

بِسْمِ اللَّهِ الرَّحْمَنِ الرَّحِيمِ
National University- Sudan
Faculty of Medicine

1. **Program Title:** MSc. in Bioinformatics.
2. **Degree to be award:** Master of Science: Bioinformatics
الماجستير في المعلوماتية الحيوية
3. **Total Credit Hours:** 45 Credit hours.
4. **Duration of program:** 3 semesters (16 weeks each).
5. **Final Program evaluation:**
 - a. Feedback of students.
 - b. External examiner.
 - c. Teacher's feedback.
6. **Methods of assessment:**
 - Continuous assessment: 30 %
 - Final examination: 70%
7. **Teaching Language:** English.
8. **Required number of seats:** 150 seats.
9. **Teaching Modules:**

Lectures, tutorials, presentations, seminars, assignments and practical sessions.
10. **Admission requires:**

Applicants must satisfy the general regulations set by the collage of graduate studies and scientific research of the National University –Sudan for registration for master degrees. Hold honors B.Sc from recognized University in: Science, Biotechnology, Agriculture, Medicine, Veterinary Science, Pharmacy, Laboratory medicine of sciences and Dentistry.

11. Career Opportunities:

The MSc programme in Bioinformatics qualifies student to become professionals within area such as:

1- A Phd programme.

2- Research Institutions, public and private and in universities.

12. Syllabus Committee : اللجنه المشاركه في اعداد البرنامج :

1- Prof . Awad Haj Ali (Professor/Computer Science).

2- Dr. Rihab Ali Omer (Associated Professor/ Molecular biology).

3- Dr. Hoida Abed Algader (Associated Professor/Speech Recognition).

4- Dr. Sofia Bashir Mohamed (PhD/Molecular biology).

5- Dr. Mariatulqabtiah Binti Abdul Razak (PhD/ Clinical Medicine Research).

6- Dr. Mohammed Abdelgader (PhD/Medical chemistry).

7- Dr. Wafaa Faisal Mukhtar (Phd/ Data Mining).

8- Dr. Mushal Allam Mohamed Alhaj Ali (Bioinformatics Scientist).

9- Dr. Mohammed Albashir Mohammed (Information Technology).

10- Dr. Abdel wahed Motwakel Eltayeb Ismaeil (Computer Science).

Introduction

Bio-Informatics is where computer science and biology join to address and solve basic problems associated with human health, environment and agriculture. Recent developments in the sciences have produced a wealth of experimental data of sequences and three-dimensional structures of biological macromolecules. With the advances of computer and information science, variety of databases is made available to the public on the internet. This master program aims at providing the learner with the required know-how for developing and using tools in bioinformatics. It integrates disciplines as varied as biochemistry, cell biology to computer programming and algorithms. Above all it gives a choice in career paths as the training provided to graduates will enable them to work in many different fields such as medical research, drug discovery, veterinary labs, agricultural research, food safety, agricultural biotechnology and biodiversity

2. General Objective

Avail:

- Apt Bioinformatics knowledge for interpretation of the rapidly expanding biological information.
- Basic concepts of bioinformatics to identify, seek, establish, maintain and exchange research information in biology.

3. Specific Objectives

Equip the students with:

- Requisite background in modern biology, Biochemistry, Cell biology, Genetics and Molecular Biology.
- Familiarity in computational methods to address problems in molecular biology.
- Knowledge on storage, retrieval, sharing and use of biological information in core areas of Bioinformatics: multiple sequence alignment, Phylogenetic trees, Genomics, Proteomics etc.
- Skills in applied Bioinformatics: Immunoinformatics, Drug designing and discovery.

4. Learning Outcomes:

Upon successful completion of the program, the successful candidates should be able to:

- Identity strategies and apply appropriate tools in Bioinformatics.
- Identify topical problems drawn from ongoing research and their applications

- Interpret data related to sequences of nucleotides and amino acids, Protein domains and protein structures.
- Develop and implement tools that enable efficient access and management of data.
- Acquire the essential programming skills.
- Demonstrate an understanding of the algorithms used in Bioinformatics

5. Study Program:

Semester One

Code	Name	Credit hours	Contact hours/week	
			Theory	Practical
BIO-611	Basic Molecular Biology اساسيات الاحياء الجزيئية	3(2+1)	2	2
BIO-612	Introduction to Proteomics مقدمة في البروتين	3	3	-
BIO-613	Object Oriented programming البرمجة الشيئية	3(2+1)	2	2
BIO-614	Database Management System نظام إدارة قواعد البيانات	2(1+1)	1	2
BIO-615	Fundamental of Algorithm أساسيات الخوارزمية	2(1+1)	1	2
Total		13	9	8

