Applications of Bioinformatics and Genomics/Proteomics. BIPG 640/840

Summary: In this final course of the BPG program, students will be familiarized with the most advanced computational techniques, programs and databases used at the frontiers of biomedical sciences. Advanced applications will be covered in four broad areas: new bioinformatics tools, genomics, proteomics, and RNomics.

Instruction: The course is team-taught by faculty from The University of Toledo and Bowling Green State University.

Course director: Dr. Alexei Fedorov, Dept. of Medicine, Vice Director BPG Program, Director of Bioinformatics Lab, (419) 383-5270, alexei.fedorov@utoledo.edu.

Format: Three credit hours course in a distance learning format (video lectures/labs) with the ability to meet lecturers every week.

Office hours: Every Tuesday and Thursday from 9 AM to 10 AM in the office of Dr. Fedorov (Room 0012 at Ruppert Center, HSC; tel: 419-383-5270). Also, students may contact remotely via Skype (Afedorov_lab) every Tuesday from 8 PM to 9 PM.

Homework time policy: Each homework assignment must be returned in seven days by noon. (For example, for a Tuesday class this homework must be returned via e-mail next Tuesday by 1 pm.) Absolutely NO excuse for a late homework return (automatic 0 points). Each lecture/lab will be available on the web in advance for at least one week, thus, ≥ 17 days will be allocated for the homework. Several EXTRA assignments will be available through the course. They are designed to improve grades. Special assignments must be returned in two weeks.

Grading principles:

- Homework 40%
- LABs+ activity 10%
- Mid-term Exam 20%
- Final Exam 30%

- Extra points for outstanding homework and SPECIAL ASSIGNMENTS are possible!
- Students receive a waiver to change one homework grade to A

Topics covered in each video lecture/lab

1. INTRODUCTION TO GENOMICS: Genome is not an instruction text but an unsupervised operating system.

2. Genome as an advanced Cellular Automaton.

3. Organization and structure of the Human genome.

4. Complex hierarchy of non-randomness in the human genome.

5. Codon bias puzzle. What forces have created unequal codon frequencies?

6. INTRONS: structure, function, and evolution.

7-8. Single-Nucleotide Polymorphism (SNP) (John Gray)

9. Introduction to computational algorithms for gene prediction.

10-11. Advanced gene predictions. Basics on Support Vector Machines (Sam Shepard)

12. Bacterial Genomics (Robert Blumenthal)

13. Transcription factor binding sites (Robert Trumbly)

14. Genomic Entropy. Origin of novel genes. Pros and cones of genomic mutations.

15. Recombination and large rearrangements in the human genome.

Take-home exam

SPRING BREAK

16. Gene arrays (Douglas Leaman)

17. Data Mining in Bioinformatics (Sadik Khuder)

18. Cluster Analysis in Bioinformatics (Sadik Khuder)

19. Pattern Recognition in Bioinformatics (Sadik Khuder)

20. Gene Regulatory Network (Sadik Khuder)

21. Profound differences between DNA and RNA molecules. Introduction to RNA World.

22. Small non-coding RNA. Part 1: snoRNA

23. Small non-coding RNA. Part 2: microRNA, siRNA, piRNA

24. Long non-coding RNA

25. Advanced Proteomics. LAB (Wendell Griffin)

26. Glycan Analysis, Imaging, and Biomarker Discovery by MALDI-MS (Dragan Isailovic)

27-28. Advanced Molecular Phylogenetics (Scott Rogers)

Final exam