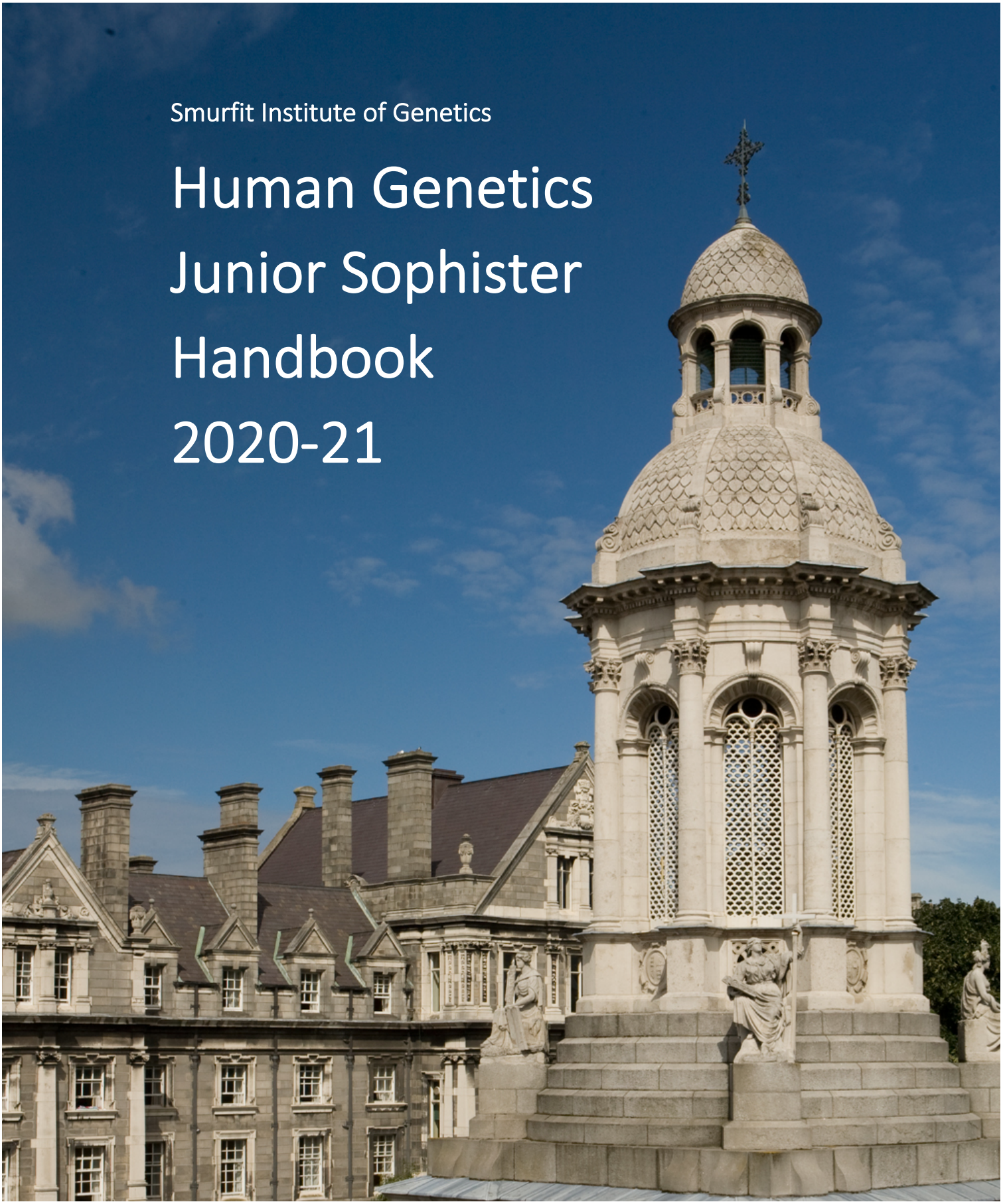
Trinity College Dublin
Coláiste na Tríonóide, Baile Átha Cliath
The University of Dublin



Smurfit Institute of Genetics

Human Genetics Junior Sophister Handbook 2020-21

Contents

A note on adapting to Covid-19 restrictions:

As we are all acutely aware, this is not going to be a normal year of College. In the Genetics Department we are determined to ensure that you receive the same high quality of education that you would have any other year. The most difficult constraint that we are facing is the reduced capacity of teaching and research spaces on campus. This has necessitated some rethinking of how we deliver lectures and how we organise laboratory practicals.

Lectures: Lectures will be delivered online through Blackboard. In the main these will be pre-recorded to avoid internet glitches etc. and they will remain available for the whole academic year. These will be supplemented with tutorial sessions delivered by the respective lecturers on each course (on average there will be a tutorial every 5 lectures). As far as possible the tutorials will be in-person on campus, but in case of health and safety concerns they may be online in specific instances. The tutorials are a wonderful opportunity to clarify points from the lectures, to engage in a class discussion, to delve deeper into the themes and to ask any questions you may have. These will work best if students come prepared (having previously watched the lectures and read some of the suggested papers), and ready to engage in discussion. If we all contribute, these could be a major asset to the course.

Laboratory practicals: This academic year, while we are still running laboratory practicals, unfortunately due to Covid-19 restrictions, designed to maximize the safety of all participants (students, demonstrators and staff), it will not be possible for this year's JS class to acquire the same amount of laboratory practical experience as in previous years. All labs have restrictions on the number of individuals who can be present, and on the nature of their participation. Nevertheless, we will explore important topics in molecular genetics relating to gene structure and the regulation of gene expression, and the relevant experimental techniques used in their analysis. Prior to the first laboratory practical, a document detailing the Covid-19 policy in place during laboratory sessions will be provided to JS students.

In case you become unwell or suspect that you are unwell we urge you to exercise an abundance of caution and stay at home. Similarly, some students may have a personal health concern or have a close family member who is vulnerable and therefore may need to stay at home to protect them. We will do everything in our power to ensure that there is no academic loss to any student who needs to stay at home.

Please note that the department building has been reconfigured in terms of access and circulation. This is detailed in a separate "return to work" document, which also details some guidelines that all students should read and adhere to. Most notably, **it will not be possible to congregate in previously 'social' spaces in the building,** and the atrium, for example, will not be available for use by students.

We are doing our best to anticipate what needs to be done. The situation is rapidly changing, and we may have to readjust our plans during the year. Please trust in us to always maintain your best interests at heart and to maintain the integrity of your education and your degrees. If any issues arise at any point in the year, please feel free to email me about this and we can arrange to talk

With best wishes for the year ahead,

Aoife McLysaght, Head of Genetics.

1. Communication

Announcements will be made by emailing you at your **tcd.ie email address**. Read this mailbox regularly or set it up to forward to an account that you read regularly. Your primary contact for each module is the module coordinator and for general queries the Course Coordinator.

2. Lectures courses and attendance

The objective during the Junior Sophister year is to provide you with a thorough grounding in the fundamentals of Human Genetics so that you will be well prepared for the challenges of the Senior Sophister year. We expect you to attend all lectures and in addition, some modules have strict attendance policy with direct consequences as a student may be deemed non-satisfactory. Please note for the 2020-21 academic year, attendance may be in person or in real-time online or lectures may be recorded depending on TCD policies relating to Covid-19.

3. Attendance at seminars

In addition to the lecture courses there are weekly departmental seminars scheduled for 1 p.m. on Fridays in the atrium (these will be announced a few days ahead of time). Whilst it is not compulsory to attend these seminars you are strongly recommended to do so.

4. JS course structure

The Junior Sophister year is comprised of modules totaling 60 European Credit Transfer System credits (ECTS). There are 40 credits of core modules compulsory for all Human Genetics students and 20 credits of open modules and Trinity Electives spread equally over two semesters in the academic year. The different possible combinations for Human Genetics are described in the module structure table below. Descriptions of the modules can be found from page 9 onwards.

Human Genetics	
Semester 1 (S1)	**Semester 2 (S2)**
Core Modules	
GEU33015 Molecular Genetics (5 credits)	GEU33215 Medical Genetics (5 credits)
GEU33007 Molecular Genetics Laboratory (5 credits)	GEU33285 Science Structure Discussion and Presentation for Human Genetics (5 credits)
GEU33075 Evolutionary and Population Genetics (5 credits)	GEU33035 Genetic Analysis of Nervous Systems (5 credits)
GEU33025 Data Handling and Bioinformatics (5 credits)	GEU33008 Analytical Genetics Laboratory (5 credits)
Open Modules Scenario I	
GEU33045 Genomics and Systems Biology (5 credits)	GEU33055 Developmental Genetics (5 credits)
Trinity Elective (5 credits)	BIU33140: Introduction to Immunology and Immunometabolism OR BIU33475 Basic Neurobiology (5 credits)
Open Modules Scenario II	
GEU33045 Genomics and Systems Biology (5 credits)	GEU33055 Developmental Genetics (5 credits)
BIU33210 Biochemistry for Biological Sciences (5 credits)	Trinity Elective (5 credits)
Open Modules Scenario III	
GEU33045 Genomics and Systems Biology (5 credits)	GEU33055 Developmental Genetics (5 credits)
Trinity Elective (5 credits)	Trinity Elective (5 credits)

5. JS Assessments

The overall Junior Sophister results will represent 30% of your final moderatorship grade. Modules are assessed by continuous assessment and/or by examination. The distribution marks between papers, continuous assessment and practical work varies for each module and is specified in the description of the module. Specific exam dates as well as submission deadlines are also specified for each module and it is vital that you submit on time. Please note: Unless accompanied by a valid medical certificate submissions after the deadline will incur a 5% deduction. Please contact the relevant module coordinator with any queries in this regard.

6. Field Trip

A field trip takes place over two days on the 6th week of Hilary term (March 8-12, 2021, dates to be confirmed). The field trip is organized by Juan Pablo Labrador and will be held in the Kippure Estate (www.kippure.com) in the Wicklow Mountains. It is a great opportunity for staff and students to meet scientifically and socially in an informal setting. Each student is expected to present a short (15 minute) seminar on a topical paper related to their review chosen together with their supervisor. Staff members will give a brief outline of their research interests.

7. Summer Vacation Research Experience outside Ireland

We encourage Junior Sophisters to gain experience working in a research laboratory during the summer vacation. Each year the Department awards 6 travel bursaries (4 Bill Vincent Awards, 1 David McConnell award and 1 James Watson award) on the basis of performance in the Senior Freshman exams, to enable students to carry out a summer research project outside of Ireland. Dr. Matthew Campbell will advise interested students about placements in various research labs. However, it is the student's responsibility alone to arrange: air travel, visas (where appropriate), work permits, and any insurance requirements. These arrangements should be made as far in advance as possible from the departure date - preferably in early January.

8. Summer Vacation Research Seminars

The current rising Senior Sophister students will present research seminars towards the end of Michaelmas term. You will be advised of the date and venue of these seminars and will be expected to attend.

9. Behaviour in the Department

We expect high standards of personal behaviour in the Department consistent with its professional status. Please do not invite students from other Departments or friends into the Smurfit Institute, and when you are in the building please keep the noise down. Alcohol and smoking are absolutely forbidden. Students are not permitted to go on the roofs of the buildings.

10. Safety

Please make sure that you have received and have read the Science Faculty Safety Manual. Remember also that you are responsible for your own safety and that you have a responsibility not to endanger others by your actions.

11. Prizes in Human Genetics

The following prizes are awarded annually to students who have excelled during the Junior Sophister year:

a. Leslie Bloomer Prize in Human Genetics - awarded to the best-qualified student of Human Genetics (based on JS exam results) who in addition wishes to carry out research in the summer vacation prior to entering the Senior Sophister year.

b. Barbara McClintock Prize in Human Genetics - awarded to a Sophister student of Human Genetics who has excelled in oral presentation of a subject of his/her choice within the field of Human Genetics. This prize is awarded based on presentations made during the field trip.