Semester Two

Code	Name	Credit hour	Contact hours/week	
			Theory	Practical
BIO-621	Fundamental of Bioinformatics اساسيات المعلوماتية الحيوية	3(1+2)	1	4
BIO-622	Computational Structural Biology علم الأحياء الهيكلية الحاسوبية	4(2+2)	2	4
BIO-623	Alignment and Sequences Analysis المقارنه و تحليل السكونس	3(2+1)	2	2
BIO-624	Data Mining and machine learning استخراج البيانات والتعلم الآلي	4(2+2)	2	4
BIO-625	Biostatistics الاحصاء الحيويه	3(2+1)	2	4
Total		17	9	18

Semester Three

Code	Name	Credit hours	Contact hours/week	
			Theory	Practical
BIO-631	Immunoinformatics المعلوماتية المناعية	4(2+2)	2	4
BIO-632	Molecular Modeling and Drug Design التصميم الجزيئي و الدوائي	4(2+2)	2	4
BIO-633	Research Methodology طرق البحث العلمي	3(3+0)	3	0
BIO-634	Research Paper البحث عن طريق الورقة العلمية	4(0+8)	0	8
Total		15	7	16

Semester One

Course Title: Basic Molecular Biology

Course Code: BIO-611

Credit hours: (3) hours

Duration: 3 weeks

Intended students: Semester: 1 (Master) / Batch No.: 1

Course Coordinator: Sofia Bashir Mohamed.

Prerequisites: Knowledge in Biochemistry, Molecular biology, Computer skills

Rationale:

Molecular biology dealing with nucleic acids and proteins and how these molecules interact within the cell to promote proper growth, division, and development. It is a large and ever-changing discipline. This course will emphasize the molecular mechanisms of DNA replication, repair, transcription, splicing, protein synthesis, and gene regulation in different organisms. In addition, the course will give an in-depth look at some rapidly evolving fields, including chromatin structure and function, genome editing techniques, back splicing, and regulation of gene expression by different types of RNAs.

Course outcomes:

By the end of the course, students are expected to:

1. Explain and give examples of how ionic, hydrophobic, and hydrogen bonding interactions determine the structure of nucleic acids and proteins and modulate the specificity of binding between them.
2. Give a particular biological question; identify which experimental techniques are best used to answer that question.
3. Recognize the cell organelles and their functions and identify differences between prokaryotic and eukaryotic cells.
4. Explain cell cycle steps and events; DNA structure, function and replication; RNA structure, function, transcription and reverse transcription; genetic code; protein synthesis; gene expression and cell signaling.
5. Understand and explain different types of mutations.

Course contents:

- 1- Genome organization.
- 2- DNA Structure; Replication; Repair & Recombination
- 3- Prokaryotic & Eukaryotic Transcription.
- 4- Post Transcriptional Modifications
- 5- Translation & Transport
- 6- Mutations; Oncogenes and Tumor suppressor genes

Practical of Molecular biology:

- DNA Extraction by different methods.
- RNA Extraction.
- Polymerase Chain Reaction.
- Real Time PCR.
- RFLP.
- Gel Electrophoresis.
- DNA sequencing (Demonstration).

Educational Strategies and Methods:

Lectures, Tutorial, Group work, Seminars

Evaluation and Assessment Methods (%):

Continuous assessment 30 %

Final exam (written (MCQs & structured questions + practical) 70 %.

Required Resources (in details):

Lecture room.. Staff (Associate Professor and Assistant Professor).

References:

Turner, P.C., Turner, M. and Bates, W. (2000) Instant notes in molecular biology. 2nd edn. New York: Garland Publishing.

Sambrook, J., Sambrook, J., Fritsch, E.F. and Maniatis, T. (1987) Molecular cloning: A laboratory manual. 2nd edn. United States: Cold Spring Harbor Laboratory Press, U.S.

Starr, C., Taggart, R. and Taggart, L. (2005) Cell biology and genetics (with 1pass for Biology Now, vMentor, how do I prepare, iLrn, and InfoTrac), Vol. 1. 11th edn. United States: Thomson/Brooks Cole.

