Course Code: CBB 501

Course Name: Algorithms in Computational Biology

Course Instructor: Dr. Vikram Singh

Credits Equivalent: 4 Credits

(One credit is equivalent to 10 hours of lectures / organised classroom activity / contact hours; 5 hours of laboratory work / practical / field work / Tutorial / teacher-led activity and 15 hours of other workload such as independent individual/ group work; obligatory/ optional work placement; literature survey/ library work; data collection/ field work; writing of papers/ projects/dissertation/thesis; seminars, etc.)

Course Objectives: The course is designed to introduce students the algorithmic principles, central to the studies in Computational Biology and Bioinformatics. Concepts from computer science like dynamic programming and graph theory will enable students to understand a variety of concepts that are used in the theoretical studies of life sciences and expose them to the underlying mechanisms of widely used softwares. Students, who are familiar with at least one programming language, will be encouraged to write their own codes for various algorithms discussed in this course.

Pre-requisite: CBB 405 Basics of Bioinformatics

Attendance Requirements:
Students are expected to attend all lectures in order to be able to fully benefit from the course. A minimum of 75% attendance is a must failing which a student will not be permitted to appear in examination.

Evaluation Criteria:
1. Mid Term Examination: 25%
2. End Term Examination: 50%
3. Continuous Internal Assessment: 25%
   - Class Participation – 5%
   - Assignments – 10%
   - Course project – 10%

Course Contents:

Unit 1: Introduction to algorithms and complexity   6 Hours

1. Basic Concepts: Algorithmic complexity, Biological vs. Computer algorithms
2. Standard Notations: Big-Oh, Omega, Theta notations; Hardness of an algorithm. Few examples: Sorting, Finding optimal change, Tower of Hanoi etc.
3. Introduction to algorithm design techniques: Exhaustive search, Greedy Algorithms, Divide and conquer etc.

Example: Motif finding problem-- using brute force algorithm, using greedy algorithm

Unit 2: Dynamic Programming and Finite State Machines   10 Hours

1. Models of DNA evolution: Jukes Cantor, Kimura and Tamura models
2. Derivation of protein evolution models: PAM and BLOSUM
3. Elements of dynamic programming: Edit distance, Longest Common Subsequences, Global and Local Sequence Alignment
4. Markov Chains and Hidden Markov Models: CpG islands, Pairwise alignment using HMMs
5. Working of BLAST: Usage of Finite State Machine, E-value, etc.

Unit 3: Pattern matching, trees and clustering   8 Hours

1. Introduction to hash table, keyword tree, suffix tree
2. Ukkonen's linear time suffix tree algorithm
3. Hierarchical and k-means clustering
4. Evolutionary trees: (I) distance based methods – UPGMA, NJ; (II) character based methods – MP, ML; (III) methods of tree evaluation

Unit 4: Algorithms for RNA and Protein Structure Prediction   8 Hours

1. RNA secondary structure: Nussinov algorithm, Energy minimization, Zuker's Algorithm; Base covariation, SCFG
2. RNA tertiary structure: Basics of "minimum free energy" based methods
3. Protein secondary structure: Chou-Fasman, GOR method
4. Protein tertiary structure: Rosetta method, Contact potential method

Unit 5: Introduction to Graph Theory and Network Biology   8 Hours

1. Elementary graph algorithms: Breadth-first search, Depth-first search, Topological sort, Strongly connected components.
2. Basics of Networks: Hamiltonian path vs. Eulerian path, Degree distribution.
3. Finding shortest path: Dijkstra's algorithm, Floyd–Warshall algorithm
4. Basics of network models: Random, Small-world, Scale-free

Text Books:
1. **Jones and Pevzner (2004)**, An Introduction to Bioinformatics Algorithms. MIT Press.
2. **Durbin *et al.* (1998),** Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids. Cambridge University Press
3. **Mount (2004)**, Bioinformatics: Sequence and Genome Analysis, CBS Publishers

Additional Readings:
1. **Gusfield (2005),** Algorithms on Strings, Trees and Sequences. Cambridge University Press.
2. **Mitchell (1998)**, An Introduction to Genetic Algorithms. MIT Press.
3. **Cormen *et al.* (2009)**, Introduction to Algorithms. MIT Press.
4. **Sung (2009),** Algorithms in Bioinformatics: A Practical Introduction. Chapman & Hall/CRC.
5. **Neapolitan and Naimipour (2011),** Foundations of Algorithms. Jones & bartlett.
6. **Korf *et al.* (2003),** BLAST. O'Reilly
7. **Junker and Schreiber (2008),** Analysis of Biological Networks. Wiley-Interscience, New Jersy.

CENTRAL UNIVERSITY OF HIMACHAL PRADESH

Course Code: CBB 522

Course Name: Elements of Synthetic Biology

Instructor: Dr. Vikram Singh

Credits Equivalent: 2 Credits

(One credit is equivalent to 10 hours of lectures / organised classroom activity / contact hours; 5 hours of laboratory work / practical / field work / Tutorial / teacher-led activity and 15 hours of other workload such as independent individual/ group work; obligatory/ optional work placement; literature survey/ library work; data collection/ field work; writing of papers/ projects/dissertation/thesis; seminars, etc.)

