

**QUALITY ASSURANCE MANUAL
DEPARTMENT OF BIOCHEMISTRY, MICROBIOLOGY AND
BIOTECHNOLOGY**

MSc PROGRAMME OUTLINE		
MSc in Bioinformatics and Computational Molecular Biology		
Course Work / Project Masters	Year: 2013	Coordinators: Prof Mike BURTON (January – June 2013) and Dr Özlem TAŞTAN BISHOP (July – December 2013)

COURSE WORK and RESEARCH PROJECT MASTERS

in

**BIOINFORMATICS and
COMPUTATIONAL MOLECULAR BIOLOGY**

2013

DEPARTMENTS

of

**BIOCHEMISTRY, MICROBIOLOGY & BIOTECHNOLOGY
CHEMISTRY, COMPUTER SCIENCE, MATHEMATICS and
STATISTICS**

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ORIENTATION DAY

(7 February 2013, Thursday)

(Place: Biochemistry Tea Room, Biological Sciences Building 5th Floor)

9:00 – 9:30	Welcoming (Tea/Coffee & Scones)
9:30 – 10:00	Introduction of students, lecturers, supervisors, rest of RUBi members
10:00-10:30	“Introduction to the programme” by Dr Özlem Tastan Bishop and Prof Mike Burton
10:30 – 11:00	Tea break
11:00 – 11:30	“Overview of bioinformatics” by Dr Özlem Tastan Bishop
11:30 – 12:00	“What is plagiarism?” by Dr Adrienne Edkins

Lunch Break

14:00 – 15:15 Research talks with some examples from previous MSc projects
(Maximum 15 min each)

- 14:00 - Prof Mike Burton
- 14:15 - Dr Adrienne Edkins
- 14:30 – Dr Kevin Lobb
- 14:45 - Prof Philip Machanick
- 15:00 - Dr Özlem Tastan Bishop

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PROPOSED PROGRAMME FOR 2013

Date	Module	Content
7 Feb, Thu	ORIENTATION DAY	
8 Feb, Fri	Research projects discussion with supervisors <i>(Time will be arranged by supervisors)</i>	<ul style="list-style-type: none"> • Ngonidzashe Faya (<i>Dr Edkins and Dr. Ö Tastan Bishop</i>) • Caleb K. Kibet (<i>Prof P. Machanick</i>) • Abdul R Moos (<i>Prof P. Machanick</i>) • Vuyani Moses (<i>Dr Ö Tastan Bishop</i>)
11 Feb, Mon - 15 Feb, Fri [20 contact hours]	Introduction to Linux Prof Philip Machanick	<ul style="list-style-type: none"> • Linux operating system and software installation • Use of Linux and Linux shell commands • Application to Bioinformatics problems
18 Feb, Mon – 22 Feb, Fri [10 hours]	Introduction to programming Dr Denis Pollney	Basics for (Python) programming
25 Feb, Mon – 1 Mar, Fri [10 hours]	Introduction to Mathematics Prof Mike Burton	Review of basic calculus and linear algebra
4 Mar, Mon – 22 Mar, Fri [75 h for biology students, 35 h for computer science students]	Python for Bioinformatics Mr Gustavo Adolfo Salazar Orejuela	<ul style="list-style-type: none"> • Introductory and advanced Python • Biopython

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11 Feb, Mon – 22 Mar, Fri [40 hours]	Introductory biochemistry Dr Adrienne Edkins	Students without an appropriate background in biology will take 2 nd year Biochemistry lectures together with additional readings, in place of other topics as determined by the Coordinators
25 Mar, Mon – 28 Mar, Thr [25 hours]	Basic Genomics – Part 1 Ms. Candice Ryan	DNA and protein databases; database searching; sequence alignment
29 Mar, Fri – 1 Apr, Mon	Easter holiday	
2 Apr, Tue	Basic Genomics – Part 1 Ms. Candice Ryan	DNA and protein databases; database searching; sequence alignment
3 Apr, Wed – 8 Apr, Mon	Python (assignment week)	
9 Apr, Tue – 11 Apr, Thu [10 hours]	Basic Genomics - Part 2 Prof Philip Machanick	Discovering features of interest in DNA including transcription factor binding sites, using genome browsers to obtain data, using web services and the command line to performance genome-wide and specific sequence analyses
12 Apr	Study day	
15 Apr, Mon – 19 Apr, Fri	Examinations: Basic Biochemistry (15 April), Linux (16 April), Basic mathematics (17 April), Python (18 April), Basic genomics (Part 1 & 2) (19 April)	
22 Apr, Mon - 26 Apr, Fri [25 hours]	Phylogenetics Dr Jane Wright	Introductory Phylogenetics covering neighbor-joining in detail and the principles of maximum likelihood and Bayesian inference. We will also look at sequence alignment, bootstrap analysis, evolutionary models and comparison of tree topologies.