Lodish, H., Darnell, J.E., Berk, A., Matsudaira, P., Kaiser, C.A. and Krieger, M. (2003) Molecular cell biology. 6th edn. New York: Freeman, W. H. & Company.

Course Title: Introduction to Proteomics

Course Code: BIO-612

Credit hours: (3) hours

Duration: 3 weeks

Intended students: Semester: 1 (Master) / Batch No.: 1

Course Coordinator: Sofia Bashir Mohamed.

Prerequisites: Knowledge in Biochemistry

Rationale:

This course introduces to the basic biology of proteins and the new advanced science called as proteomics which aims to look into the protein properties from a global perspective

Course outcomes:

By the end of the course, students are expected to:

Fundamental knowledge in proteomics.

Course contents:

- 1- Protein structure and function
 - Amino acids and their properties.
 - Amino acids form polypeptides.
 - Protein structure – four levels of organization.
 - Cellular functions performed by protein.
- 2- Protein folding & misfolding
- 3- Protein-protein interaction

Educational Strategies and Methods:

Lectures, Tutorial, Group work, Seminars

Evaluation and Assessment Methods (%):

Continuous assessment 30 %

Final exam (written (MCQs & structured questions + practical) 70 %.

Required Resources (in details):

Lecture room. Computer lab. Staff (Associate Professor and Assistant Professor).

References:

Nature Insight: Proteomics. Nature 422: 191-237.

Zhu, H. *et al.* Proteomics. Annual Review of Biochemistry 72: 783-812.

Griffiths *et al.* Modern Genetic Analysis. Online: <http://ncbi.nih.gov>

Course Title: Object Oriented programming

Course Code: BIO-613

Credit hours: Hours (3)

Duration: 3 weeks

Intended students: Semester: 1 (Master) / Batch No.: 1

Course Coordinator: Sofia Bashir Mohamed

Prerequisites:

Bioinformatics

Rationale:

This is an introductory course designed for any student interested in using computation to enhance their problem solving abilities. No prior experience in programming is necessary. Students will use their problem solving abilities to implement programs in Java and Python.

Course out comes:

By the end of the course, students are expected to:

- Demonstrate the application of Python and Java in distributed computing and database technologies.
- Explain the difference between event-driven programming and command-line programming.
- Design, code, test, and debug simple event-driven programs that respond to user events.
- Develop code that responds to exception conditions raised during execution.
- Understand multithreading concepts and how to apply them in the Java environment.

Course contents:

- 1- Java Basics
- 2- Multithreading and Communication AWT & Event Handling
- 3- BioJava
- 4- Introduction to scripting with python.
- 5- Writing python scripting.
- 6- Making plot with matplotlib

7- Scientific computing with python

8- Data clustering and classification.

9- Searching and sorting.

Educational Strategies and Methods:

Lectures, Tutorial, Group work, Seminars

Evaluation and Assessment Methods (%):

Continuous assessment 30 %

Final exam (written (MCQs & structured questions + practical) 70 %.

Required Resources (in details):

Lecture room. Computer lab. Staff (Associate Professor and Assistant Professor).

Reference Books:

1. Computing Concepts with Java 2 Essentials (2nd Ed.) by Horseman, C.S., John Wiley Publishers. 2000
2. Object Oriented Design and Applications (2nd Ed.) by Benjamin, Cummings and Brooch, G., Addison Wesley Publishers. 1994
3. Think Python: How to think like a Computer Scientist by Allen B. Downey <http://w.wow.greenteapress.com/thinkpython/thinkpython.html>

Course Title: Database Management System

Course Code: BIO-614

Credit hours: Hours (2)

Duration: 3 weeks

Intended students: Semester: 1 (Master) / Batch No.: 1

Course Coordinator: Sofia Bshir Mohamed

Prerequisites:

Bioinformatics

Course out comes:

By the end of the course, students are expected to

- Accomplish and identify both the principles and concepts of File Management and databases.
- Explain the characteristics, goals, functions, models, components, applications, and social impact of database systems.

- Describe the modeling concepts and notation of the entity-relationship model and UML, including their use in data modeling.
- Describe the main concepts of relational data model.
- Demonstrate queries in the relational algebra and relational calculus.
- Explain and demonstrate the concepts of entity integrity constraint and referential integrity constraint
- Prepare a relational schema from a conceptual model developed using the entity relationship model
- Explain the concepts of Physical database design

Course contents:

1. Introduction to Database Management System
2. Data models
3. Structured Query Language
4. Relational Database and Storage
5. Concurrency control techniques & Information retrieval

Educational Strategies and Methods:

Lectures, Tutorial, Group work, Seminars

Evaluation and Assessment Methods (%):

Continuous assessment 30 %

Final exam (written (MCQs & structured questions + practical) 70 %.