12. Passing the Junior Sophister Year

It is important that you aim to achieve high grades in your continuous assessments and exams because 30% of the marks obtained in the JS year will contribute directly to your Senior Sophister BA Moderatorship grade. Also, when **project and review topics for Senior Sophister year** are assigned next year, students with higher marks in the JS year will tend to get their higher preference choices of topic.

The regulations below are extracted from the 2019-20 TCD Calendar. Please check the most recent version of the calendar for any updates:

"*58 ...*
In order to rise with their class, students must obtain credit for the academic year by satisfactory attendance at lectures and tutorials and by carrying out, submitting and sitting the required assessment components. In addition, students must pass the year by achieving, at a minimum, an overall credit-weighted average pass mark for the year (40 per cent or 50 per cent, as per programme regulations) and either:

(a) accumulate 60 credits by achieving at least the pass mark in all modules
or
(b) pass by compensation. All modules and components within modules are compensatable).

To pass a year by compensation, in programmes that locate the pass mark at 40 per cent, a student must achieve the pass mark in modules carrying a minimum of 50 credits and obtain a module mark of at least 35 per cent in any remaining module(s). A student may accumulate a maximum of 10 credits at qualified pass where the mark lies between 35-39 per cent.

59 Progression is on an annual basis. Within a year, students may carry failed modules from one semester to the next but not from one academic year to another; that is, they will not be able to rise to the next year of their programme until they have successfully completed the preceding year(s). Students who have not passed their year are required to present for reassessment when:
(a) they obtain in excess of 10 credits at qualified pass (i.e. marks between 35-39 per cent);
(b) they fail any module (i.e. achieving marks below 35 per cent;
(c) they do not obtain an overall pass mark for the year;

(d) any combination of (a) - (c) occurs.

60 If a student has achieved both fail and qualified pass grades at the first sitting or has exceeded the 10 credit limit allowed for compensation and is not permitted to rise with their year, they must present for reassessment in all failed components of all modules for which they obtained a fail and/or a qualified pass.
61 Different modalities of assessment to the first sitting are permitted in the reassessment session as determined by the programme.

62 The same progression and compensation regulations as outlined above apply at the reassessment session. The overall credit-weighted average for the academic year will be calculated using the most recent marks achieved.

63 Students who fail to satisfy the requirements of their year at the reassessment session are required to repeat the year in full (i.e. all modules and all assessment components)."

There is one reassessment session which is held at the beginning of Michaelmas term. Students are assessed in all failed modules from both semesters during the reassessment session. Students are not permitted to repeat successfully completed assessments or examinations in order to improve their performance. In exceptional circumstances such as illness, if a student does not attempt exams at the end of the semester, they can defer until the reassessment examining period. Applications to defer exams should be made to the Senior Lecturer's Office via your tutor.

You are strongly advised to submit all the lab reports during the year, and not to miss the continuous assessment tests, because if you obtain a mark of < 35% in 3 modules you will be unable to progress to the Senior Sophister year (you'll have to repeat the JS year or leave College). If you fail to submit coursework on time, you will get a mark of zero for it.

13. Textbook:
We recommend Introduction to Genetic Analysis by Anthony J. F. Griffiths, Susan R. Wessler, Sean B. Carroll, and John Doebley (current edition is 12th edition, 2020).

Department's web address: http://www.tcd.ie/Genetics
Keys - from the Human Genetics secretary, €10 deposit.
Photocopier - in the atrium of the Smurfit Institute.
Printer and PCs - in Genetics Library (upstairs in Westland Row building). Spare paper and toner from the genetics administrator.

Course Coordinator: Jane Farrar (gjfarrar@tcd.ie)
Email for administrator: genetics@tcd.ie **Phone:** 01 896 1140

Minor changes to that described in the JS Human Genetics Handbook may be undertaken during the academic year.

Module code	Module	Coordinator	email
GEU33007	Molecular Genetics Laboratory	Tony Kavanagh	tony.kavanagh@tcd.ie
GEU33008	Analytical Genetics Laboratory	Juan Pablo Labrador	labradoj@tcd.ie
GEU33015	Eukaryotic Molecular Genetics	Tony Kavanagh	tony.kavanagh@tcd.ie
GEU33025	Data Handling and Bioinformatics	Karsten Hokamp	kahokamp@@tcd.ie
GEU33035	Genetic Analysis of Nervous Systems	Juan Pablo Labrador	labradoj@tcd.ie
GEU33045	Genomics & Systems Biology	Frank Wellmer	wellmerf@tcd.ie
GEU33055	Developmental Genetics	Frank Wellmer	wellmerf@tcd.ie
GEU33075	Evolutionary and Population Genetics	Russell McLaughlin	russell.mclaughlin@tcd.ie
GEU33085	Science Structure, Discussion and Presentation for Genetics	Kevin Devine	kdevine@tcd.ie
GEU33285	Science Structure, Discussion and Presentation for Human Genetics	Juan Pablo Labrador	labradoj@tcd.ie
GEU33215	Medical Genetics	Jane Farrar	gjfarrar@tcd.ie

CORE MODULES

1. Module Code GEU33015
2. Module Name Eukaryotic Molecular Genetics
3. Semester taught Semester 1
4. Contact Hours 24
5. Module Personnel Tony Kavanagh; others TBA
6. Learning Aims The aim of this module is to introduce students to advanced concepts in the molecular genetics of eukaryotes. A major focus will be on the complexities of gene expression and its regulation. This will include transcription by RNA polymerase II, the role of the Mediator complex, and the processing steps involved in the maturation of pre-mRNAs: capping, polyadenylation and splicing. The regulation of gene expression and its critical importance in differentiation and development will be explored at the level of chromatin and nucleosome modifications, and in relation to the combinatorial interactions between transcription factors and *cis*-acting upstream regulatory elements such as enhancers. Approximately one-third of the course will explore recombinant DNA techniques used in gene expression and genome analysis.
7. Module content: Programme of lectures

Week	Lecture Topic & Lecturer
10	Chromatin and the nucleosome: the histone code hypothesis.
10	Histone modifications: writers, readers and erasers.
10	The 'Epigenome'; role of enhancers; genomic imprinting.
10	Chromatin: local and higher order structure of chromosomes.
10	Polycomb repressor complexes and DNA methylation systems: roles In development and Disease.
11	Study/Review week
12	Transcription of mRNAs by RNA polymerase II; the Mediator complex.
12	Combinatorial control of gene expression: role of transcription factors.
12	Importance of gene regulation in differentiation and development.
12	Processing of pre-mRNAs, capping, polyadenylation, splicing. (Mani?)
12	Transcription, processing, and function of rRNA, tRNA, snoRNA, miRNA piRNA.
13	mRNA translation, localization and translational control.
13	RNA quality control (NMD) and mRNA turnover.
13	Protein folding and posttranslational modifications
13	Protein localization and targeted degradation
13	Tutorial 1
14	Recombinant DNA techniques: DNA-modifying enzymes.
14	Cloning vectors and strains.
14	PCR and cloning strategies.
14	Cloning by recombination: Gateway cloning.
14	Monoclonal antibodies and their uses
15	Making genomic libraries
15	Expressing recombinant proteins in bacteria
15	Expressing recombinant proteins in eukaryotes
15	Tutorial 2
16	
19	Revision Week Open MCQ
20	Assessment Week

8. Learning Outcomes: Upon successful completion of this module, students will be able to describe the critical features of gene expression and its regulation in eukaryotes. They will, for example, understand how pre-mRNAs are transcribed in the nucleus and processed to give mature mRNAs. Students will also have gained knowledge and an appreciation of the complexities of gene regulation at the level of chromatin and the nucleosome, and the binding of transcription factors to upstream *cis*-acting regulatory elements in DNA. In addition, students will have acquired an in-depth knowledge of the key recombinant DNA techniques that underpin molecular genetics analyses.

9. Recommended Reading List: Anthony J.F. Griffiths; Susan R. Wessler; Sean B. Carroll; John Doebley. Introduction to Genetic Analysis. New York, NY :W.H. Freeman & Company, 2015.
Further reading on specialist topics may also be provided during presentation of the module.

10. Assessment Details: One 1.5-hour exam paper at the end of semester 1

11. Module Coordinator Tony Kavanagh
Email: tony.kavanagh@tcd.ie
Phone x1035
Executive Officer: Genetics
Email: genetics@tcd.ie
Phone x1140

12. Module Website (not applicable)

1. Module Code GEU33007
2. Module Name Molecular Genetics Laboratory
3. Semester taught Semester 1
4. Contact Hours 5 hours per week
5. Module Personnel Prof. Tony Kavanagh
Dr. David Noone (+ 3 demonstrators)
6. Learning Aims This comprises a set of robust experiment-based projects in molecular genetics that have given us consistently good results in the Junior Sophister class environment for many years. The central theme of the module is: gene expression and its regulation.

Aims: To provide hands-on training and experience of widely used experimental strategies and techniques in molecular genetics/ molecular biology, which include: the isolation and purification of genomic and plasmid DNA; the polymerase chain reaction (PCR); the use of agarose and polyacrylamide gel electrophoresis in the analysis of DNA, RNA and proteins; genetic transformation of *E. coli*; gene cloning and analysis in plasmid vectors; *lacZ*, GUS and GFP reporter gene assays.

7. Module content: Programme of laboratory practicals

Week	Lecture Topic & Lecturer	Practical
5		Exploring gene regulation in *E. coli*: the *lac* operon
5		Gene transfer and expression in plant cells
5		Induction of the lac operon: measuring lacZ expression
5		Transformation of Agrobacterium
6		PCR amplification of the lac operon intergenic region
6		Exploring the genome and proteome of phage lambda
6		Agarose gel electrophoresis of lac operon PCR products
6		Growth and precipitation of phage lambda virions
7		Purification of phage lambda virions via CsCl step gradient
7		Extraction of phage DNA from purified virions; restriction digestion
7		Transformation of leaf tissue using Agrobacterium
7		Sequence analysis of lac operon intergenic region
8		Creating a library of phage genes in the plasmid vector pUC19
8		Isolation of pUC19 plasmid DNA; digestion with restriction enzyme
8		Gel analysis of pUC19 digests
8		Ligation of phage Pst1 restriction fragments and pUC19
9		SDS-PAGE analysis of phage lambda virion proteins
9		Preparation of competent E. coli cells; transformation of E. col
9		Blue-white identification of recombinant E. coli colonies
9		Miniprep cultures for recombinant plasmid isolation
10		Isolation of recombinant plasmid DNA minipreps
10		Restriction digest analysis of recombinant plasmid DNA
10		Agarose gel analysis of recombinant plasmids
10		Analysis and discussion of phage library cloning results
11	Study/Review week	
12		Exploring light-induced gene expression in plants
12		Regulation of cytoplasmic vs chloroplastic rRNA gene expressi
12		Agarose gel analysis of light-induced vs constitutive rRNAs

12		Detection of GUS and KanR transgenes
13		Regulation of RUBISCO protein synthesis in plants
13		SDS-PAGE analysis of light-induced RUBISCO expression
13		Regulatory properties of the rbcS promoter (fused with GUS)
13		Analysis and discussion of RUBISCO protein gels
14		GUS assays of putative transgenic shoots
14		Sequence analysis of pUC19-lambda recombinant clones
14		Review of lac operon data
14		Review of phage lambda library cloning data
15		Writing laboratory reports
15		Writing laboratory reports
15		Writing laboratory reports
15		Writing laboratory reports
16		
19	Revision Week	
20	Assessment Week	

8. Learning Outcomes: On successful completion of the module, students will be able to:
a. isolate and purify genomic and plasmid DNA;
b. assemble the reagents required to amplify DNA using the polymerase chain reaction (PCR);
c. analyse DNA and RNA using agarose gel electrophoresis;
d. make protein extracts and analyse them using SDS-polyacrylamide gel electrophoresis;
e. transform *E. coli* and *Agrobacterium* using plasmid DNA;
f. grow, isolate and purify bacteriophage;
g. clone DNA fragments in plasmid vectors;
h. use Agrobacterium to introduce genes into the plant nucleus;
i. perform *lacZ*, GUS and GFP reporter gene assays.