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29 Apr , Mon - 3 May , Fri [25 hours]	Structural Bioinformatics Ms. Crystal-Leight Clitheroe	Protein visualization programs; structural biology techniques; template and non-template based protein structure prediction methods; homology modeling; Modeler.
6 May , Mon – 10 Mar , Fri	Study week	
13 May , Mon - 17 May , Fri [25 hours]	Comparative genomics Prof Oleg Reva	Introduction to pairwise and multiple complete genome alignment; phylogenomics; genome evolution; and horizontal gene transfer. New approaches, techniques and challenges.
20 May , Mon - 24 May , Fri [15 hours]	Mathematical Programming Prof Mike Burton	The MATLAB computational environment, MATLAB scripts, graphical output, functions, systems of linear and non-linear equations, differential equations. Use of the Bioinformatics Toolbox.
27 May , Mon– 31 May , Fri [25 hours]	Statistics Mr Jeremy Baxter	Introductory statistics; R: statistical software
3 Jun , Mon - 7 Jun Fri [25 hours]	Neural Networks Prof Mike Burton	Origins of artificial neural networks, perceptrons: their construction and deployment, convergence of perceptrons, gradient descent for optimisation, general feed-forward networks with differentiable transfer functions, backpropagation, training, assessing performance, construction and deployment of feed-forward neural networks for prediction and pattern recognition, various applications, problems.

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10 June, Mon – 14 June, Fri	Study week
18 Jun, Tue – 27 Jun, Wed	EXAMINATIONS: <ul style="list-style-type: none"> • Structural Bioinformatics (18 June) • Phylogenetics (19 June) • Comparative genomics (21 June) • Mathematical programming (24 June) • Statistics (25 June) • Neural Networks (26 June)
27 Jun, Thr – 7 Jul, Sun	BREAK
16 Jul, Tue	PROJECTS: Hand-in Literature Review and Project Proposal to Supervisor and Co-supervisor – Project starts!
22 Jul, Mon	PROJECTS: Project Proposal Presentations
5 Aug, Wed – 15 Nov, Fri	BIOINFORMATICS JOURNAL CLUB
Week of 23 Sep	1 st Presentation of Project Progress
Week of 21 Oct	2 nd Presentation of Project Progress
Week of 25 Nov	Presentation of project results
10-14 Dec	Thesis submission (If thesis on time)

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OVERALL TEACHING HOURS

	Contact Hours	Lecturing Hours	Practicals and tutorials
Introduction to Linux	20	9	11
Introduction to Mathematics	10	4	6
Basic Biochemistry	40		
Python for Bioinformatics	75	35	40
Python for Bioinformatics (Comp sci background)	35		
Basic Genomics - Part 1	25	12	13
Basic Genomics - Part 2	10	4	6
Structural Bioinformatics	25	12	13
Phylogenetics	25	12	13
Comparative genomics	25	12	13
Mathematical programming	15	7	8
Statistics	25	12	13
Neural network	25	12	13
TOTAL	280	131	149

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COURSE OUTCOMES

CRITICAL OUTCOMES ADDRESSED

1. Identify and solve problems and make decisions using critical and creative thinking
2. Work effectively with others as a team
3. Organise and manage time and activities effectively
4. Collect, analyse, organise, and critically evaluate information
5. Communicate effectively using written, electronic and language skills
6. Use science and technology effectively and critically showing responsibility towards the environment and others
7. Demonstrate an understanding of the world as a set of related systems

SPECIFIC OUTCOMES ADDRESSED:

1. Develop a broad understanding of what the field of Bioinformatics and Computational Molecular Biology comprises
2. Develop an in-depth knowledge of certain major areas of Bioinformatics and Computational Molecular Biology
3. Demonstrate the ability to conduct research by designing and carrying out a piece of research in Bioinformatics and Computational Molecular Biology, including design of computational experiments and collection and analysis of data
4. Demonstrate expertise in scientific writing, oral presentation and communication
5. Demonstrate an understanding of the relationship between Bioinformatics and Computational Molecular Biology, the community and the environment
6. Demonstrate the competence required for recognition as a professional Bioinformaticist or Computational Molecular Biologist in South Africa
7. Develop professional attitudes and values including scientific ethics and integrity

PARTICULAR SKILLS TO BE ACQUIRED:

