



Special Topics: Literature Analysis in Bioinformatics

This course is designed to teach GBCB students the important skills of reading, analyzing, and interpreting primary literature in the field of bioinformatics. The proposed topic for Spring 2008 is Host-Pathogen Interactions. The class is 1 credit and will meet weekly for one hour.

Structure

Each class meeting will be devoted to the presentation and analysis of a published paper relevant to the semester's topic. Each student in the class will be required to present at least one paper, and to lead the discussion of that paper. Students who are not presenting will be required to write a brief summary of the paper, and to participate in the class discussion. Students may choose their own papers, but all papers must be approved by the professor at least one week in advance of presentation.

Content

The topic for this semester will be "Host-Pathogen Interactions." This includes bacterial or viral pathogens of animals or plants. It also covers non-pathogenic symbioses (i.e., *Sinohizobium-Medicago*). Acceptable papers will address research questions in this area using computational, mathematical, biological, or statistical approaches. Particularly good papers will combine one or more of these approaches. Review and opinion papers are not acceptable.

Grading

Course grades will be based on three criteria:

1. **Paper presentation (40%).** Each student is required to deliver a 45 minute presentation of an approved paper. In addition, the presenter will lead the discussion of the paper during class. Satisfactory presentations will include, at a minimum, an introduction to the relevant background, a summary of the methodology, an explanation of the results and conclusions, and an analysis of the paper's strengths and weaknesses. Presenters will be expected to consult background literature and other relevant sources in order to properly present their paper. Part of the grade for this presentation will take into account written feedback from your classmates.
2. **Weekly written summaries (30%).** Each week, every student except the presenter will be required to complete a brief (1 page) summary of the paper. Satisfactory summaries will include a brief introduction to the paper's topic, summary of methods and results, statement of conclusions, and at least two questions that arose from reading the paper. These questions will be used during

class discussion. Students are encouraged, but not required to consult outside sources for their summaries; however, students will be expected to turn in their own summaries; collaboration with fellow classmates will not be allowed.

3. ***Class attendance and participation (30%)***. All students will be expected to attend class and participate in class discussions. In addition, students will evaluate the presentations of their fellow classmates. Participation is crucial to the success of the course; therefore, **only one unexcused absence** will be tolerated. Students who expect to miss multiple classes should consider re-enrolling in another semester.

Note that the grading for this course includes peer review. Peer review is a crucial component of scientific publication. Students are expected to provide honest, thoughtful, and constructive criticism of their peers. Personal attacks and destructive criticism will not be tolerated. You will be graded both on your ability to provide feedback, as well as the feedback that you receive from your classmates.

Selected Literature

1. Singhal M and Resat H. A domain-based approach to predict protein-protein interactions. *BMC Bioinformatics* 2007, 8: 199.
<http://www.biomedcentral.com/1471-2105/8/199>
2. Dyer MD, Murali TM, Sobral BW. Computational prediction of host-pathogen protein protein interactions. *Bioinformatics* 2007, 23(13): 159-166.
<http://bioinformatics.oxfordjournals.org/cgi/content/abstract/23/13/i159>
3. Rajashekara G, Glasner JD, Glover DA, Splitter GA. Comparative whole-genome hybridization reveals genomic islands in *Brucella* species. *J. Bacteriol.* 2004 Aug, 186(15): 5040-51.
<http://jb.asm.org/cgi/content/full/186/15/5040?view=long&pmid=15262941>
4. Paulsen IT, et al. The *Brucella suis* genome reveals fundamental similarities between animal and plant pathogens and symbionts. *Proc Natl Acad Sci USA.* 2002 Oct 1, 99(20): 13148-53. <http://www.pnas.org/cgi/content/full/99/20/13148>
5. Beres SB, et al. Genome-wide molecular dissection of serotype M3 group A *Streptococcus* strains causing two epidemics of invasive infections. *Proc Natl Acad Sci USA.* 2004 Aug 10, 101(32): 11833-8.
<http://www.pnas.org/cgi/content/full/101/32/11833>
6. Rengarajan J, Bloom BR, and Rubin EJ. Genome-wide requirements for *Mycobacterium tuberculosis* adaptation and survival in macrophages. *Proc Natl Acad Sci USA* 2005, 102: 8327–8332. <http://www.pnas.org/cgi/content/full/102/23/8327>
7. Davis FP, et al. Host pathogen protein interactions predicted by comparative modeling. *Protein Sci.* 2007 Dec, 16(12): 2585-96.
<http://www.proteinscience.org/cgi/content/full/16/12/2585>