9. Recommended Reading List: published primary research papers and reviews

10. Assessment Details:
Students prepare two Laboratory Reports of equal weighting
Students are notified of the first Laboratory Report during Week 12; and the second report during the last week. Both reports are due at the end of Week 21.

11. Module Coordinator: Prof Tony Kavanagh
Email: tony.kavanagh@tcd.ie
Phone: 01 8961035

Executive Officer: Genetics
Email: genetics@@tcd.ie
Phone: 01 896 1140

12. Module Website N/A

1. Module Code GEU33075
2. Module Name Evolutionary and Population Genetics
3. Semester taught Semester 1
4. Contact Hours 24
5. Module Personnel Lara Cassidy
Russell McLaughlin
Ross McManus
6. Learning Aims This module provides an in-depth exploration of genetic variation, from its origins to its evolutionary consequences. The information in DNA is not always transmitted accurately from one generation to the next. DNA sequences can change spontaneously by the process of mutation and inaccurate DNA repair, resulting in genetic variation (polymorphism) within populations. Variable sites at different positions in the genome get shuffled into new combinations by the process of genetic recombination that occurs during sexual reproduction. Whether a particular allele survives for a long time in a population or goes extinct depends on the evolutionary forces acting on the population. If a new allele is advantageous to the population, Darwinian natural selection will tend to increase its frequency in the population; alternatively, if the new allele is disadvantageous natural selection will tend to eliminate it. However, selection is only one of several evolutionary processes that change allele frequencies within populations over generations. In this module, students will learn about the origin of genetic variation, its distribution within populations and long-term changes brought about by evolutionary processes.
7. Module content

Week	Lecture Topic & Lecturer
5	**Introduction to evolutionary and population genetics** (Cassidy)
5	**Spectrum and mechanisms of DNA mutation I** (McManus)
5	**Spectrum and mechanisms of DNA mutation II** (McManus)
5	**Exogenous and structural causes of mutation** (McManus)
5	**Mutation and health** (McManus)
6	**Genetic variation and its detection I** (McLaughlin)
6	**Genetic variation and its detection II** (McLaughlin)
6	**Alleles and genotypes: Hardy-Weinberg equilibrium** (McLaughlin)
6	**Alleles and genotypes: inbreeding** (McLaughlin)
6	**Effective population size** (McLaughlin)
7	**Genetic drift, fixation F-statistics and population structure** (McLaughlin)
7	**Linkage disequilibrium** (McLaughlin)
7	**Applied population genetics: complex traits and GWAS** (McLaughlin)
7	**Applied population genetics: population structure and PCA** (McLaughlin)
7	**The neutral theory and random genetic drift** (Cassidy)
8	**Evolutionary change in sequences: patterns and models**
8	**Evolution of protein-coding sequences** (Cassidy)
8	**The molecular clock** (Cassidy
8	**Phylogenetics I** (Cassidy)
8	**Concerted evolution** (Cassidy)

9	**Codon usage bias** (Cassidy)
9	**Evolution by transposition (mobile genetic elements)** (Cassidy)
9	**Gene and genome duplication** (Cassidy)
9	**Gene loss** (Cassidy)
10	
11	Study/Review week
12	
13	
14	
15	
16	
19	Revision Week
20	Assessment Week

Description of each Lecture

1. Introduction to evolutionary and population genetics (Cassidy)
   This lecture introduces molecular evolution and provides historical context, including ideas presented by Lamarck, Weissmann and Darwin. Core principles, including selection and neutral mutations, are also introduced.
2. Spectrum and mechanisms of DNA mutation I (McManus)
3. Spectrum and mechanisms of DNA mutation II (McManus)
   These two lectures explore the different ways that DNA can change (mutate) between individuals, leading to genetic variation within a population and a substrate on which evolution acts. Types of DNA mutation are described, along with the molecular biological mechanisms bringing about these changes.
4. Exogenous and structural causes of mutation (McManus)
   This lecture extends our view of the origin of mutation beyond molecular mechanisms to include exogenous (eg environmental) factors and structural changes.
5. Mutation and health (McManus)
   The consequences of mutation on human health are discussed.
6. Genetic variation and its detection I (McLaughlin)
7. Genetic variation and its detection II (McLaughlin)
   These two lectures describe in detail some core methodologies and technologies used in the identification and study of genetic variation in DNA. Methods include polymerase chain reaction, electrophoresis, Sanger sequencing, whole-genome SNP genotyping and next-generation sequencing. Technologies are also compared and contrasted for their relative advantages and constraints in the context of conducting population genetic studies on genetic variation.
8. Alleles and genotypes: Hardy-Weinberg equilibrium (McLaughlin)
   In this lecture, we define the expected relationship between allele and genotype frequencies in an idealized population, and the interpretation when observation deviates from expectation. Statistical methods for assessing the probability of observed data under a null model are detailed, and the conclusions that can be drawn from the results of these tests are discussed.
9. Alleles and genotypes: inbreeding (McLaughlin)
   The concept of inbreeding (mating between related individuals) is introduced and our model for expected genotype frequencies under various inbreeding scenarios is updated. This forms the basis of ensuing lectures.

10. Effective population size (McLaughlin)
    In this lecture we state how populations are modelled as idealized populations with effective sizes that can – sometimes counterintuitively – be far from actual census sizes. We discuss the various parameters that affect effective population size and their consequences in the population, including resilience in agriculture and animal breeding.
11. Genetic drift, fixation, F-statistics and population structure (McLaughlin)
    Here we explore genetic drift (the random long-term change in allele frequencies) and the ultimate long-term fate for all genetic variation: either loss or fixation. We explore the role of parameters such as population size on defining the rate of fixation of an allele in a population. We then set a statistical framework for the analysis of variance of genotype frequencies in a population and their use in defining the fixation index, a useful tool for identifying genetic structure (non-random patterns) in populations.
12. Linkage disequilibrium (McLaughlin)
    This lecture introduces the new concept of linkage disequilibrium – the statistical correlation of adjacent alleles – and its uses in modern genomics.
13. Applied population genetics: complex traits and GWAS (McLaughlin)
14. Applied population genetics: population structure and PCA (McLaughlin)
    In these final three lectures, we apply some of the techniques and methods that have been discussed in previous lectures to understand the genetic basis of traits in a population and genomic descriptors of population differentiation. We explore the design and typical execution of a genome-wide association study (GWAS), from its motivation to the statistical considerations in controlling false positives and technical bias. We qualitatively discuss the application of principal component analysis (PCA) in delineating population structure and controlling GWAS, and finish with a tour of modern, population-scale genome sequencing studies such as the UK Biobank.
15. The neutral theory and random genetic drift (Cassidy)
    In this lecture we define and introduce the neutral theory of molecular evolution and explore the relative rates of neutral and non-neutral genetic variation between species.
16. Evolutionary change in sequences: patterns and models (Cassidy)
    Molecular evolution describes the long-term changes in DNA, RNA or protein sequences over many successive generations. In this lecture, we explore the various models of molecular evolution and the expected patterns observed in sequence data as a consequence of evolutionary processes.
17. Evolution of protein-coding sequences (Cassidy)
    This lecture defines different types of genetic variants present in protein coding sequences (synonymous and nonsynonymous changes) and how these are used to infer evolutionary processes (eg selection) by studying functional constraint and Ka/Ks ratio.
18. The molecular clock (Cassidy)
    The concept of the molecular clock is introduced, defining the relationship between rate of accumulation of neutral substitutions and evolutionary time. In this lecture, we cover principles of, exceptions to and factors influencing the molecular clock and how this paradigm can be harnessed to study evolution in different scenarios.
19. Phylogenetics (Cassidy)
    This lectures explains the construction of phylogenetic trees from sequence data to describe the evolutionary relationships between species, providing applied examples in defining the tree of life and tracking disease outbreaks such as the 2014 West African Ebola virus epidemic.

20. Concerted evolution (Cassidy)
    This lecture defines and explores concerted evolution, the process which results in paralogous (similar) genes remaining more closely related within a species than between species.
21. Codon usage bias (Cassidy)
    In this lecture we identify and explain the phenomenon of codon usage bias, whereby synonymous codons appear to be used at different frequencies within genes.
22. Evolution by transposition (mobile genetic elements) (Cassidy)
    Transposition is discussed in this lecture – the process by which genetic elements are transferred "horizontally" between organisms rather than the more conventional "vertical" inheritance of genetic material from parent to offspring.
23. Gene and genome duplication (Cassidy)
    Duplication of genetic material – either in segments or entire genomes – is a strong driver of rapid evolutionary change. This lecture explores the role of duplication in evolution and speciation.
24. Gene loss (Cassidy)
    This lecture discusses gene loss, which, like duplication, can be an agent of rapid evolutionary change.

8. Learning Outcomes

On completion of this module, students will be able to:

1. Describe and explain the origin of genetic variation through mutation
2. Describe and explain the consequences of genetic variation in health and disease
3. Identify suitable technological approaches to the detection and study of different types of genetic variation
4. Describe the relationship between population genotype and allele frequencies under panmixia and inbreeding
5. Define effective population size (N_e), identify population parameters that influence N_e and describe practical consequences of low N_e even in large census populations
6. Specify the long-term evolutionary trajectories of alleles under genetic drift and define fixation
7. Define and quantitatively describe population structure using F-statistics
8. Define linkage disequilibrium and describe its use in population genomics
9. Explain the design of genome-wide association studies for complex traits and their use of population genetic principles to control bias
10. Discuss modern population-scale genome sequencing efforts to understand human health and disease
11. State the neutral theory of molecular evolution
12. Describe the nature and consequences of evolutionary change in DNA and protein sequences, including codon usage bias
13. Define the relationship between mutation accumulation and evolutionary time and its use in the molecular clock
14. Construct phylogenetic trees based on evolutionary relationships between related sequences
15. Define homolog, paralog, ortholog and ohnolog and describe concerted evolution of paralogous genes within species
16. Describe large-scale evolutionary changes to genetic sequences, including transposition, gene and genome duplication and gene loss

9. Recommended Reading List

Introduction to Genetic Analysis, 11th ed. (Griffiths, Wessler, Carroll, Doebley) – chapters 15-18
Principles of Population Genetics, 4th ed. (Hartl & Clark)

10. Assessment Details

Students will sit an essay-style examination at the end of semester 1.