Required Resources (in details):

Lecture room. Computer lab. Staff (Associate Professor and Assistant Professor).

Reference books:

1. An Introduction to Database Systems (7th Ed.) by Date, C.J., Addison Wesley Publishers. 2000
2. Fundamentals of Database Systems (4th Ed.) by Elmasri and Navathe, Addison Wesley Publishers. 2004
3. Principles of Database Systems (2nd Ed.) by Ullman, J. D., Galgotia Publications. 2001

Course Title: fundamental of algorithms

Course Code: BIO-615

Credit hours: Hours (2)

Duration: 3weeks

Intended students: Semester: 1 (Master) / Batch No.: 1

Course Coordinator: Sofia Bashir Mohamed

Prerequisites:

Bioinformatics

Rationale:

Algorithm design and analysis provide the theoretical backbone of computer science and are a must in the daily work of the successful programmer. The goal of this course is to provide a solid background in the design and analysis of the major classes of algorithms.

Course out comes:

By the end of the course, students are expected to:

Will be able to develop their own versions for a given computational task and to compare and contrast their performance.

Course contents:

- 1- Computing Algorithms
- 2- Sorting, Searching & Strings Matching
- 3- Graphs
- 4- Trees
- 5- Algorithm Design and Analysis.

Educational Strategies and Methods:

Lectures, Tutorial, Group work, Seminars

Evaluation and Assessment Methods (%):

Continuous assessment 30 %

Final exam (written (MCQs & structured questions + practical) 70 %.

Required Resources (in details):

Lecture room. Computer lab. Staff (Associate Professor and Assistant Professor).

Reference:

- 1- Fundamentals of Algorithms by E. Horowitz and S. Sahani., Galgotia Book source Pvt. Ltd. 1999
- 2- Data Structures by Seymour Lipschutz., Tata Mc-Graw-Hill publication. 2007
- 3- Introduction to Algorithms (3rd Ed.) by T .H. Cormen, C. E. Leiserson, R .L. Rivest., The MIT Press. 2007

Semester Two

Course Title: Fundamental of Bioinformatics

Course Code: BIO-621

Credit hours: (3) Hours

Duration: 3 weeks

Intended students: Semester: 2 (Master) / Batch No.: 1

Course Coordinator: Sofia Bashir mohamed

Prerequisites:

Molecular biology and computer skill

Rationale:

Introduce the basics, models and applications of different biological sequence describe the database designing concepts and the languages used to describe the widely used relational database model and biological sequence databases.

Course outcomes:

By the end of the course, students are expected to:

- Equip the students with the requisite background in areas of modern biology (Biochemistry, cell biology, genetics and molecular biology) and computer science (Programming languages, databases, algorithms, graphics, data mining, data Security, etc.).
- Gain familiarity with computational methods in order to address problems in Molecular biology.
- Become knowledgeable about the storage, retrieval, sharing and use of biological data, information, and tools.

Course contents:

- 1- Introduction to Bioinformatics:
- 2- Bioinformatics Resources
- 3- Open access bibliographic resources and literature databases

- 4- Databases
- 5- Bioinformatics Softwares and tools
- 6- Sequence file formats
- 7- Protein and nucleic acid sequence
- 8- Submitting DNA Sequence to the Database
- 9- Taxonomy and phylogeny
- 10- Sequence patterns and profiles

11- Bioinformatics database and tools practical :

- 1. Entrez and Literature Searches.
 - a. PubMed
 - b. PubMed central
 - c. OMIM / OMIA
 - d. Citation matcher
- 2. SRS of Biological Databases
 - a. Nucleotide/ Genome Databases.
 - b. Protein Sequence Database.
 - c. Structure databases.
 - d. Protein Pattern Databases
- 3. File format conversion
 - a. FmtSeq
 - b. ReadSeq
- 6. Sequence file formats: GenBank, FASTA
- 7. Protein and nucleic acid properties: Proteomics tools at the ExPASy server, EMBOSS
- 8. Softwares
 - a. BioEdit.
 - b. GeneDoc
 - c. ClustalW / X, MEGA, MEME

Educational Strategies and Methods:

Lectures, Tutorial, Group work, Seminars

Evaluation and Assessment Methods (%):

Continuous assessment 30 %

Final exam (written (MCQs & structured questions + practical) 70 %.

