Welcome to Bioinformatics Applications 2017 Spring

Overview

Bioinformatics Applications (PLPTH813)

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1/19/2017

Course materials are online

Course site at Github

- Course information
- Lecture slide files
- Labs slide files

Goal

PLPTH813 will cover the basic principle of regular bioinformatics applications and emphasize **the practice of bioinformatics**.

The ultimate goal of this course is to help you to be prepared for next-generation biological research that often generates large data and requires researchers to have the capability in data management and data mining.

Lecture topics

1. Basic Unix
2. Basic R
3. Introduction of NGS and NGS bioinformatics tools
4. DNA sequence alignment
5. Genome variants
6. Phylogeny
7. Construction of a genetic map
8. QTL and GWAS
9. RNA-Seq and RNA-Seq assembly
10. Identification of differential expression via RNA-Seq
11. Genome assembly

Grading and schedule

- **Grading**

Class participation 10%, Homework 30%, Midterm Exam 20%, Paper presentation 5%, Project 10%, Final Exam 25%

- Homework: ~6 times
- Paper presentation
  three topics: GWAS, RNA-Seq, Genome assembly
- Two exams (midterm and final)
- Oral project presentation

Projects

- A project requiring the skills for data analysis

  Examples:

  1. your own project (e.g., RNA-Seq or genome assembly)

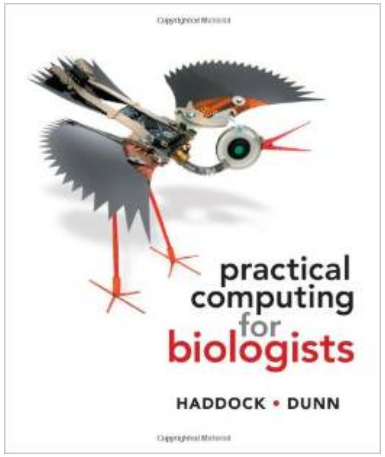
  2. A survey of several software packages (e.g., genotype imputation)

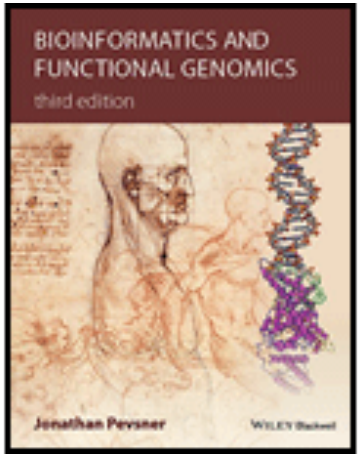
  3. Implementation of a classical study through re-analysis (need a good justification)

- Oral presentation: each project 15-20 min

References

- Papers
- Online resources (e.g., Wikipedia)
- Practical computing for biologists, Haddock and Dunn, 2010
- Bioinformatics and Functional Genomics, Pevsner, 2015





Lecture: 10:30am-11:20pm, Tuesday, Thursday

Lab: 12:30-2:30pm (typically finished in 2 hours), Thursday

Office hours: 3:00am-4:00pm Wednesday