Course Objectives: The course is designed to introduce students the concepts of synthetic biology – a field of study at the interface of (i) complexity of biological systems and (ii) techniques of traditional engineering. This course is designed to acquaint students about the following basic questions:

- Can we study and understand biology as an engineering discipline?
- Why is it necessary to consider stochasticity while modeling biological processes?
- What are the basic parts and devices that have been successfully bioengineered?
- What are the implications of Synthetic Biology on the society?

Attendance Requirements: Students are expected to attend all lectures in order to be able to fully benefit from the course. A minimum of 75% attendance is a must failing which a student will not be permitted to appear in examination.

Evaluation Criteria:
1. Mid Term Examination: 25%
2. End Term Examination: 50%
3. Continuous Internal Assessment: 25%
   - 5% class participation,
   - 20% assignment and presentation

Course Contents

UNIT I: Introductory Interdisciplinary Concepts   (4 Hours)

- Definition and scope of Systems biology and Synthetic biology.
- Engineering concepts: parts, devices, circuits -- digital vs. analog, logic gates.
- Biological complexity: Self organization, Emergence, Robustness.
- Introduction to genetic engineering and metabolic engineering.

UNIT II: Modeling methods for Biological Systems   (4 Hours)

- Review of kinetic chemistry
- Aspects of noise in designing biological systems.
- Brief overview of deterministic modeling, master equation and Gillespie's Stochastic Simulation Algorithm.
- Lambda switch and Chemotactic module in *E coli*.
- SBML, CellML, CAD and open source programs: Copasi, CellDesigner, JDesigner, eCell, mCell, StochSim, BioNets, etc

UNIT III: Standards and parts in Synthetic Biology   (4 Hours)

- Lac operon, Quorum sensing, Promoter designing
- MIT Registry of standard biological parts
- Bio-brick and non-biobrick initiatives, iGEM events.
- DNA writing technologies, artificial genes, zinc fingers, never born proteins.

UNIT IV: Bio-engineered Synthetic Circuits   (4 Hours)

- Gates: AND gate
- Counters: Pulse generators
- Switches: Toggle switch
- Oscillators: Repressilator, mammalian oscillator
- Brief overview of cascades, time delayed circuits, spatial patterning, biosensors, and other logical formula driven circuits.

UNIT V: From Modules to Systems (4 Hours)

- Integrating gene circuits
- DNA Origami, Genome Synthesis
- Minimal synthetic cell, Multicellular synthetic systems
- Bio-energetics and Bio-fuels
- **Safety and Legal issues:** Bio-security, Bio-safety

Text Books:

1. **Chris Myers (2009).** Engineering Genetic Circuits. Chapman & Hall.
2. **Edda Klipp *et al.* (2009).** Systems Biology: A Textbook. Wiley-VCH.
3. **Huimin Zhao (2013).** Synthetic Biology: Tools and Applications. Academic Press.

Additional Readings:

4. **Freemont and Kitney (2012).** Synthetic Biology: A Primer. World Scientific
5. **Fu and Panke (2009).** Systems Biology and Synthetic Biology. Wiley, New Jersy.
6. Presidential Commission for the Study of Bioethical Issues (2010). NEW DIRECTIONS: Ethics of Synthetic Biology and Emerging Technologies. (http://bioethics.gov)

CENTRAL UNIVERSITY OF HIMACHAL PRADESH

[Established under the Central Universities Act 2009]
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Course Code: CBB 523

Course Name: Practical Course on Systems Biology

Instructor: Dr. Vikram Singh

Credits Equivalent: 2 Credits

(One credit is equivalent to 10 hours of lectures / organised classroom activity / contact hours; 5 hours of laboratory work / practical / field work / Tutorial / teacher-led activity and 15 hours of other workload such as independent individual/ group work; obligatory/ optional work placement; literature survey/ library work; data collection/ field work; writing of papers/ projects/dissertation/thesis; seminars, etc.)

Course Objectives: The course is designed to give students an opportunity for learning the computational techniques to understand biological complexity at systems level. They will be introduced to the softwares implementing deterministic and stochastic modeling algorithms. At the same time they will also be acquainted with the network visualization and analysis softwares.

Students having working knowledge of any programming language will be encouraged to write their own codes for simulating and analysing model biological systems.

Pre-requisite: CBB 518 – Elements of Systems Biology

Attendance Requirements: Students are expected to attend all lectures in order to be able to fully benefit from the course. A minimum of 75% attendance is a must failing which a student will not be permitted to appear in examination.

Evaluation Criteria:
1. Mid Term Examination: 25%
2. End Term Examination: 50%
3. Continuous Internal Assessment: 25%
   - 5% attendance,
   - 5% class participation,
   - 15% assignment and presentation

Contents:
1. Deterministic simulation of a biological system.
2. Implementation of Gillespie's stochastic simulation algorithm to model chemical reaction system.
3. To construct and visualize simple biological network.
4. To analyze a given biological network by calculating followings
   a. Degree centrality
   b. Closeness centrality
   c. Eccentricity centrality
   d. Between centrality
      Etc.
5. Stability analysis of 1-dimensional systems
6. Stability analysis of 2-dimensional biological systems
7. A minor project

   Students will be required to learn the following modeling suites
   1. CellDesigner
   2. Cytoscape
   3. XPPAut