Agenda Today

• Introductions
• Course information
• Overview of topics
Course Web Site

- www.biostat.wisc.edu/bmi776/
- Syllabus and policies
- Readings
- Tentative schedule
- Lecture slides (draft posted before lecture)
- Announcements
- Homework
- Project information
- Link to Piazza discussion board
Your Instructor: Anthony Gitter

- Email: gitter@biostat.wisc.edu
- Office: room 3268, Discovery Building
- Assistant professor, Biostatistics & Medical Informatics
- Affiliate faculty, Computer Sciences
- Investigator, Morgridge Institute for Research
- Research interests: biological networks, time series analysis, computational problems related to cancer and virology
Your TA: Li Liu

• Email: lliu262@wisc.edu

• Office: CS building, room to be announced

• Graduate student, Computer Sciences
Office Hours

• Instructor: Tuesday and Thursday, 2:30-3:30 PM
  – Immediately after class

• TA: Will be announced soon
Finding My Office: Discovery Building

- 3rd floor has restricted access
- See Piazza if you need building access
- Stop at visitor desk to call my office if card does not work
You

• So that we can all get to know each other better, please tell us your
  – name
  – major or graduate program
  – research interests and/or topics you’re especially interested in learning about
  – favorite programming language
Course Requirements

• 4 or 5 homework assignments: ~40%
  – Written exercises
  – Programming (Python)
  – Computational experiments (e.g. measure the effect of varying parameter \( x \) in algorithm \( y \))
  – Five late days permitted

• Project: ~25%
• Midterm: ~15%
• Final exam: ~15%
• Class participation: ~5%
Exams

• Midterm: March 7, in class
• Final: Sunday May 7, 2:45-4:45 PM

• Let me know immediately if you have a conflict with either of these exam times
Computing Resources for the Class

• Linux workstations in Dept. of Biostatistics & Medical Informatics
  – No “lab”, must log in remotely (use WiscVPN)
  – Will create accounts for everyone on course roster
  – Two machines
    - mi1.biostat.wisc.edu
    - mi2.biostat.wisc.edu
  – HW0 tests your access to these machines
  – Homework must be able to run on these machines

• CS department usually offers Unix orientation sessions at beginning of semester
Programming Assignments

• Piazza poll supports using Python
  – 4 have used Python
  – 8 willing to learn
  – 0 strongly opposed
  – Many abstained, any more input?

• Will set up Python environment on biostat servers
  – Debating Python 2 vs. Python 3
  – Will install permitted packages and post the list

• HW0 will be Python introduction

• Use Piazza for Python discussion
Project

- Design and implement a new computational method for a task in molecular biology
- Improve an existing method
- Perform an evaluation of several existing methods
- Run on real biological data
- Suggestions will be provided
- Each student works individually
- Not directly related to your existing research
Participation

• Do the assigned readings
• Show up to class
• No one will have the perfect background
  – Ask questions about computational or biological concepts
• Correct me when I am wrong
• Piazza discussion board
Piazza Discussion Board

• Instead of a mailing list
• http://piazza.com/wisc/spring2017/bmics776/home
• Post your questions to Piazza instead of emailing the instructor or TA
  • Unless it is a private issue
• Answer your classmates’ questions
• Announcements will also be posted to Piazza
• Supplementary material for lecture topics
Course Readings

• Mostly articles from the primary literature
• Must be using a campus IP address to download some of the articles (can use WiscVPN from off campus)
Prerequisites

• BMI/CS 576 or equivalent
• Knowledge of basic biology and methods from that course will be assumed
• May want to go over the material on the 576 website to refresh
• http://www.biostat.wisc.edu/bmi576/
What you should get out of this course

• An understanding of some of the major problems in computational molecular biology
• Familiarity with the algorithms and statistical techniques for addressing these problems
• How to think about different data types
• At the end you should be able to
  – Read the bioinformatics literature
  – Apply the methods you have learned to other problems both within and outside of bioinformatics
Major Topics to be Covered (the algorithms perspective)

• Expectation Maximization
• Gibbs sampling
• Mutual information
• Multiple hypothesis testing correction
• Convolutional neural networks
• Linear programming
• Interpolated Markov models
• Duration modeling and semi-Markov models
• Tries and suffix trees
• Markov random fields
• Stochastic context free grammars
• Branch and bound search
Major Topics to be Covered
(the task perspective)

• Modeling of motifs and cis-regulatory modules
• Identification of transcription factor binding sites
• Genotype analysis and association studies
• Regulatory information in epigenomic data
• Transcriptome quantification
• Mass spectrometry peptide and protein identification
• Pathways in cellular networks
• Gene finding
• Large-scale sequence alignment
• RNA sequence and structure modeling
• Protein structure prediction
Motif Modeling

What sequence motif do these promoter regions have in common?
cis-Regulatory Modules

What configuration of sequence motifs do these promoter regions have in common?
Genome-wide Association Studies

Which genes are involved in diabetes?

Type 2 diabetes association P values by chromosome (386,731 markers). The x-axis is the genomic position by chromosome 1-22 and X (by color), and the y-axis is the negative base 10 logarithm of the P value.
Noncoding Genetic Variants

How do genetic variants outside protein coding regions impact phenotypes?

Transcriptome Analysis with RNA-Seq

What genes are expressed and at what levels?
Proteomic Analysis with Mass Spectrometry

What proteins are expressed and at what levels?

Identifying Signaling Pathways

How do proteins coordinate to transmit information?

Yeger-Lotem et al.,
*Nature Genetics*, 2009
Gene Finding

Where are the genes and functional elements in a genome?
Large Scale Sequence Alignment

What is the best alignment of these 6 genomes?
RNA Sequence and Structure Modeling

How can we identify sequences that encode this RNA structure?

E. coli

H. influenzae

B. subtilis
Protein Structure Prediction

Can we predict the 3D shape of a protein from its sequence?

\[ E = \varepsilon \sum_i \left| c_i - c_i^{\text{target}} \right| + E_{\text{steric}} \]
Other Topics

• Many topics we aren’t covering
  – Protein function annotation
  – Modeling long reads
  – Metagenomics
  – Metabolomics
  – Sequence compression
  – Graph genomes
  – Single-cell sequencing
  – Pseudo- and quasi-alignment
  – Text mining
  – Others?
Reading Groups

• Computational Systems Biology Reading Group
  – http://lists.discovery.wisc.edu/mailman/listinfo/compsysbiojc

• AI Reading Group
  – http://lists.cs.wisc.edu/mailman/listinfo/airg

• Will also announce relevant seminars