Genome 540

Introduction to Computational Molecular Biology:
Genome and protein sequence analysis

Lecture 0

- Course resources & requirements

Course Resources

- Instructors (contact/office hr info is on web page):
  - Me (Phil)
  - TA: Danielle Faivre (Dani)
- Web site (we don't use Canvas!)
  http://bozeman.mbt.washington.edu/compbio/mbt599
  - Admin info
  - HW assignments
    - posted approx 1.5 weeks in advance
  - zoom lecture recording & pdf of lecture slides
    - posted ≥1 day prior to corresponding discussion session
  - links to texts, various papers, C++ tutorials
  - new postings (of HW or lectures) will be announced by email

- Discussions (***not*** recorded!) Tu Th 10:30 – 12
  - led by me:
    - review & discuss lecture slides
  - led by Dani:
    - discuss homework & programming issues
    - review background material
    - *related topics* (next-gen sequencing?)

- Recommended texts:
  - Durbin *et al*. (HMMs, alignment algorithms)
  - Ewens & Grant (probabilities)
  - web page has links to rent or buy (new, used, e-book)

Course Requirements

- Homework (no tests or exams)

- Ask questions!
  - in discussion sessions
  - by email

Homework

- Due weekly, Sun at midnite
  - See web site for late penalty / redo / sharing policy
- Readings (journal articles)
- Write computer program to analyze a genomic data set, and run it (on your own computer)
- Submit by email, *in computer-readable format*:
  - results of analysis
  - your program
  - (in some cases) a written interpretation of the results

- You must use a general-purpose programming language (not R or Matlab)
  - a compiled language (e.g. C, C++) is recommended for efficiency reasons
  - Python + Cython also works
  - interpreted language may work, but risky!

- Your program must be written “from scratch”, i.e. not using prewritten routines from elsewhere
  - OK to use ‘built-in’ functions for sorting, random-number generation etc.

- This course does *not* cover how to use *existing* software tools
  - even though most comp bio research is done using pre-existing programs!
  - we do describe the ideas behind some programs
    - (BLAST, PhastCons …)
- Rather, our goal is to empower you to write your own programs when existing ones are inadequate!