1. Scientific communication and presentation skills including computer skills
2. Ability to use the scientific literature efficiently and effectively
3. Practical skills required for use and application of computers and software
4. Organisational skills required to acquire, manage and utilise data and information
5. Ability to analyse and evaluate scientific data
6. Good computer practice

GENERAL BACKGROUND & OUTCOMES

Bioinformatics and computational molecular biology is the systematic development and application of information technologies and data mining techniques for analysing biological data obtained by experiments, modelling, database searching and instrumentation to make novel observations and predictions about biological function. This course will be taught in an

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interdisciplinary manner and focussing on the interface between the computational sciences and the biological, physical and chemical sciences. Graduates who complete this course will be skilled in the assimilation of biological information through the use and development of computational tools for a range of applications including simple pattern recognition, molecular modelling for the prediction of structure and function, gene discovery and drug target discovery, the analysis of phylogenetic relationships, whole genome analysis and the comparison of genetic organization.

COURSE STRUCTURE, TEACHING METHODS & APPROACH

The Masters programme will be offered over 11 months and incorporate a number of course work modules and a research project running concurrently throughout the programme. The course work modules will involve an integration of formal lectures, self-learning computer-based tutorials and practicals. In addition, problem solving tutorials would be designed to guide the student through current information-based problems and involve the assimilation and reduction of biological information. A number of the tutorials and practical components will be assessed and contribute towards a course work year mark. The assessment of the course work component would be through assignments, tutorials, tests etc., and examinations. Each examination will have an external examiner, appointed by the lecturer's home Department (for lecturers from Rhodes), or by the Department of Biochemistry, Biotechnology and Microbiology (for external lecturers).

The research projects will be computer based. The projects will be assessed by seminar presentations of the proposed and final work, and by a written thesis. Each thesis will be examined by two external examiners.

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ASSESSMENT

OVERALL

The course-work and the research work will each contribute 50% to an overall mark. Successful completion of the course will be subject to a final mark of at least 50%, provided that a candidate obtains at least 50% for the course work, with a sub-minimum of at least 40% from each module, and at least 50% for the project report.

COURSE WORK

The course-work modules will be assessed by internal grading of tutorials, assignments, tests and practicals, etc. to give a class mark; and by internal and external grading of examinations. The calculation of the class mark for each module is given later in this manual under the detailed entry for the module. The examinations will be given during the period specified in the course programme earlier in this manual. For each module, the weighting between class mark and examination towards the module mark will be

- Class mark 40%
- Examinations 60%

The weightings of the various modules in the calculation of the overall course work mark will be proportional to the number of lectures given. For each module the weighting, and the duration of the examination, will be

Module	Weighting	Duration (hours)
Introduction to Linux	7.0%	2
Python for Bioinformatics	29.3%	4
or		
<i>(Python for com sci students)</i>	<i>14%</i>	<i>2</i>
<i>Introductory biochemistry</i>		
<i>for non-biology background students)</i>	<i>15.3%</i>	<i>2</i>
Basic Genomics	12.1%	2.5
Phylogenetics	8.6%	2
Mathematics	3.4%	1
Mathematical programming	5.2%	1.5
Structural Bioinformatics	8.6%	2
Comparative genomics	8.6%	2
Statistics	8.6%	2
Neural Network	8.6%	2

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PROJECT

The project will be graded internally and externally with the following weightings:

- Project proposal and presentation 10%
- Project results and presentations 30%
- Thesis 60%

PROPOSAL:

Guidelines

Preparation for the Research Project Proposal (written and oral) should be commenced as soon as the projects have been allocated.

Written

Style: Follow the style of any journal article on Bioinformatics

Length: Around 20 typed pages. Include sections on: Literature review (around 15 pgs); problem statement and hypothesis (1 pg); aims and objectives (1 page); outline of approach and methodology (1–2 pgs).

References: Follow the citation and listing style of the journal, (references may be single-spaced).

Oral

Length: 30 minutes; 25 minutes presentation and 5 minutes questions.

Dates

As specified in the programme earlier in this manual.

Marks Breakdown

- Proposal presentation: 50%
- Written proposal: 50%

PRESENTATION OF PROJECT RESULTS:

Guidelines

The Research Project Results presentation should include:

- **Introduction** - an explanation of the background to the project, the current status of the scientific field, a clear hypothesis statement, and the overall aims & objectives of the project.

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- **Description of the approach**, the techniques and methodology, including reasons for why these computations were done.
- **Presentation and Explanation of Results.**
- **Critical discussion of results** including analysis of their implications, and any problem areas.
- **Conclusion** that includes the overall outcome of the project and where future research should be directed.