11. Module Coordinator: Russell McLaughlin
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Executive Officer:
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12. Module Website N/A

1. Module Code **GEU33025**
2. Module Name **Data Handling and Bioinformatics**
3. Semester taught Semester 1
4. Contact Hours 45 Hours
5. Module Personnel Dr Fiona Roche (FR), Dr Karsten Hokamp (KH)
6. Learning Aims

This module contains web-based bioinformatics, Python programming and a data handling component. The bioinformatics component provides a practical introduction to the use of commonly used bioinformatic databases and tools with a focus on web-based applications. Students will become familiar with accessing biological sequence databases and exploring various sequence analysis tools to understand evolutionary relationships and how this can help to draw protein functional and structural inferences. The Python programming component introduces students to computer programming in Python using bioinformatics-related examples and exercises. The data handling part covers basic techniques for processing next-generation sequencing data and, more specifically, approaches for the analysis of ChIP-Seq data.
This module runs for 5 x 1 hour and 20 x 2 hours (combined lecture and practical sessions) in Term 1.
As learning aims of this module students will

- learn how to search a range of biological databases
- understand how proteins are annotated and classified
- get to know which tools can be used to explore unknown sequences of interest
- master the concept of sequence alignment and homology searching
- understand the process of programming
- acquire basic Python programming skills
- gain a thorough understanding of next-generation sequencing data
- be familiar with the steps and tools required to process, map and visualise NGS data
- become familiar with the specifics of ChIP-Seq data analysis
- understand how to enhance NGS results with annotation data

7. Module content: Programme of lectures and practicals

Week	Lecture Topic & Lecturer	Practical
5	Introduction to the GEU33025 Module (FR, KH, 1 hour)	
5	Bioinformatics 1 - Biological Databases (FR, 2 hours)	
5	Bioinformatics 2 - Protein Classification (FR, 2 hours)	
6	Bioinformatics 3 - Introduction to Sequence Alignments (FR, 1 hour)	
6	Bioinformatics 4 - Pairwise Sequence Similarity and BLAST (FR, 2 hours)	
6	Bioinformatics 5 - Multiple Sequence Alignment (FR, 2 hours)	
7	Bioinformatics 6 - Genetic Variation Resources (FR, 1 hour)	
7	Bioinformatics 7 - Genome Browsers (FR, 2 hours)	
7	Bioinformatics 8 - Recap (FR, 2 hours)	
8	Programming 1 - Introduction	

8	Programming 2 - Strings and Loops (KH, 2 hours)	
8	**Bioinformatics Exam (FR, 2 hours)**	
9	Programming 3 - Input/Output (KH, 1 hour)	
9	Programming 4 - Branching (KH, 2 hours)	
9	Programming 5 - Lists, Tuples, Sets (KH, 2 hours)	
10	Programming 6 - Dictionaries (KH, 2 hours)	
10	Programming 7 - Functions (KH, 2 hours)	
11	Study/Review week	
12	Programming 8 - Regular Expressions (KH, 2 hours)	
12	Data Handling 1 - Introduction to ChIP-Seq Data Analysis (KH, 2 hours)	
13	**Python Exam (KH, 2 hours)**	
13	Data Handling 2 - Quality Control, Trimming (KH, 2 hours)	
14	Data Handling 3 - Short Read Mapping (KH, 2 hours)	
14	Data Handling 4 - Peak Calling, Motif Detection (KH, 2 hours)	
15	Data Handling 5 - Data Filtering (KH, 2 hours)	
15	Data Handling 6 - Gene Lists (KH, 2 hours)	
16		
19	Revision Week	
20	Assessment Week	

Description of each Lecture

Introduction to the GEU33025 Module (FR, 1 hour)
This class serves to introduce the module and its components and also to familiarise students with the computer setup.

Bioinformatics 1 - Biological Databases (FR, 2 hours)
This lecture covers how bioinformatics data are stored and organised with a focus on resources found at NCBI and the EBI. Students will learn about the different types of data and tools found within these resources, delving deeper into the PubMed and Gene databases.

Bioinformatics 2 - Protein Classification (FR, 2 hours)
This lecture describes how protein sequence data are stored, annotated and classified. Students will learn about different levels of classifying proteins and use the UniProt resource to access a wealth of rich annotations.

Bioinformatics 3 - Introduction to Sequence Alignment (FR, 2 hour)
This lecture introduces the concept of sequence alignment, the process of comparing sequences to determine if they are evolutionarily related to one another.
It discusses how sequence alignment methods use evolutionary theory to detect related proteins and how these methods can be used to help predict protein function and structure.

Bioinformatics 4 - Pairwise Sequence Similarity and BLAST (FR, 2 hours)
This lecture explores the basic principles of pairwise sequence alignment with a particular focus on the BLAST algorithm to search for significantly similar sequences.

Bioinformatics 5 - Multiple Sequence Alignment (FR, 2 hours)
This lecture covers multiple sequence alignment and discusses its many applications including its role in inferring function from sequence comparison.

Bioinformatics 6 - Genetic Variation Resources (FR, 1 hour)
This lecture introduces bioinformatic resources developed to capture genetic variation data and how these data can be accessed and interpreted for the purpose of personal genomics.

Bioinformatics 7 - Genome Browsers (FR, 2 hours)
This lecture introduces genome browsers and teaches students how to interactively explore and visualise biological data in the context of the genome.

Bioinformatics 8 - Recap (FR, 2 hours)
This lecture focuses on recapping on all material covered in this module through exercises and case studies.

Programming 1 - Introduction (KH, 1 hour)
This lecture introduces students to the concepts of programming. It covers the use of operators and variables. Students will learn some basic Python statements and write simple scripts using the IDLE software development environment.

Programming 2 - Strings and Loops (KH, 2 hours)
This lecture covers string variables, string formatting, as well as built-in functions and methods for strings. This is followed by the use of 'while' and 'for' loops for repeated application of programming steps.

Programming 3 - Input/Output (KH, 1 hour)
This lecture deals with ways of reading experimental data from files into a Python script and how to store results generated by a script in a file.

Programming 4 - Branching (KH, 2 hours)
This lecture introduces ways of making decisions in a Python script through branching. With this additional skill set students will be able to write more elaborate scripts and tackle processing of sequence data in Fasta format.

Programming 5 - Lists, Tuples, Sets (KH, 2 hours)
Lists are a very common feature in data science. They are represented in Python through various types of iterable variables, which are covered in this lecture together with their built-in functions and methods.

Programming 6 - Dictionaries (KH, 2 hours)
This lecture is dedicated to dictionaries, a collection of key-value pairs, which enables students to implement a DNA translation script.

Programming 7 - Functions (KH, 2 hours)
With the introduction of functions the repertoire of programming skills is expanded so that scripts can be written more efficiently.

Programming 8 - Regular Expressions (KH, 2 hours)
Regular expressions provide elaborate text processing capabilities. This will be practiced through an interactive website first and then applied in Python scripts to extract and clean biological data and to carry out motif searches in DNA or protein sequences.

Data Handling 1 - Introduction to ChIP-Seq Data Analysis (KH, 2 hours)
The last part of the module deals with Next-Generation Sequencing (NGS) data. At the example of a ChIP-Seq experiment with bacterial data the whole process of NGS data analysis is demonstrated in a nutshell.

Data Handling 2 - Quality Control, Trimming (KH, 2 hours)
Students will start working on individual ChIP-Seq data sets and learn about the FastQ data format, how to carry out Quality Control with FastQC, and how to trim contaminated or low-quality data from the sequence reads.

Data Handling 3 - Short Read Mapping, Visualisation (KH, 2 hours)
Mapping short reads against a reference sequence is a common processing step in NGS analyses. This lecture covers the popular Bowtie2 mapping tool and the Integrated Genome Viewer for visualisation of BAM and BigWig files in an interactive browser.

Data Handling 4 - Peak Calling, Motif Detection (KH, 2 hours)
Students will learn about peak calling software and apply the GEM tool to their mapped reads to detect peaks that represent potential binding sites of a transcription factor. This tool also allows the detection of overrepresented motifs which will be compared to known transcription factor binding motifs.

Data Handling 5 - Data Filtering (KH, 2 hours)
This lecture covers details of the SAM output, which will enable students to apply Python scripts to further analyse their mapped reads and remove low quality results. They will also apply the samtools software to remove PCR duplicates and check for improvements in the peak calling step.

Data Handling 6 - Gene Lists (KH, 2 hours)
This lecture deals with the importance of data integration by teaching students how to use external annotation and a Python script to overlay additional data onto the ChIP-Seq results, therefore generating enriched gene lists that can be compared to published results.

8. Learning Outcomes:
On successful completion of the module students should be able to:

MLO1. Query a range of bioinformatic databases

MLO2. Apply tools to investigate unknown sequences

MLO3. Carry out sequence alignment and homology searching

MLO4. Visualise biological data through a genome browser

MLO5. Approach programming tasks in a structured way

MLO6. Write Python scripts following good coding practice

MLO7. Apply regular expressions and use functions within Python scripts

MLO8. Solve entry-level bioinformatics problems using Python scripts

MLO9. Assess the quality of NGS data

ML1O. Apply bioinformatics tools for processing NGS data

ML11. Visualise NGS data through genome browser resources

ML12. Carry out basic ChIP-Seq analyses resulting in binding site locations and motifs

ML13. Integrate external annotation data with analysis results through Python scripts

9. Recommended Reading List:
The Biostar Handbook, 2nd Edition (https://www.biostarhandbook.com/)
Bioinformatics, 4th Edition, John Wiley and Sons Ltd, by Andreas D. Baxevanis, Gary Bader, David Wishart
A Critical Guide to BLAST, TK Attwood
https://www.mygoblet.org/about-us/publication/critical-guide-blast

10. Assessment Details: One exam on the bioinformatics topics, one Python programming exam and one ChIP-Seq analysis report, based on analyses carried out in weeks 13-15, to be submitted by the end of week 21; each part contributing ⅓ to the overall module mark.

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12. Module Website: bioinf.gen.tcd.ie/GEU33025

1. Module Code GEU33215
2. Module Name Medical Genetics
3. Semester taught Semester 2
4. Contact Hours 20
5. Module Personnel Jane Farrar, Pete Humphries, Russell McLaughlin
6. Learning Objectives The model provides an introduction to core concepts in medical genetics highlighting the importance and power of genetic information in the era of genomic medicine and the impact of such information for all of us. Learning objectives include: (1) discussion of the genetic basis of single gene disorders (Mendelian) and complex disorders; (2) overview of the history of medical genetics; (3) insights into key developments in medical genetics up to 2020 including state-of-art technologies and novel innovative therapies; (4) discussion of the key technologies and methodologies currently used to elucidate the genetic basis of human traits; (5) discussion of the individualisation of medicine and the important roles of genetic information in disease diagnosis, prognosis and the design and choice of therapy. In summary, the module provides an introduction to:

- The genetic basis of mendelian & complex disorders
- Genetic technologies & methodologies used to elucidate the genetic basis of human traits
- The exploitation of genomic data in diagnosis, prognosis & treatment of disease
- The individualization of medicine using genetic information

7. Module content: Programme of lectures

Week	Lecture Topic & Lecturer
30	Importance of medical genetics and history of developments in the field. Pete Humphries
30	Introduction to complex traits. Russell McLaughlin
30	Introduction to genetic variation and effects on drug response – pharmacogenomics. Jane Farrar
30	Quantitative traits and complex disorders. Russell McLaughlin
31	Mendelian genetics: Types of mutation in human disease; prevalence and diversity of mendelian diseases; clinical manifestations of autosomal dominant diseases. Pete Humphries
31	Variance components and heritability Russell McLaughlin
31	Genetic variation in drug metabolising enzyme (DME) genes. Monogenic pharmacogenetic traits. Jane Farrar
31	Mendelian genetics: Clinical spectrum of autosomal recessive and X-linked recessive diseases. Pete Humphries
32	Genetic variation in cytochrome P450s and influence on drug response. Jane Farrar
32	Dominance, additivity and interaction. Russell McLaughlin
32	On the genetics of multifactorial diseases. Pete Humphries
32	Pharmacodynamic effects and drug response. Tracking on polygenic pharmacogenetic traits - GWAS, high throughput analysis. Jane Farrar
33	Variants in pharmacogenes can influence disease risk. Actionable pharmacogenetic traits in clinical practice –- the individualisation of medicine. Jane Farrar
33	Selection on complex traits and the liability scale for complex disorders. Russell McLaughlin
33	Development of human physical & genetic linkage maps. Early successes In mapping - predictive testing for Huntington disease. Pete Humphries
33	Mapping complex disease genes I: GWAS and polygenic risk.

