Syllabus
BINF 701-702
Computational Biology Core Course

Course Description

BINF 701/702 is the Computational Biology core course developed at the KU Center for Computational Biology. The course is designed to introduce the most important and basic concepts, methods, and tools used in computational biology. Topics include (but not limited to) bioinformatics databases, sequence and structure alignment, protein structure prediction, protein folding, protein-protein interaction, Monte Carlo simulation, protein design, dynamical systems, and systems biology. Emphasis will be put on the understanding and utilization of these concepts and algorithms. We also discuss in detail the application of these algorithms to interesting problems in gene regulation, signaling networks, macromolecular self-assembly, and drug design. The objective is to help the students to rapidly reach the frontier of computational biology and be able to use the computational tools to solve problems in their own research.

Instructors

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- Eric Deeds, Email: deeds@ku.edu, Phone: 785-864-1057

Schedule

2:00-2:50pm, MWF

Homework & Exams

Take-Home Exams: 400 points (80% of total grade)

A total of 4 take-home exams will be assigned over the course of each semester; each is worth 100 points. These exams will generally be due about two weeks after they are assigned. Due dates will be provided for each exam when it is handed out.

Late policy: We will deduct 10% from the grade if the exam is late. We will not accept take-home exams more than a week after the due date, except in emergency situations, which will be dealt with on a case-by-case basis.

Literature Reports: 100 points (20% of total grade)

Each week throughout the semester, we will focus on reading and writing about relevant literature. We will have one or two papers each week, depending on the length of the paper. In a brief written report, the student will be responsible for introducing the paper, providing a scientific context for the work and setting up the main problems or issues the paper addresses, describe each figure, and provide a brief summary of the results at the end.

Student evaluation and grades

The grading scale will be:
A = 90-100%
B = 80-89
C = 70-79
D = 60-69
F = below 60

Textbook

A textbook is not required for this course. Assigned materials will either be handed out to the class or posted on the blackboard website.

Course Policies

Attendance and class participation are expected. Repeated absences without approval or valid justification will result in the reduction of the grade for the course.

Late assignments will be docked 10% for being late, and an additional 10% for each additional day they are late.

Cheating and Plagiarism will be considered academic misconduct and therefore subject to the University Senate Rules and Regulations Section 2.6.1-7. Briefly, if a student represents someone else's work for their own (either by cheating or plagiarism) in any classroom examination or assignment without making the proper acknowledgement of that work, it will be deemed academic misconduct. All work, either in class or on an assignment, is expected to be your own work. Homework: the penalty for the first offense will be a reduction in grade to a zero (F) for that specific work. The penalty for a second offense will be a reduction in grade assignment to F for the course. Exams: the penalty for the first offense will be a reduction in grade to F for the course. For more information on academic misconduct, please see
http://www.clas.ku.edu/faculty/policies/misconduct.pdf.

Class Content

I. Computational Biology Basics

1. Introduction (Ilya Vakser and Christian Ray)
    - 1.1 What is computational biology?
        - 1.1.1 Principles of protein structure
        - 1.1.2 Tertiary structure
        - 1.1.3 Quaternary structure
        - 1.1.4 Similarity of ternary and quaternary structure
    - 1.2 What is systems biology?
        - 1.2.1 Dynamics and the birth-death process
        - 1.2.2 Chemical reaction networks
        - 1.2.3 Dynamical regulation, feedback, and noise

2. Bioinformatics Databases (Ilya Vakser and Joanna Slusky)
    - 2.1 Databases of sequences
    - 2.2 Databases of structures
    - 2.3 Databases of interactions

3. Biophysics Fundamentals (Joanna Slusky)
    - 3.1 Rotamers
    - 3.2 van der Waals
    - 3.3 Electrostatics
    - 3.4 Hydrogen bonding
    - 3.5 Solvation and solvent accessible surface area
    - 3.6 Knowledge based (statistical) energy functions

4. Alignment (Ilya Vakser)
    - 4.1 Sequence alignment
    - 4.2 Multiple alignments
    - 4.3 Structure alignment

II. Protein Structure Modeling

5. Modeling of tertiary structure (Ilya Vakser)
    - 5.1 Optimization
    - 5.2 Energy landscapes
    - 5.3 Molecular dynamics
    - 5.4 Conformational analysis
    - 5.5 Secondary structure prediction
    - 5.6 CASP
    - 5.7 Homology modeling
    - 5.8 Threading
    - 5.9 Ab initio

6. Modeling of quaternary structure (Ilya Vakser)
    - 6.1 Basic concepts
    - 6.2 Intermolecular energy landscapes
    - 6.3 Docking algorithms – foundation
    - 6.4 Docking algorithms – current & future

6.5 Docking examples
6.6 CAPRI
6.7 Protein Structure Initiative

7. Search space (Joanna Slusky)
    7.1 Search space I (global)
    7.2 Search space II (global and local)

III. Protein and Drug Design; Proteomics

8. Introduction to protein design (Joanna Slusky)
    9.1 Backbone selection
    9.2 Flexible backbones
    9.3 Directed evolution
    9.4 Membrane design
    9.5 Enzyme design
    9.6 Antibody design
    9.7 Academic impropriety!
    9.8 Design with peptide mimetics and non natural amino acids

9. Computational proteomics (Ilya Vakser)
    10.1 Protein interaction networks
    10.2 Genome-wide modeling of protein interactions

10. Drug design (Ilya Vakser)
    11.1 QSAR and biological activity
    11.2 Inhibition of protein interactions

IV. Dynamical Systems Biology

11. Introduction to dynamics and graphs (Eric Deeds)
    8.1 Intro to Dynamical Systems Biology
    8.2 Graph Theory I: Introduction
    8.3 Properties of Graphs
    8.4 Networks in Biology

12. Deterministic dynamical network modeling (Christian Ray and Eric Deeds)
    12.1 Chemical reaction networks
    12.2 Mapping CRNs to ODEs
    12.3 Stability of 1 dimensional systems
    12.4 Multidimensional systems
    12.5 Sensitivity
    12.6 Multistability
    12.7 Mathematical biology
    12.8 Sensitivity and diffusion

13. Network structure (Christian Ray and Eric Deeds)
    13.1 Feedback loops in systems biology
        13.1.1 Representative ODE models
        13.1.2 Canonical nonlinear models
        13.1.3 Evolutionary design principles

- 13.2 Chemical reaction network motifs
  - 13.2.1 Michaelis-Menten
  - 13.2.2 Futile cycles
  - 13.2.3 Goldbeter-Koshland loops

14. Numerical integration (Eric Deeds)
    - 14.1 Introduction
    - 14.2 Advanced numerics

15. Stochastic network biology (Christian Ray and Eric Deeds)
    - 15.1 Stochastic CRNs and the Chemical Master Equation
    - 15.3 Unifying sensitivity and noise
    - 15.4 Noise approximations: omega expansion, Wiener process, Fokker Planck
    - 15.5 Simulating molecular distributions
    - 15.6 Single cell networks
    - 15.7 Theory-driven experimental systems biology
    - 15.8 Networks and Information Transmission

16. Rule-based modeling (Eric Deeds)
    - 16.1 Introduction to rule-based modeling with Kappa
    - 16.2 Rule-based modeling with Kappa
    - 16.3 Scalable agent-based simulations
    - 16.4 Contact maps, reachables and fragments
    - 16.5 Stories and causal flows in Kappa
    - 16.6 Combinatorial complexity and network dynamics