Required Resources (in details):

Lecture room. Computer lab. Staff (Associate Prof and Lecturer).

References:

1. Introduction to Bioinformatics, (Atwood, T. K. and Parry-Smith, D. J).
2. An introduction to Computational Biochemistry. (C. Stain Tsai, A. John Wiley and Sons, Inc., publications).

Course Title: Computational Structural Biology

Credit hours: Hours (4)

Course Code: BIO-622

Duration: 4 weeks

Intended students: Semester: 2 (Master) / Batch No.: 1

Course Coordinator: Sofia Bashir Mohamed

Prerequisites:

Bioinformatics

Rationale:

To acquire information from biological databases. Use of computational approaches to analyze this information. To interpret the results as a guide to experiments in Biology, and use advance software to analysis different type of SNPs.

Course out comes:

By the end of the course, students are expected to:

- Evaluate the results from different types of sequence-based analyses such as relations of homology based on primary sequence, domain comparisons, profile- or secondary structure analyses and 3D structure of protein
- Design PCR Primers by software.
- A apply some areas of Bioinformatics like Protein-protein interaction, drug design, metabolic pathway engineering etc.
 - Be able to pursue project work in an identified area of Bioinformatics.

Course contents:

- 1- Prediction of genes.
- 2- Primer Design.
- 3- Proteomics.
- 4- Xray Crystallography.
- 5- Predicting Protein structure and function from sequence
- 6- Structure Prediction Strategies – Secondary structure prediction.
- 7- Protein modeling.
- 8- Classification and comparison of protein 3D structures.
- 9- Protein –Protein Interaction.
- 10- Basic concepts on identification of disease genes (SNP).

11- Bioinformatics Practical:

- Proteomics tools at the ExPASy server.
- Primer analysis using OLIGO, Primer3
- SNP database (dbSNP) and Software.
- ORF finding database and software.
- Secondary structure predicated tool.
- Structure visualization using Chimera.
- Evaluation of protein structure by Swiss PDB viewer and by other molecular visualization tools.
- Homology modeling of a given protein sequence.
- Active site and ligand predication software.

Educational Strategies and Methods:

Lectures, Tutorial, Group work, Seminars

Evaluation and Assessment Methods (%):

Continuous assessment 30 %

Final exam (written (MCQs & structured questions + practical) 70 %.

Required Resources (in details):

Lecture room. Computer lab. Staff (Associate Professor and Assistant Professor).

References:

1. Claverie, J.M. and Notredame C. 2003 Bioinformatics for Dummies. Wiley Editor.
2. Letovsky, S.I. 1999 Bioinformatics. Kluwer Academic Publishers.
3. Baldi, P. and Brunak, S. 1998 Bioinformatics. The MIT Press.

4. Setubal, J. and Meidanis, J. 1996 Introduction to Computational Molecular Biology. PWS Publishing Co., Boston.

Course Title: Alignment and sequences analysis

Course code: BIO-623

Credit hours: Hours (3)

Duration: 3 weeks

Intended students: Semester: 2 (Master) / Batch No.: 1

Course Coordinator: Sofia Bashir Mohamed

Prerequisites:

Bioinformatics

Rationale:

To learn how to analyze s sequences and increase the knowledge about alignment and algorithms. Use of computational approaches to phylogeny and taxonomy information.

Course out comes:

By the end of the course, students are expected to:

- Understand the theoretical basis behind Alignment.
- launch the students into core areas of Bioinformatics like multiple sequence alignment and Phylogenetic trees.
- Manipulate DNA and protein sequences using software and tool available on the internet.

