

Module Specification

Module Title Module Code
Credit Value Level Mode of Delivery Semester A

Pre-requisite modules	Co-requisite modules	Overlapping modules
SBS110 Evolution; SBS633 Evolutionary Genetics		

1) Content Description

Provide a description of the module, as it will appear in the Module Directory and on the Student Information System (approx. 70-80 words).

This module will introduce strategies and methods for identifying the molecular genetic basis of inherited human disorders and other traits in particular how linkage disequilibrium (LD) is used to identify the loci involved. It will use examples from the current literature to better understand genetic variation at a population and species level. It will examine quantitative traits in humans and other species; in particular the heritability estimates to infer the relative contribution of genes and the environment to important quantitative traits and disorders. Together the information will lead to an understanding of genetic drift and natural selection acting on the DNA sequence, the chromosome and genome organisation. The course will explore the evolution of genomic sequences and of chromosomes. Particular attention is paid to evolutionary processes observed at repetitive DNA sequences and the role of chromosomes in transmitting genetic material through mitosis and meiosis. It explores the role and evolution of sex chromosomes, the evolution of sex and of sexual selection. The course should students to achieve a critical understanding of thinking and research in the genetic processes of evolution.

2) Module Aims

Specify the aims of the module, i.e. the broad educational purposes for offering this module.

To show how patterns of chromosome and sequence divergence can be used to resolve species relationships.
To demonstrate approaches in population genetics to show how linkage disequilibrium (LD) is generated during evolution, and how it can be used to make inferences about population history and the genetic basis of important traits.
To use quantitative genetics and heritability estimates to infer the contribution of genetic variation to important traits.
To explore the evolution of genomic sequences and of chromosomes.
To study evolutionary processes acting on repetitive DNA sequences and the role of chromosomes in transmitting genetic material through mitosis and meiosis.
To explore the role and evolution of sex chromosomes, the evolution of sex and of sexual selection.

3) Learning Outcomes

Identify the learning outcomes for this module, i.e. knowledge, skills and attributes to be developed through completion of this module. Outcomes should be referenced to the relevant [QAA benchmark statements](#) and the [Framework for Higher Education Qualifications in England, Wales and Northern Ireland \(2008\)](#). The [SEEC Credit Level Descriptors for Further and Higher Education 2003](#) and [Queen Mary Statement of Graduate Attributes](#) should also be used as a guiding framework for curriculum design.

Academic Content:	
A1	Apply simple genealogical reasoning to the genetic variation within and between populations, including human populations

A2	Assess measures of heritability and use them to evaluate arguments about modes of evolution, behaviour and conservation.
A3	Be aware of the range of genetic markers and methods available, the type of genetic information they provide, and make appropriate choices in applying them to particular problems and experimental
A4	Predict the effects of the fundamental evolutionary process on the evolution of chromosomes and DNA sequences and hence be able to draw inferences about evolution from sequences and their
A5	Make comparisons between genome structures from different organisms
A6	Assess the roles of specific sequences and whole chromosomes in evolutionary processes
A7	Propose how evolutionary processes act on different sequences, chromosomes and can be modified by chromosome structure and genetic linkage, population subdivision and interactions between and within loci.

Disciplinary skills - able to:	
B1	To read, assess and critically analyse current research papers

Attributes:	
C1	To develop group working skills
C2	To prepare in advance of lectures

4) Reading List

Provide an indicative reading list for the module. This should include key texts and/or journals but **should not** be an exhaustive list of materials.

- Alberts B, Johnson A, Lewis J, Raff M, Roberts K, Walter P. 2002. *Molecular biology of the cell*. New York: Garland Science.
- Franklin, F.C.H., Higgins, J.D., Sanchez-Moran, E., Armstrong, S., Osman, K., Jackson, N. and Jones, G. (2006) Control of meiotic recombination in *Arabidopsis*: role of MutL and MutS homologues. *Biochemical Society Transactions*, 34, 542-544.
- Kejnovsky, E., Leitch, I.J. and Leitch, A.R. (2009) Contrasting evolutionary dynamics between angiosperm and mammalian genomes. *Trends in Ecology and Evolution*, 24, 572-582.
- Leitch, A.R. and Leitch, I.J. (2008) Genomic plasticity and the diversity of polyploid plants. *Science*, 320, 481-483.
- Tucker, S., Vitins, A. and Pikaard, C.S. Nucleolar dominance and ribosomal RNA gene silencing. *Current Opinion in Cell Biology*, 22, 351-356.
- Van de Peer, Y., Fawcett, J.A., Proost, S., Sterck, L. and Vandepoele, K. (2009) The flowering world: a tale of duplications. *Trends in Plant Science*, 14, 680-688.
- Yousafzai, F.K., Al-Kaff, N. and Moore, G. (2010) The molecular features of chromosome pairing at meiosis: the polyploid challenge using wheat as a reference. *Functional & Integrative Genomics*, 10, 147-156.
- Boomsma, D., Busjahn, A. and Peltonen, L. (2002) Classical twin studies and beyond. *Nature Reviews Genetics*, 3, 872-882.
- Burton, et al. (2007) Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. *Nature*, 447, 661-678.
- Lahn, B.T., Pearson, N.M. and Jegalian, K. (2001) The human Y chromosome, in the light of evolution. *Nature Reviews Genetics*, 2, 207-216

5) Teaching and Learning Profile

Provide details of the method of delivery (lectures, seminars, fieldwork, practical classes, etc.) used to enable the achievement of learning outcomes and an indicative number of hours for each activity to give an overall picture of the workload a student taking the module would be expected to undertake. This information will form the Key Information Set for each undergraduate programme and will be used to populate the KIS widget found on the QMUL programme information pages. More information can be found [online](#) about KIS. You may also wish to refer to the [QAA guidance on contact hours](#) when completing this section.

Activity Type	KIS Category	Time Spent (in hours)
Lecture	Scheduled	22
Classes and workshops	Scheduled	10
Total		32

Specify the total module notional study hours. This should be a total of the hours given for each activity. The notional study hours for each academic credit point is 10. A 15 credit point module therefore represents 150 notional study hours.

Activity Type	Total Time Spent (in hours)	Percentage of Time Spent
Scheduled learning and teaching	32	21
Placement	0	0
Independent Study	118	79
Total	150	100

Use the information provided in the box above to specify the total time spent and the percentage time spent in each category of teaching and learning activity.

6) Assessment Profile

Provide details of the assessment methods used to assess the achievement of learning outcomes.

Description of Assessment	Assessment Type	KIS Category	Duration/Length	Percentage Weighting	Final element of assessment	Qualifying Mark
Written Examination	Examination	Composite Written Exam: Essays answers and MCQ	3 Hours	80%	Yes	
Coursework	Written Assessment	Coursework		20%	No	

Final element of assessment: The assessment that takes place last. **There should normally be only one element of assessment marked as final unless two assessment or submission dates occur on the same day.**

Qualifying mark: A specified minimum mark that must be obtained in one or more elements of assessment in order to pass a module. **This is in addition to, and distinct from, the requirement to achieve a pass in the module mark to pass the module.**

Reassessment

Provide details of the reassessment methods used, specifying whether reassessment is either standard reassessment or synoptic reassessment.

- Standard Reassessment
 Synoptic Reassessment

Synoptic reassessment details (if you have indicated synoptic reassessment above, please give details)

Brief Description of Assessment	Assessment Type	Duration/Length of Examination/ Coursework
Resit Examination	Written Exam	3 Hours