**UNIVERSITY OF GONDAR**

**INSTITUTE OF BIOTECHNOLOGY**

**DEPARTMENT OF BIOTECHNOLOGY**

**COURSE SYLLABUS FOR BIOINFORMATICS**

**Course title: Bioinformatics**

**Course code: Biot. 606**

**ECTS: 5**

**Lecture: 4 hours/week**

**Independent learning: 3 hours/week**

**Collaborative learning: 2 hours/week**

**Length of time to complete module: 16**

**Pre-requisite module: None**

**Co-requisite: Molecular Biology (Biot. 603)**

**Barred combination module: None**

**Course Description**

**Module objectives:**

This course is designed for graduate students with a solid background in molecular genetics, a fair amount of statistical know-how and strong computer & internet experience. This course is designed with the objective of introducing the principles, basic tools and strategies of bioinformatics for use in research and applications of biology.

**Mode of delivery:**

Lectures will the means by which important principles of bioinformatics will be imparted. The lecture content will be supplemented with practicum laboratory sessions where students will use the latest publicly available sequence databases and analytical tools towards solving assigned questions presented in the form of laboratory reports. Current and seminal research articles literature will be reviewed and serve as a basis for group discussions. A project will be assigned where students will be required to take real world data and perform an analysis, generate results, interpret the results and present it in a form of a report. Reading assignment will be given, generally from the textbook or review articles.

**Learning outcome:**

* understand DNA and protein sequence as information carriers
* obtain an in depth understanding of gene structure and regulatory sequences
* familiarize with the mechanics and limitations of pairwise and multiple sequence alignments
* perform and interpret graphic means of sequence analysis using publicly available internet based tools
* perform and interpret pair wise and multiple sequence alignments using publicly available internet based tools
* query and analyze sequence data using publicly available internet based major sequence data repositories
* perform gene finding and regulatory sequence discovery using publicaly available internet based tools
* understand the principles and limitations of various phylogenetic analysis tools
* perform and interpret phylogenetic relationships using publicly available internet based analysis tools
* Classroom teaching 40% and independent learning 60%
* Modes of Evaluation

Examination – 50%

Seminar paper and/or group assignments– 50%

**Course content:**

The genetic material:

Genetic information

Sequences

Codons

Deciphering the information

Molecular biology tools

Bioinformatics

Genomic information content

Mutation and conservation

Gene families

Genome complexity

Bioinformatics

Definition

Terminologies

Tools and considerations

Comparing sequences

Edit operations

Edit distance

Edit transcript

Dot matrix plots

Simple algorithm

Filtering noise

Pattern recognition

Estimation of statistical significance

Gaps

Simple gap penalty

Origination and length penalty

Scoring matrices

For nucleic acid

Point accepted mutation (PAM) – amino acid

BLOSUM – amino acid

Dynamic programming (DP) - Pairwise alignment

Principle of Optimality

The biological problem

Illustrative description of DP

Formal description of DP

Global alignment (Needleman & Wunsch)

Local alignment (Smith & Waterman)

Multiple sequence alignment (msa)

Uses of msa

msa as an extension of pairwise alignment

Progressive msa

Substitutions and mutations

Mutation rates

Synonymous and non-synonymous substitutions

Substitution vs mutation

Jukes-Cantor one-parameter model

Kimuar’s two-parameter model

Principles of phylogenetics

Phylogenetic tree; Distance matrix method (UPGMA)

Character based method (Parsimony)

Evolution in organelles

**Mode of evaluation:**

Exam: There is one exam at the end of the semester. This exam will carry 50% of the final grade. The formulation of the questions for the exam will be such that a student will need to understand and digest the information provided during the lectures and reading assignments. The questions will test: (1) depth of understanding, (2) ability to apply what was learned to a real world scenario, and (3) relational thinking, where a student is expected to pull together various aspects of what s/he has learned. Rot memorization by itself is not a desirable approach in order to do well on the exam.

Laboratory Reports: The lab reports will comprise 10% of the final grade. The lab reports will be answers to the questions provided at each lab session. The la report shall be a full length report with the introduction, methods, results and conclusion.

Laboratory exam: After completing all the lab sessions there will be a lab exam which will constitute 20% of your final grade. The lab exam will test the students ability to solve problems related to sequence analysis, alignments, database mining, etc acquired during the semester. The lab exam is open book and any material in print or over the internet may be used (except getting help or helping fellow classmates).

Project: The project will constitute 10% of your grade. You are expected to do the project independently but you can use any resource that you want. You will be given a set of guidelines on how to prepare your project paper. As always, plagiarism is unacceptable, and maybe grounds for invalidating the whole report!

Literature presentation/discussion participation: An original research article will be assigned for the student to review and present to the class. The depth of understanding of the material being presented, the ability to present core findings, the ability to answer questions, and the overall participation in the presentation/discussion will be used to evaluate a student from 10%.

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**References**

David W. Mount, 2001. *Bioinformatics: Sequence and Genome Analysis,* Cold Spring Harbor Laboratory Press.

Dan E Krane and Michael L. Raymer, 2003. *Fundamental concepts of bioinformatics.* Pearson Education Inc.

**Rissler, J. and Mellon**, M. (1996). The Ecological Risks of Engineered Crops. The MIT press, Cambride, Massachusetts

**Tzotzos, G.T**. (1995). Genetically Modified Organisms: A Guide to Biosafety. United Nations Industrial Development organization (UNIDO) and CAB International, Wallingford, UK.

**Kjellsson, G. and Simonsen, V**. (1994). Methods for Risk Assessment of Transgenic Plants I. Competition, Establishment and Ecosystem Effects. Birkhäuser Verlag, Basel.

, USA.