CS2220: Introduction to Computational Biology

Course Briefing, 18/1/08

Limsoon Wong

Recommended "Pre-requisites"

- **CS1102: Data Structures and Algorithms**
- **LSM1102: Molecular Genetics**

Objectives

- **Develop flexible and logical problem solving skill**
- **Understand bioinformatics problems**
- **Appreciate techniques and approaches to bioinformatics**

To achieve the goals above, we expose the students to a series of case studies spanning gene feature recognition, gene expression and proteomic analysis, gene finding, sequence homology interpretation, phylogeny analysis, physical mapping, and genome sequencing

What to Expect

- **Time Table**
- **Course Syllabus**
- **Course Homepage**
- **Teaching Style**
- **Project, Assignments, Exams**
- **Readings**
- **Assessment**

Time Table

- **Lecture**
  - Friday 2:00pm – 4:00pm, COM1-212
- **Tutorial**
  - T. B. A.
- **Consultation**
  - Any time, just drop by my office ☺
- **Office**
  - COM1, Level 3, Room 34
- **Email**
  - wongls@comp.nus.edu.sg

Course Syllabus

- **Essence of Bioinformatics**
  - molecular biology
  - tools and instruments for molecular biology
  - themes and applications of bioinformatics
- **Essence of Knowledge Discovery**
  - classification performance measures
  - feature selection techniques
  - machine learning techniques
- **Gene Feature Recognition from Genomic DNA**
  - feature generation, selection, & integration
  - translation initiation site (TIS) recognition
  - Transcription start site (TSS) recognition
- **Gene Expression and Proteome Analysis**
  - Microarray and mass-spec basics
  - classification of gene expression profiles
  - classification of proteomic profiles
  - clustering of gene expression profiles
  - molecular network reconstruction
- **Essence of Seq Comparison**
  - Dynamic programming basics
  - Sequence comparison and alignment basics
  - Needleman-Wunsh global alignment algorithm
  - Smith-Waterman local alignment algorithm
- **Seq Homology Interpretation**
  - protein function prediction by sequence alignment
  - protein function prediction by phylogenetic profiling
  - active site and domain prediction
  - key mutation sites prediction
- **Gene Finding**
  - Overview of gene finding
  - GRAIL
  - Handling of frame shifts and in-dels
- **Phylogenetic Trees**
  - Phylogeny reconstruction method basics
  - origin of Polynesians & Europeans
  - Large-scale sequencing basics
- **Physical Mapping and Genome Sequencing**
  - Physical mapping basics
  - sequence assembly algorithm
  - shortest common superstring problem

Course Homepage

- **IVLE**
  - http://ivle.nus.edu.sg/Lms/course/course_studentview.aspx?CourseID=%7b89a84ffe-68a0-4ed6-aebe-f0f70311ca91%7d
- **Lecture Slides & etc**
  - http://www.comp.nus.edu.sg/~wongls/courses/cs2220/2008

Teaching Style

- **Bioinformatics is a broad area**
- **Need to learn a lot of material by yourself**
  - Reading books
  - Reading papers
  - Practice on the web
- **Don't expect to be told everything**

Assignments, Project, & Exam

- **Assignments**
  - Probably 4 assignments
  - Some are simple programming assignments
- **Project**
  - Based on a case study in the class
  - 8-10 pages of report expected
- **Exam**
  - No mid-term exam … I hope!
  - 1 final open-book exam

Be Honest

- **Exam**
  - Absence w/o good cause results in ZERO mark
  - Cheating results in ZERO mark
- **Discussion on assignments is allowed**
- **Blatant plagiarism is not allowed**
  - Offender gets ZERO mark for assignment or exam
  - Penalty applies to those who copied AND those who allowed their assignments to be copied

Background Readings

- Limsoon Wong, *The Practical Bioinformatician*, WSPC, 2004
- Marketa Zvelebil and Jeremy Baum, *Understanding Bioinformatics*, Garland, 2007
- Peter Clote and Rolf Backofen, *Computational Molecular Biology: An Introduction*, John Wiley, 2000
- Pierre Baldi and Soren Brunak, Bioinformatics: the Machine Learning Approach, MIT Press, 1998
- Pavel Pevner, *Computational Molecular Biology: An Algorithmic Approach*, MIT Press, 2000
- Dan Gusfield, *Algorithms on Strings, Trees, and Sequences - Computer Science and Computational Biology*, Cambridge University Press, 1997
- Malcolm Campbell and Laurie Heyer, *Genomics, Proteomics, and Bioinformatics, Pearson*, 2007

Assessment

- **Continuous Assessment: 50%**
- **Final Exam: 50%**

What comes after CS2220

- **CS2220 Introduction to Computational Biology**
  - Understand bioinformatics problems; interpretational skills
- **CS3225 Combinatorial Methods in Bioinformatics**
- **CS4220 Knowledge Discovery Methods in Bioinformatics**
  - Clustering; classification; association rules; SVM; HMM; Mining of seq, trees, & graphs
- **CS5238 Advanced Combinatorial Methods in Bioinformatics**
  - Seq alignment, whole-genome alignment, suffix tree, seq indexing, motif finding, RNA sec struct prediction, phylogeny reconstruction
- **CS6280 Computational Systems Biology**
  - Dynamics of biochemical and signaling networks; modeling, simulating, & analyzing them
- **Etc …**

Any questions?

I hope you will enjoy this class ☺