Dates

As specified in the programme earlier in this manual.

THESIS:

Structure

There is some flexibility in the choice of format for a thesis, but as a guide, it should contain the following sections in the order given:

Abstract
Table of Contents
Table of Figures
List of Tables
List of Abbreviations
Acknowledgements
Chapters 1 (Literature review)
Chapter 2, 3, etc
Conclusion
References

Each Chapter following Chapter 1 would normally contain
Introduction
Methods
Results and Discussion

Dates

As specified in the programme earlier in this manual.

ASSESSMENT CRITERIA & PROCEDURE

The thesis will be assessed by two external examiners. Preferably, at least one of the external

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examiners should be international.

NUMBER OF COPIES OF THE RESEARCH REPORT

You should prepare two copies of your thesis for external examiners. After corrections are done, one final copy should be prepared for RUBi.

DESCRIPTION OF THE MAJOR SECTIONS OF THE THESIS

1. ABSTRACT

An abstract has to stand alone and should: (i) state the principal objectives and scope of the investigation; (ii) state the methodology used; (iii) summarize the results; (iv) state the principal conclusions. It should not exceed a page.

2. CHAPTER 1

Literature review

This should be a concise summary that describes the current status of the research field. It should be current and comprehensive.

Project aims, objectives and motivation

A clear statement of the aims & objectives of the project and motivation for these should be given. Knowledge gap should be explained.

3. FURTHER CHAPTERS

Introduction

This should be a concise summary that describes the current status of the literature related to the chapter.

Methodology

This should give a logical account of the methodology. It should be precise and complete.

Results and Conclusion

This section should give a description of the results of the experiments together with an explanation of why they were done. It should include critical analysis of the data and interpretation of the implications of the results.

5. CONCLUSION

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Should be a concise and relevant summary, including the contribution the research makes to the current status of the field. A statement of the direction of future research arising from the project should be given.

6. REFERENCES

Current research articles should be used and cited in the text of the thesis using the style of a bioinformatics journal.

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EVALUATION FORMS

MSc Proposal Presentation Evaluation Criteria

Criterion	Weight
1. Concise, accurate & up-to-date literature review	20
2. Knowledge gap and/or problem clearly identified and stated	20
3. Clear research hypothesis & objectives; Concise description of approach and methods	20
4. Research objectives, approach & methods. Realistic? Feasible?	15
5. Time management, visual media and speaker – audience contact	10
6. Ability of speaker to answer questions in a clear & meaningful manner.	15

MSc Written Proposal Evaluation Form

Criterion	Weight
1. Concise, accurate & up-to-date literature review	30
2. Knowledge gap and/or problem clearly identified and stated	20
3. Clear research hypothesis & objectives; Concise description of approach and methods	20
4. Research objectives, approach & methods. Realistic? Feasible?	15
5. Quality of scientific writing	15

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MSc Project Progress Presentation Evaluation Criteria

Criterion	Weight
1. Clear research hypothesis & objectives	10
2. Concise description of approach and methods	15
3. Results and discussion: interpretation of results and critical analysis of their meaning and impact	45
4. Summary of findings and future plans	10
5. Ability of speaker to answer questions in a clear & meaningful manner.	10
6. Time management, visual media and speaker – audience contact	10

MSc Final Project Presentation Evaluation Criteria

Criterion	Weight
1. Concise, accurate & up-to-date literature review	15
2. Knowledge gap and/or problem clearly identified and stated	15
3. Clear research hypothesis & objectives; Concise description of approach and methods	15
4. Results and discussion: interpretation of results and critical analysis of their meaning and impact	25
5. Summary of findings and future plans	5
6. Time management, visual media and speaker – audience contact	10
7. Ability of speaker to answer questions in a clear & meaningful manner.	15

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PLAGIARISM

Plagiarism is a serious offence. All students are expected to familiarize themselves with the Rhodes University Policy on Plagiarism:

http://www.ru.ac.za/intranet/policies/plagiarism_policy.doc

Before lectures start, each student must sign the plagiarism declaration page and return to the course coordinator.

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Student Name:

Student No:

PLAGIARISM DECLARATION FORM

1. I am aware of Rhodes University Policy on Plagiarism webpage and I have familiarized myself (http://www.ru.ac.za/intranet/policies/plagiarism_policy.doc)
2. I know that “plagiarism” means using another person’s work and ideas without acknowledgement, and pretending that it is one’s own. I know that plagiarism not only includes verbatim copying, but also the extensive (albeit paraphrased) use of another person’s ideas without acknowledgement. I know that plagiarism covers this sort of use of material found in theses, textbooks, journal articles AND on the internet.
3. I acknowledge and understand that plagiarism is wrong, and that it constitutes academic theft.
4. I understand that my research must be accurately referenced.
5. All the assignments that I submit during my MSc degree are my own work, or the unique work of a group, if a group assignment.
6. I have not allowed, nor will I in the future allow, anyone to copy my work with the intention of passing it off as his or her own work. I also accept that submitting identical work to someone else (a syndicate essay) constitutes a form of plagiarism.