	Russell McLaughlin
34	Gene therapy - successes and setbacks. Pete Humphries.
34	Use of genetic information to design targeted therapies. Jane Farrar
34	On the genetics of cancer Pete Humphries
34	Mapping complex disease genes II: missing heritability and rare variants Russell McLaughlin

Description of Lectures:

Pete Humphries

An overview of the importance of medical genetics: Topics including disease prevalence (congenital, Mendelian and multifactorial disorders including cancer), the practical value of genetic information, inter alia, the role of genetic counseling and the potential of emerging new therapeutics based on knowledge of disease etiology, are outlined.

Mendelian genetics (x2 lectures): A reminder on nomenclature is given including transition, transversion, missense, nonsense, frameshift, dynamic, dominant-negative, haploinsufficiency etc. A brief description of phenotypes associated with autosomal dominant, recessive and X-linked disorders is provided, emphasising that the majority of such conditions are clinically significant with many being highly distressing, serious and life-threatening.

On the genetics of multifactorial diseases: The genetics underpinning multifactorial disorders and the methods used to elucidate these genetic factors will be outlined.

Development of human physical & genetic linkage maps. Early successes In mapping - predictive testing for Huntington disease: On the development of the human genetic linkage map - from somatic cell genetics to modern DNA-based genetic markers. Lod-scores. First success in use of modern linkage map – localization of the Huntington disease gene and to gene's identification – a dynamic expanding repeat. Function of the HD protein. Implications of predictive testing.

Gene therapy - successes and setbacks: Number of current disease targets; number of registered trials; Basic requirements (knowledge of genetic basis of disease, efficient delivery, availability of animal models (with note on regulations governing use of animal models), Vectorology concentrating on AAV; examples successes and drawbacks in gene therapy – Familial hypercholesterolaemia, ornithine transcarbamylase deficiency, Severe combined immunodeficiency, Haemophila A/B, Leber congenital amaurosis, Retinitis Pigmentosa, Duchenne Muscular Dystrophy, haemoglobinopathies, sensorineural deafness.

On the genetics of cancer: Prevalence; genetic basis including hereditary syndromes and well known chromosomal aberrations; viruses as carcinogens; examples of modern cancer therapies that have been developed through our knowledge of the genetic changes occurring in cancer cells, including Crizotinib, Gleevec, Herceptin, PLX4032 and others. Bottom line: as our knowledge of genetic aetiologies increases, so will new and effective drugs continue to emerge.

Russell McLaughlin

Introduction to complex traits: In this lecture we define the concept of complex traits, framed against classical Mendelian genetics and alternative models of genetic architecture. This lecture also explores the problem of defining phenotypes in the presence of clinical and genetic heterogeneity.

Quantitative traits and complex disorders: This lecture sets the statistical framework for following lectures, defining basic population parameters including mean, variance and distribution, using a worked example of human height. The liability scale is introduced as a prototype for modelling complex disorders as quantitative traits.

Variance components and heritability: Here we demonstrate how phenotypic variance can be decomposed into genetic and non-genetic components, allowing the estimation of heritability (the fraction of phenotypic variance due to genetic variance). Methods for estimating heritability are discussed, including worked examples with inbred plant lines and monozygotic twins.
Dominance, additivity and interaction: Our genetic model for complex traits is further decomposed to explicitly define variance conferred by dominance effects, gene-gene and gene-environment interactions and additive effects of trait-increasing alleles. Methods for heritability estimation using non-twin pedigree data are defined.
Selection on complex traits and the liability scale for complex disorders: This lecture discusses the practical application of statistical models for complex traits, explaining models of variance components established in previous lectures through the lens of plant and animal breeding. The equivalence between this and the liability scale for complex disease is delineated.
Mapping complex disease genes I: GWAS and polygenic risk: Having established the overall model for complex diseases, this lecture now lays out a key method used to understand the genetics of complex disease: the genome-wide association study (GWAS). We also describe and explain how GWAS data can be used to understand the genetic architecture of complex diseases (e.g., polygenic/non-polygenic) and to estimate the fraction of overall heritability explained by common variants.
Mapping complex disease genes II: missing heritability and rare variants: This lecture defines the missing heritability problem along with explanations and solutions for understanding the genetic architecture of disease in the post-GWAS era, specifically in the context of rare variants.
We shift our focus from GWAS and rare single-nucleotide variants to some other types of genetic variation that are likely to play a major role in the aetiology of complex diseases. The lecture takes a dive into a worked example of the role of repeat expansions in the neurodegenerative disease amyotrophic lateral sclerosis.

Jane Farrar
Introduction to genetic variation and pharmacogenomics: Students will be introduced to the concept that genetic variation between individuals greatly influences drug response, drug efficacy and / or drug toxicity and indeed is relevant to all of us - on average every human carries a number of actionable pharmacogenetic variants. Such genetic information is leading to the individualisation of medicine and has enormous ramifications for medicine and drug development. An introduction to the methods used to identify genetic variants which cause or can influence pharmacogenetic traits will be provided - monogenic and polygenic pharmacogenetic traits will be discussed (analogous to methods used to identify genes involved in Mendelian disorders and complex disorders). A brief introduction to the history of the field of pharmacogenomics will also be outlined.
Genetic variation in drug metabolising enzyme (DME) genes - monogenic pharmacogenetic traits: Concepts of pharmacokinetic and / or pharmacodynamic effects will be introduced. Mechanisms by which genetic variation can modulate pharmacokinetics and thereby influence drug response will be detailed. Genes encoding drug metabolising enzymes (DMEs) will be introduced including Phase I and Phase II DMEs. The significant effects of genetic variants in the thiopurine methyltransferase (TPMT) gene (a Phase II DME) on response(s) to thiopurine drugs (major chemotherapeutic and immunosuppressant drugs) will be outlined. Data suggesting that TPMT operates as a monogenic trait from genome wide association studies (GWAS) will be discussed.
Genetic variation in cytochrome P450s and drug response: A family of genes encoding the cytochrome P450 enzymes, a group of Phase I DMEs will be introduced including CYP2C9, CYP4F2 and CYP2D6, among others. Genetic variants in these DME genes influence the metabolism of drugs, including commonly used medications such as warfarin, codeine and tramadol, among others. A summary of the many genetic

studies which underpin the now actionable pharmacogenomic outcomes associated with warfarin and codeine therapies will be provided. Genetic information can be used to target the optimal therapy at the right dose to patients.

Pharmacogenetics and pharmacodynamics effects. Tracking on polygenic pharmacogenetic traits: Examples of clear pharmacodynamic traits that involve variants in genes encoding receptors will be outlined. Variants in the ryanodine receptor gene and risk of malignant hyperthermia upon administration of anaesthetic (causing fever, increased pulse rate and muscle breakdown) will be discussed. Methods used to identify genetic factors that determine the variation in drug response between individuals will be reviewed. Parallels between such pharmacogenomic studies and the use of GWAS to decipher the genetic determinants of complex disorders will be drawn.

Variants in pharmacogenes influence disease risk. Actionable pharmacogenetic traits in clinical practice - the individualisation of medicine:
While pharmacogenetic traits underpin much of the variance between individuals in response to medications, genetic variants in pharmacogenes can also influence disease risk. Many DMEs metabolise not just exogenous compounds (therapeutics) but also endogenous compounds, and therefore it is not surprising that genetic variants in these genes can contribute to disease risk - the mounting evidence that genetic variants in pharmacogenes can impact disease risk will be reviewed. Actionable outcomes from pharmacogenomic studies will be discussed highlighting that genetic factors greatly impact how each of us responds to medication with enormous implications for medicine and drug development. An overview will be provided of pharmacogenetic traits that have obtained FDA/EMA backing with actionable outcomes in clinical practise. Barriers that have hindered translation of pharmacogenetic information from the laboratory into clinical practise will be reviewed.

Use of genetic information to design targeted therapies: The use of genetic information to design a diverse array of innovative targeted therapies will be discussed. Included in this discussion will be novel gene therapies employing gene editing technologies (CRISPR/Cas) and new classes of CAR-T cell therapies in development for haematological disorders.

8. Learning Outcomes:

On completion of the module students will:

- Have gained an overview of the history of medical genetics and understand the current state-of-the art in this rapidly changing and exciting field
- Have knowledge regarding the genetic basis of mendelian and complex disease
- Have gained insights into methods of analyses used in medical genetics; linkage studies, genome-wide association studies (GWAS), next generation sequencing (NGS), data analyses tools etc
- Understand the genetics of polygenic traits, the concept of heritability and methods to estimate it
- Have insights into emerging themes in personalized medicine that influence drug design, drug choice and drug response and the importance of genetic information for medicine and drug development
- Understand the relevance of medical genetics to diagnosis, prognosis and treatment of disease

9. Recommended Reading List:

‘Genetic and Genomics and Medicine’, (Garland Science) - Tom Strachan, Judith Goodship and Patrick Chinnery
‘Introduction to Genetic Analysis’ (Macmillan Education) Griffiths, Wessler, Carroll & Doebly

Primary references will be provided in lecture materials

10. Assessment Details:

Examination:
After the end of semester 2 (75% of module grade)

Continuous Assessment:
One assignment will be given during week 30 (semester 2) and will be due at the end of week 32 (25% of module grade)

11. Module Coordinator

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1. Module Code GEU33285
2. Module Name Science Structure, Discussion and Presentation for Human Genetics
3. Semester taught Semester 2
4. Contact Hours 12
5. Module Personnel Adrian Bracken, Dan Bradley, Matthew Campbell, Lara Cassidy, Kevin Devine, Jane Farrar, Seamus Martin, Kevin Mitchell, Juan Pablo Labrador, Aoife Mc Lysaght, Russell Mc Laughlin, Mani Ramaswami, Tony Kavanagh, Frank Wellmer.

6. Learning Objectives: The module has the following learning objectives: (1) discussion of the design and implementation of genetic analysis of biological phenomena relevant to human genetics; (2) discussion of genetic analysis in cell and animal models - their strengths and weaknesses; (3) discussion of mathematical genetics; (4) discussion of how to research, design and write a literature review on a human genetics subject; (5) to write a 4,000 literature review on an assigned human genetics topic; (6) discussion of science communication: how to assemble and present a talk on a human genetics topic. Students will make a 15 minute presentation on the topic of their literature review at the annual genetics/human genetics field trip.

7. Module content:

Week	Programme of Tutorials
23	Review I: How to write a literature review on a genetics/human genetic topic
23	Review II: Supervisor and student meet to discuss the topic and how to structure the review
24	How to make an oral presentation:
25	Review III: Supervisor and student meet to discuss review structure produced by the student.
25	Human Genetic Analysis I: In search of human disease genes
26	Human Genetic Analysis II: In search of human disease genes
27	Human Genetic Analysis III: Simulating human disorders in animal models
28	Human Genetic Analysis IV: Emerging methodologies in elucidating the molecular basis of human disease
29	Reading Week
30	Mathematical Genetics I: Bayesian statistics
31	Mathematical Genetics II: Game theory
32	Mathematical Genetics III: Evolution of co-operation/altruism
33	Mathematical Genetics IV: Networks/graph theory

Week 23 Review I: How to write a literature review on a genetics/human genetics topic:
Discussion under the following headings: Topic / focus, structure of review, themes, progression of ideas, literature survey, search databases, references.

Week 23 Review II: Discussion of the review topic assigned to each student and review with the supervisors under the headings listed above.
This is arranged by the supervisor / student at their mutual convenience.