Course contents:

- 1- Sequence Analysis
- 2- Scoring matrices
- 3- Pairwise sequence alignments.
- 4- Multiple sequence alignments (MSA).
- 5- Comparative Genomics
- 6- Sequence patterns and profiles
- 7- Algorithms for derivation and searching sequence patterns

8- Taxonomy and phylogeny

9- BIOSEQUENCE ANALYSIS Practical:

1. Sequence Analysis Packages: EMBOSS, NCBI ToolKit, SMS

2. Pair wise alignment:

a. Search tools against Databases:

i. BLAST

ii. FASTA

3. Multiple sequence alignment:

a. Clustal

b. Dialign

c. Multalign

4. Sequence patterns and profiles:

a. generation of sequence profiles

i. PSI-BLAST

b. derivation of and searching sequence patterns:

i. MEME/MAST

ii. PHI-BLAST

iii. SCanProsite

iv. PRATT

5. Protein motif and domain analysis:

a. MEME/MAST

b. eMotif

c. InterproScan

d. ProSite

e. ProDom

f. Pfam

6. Phylogenetic analysis – MEGA, PAUP, PHYLIP.

Educational Strategies and Methods:

Lectures, Tutorial, Group work, Seminars

Evaluation and Assessment Methods (%):

Continuous assessment 30 %

Final exam (written (MCQs & structured questions + practical) 70 %.

Required Resources (in details):

Lecture room. Computer lab. Staff (Associate Professor and Assistant Professor).

References:

1. Bioinformatics: Sequence and Genome Analysis by Mount D., Cold Spring Harbor Laboratory Press, New York. 2004
2. Bioinformatics- a Practical Guide to the Analysis of Genes and Proteins by Baxevanis, A.D. and Francis Ouellette, B.F., Wiley India Pvt Ltd. 2009

Course Title: Data Mining and Machine Learning

Course Code: BIO-624

Credit hours: Hours (4)

Duration: 4 weeks

Intended students: Semester: 2 (Master) / Batch No.: 1

Course Coordinator: Sofia Bashir Mohamed

Course out comes:

By the end of the course, students are expected to:

1. Understand Data Warehouse and OLAP technology for data mining: Data preparation, data mining primitives, languages, and system architectures.
2. Make mining association with rules in large databases, do classification and prediction (with various techniques: Cluster analysis, neural nets, and genetic algorithms.
3. Develop and understand data mining applications and trends of data mining,
4. Deal with warehousing strategy, warehouse management and support processes,
5. Have skills in data warehouse planning, data warehouse implementation, data warehouse maintenance and evolution,
6. Use some warehouse software related to some warehouse applications, and be acquainted with recent warehouse trends.

Course contents:

1. Introduction, Importance of Data Mining.

2. Primitives and System Architectures.
3. Concept Description and Association Rules.
4. Classification and Prediction.
5. Clustering Methods.

Educational Strategies and Methods:

Lectures, Tutorial, Group work, Seminars

Evaluation and Assessment Methods (%):

Continuous assessment 30 %

Final exam (written (MCQs & structured questions + practical) 70 %.

Required Resources (in details):

Lecture room. Computer lab. Staff (Associate Professor and Assistant Professor).

Reference:

1. Margaret H. Dunham "Data Mining: Introductory and Advanced Topics", Prentice Hall; 1st edition, 2002, ISBN: 0130888923.
2. M.Humphries, M.W.Hawkins, M. C.Dy. Harrys, "Data Warehousing: Architecture and Implementation", Prentice Hall, 1999, ISBN: 0130809020. 0262232138.

Course Title: Biostatistics

Credit hours: Hours (3)

Course Code: BIO-625

Duration: 3 weeks

Intended students: Semester: 2 (Master) / Batch No.: 1

Course Coordinator: Sofia BashirMohamed

Rationale:

Introduction to Biostatistics provides an introduction to selected important topics in biostatistical concepts and reasoning. This course represents an introduction to the field and provides a survey of data and data types. Specific topics include tools for describing central tendency and variability in data; methods for performing inference on population means and proportions via sample data; statistical hypothesis testing and its application to group comparisons; issues of power and sample

size in study designs; and random sample and other study types. While there are some formulae and computational elements to the course, the emphasis is on interpretation and concepts.

Course outcomes:

By the end of the course, students are expected to:

1. Recognize and give examples of different types of data arising in public health and clinical studies
2. Interpret differences in data distributions via visual displays, Calculate standard normal scores and resulting probabilities
3. Understand and interpret results from Analysis of Variance (ANOVA), a technique used to compare means amongst more than two independent populations
4. Understand why survival (timed to event) data requires its own type of analysis techniques
5. Construct a Kaplan-Meier estimate of the survival function that describes the "survival experience" of a cohort of subjects
6. Interpret the result of a log-rank test in the context of comparing the "survival experience" of multiple cohorts
7. Use SPSS/STATA package to
 - a. Perform two sample comparisons of means and create confidence intervals for the population mean differences
 - b. Compare proportions amongst two independent populations
 - c. Interpret output from the statistical software package STATA related to the various estimation and hypothesis testing procedures covered in the course