Signed _____

Date _____

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COURSE WORK MODULES

INTRODUCTION TO LINUX

Lecturer: Prof Philip Machanick

Contact hours: 20

SPECIFIC OUTCOMES ADDRESSED

1. To be able to install a Linux operating system
2. To be able to install various programs
3. Log in and out of a Linux system
4. Work with directories and files and change file permissions
5. Master several shell commands
6. Redirect input and output and print documents

BACKGROUND KNOWLEDGE REQUIRED

Basic computer literacy: proficiency with word-processing, spreadsheets and graphics programmes, exposure to standard bench-top computational tools and the web

TEACHING METHODS/APPROACH

The lectures will be complemented by tutorials and self-study.

BOOKS & OTHER SOURCES USED

Introduction to Linux – A Hand on Guide by Machtelt Garrels (tldp.org/LDP/intro-linux/intro-linux.pdf)

COURSE CONTENT

1. What is Linux?
2. How to install an operating system
3. Quick start
4. About files and file systems
5. Processes
6. I/O redirection
7. Text editors
8. Home
9. Printers and printing
10. Fundamental backup systems
11. Networking
12. Installation of various programs

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ASSESSMENT ACTIVITIES AND THEIR WEIGHTS

1. Test 1: 40%
2. Test 2: 60%

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INTRODUCTION TO PROGRAMMING

Lecturer: Dr. Denis Pollney

Contact hours: 10

This is an introductory module to prepare students for programming. Students will not be examined on this module.

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MATHEMATICS – PART 1: (INTRODUCTION TO MATHEMATICS WITH BIOLOGICAL APPLICATIONS)

Lecturer: Prof Mike Burton

Contact hours: 10

SPECIFIC OUTCOMES ADDRESSED

1. Describe biological/bioinformatics problems using mathematics.
2. Solve these problems using calculus, linear algebra.
3. Acquire background for Matlab and Statistics courses

BACKGROUND KNOWLEDGE REQUIRED

Basic calculus, algebra, linear algebra

TEACHING METHODS/APPROACH

The lectures will be complemented by self-study and tutorials.

BOOKS & OTHER SOURCES USED

Lecture notes

Any Calculus, Linear Algebra books

COURSE CONTENT

1. Calculus (Differentiation and integration)
2. Linear Algebra (Matrices, eigenvalue / eigenvector problems)

ASSESSMENT ACTIVITIES AND THEIR WEIGHTS

1. Assignment 1: 25%
2. Assignment 2: 25%
3. Test: 50%

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BIOTECHNOLOGY**

MSc PROGRAMME OUTLINE		
MSc in Bioinformatics and Computational Molecular Biology		
Course Work / Project Masters	Year: 2013	Coordinators: Prof Mike BURTON (January – June 2013) and Dr Özlem TAŞTAN BISHOP (July – December 2013)

PYTHON AND BIOPYTHON

Lecturer: Gustavo Salazar

Contact hours: 75

SPECIFIC OUTCOMES ADDRESSED

1. To be able to write short Python program to manipulate data
2. To understand the differences between numbers, strings, lists and arrays
3. To master the use of various control structures and functions within Python program
4. To understand the concepts of the Object Oriented paradigm and how to use it in python
5. To retrieve and manipulate data from databases and files
6. To use the most common procedures in Biopython

BACKGROUND KNOWLEDGE REQUIRED

Basic computer literacy: proficiency with word-processing, spreadsheets and graphics programmes, exposure to standard bench-top computational tools and the web

TEACHING METHODS/APPROACH

Lectures: utilizing self-study tutorials and demonstration programmes
Numerous small exercises to build up experience and skills progressively

BOOKS & OTHER SOURCES USED

Python documentation: <http://docs.python.org/index.html>

Biopython <http://biopython.org/wiki/Biopython>

COURSE CONTENT

1. Introduction to Python (Thinking, writing and running)
2. Flow Control
3. Data Structures
4. Strings in Depth
5. Functions
6. Importing Standard Modules
7. Files for Input and Output
8. Regular Expressions
9. Basic Parsing
10. Exceptions and error handling
11. Recursion
12. Classes and Objects
13. Database Theory and Relational Databases
14. Biopython