Weeks 24 Human Genetic Analysis I: In search of human disease genes
How to design and perform a genetic analysis searching for Mendelian disease genes (single gene disorders). Pedigree/segregation analysis and genetic linkage, next generation sequencing (NGS). Novel variants in known disease genes and methods to explore disease pathogenicity. Brief

discussion of analysis of complex disorders and associated methods. Examples of disorders where disease genes have been identified using these methods.
Review: Nat Rev Genet. 2015 16(5): 275–284 Genetic linkage analysis in the age of whole-genome sequencing. Jurg Ott, Jing Wang and Suzanne M. Leal.

Week 25 **Review III:** Meeting with supervisor to discuss the review structure produced by the student and to decide on the paper/review for the field trip presentation. This meeting is arranged by the supervisor / student at their mutual convenience.

Week 26: **How to make an oral presentation:**
Discussion of how to prepare a talk, focusing on the topic, judging your audience, slide preparation and the general do's and don'ts of preparing and giving an oral presentation. Discussion will be centred on "*Giving a seminar: Suggestions for Graduate Students"* by John Roth.
Each student will give a 15 minute presentation on the topic of the review at the Junior Sophister field trip.

Weeks 26 **Human Genetic Analysis II: Simulating human disorders in animal models**
How to design and generate animal models of human genetic disorders. Discussion of methodologies including ES cell technology, gene targeting and gene editing etc. Consideration of species suitability for human disease target. Examples of transgenic animal models of human disorders.
Review: Adv Exp Med Biol 2020;1236:1-38. A History of Mouse Genetics: From Fancy Mice to Mutations in Every Gene. María J García-García

Weeks 27 **Human Genetic Analysis III: Generating human cell and organoid models of disease**
Methods to generate cell models of human diseases including mutagenizing or editing cell lines, generating cell lines from patient biopsies, generating induced pluripotent stem cells (iPS) cells etc. Generation of 3-D models from iPS cells to create human organoids with 3-D structures and multiple cell types. Discussion of the value of human cell and organoid models of disease versus non-human models of disease. Examples of cell and organoid models of human disorders.
Review: Nat Rev Mol Cell Biol. 2020 Jul 7:1-14 Human organoids: model systems for human biology and medicine. Kim J, Koo BK, Knoblich JA.
Review: Nat Rev Genet. 2019 Jul;20(7):377-388. Induced pluripotent stem cells in disease modelling and drug discovery. Rowe RG, Daley GQ.

Week 28 **Human Genetic Analysis IV: Emerging methodologies in elucidating the molecular basis of human disease**
Discussion of innovative methods enabling in depth exploration of the coding and non-coding human genome and the effects of genetic variants in disease. The ENCODE project and resources, functional genomics, genome editing etc. Examples of the application of functional genomics enabling elucidation of the genetic basis of disease.
Review: Nat Rev Neurol. Jul 2020 CRISPR-based functional genomics for neurological disease. Kampmann M.
(Additional reading may be provided before tutorials 25-28)

Week 30 **Mathematical Genetics I- Bayesian statistics, Game Theory, Evolution of co-operation/altruism Networks**
Bayesian statistics : making decisions based on the data

Week 31 **Mathematical Genetics II - Bayesian statistics, Game Theory, Evolution of co-operation/altruism Networks**
Game theory

Week 32 **Mathematical Genetics III - Bayesian statistics, Game Theory, Evolution of co-operation/altruism Networks**
Evolution of co-operation/altruism

Week 33 **Mathematical Genetics IV - Bayesian statistics, Game Theory, Evolution of co-operation/altruism Networks**
Networks/graph theory – Network architectures in Biology

8. Learning Outcomes: Students will have the following skills: (1) to research and write a scientific literature review; (2) to research, prepare and give a scientific oral presentation; (3) to design and perform a genetic analysis of a biological phenomenon relevant to human genetics; (4) to choose an appropriate model organism in which to study specific biological phenomena; (5) to perform mathematical genetic analysis.

9. Recommended Reading List:
Tutorials in weeks 25-28 will be based on the following reviews:
Nat Rev Genet. 2015 16(5): 275–284 Genetic linkage analysis in the age of whole-genome sequencing. Jurg Ott, Jing Wang and Suzanne M. Leal
Adv Exp Med Biol 2020;1236:1-38. A History of Mouse Genetics: From Fancy Mice to Mutations in Every Gene. María J García-García
Nat Rev Mol Cell Biol. 2020 Jul 7:1-14 Human organoids: model systems for human biology and medicine. Kim J, Koo BK, Knoblich JA
Nat Rev Genet. 2019 Jul;20(7):377-388. Induced pluripotent stem cells in disease modelling and drug discovery. Rowe RG, Daley GQ
Nat Rev Neurol. Jul 2020 CRISPR-based functional genomics for neurological disease. Kampmann M.
How to make a scientific presentation will be based on "*Giving a seminar: Suggestions for Graduate Students"* by John Roth. Reading material for the Mathematical genetics tutorials will be presented during the first tutorial.

10. Assessment Details: 70% Written review, 4,000 words (deadline, Friday of week 29);
5% Field trip presentation
25% Assignments on a model organism / mathematical genetics.

11. Module Co-ordinator Juan Pablo Labrador
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1. Module Code GEU33035
2. Module Name Genetic Analysis of Nervous Systems
3. Semester taught Semester 2
4. Contact Hours 24
5. Module Personnel Juan Pablo Labrador, Mani Ramaswami
6. Learning Aims The module is focused on understanding how experimental genetics are used to manipulate genes in organisms to address problems in biology. Areas covered are 1) Experimental Genetics: structure and conservation of genes, nature of mutations and their effects on protein structure and function, model organisms in genetic research and experimental manipulation of animal genomes. 2) Developmental Neurogenetics: the purpose and design of genetic screens, genetic analysis of neurogenesis and genetic analysis of axon guidance 3) Behavioral Genetics: cell organization and methods of cell biology, cell biology of neurons and synapses, creation and use of molecular reporters of specific gene or cell activity, methods to study nervous systems, sensory circuits, sensation; transduction; perception; coding; behavior, learning and memory, sleep and circadian rhythms.
7. Module content: Program of lectures

Week	Lecture Topic & Lecturer
23	Experimental Genetics - Introduction - Structure and conservation of genes, nature of mutations and their effects on protein structure and function.
23	Experimental Genetics - Model organisms in genetic research
23	Experimental Genetics - Experimental manipulation of animal genomes
23	Experimental Genetics - Creation and use of transgenic animals to probe gene function in vivo.
23	Experimental Genetics – Flip lecture/ Tutorial.
24	Developmental Neurogenetics - The purpose and design of genetic screens.
24	Developmental Neurogenetics - genetic screens – mapping genes.
24	Developmental Neurogenetics - Genetic analysis of neurogenesis
24	Developmental Neurogenetics - Genetic analysis of axon guidance
24	Developmental Neurogenetics - Flip lecture/ Tutorial
25	Behavioral Genetics - Introduction to Behavioral Genetics - Cell organization and methods of cell biology.
25	Behavioral Genetics - Cell biology of neurons and synapse. Structures, electrical properties
25	Behavioral Genetics - Cell biology of neurons and synapse. Synaptic transmission and molecular determinants
25	Behavioral Genetics - Methods to study nervous systems (behavior, imaging, electrophysiology, anatomy)
25	Behavioral Genetics - Flip lecture/ Tutorial
26	Behavioral Genetics- Sensory circuits: vision; taste and smell.
26	Behavioral Genetics - Sensation; Transduction; Perception; Coding;
26	Behavioral Genetics - Behavioral Plasticity.
26	Behavioral Genetics - Learning and memory.
26	Behavioral Genetics- Sleep and Circadian Rhythms.
27	Behavioral Genetics – Flip lecture/ Tutorial
27	Final written exam
28	Study/Review week

8. Learning Outcomes: Upon successful completion of this module, students will be able to understand and describe how model organisms are used in genetic research and common technologies and methods

employed to genetically modify organisms. Students should also understand the basis of genetic screens and mapping. They will be able to explain epistasis through the analysis of different genetic interactions in neurogenesis and axon guidance. Students will become familiar with the cell biology of neurons and synapse as well as methods to probe synaptic activity. Students will also learn about circuitry underlying perception.

9. Recommended Reading List: Anthony J.F. Griffiths; Susan R. Wessler; Sean B. Carroll; John Doebley. Introduction To Genetic Analysis. New York, NY :W.H. Freeman & Company, 2015

10. Assessment Details: Final exam. Week 27

11. Module Coordinator Juan Pablo Labrador
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Executive Officer: Genetics
Email: genetics@tcd.ie
Phone 01 896 1140

1. Module Code GEU33008
2. Module Name Analytical Genetics Laboratory
3. Semester taught Semester 2
4. Contact Hours 5 hours per week
5. Module Personnel Juan Pablo Labrador
6. Learning Aims

This module is a practical module that introduces the fundamentals of genetic analysis and the use of *Drosophila melanogaster* as a genetic model organism .The module will cover different aspects of model organisms handling and segregation. Virtual crosses are employed to understand Mendelian genetics and non-Mendelian inheritance including segregation, recombination, gene mapping, lethal genes and sex-linked inheritance.

7. Module content: Programme of lectures

Week	Lecture Topic & Lecturer
23	Drosophila husbandry, identification of phenotypes, setting up crosses Mendelian inheritance tutorial. P-elements tutorial Monohybrid, dihybrid crosses
24	Drosophila husbandry, identification of phenotypes, setting up crosses Non-Mendelian inheritance tutorial, Lethal mutations. Short Quiz 1: Monohybrid/dihybrid crosses
25	Segregation in Drosophila, identification of males carrying P-elements Lethal mutations , Sex linked inheritance. Short Quiz 2: Lethal mutations
26	Segregation in Drosophila - fly husbandry Sex linked inheritance , Linkage, recombination and mapping. Linkage and mapping tutorial Short Quiz 3: Sex linked inheritance
27	Segregation in Drosophila analysis of crosses Linkage and mapping Short Quiz 4: Linkage, Recombination and mapping
28	Fly husbandry -Set up crosses if required Review Mendelian and non-Mendelian inheritance Quiz: Mendelian and non-Mendelian inheritance, lethal mutations, linkage and mapping
29	Reading Week
30	Segregation in Drosophila – Review of results P-element mapping in Drosophila Tutorial Fly husbandry
31	Analysis and review of P-element results Fly husbandry
32	Lab report writing

8. Learning Outcomes: Upon successful completion of this module, students will be able to understand how model organisms are used in genetic research in a laboratory setting. Students should be able to set-up crosses and plan experiments using *Drosophila melanogaster*. Students will be able to design crosses and analyse ratios in the progeny. Mendelian inheritance ratios through the analysis of monohybrid, dihybrid and trihybrid crosses involving two or 3 chromosomes should be understood. Students will appreciate non-Mendelian inheritance involving sex linked loci or linked loci in autosomes or sex chromosomes.

9. Recommended Reading List:

Anthony J.F. Griffiths; Susan R. Wessler; Sean B. Carroll; John Doebley. Introduction To Genetic Analysis. New York, NY :W.H. Freeman & Company, 2015

Greenspan, R.J. (2004). Fly pushing: the theory and practice of Drosophila genetics, 2nd edn (Cold Spring Harbor, N.Y.: Cold Spring Harbor Laboratory Press).

10. Assessment Details: MCQs/Final MCQ 50%. Lab report 50% (submission deadline Monday on week 30)

11. Module Coordinator Juan Pablo Labrador
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12. Module Website (not applicable)

OPEN MODULES

1. Module Code GEU33045
2. Module Name Genomics & Systems Biology
3. Semester taught 1
4. Contact Hours 24
5. Module Personnel Adrian Bracken, Carsten Kröger, Kenneth Mok, Frank Wellmer
6. Learning Aims The aim of this module is to provide students with a general overview of methods used in the fields of genomics, proteomics and metabolomics and to explain how these methods are used for basic research, biotechnology, agriculture and medicine. To this end, a number of examples from work with diverse organisms (bacteria, fungi, plants, animals including humans) will be presented. The module further introduces students to the field of systems biology and outlines how systems biology differs from the classic reductionist approach used in biology.

