MTH6134 2022 Exam

1. **Gaussian**

   ESSAY | 1.0 point | 0.10 penalty | editor

   An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 66.8, 65.7; while for $x = 0$ were 58.4, 58.9, 61, 59.8, 61.4 and for $x = 1$ were 53.9, 54.7, 54.4.

   You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

   (a) Write the estimated coefficient of catalyst.

   (b) Write the residual deviance.

   (c) Compute the pvalue of the residual deviance.

   (d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

   Notes for grader:

   - (a) the estimated is coefficient of catalyst -5.9183673; (b) the residual deviance is 8.0273469, with (c) pvalue 0.4308033544; (d) concerning the hypothesis, we do not reject H_0.

2. **Gaussian**

   ESSAY | 1.0 point | 0.10 penalty | editor

   An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 62.9, 63.2, 64.5, 65; while for $x = 0$ were 70.2, 70.9, 69.5, 70 and for $x = 1$ were 75.8, 77.1, 74.3, 72.5.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 69.6583333; (b) the residual deviance is 17.2879167, with (c) pvalue 0.0682309793; (d) concerning the hypothesis, we do not reject H_0.

3. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,9,-1), (45,20,-0.5), (35,16,0), (40,27,0.5), (30,19,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0745$, $\hat{\beta}_1 = 0.6596$

The null deviance was 9.6852 on 4 degrees of freedom.
The residual deviance was 1.7509 on 3 degrees of freedom.
AIC: 25.4551

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.0460778900 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

$-9.8520793 \pm 5\text{e-}1$ ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.5$:

NUMERICAL | 1 point

$0.4365249 \pm 5\text{e-}2$ ✓	

4. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,22,-1), (40,27,-0.6), (35,16,-0.2), (30,12,0.2), (40,13,0.6), (40,10,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0239$, $\hat{\beta}_1 = -1.2897$

The null deviance was 37.7759 on 5 degrees of freedom.
The residual deviance was 3.5949 on 4 degrees of freedom.
AIC: 30.2234

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.0000004200 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

$-11.3142472 \pm 5\text{e-}1$ ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.2$:

NUMERICAL | 1 point

$0.5582338 \pm 5\text{e-}2$ ✓	

5. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	62	3
Clinic B	51	11
Clinic C	17	15

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$24.5343222 \pm 5e\text{-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1e\text{-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

6. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	75	11
Clinic B	80	19
Clinic C	81	19

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

$1.7556291 \pm 5e\text{-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

$2 \pm 1e\text{-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

7. **Exponential**

CLOZE 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$2, 2, 4, 7, 9+, 10+, 11+, 12+, 14+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$6 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$86 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0697674 \pm$ 5e-1 ✓	

8. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0+, 1, 2, 2, 3, 3, 4, 5+, 5, 6, 7+, 8.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$46 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL   1 point

$0.0652174 \pm$ 5e-1 ✓	

9. **Gaussian**

ESSAY   1.0 point   0.10 penalty   editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 66.1, 66.5, 68; while for $x = 0$ were 60.7, 60.7, 60.2, 58.1, 58.3 and for $x = 1$ were 53.9, 53.1.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -6.7428571; (b) the residual deviance is 9.88, with (c) pvalue 0.2735496105; (d) concerning the hypothesis, we do not reject H_0.

10. **Gaussian**

ESSAY   1.0 point   0.10 penalty   editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst

x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.7, 63.4, 65.5, 63.3, 66; while for $x = 0$ were 72.3, 69, 71.5, 69.5 and for $x = 1$ were 74.1, 76.3, 75.9.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 5.3673913; (b) the residual deviance is 17.7343478, with (c) pvalue 0.0596136040; (d) concerning the hypothesis, we do not reject H_0.

11. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,7,-1), (30,11,-0.5), (30,13,0), (35,21,0.5), (40,35,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0687$, $\hat{\beta}_1 = 1.5914$

The null deviance was 52.6968 on 4 degrees of freedom.
The residual deviance was 2.7002 on 3 degrees of freedom.
AIC: 25.3176

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.0000000000 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-9.3086626 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0$:

NUMERICAL 1 point

0.4828406 ± 5e-2 ✓	

12. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (40,26,-1), (35,23,-0.6), (45,30,-0.2), (25,9,0.2), (20,11,0.6), (20,8,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.2253$, $\hat{\beta}_1 = -0.5576$

The null deviance was 10.6969 on 5 degrees of freedom.
The residual deviance was 4.9887 on 4 degrees of freedom.
AIC: 31.6283

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL 1 point

0.0577319600 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the model with common probability	
We do not reject the model with common probability ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-11.319777 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.2$:

NUMERICAL 1 point

0.583424 ± 5e-2 ✓	

13. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	11	3
Clinic B	94	7
Clinic C	17	11

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$16.3815653 \pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

14. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	86	11
Clinic B	92	16
Clinic C	91	18

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$1.1795173 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

15. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 2, 11+, 11+, 12+, 13+, 13+, 14+, 15+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$8 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$107 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0747664 \pm$ 5e-1 ✓	

16. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 1+, 1, 1, 1, 3, 3, 5, 5, 5+, 8, 9+ .$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$42 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0714286 \pm$ 5e-1 ✓	

17. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 68.3, 66.2, 66, 66.1; while for $x = 0$ were 58.5, 60.7, 61.8, 60.4 and for $x = 1$ were 51.2, 56.3.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 60.2642857; (b) the residual deviance is 22.3564286, with (c) pvalue 0.0042966619; (d) concerning the hypothesis, we reject H_0.

18. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 64.1, 63.9, 65.7, 60.2, 60.5; while for $x = 0$ were 70.2, 68.8, 72.8, 70.4, 68.4 and for $x = 1$ were 77.1, 76.3.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 69.944; (b) the residual deviance is 35.9064, with (c) pvalue 0.0000873511; (d) concerning the hypothesis, we reject H_0.

19. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (30,6,-1), (35,13,-0.5), (25,14,0), (25,17,0.5), (45,34,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.042$, $\hat{\beta}_1 = 1.2262$

The null deviance was 29.5096 on 4 degrees of freedom.
The residual deviance was 0.6783 on 3 degrees of freedom.
AIC: 23.2719

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL 1 point

0.0000061600 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the R function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.2967774 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0$:

NUMERICAL | 1 point

0.5105038 ± 5e-2 ✓	

20. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,32,-1), (35,24,-0.6), (30,18,-0.2), (30,11,0.2), (45,10,0.6), (45,6,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.2667$, $\hat{\beta}_1 = -1.4668$

The null deviance was 54.9282 on 5 degrees of freedom.
The residual deviance was 2.2528 on 4 degrees of freedom.
AIC: 29.2535

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

$0.6893751700 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

$-11.5003393 \pm 5\text{e-}1$ ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.2$:

NUMERICAL 1 point

$0.3635352 \pm$ 5e-2 ✓	

21. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	70	0
Clinic B	78	1
Clinic C	34	8

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

$20.9331217 \pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

$2 \pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

22. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	100	15
Clinic B	106	19
Clinic C	108	21

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$0.5216534 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

23. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$2, 2, 2, 3, 3, 8, 9+, 11+, 12+, 12+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$4 \pm 5\text{e-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$64 \pm 5\text{e-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0625 \pm 5\text{e-}1$ ✓	

24. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$1+, 1, 1, 1, 2, 2, 4, 4, 5, 12.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$1 \pm 5\text{e-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$33 \pm 5\text{e-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.030303 \pm 5\text{e-}1$ ✓	

25. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 68.2; while for $x = 0$ were 58.3, 59.6, 60.2, 62.1 and for $x = 1$ were 50.1, 52.8, 49.8, 52.3, 53.5.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -8.2863636; (b) the residual deviance is 18.4881818, with (c) pvalue 0.0178499640; (d) concerning the hypothesis, we reject H_0.

26. **Gaussian**

ESSAY 1.0 point 0.10 penalty editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 62.8, 64.3, 65.8, 63.4, 63.6, 63.8, 65.1; while for $x = 0$ were 69.4, 69.2 and for $x = 1$ were 78.1, 78.6, 74.1.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 6.3153846; (b) the residual deviance is 21.0546154, with (c) pvalue 0.0207159314; (d) concerning the hypothesis, we reject H_0.

27. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (30,7,-1), (40,12,-0.5), (30,15,0), (20,16,0.5), (35,22,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.1221$, $\hat{\beta}_1 = 1.0432$

The null deviance was 24.8441 on 4 degrees of freedom.
The residual deviance was 5.4066 on 3 degrees of freedom.
AIC: 27.8002

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0000540800 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-9.1968179 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL 1 point

0.2377195 ± 5e-2 ✓	

28. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,18,-1), (40,25,-0.6), (30,15,-0.2), (30,13,0.2), (20,9,0.6), (20,4,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0648$, $\hat{\beta}_1 = -0.9667$

The null deviance was 15.9269 on 5 degrees of freedom.
The residual deviance was 1.52 on 4 degrees of freedom.
AIC: 27.3198

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

$0.8231012400 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

$-10.8999175 \pm 5\text{e-}1$ ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.6$:

NUMERICAL 1 point

$0.3441508 \pm 5\text{e-}2$ ✓	

29. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	24	5
Clinic B	29	9
Clinic C	18	7

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

$0.9254046 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

30. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	60	1
Clinic B	67	6
Clinic C	67	7

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$4.5807718 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

31. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$2, 6, 6, 6, 7, 8, 10+, 12+, 12+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$4 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$83 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0481928 \pm$ 5e-1 ✓	

32. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 0, 0+, 1+, 2, 2, 5+, 6, 7+, 14+ .$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$5 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$37 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.1351351 \pm$ 5e-1 ✓	

33. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.9, 65, 65.2, 66.5, 65.9; while for $x = 0$ were 60 and for $x = 1$ were 52.6, 52.9, 52, 52.8.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -6.552809; (b) the residual deviance is 2.6161798, with (c) pvalue 0.9560929711; (d) concerning the hypothesis, we do not reject H_0.

34. **Gaussian**

ESSAY 1.0 point 0.10 penalty editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 64.7, 65.3, 63.7, 63.8, 63.9; while for $x = 0$ were 69.5, 68.5 and for $x = 1$ were 73.9, 77.3, 78, 76.5, 77.8.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 70.2416667; (b) the residual deviance is 17.2681667, with (c) pvalue 0.0686367730; (d) concerning the hypothesis, we do not reject H_0.

35. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,6,-1), (35,15,-0.5), (25,8,0), (40,20,0.5), (25,18,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.1991$, $\hat{\beta}_1 = 0.7257$

The null deviance was 11.4963 on 4 degrees of freedom.
The residual deviance was 3.6273 on 3 degrees of freedom.
AIC: 26.1228

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0215172400 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.2477602 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.5$:

NUMERICAL | 1 point

0.3631088 ± 5e-2 ✓	

36. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,31,-1), (20,17,-0.6), (20,7,-0.2), (40,17,0.2), (25,11,0.6), (40,9,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.058$, $\hat{\beta}_1 = -1.0194$

The null deviance was 33.1034 on 5 degrees of freedom.
The residual deviance was 8.9531 on 4 degrees of freedom.
AIC: 34.8898

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.0000035900 \pm$ 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

$-10.9683843 \pm$ 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.6$:

NUMERICAL 1 point

$0.3385751 \pm 5\text{e-}2$ ✓	

37. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	100	2
Clinic B	8	11
Clinic C	82	1

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

$45.652872 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

38. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	100	11
Clinic B	106	16
Clinic C	107	16

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$0.7379521 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

39. **Exponential**

CLOZE 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$2, 3, 5, 7, 7, 8, 9+, 10+, 12+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL 1 point

$4 \pm 5\text{e-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL 1 point

$77 \pm 5\text{e-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL 1 point

$0.0519481 \pm 5\text{e-}1$ ✓	

40. **Exponential**

CLOZE 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 1, 1, 2, 3, 4, 4+, 6+, 7, 7, 7, 9.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$2 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$51 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0392157 \pm$ 5e-1 ✓	

41. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 68.9, 67.3, 65.7; while for $x = 0$ were 58.3, 58.5, 61, 62.5 and for $x = 1$ were 51.9, 49.9, 51.9.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -8.0333333; (b) the residual deviance is 21.7223333, with (c) pvalue 0.0054570642; (d) concerning the hypothesis, we reject H_0.

42. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 63.3, 63.8; while for $x = 0$ were 71.4, 68.9, 70, 69.3, 69.8 and for $x = 1$ were 75.7, 74.6, 76, 76.4, 77.1.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 69.8133333; (b) the residual deviance is 7.2066667, with (c) pvalue 0.7058009242; (d) concerning the hypothesis, we do not reject H_0.

43. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (30,11,-1), (45,23,-0.5), (45,15,0), (25,15,0.5), (25,18,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0201$, $\hat{\beta}_1 = 0.5889$

The null deviance was 13.0832 on 4 degrees of freedom.
The residual deviance was 7.1246 on 3 degrees of freedom.
AIC: 30.4767

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL 1 point

0.0108762400 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.6760393 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.5$:

NUMERICAL | 1 point

0.5681643 ± 5e-2 ✓	

44. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,17,-1), (35,21,-0.6), (45,30,-0.2), (25,10,0.2), (35,12,0.6), (25,3,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0768$, $\hat{\beta}_1 = -1.1993$

The null deviance was 30.5704 on 5 degrees of freedom.
The residual deviance was 5.9509 on 4 degrees of freedom.
AIC: 32.0761

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

0.2028476000 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.0625927 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL | 1 point

$0.7544405 \pm 5e\text{-}2$ ✓	

45. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	75	9
Clinic B	28	1
Clinic C	20	10

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$11.6524034 \pm 5e\text{-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1e\text{-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

46. **Poissson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	64	2
Clinic B	68	7
Clinic C	71	8

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$3.4518561 \pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

47. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$2, 2, 4, 4, 8, 8, 8, 9+, 10+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm 5e\text{-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$70 \pm 5e\text{-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0428571 \pm 5e\text{-}1$ ✓	

48. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 0, 1, 2+, 3, 3, 4+, 5+, 6, 6, 7, 19+.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$4 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$56 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0714286 \pm$ 5e-1 ✓	

49. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.9; while for $x = 0$ were 59.7, 60.9, 60 and for $x = 1$ were 52, 53.6, 54.4, 53.4, 53.7, 56.5.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 60.0488889; (b) the residual deviance is 11.9017778, with (c) pvalue 0.1556404162; (d) concerning the hypothesis, we do not reject H_0.

50. **Gaussian**

ESSAY 1.0 point 0.10 penalty editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 62.5, 64.2, 62.1, 64.9, 62.8; while for $x = 0$ were 72.6, 71.6, 67.7 and for $x = 1$ were 76.9, 76.9, 75.7, 74.7.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 6.4018692; (b) the residual deviance is 24.5566355, with (c) pvalue 0.0062523401; (d) concerning the hypothesis, we reject H_0.

51. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,6,-1), (30,15,-0.5), (20,16,0), (30,18,0.5), (35,22,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1636$, $\hat{\beta}_1 = 0.6717$

The null deviance was 16.9594 on 4 degrees of freedom.
The residual deviance was 9.0185 on 3 degrees of freedom.
AIC: 31.1014

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL 1 point

0.0290462100 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the logistic regression model ✓	
We do not reject the logistic regression model	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-9.0414457 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL 1 point

0.3756382 ± 5e-2 ✓	

52. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,17,-1), (30,14,-0.6), (25,14,-0.2), (35,18,0.2), (20,10,0.6), (20,5,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0631$, $\hat{\beta}_1 = -0.7957$

The null deviance was 16.3328 on 5 degrees of freedom.
The residual deviance was 7.3453 on 4 degrees of freedom.
AIC: 32.4059

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL 1 point

$0.0059553900 \pm 5e\text{-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-10.5303198 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.6$:

NUMERICAL 1 point

0.6319285 ± 5e-2 ✓	

53. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	9	14
Clinic B	8	1
Clinic C	24	0

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

28.0169098 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

5.9914645 ± 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

54. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	96	5
Clinic B	101	14
Clinic C	104	10

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$3.6578247 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

55. **Exponential**

CLOZE 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 1, 1, 5, 5, 7, 8, 10+, 13+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL 1 point

$3 \pm 5e\text{-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL 1 point

$66 \pm 5e\text{-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL 1 point

$0.0454545 \pm 5e\text{-}1$ ✓	

56. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0+, 1, 1+, 2, 2, 2, 3+, 4, 5, 6, 6, 12+.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$4 \pm 5\text{e-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$44 \pm 5\text{e-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0909091 \pm 5\text{e-}1$ ✓	

57. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 66.7, 67.3, 66.6; while for $x = 0$ were 60.8, 62.4, 60.9, 61.6 and for $x = 1$ were 54.4, 51.4, 53.4.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -6.9; (b) the residual deviance is 11.705, with (c) pvalue 0.1648593116; (d) concerning the hypothesis, we do not reject H_0.

58. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 62.8, 63.3; while for $x = 0$ were 70.9, 70.5, 70.2 and for $x = 1$ were 75.1, 75.5, 76.2, 75.9, 74.4, 78.3, 76.7.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 69.8578313; (b) the residual deviance is 11.8491566, with (c) pvalue 0.2952787721; (d) concerning the hypothesis, we do not reject H_0.

59. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,6,-1), (45,17,-0.5), (45,24,0), (20,14,0.5), (35,25,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0479$, $\hat{\beta}_1 = 1.0624$

The null deviance was 19.9291 on 4 degrees of freedom.
The residual deviance was 0.7476 on 3 degrees of freedom.
AIC: 23.7332

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL 1 point

0.0005157600 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-9.4927736 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.5$:

NUMERICAL 1 point

0.640857 ± 5e-2 ✓	

60. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (35,20,-1), (20,14,-0.6), (20,12,-0.2), (45,15,0.2), (35,12,0.6), (45,14,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.1887$, $\hat{\beta}_1 = -0.7157$

The null deviance was 16.6217 on 5 degrees of freedom.
The residual deviance was 4.6117 on 4 degrees of freedom.
AIC: 31.5404

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

$0.3295045400 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.4643509 $\pm$ 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.2$:

NUMERICAL | 1 point

0.4177815 $\pm$ 5e-2 ✓	

61. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	32	13
Clinic B	98	14
Clinic C	95	12

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

7.4867764 $\pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 $\pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

62. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	37	13
Clinic B	44	22
Clinic C	43	18

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

$0.7406541 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

63. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 1, 1, 3, 4, 8, 10+, 12+, 14+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$4 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$68 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0588235 \pm$ 5e-1 ✓	

64. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0+, 0+, 1+, 1, 3, 3, 3+, 4, 4, 7, 11, 13+ .$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$5 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$50 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.1 \pm$ 5e-1 ✓	

65. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 67.4, 66.3, 67; while for $x = 0$ were 59.6, 61.3, 59 and for $x = 1$ were 53.9, 52.4, 54, 51.6.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 59.9463768; (b) the residual deviance is 7.595942, with (c) pvalue 0.4739000383; (d) concerning the hypothesis, we do not reject H_0.

66. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 67.4, 64.5, 66.6; while for $x = 0$ were 68.5, 68.4, 72.6, 68.4, 69.6, 70.2 and for $x = 1$ were 78.2, 78.5, 74.9.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 5.5166667; (b) the residual deviance is 38.7283333, with (c) pvalue 0.0000283251; (d) concerning the hypothesis, we reject H_0.

67. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,5,-1), (30,8,-0.5), (45,29,0), (30,17,0.5), (35,24,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0108$, $\hat{\beta}_1 = 0.9758$

The null deviance was 21.0921 on 4 degrees of freedom.
The residual deviance was 6.227 on 3 degrees of freedom.
AIC: 28.964

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.0003036300 \pm$ 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

$-9.3684892 \pm$ 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0$:

NUMERICAL | 1 point

$0.4972892 \pm$ 5e-2 ✓	

68. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,15,-1), (40,27,-0.6), (40,20,-0.2), (35,18,0.2), (40,16,0.6), (40,8,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0263$, $\hat{\beta}_1 = -1.1061$

The null deviance was 27.0688 on 5 degrees of freedom.
The residual deviance was 2.3309 on 4 degrees of freedom.
AIC: 29.5535

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL 1 point

$0.0000553100 \pm$ 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.6112767 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.6$:

NUMERICAL | 1 point

0.3458301 ± 5e-2 ✓	

69. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	32	11
Clinic B	90	14
Clinic C	15	13

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

13.3941285 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

70. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	46	11
Clinic B	51	19
Clinic C	53	16

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$1.0888558 \pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

71. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 1, 8, 9+, 10+, 11+, 13+, 13+, 14+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$7 \pm 5e\text{-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$94 \pm 5e\text{-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0744681 \pm 5e\text{-}1$ ✓	

72. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 1, 1, 2, 2, 3, 3+, 4+, 4, 11, 12+, 26.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$69 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0434783 \pm$ 5e-1 ✓	

73. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 67.4, 66.5, 65.9, 67.9, 65.6, 66.8; while for $x = 0$ were 59.2, 59.1, 59 and for $x = 1$ were 51.8.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -7.4888889; (b) the residual deviance is 3.8804444, with (c) pvalue 0.8677457953; (d) concerning the hypothesis, we do not reject H_0.

74. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 65, 64.1, 63.1, 63.5, 64.9; while for $x = 0$ were 68.4, 71.3, 71.2 and for $x = 1$ were 74.8, 73.4, 76, 77.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 5.6065421; (b) the residual deviance is 16.248785, with (c) pvalue 0.0927286832; (d) concerning the hypothesis, we do not reject H_0.

75. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,8,-1), (20,6,-0.5), (30,14,0), (30,15,0.5), (35,25,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.3233$, $\hat{\beta}_1 = 1.1498$

The null deviance was 26.7152 on 4 degrees of freedom.
The residual deviance was 0.8327 on 3 degrees of freedom.
AIC: 23.4373

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0000227000 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.3022845 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 1$:

NUMERICAL | 1 point

0.6956222 ± 5e-2 ✓	

76. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (35,25,-1), (25,15,-0.6), (30,21,-0.2), (25,13,0.2), (35,16,0.6), (20,4,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1789$, $\hat{\beta}_1 = -0.8957$

The null deviance was 18.683 on 5 degrees of freedom.
The residual deviance was 4.3025 on 4 degrees of freedom.
AIC: 30.2226

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL 1 point

$0.3666176400 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-10.9600912 $\pm$ 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.2$:

NUMERICAL 1 point

0.588565 $\pm$ 5e-2 ✓	

77. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	28	7
Clinic B	45	8
Clinic C	76	14

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

0.4266951 $\pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

2 $\pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

5.9914645 ± 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

78. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	82	3
Clinic B	86	11
Clinic C	89	11

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

5.0140396 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

79. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 2, 6, 7, 9+, 10+, 10+, 14+, 14+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$6 \pm 5\text{e-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$87 \pm 5\text{e-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0689655 \pm 5\text{e-}1$ ✓	

80. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 0+, 1+, 2, 4, 5+, 8, 10, 13+, 18.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$4 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$61 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0655738 \pm$ 5e-1 ✓	

81. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 67.9, 66.1, 68; while for $x = 0$ were 59.9, 61.1, 60.3, 62.1 and for $x = 1$ were 53.8, 52.8, 52.6.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 60.46; (b) the residual deviance is 6.9573333, with (c) pvalue 0.5412430271; (d) concerning the hypothesis, we do not reject H_0.

82. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 61.4, 65.3; while for $x = 0$ were 68.8, 72.7, 70, 69.5, 70.5 and for $x = 1$ were 77.4, 75, 76, 75.7, 73.9.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 5.96; (b) the residual deviance is 24.86, with (c) pvalue 0.0056172832; (d) concerning the hypothesis, we reject H_0.

83. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (35,7,-1), (30,13,-0.5), (35,19,0), (30,20,0.5), (35,27,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1009$, $\hat{\beta}_1 = 1.2239$

The null deviance was 28.2776 on 4 degrees of freedom.
The residual deviance was 0.9547 on 3 degrees of freedom.
AIC: 23.8407

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL 1 point

0.0000109600 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-9.4429964 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.5$:

NUMERICAL 1 point

0.6710227 ± 5e-2 ✓	

84. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (35,30,-1), (35,24,-0.6), (45,28,-0.2), (40,19,0.2), (35,13,0.6), (30,6,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1781$, $\hat{\beta}_1 = -1.4134$

The null deviance was 39.6592 on 5 degrees of freedom.
The residual deviance was 0.9174 on 4 degrees of freedom.
AIC: 27.8694

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0000001700 $\pm$ 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.4760122 $\pm$ 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 1$:

NUMERICAL | 1 point

0.2252556 $\pm$ 5e-2 ✓	

85. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	76	6
Clinic B	95	5
Clinic C	82	14

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

5.7267518 $\pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 $\pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

5.9914645 ± 1e-1 ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

86. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	64	11
Clinic B	69	18
Clinic C	69	17

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

1.1332982 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

87. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$5, 5, 7, 8, 9+, 9+, 11+, 13+, 14+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$6 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$96 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0625 \pm$ 5e-1 ✓	

88. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 0+, 1, 2, 2, 4, 4, 4, 7, 13.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$1 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$37 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.027027 \pm$ 5e-1 ✓	

89. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 64.9, 64.9, 66.3, 66.2; while for $x = 0$ were 59.9, 59.8, 61.3, 61.5 and for $x = 1$ were 54.4, 54.3.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 60.2464286; (b) the residual deviance is 5.2632143, with (c) pvalue 0.7291085729; (d) concerning the hypothesis, we do not reject H_0.

90. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 63, 65.5, 62.2, 64.5, 63.3, 64.9; while for $x = 0$ were 71.6, 69.1, 72.4, 70.2, 72 and for $x = 1$ were 75.7.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 6.4338983; (b) the residual deviance is 18.7610169, with (c) pvalue 0.0434052491; (d) concerning the hypothesis, we reject H_0.

91. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (35,7,-1), (20,8,-0.5), (40,21,0), (30,20,0.5), (25,23,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1867$, $\hat{\beta}_1 = 1.6021$

The null deviance was 38.0876 on 4 degrees of freedom.
The residual deviance was 1.7895 on 3 degrees of freedom.
AIC: 23.2438

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0000001100 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-8.7271673 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.5$:

NUMERICAL | 1 point

0.7286415 ± 5e-2 ✓	

92. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,36,-1), (25,14,-0.6), (45,21,-0.2), (20,8,0.2), (25,9,0.6), (20,2,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.2461$, $\hat{\beta}_1 = -1.3775$

The null deviance was 35.4225 on 5 degrees of freedom.
The residual deviance was 3.5885 on 4 degrees of freedom.
AIC: 28.9144

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

$0.4645457500 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-10.6629567 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL | 1 point

0.7560937 ± 5e-2 ✓	

93. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	58	15
Clinic B	93	8
Clinic C	18	1

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

7.0368083 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

94. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	88	7
Clinic B	94	15
Clinic C	96	13

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$2.3056903 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

95. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 1, 6, 6, 7, 7, 9+, 12+, 13+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$4 \pm 5\text{e-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$76 \pm 5\text{e-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0526316 \pm 5\text{e-}1$ ✓	

96. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0+, 0+, 1, 1+, 1+, 3+, 4, 4, 5, 6, 7, 14+ .$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$6 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$46 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.1304348 \pm$ 5e-1 ✓	

97. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 67.3, 67.1, 65.1, 66.2, 66.6, 68.2; while for $x = 0$ were 59.4, 59.6 and for $x = 1$ were 51.7, 53.1.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -7.184375; (b) the residual deviance is 6.5834375, with (c) pvalue 0.5821683058; (d) concerning the hypothesis, we do not reject H_0.

98. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 63.3, 62.2, 62.8, 63.6; while for $x = 0$ were 69.3, 69.4, 70.2, 67.9, 69.1 and for $x = 1$ were 75.3, 78.4, 78.3.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 7.1204819; (b) the residual deviance is 12.8262651, with (c) pvalue 0.2335484277; (d) concerning the hypothesis, we do not reject H_0.

99. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,6,-1), (40,14,-0.5), (35,16,0), (45,29,0.5), (45,35,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0294$, $\hat{\beta}_1 = 1.2225$

The null deviance was 29.0096 on 4 degrees of freedom.
The residual deviance was 0.2549 on 3 degrees of freedom.
AIC: 23.8046

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0000077800 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.7748802 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.5$:

NUMERICAL | 1 point

0.3450948 ± 5e-2 ✓	

100. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,22,-1), (35,25,-0.6), (25,14,-0.2), (25,13,0.2), (40,15,0.6), (25,8,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.2775$, $\hat{\beta}_1 = -1.2274$

The null deviance was 27.1271 on 5 degrees of freedom.
The residual deviance was 1.5025 on 4 degrees of freedom.
AIC: 27.2003

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL 1 point

$0.8262047200 \pm 5e\text{-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-10.8489283 $\pm$ 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.2$:

NUMERICAL | 1 point

0.5080137 $\pm$ 5e-2 ✓	

101. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	80	9
Clinic B	85	6
Clinic C	90	14

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

2.5682671 $\pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 $\pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

102. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	36	2
Clinic B	44	7
Clinic C	42	7

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$2.3612634 \pm 5e\text{-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1e\text{-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

103. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 5, 7, 7, 7, 8, 8, 10+, 11+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm 5\text{e-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$79 \pm 5\text{e-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0379747 \pm 5\text{e-}1$ ✓	

104. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$1, 2, 2, 3, 3+, 4, 5, 10+, 13, 13+ .$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$56 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0535714 \pm$ 5e-1 ✓	

105. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 67.7, 66.4, 67.8; while for $x = 0$ were 60.2, 59.8, 59.3, 60.4 and for $x = 1$ were 53.8, 52.8, 51.6.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 59.98; (b) the residual deviance is 4.3743333, with (c) pvalue 0.8218700293; (d) concerning the hypothesis, we do not reject H_0.

106. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 64.6, 63.2, 64.6; while for $x = 0$ were 68.4, 69.9, 72.2, 68.1, 69.9 and for $x = 1$ were 76.8, 75.2, 76.7, 78.1.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 6.326506; (b) the residual deviance is 17.5918072, with (c) pvalue 0.0622522255; (d) concerning the hypothesis, we do not reject H_0.

107. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (30,10,-1), (30,11,-0.5), (30,16,0), (20,12,0.5), (40,30,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0887$, $\hat{\beta}_1 = 0.9244$

The null deviance was 16.5343 on 4 degrees of freedom.
The residual deviance was 0.516 on 3 degrees of freedom.
AIC: 23.2366

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0023799600 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.3602998 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0$:

NUMERICAL | 1 point

0.5221541 ± 5e-2 ✓	

108. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,11,-1), (25,16,-0.6), (20,16,-0.2), (45,18,0.2), (40,16,0.6), (40,11,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0097$, $\hat{\beta}_1 = -0.8009$

The null deviance was 20.6854 on 5 degrees of freedom.
The residual deviance was 8.6321 on 4 degrees of freedom.
AIC: 35.0234

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

$0.0709812900 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.1956282 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL | 1 point

0.6880846 ± 5e-2 ✓	

109. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	29	4
Clinic B	94	15
Clinic C	6	0

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

1.7456522 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

110. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	48	9
Clinic B	55	18
Clinic C	54	16

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$1.6767862 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

111. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 3, 10+, 11+, 11+, 12+, 12+, 13+, 13+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$8 \pm 5e\text{-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$101 \pm 5e\text{-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0792079 \pm 5e\text{-}1$ ✓	

112. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$2, 3, 3, 3, 4, 5+, 5, 6, 10, 30.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$1 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$71 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0140845 \pm$ 5e-1 ✓	

113. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 63.8, 66.8, 65.6; while for $x = 0$ were 62.1, 59.7, 59.7 and for $x = 1$ were 52.8, 52.6, 53.4, 50.3.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -6.6347826; (b) the residual deviance is 19.7156522, with (c) pvalue 0.0114670663; (d) concerning the hypothesis, we reject H_0.

114. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 64.2, 64.9, 62.2, 63.7, 63.1; while for $x = 0$ were 70.6, 70.1, 69.6, 70.4 and for $x = 1$ were 75.9, 77.5, 78.6.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 6.8304348; (b) the residual deviance is 8.7595652, with (c) pvalue 0.5550637207; (d) concerning the hypothesis, we do not reject H_0.

115. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (35,8,-1), (20,10,-0.5), (20,14,0), (25,16,0.5), (40,33,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.3168$, $\hat{\beta}_1 = 1.2519$

The null deviance was 31.0521 on 4 degrees of freedom.
The residual deviance was 2.9952 on 3 degrees of freedom.
AIC: 24.679

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0000029900 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-8.8418981 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.5$:

NUMERICAL | 1 point

0.7196624 ± 5e-2 ✓	

116. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (35,25,-1), (30,23,-0.6), (20,13,-0.2), (20,10,0.2), (45,11,0.6), (25,4,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0441$, $\hat{\beta}_1 = -1.4438$

The null deviance was 42.4142 on 5 degrees of freedom.
The residual deviance was 4.0404 on 4 degrees of freedom.
AIC: 29.3246

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.0000000500 \pm$ 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-10.6420981 $\pm$ 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.6$:

NUMERICAL 1 point

0.6946927 $\pm$ 5e-2 ✓	

117. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	54	9
Clinic B	10	10
Clinic C	80	0

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

37.9671107 $\pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

2 $\pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

118. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	51	1
Clinic B	57	9
Clinic C	57	6

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

$6.0853912 \pm 5e\text{-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

$2 \pm 1e\text{-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

5.9914645 ± 1e-1 ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

119. **Exponential**

CLOZE 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$4, 6, 6, 9+, 11+, 12+, 14+, 15+, 15+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL 1 point

7 ± 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL 1 point

107 ± 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL 1 point

0.0654206 ± 5e-1 ✓	

120. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$1, 1, 1+, 1, 1+, 5+, 6+, 7, 7, 9, 46.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$4 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$85 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0470588 \pm$ 5e-1 ✓	

121. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 67.4, 67.4, 66.9; while for $x = 0$ were 60.5, 60.1, 60.5, 60.1, 58.7 and for $x = 1$ were 53.5, 52.4.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -7.1530612; (b) the residual deviance is 3.0102041, with (c) pvalue 0.9337155522; (d) concerning the hypothesis, we do not reject H_0.

122. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 62.5, 64.2, 65.7, 64.5, 62.9, 63.3; while for $x = 0$ were 70.8, 70.5, 70.4 and for $x = 1$ were 76.4, 77.7, 75.7.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command **`glm`** and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 6.4060606; (b) the residual deviance is 9.3963636, with (c) pvalue 0.4949450592; (d) concerning the hypothesis, we do not reject H_0.

123. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,11,-1), (35,9,-0.5), (35,21,0), (35,25,0.5), (40,30,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0621$, $\hat{\beta}_1 = 1.2881$

The null deviance was 39.4417 on 4 degrees of freedom.
The residual deviance was 3.5117 on 3 degrees of freedom.
AIC: 26.9161

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL 1 point

0.3192439400 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-9.7021982 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.5$:

NUMERICAL 1 point

0.6695436 ± 5e-2 ✓	

124. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,18,-1), (30,21,-0.6), (30,18,-0.2), (35,17,0.2), (40,15,0.6), (45,9,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0647$, $\hat{\beta}_1 = -1.191$

The null deviance was 30.6619 on 5 degrees of freedom.
The residual deviance was 1.3802 on 4 degrees of freedom.
AIC: 28.332

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0000109200 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.4759373 $\pm$ 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.2$:

NUMERICAL | 1 point

0.5751403 $\pm$ 5e-2 ✓	

125. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	97	10
Clinic B	99	12
Clinic C	2	7

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

21.4517404 $\pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 $\pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

126. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	69	2
Clinic B	76	11
Clinic C	77	7

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$5.5752607 \pm 5e\text{-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1e\text{-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

127. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 2, 6, 8, 9+, 13+, 13+, 13+, 13+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$6 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$92 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0652174 \pm$ 5e-1 ✓	

128. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0+, 0+, 1, 1+, 2, 2, 2, 2, 4, 5, 6, 8+.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$4 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$33 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.1212121 \pm$ 5e-1 ✓	

129. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 67.2, 66.9, 66.1; while for $x = 0$ were 59.7, 58.4, 60.6 and for $x = 1$ were 54.5, 54.8, 53.1, 52.9.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 60.0623188; (b) the residual deviance is 6.9402899, with (c) pvalue 0.5430884804; (d) concerning the hypothesis, we do not reject H_0.

130. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 62.5, 63.8; while for $x = 0$ were 68.9, 71.2 and for $x = 1$ were 77.3, 76.7, 77.6, 78.2, 76.7, 73, 76.4, 74.2.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 69.7880952; (b) the residual deviance is 25.5888095, with (c) pvalue 0.0043344036; (d) concerning the hypothesis, we reject H_0.

131. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (30,6,-1), (40,12,-0.5), (25,18,0), (20,11,0.5), (25,16,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.1076$, $\hat{\beta}_1 = 1.021$

The null deviance was 23.9415 on 4 degrees of freedom.
The residual deviance was 7.891 on 3 degrees of freedom.
AIC: 29.8637

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0000820600 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-8.9863736 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.5$:

NUMERICAL | 1 point

0.5993962 ± 5e-2 ✓	

132. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,17,-1), (25,14,-0.6), (30,18,-0.2), (20,8,0.2), (30,15,0.6), (30,11,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0991$, $\hat{\beta}_1 = -0.5617$

The null deviance was 7.6226 on 5 degrees of freedom.
The residual deviance was 1.78 on 4 degrees of freedom.
AIC: 27.9412

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.1782969400 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability	
We do not reject the model with common probability ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.0805944 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.6$:

NUMERICAL | 1 point

0.4408087 ± 5e-2 ✓	

133. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	21	0
Clinic B	42	8
Clinic C	8	4

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

9.3459108 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

5.9914645 ± 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

134. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	75	6
Clinic B	84	10
Clinic C	82	11

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

1.0269283 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

135. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$3, 4, 5, 9+, 10+, 13+, 13+, 14+, 14+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$7 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$99 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0707071 \pm$ 5e-1 ✓	

136. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 1, 1, 2+, 2+, 3, 5+, 6, 7, 15, 17.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$59 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0508475 \pm$ 5e-1 ✓	

137. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.1, 67.3, 64.2; while for $x = 0$ were 58.7, 61.1, 59.8 and for $x = 1$ were 53.1, 53.2, 53.2, 51.1.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 59.3275362; (b) the residual deviance is 12.4368116, with (c) pvalue 0.1327525575; (d) concerning the hypothesis, we do not reject H_0.

138. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 64.1, 63.2, 65.2, 64.7; while for $x = 0$ were 69.8, 71.1, 71.6, 68.3, 72.6, 72.7 and for $x = 1$ were 76.3, 75.1.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 70.5382353; (b) the residual deviance is 20.4067647, with (c) pvalue 0.0256318147; (d) concerning the hypothesis, we reject H_0.

139. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,4,-1), (25,7,-0.5), (20,11,0), (35,18,0.5), (35,25,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.258$, $\hat{\beta}_1 = 1.0976$

The null deviance was 19.4046 on 4 degrees of freedom.
The residual deviance was 1.6663 on 3 degrees of freedom.
AIC: 23.4982

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0006543700 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-8.9159599 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.5$:

NUMERICAL | 1 point

0.3085717 ± 5e-2 ✓	

140. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (30,19,-1), (40,26,-0.6), (40,24,-0.2), (40,21,0.2), (40,11,0.6), (45,20,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1031$, $\hat{\beta}_1 = -0.6327$

The null deviance was 16.2727 on 5 degrees of freedom.
The residual deviance was 6.0797 on 4 degrees of freedom.
AIC: 34.3887

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL 1 point

$0.1932765300 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-12.1545207 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 1$:

NUMERICAL | 1 point

0.3706025 ± 5e-2 ✓	

141. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	18	0
Clinic B	44	8
Clinic C	86	13

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

5.2140839 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

5.9914645 ± 1e-1 ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

142. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	87	6
Clinic B	93	15
Clinic C	93	11

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

3.0656677 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

143. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 1, 2, 2, 4, 7, 9+, 13+, 13+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$4 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$66 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0606061 \pm$ 5e-1 ✓	

144. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 0, 1, 1, 4, 5, 5+, 7, 10, 13+, 18.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$2 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$64 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.03125 \pm$ 5e-1 ✓	

145. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.8, 67.2; while for $x = 0$ were 60, 60.4 and for $x = 1$ were 54.9, 55.3, 53.7, 53.8, 52.9, 52.4.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 60.175; (b) the residual deviance is 7.295, with (c) pvalue 0.5051645313; (d) concerning the hypothesis, we do not reject H_0.

146. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 64.9, 65.2, 63.2; while for $x = 0$ were 72, 71.4, 68.6, 69.9, 68.9 and for $x = 1$ were 75.5, 76, 78.8, 76.4.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 70.3879518; (b) the residual deviance is 18.2154217, with (c) pvalue 0.0514367011; (d) concerning the hypothesis, we do not reject H_0.

147. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,11,-1), (35,7,-0.5), (20,10,0), (25,16,0.5), (45,33,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.1896$, $\hat{\beta}_1 = 1.2227$

The null deviance was 36.4912 on 4 degrees of freedom.
The residual deviance was 3.0997 on 3 degrees of freedom.
AIC: 25.7684

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.0000002300 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

$-9.3343418 \pm 5\text{e-}1$ ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.5$:

NUMERICAL | 1 point

$0.3098365 \pm 5\text{e-}2$ ✓	

148. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,20,-1), (20,11,-0.6), (25,13,-0.2), (40,23,0.2), (35,13,0.6), (45,15,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1509$, $\hat{\beta}_1 = -0.8621$

The null deviance was 18.2184 on 5 degrees of freedom.
The residual deviance was 3.2736 on 4 degrees of freedom.
AIC: 29.9224

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

$0.5131193500 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.3243875 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.2$:

NUMERICAL | 1 point

0.5801385 ± 5e-2 ✓	

149. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	34	13
Clinic B	72	15
Clinic C	66	10

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

3.9859138 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

5.9914645 ± 1e-1 ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

150. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	60	9
Clinic B	68	16
Clinic C	66	14

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

1.0642719 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

151. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 3, 4, 4, 4, 6, 6, 9+, 12+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$63 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.047619 \pm$ 5e-1 ✓	

152. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0+, 0+, 1, 2, 2, 3+, 5+, 5, 8, 8+, 9, 14.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$5 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$57 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0877193 \pm$ 5e-1 ✓	

153. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.7, 68.3, 67.2, 67.2; while for $x = 0$ were 59.7, 60.4, 60.1 and for $x = 1$ were 53, 51.7, 51.9.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 59.7768116; (b) the residual deviance is 5.0089855, with (c) pvalue 0.7566153185; (d) concerning the hypothesis, we do not reject H_0.

154. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 66, 63, 64.4, 64.9, 61.9; while for $x = 0$ were 69.6, 69.4, 70.4, 68.8 and for $x = 1$ were 74.6, 74, 77.3.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 5.6195652; (b) the residual deviance is 17.8995652, with (c) pvalue 0.0566816515; (d) concerning the hypothesis, we do not reject H_0.

155. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (30,7,-1), (40,19,-0.5), (25,10,0), (40,25,0.5), (35,26,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0229$, $\hat{\beta}_1 = 0.9751$

The null deviance was 21.1489 on 4 degrees of freedom.
The residual deviance was 2.7769 on 3 degrees of freedom.
AIC: 25.9692

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL 1 point

0.4273208800 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-9.5961752 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL 1 point

0.2784411 ± 5e-2 ✓	

156. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,14,-1), (30,18,-0.6), (40,19,-0.2), (40,18,0.2), (30,9,0.6), (30,10,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.1142$, $\hat{\beta}_1 = -0.8013$

The null deviance was 12.3026 on 5 degrees of freedom.
The residual deviance was 1.1231 on 4 degrees of freedom.
AIC: 28.0042

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

$0.8905937500 \pm 5e\text{-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.4405813 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.6$:

NUMERICAL | 1 point

0.5906328 ± 5e-2 ✓	

157. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	58	3
Clinic B	16	4
Clinic C	53	13

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

7.4999244 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

158. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	41	8
Clinic B	47	15
Clinic C	46	16

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

$1.6295025 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

159. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 3, 7, 7, 8, 9+, 9+, 9+, 12+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$5 \pm 5\text{e-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$80 \pm 5\text{e-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0625 \pm 5\text{e-}1$ ✓	

160. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0+, 0, 1+, 2+, 3+, 4, 5+, 6+, 6, 8, 10.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$6 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$45 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.1333333 \pm$ 5e-1 ✓	

161. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 66.5, 67.3, 68.2, 66.5, 65.3, 68.2; while for $x = 0$ were 61.4, 58.8 and for $x = 1$ were 52.3, 49.6.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 59.25625; (b) the residual deviance is 15.2834375, with (c) pvalue 0.0538629223; (d) concerning the hypothesis, we do not reject H_0.

162. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 61.8, 62, 63.2, 64.6, 63.2, 63.9; while for $x = 0$ were 67.2, 68.6, 69.9, 70.5 and for $x = 1$ were 76.2, 73.5.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 69.01; (b) the residual deviance is 15.914, with (c) pvalue 0.1021208561; (d) concerning the hypothesis, we do not reject H_0.

163. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,8,-1), (30,13,-0.5), (25,10,0), (30,20,0.5), (30,18,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0537$, $\hat{\beta}_1 = 0.651$

The null deviance was 9.4331 on 4 degrees of freedom.
The residual deviance was 2.3532 on 3 degrees of freedom.
AIC: 24.9955

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

0.5024019300 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.321123 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0$:

NUMERICAL | 1 point

0.4865744 ± 5e-2 ✓	

164. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,39,-1), (30,22,-0.6), (40,22,-0.2), (25,11,0.2), (25,7,0.6), (35,9,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1203$, $\hat{\beta}_1 = -1.476$

The null deviance was 46.2214 on 5 degrees of freedom.
The residual deviance was 1.621 on 4 degrees of freedom.
AIC: 27.8249

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

$0.8050205500 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-11.101979 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 1$:

NUMERICAL 1 point

0.2049328 ± 5e-2 ✓	

165. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	77	4
Clinic B	28	6
Clinic C	51	10

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

6.6449833 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

166. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	57	8
Clinic B	65	17
Clinic C	62	16

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

$2.283045 \pm 5e\text{-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

$2 \pm 1e\text{-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

167. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 1, 2, 4, 6, 6, 7, 8, 10+, 11+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$2 \pm 5\text{e-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$56 \pm 5\text{e-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0357143 \pm 5\text{e-}1$ ✓	

168. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$1+, 1, 1, 3, 4, 5, 6, 7, 7, 11, 12.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$1 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$58 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0172414 \pm$ 5e-1 ✓	

169. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 68.3, 64.2; while for $x = 0$ were 58.7, 58.5, 60.7, 61.1 and for $x = 1$ were 53, 53.9, 53.2, 51.2.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -6.7428571; (b) the residual deviance is 17.8657143, with (c) pvalue 0.0222560890; (d) concerning the hypothesis, we reject H_0.

170. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.3, 66.5, 59.6, 63.2; while for $x = 0$ were 73.1, 70.4 and for $x = 1$ were 75.4, 77.1, 76.4, 72.7, 74.4, 74.1.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 69.75; (b) the residual deviance is 53.75, with (c) pvalue 0.0000000540; (d) concerning the hypothesis, we reject H_0.

171. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,13,-1), (35,15,-0.5), (30,21,0), (30,15,0.5), (45,37,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.2285$, $\hat{\beta}_1 = 1.0409$

The null deviance was 32.6314 on 4 degrees of freedom.
The residual deviance was 7.2486 on 3 degrees of freedom.
AIC: 30.6378

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0000014200 $\pm$ 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.6945867 $\pm$ 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL | 1 point

0.3073764 $\pm$ 5e-2 ✓	

172. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,33,-1), (35,20,-0.6), (40,20,-0.2), (20,10,0.2), (20,8,0.6), (25,7,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0313$, $\hat{\beta}_1 = -0.8633$

The null deviance was 16.0683 on 5 degrees of freedom.
The residual deviance was 1.1455 on 4 degrees of freedom.
AIC: 27.7142

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.0066517800 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.2843278 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.2$:

NUMERICAL | 1 point

0.4491789 ± 5e-2 ✓	

173. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	39	7
Clinic B	88	4
Clinic C	56	5

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

4.6057843 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

174. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	99	12
Clinic B	108	19
Clinic C	107	18

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

$1.0408844 \pm 5e\text{-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

$2 \pm 1e\text{-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

175. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 1, 6, 6, 7, 9+, 9+, 10+, 14+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$5 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$77 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0649351 \pm$ 5e-1 ✓	

176. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$1, 1+, 1, 2+, 2, 5+, 6, 8+, 10, 11.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$4 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$47 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0851064 \pm$ 5e-1 ✓	

177. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.7, 67.5; while for $x = 0$ were 59.9, 60.5, 60.5, 59.3 and for $x = 1$ were 53, 51.9, 51.4, 52.4.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -7.3071429; (b) the residual deviance is 5.0207143, with (c) pvalue 0.7553598834; (d) concerning the hypothesis, we do not reject H_0.

178. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 64.4, 61.3; while for $x = 0$ were 70.2, 68.2, 70.9, 69.7 and for $x = 1$ were 76.5, 74.5, 74.4, 74.7, 77.2, 74.3.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 6.07; (b) the residual deviance is 17.7365, with (c) pvalue 0.0595745483; (d) concerning the hypothesis, we do not reject H_0.

179. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,8,-1), (35,12,-0.5), (20,7,0), (40,18,0.5), (45,34,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.2223$, $\hat{\beta}_1 = 0.904$

The null deviance was 21.0918 on 4 degrees of freedom.
The residual deviance was 5.0906 on 3 degrees of freedom.
AIC: 28.0617

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0003036700 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.4855463 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL | 1 point

0.2448534 ± 5e-2 ✓	

180. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,18,-1), (30,22,-0.6), (45,28,-0.2), (35,20,0.2), (45,15,0.6), (25,8,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.222$, $\hat{\beta}_1 = -1.0563$

The null deviance was 22.2362 on 5 degrees of freedom.
The residual deviance was 2.2386 on 4 degrees of freedom.
AIC: 29.269

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

$0.6919695800 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.5151943 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.6$:

NUMERICAL | 1 point

0.3984777 ± 5e-2 ✓	

181. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	23	9
Clinic B	12	3
Clinic C	32	15

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

0.8337524 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

182. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	97	1
Clinic B	101	6
Clinic C	104	7

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$5.0082911 \pm 5e\text{-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1e\text{-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

183. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 3, 3, 5, 5, 6, 6, 10+, 11+, 12+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$62 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0483871 \pm$ 5e-1 ✓	

184. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0+, 0, 0, 1+, 1, 1, 1+, 3, 5, 10, 13+ .$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$4 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$35 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.1142857 \pm$ 5e-1 ✓	

185. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 66.2, 66.2, 69.8, 66.2; while for $x = 0$ were 62.5, 60.4, 59 and for $x = 1$ were 54.3, 53.5, 53.6.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -6.642029; (b) the residual deviance is 16.3768116, with (c) pvalue 0.0372935706; (d) concerning the hypothesis, we reject H_0.

186. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 66.9, 65.2; while for $x = 0$ were 67.7, 70.1, 71.4, 70.2, 69 and for $x = 1$ were 76.7, 77.1, 77.5, 77.2, 74.9.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 5.652; (b) the residual deviance is 21.0922667, with (c) pvalue 0.0204592922; (d) concerning the hypothesis, we reject H_0.

187. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,5,-1), (25,10,-0.5), (25,7,0), (20,14,0.5), (35,26,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.1834$, $\hat{\beta}_1 = 1.2153$

The null deviance was 27.285 on 4 degrees of freedom.
The residual deviance was 4.8637 on 3 degrees of freedom.
AIC: 26.3175

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

0.1820560600 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-8.7269148 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 1$:

NUMERICAL | 1 point

0.7372768 ± 5e-2 ✓	

188. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (40,36,-1), (30,19,-0.6), (45,20,-0.2), (30,11,0.2), (20,5,0.6), (45,18,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0625$, $\hat{\beta}_1 = -1.0653$

The null deviance was 41.0604 on 5 degrees of freedom.
The residual deviance was 14.2905 on 4 degrees of freedom.
AIC: 40.7281

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

$0.0064233500 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model ✓	
We do not reject the logistic regression model	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.2187884 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.2$:

NUMERICAL | 1 point

0.5684641 ± 5e-2 ✓	

189. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	84	1
Clinic B	73	15
Clinic C	98	13

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

15.8602192 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

190. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	53	9
Clinic B	62	14
Clinic C	60	14

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

$0.5460057 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

191. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 5, 7, 8, 10+, 11+, 11+, 14+, 15+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$6 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$97 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0618557 \pm$ 5e-1 ✓	

192. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$1+, 1, 2, 3+, 3+, 3+, 3, 4, 4, 5+ .$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$5 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$29 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.1724138 \pm$ 5e-1 ✓	

193. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 67.3, 65.3, 68, 69.2, 70.1; while for $x = 0$ were 59.9, 60.2, 60.8, 59.3 and for $x = 1$ were 53.8.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 60.4318182; (b) the residual deviance is 16.0809091, with (c) pvalue 0.0412365864; (d) concerning the hypothesis, we reject H_0.

194. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 64.6, 64.5, 64.7; while for $x = 0$ were 71.5, 70.4, 66.7 and for $x = 1$ were 77.5, 76.5, 74.5, 74.8, 74.8, 79.3.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 70.1757576; (b) the residual deviance is 32.5624242, with (c) pvalue 0.0003225420; (d) concerning the hypothesis, we reject H_0.

195. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (30,11,-1), (35,20,-0.5), (45,25,0), (20,16,0.5), (40,29,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.3966$, $\hat{\beta}_1 = 0.7515$

The null deviance was 13.4813 on 4 degrees of freedom.
The residual deviance was 2.8086 on 3 degrees of freedom.
AIC: 25.8397

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0091487000 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.5155476 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 1$:

NUMERICAL | 1 point

0.7591684 ± 5e-2 ✓	

196. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (40,32,-1), (40,25,-0.6), (45,29,-0.2), (45,15,0.2), (25,8,0.6), (20,8,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0436$, $\hat{\beta}_1 = -1.1026$

The null deviance was 29.2909 on 5 degrees of freedom.
The residual deviance was 6.7228 on 4 degrees of freedom.
AIC: 33.8538

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.0000203300 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.5655184 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.2$:

NUMERICAL | 1 point

0.5656426 ± 5e-2 ✓	

197. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	85	11
Clinic B	2	6
Clinic C	30	12

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

17.9588237 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

198. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	61	4
Clinic B	66	10
Clinic C	68	12

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

$3.2248935 \pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

$2 \pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

5.9914645 ± 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

199. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$4, 4, 4, 5, 8, 9+, 9+, 11+, 12+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

5 ± 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

81 ± 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

0.0617284 ± 5e-1 ✓	

200. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$1, 2, 3, 3+, 6, 6+, 6, 7, 9, 10+\,.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

3 ± 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

53 ± 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

0.0566038 ± 5e-1 ✓	

201. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.7, 65.3; while for $x = 0$ were 62.1, 60.7, 57.9, 59.6 and for $x = 1$ were 52.1, 53.8, 51.5, 52.6.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 59.4607143; (b) the residual deviance is 15.0289286, with (c) pvalue 0.0585853967; (d) concerning the hypothesis, we do not reject H_0.

202. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 64, 65.2, 63.5; while for $x = 0$ were 69.9, 69.6, 68.4, 68.7 and for $x = 1$ were 77.1, 76.1, 76.5, 72.6, 75.1.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 69.6108696; (b) the residual deviance is 16.8473913, with (c) pvalue 0.0778097672; (d) concerning the hypothesis, we do not reject H_0.

203. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,7,-1), (40,16,-0.5), (25,13,0), (35,27,0.5), (45,36,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.3059$, $\hat{\beta}_1 = 1.1704$

The null deviance was 25.0734 on 4 degrees of freedom.
The residual deviance was 1.4858 on 3 degrees of freedom.
AIC: 24.1803

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL 1 point

0.0000486300 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-9.3472231 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.5$:

NUMERICAL 1 point

0.4306236 ± 5e-2 ✓	

204. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,29,-1), (30,17,-0.6), (25,17,-0.2), (25,9,0.2), (30,11,0.6), (30,10,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0472$, $\hat{\beta}_1 = -0.7079$

The null deviance was 15.1968 on 5 degrees of freedom.
The residual deviance was 3.6041 on 4 degrees of freedom.
AIC: 30.358

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

$0.4622330900 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.3769838 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.2$:

NUMERICAL | 1 point

0.5235705 ± 5e-2 ✓	

205. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	16	8
Clinic B	62	11
Clinic C	60	13

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

3.6039073 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

206. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	90	11
Clinic B	94	18
Clinic C	96	16

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$1.2526588 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

207. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 7, 7, 9+, 9+, 11+, 12+, 12+, 14+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$7 \pm 5e\text{-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$96 \pm 5e\text{-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0729167 \pm 5e\text{-}1$ ✓	

208. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$1, 1, 2, 2, 2, 2, 3, 5+, 6, 8, 9.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$1 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$41 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0243902 \pm$ 5e-1 ✓	

209. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 66.8, 68.1, 70.3, 67.6, 65.5; while for $x = 0$ were 59, 58.3, 59.6 and for $x = 1$ were 53.4, 53.2.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 59.9590164; (b) the residual deviance is 17.9439344, with (c) pvalue 0.0216507683; (d) concerning the hypothesis, we reject H_0.

210. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 63, 63.4, 61.6, 65.1, 63.4; while for $x = 0$ were 69.3, 69.7, 71.5, 70 and for $x = 1$ were 76.7, 76.5, 75.7.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 69.9130435; (b) the residual deviance is 9.8430435, with (c) pvalue 0.4543699880; (d) concerning the hypothesis, we do not reject H_0.

211. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,2,-1), (35,16,-0.5), (45,22,0), (30,19,0.5), (40,32,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0275$, $\hat{\beta}_1 = 1.3311$

The null deviance was 31.7334 on 4 degrees of freedom.
The residual deviance was 3.8779 on 3 degrees of freedom.
AIC: 26.1835

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL 1 point

0.2749493000 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-9.1527686 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL 1 point

0.2135615 ± 5e-2 ✓	

212. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,40,-1), (20,11,-0.6), (40,24,-0.2), (45,17,0.2), (40,19,0.6), (45,13,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.2018$, $\hat{\beta}_1 = -1.1782$

The null deviance was 43.1758 on 5 degrees of freedom.
The residual deviance was 9.0123 on 4 degrees of freedom.
AIC: 36.3864

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.0000000300 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-11.6870565 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL 1 point

0.7989861 ± 5e-2 ✓	

213. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	66	3
Clinic B	22	1
Clinic C	96	12

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

3.2525521 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

214. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	44	7
Clinic B	52	16
Clinic C	49	15

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

$2.2698124 \pm 5e\text{-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

$2 \pm 1e\text{-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

215. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 5, 5, 10+, 10+, 10+, 11+, 12+, 14+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$7 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$93 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0752688 \pm$ 5e-1 ✓	

216. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0+, 0, 0, 0+, 2, 2, 2, 2, 3+, 13, 13.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$35 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0857143 \pm$ 5e-1 ✓	

217. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 68.1, 67.1; while for $x = 0$ were 60.6, 60.6 and for $x = 1$ were 52.2, 53, 53.4, 53.4, 54.8, 51.6.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 60.4; (b) the residual deviance is 6.74, with (c) pvalue 0.5649269007; (d) concerning the hypothesis, we do not reject H_0.

218. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 64.6, 66, 63.8, 62.5, 66.5; while for $x = 0$ were 68.9, 71.5, 69.1, 71.2 and for $x = 1$ were 75.2, 76.2, 74.5.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 5.326087; (b) the residual deviance is 17.7247826, with (c) pvalue 0.0597874641; (d) concerning the hypothesis, we do not reject H_0.

219. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (40,7,-1), (45,13,-0.5), (30,16,0), (45,34,0.5), (25,17,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0229$, $\hat{\beta}_1 = 1.4489$

The null deviance was 41.7558 on 4 degrees of freedom.
The residual deviance was 4.3019 on 3 degrees of freedom.
AIC: 27.3868

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0000000200 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.5424172 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.5$:

NUMERICAL | 1 point

0.3214097 ± 5e-2 ✓	

220. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,31,-1), (20,12,-0.6), (30,16,-0.2), (25,15,0.2), (35,11,0.6), (25,8,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0181$, $\hat{\beta}_1 = -0.8067$

The null deviance was 16.5901 on 5 degrees of freedom.
The residual deviance was 2.6983 on 4 degrees of freedom.
AIC: 29.1962

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

$0.6095142900 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.2489775 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.2$:

NUMERICAL | 1 point

0.5447328 ± 5e-2 ✓	

221. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	3	4
Clinic B	85	10
Clinic C	39	14

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

11.7403771 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

222. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	73	14
Clinic B	79	21
Clinic C	78	22

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$1.1782098 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

223. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$2, 4, 4, 5, 7, 8, 9+, 11+, 13+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$4 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$77 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0519481 \pm$ 5e-1 ✓	

224. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 1, 1, 1, 4, 6+, 9+, 9, 10+, 13, 13, 14.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$81 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.037037 \pm$ 5e-1 ✓	

225. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.6; while for $x = 0$ were 61.2, 59.2, 59.6, 59, 58.8 and for $x = 1$ were 54.1, 54.1, 53.3, 51.6.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -6.2073171; (b) the residual deviance is 7.9087805, with (c) pvalue 0.4424311607; (d) concerning the hypothesis, we do not reject H_0.

226. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.2, 63, 62.6, 62.7, 63.5, 61.1; while for $x = 0$ were 69.3, 70.1, 69.4 and for $x = 1$ were 77.2, 76.5, 77.3.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 6.9545455; (b) the residual deviance is 10.0721212, with (c) pvalue 0.4341888053; (d) concerning the hypothesis, we do not reject H_0.

227. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,2,-1), (30,9,-0.5), (45,29,0), (45,36,0.5), (35,26,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1594$, $\hat{\beta}_1 = 1.7127$

The null deviance was 52.22 on 4 degrees of freedom.
The residual deviance was 8.9084 on 3 degrees of freedom.
AIC: 30.9116

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL 1 point

0.0305334500 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the logistic regression model ✓	
We do not reject the logistic regression model	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-9.0015918 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0$:

NUMERICAL 1 point

0.5397631 ± 5e-2 ✓	

228. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,32,-1), (20,14,-0.6), (45,17,-0.2), (25,15,0.2), (40,13,0.6), (20,7,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0618$, $\hat{\beta}_1 = -0.8297$

The null deviance was 22.122 on 5 degrees of freedom.
The residual deviance was 7.9555 on 4 degrees of freedom.
AIC: 34.6013

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL 1 point

$0.0004963600 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.3229108 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 1$:

NUMERICAL | 1 point

0.2908067 ± 5e-2 ✓	

229. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	99	8
Clinic B	36	6
Clinic C	41	14

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

9.4486567 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

230. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	94	5
Clinic B	100	9
Clinic C	99	13

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$3.0180732 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

231. **Exponential**

CLOZE 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$2, 2, 4, 6, 6, 7, 7, 10+, 12+, 13+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL 1 point

$3 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL 1 point

$69 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL 1 point

$0.0434783 \pm$ 5e-1 ✓	

232. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$1, 1, 1, 1+, 2, 2, 3, 3, 5+, 9.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$2 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$28 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0714286 \pm$ 5e-1 ✓	

233. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 67.2, 66.7, 66.8; while for $x = 0$ were 60.2, 60.1, 59.2, 59.3 and for $x = 1$ were 51.4, 53.2, 52.8.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -7.2166667; (b) the residual deviance is 2.7473333, with (c) pvalue 0.9491997824; (d) concerning the hypothesis, we do not reject H_0.

234. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 64.2, 63.8, 63.1, 66.6; while for $x = 0$ were 69.6, 69.6, 68, 68.4, 71.1 and for $x = 1$ were 76.2, 76, 75.1.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 69.7771084; (b) the residual deviance is 15.1780723, with (c) pvalue 0.1257032764; (d) concerning the hypothesis, we do not reject H_0.

235. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,21,-1), (35,15,-0.5), (40,22,0), (35,25,0.5), (25,16,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.2671$, $\hat{\beta}_1 = 0.5329$

The null deviance was 8.1424 on 4 degrees of freedom.
The residual deviance was 2.343 on 3 degrees of freedom.
AIC: 26.1857

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL 1 point

0.5043296800 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-9.9213339 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 1$:

NUMERICAL 1 point

0.6899886 ± 5e-2 ✓	

236. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (30,26,-1), (30,22,-0.6), (25,16,-0.2), (45,22,0.2), (45,11,0.6), (20,7,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.199$, $\hat{\beta}_1 = -1.4949$

The null deviance was 40.1215 on 5 degrees of freedom.
The residual deviance was 3.795 on 4 degrees of freedom.
AIC: 29.7815

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL 1 point

$0.4344649300 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-10.9932774 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.6$:

NUMERICAL | 1 point

0.7494934 ± 5e-2 ✓	

237. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	76	8
Clinic B	43	15
Clinic C	74	5

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

11.5679378 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

238. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	66	2
Clinic B	70	11
Clinic C	74	7

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$5.8418747 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

239. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$3, 5, 7, 9+, 10+, 12+, 13+, 13+, 13+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$7 \pm 5\text{e-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$99 \pm 5\text{e-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0707071 \pm 5\text{e-}1$ ✓	

240. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0+, 1, 1+, 1, 2, 8, 8, 11, 12, 17+, 18.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$79 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0379747 \pm$ 5e-1 ✓	

241. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 66.9, 67.9, 66.8, 67.7, 65.6; while for $x = 0$ were 60.1, 60.6 and for $x = 1$ were 52, 52.4, 54.3.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 60.0263158; (b) the residual deviance is 6.7184211, with (c) pvalue 0.5672951168; (d) concerning the hypothesis, we do not reject H_0.

242. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.5, 63.2, 61.1; while for $x = 0$ were 71.8, 68.6, 70.8, 68.1 and for $x = 1$ were 76.3, 76.7, 75.7, 77.2, 75.1.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 6.4586957; (b) the residual deviance is 21.756087, with (c) pvalue 0.0163965642; (d) concerning the hypothesis, we reject H_0.

243. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (35,10,-1), (25,7,-0.5), (25,12,0), (25,16,0.5), (25,20,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0054$, $\hat{\beta}_1 = 1.1821$

The null deviance was 23.1296 on 4 degrees of freedom.
The residual deviance was 1.3596 on 3 degrees of freedom.
AIC: 23.2229

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

0.7150304800 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-8.9316602 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.5$:

NUMERICAL | 1 point

0.3576277 ± 5e-2 ✓	

244. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,14,-1), (40,30,-0.6), (20,10,-0.2), (45,24,0.2), (40,6,0.6), (20,4,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.1657$, $\hat{\beta}_1 = -1.2343$

The null deviance was 39.3383 on 5 degrees of freedom.
The residual deviance was 13.7827 on 4 degrees of freedom.
AIC: 39.6074

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL 1 point

$0.0000002000 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-10.9123682 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL | 1 point

0.7443396 ± 5e-2 ✓	

245. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	95	6
Clinic B	69	9
Clinic C	64	3

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

2.9815647 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

246. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	60	12
Clinic B	66	19
Clinic C	67	20

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

$1.1551353 \pm 5e\text{-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

$2 \pm 1e\text{-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

247. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$2, 2, 4, 6, 10+, 10+, 10+, 10+, 11+, 13+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$6 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$78 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0769231 \pm$ 5e-1 ✓	

248. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0+, 1+, 1+, 1+, 2, 3, 6, 8, 8, 26.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$4 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$56 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0714286 \pm$ 5e-1 ✓	

249. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.3, 67, 66.1; while for $x = 0$ were 58.6, 60, 58.8, 59.7 and for $x = 1$ were 53.1, 52.7, 51.9.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 59.32; (b) the residual deviance is 3.5943333, with (c) pvalue 0.8917464082; (d) concerning the hypothesis, we do not reject H_0.

250. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 63.8, 62, 63.1, 62.3, 63.5, 62.6, 65.9; while for $x = 0$ were 67.3, 70.8, 69.4, 70 and for $x = 1$ were 76.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 69.5066667; (b) the residual deviance is 17.1446667, with (c) pvalue 0.0712235417; (d) concerning the hypothesis, we do not reject H_0.

251. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (35,9,-1), (30,11,-0.5), (30,13,0), (35,25,0.5), (40,30,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0273$, $\hat{\beta}_1 = 1.1616$

The null deviance was 28.2059 on 4 degrees of freedom.
The residual deviance was 1.4528 on 3 degrees of freedom.
AIC: 24.5535

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL 1 point

$0.6932108900 \pm$ 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

$-9.5503398 \pm$ 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 1$:

NUMERICAL 1 point

$0.7665555 \pm$ 5e-2 ✓	

252. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,21,-1), (30,19,-0.6), (40,18,-0.2), (40,27,0.2), (20,5,0.6), (20,6,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1467$, $\hat{\beta}_1 = -1.0191$

The null deviance was 27.109 on 5 degrees of freedom.
The residual deviance was 11.7345 on 4 degrees of freedom.
AIC: 37.2922

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

$0.0194391400 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model ✓	
We do not reject the logistic regression model	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-10.7788578 $\pm$ 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.6$:

NUMERICAL | 1 point

0.6809622 $\pm$ 5e-2 ✓	

253. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	90	0
Clinic B	94	6
Clinic C	73	9

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

13.9513701 $\pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 $\pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

5.9914645 ± 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

254. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	58	5
Clinic B	62	10
Clinic C	65	13

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

2.5350434 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

255. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$3, 3, 7, 10+, 10+, 12+, 13+, 15+, 15+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$7 \pm 5\text{e-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$103 \pm 5\text{e-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0679612 \pm 5\text{e-}1$ ✓	

256. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 0, 1, 3+, 5, 6, 7+, 7, 11, 12.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$2 \pm 5\text{e-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$52 \pm 5\text{e-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0384615 \pm 5\text{e-}1$ ✓	

257. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 66, 66.2, 64.8; while for $x = 0$ were 60.4, 59, 60.5, 59.8 and for $x = 1$ were 53.3, 55.1, 53.3.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 59.84; (b) the residual deviance is 4.7823333, with (c) pvalue 0.7805671532; (d) concerning the hypothesis, we do not reject H_0.

258. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 64.2, 65; while for $x = 0$ were 71.5, 69.3, 69.5, 69.3, 70.5, 70.2 and for $x = 1$ were 76.6, 74.4, 76.4, 76.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 5.6558824; (b) the residual deviance is 7.1514706, with (c) pvalue 0.7110720135; (d) concerning the hypothesis, we do not reject H_0.

259. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,6,-1), (30,16,-0.5), (35,17,0), (25,16,0.5), (20,10,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0077$, $\hat{\beta}_1 = 0.3952$

The null deviance was 5.4398 on 4 degrees of freedom.
The residual deviance was 3.3761 on 3 degrees of freedom.
AIC: 25.6492

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL 1 point

0.3371965500 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-9.1365824 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.5$:

NUMERICAL 1 point

0.452672 ± 5e-2 ✓	

260. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (30,24,-1), (40,25,-0.6), (40,22,-0.2), (40,20,0.2), (35,13,0.6), (30,10,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1181$, $\hat{\beta}_1 = -0.94$

The null deviance was 19.444 on 5 degrees of freedom.
The residual deviance was 1.142 on 4 degrees of freedom.
AIC: 28.6718

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

$0.8875482500 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.7648971 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL | 1 point

0.7423288 ± 5e-2 ✓	

261. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	52	3
Clinic B	48	7
Clinic C	31	1

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

3.2853574 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

262. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	39	6
Clinic B	46	12
Clinic C	44	13

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

$1.6270172 \pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

$2 \pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

263. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 1, 1, 2, 2, 7, 11+, 12+, 13+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$4 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$64 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0625 \pm$ 5e-1 ✓	

264. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0+, 0, 2, 2+, 2, 2, 2, 6+, 8, 10, 14.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$48 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0625 \pm$ 5e-1 ✓	

265. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 68, 67.7, 67.6; while for $x = 0$ were 59.6, 60.6, 59.9, 59.2 and for $x = 1$ were 54.8, 51.7, 53.1.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -7.2833333; (b) the residual deviance is 6.9943333, with (c) pvalue 0.5372441836; (d) concerning the hypothesis, we do not reject H_0.

266. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 63.5, 62, 62.8, 61.8; while for $x = 0$ were 70.7, 70.4, 68.5, 68.8, 67.9 and for $x = 1$ were 77.6, 75.3, 75.8.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 69.3289157; (b) the residual deviance is 10.8072289, with (c) pvalue 0.3727326577; (d) concerning the hypothesis, we do not reject H_0.

267. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,10,-1), (30,16,-0.5), (20,10,0), (20,15,0.5), (30,22,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1844$, $\hat{\beta}_1 = 1.1148$

The null deviance was 26.8626 on 4 degrees of freedom.
The residual deviance was 3.9107 on 3 degrees of freedom.
AIC: 25.9806

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0000211900 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.0349826 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0$:

NUMERICAL | 1 point

0.5459652 ± 5e-2 ✓	

268. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,16,-1), (40,28,-0.6), (45,27,-0.2), (30,18,0.2), (25,14,0.6), (25,7,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.2885$, $\hat{\beta}_1 = -0.6791$

The null deviance was 12.2032 on 5 degrees of freedom.
The residual deviance was 3.9833 on 4 degrees of freedom.
AIC: 30.7929

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL 1 point

$0.0321065200 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-11.4047789 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.2$:

NUMERICAL 1 point

0.538091 ± 5e-2 ✓	

269. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	47	8
Clinic B	19	5
Clinic C	7	0

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

2.8667386 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

5.9914645 ± 1e-1 ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

270. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	51	5
Clinic B	58	9
Clinic C	56	11

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

1.5614491 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

271. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$6, 6, 7, 8, 9+, 9+, 9+, 14+, 14+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$6 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$96 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0625 \pm$ 5e-1 ✓	

272. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$1, 1, 2, 2, 3+, 6, 7, 8, 10, 12, 13+.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$2 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$65 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0307692 \pm$ 5e-1 ✓	

273. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.6, 66.2, 66.6; while for $x = 0$ were 59, 58.6, 59.1, 60.3 and for $x = 1$ were 51.8, 52.7, 51.9.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -7; (b) the residual deviance is 2.636, with (c) pvalue 0.9550871569; (d) concerning the hypothesis, we do not reject H_0.

274. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 66, 64.9, 61.9, 63.6; while for $x = 0$ were 71.3, 67.7, 70.2 and for $x = 1$ were 75.6, 77.4, 76, 77.9, 75.7.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 70.164486; (b) the residual deviance is 21.3605607, with (c) pvalue 0.0187150208; (d) concerning the hypothesis, we reject H_0.

275. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (35,16,-1), (35,15,-0.5), (30,19,0), (35,20,0.5), (35,25,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.2453$, $\hat{\beta}_1 = 0.5443$

The null deviance was 8.1333 on 4 degrees of freedom.
The residual deviance was 1.9391 on 3 degrees of freedom.
AIC: 25.575

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0868145700 $\pm$ 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability	
We do not reject the model with common probability ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.8179488 $\pm$ 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.5$:

NUMERICAL | 1 point

0.6265558 $\pm$ 5e-2 ✓	

276. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,16,-1), (35,26,-0.6), (25,11,-0.2), (40,20,0.2), (45,14,0.6), (35,9,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0676$, $\hat{\beta}_1 = -1.2545$

The null deviance was 31.569 on 5 degrees of freedom.
The residual deviance was 2.9202 on 4 degrees of freedom.
AIC: 29.428

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.0000072300 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-11.2539216 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.6$:

NUMERICAL 1 point

0.3351148 ± 5e-2 ✓	

277. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	23	0
Clinic B	56	12
Clinic C	80	11

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

7.6397923 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

278. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	67	7
Clinic B	72	11
Clinic C	74	13

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$1.1587247 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

279. **Exponential**

CLOZE 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$2, 2, 2, 3, 4, 5, 5, 6, 10+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL 1 point

$2 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL 1 point

$54 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL 1 point

$0.037037 \pm$ 5e-1 ✓	

280. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 0+, 1, 1, 2+, 3, 3, 3, 3, 4, 5, 8, 20+ .$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

3 ± 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

50 ± 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

0.06 ± 5e-1 ✓	

281. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 67, 68.5; while for $x = 0$ were 59.8, 59.8, 60.6, 60.1, 60.5 and for $x = 1$ were 53.4, 52.9, 52.9.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 60.2816327; (b) the residual deviance is 2.0146939, with (c) pvalue 0.9805580649; (d) concerning the hypothesis, we do not reject H_0.

282. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 64.1, 64.6, 66.1, 67; while for $x = 0$ were 67.4, 68, 71.6, 70.9, 68.8 and for $x = 1$ were 75.6, 74.8, 76.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 4.9409639; (b) the residual deviance is 23.1250602, with (c) pvalue 0.0102942549; (d) concerning the hypothesis, we reject H_0.

283. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (30,7,-1), (25,5,-0.5), (25,14,0), (45,29,0.5), (45,32,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.1385$, $\hat{\beta}_1 = 1.2023$

The null deviance was 30.9855 on 4 degrees of freedom.
The residual deviance was 3.324 on 3 degrees of freedom.
AIC: 26.0628

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0000030800 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.3694064 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 1$:

NUMERICAL | 1 point

0.7434018 ± 5e-2 ✓	

284. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,16,-1), (20,14,-0.6), (35,17,-0.2), (25,9,0.2), (25,11,0.6), (30,7,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0202$, $\hat{\beta}_1 = -1.1288$

The null deviance was 22.0532 on 5 degrees of freedom.
The residual deviance was 2.9194 on 4 degrees of freedom.
AIC: 28.1198

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL 1 point

$0.0005115400 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-10.6001847 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.2$:

NUMERICAL | 1 point

0.5512007 ± 5e-2 ✓	

285. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	65	1
Clinic B	53	0
Clinic C	17	14

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

44.4764634 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

286. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	50	13
Clinic B	59	17
Clinic C	58	20

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$0.5205334 \pm 5e\text{-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1e\text{-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

287. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$4, 6, 7, 9+, 9+, 9+, 13+, 13+, 14+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$7 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$99 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0707071 \pm$ 5e-1 ✓	

288. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 0, 1+, 1, 1+, 2, 4, 5+, 7+, 8+.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$5 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$29 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.1724138 \pm$ 5e-1 ✓	

289. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 68.3, 67.8; while for $x = 0$ were 60.7, 58.9, 60.3, 59.9 and for $x = 1$ were 53.2, 55.5, 51.1, 52.8.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -7.3571429; (b) the residual deviance is 12.7307143, with (c) pvalue 0.1214568913; (d) concerning the hypothesis, we do not reject H_0.

290. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.9, 64.3, 63.7; while for $x = 0$ were 68.8, 70.1, 71.1, 69.8, 68.5 and for $x = 1$ were 74.6, 75, 76.6, 75.7.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 5.4445783; (b) the residual deviance is 9.7154217, with (c) pvalue 0.4658050746; (d) concerning the hypothesis, we do not reject H_0.

291. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,12,-1), (35,9,-0.5), (30,15,0), (45,34,0.5), (35,30,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1758$, $\hat{\beta}_1 = 1.5408$

The null deviance was 50.4233 on 4 degrees of freedom.
The residual deviance was 3.1357 on 3 degrees of freedom.
AIC: 26.0901

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

0.3711760200 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.4771886 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 1$:

NUMERICAL | 1 point

0.847691 ± 5e-2 ✓	

292. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,14,-1), (30,21,-0.6), (25,12,-0.2), (20,5,0.2), (20,9,0.6), (40,11,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0776$, $\hat{\beta}_1 = -0.9549$

The null deviance was 21.3181 on 5 degrees of freedom.
The residual deviance was 4.9688 on 4 degrees of freedom.
AIC: 30.2505

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL 1 point

$0.2905185900 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-10.6408513 $\pm$ 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 1$:

NUMERICAL | 1 point

0.2625966 $\pm$ 5e-2 ✓	

293. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	71	6
Clinic B	34	14
Clinic C	97	11

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

11.5502888 $\pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 $\pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

5.9914645 ± 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

294. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	96	7
Clinic B	103	12
Clinic C	104	13

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

1.4125329 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

295. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$2, 2, 3, 4, 7, 7, 8, 12+, 14+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$74 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0405405 \pm$ 5e-1 ✓	

296. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 1, 1, 5, 5+, 6, 7, 7, 13, 13.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$1 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$58 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0172414 \pm$ 5e-1 ✓	

297. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 67.3, 65.3, 67.8; while for $x = 0$ were 59.2, 60.5, 58.6 and for $x = 1$ were 52.7, 53.5, 52.5, 52.3.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 59.6710145; (b) the residual deviance is 6.4602899, with (c) pvalue 0.5958155954; (d) concerning the hypothesis, we do not reject H_0.

298. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 64.9, 63.7, 64.5, 65.3; while for $x = 0$ were 70, 70.6, 68.2, 70.5, 69.5, 68.5 and for $x = 1$ were 75.9, 77.3.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 70.0441176; (b) the residual deviance is 10.6279412, with (c) pvalue 0.3872294593; (d) concerning the hypothesis, we do not reject H_0.

299. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,13,-1), (40,13,-0.5), (20,7,0), (35,24,0.5), (30,20,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.1089$, $\hat{\beta}_1 = 0.9476$

The null deviance was 21.9488 on 4 degrees of freedom.
The residual deviance was 3.149 on 3 degrees of freedom.
AIC: 26.2614

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

0.3692177700 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.5561782 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0$:

NUMERICAL | 1 point

0.4727944 ± 5e-2 ✓	

300. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (30,22,-1), (20,14,-0.6), (45,25,-0.2), (35,23,0.2), (45,18,0.6), (35,11,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.244$, $\hat{\beta}_1 = -0.8825$

The null deviance was 19.6966 on 5 degrees of freedom.
The residual deviance was 3.6524 on 4 degrees of freedom.
AIC: 30.8681

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.0014246100 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.6078329 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL | 1 point

0.755196 ± 5e-2 ✓	

301. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	28	1
Clinic B	23	12
Clinic C	34	13

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

11.7077192 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

302. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	67	7
Clinic B	76	14
Clinic C	74	12

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$1.4464185 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

303. **Exponential**

CLOZE 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 2, 5, 7, 7, 9+, 10+, 11+, 12+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL 1 point

$5 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL 1 point

$78 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL 1 point

$0.0641026 \pm$ 5e-1 ✓	

304. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$1+, 2, 5, 5, 6, 7, 7, 9, 12, 12, 12.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$1 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$78 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0128205 \pm$ 5e-1 ✓	

305. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 66.7; while for $x = 0$ were 59.1, 60.5, 60.2, 61.7, 61.7 and for $x = 1$ were 53.7, 53.4, 56.1, 51.7.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 60.4731707; (b) the residual deviance is 15.0360976, with (c) pvalue 0.0584473542; (d) concerning the hypothesis, we do not reject H_0.

306. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 65, 61.7, 63.4, 64.6; while for $x = 0$ were 69.1, 69.9, 70.3, 68.5 and for $x = 1$ were 75.5, 77, 78, 75.6.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 6.425; (b) the residual deviance is 13.9716667, with (c) pvalue 0.1742879066; (d) concerning the hypothesis, we do not reject H_0.

307. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (35,14,-1), (25,9,-0.5), (20,11,0), (30,20,0.5), (30,22,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.2012$, $\hat{\beta}_1 = 0.795$

The null deviance was 12.7583 on 4 degrees of freedom.
The residual deviance was 1.2081 on 3 degrees of freedom.
AIC: 23.6474

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0125190100 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.219646 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0$:

NUMERICAL | 1 point

0.5501199 ± 5e-2 ✓	

308. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (30,22,-1), (35,23,-0.6), (45,27,-0.2), (25,13,0.2), (40,12,0.6), (40,9,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0176$, $\hat{\beta}_1 = -1.1754$

The null deviance was 31.502 on 5 degrees of freedom.
The residual deviance was 1.298 on 4 degrees of freedom.
AIC: 28.5471

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.0000074500 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.6245304 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.6$:

NUMERICAL | 1 point

0.3345602 ± 5e-2 ✓	

309. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	100	5
Clinic B	47	0
Clinic C	24	1

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

3.8064908 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

310. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	35	5
Clinic B	43	14
Clinic C	42	11

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$2.2950859 \pm 5e\text{-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1e\text{-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

311. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 3, 4, 7, 8, 9+, 12+, 12+, 12+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$5 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$82 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0609756 \pm$ 5e-1 ✓	

312. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 0, 2, 2, 3+, 3, 3, 3, 4, 8+, 16, 18.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$2 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$62 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0322581 \pm$ 5e-1 ✓	

313. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 66.6, 63.7, 68; while for $x = 0$ were 59.5 and for $x = 1$ were 55.3, 51.9, 52.5, 54.1, 53.3, 52.1.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 59.6333333; (b) the residual deviance is 18.26, with (c) pvalue 0.0193594973; (d) concerning the hypothesis, we reject H_0.

314. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 64.4, 62.8, 63.1; while for $x = 0$ were 72.7, 71.3, 69.9, 69.2, 69.8, 70.8 and for $x = 1$ were 76.6, 76.9, 74.6.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 6.3; (b) the residual deviance is 14.9425, with (c) pvalue 0.1341723080; (d) concerning the hypothesis, we do not reject H_0.

315. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (35,11,-1), (45,18,-0.5), (20,9,0), (20,8,0.5), (25,17,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.1781$, $\hat{\beta}_1 = 0.6128$

The null deviance was 8.5812 on 4 degrees of freedom.
The residual deviance was 2.0448 on 3 degrees of freedom.
AIC: 24.6008

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0724630000 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability	
We do not reject the model with common probability ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.2780161 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0$:

NUMERICAL | 1 point

0.4555933 ± 5e-2 ✓	

316. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,13,-1), (45,26,-0.6), (25,12,-0.2), (25,12,0.2), (30,11,0.6), (45,11,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.1588$, $\hat{\beta}_1 = -0.8267$

The null deviance was 15.3814 on 5 degrees of freedom.
The residual deviance was 0.6882 on 4 degrees of freedom.
AIC: 27.4617

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.0088511400 \pm 5e\text{-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.3867464 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL | 1 point

0.6610346 ± 5e-2 ✓	

317. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	44	11
Clinic B	16	7
Clinic C	66	3

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

12.5821803 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

5.9914645 ± 1e-1 ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

318. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	47	0
Clinic B	55	6
Clinic C	55	7

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

8.8874837 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

319. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 2, 2, 3, 3, 5, 6, 11+, 11+, 13+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$57 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0526316 \pm$ 5e-1 ✓	

320. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$1+, 1, 1, 2+, 4, 5+, 5, 6, 6, 9, 12, 16.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$68 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0441176 \pm$ 5e-1 ✓	

321. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 67.8, 69.4, 67.3, 67.3; while for $x = 0$ were 59.6, 61.2 and for $x = 1$ were 54.2, 54.1, 53.1, 52.3.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 60.63; (b) the residual deviance is 6.80975, with (c) pvalue 0.5572916033; (d) concerning the hypothesis, we do not reject H_0.

322. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.3, 64.1; while for $x = 0$ were 70.8, 67.4, 70.1, 67.7, 71.2 and for $x = 1$ were 76, 77.9, 76.8, 76.6, 77.5.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 70.1813333; (b) the residual deviance is 20.6962667, with (c) pvalue 0.0233139513; (d) concerning the hypothesis, we reject H_0.

323. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,11,-1), (45,21,-0.5), (35,22,0), (30,17,0.5), (35,27,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1723$, $\hat{\beta}_1 = 1.0225$

The null deviance was 26.1081 on 4 degrees of freedom.
The residual deviance was 3.4341 on 3 degrees of freedom.
AIC: 27.157

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

0.3294137700 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.8614419 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.5$:

NUMERICAL | 1 point

0.4160573 ± 5e-2 ✓	

324. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,13,-1), (45,28,-0.6), (45,32,-0.2), (20,6,0.2), (25,6,0.6), (25,8,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0013$, $\hat{\beta}_1 = -1.0158$

The null deviance was 26.3323 on 5 degrees of freedom.
The residual deviance was 9.3955 on 4 degrees of freedom.
AIC: 35.3066

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

$0.0519393400 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-10.9555725 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL 1 point

0.7339132 ± 5e-2 ✓	

325. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	29	10
Clinic B	26	5
Clinic C	10	14

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

11.7698831 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

326. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	79	14
Clinic B	86	22
Clinic C	84	21

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

$1.1663045 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

327. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$5, 6, 7, 8, 8, 9+, 10+, 11+, 11+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$5 \pm 5e\text{-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$89 \pm 5e\text{-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0561798 \pm 5e\text{-}1$ ✓	

328. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 0, 1+, 1, 2+, 2, 2, 4+, 6, 7+, 8+, 11.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$5 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$44 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.1136364 \pm$ 5e-1 ✓	

329. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 67.1, 67.3, 67.9, 68.2, 65, 68.5; while for $x = 0$ were 59.9, 59.3, 60.7 and for $x = 1$ were 53.3.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the R command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 60.1533333; (b) the residual deviance is 9.116, with (c) pvalue 0.3326051023; (d) concerning the hypothesis, we do not reject H_0.