Course contents:

1. Introduction to biostatistics: significance and basic concepts.
2. Descriptive statistics: measures of central tendency and dispersion.
3. Introduction to Inference; Sampling Distribution and Confidence intervals
4. Sampling Variability, Confidence Intervals, and p-values for Means and Differences in Means
5. Sampling Variability and Confidence Intervals
6. An Introduction to Hypothesis Testing: The Paired t-Test
7. Comparing Means among Two (or More) Independent Populations
8. Measures of Association, Sampling Variability, Confidence Intervals and p-values for Binary Outcomes
9. Simple Linear Regression

10. Comparing Proportions Between Two Independent Populations
11. Non-parametric alternatives: Analysis of Variance
12. Analyzing categorical data: Goodness-of-fit and Contingency tables

Educational Strategies and Methods:

Lectures, Tutorial, Group work, Seminars

Evaluation and Assessment Methods (%):

Continuous assessment 30 %

Final exam (written (MCQs & structured questions + practical) 70 %.

Required Resources (in details):

Lecture room. Computer lab. Staff (Associate Professor and Assistant Professor).

References:

Biostatistics: A methodology for the Health Sciences (2004), Belle, G., Fisher, L., Heagerty, P., and Lumley, T., Wiley: New York.

Semester Three

Course Title: Immunoinformatics

Course Code: BIO-631

Credit hours: Hours (4)

Duration: 4 weeks

Intended students: Semester: 3 (Master) / Batch No.: 1

Course Coordinator: Sofia BashirMohamed

Prerequisites: Basic knowledge about immunology & bioinformatics

Rational:

Develops the concepts in molecular bacteriology and virology, identifying key targets for rational vaccine design, use of bioinformatics tools to determine immune responses of vaccines and assessment of efficacy, development of new generation vaccines, and regulation of vaccine production

Course out comes:

By the end of the course, students are expected to:

- Have knowledge of immune responses to various pathogens by integrating genomics and proteomics with bioinformatics strategies.
- Be proficient in computer aided vaccine design.

Course contents:

Section 1: Basic in Immunology

- 1- Introduction to Immunology
- 2- Antigens and Antibodies
- 3- Major Histocompatibility Complex
- 4- Disorders of Human Immune System.

Section 2: Immunoinformatics

- 1- Introduction to Immunoinformatics and Immunological Database
- 2- Computational vaccinology.

Educational Strategies and Methods:

Lectures, Tutorial, Group work, Seminars

Evaluation and Assessment Methods (%):

Continuous assessment 30 %

Final exam (written (MCQs & structured questions + practical) 70 %.

Required Resources (in details):

Lecture room. Computer lab. Staff (Associate Professor and Assistant Professor).

References:

- Immunoinformatics: Bioinformatic Strategies for Better Understanding of Immune (2008) Wiley Publications. ISBN: 978-0470853566.
- Predicting Immunogenicity In Silico Series (2013): Methods in Molecular Biology, Flower, Darren R. ISBN:978-1588296993.

Immunoinformatics – Practical

1- ONLINE TOOLS

- SOSUI-GRAMM
- VAXIJEN
- BLASTP
- SWISS MODEL
- PROCHECK
- BCPRED
- IEDB
- PATCHDOCK
- SOPMA

2- OFFLINE TOOLS

- MODELLER
- CHIMERA
- RASMOL
- CLC

Course Title: Molecular Modeling and Drug Design

Course Code: BIO-632

Credit hours: Hours (4)

Duration: 4weeks

Intended students: Semester: 3 (Master) / Batch No.: 1

Course Coordinator: Sofia Bashir Mohamed

Prerequisites:

Bioinformatics

Rationale:

This course will explore the process of drug development, from target identification to final drug registration. It will present drug development as a process involving target selection, lead discovery using computer-based methods and combinatorial chemistry/high-throughput screening. Safety evaluation, bioavailability, clinical trials, and the essentials of patent law will also be discussed. Along the way you will learn about molecular recognition, computer-aided drug design, and toxicology as applied to the development of new medicines

Course outcomes:

By the end of the course, students are expected to:

- be able to discuss the challenges faced in each step of the drug discovery process
- be able to describe the process of drug discovery and development
- have the basic knowledge of computational methods used in drug discovery
- be able to organize information into a clear report
- be able to demonstrate their ability to work in teams and communicate scientific information effectively