7. Module content:

Week	Lecture Topic & Lecturer
5	Overview of genomic approaches (Wellmer)
5	Systems approaches versus reductionism (Wellmer)
6	First and second generation methods: Sanger and pyrosequencing (Wellmer)
6	Second and third generation methods: Illumina and Nanopores (Wellmer)
7	Genome sequencing and the history of the Human Genome project (Wellmer)
7	Genome sequencing and the history of the Human Genome project (Wellmer)
8	Genome annotation and gene finding (Wellmer)
8	Genome comparisons across species and within populations (Wellmer)
9	Transcriptomics and data analysis (Wellmer)
9	Gene ontologies; Identification of co-expressed genes (Wellmer)
10	Networks in biology (Wellmer)
10	Data integration and modelling (Wellmer)
10	*Revision of material, discussion and answering student questions (Wellmer)*
11	Study/Review week
12	Bacterial genomes and comparative genomics (Kröger)
12	Functional genomics in bacteria (Kröger)
13	Introduction into the epigenome: histone and DNA modifications (Bracken)
13	Methods to analyse the epigenome; the ENCODE project (Bracken)
14	Cancer profiling and classification of tumour types (Bracken)
14	Using genomic information for the development of cancer therapies (Bracken)
15	Proteomics: Identify/characterise/quantify; Mass Spec and other technologies (Mok)
15	Quantitative proteomics; clinical proteomics (Mok)
16	Interaction/affinity proteomics; metabolomics introduction (Mok)
16	Metabolomics technologies (Mok)
16	*Revision of material, discussion and answering student questions (all lecturing staff)*
19	Revision Week
20	Assessment Week

8. Learning Outcomes: Upon successful completion of this module, students will be able to describe experimental approaches used in the fields of genomics, proteomics and metabolomics. They will understand the difference between functional, comparative and structural genomics and will be

familiar with the use of genomic technologies in fundamental and medical research, biotechnology and agriculture. Students will be able to describe how genome sequences are being deciphered and annotated. They will further understand the difference between reductionist and systems approaches in biology.

9. Recommended Reading List: none

10. Assessment Details: One 1.5-hour exam paper at the end of semester 1

11. Module Coordinator Frank Wellmer
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Phone x3729

Executive Officer: Genetics
Email: genetics@tcd.ie
Phone x1140

12. Module Website (not applicable)

1. Module Code BIU33150
2. Module Name Biochemistry for Biosciences
3. Semester taught Semester 1
4. Contact Hours 20 hours
5. Module Personnel Amir Khan, K.H. Mok, Vincent kelly, Martin Caffrey, Paul Voorheis, Derek Nolan, Emma Creagh, Danny Zisterer.

6. Learning Aims

This module follows on from the biochemistry/cell biology component of the "Molecules to Cells" BIU22201 module of year 2. The aim is to provide Junior Sophister students of other disciplines with the grounding in biochemistry necessary to (i) understand biology at a molecular level, (ii) form a mechanistic view of biological processes and (iii) appreciate the pathobiochemical basis of disease. The module covers four major themes in biochemistry: Proteins and Nucleic Acids , Membranes, Cytoskeleton and Signalling. The module will be assessed through a combination of in course assessment and an individual end of term exam.

7. Module content: Programme of lectures and practicals –

Week	Lecture Topic & Lecturer
Semester 1	
	Proteins and Nucleic Acids
1	Amino acids and peptide bond (AK)
1	Structures , motifs and folds (AK)
2	Structure and mechanism: serine proteases (AK)
2	Spetrophotometry of biomolecules (KHM)
3	Protein folding and pathologies (KHM)
3	The proteome (KHM)
4	DNA, chromatin & the nucleus (VK)
4	RNA structure, folds & function (VK)
	Membranes
5	An introduction to cellular and model membranes (MC)
5	Membrane composition and therapeutic approaches (MC)
6	The Synthetic & Assembly Mechanisms for Membrane Proteins that Form Specific Topologies (HPV)
6	Membrane transport of small molecules, specificity, mechanisms, energy Coupling (HPV)
	Cytoskeleton
8	Structure of tubulin and microtubules and the Assembly / Disassembly of Microtubular Structures (HPV)
8	Microtubular motors, types, mechanism of movement, regulation, physiological roles (HPV)
9	Introduction to actin and the actin cytoskeleton (DN)
9	F-actin nucleation & pathologies associated with actin cytoskeleton (DN)
	Signalling
10	Signalling 1: Introduction to cell signalling & GPCRs (EC)

10	Signalling 2: G-Protein coupled Receptor (GPCR) regulation (EC)
11	Signalling 3: Receptor tyrosine kinases (RTKs)-PDGF and EGF (DZ)
11	Signalling 4: RTK signalling – PKB and PDK1 (DZ).

8. Learning Outcomes:

On completion of this module, the student will be able to: (Please suggest some learning outcomes)
Recall and comprehend key knowledge and concepts of the hierarchy of polypeptide structure and the forces that stabilize the three-dimensional shape of proteins
Explain the link between a protein structure and its biological activity, and with appropriate examples, how human diseases arise from a deviation in structure
Appreciate the principles of spectrophotometry and its applications to biomolecules
Understand the concept of the proteome and its importance in disease
Integrate key concepts about nucleic acid structure and function
Demonstrate an understanding of the biochemical processes of nucleic acids in the cell
Recall and integrate key knowledge and concepts concerning the role of lipids in membrane structure and function
Describe how model membranes are formed and their applications
Describe how an understanding of membrane composition and structure can be used in the design of vaccines, antibiotics and beta-blockers.
Demonstrate a knowledge of the biosynthesis of membrane proteins, including the mechanisms of insertion and transport to their various locations.
Explain the types of membrane transport and how this process is coupled to energy and assayed.
Describe the structure of microtublules, their assembly and disassembly and their polarity.
Describe the structure of microtublule motors and the processes of directed vesicle transport and cytoplasmic streaming.
Describe the structure of monmeric actin and how it is assembled into filaments
Explain how actin nucleation is linked to pathological states.
Describe the general principles of G-protein coupled receptor (GPCR) signalling and its regulation, the initial discovery of G-proteins linked to cyclase, the functional effects of cAMP and the activation of GPCR-linked signal-activated phospholipases.
Discuss Receptor Tyrosine Kinase (RTK) signalling and details of MAP kinase cascades, using PDGF and EGF as examples. Explain RTK and PI3K pathways in the context of PKB (Akt) and PDK1 signalling.
Describe the principles of steroid hormone receptor signalling mechanisms.

9. Recommended Reading List:

A reading list will be given out by lecturers during the module.

10. Assessment Details:

60% End of year examination, 40% in course assessed.
In course assessment: Two online MCQ assessments.

11. Module Coordinator: Dr D Nolan
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Executive Officer: Úna Murphy
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1. Module Code GEU33055
2. Module Name Developmental Genetics
3. Semester taught Semester 2
4. Contact Hours 24
5. Module Personnel Seamus Martin, Adrian Bracken, Frank Wellmer
6. Learning Aims This module aims at introducing students to fundamental concepts in developmental genetics and to experimental approaches that are used to study development. To this end, the module takes a comparative approach: the development of different organisms (insects, vertebrates, plants) will be taught together to demonstrate differences and commonalities in the genetic mechanisms controlling morphogenesis. Students will be introduced to important developmental control mechanisms, including morphogens, homeotic selector genes and signal transduction cascades. The module will also introduce students to stem cell biology and how stem cells are programmed to undergo growth and differentiation.

7. Module content:

Week	Lecture Topic & Lecturer
23	Introduction to development and developmental genetics (Wellmer)
23	Overview of genetic mechanisms controlling development (Wellmer)
23	Stem cells (Bracken)
23	Cell fate determination (Bracken)
24	Genetic control of cell differentiation and growth (Bracken)
24	The cell cycle: dissection in different experimental systems. Discovery of the cyclins and cyclin-dependent kinases (Martin)
24	The cell cycle: role of Cyclins and Cyclin-dependent kinases (Martin)
24	The cell cycle: how Cyclin activity is regulated by kinases and phosphates (Martin)
25	The cell cycle: role of Rb and CDK inhibitors. p53 and the DNA damage cell cycle checkpoint (Martin)
25	Introduction to *Drosophila* development and embryogenesis (Martin)
25	*Drosophila* development: anterior-posterior axis specification (Martin)
25	*Drosophila* development: role of maternal effect genes (Martin)
26	*Drosophila* development: activation and function of gap genes (Martin)
26	*Drosophila* development: activation and function of pair-rule genes (Martin)
26	*Drosophila* development: activation and function of segment polarity genes (Martin)
26	*Drosophila* development: dorso-ventral axis specification (Martin)
27	*Drosophila* development: homeotic selector genes and the control of segment identity (Martin)
27	Tutorial: revision of material, discussion and answering student questions (Martin, Bracken)
27	Organogenesis: genetic control of vertebrate limb development (Wellmer)
27	Organogenesis: genetic control of vertebrate limb development (Wellmer)
28	Organogenesis: Genetic control of *Drosophila* eye development (Wellmer)
28	Principles of plant development (Wellmer)
28	Stem cells, cell fate determination and organogenesis in plants (Wellmer)
28	Tutorial: revision of material, discussion and answering student questions (Wellmer)

8. Learning Outcomes: Upon successful completion of this module, students will be able to describe fundamental mechanisms underlying the control of development in animals and plants. They will have acquired knowledge to outline key events during development including embryogenesis and the formation of organs and will be able to describe how these events are regulated at a molecular level. Students will be familiar with the biology of stem cells and how these cells are programmed to undergo

growth and differentiation. They will be able to describe experimental approaches that are used by researchers to dissect developmental processes and mechanisms.

9. Recommended Reading List: Anthony J.F. Griffiths; Susan R. Wessler; Sean B. Carroll; John Doebley. Introduction to Genetic Analysis. New York, NY :W.H. Freeman & Company, 2015.

10. Assessment Details: One 1.5-hour exam paper at the end of semester 2

11. Module Coordinator Frank Wellmer
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Executive Officer: Genetics
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Phone x1140

12. Module Website (not applicable)

1. Module Code BIU33250
2. Module Name Introduction to Immunology & Immunometabolism
3. Semester taught Semester 2
4. Contact Hours 22
5. Module Personnel Cliona O'Farrelly (COF), Frederick Sheedy (FS), Jean Fletcher (JF), Richard Porter (RP), Luke O'Neill (LON),
6. Learning Aims This module introduces to the basic components and function of the immune system – the molecules, cells, tissues and organs that make up the immune system. It will illustrate the immune responses to infection. Additionally, it will introduce students to the importance of central energy and intermediary metabolic pathways before considering how they are dysregulated in diseases like cancer and also how we can harness this knowledge for new immunotherapies.

