# 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
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- Project, Assignments, Exams
- Readings
- Assessment
- Quick Overview of Themes and Applications of Bioinformatics

## Time Table



- Lecture
  - Tuesday 12nn-3pm at COM1-204
- "Tutorial" (it is integrated into lecture)
- Emails
  - wongls@comp.nus.edu.sg
  - nagarajann@gis.a-star.edu.sg
- Consultation
  - Any time; just make appt

# 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

### 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

# **Teaching Style**



- Bioinformatics is a broad area
- Need to learn a lot of material by yourself
  - Reading books
  - Reading papers
  - Try the exercises
  - Practise on the web

Don't expect to be told everything

And do this before each lecture

# Assignments, Project, & Exam



- Assignments (30-40% of marks)
  - 3 to 4 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
  - 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 ...

# Any questions?



I hope you will enjoy this class ©

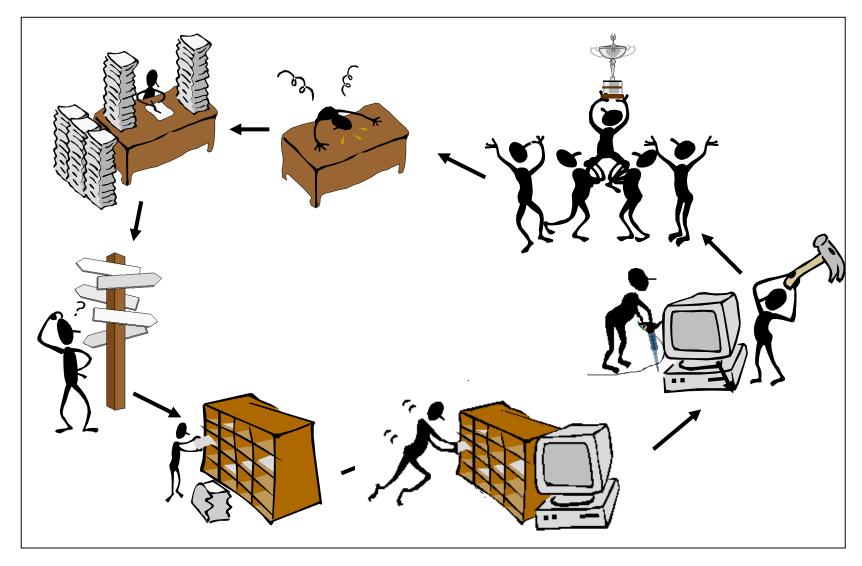
# Themes and Applications of Bioinformatics

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



## What is Bioinformatics?





# 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

Fulfilling the Promise via Drugs

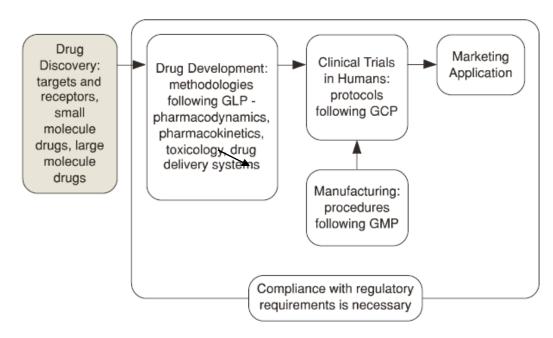


Figure from Rick Ng, Drugs: From Discovery to Approval

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

## 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

### 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 Databas National University of Singapore

- Proteins are true workhorses
  - Lots of cell's activities are performed thru PPI, e.g., message passing, gene regulation, etc.
- Function of a protein depends on proteins it interacts with

- Methods for generating PPI db
  - biochemical purifications,
     Y2H, synthetic lethals, in
     silico predictions, mRNA co-expression
- 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, http://www.as.wvu.edu/~dray/Bio 219.html

• Materials from CS2220, http://www.comp.nus.edu.sg/~wongls/courses/cs2220/2015