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15. Graphical User Interfaces

ASSESSMENT ACTIVITIES AND THEIR WEIGHTS

1. Test: 30%
2. Mini-project: 30%
3. Assignments: 40%

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BASIC GENOMICS – PART 1

Lecturer: Candice Ryan

Contact hours: 25

SPECIFIC OUTCOMES ADDRESSED

1. Ability to retrieve data from databases and analyse the data
2. To be able to align homologous sequences in DNA or protein format and understand the advantages and disadvantages of the two approaches
3. Understand various alignment algorithms

BACKGROUND KNOWLEDGE REQUIRED

Basic biochemistry and genetics knowledge.

TEACHING METHODS/APPROACH

The lectures will be complemented by tutorials, self study and article discussions.

BOOKS & OTHER SOURCES USED

1. Essential Bioinformatics by Jin Xiong
2. Introduction to bioinformatics by Anna Tramontano
3. Bioinformatics – A practical guide to the analysis of genes and proteins by Andreas Baxevanis and Francis Ouellette
4. Research articles and other bioinformatics books in the library

COURSE CONTENT

1. Biological databases
2. Sequence alignment
 - a. Pairwise sequence alignment
 - b. Database similarity search
 - c. Multiple sequence alignment
 - d. Profiles and HMMs

ASSESSMENT ACTIVITIES AND THEIR WEIGHTS

1. Assignment 1: 25%
2. Assignment 2: 25%
3. Test: 50%

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BASIC GENOMICS – PART 2

Lecturer: Prof Philip Machanick

Contact hours: 10

SPECIFIC OUTCOMES ADDRESSED

Understanding how DNA is computationally analysed for features of interest, including but not limited to transcription factor binding sites.

BACKGROUND KNOWLEDGE REQUIRED

Role of DNA in genetics, basic understanding of developmental biology.

TEACHING METHODS/APPROACH

Lecturing, demonstrating techniques and problem-solving.

BOOKS & OTHER SOURCES USED

Web searches and academic literature.

COURSE CONTENT

1. Transcription factors and DNA sequence analysis
2. Coding and non-coding DNA
3. Conservation and its role in sequence analysis
4. Use of the UCSC genome browser
5. Other web-based tools for sequence analysis

ASSESSMENT ACTIVITIES AND THEIR WEIGHTS

1. Assignment 1: 20%
2. Assignment 2: 30%
3. Write short paper: 50%

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PHYLOGENETIC ANALYSIS

Lecturer: Dr Jane Wright

Contact hours: 25

SPECIFIC OUTCOMES ADDRESSED

Basic understanding of phylogenetic methods and evolutionary models. Use of various phylogenetic software.

BACKGROUND KNOWLEDGE REQUIRED

Basic computer literacy and a basic knowledge of genetics, DNA and proteins.
Database mining.

TEACHING METHODS/APPROACH

Workshops comprising presentations, demonstration of software and computer exercises.

BOOKS & OTHER SOURCES USED

Molecular Evolution: A Phylogenetic Approach by Rod Page & Eddie Holmes
Inferring Phylogenies by Joseph Felsenstein
Molecular Evolution and Phylogenetics by Nei and Kumar
Molecular Systematics by David M. Hillis
Phylogenetic Trees Made Easy: A How-to manual by Barry G.Hall
Web searches and research articles.

COURSE CONTENT

1. Overview of phylogenetics.
2. Distance analysis.
3. Bootstrap analysis.
4. Maximum likelihood analysis.
5. Bayesian inference.

ASSESSMENT ACTIVITIES AND THEIR WEIGHTS

1. Assignment 1: 25%
2. Assignment 2: 25%
3. Test: 50%

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STRUCTURAL BIOINFORMATICS

Lecturer: Crystal Clitheroe

Contact hours: 25

SPECIFIC OUTCOMES ADDRESSED

1. To understand structural biology terminology, especially X-ray crystallography, and to be able to follow the literature
2. To learn how to use different protein visualization programs
3. To understand various secondary and tertiary structure prediction algorithms
4. To understand the range, applications and limitations of modeling methods
5. To learn modeling by using Modeller

BACKGROUND KNOWLEDGE REQUIRED

1. Knowledge on biochemical properties of amino acids
2. Basic understanding of the primary, secondary, tertiary and quaternary structure of proteins.
3. Knowledge on non-covalent bond formations

TEACHING METHODS/APPROACH

The lectures will be complemented by tutorials, self study and article discussions.