7. Module content:

Week	Lecture Topic & Lecturer	
23	Introduction – The Immune System	(COF)
23	Innate Immunity 1 – Innate Defences	(FS)
23	Innate Immunity 2 – Cellular Response to infection	(FS)
23	Innate Immunity 3 – PRR Signalling	(FS)
24	Innate Immunity 4 – Cytokines	(FS)
24	T-cells 1 – DCs & Antigen Presentation	(JF)
24	T-cells 2 – T-cell Receptor	(JF)
24	T-cells 3 – T-cell Signalling	(JF)
24	T-cells 4 – Effector T-cells	(JF)
25	B-cells 1 – B-lymphocytes & Plasma Cells	(COF)
25	B-cells 2 – Antibodies	(COF)
25	B-cells 3 – Disorders of the immune system	(COF)
26	Advanced Metabolism 1 – Central Energy Metabolism	(RKP)
26	Advanced Metabolism 2 – Intermediary Metabolism	(RKP)
26	Advanced Metabolism 3 – PPARs	(RKP)
26	Advanced Metabolism 4 – Nucleotide Metabolism	(RKP)
27	Advanced Metabolism 5 – Cancer Cell Metabolism	(RKP)
27	Advanced Metabolism 6 – Immune Cell Metabolism	(RKP)
27	Immunometabolism 1	(LON)
27	Immunometabolism 2	(LON)
28	*In-class MCQ*	
29	Reading Week	
35	Trinity Week	
36	Revision Week	
37/38	Assessment	

8. Learning Outcomes:

On successful completion of this module students will be able to:

- Identify cells, receptors and soluble component of the innate immune system and how they function to eliminate pathogen.

- Define how an adaptive immune response is initiated and how different types of adaptive immune responses are used to eliminate particular pathogens.
- Identify how the immune system can cause disease and how it can be exploited therapeutically
- Recall key central energy and intermediary metabolic pathways and appreciate their importance in cellular function
- Apply knowledge on cellular metabolism to diseases including cancer and inflammation

9. Recommended Reading List:

The recommended text for this module is Janeway's Immunobiology published by Norton's Books, currently in its 10th Edition.
Further reading will be given out by lecturers during the module.

10. Assessment Details:

70% End of year examination, 30% in course assessed.
In course assessment: In-class end of module MCQ exam covering lecture material

11. Module Coordinator Frederick J Sheedy
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Executive Officer: Úna Murphy
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12. Module Website NA

REVIEW INSTRUCTIONS:

Please note: due to the length and number of reviews to be assessed, we may not be able to return marks to you before the annual exams in May.

Format

Your review must not exceed 4,000 words (i.e. all text, including figure legends and tables; but excluding the References section). It must be typed in Times New Roman 12 point font, with a line spacing of 1.5. It must be submitted not later than Friday, on week 29 (March 19th, 2021), with the word count verified and included in the submitted version (see last page of this handbook).

- The work should be divided into: Abstract; Introduction; Main text in sections according to topic; Conclusion; References.
- Pages must be numbered.
- Figures and Tables: Each Figure/Table must be numbered (Figure 1, etc.). Figures must have a legend (text attached to the Figure that explains what it shows). Each Figure/Table must be referred to from a sentence in the main text, to tell the reader when to look at it. You are allowed to copy Figures and Tables from papers or websites, provided that the legend cites the source clearly ("Figure taken from Smith et al., 2011").
- Citations: When the text refers to a published paper, the citations in the text must use a format like these examples:
    - XYZ was observed (Behan, 2011). For papers with 1 author.
    - XYZ was observed (Behan and Murphy, 2011). For papers with 2 authors.
    - XYZ was observed (Behan et al., 2011). For papers with 3 or more authors.
    - Most references are cited at the ends of sentences like this (Behan et al., 2011). However, it is sometimes more useful to write something like Behan et al. (2011) found that XYZ was not true.
    - Do not use a citation system based on numbers.
    - Do not include the initials of the authors in the citations in the main text.
- References section: The references section (also called the bibliography) is the list of papers that have been cited in the text. It appears at the end of the review. It gives more details of the papers that have been cited: complete list of authors (initials and surname); year of publication; title of the article; journal name; volume number; page numbers (first and last). Example:
    - Behan M, Cahill S, Murphy C (2011) The plastid genome of higher plants. Nature Reviews Genetics 103: 56-58.
- References to websites should not be used as a substitute for the primary published literature in the field under review and should only be cited if there is no published paper as an alternative. If you need to cite a website, put the address (URL) directly in the text of as a footnote, not in the references section.
- The work must be bound (e.g. by ring binding), not stapled or clipped together. Read's print centre on Nassau Street (back of courtyard beside the Kilkenny shop) do binding quickly and cheaply.
- The review's title and your name should be on the front cover.

You must also upload an electronic copy of your review to *Blackboard* before the deadline.

Plagiarism – Trinity College's regulations (from the TCD Calendar)

70 Plagiarism is interpreted by the University as the act of presenting the work of others as one's own work, without acknowledgement.

Plagiarism is considered as academically fraudulent, and an offence against University discipline. The University considers plagiarism to be a major offence, and subject to the disciplinary procedures of the University.

71 Plagiarism can arise from deliberate actions and also through careless thinking and/or methodology. The offence lies not in the attitude or intention of the perpetrator, but in the action and in its consequences.

Plagiarism can arise from actions such as:

(a) copying another student's work;

(b) enlisting another person or persons to complete an assignment on the student's behalf;

(c) quoting directly, without acknowledgement, from books, articles or other sources, either in printed, recorded or electronic format;

(d) paraphrasing,without acknowledgement, the writings of other authors.

Examples (c) and (d) in particular can arise through careless thinking and/or methodology where students:

(i) fail to distinguish between their own ideas and those of others;

(ii) fail to take proper notes during preliminary research and therefore lose track of the sources from which the notes were drawn;

(iii) fail to distinguish between information which needs no acknowledgement because it is firmly in the public domain, and information which might be widely known, but which nevertheless requires some sort of acknowledgement;

(iv) come across a distinctive methodology or idea and fail to record its source.

All the above serve only as examples and are not exhaustive.

Students should submit work done in co-operation with other students only when it is done with the full knowledge and permission of the lecturer concerned. Without this, work submitted which is the product of collusion with other students may be considered to be plagiarism.

72 It is clearly understood that all members of the academic community use and build on the work of others. It is commonly accepted also, however, that we build on the work of others in an open and explicit manner, and with due acknowledgement. Many cases of plagiarism that arise could be avoided by following some simple guidelines:

(i) Any material used in a piece of work, of any form, that is not the original thought of the author should be fully referenced in the work and attributed to its source. The material should either be quoted directly or paraphrased. Either way, an explicit citation of the work referred to should be provided, in the text, in a footnote, or both. Not to do so is to commit plagiarism.

(ii) When taking notes from any source it is very important to record the precise words or ideas that are being used and their precise sources.

(iii) While the Internet often offers a wider range of possibilities for researching particular themes, it also requires particular attention to be paid to the distinction between one's own work and the work of others. Particular care should be taken to keep track of the source of the electronic information obtained from the Internet or other electronic sources and ensure that it is explicitly and correctly acknowledged.

73 It is the responsibility of the author of any work to ensure that he/she does not commit plagiarism.

74 Students should ensure the integrity of their work by seeking advice from their lecturers, tutor or supervisor on avoiding plagiarism. All schools and departments should include, in their handbooks or other literature given to students, advice on the appropriate methodology for the kind of work that students will be expected to undertake.

75 If plagiarism as referred to in §70 above is suspected, in the first instance, the head of school will write to the student, and the student's tutor advising them of the concerns raised and inviting them to attend an informal meeting with the head of school,[7] and the lecturer concerned, in order to put their suspicions to the student and give the student the opportunity to respond. The student will be requested to respond in writing stating his/her agreement to attend such a meeting and confirming on which of the suggested dates and times it will be possible for the student to attend. If the student does not in this manner agree to attend such a meeting, the head of school may refer the case directly to the Junior Dean, who will interview the student and may implement the procedures as referred to under CONDUCT AND COLLEGE REGULATIONS §2.

76 If the head of school forms the view that plagiarism has taken place, he/she must decide if the offence can be dealt with under the summary procedure set out below. In order for this summary procedure to be followed, all parties attending

[7] *The director of teaching and learning (undergraduate) may also attend the meeting as appropriate. As an alternative to their tutor, students may nominate a representative from the Students' Union to accompany them to the meeting.*

the informal meeting as noted in §75 above must state their agreement in writing to the head of school. If the facts of the case are in dispute, or if the head of school feels that the penalties provided for under the summary procedure below are inappropriate given the circumstances of the case, he/she will refer the case directly to the Junior Dean, who will interview the student and may implement the procedures as referred to under CONDUCT AND COLLEGE REGULATIONS §2.

77 If the offence can be dealt with under the summary procedure, the head of school will recommend to the Senior Lecturer one of the following penalties:

(a) that the piece of work in question receives a reduced mark, or a mark of zero; or

(b) if satisfactory completion of the piece of work is deemed essential for the student to rise with his/her year or to proceed to the award of a degree, the student may be required to resubmit the work. However the student may not receive more than the minimum pass mark applicable to the piece of work on satisfactory re-submission.

TRINITY COLLEGE DUBLIN
THE UNIVERSITY OF DUBLIN

SCHOOL OF GENETICS AND MICROBIOLOGY

SMURFIT INSTITUTE OF GENETICS

DECLARATION FOR REVIEW

(to be bound into your Review)

I have read and I understand the plagiarism provisions in the General Regulations of the University Calendar for the current year, found at http://www.tcd.ie/calendar.

I have also completed the Online Tutorial on avoiding plagiarism 'Ready Steady Write', located at http://tcd-ie.libguides.com/plagiarism/ready-steady-write.

I declare that this Review does not contain material which has been **PLAGIARISED**.

Signed.....

Dated .....

The **word count** of this document (with the exception of the References section is: [ ]

Signed.....

Dated .....

Careers Advisory Service

What do you want to do? How will you get there? We are here to support you in answering these and other questions about your career.

Junior and Senior Fresh Students

Get Involved: Remember that your course of study, extra- curricular activities, voluntary and part-time work all provide opportunities for developing skills and gaining an insight into your career preferences. In your Senior Fresh year, look out for short-term internship opportunities.

MyCareer: Log in to MyCareer to keep abreast of jobs, study and careers events of interest to you.

Junior Sophisters

Attend class seminar: Typically this takes place in Hilary term and includes information on applying for work experience and internships and postgraduate study.

Get work experience: The programme of summer work experience and internships is particularly relevant to Junior Sophisters. Personalise your MyCareer profile to receive email alerts tailored to your preferences.

MyCareer: Log in to MyCareer to keep abreast of jobs, study and careers events of interest to you.

Finalists and Senior Sophisters

Meet Employers and/or Explore Further Study: You may have decided to seek employment directly after graduation and many employers visit Dublin to actively seek out talented graduates. For others, further study may be their preferred option. Your MyCareer dashboard will keep you informed.

Find Jobs: Personalise your MyCareer profile to receive email alerts tailored to your interests.

Attend class seminar: Typically this takes place in Michaelmas term and includes information on applying for postgraduate study and jobs.

GradLink Mentoring: An opportunity to get advice and support from a Trinity graduate.

Drop-In CV/ LinkedIn Clinics: We also provide support at a practical level, helping you to improve your applications, which will benefit you in securing your future, whether in employment or further study.

Practice Interviews: A practice interview tailored to the job/ course of your choice with practical feedback.

MyCareer: Log in to MyCareer to keep abreast of jobs, study and careers events of interest to you.

MyCareer

An online service that you can use to:

- Apply for opportunities which match your preferences - vacancies including research options
- Search opportunities- postgraduate courses and funding
- View and book onto employer and CAS events
- Submit your career queries to the CAS team
- Book an appointment with your Careers Consultant

Simply login to MyCareer using your Trinity username and password and personalise your profile.

Careers Advisory Service
Trinity College Dublin, 7-9 South Leinster Street, Dublin 2
01 896 1705/1721 | Submit a career query through MyCareer

MyCareer: mycareerconnect.tcd.ie

TCD.Careers.Service

TCDCareers

www.tcd.ie/Careers/students/postgraduate/

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Opening Hours

During term: 9.30am - 5.00pm, Monday - Friday

Out of Term: 9.30am - 12.30pm & 2.15 - 5.00pm, Monday - Friday