Course contents:

Section 1: Introduction to Organic Chemistry

- 1- Atomic and Molecular Structure
- 2- Chemical bonding
- 3- Conformational analysis
- 4- Stereochemistry
- 5- Heteroaromatics

Section 2: Molecular modeling and Drug design

- 1- Introduction to Drug Discovery and Development
2. Drug targets
3. Lead Identification and Modification
4. Computer-Aided Drug Design
5. Drug Delivery
6. Pre-clinical and Clinical Testing

Molecular Modeling and Drug Design Practical:

1. Molecular Visualization Softwares: Pymol and Rasmol
2. Geometry Optimization
4. Binding Site Identification
5. Structure based Drug Design(Molecular Docking)
6. Ligand based Drug Design:- QSAR

Educational Strategies and Methods:

Lectures, Tutorial, Group work, Seminars

Evaluation and Assessment Methods (%):

Continuous assessment 30 %

Final exam (written (MCQs & structured questions + practical) 70 %.

Required Resources (in details):

Lecture room. Computer lab. Staff (Associate Professor and Assistant Professor).

References:

1. Computational Chemistry and Molecular Modeling-Principles and Applications by Ramachandran, Deepa and Namboori. 2008, Springer_Verlag. Reference for Unit 1 and 2.

2. Molecular Modeling Principles and Applications (2nd Ed.) by Andrew R. Leach., Prentice Hall, USA. 2001

Course Title: Research Methodology.

Course Code: BIO- 633

Credit hours: Hours (3)

Duration: 3 weeks

Intended students: Semester: 2 (Master) / Batch No.: 1

Course Coordinator: Sofia BashirMohamed

Rationale:

The course is designed to impart education in the foundational methods and techniques of scientific research. Research scholars would examine and be practically exposed to the main components of a research framework i.e. Problem definition; Research design; Data collection; Ethical issues in research; in addition to different types of scientific writing.

Course out comes:

By the end of the course students are expected to be

well placed to conduct disciplined research under supervision in an area of their choice. In addition to their application in an academic setting, many of the methodologies discussed in this course would be similar to those deployed in professional research environments.

Course contents:

6- Foundations of research methodology and introduction to different types of research

- What is research?
- Finding research gaps, research topic
- Proposal writing
- Pilot studies
- Ethical considerations in Research
- Ways of data collection
- Obstacles in Research
- Scientific writing

Educational Strategies and Methods:

Lectures, Tutorial, Group work, Seminars

Evaluation and Assessment Methods (%):

Continuous assessment 30 %

Final exam (written (MCQs & structured questions + practical) 70 %.

Required Resources (in details):

Lecture room. Computer lab. Staff (Associate Professor and Assistant Professor).

References:

1. from Research to Manuscript: A Guide to Scientific Writing by Michael Jay Katz, by Springer. 2006
2. Writing and Presenting Scientific Papers, 2nd Edition by Brigitta Malmfors, Phil Garnsworthy and Michel Grossman, Nottingham University Press, 2004, Viva Books Pvt. Ltd. 2011
3. Scientific Writing- A Reader and Writer's Guide, by Jean Luc- Lebrun, World Scientific Publishers, 2007

Course Title: Research Paper

Course Code: BIO-634

Credit hours: Hours (4)

Duration: 7 weeks

Intended students: Semester: 3 (Master) / Batch No.: 1

Course Coordinator: Sofia Bashir Mohamed

Rationale:

The seminar will provide the students with the opportunity to present write and publish scientific manuscripts in bioinformatics. The students will read and present papers in frontier bioinformatics conferences, and in peer reviewed journals with high impact factor. This course will be an attractive venue for discussing recent breakthroughs and brainstorming of new research ideas.

Seminar in Bioinformatics I

This is a variable-content course that allows participants to be engaged in current research in bioinformatics and develops their own skills of oral presentations and scientific research.

Senior Project in Bioinformatics II

This course is the first part of a two-part series that allows students to work on a guided research project on a specific topic in bioinformatics. The goal of this course is for the student to decide on a research topic and to write a detailed proposal based on this topic that outlines the goals and objectives of the proposed research.

Senior Project in Bioinformatics III

This course is the second part of a two-part series that allows the student to work on a guided research project on a specific topic in bioinformatics. The goal of this course is for the student to perform the research proposed in Part I of the course and to present the results of his or her work. Presentations will be made in the form of a scientific research paper.