BOOKS & OTHER SOURCES USED

1. Essential Bioinformatics by Jin Xiong
2. Introduction to bioinformatics by Anna Tramontano
3. Bioinformatics – A practical guide to the analysis of genes and proteins by Andreas Baxevanis and Francis Ouellette
4. Manuals and tutorials of various modeling and visualization programs

COURSE CONTENT

1. Structural biology techniques
2. Protein visualization programs
3. Protein secondary structure prediction
4. Protein tertiary structure prediction
5. Homology modeling; Modeller

ASSESSMENT ACTIVITIES AND THEIR WEIGHTS

1. Assignment: 20%
2. Short project: 40%
3. Test: 40%

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COMPARATIVE GENOMICS

Lecturer: Prog Oleg Reva

Contact hours: 25

SPECIFIC OUTCOMES ADDRESSED

1. To understand opportunities, challenges and possible pitfalls of comparison of complete genomes;
2. To get known available resources (databases and open source programs);
3. To learn how to use different genome comparison programs;
4. To understand the concepts of genomic polymorphism; gene homology; genomic evolution and horizontal gene transfer;
5. To gain practical skills in using genome comparison programs and techniques.

BACKGROUND KNOWLEDGE REQUIRED

1. Basic knowledge of genetics of eukaryotes and prokaryotes.
2. Basic computer skills on Windows PC.

TEACHING METHODS/APPROACH

The lectures will be complemented by tutorials.

BOOKS & OTHER SOURCES USED

1. Analysis of genes and genomes by Richard J. Reece;
2. Bioinformatics – a practical guide to the analysis of genes and proteins by Andreas Baxevanis and Francis Ouellette;
3. Systems and computational biology – molecular and cellular experimental systems by Ning-Sun Yang;
4. Manuals and tutorials of various modeling and visualization programs.

COURSE CONTENT

1. Introduction to genome alignment approaches;
2. Introduction to the concepts of genome polymorphism;
3. Introduction to genome evolution and horizontal gene transfer;
4. Introduction to phylogenomics;
5. Selection and use of various software tools for comparative genomics: practical course.

ASSESSMENT ACTIVITIES AND THEIR WEIGHTS

1. Assignment: 40%
2. Test: 60%

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MATHEMATICAL PROGRAMMING WITH MATLAB

Lecturer: Prof Mike Burton

Contact hours: 15

SPECIFIC OUTCOMES ADDRESSED

1. Introduction to mathematical programming with MATLAB.
2. Solve problems using mathematical programming.

BACKGROUND KNOWLEDGE REQUIRED

Matrix algebra, basic calculus.

TEACHING METHODS/APPROACH

Lectures will be mainly in the form of demonstrations of MATLAB features, with discussion. Relevant notions from various aspects of mathematics will be discussed as necessary. At each lecture a set of exercises will be presented, which students should complete and submit by the next lecture.

BOOKS & OTHER SOURCES USED

Course notes.

Essential MATLAB for Scientists and Engineers, B Hahn, Pearson, 3 rd edition ISBN 1 868 91143 82

COURSE CONTENT

The purpose of the course is to enable the student to construct a computational environment with MATLAB in which to model, study and simulate real-world processes. It is intended that the student learn this skill by hands-on experience with the computer. The lectures are meant to provide an overview and a forum for discussion. The exercises are there to provide practical experience. Most of the real learning will be accomplished by doing the exercises.

1. Introduction to the MATLAB environment; programming in MATLAB: statements, data structures, input / output, flow control, functions, graphics
2. Linear algebra with MATLAB and maxima: systems of equations, over-determined systems and linear regression, eigenvalues and eigenvectors
3. Other applications of MATLAB: differentiation, integration, solving nonlinear equations and differential equations.

ASSESSMENT ACTIVITIES AND THEIR WEIGHTS

1. Assignment 1: 20%
2. Assignment 2: 20%
3. Project: 60%

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INTRODUCTORY STATISTICS

Lecturer: Mr. Jeremy Baxter

Contact hours: 25

SPECIFIC OUTCOMES ADDRESSED

The aims of this course are:

1. To provide students with the basics of probability theory (probability, probability axioms, conditional probability, probability density function, cumulative distribution function, expectation, variance, discrete random variable, continuous random variable) and statistical background, concepts and techniques (statistical experiment, descriptive statistics, inference statistics) that are most useful to Bioinformaticians.

