CS4220: Knowledge Discovery Methods in Bioinformatics Course Briefing

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Recommended "Pre-requisites"

- Completed modules on
 - Programming
 - Algorithms
 - Basic molecular biology
 - ST2334 Probability & Statistics
 - CS2220 Introduction to Computational Biology



Objectives



- Exposure to knowledge-discovery techniques
- Enhance flexible & logical problem-solving skill
- Understand bioinformatics problems and their solution in depth
 - A modern network-based perspective
- To achieve goals above, we expose students to case studies spanning gene expression and proteomic analysis, protein functional prediction, epistatic interaction analysis, etc.



Contents of Course Overview

- Time Table
- Course Syllabus
- Course Homepage
- Teaching Style
- Project, Assignments, Exams
- Readings
- Assessment
- Quick Overview of Themes and Applications of Bioinformatics



Time Table



- Lecture
 - Thursday 9am 11am, COM1-208
- "Tutorial"
 - Thursday 11am 12nn, COM1-208
- Emails
 - wongls@comp.nus.edu.sg
 - nagarajann@gis.a-star.edu.sg
- Consultation
 - Any time; just make appt



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Course Syllabus

Essence of Biostatistics

- Statistical estimation
- Hypothesis testing
- Principle component analysis

Essence of Data Mining

- Clustering
- Association rules
- Classification
- Class-imbalance learning

Gene Expression Analysis

- Basic gene expression analysis
- Batch effect & normalization
- Improving reproducibility
- Dealing with small sample

Proteomic Profile Analysis

- Basic proteomic profile analysis
- Improving consistency
- Improving coverage

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Protein Interaction Network

- Consistency, comprehensiveness of pathway databases
- Integration of pathway databases
- Reliability of PPI network
- Protein Complex Prediction
 - Basic approaches
 - Overlapping complexes
 - Low-density complexes
 - Small complexes
- Network Perturbations in
 Disease Context
- Transcription Factor
 Interaction Identification



Course Homepage

- IVLE
 - https://ivle.nus.edu.sg/v1/Module/Student/default.a
 spx?CourseID=b8292ca8-7ade-4c10-b72f 50d7a6f008c3
- Lecture Slides & etc
 - http://www.comp.nus.edu.sg/~wongls/courses/cs4 220/2016





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Teaching Style

- Bioinformatics is a broad area
- Need to learn a lot of material by yourself
 - Reading books
 - Reading papers

And do this before each lecture!

- Practise on the web
- Don't expect to be told everything



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Assignments, Project, & Exam

- Assignments (30-40% of marks)
 - 2 to 3 assignments
 - Some are simple programming assignments
- Project (20-30% of marks)
 - Based on a case study in the class
 - 8-10 pages of report / ppt slides expected
- Exam (40% of marks)
 - 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 & project 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

- Every lecture will be accompanied by a small set of "must-read" and "good-to-read" articles
 - The "must-read" articles are considered lecture notes and are examinable





Related Courses

- CS2220 Introduction to Computational Biology
 - Understand bioinformatics problems; interpretational skills
- CS3225 Combinatorial Methods in Bioinformatics
- CS4220 Knowledge
 Discovery Methods in
 Bioinformatics

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 Gene expression, proteomic profiling, protein interaction, transcription factor interaction, pathway perturbation

- CS5238 Advanced Combinatorial Methods in Bioinformatics
 - Seq alignment, whole-genome alignment, suffix tree, seq indexing, motif finding, RNA sec struct prediction, phylogeny reconstruction
- CS6222 Computational frontier in precision medicine
- Etc ...



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Any questions?

I hope you will enjoy this class ③



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Themes and Applications of Bioinformatics

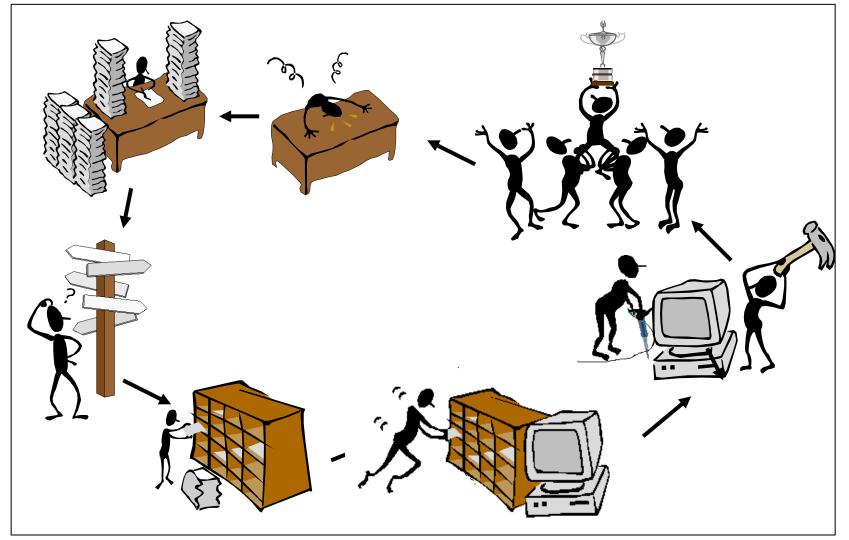
These slides are for those who have not taken CS2220 to read at your own leisure





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What is Bioinformatics?