330. **Gaussian**

ESSAY 1.0 point 0.10 penalty editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 64.8, 61.9, 63.4; while for $x = 0$ were 68.8, 69.2, 69.9 and for $x = 1$ were 76, 76.3, 74.6, 75.7, 76.1, 77.2.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 69.5727273; (b) the residual deviance is 8.7218182, with (c) pvalue 0.5586918809; (d) concerning the hypothesis, we do not reject H_0.

331. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (35,9,-1), (20,7,-0.5), (20,13,0), (40,27,0.5), (20,15,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.16$, $\hat{\beta}_1 = 1.164$

The null deviance was 22.1477 on 4 degrees of freedom.
The residual deviance was 1.382 on 3 degrees of freedom.
AIC: 23.1228

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

0.7097673900 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-8.8704411 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.5$:

NUMERICAL | 1 point

0.3960461 ± 5e-2 ✓	

332. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (30,24,-1), (25,18,-0.6), (20,15,-0.2), (20,9,0.2), (30,9,0.6), (40,10,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1956$, $\hat{\beta}_1 = -1.3663$

The null deviance was 37.2576 on 5 degrees of freedom.
The residual deviance was 2.2373 on 4 degrees of freedom.
AIC: 27.383

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.0000005300 \pm$ 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-10.57287 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.6$:

NUMERICAL | 1 point

0.3488373 ± 5e-2 ✓	

333. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	59	2
Clinic B	49	15
Clinic C	15	1

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

12.9164776 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

334. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	38	9
Clinic B	43	13
Clinic C	44	14

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$0.4165313 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

335. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 2, 4, 7, 10+, 11+, 11+, 12+, 13+, 14+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$6 \pm 5\text{e-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$85 \pm 5\text{e-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0705882 \pm 5\text{e-}1$ ✓	

336. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 0, 1, 1, 1, 1, 2+, 7+, 10+, 18.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

3 ± 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

41 ± 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

0.0731707 ± 5e-1 ✓	

337. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 67, 66.1, 69.3; while for $x = 0$ were 59.9, 59.5, 58.3, 60.6 and for $x = 1$ were 54.1, 52.2, 52.5.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 59.95; (b) the residual deviance is 11.2583333, with (c) pvalue 0.1874869046; (d) concerning the hypothesis, we do not reject H_0.

338. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.2, 63.7; while for $x = 0$ were 70.3, 69.3, 70.8 and for $x = 1$ were 75.3, 75.1, 75, 77.1, 77.1, 74.1, 77.5.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 5.7240964; (b) the residual deviance is 12.7826506, with (c) pvalue 0.2360792504; (d) concerning the hypothesis, we do not reject H_0.

339. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (35,16,-1), (20,6,-0.5), (30,20,0), (40,27,0.5), (30,22,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.35$, $\hat{\beta}_1 = 0.7216$

The null deviance was 14.0187 on 4 degrees of freedom.
The residual deviance was 4.3861 on 3 degrees of freedom.
AIC: 27.1134

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0072357300 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.3636573 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0$:

NUMERICAL | 1 point

0.586617 ± 5e-2 ✓	

340. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,17,-1), (40,30,-0.6), (20,10,-0.2), (30,7,0.2), (45,21,0.6), (35,13,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1819$, $\hat{\beta}_1 = -1.014$

The null deviance was 32.6261 on 5 degrees of freedom.
The residual deviance was 12.6764 on 4 degrees of freedom.
AIC: 38.613

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.0000044600 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-10.9683092 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.2$:

NUMERICAL | 1 point

0.4947733 ± 5e-2 ✓	

341. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	93	15
Clinic B	0	6
Clinic C	40	7

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

22.1797754 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

342. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	98	5
Clinic B	103	13
Clinic C	103	11

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

$3.225283 \pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

$2 \pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

343. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 4, 5, 8, 9+, 10+, 14+, 15+, 15+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$6 \pm 5\text{e-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$96 \pm 5\text{e-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0625 \pm 5\text{e-}1$ ✓	

344. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0+, 1, 1, 2, 2+, 2, 3+, 3, 4+, 7+, 12, 17+.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$6 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$54 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.1111111 \pm$ 5e-1 ✓	

345. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 66.2, 65.3, 66.6, 68.4, 68.3; while for $x = 0$ were 60.7, 62.1 and for $x = 1$ were 53.4, 52.4, 52.6.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -7; (b) the residual deviance is 12.52, with (c) pvalue 0.1294668907; (d) concerning the hypothesis, we do not reject H_0.

346. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 67.5, 63.7, 62.3; while for $x = 0$ were 71.5, 70.1, 70.9 and for $x = 1$ were 78.8, 74.2, 75.1, 76.2, 75.8, 74.6.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 5.5787879; (b) the residual deviance is 30.1587879, with (c) pvalue 0.0008068750; (d) concerning the hypothesis, we reject H_0.

347. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (40,10,-1), (45,19,-0.5), (30,14,0), (45,24,0.5), (40,26,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.1504$, $\hat{\beta}_1 = 0.7539$

The null deviance was 14.5671 on 4 degrees of freedom.
The residual deviance was 0.8881 on 3 degrees of freedom.
AIC: 25.1945

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0056886500 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-10.1532053 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0$:

NUMERICAL | 1 point

0.4624813 ± 5e-2 ✓	

348. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (35,24,-1), (25,18,-0.6), (30,15,-0.2), (45,27,0.2), (35,14,0.6), (35,8,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1191$, $\hat{\beta}_1 = -0.9315$

The null deviance was 23.8307 on 5 degrees of freedom.
The residual deviance was 5.1575 on 4 degrees of freedom.
AIC: 32.2748

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

$0.2715139600 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.5586484 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL | 1 point

0.7408786 ± 5e-2 ✓	

349. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	52	3
Clinic B	92	14
Clinic C	26	2

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

2.8783636 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

350. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	81	6
Clinic B	88	12
Clinic C	88	12

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

$1.8097088 \pm 5e\text{-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

$2 \pm 1e\text{-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

351. **Exponential**

CLOZE 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$2, 2, 3, 3, 4, 5, 6, 12+, 12+, 13+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL 1 point

$3 \pm 5e\text{-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL 1 point

$62 \pm 5e\text{-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL 1 point

$0.0483871 \pm 5e\text{-}1$ ✓	

352. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0+, 0+, 1, 3, 3, 3+, 5, 6, 12, 13+, 17.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$4 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$63 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0634921 \pm$ 5e-1 ✓	

353. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.9, 65.6, 69.5, 67.5; while for $x = 0$ were 60.9, 61.3, 58.5, 59.4 and for $x = 1$ were 53.2, 54.9.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 60.3464286; (b) the residual deviance is 16.8832143, with (c) pvalue 0.0313483961; (d) concerning the hypothesis, we reject H_0.

354. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 63.1, 63.6, 64.5, 65.1; while for $x = 0$ were 70.3, 70.3, 70.3, 72.2 and for $x = 1$ were 77, 77.4, 76.5, 74.5.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 70.4; (b) the residual deviance is 10.92875, with (c) pvalue 0.3630959447; (d) concerning the hypothesis, we do not reject H_0.

355. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,6,-1), (25,8,-0.5), (40,17,0), (40,24,0.5), (40,27,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.1692$, $\hat{\beta}_1 = 0.9056$

The null deviance was 14.1187 on 4 degrees of freedom.
The residual deviance was 0.6245 on 3 degrees of freedom.
AIC: 23.7525

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

0.8907911100 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.5639636 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.5$:

NUMERICAL | 1 point

0.5704234 ± 5e-2 ✓	

356. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i-th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (35,21,-1), (20,9,-0.6), (45,21,-0.2), (20,9,0.2), (35,15,0.6), (25,5,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.2532$, $\hat{\beta}_1 = -0.6133$

The null deviance was 10.1375 on 5 degrees of freedom.
The residual deviance was 2.7908 on 4 degrees of freedom.
AIC: 29.2222

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL 1 point

$0.0714327800 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the model with common probability	
We do not reject the model with common probability ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.2157262 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL | 1 point

0.5890682 ± 5e-2 ✓	

357. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	59	1
Clinic B	7	5
Clinic C	64	4

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

15.1509935 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

358. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	66	6
Clinic B	70	15
Clinic C	73	12

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$3.0505122 \pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

359. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$3, 4, 4, 7, 10+, 10+, 11+, 11+, 11+, 11+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$6 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$82 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0731707 \pm$ 5e-1 ✓	

360. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 1, 1+, 2+, 2, 4+, 7, 9, 12, 13.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$51 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0588235 \pm$ 5e-1 ✓	

361. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 69.5, 65.7; while for $x = 0$ were 61.3, 60.8, 60.6, 59.5 and for $x = 1$ were 53.1, 52.4, 52.5, 51.8.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 60.25; (b) the residual deviance is 10.43, with (c) pvalue 0.2361324642; (d) concerning the hypothesis, we do not reject H_0.

362. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 62.5, 64.3, 63.1, 63.8, 66.8; while for $x = 0$ were 69.2, 67.5, 71.5, 69.4, 67.1 and for $x = 1$ were 76.3, 76.3.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 69.612; (b) the residual deviance is 27.5056, with (c) pvalue 0.0021650293; (d) concerning the hypothesis, we reject H_0.

363. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (30,9,-1), (30,10,-0.5), (35,20,0), (45,28,0.5), (45,30,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -6 \times 10^{-4}$, $\hat{\beta}_1 = 0.8394$

The null deviance was 16.427 on 4 degrees of freedom.
The residual deviance was 1.5068 on 3 degrees of freedom.
AIC: 25.3237

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL 1 point

0.0024966100 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-9.9084263 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 1$:

NUMERICAL 1 point

0.698206 ± 5e-2 ✓	

364. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,15,-1), (30,19,-0.6), (45,23,-0.2), (35,15,0.2), (20,6,0.6), (45,15,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0243$, $\hat{\beta}_1 = -0.8695$

The null deviance was 16.1036 on 5 degrees of freedom.
The residual deviance was 1.2497 on 4 degrees of freedom.
AIC: 27.9704

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

$0.8698482700 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.360322 $\pm$ 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.2$:

NUMERICAL | 1 point

0.5373396 $\pm$ 5e-2 ✓	

365. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	89	14
Clinic B	66	8
Clinic C	91	6

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

3.1718123 $\pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 $\pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

366. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	57	3
Clinic B	65	10
Clinic C	64	9

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$3.18921 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

367. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$1, 2, 3, 4, 4, 6, 11+, 13+, 13+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$4 \pm 5e\text{-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$72 \pm 5e\text{-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0555556 \pm 5e\text{-}1$ ✓	

368. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0+, 0, 1+, 1, 2, 2, 3, 5, 8+, 11+ .$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$4 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$33 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.1212121 \pm$ 5e-1 ✓	

369. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 68.5, 69.5, 68, 67.3; while for $x = 0$ were 60.7, 58.9, 62.1 and for $x = 1$ were 53.1, 54.7, 54.8.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 61.0507246; (b) the residual deviance is 10.5446377, with (c) pvalue 0.2288586597; (d) concerning the hypothesis, we do not reject H_0.

370. **Gaussian**

ESSAY 1.0 point 0.10 penalty editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 66, 64.3; while for $x = 0$ were 70.4, 70.9, 68.9, 69.7, 71, 68.7 and for $x = 1$ were 75.8, 76.4, 76.5, 77.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 70.3352941; (b) the residual deviance is 9.1658824, with (c) pvalue 0.5164365352; (d) concerning the hypothesis, we do not reject H_0.

371. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,5,-1), (25,13,-0.5), (45,22,0), (30,22,0.5), (45,36,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.2347$, $\hat{\beta}_1 = 1.1532$

The null deviance was 23.5767 on 4 degrees of freedom.
The residual deviance was 2.352 on 3 degrees of freedom.
AIC: 24.9669

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0000971000 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.3074317 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 1$:

NUMERICAL | 1 point

0.8002528 ± 5e-2 ✓	

372. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,38,-1), (25,15,-0.6), (30,17,-0.2), (45,17,0.2), (45,14,0.6), (45,8,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0704$, $\hat{\beta}_1 = -1.4665$

The null deviance was 53.3571 on 5 degrees of freedom.
The residual deviance was 1.939 on 4 degrees of freedom.
AIC: 29.1505

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL 1 point

$0.7469802000 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.6057753 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL | 1 point

0.8015638 ± 5e-2 ✓	

373. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	68	5
Clinic B	1	12
Clinic C	79	8

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

45.9855051 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

374. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	56	13
Clinic B	64	22
Clinic C	64	19

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$1.0089225 \pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

375. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$2, 3, 4, 6, 8, 8, 8, 8, 10+, 12+, 13+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$74 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0405405 \pm$ 5e-1 ✓	

376. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$1, 1+, 2, 3, 3, 3, 4, 4, 4+, 4, 5, 5.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$2 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$39 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0512821 \pm$ 5e-1 ✓	

377. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 67.6, 65.9, 67.2, 68; while for $x = 0$ were 60, 59 and for $x = 1$ were 54, 53.2, 54.2, 52.4.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -6.8625; (b) the residual deviance is 6.07375, with (c) pvalue 0.6389709674; (d) concerning the hypothesis, we do not reject H_0.

378. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 64.4, 63; while for $x = 0$ were 70.5, 68.4, 71 and for $x = 1$ were 76.1, 76.7, 75.7, 76.6, 75.4, 77.2, 78.2.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 70.0759036; (b) the residual deviance is 10.2568675, with (c) pvalue 0.4182539277; (d) concerning the hypothesis, we do not reject H_0.

379. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,5,-1), (45,13,-0.5), (25,13,0), (20,15,0.5), (25,17,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.1077$, $\hat{\beta}_1 = 1.2664$

The null deviance was 25.1007 on 4 degrees of freedom.
The residual deviance was 2.6504 on 3 degrees of freedom.
AIC: 24.426

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

0.4487220300 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-8.8877792 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -1$:

NUMERICAL | 1 point

0.2019587 ± 5e-2 ✓	

380. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (45,34,-1), (40,27,-0.6), (25,14,-0.2), (35,16,0.2), (25,9,0.6), (25,9,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.126$, $\hat{\beta}_1 = -0.9403$

The null deviance was 19.2072 on 5 degrees of freedom.
The residual deviance was 0.6153 on 4 degrees of freedom.
AIC: 27.5242

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.0017585700 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.4544458 $\pm$ 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.6$:

NUMERICAL | 1 point

0.3921885 $\pm$ 5e-2 ✓	

381. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	75	7
Clinic B	55	14
Clinic C	68	15

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

5.0477478 $\pm$ 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 $\pm$ 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1e\text{-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

382. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	57	7
Clinic B	62	16
Clinic C	65	14

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

$2.5292972 \pm 5e\text{-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

$2 \pm 1e\text{-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

383. **Exponential**

CLOZE 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$5, 6, 7, 8, 8, 8, 10+, 11+, 12+, 13+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL 1 point

$4 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL 1 point

$88 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL 1 point

$0.0454545 \pm$ 5e-1 ✓	

384. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0+, 1, 2, 3+, 4, 4, 4, 4, 5, 6+, 10+, 11+, 13+.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$6 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$63 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0952381 \pm$ 5e-1 ✓	

385. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 67, 66.8, 68.2; while for $x = 0$ were 58.1, 61.3, 60 and for $x = 1$ were 53.5, 53.2, 53.1, 51.9.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -7.1898551; (b) the residual deviance is 8.0402899, with (c) pvalue 0.4295444134; (d) concerning the hypothesis, we do not reject H_0.

386. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 65.4, 64.4, 64.2, 65.7, 62.6, 62.5, 63.7, 65.6; while for $x = 0$ were 70, 68.9 and for $x = 1$ were 75.6, 74.4.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated intercept.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is intercept 69.5880952; (b) the residual deviance is 12.7338095, with (c) pvalue 0.2389379711; (d) concerning the hypothesis, we do not reject H_0.

387. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,11,-1), (25,10,-0.5), (45,25,0), (25,13,0.5), (40,30,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1743$, $\hat{\beta}_1 = 0.6659$

The null deviance was 10.4 on 4 degrees of freedom.
The residual deviance was 2.4247 on 3 degrees of freedom.
AIC: 25.5686

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

0.0342022800 $\pm$ 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-9.5719605 $\pm$ 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0$:

NUMERICAL | 1 point

0.543473 $\pm$ 5e-2 ✓	

388. **Logistic**

CLOZE | 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (35,20,-1), (40,27,-0.6), (20,12,-0.2), (35,15,0.2), (40,17,0.6), (20,5,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = -0.0217$, $\hat{\beta}_1 = -0.6927$

The null deviance was 13.359 on 5 degrees of freedom.
The residual deviance was 3.5728 on 4 degrees of freedom.
AIC: 30.3585

Examine the information given and do computations before answering the questions below.

A) We use the null deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis)	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the model with common probability (null hypothesis) against the maximal model (alternative hypoyhesis).

NUMERICAL | 1 point

$0.0202369100 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the model with common probability ✓	
We do not reject the model with common probability	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL | 1 point

-11.3928732 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0.2$:

NUMERICAL | 1 point

0.4600185 ± 5e-2 ✓	

389. **Poisson**

CLOZE | 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	90	7
Clinic B	46	13
Clinic C	43	9

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL | 1 point

7.6012964 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL | 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

390. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	64	7
Clinic B	71	12
Clinic C	69	15

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

$2.0763444 \pm 5\text{e-}1$ ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

$2 \pm 1\text{e-}1$ ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm$ 1e-1 ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

391. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$2, 3, 5, 7, 9+, 9+, 10+, 12+, 13+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$6 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$85 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0705882 \pm$ 5e-1 ✓	

392. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$0, 1, 1, 1, 1, 2, 2, 2, 2, 3, 6, 6+.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$1 \pm$ 5e-1 ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$27 \pm$ 5e-1 ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.037037 \pm$ 5e-1 ✓	

393. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 10$ experiments carried out, and the yield values y measured for when $x = -1$ were 68.9, 68, 67.4, 67.2; while for $x = 0$ were 61.2, 59.1 and for $x = 1$ were 51.5, 55.2, 52.4, 54.6.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst -7.225; (b) the residual deviance is 13.64, with (c) pvalue 0.0916448345; (d) concerning the hypothesis, we do not reject H_0.

394. **Gaussian**

ESSAY | 1.0 point | 0.10 penalty | editor

An experiment was conducted on the yield y of a chemical process, depending on the addition of catalyst x used. Three levels of catalyst x were considered in the experiment, which were coded as $-1, 0, 1$. There were $n = 12$ experiments carried out, and the yield values y measured for when $x = -1$ were 64.3, 63.4, 62.9, 63.5; while for $x = 0$ were 71.6, 70.1, 69.7, 70.5, 70.8 and for $x = 1$ were 76.1, 79.4, 76.9.

You are required to analyze the data using a generalized linear model with a normal distribution and the identity link. Run the `R` command `glm` and examine the output before answering the questions in the textbox below:

(a) Write the estimated coefficient of catalyst.

(b) Write the residual deviance.

(c) Compute the pvalue of the residual deviance.

(d) Consider the test that H_0 that data supports the regression model against the hypothesis H_1 that data backs the maximal model. Using your results, perform the test and write your conclusions. Use $\alpha = 0.05$.

Notes for grader:

- (a) the estimated is coefficient of catalyst 6.973494; (b) the residual deviance is 9.0318072, with (c) pvalue 0.5290876397; (d) concerning the hypothesis, we do not reject H_0.

395. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 5$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (20,3,-1), (25,10,-0.5), (45,22,0), (35,30,0.5), (25,19,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.1797$, $\hat{\beta}_1 = 1.6159$

The null deviance was 36.5968 on 4 degrees of freedom.
The residual deviance was 6.1044 on 3 degrees of freedom.
AIC: 27.5671

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI 1 point Single Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL 1 point

0.1066409100 ± 5e-2 ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI 1 point Single Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-8.731355 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = 0$:

NUMERICAL 1 point

0.544815 ± 5e-2 ✓	

396. **Logistic**

CLOZE 0.10 penalty

A study was carried out in $n = 6$ small apple orchards. The $i - th$ orchard has r_i trees which were all given a dose of additive x_i. After one month, y_i, the number of trees that did not have certain fungus was recorded. The following is the data per orchard, presented in the format (r_i, y_i, x_i): (25,18,-1), (35,26,-0.6), (45,25,-0.2), (40,18,0.2), (40,16,0.6), (45,11,1). In this problem, the values of doses of additive are coded, hence the negative x_i values.

The following are outputs from the analysis of these data after fitting a glm model with logit link and binomial distribution.

$\hat{\beta}_0 = 0.0897$, $\hat{\beta}_1 = -1.1099$

The null deviance was 28.5074 on 5 degrees of freedom.
The residual deviance was 1.4771 on 4 degrees of freedom.
AIC: 29.2017

Examine the information given and do computations before answering the questions below.

A) We use the residual deviance to test

MULTI | 1 point | Single | Shuffle

the model with common p (null hypothesis) against the maximal model (alternative hypothesis)	
the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis) ✓	
the model with common p (null hypothesis) against the logistic regression model (alternative hypothesis)	

B) Compute the p-value for comparing (i.e. testing) the logistic regression model (null hypothesis) against the maximal model (alternative hypothesis).

NUMERICAL | 1 point

$0.8306822000 \pm 5\text{e-}2$ ✓	

C) For the hypothesis described in B), use the p-value you computed also in B) and $\alpha = 0.05$ to select the correct statement below.

MULTI | 1 point | Single | Shuffle

We reject the logistic regression model	
We do not reject the logistic regression model ✓	

D) Compute the log-likelihood of the maximal model. Hint: Use the `R` function `dbinom` and estimate the probability using the observed proportion of trees with no fungi in each orchard.

NUMERICAL 1 point

-11.8622617 ± 5e-1 ✓	

E) Compute the predicted proportion of trees without fungus when the dose of additive is $x = -0.2$:

NUMERICAL 1 point

0.5772982 ± 5e-2 ✓	

397. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	49	13
Clinic B	94	5
Clinic C	13	8

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

18.0946221 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL 1 point

5.9914645 ± 1e-1 ✓	

D) Which statement is correct?

MULTI 1 point Single Shuffle

There is strong evidence that the chances of survival are not independent on the clinic. ✓	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic.	

398. **Poisson**

CLOZE 0.10 penalty

Patients were classified according to the clinic they were treated. The contingency table below shows the number of patients (y) that were treated at each clinic and whether they survived.

	Survived	Died
Clinic A	96	7
Clinic B	102	16
Clinic C	103	12

The null hypothesis is that survival is independent of the clinic attended.

Analyze the data to answer the questions below.

A) What is the deviance value to test the alternative hypothesis that the chances of survival depend on the clinic?

NUMERICAL 1 point

2.7806424 ± 5e-1 ✓	

B) What are the degrees of freedom for the deviance above?

NUMERICAL 1 point

2 ± 1e-1 ✓	

C) What is the limit of the critical region for the deviance above for a significance level of 0.05?

NUMERICAL | 1 point

$5.9914645 \pm 1\text{e-}1$ ✓	

D) Which statement is correct?

MULTI | 1 point | Single | Shuffle

There is strong evidence that the chances of survival are not independent on the clinic.	
We cannot reject the null hypothesis that the chances of survival are independent on the clinic. ✓	

399. **Exponential**

CLOZE | 0.10 penalty

From February 1972 to February 1975, 10 severe viral hepatitis patients from various hospitals in California were placed on steroids therapy. The survival times were

$$4, 4, 5, 7, 8, 12+, 13+, 13+, 14+, 15+,$$

where the symbol "+" represents a censored observation. Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$5 \pm 5\text{e-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$95 \pm 5\text{e-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.0526316 \pm 5\text{e-}1$ ✓	

400. **Exponential**

CLOZE | 0.10 penalty

The following data are number of months in service of air conditioning units in airplanes before the units develop a fault. In below, the symbol "+" represents a censored observation, that is, the corresponding unit is still working at the time of data collection:

$$1, 1+, 2, 2, 3, 3+, 6+, 10, 11, 11.$$

Assume that survival times are exponentially distributed $S(t) = e^{-\mu t}$.

A) Compute $\sum_{i=1}^{n} \delta_i$.

NUMERICAL | 1 point

$3 \pm 5\text{e-}1$ ✓	

B) Compute $\sum_{i=1}^{n} t_i$.

NUMERICAL | 1 point

$50 \pm 5\text{e-}1$ ✓	

C) Estimate μ by maximum likelihood.

NUMERICAL | 1 point

$0.06 \pm 5\text{e-}1$ ✓	

401. **Theory**

MATCHING | 1.0 point | 0.10 penalty | Shuffle

Match the following concepts.

$\log\left(\frac{\pi_i}{1-\pi_i}\right) = \beta_0 + \beta_1 x_i$ •	······	• is an example of logistic regression model.
$\log(\mu_i) = \beta_0 + \beta_1 x_i$ •	······	• is an example of Poisson regression model.
$\mu_i = \beta_0 + \beta_1 x_i$ •	······	• is an example of linear regression model.
$\mu_i = \beta_0 + \beta_1^2 x_i$ •	······	• is not an example of a generalised linear model.

402. **Theory**

MULTI | 1.0 point | 0.10 penalty | Single | Shuffle

Which statement below is correct?

(a) We usually find the maximum likelihood estimates by maximising the log-likelihood.
(b) In the context of the logistic regression model, the method of least squares does not have a closed form solution.
(c) In the context of the Normal linear model, the method of least squares and the method of maximising the likelihood are two alternative methods of estimation.
(d) None of the above.
(e) All of the above. (100%)

403. **Theory**

MATCHING | 1.0 point | 0.10 penalty | Shuffle

Match the following concepts.

The deviance •	······	• is the sum of squares of the deviance residuals.
The maximal model •	······	• has the same number of parameters as observations.
$\log(\mu_i) = \beta_0$ •	······	• is an example of null model.
The Poisson distribution •	······	• belongs to the exponential family.
The link function •	······	• is a monotonic differentiable function.

404. **Theory**

MULTI | 1.0 point | 0.10 penalty | Single | Shuffle

Which statement below is correct?

(a) $\log(\mu_i) = \beta_0$ is an example of null model.
(b) $\log(\mu_i) = \beta_0 + 35$ is an example of null model.
(c) $\log(\mu_i) = \beta_0 + 35\pi$ is an example of null model.
(d) None of the above.
(e) All of the above. (100%)

405. **Theory**

MULTI | 1.0 point | 0.10 penalty | Single | Shuffle

The link $g(\mu_i) = \tan(\pi(\mu_i - 1/2))$ is known as the Cauchy link. This link works best (select only one from below)

(a) with normal data as it transforms real inputs into the whole real line.
(b) with Poisson data as it transforms positive inputs into the whole real line.
(c) with binomial data as it transforms proportions into the whole real line. (100%)

406. **Theory**

MATCHING | 1.0 point | 0.10 penalty | Shuffle

Match the statements below

The conditional probability density function of T given survival up to time t is the •	······	• hazard function.
The censoring variable •	······	• indicates whether the survival time is censored.
Survival analysis •	······	• is a branch of statistics for analyzing the expected duration of time until one event occurs.
The probability that a subject survives longer than time t is the •	······	• survival function.

407. **Theory**

MULTI | 1.0 point | 0.10 penalty | Single | Shuffle

Suppose that $T \sim \text{Exp}(3)$.

(a) The hazard function is 3.
(b) The hazard function is a constant.
(c) The survivor function is $S(t) = e^{-3t}$.
(d) All of the above. (100%)
(e) None of the above.

408. **Theory**

MATCHING | 1.0 point | 0.10 penalty | Shuffle

What do these `R` commands do?

`fitted` •	······	• extracts fitted values from objects returned by modeling function.
`lm` •	······	• fits linear models.
`glm` •	······	• fits generalized linear models.
`residuals` •	······	• extracts model residuals from objects returned by modeling functions.

409. **Theory**

MULTI | 1.0 point | 0.10 penalty | Single | Shuffle

One of the following statements is correct. Which one?

(a) By Wilks' theorem, for large n, if the model is a good fit, then the deviance is distributed according to χ^2_{n-p}, where n is the number of parameters and p is the number of observations.
(b) For large n, if the model is a good fit, the Pearson's goodness of fit test is distributed according to χ^2_{n-p}, where n is the number of parameters and p is the number of observations.
(c) The χ^2 approximation is not very accurate for the deviance; it is a much better approximation for the difference in deviances. (100%)

410. **Theory**

CLOZE | 0.10 penalty

Recall the general linear model given by

$$Y = X\beta + \epsilon,$$

where $Y = (Y_1, \dots, Y_n)^\top$ is the vector of responses, X is the $n \times p$ design matrix, $\beta = (\beta_0, \dots, \beta_{p-1})^\top$ is the parameter vector and $\epsilon = (\epsilon_1, \dots, \epsilon_n)^\top$ is the error vector.
Say that you have 145 observations and you want to write the simple linear model

$$y = \beta_0 + \beta_1 x + \epsilon$$

in matrix form. How many rows does X have?

NUMERICAL | 1 point

$145 \pm$ 1e-1 ✓	

What is the value of the first element of X (ie $X_{(1,1)}$)?

NUMERICAL | 1 point

$1 \pm$ 1e-1 ✓	

411. **Theory**

MULTI | 1.0 point | 0.10 penalty | Single | Shuffle

Select the correct statement below. In a generalised linear model, the natural parameter

(a) guarantees good fit of model to data.
(b) does not guarantee good fit of model to data.
(c) is just one among several possibilities to model data. (100%)
(d) is the only way to model data.

Total of marks: 1312