On completion of the course students should, inter alia, be able to:

1. Explain the differences between a population and a sample.
2. Collect, summarise and describe data using suitable numerical and graphical techniques.
3. Explain the concepts of probability, interpret probabilities and use suitable theory to calculate simple and conditional probabilities.
4. Identify discrete and continuous probability distributions.
5. Demonstrate the use of the binomial, Poisson, normal, Student t, chi-square and F distributions.
6. Calculate point and interval estimates, one- and two-sample, for the population mean(s), proportion(s) and variance(s) and interpret the meaning of each.
7. Perform suitable hypothesis tests (parametric and or non-parametric procedure) for one- and two-sample analyses and draw meaningful conclusions and decisions for the population mean(s), proportion(s) and variance(s).
8. Estimate, interpret and make predictions using linear models. Perform suitable statistical inference and model diagnostics for linear models.

BACKGROUND KNOWLEDGE REQUIRED

1. Basic Calculus: Differentiation and integration
2. Linear algebra: Matrices, vectors
3. Matlab literacy, specifically matrix operations.
4. Basic programming experience, in python or perl

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TEACHING METHODS/APPROACH

This course will be taught using formal lectures, typically in the morning, and self-study tutorials and practicals. Use of hand-outs, notes, text books, board-work and overheads. Relevant notions from linear algebra and statistics will be discussed and the student will then be required to read portions of prescribed texts on his/her own. At each lecture a set of exercises will be presented and completed ready for assessment by the next lecture.

BOOKS & OTHER SOURCES USED

1. J Baxter, Introductory Statistics for Bioinformaticians using R (course notes/slides).
2. Wim P. Krijnen, 2009, Applied Statistics for Bioinformatics using R, CRAN

COURSE CONTENT

1. A brief introduction to R.
2. Descriptive statistics (Graphical and numerical summaries of univariate, bivariate and multivariate data).
3. An introduction to statistical distributions.
4. Estimation and inference for one/ two random samples (Parametric and non parametric methods.)
5. An introduction to correlation, linear regression and linear models: (One and Two Way ANOVA)

ASSESSMENT ACTIVITIES AND THEIR WEIGHTS

1. Daily assignments/exercises: 40%
2. Tests: 60%

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NEURAL NETWORK

Lecturer: Prof Mike Burton

Contact hours: 25

SPECIFIC OUTCOMES ADDRESSED

1. The ability to construct and deploy perceptrons in the MATLAB environment.
2. A knowledge of their limitations.
3. The ability to construct and deploy feed-forward neural networks in the MATLAB environment.
4. The ability to modify the architecture of a neural network to improve performance while preserving generalisation properties.
5. The ability to pose a prediction or pattern-recognition problem as a neural network problem.

BACKGROUND KNOWLEDGE REQUIRED

1. Multivariate calculus: gradient, total differential.
2. Linear Algebra: matrix manipulation, inverses, transpose, eigenvalues.

TEACHING METHODS/APPROACH

1. Power Point presentations.
2. A full set of notes.
3. Computer exercises.
4. A wide range of research-level problems

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BOOKS & OTHER SOURCES USED

1. Haykin, S., (1998), Neural Networks: A Comprehensive Foundation, 2 nd. ed., Prentice Hall.
2. Zupan, J., Gasteiger, J., (1999), Neural Networks in Chemistry and Drug Design, Wiley.
3. Baughman, D. R., (1995), Neural Networks in Bioprocessing and Chemical Engineering, Academic Press.
4. Jain, L., Vemuri, V. R., (1999), Industrial Applications of Neural Networks, CRC.
5. VerDuin, W., (1995), Better Products Faster, Irwin.
6. Hagan, M. T., Demuth, H. B., Beale, (1995), M., Neural Network Design, PWS Publishing.
7. Patterson, D., W., (1996), Artificial Neural Networks-- Theory and Applications, Simon and Schuster.
8. Reed, R., Marks, R. J., (1999), Neural Smithing, Bradford.
9. Skapura, (1995), D., Building Neural Networks, ACM.
10. Beale, R., Jackson, J., (1990), Neural Computing -- An Introduction, IOP Publishing.
11. Wu, C. H., McLarty, J. W., (2000), Neural Networks and Genome Informatics, Methods in Computational Biology and Biochemistry, Konopka, A. K., (ed). Elsevier.

COURSE CONTENT

1. Biological background: biological neural networks.
2. Perceptrons: construction and deployment.
3. Convergence of perceptrons.
4. Limitations of perceptrons.
5. Gradient descent techniques for optimization.
6. Backpropagation.
7. General feed-forward artificial neural networks: construction and deployment.
8. Various training methods.
9. Various applications to prediction and pattern-recognition problems.

ASSESSMENT ACTIVITIES AND THEIR WEIGHTS

1. Exercises from the notes: 20%
2. Projects to be solved and submitted: 40%
3. Examination problem: 40%

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