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Themes of Bioinformatics Themes of This Course

Bioinformatics involves Data Mgmt + Knowledge Discovery + Sequence Analysis + Physical Modeling + ...

Knowledge Discovery = Statistics + Algorithms + Databases





The Promises of Bioinformatics

To the patient: Better drug, better treatment

To the pharma: Save time, save cost, make more \$

To the scientist: Better science



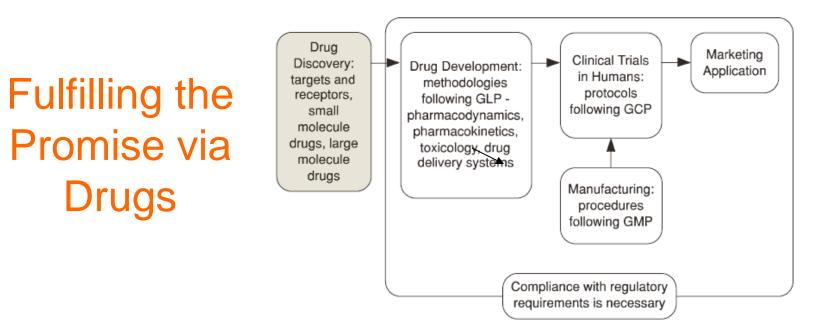


Figure from Rick Ng, Drugs: From Discovery to Approval

- Bioinformatics is applicable to drug development
- Drug discovery: Design small molecules that bind target proteins
 - Which proteins?
 - What should binding accomplish?
- Biomarkers



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Pervasiveness of Bioinformatics

- Bioinformatics is mandatory for large-scale biology
 - e.g., High-throughput, massively-parallel measurements, or "lab on a chip" miniaturization
- Computational data analysis is mandatory for indirect experimental methods
 - e.g., reconstruction based on phase contrast or wave diffraction.
- What about the rest of biology (and medicine) ?
- Limitless opportunities!



Some Bioinformatics Problems

- Biological Data Searching
- Biological Data Integration
- Gene/Promoter finding
- Cis-regulatory DNA
- Gene/Protein Network
- Protein/RNA Structure Prediction
- Evolutionary Tree reconstruction
- Infer Protein Function
- Disease Diagnosis
- Disease Prognosis
- Disease Treatment Optimization, ...

Commonly Used Data Sources

These slides are for those who have not taken CS2220 to read at your own leisure





Type of Biological Databases

- Micro Level
 - Contain info on the composition of DNA, RNA, Protein Sequences
- Metadata
 - Ontology
 - Literature

Macro Level

- Contain info on interactions
 - Gene Expression
 - Metabolites
 - Protein-Protein
 Interaction
 - Biological Network

Exercise: Name a protein seq db and a DNA seq db





Transcriptome Database

- Complete collection of all possible mRNAs (including splice variants) of an organism
- Regions of an organism's genome that get transcribed into messenger RNA
- Transcriptome can be extended to include all transcribed elements, including non-coding RNAs used for structural and regulatory purposes

Exercise: Name a transcriptome database



Gene Expression Databases

- Detect what genes are being expressed or found in a cell of a tissue sample
- Single-gene analysis
 - Northern Blot
 - In Situ Hybridization
 - RT-PCR
- Many genes: High throughput arrays
 - cDNA Microarray
 - Affymetrix GeneChip® Microarray

Exercise: Name a gene expression database



Metabolites Database

- A metabolite is an organic compound that is a starting material in, an intermediate in, or an end product of metabolism
- Metabolites dataset are also generated from mass spectrometry which measure the mass the these simple molecules, thus allowing us to estimate what are the metabolites in a tissue

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Starting metabolites

- Small, of simple structure, absorbed by the organism as food
- E.g., vitamins and amino acids

Intermediary metabolites

- The most common metabolites
- May be synthesized from other metabolites, or broken down into simpler compounds, often with the release of chemical energy
- E.g., glucose

End products of metabolism

- Final result of the breakdown of other metabolites
- Excreted from the organism without further change
- E.g., urea, carbon dioxide



Protein-Protein Interaction Databases

- Proteins are true workhorses
 - Lots of cell's activities are performed thru PPI, e.g., message passing, gene regulation, etc.
- Methods for generating PPI db
 - biochemical purifications, Y2H, synthetic lethals, in silico predictions, mRNAco-expression

- Function of a protein depends on proteins it interacts with
- Contain many false
 positives & false
 negatives

Exercise: Name a PPI database



Introductory References

- S.K. Ng, "Molecular Biology for the Practical Bioinformatician", *The Practical Bioinformatician*, Chapter 1, pages 1-30, WSPC, 2004
- Lots of useful videos, <u>http://www.as.wvu.edu/~dray/Bio_219.html</u>

Materials from CS2220,

http://www.comp.nus.edu.sg/~wongls/courses/cs2220/2015

