Human Genetics 551: Computational Genomics
Winter 2018

Course description
This course provides an introduction to the theory and practice of genomic data analysis including DNA sequence mapping, variant calling, gene expression analysis, and functional genomics. This course will introduce basic programming concepts using Python. A final course project will require applying standard genomics tools to existing data sets. This course is appropriate for students with no background in computer programming.

Students are required to bring their own laptop computers to class. Students should have the ability to install software on their computer.

Course Objectives
1. Learn the fundamentals of Python programming for manipulating genomics data
2. Develop an understanding of the computational principles underlying common genomics analyses
3. Apply computational tools to address important questions in genomics

Suggested Text Books and Other Resources
Learning Python by Mark Lutz (O'Rielly publishing). We will focus on Python v 2.x (not 3.x).
Bioinformatics Data Skills by Vince Buffalo
Bioinformatics Programming Using Python by Mitchell Model
http://www.ee.surrey.ac.uk/Teaching/Unix/index.html
https://github.com/blahah/command_line_bootcamp
http://www.openbookproject.net/thinkcs/python/english2e/index.html
http://rosalind.info/problems/locations/
http://opentechschool.github.io/python-data-intro/

Additional material including papers and web-resources will be made available using Canvas.

Start Date: January 4, 2018
Time: 10:10am-11:30am (Tuesdays and Thursdays)
An optional practicum will also be scheduled based on student availability.
Location: Taubman Library 5000
Credits: 3

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Conflict of Interest: The instructors, Jeff Kidd and Jacob Kitzman, have no industry relationships.

Grading
Course grades will be based on programming/analysis assignments (65%), a final course project and presentation (25%) and active and thoughtful participation during lectures and discussions (10%).

Lectures (Note assignment dates are subject to change -- refer to Canvas for uptodate information)**:**

1. 1/4 (Th) Introduction to Computational Genomics

Motivation for learning computation, programs vs data, manipulating text files, file transfer, and using unix.

Reading:

Sean Eddy: High Throughput Sequencing for Neuroscience
http://cryptogenomicon.org/2014/11/01/high-throughput-sequencing-for-neuroscience/

Noble, WS *Plos Comp* Biol 2009
http://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1000424

Introduction to UNIX commands
https://swcarpentry.github.io/shell-novice/01-intro/
https://swcarpentry.github.io/shell-novice/02-filedir/
https://swcarpentry.github.io/shell-novice/03-create/
https://swcarpentry.github.io/shell-novice/04-pipefilter/

Additional Unix tutorial (with built-in interface):
http://rik.smith-unna.com/command_line_bootcamp

Unix quick reference sheet:
https://www.rain.org/~mkummel/unix.html

2. 1/9 (Tu) Intro to Python I

iPython notebooks, visualization, configuration, interactive vs saved-file computing. Variables, objects, concept of immutability. Numbers and strings

Reading:

How to Think Like a Computer Scientist: Learning with Python.
Chapter 1: The way of the program
http://www.openbookproject.net/thinkcs/python/english2e/ch01.html
Chapter 2: Variables, expressions, and statements.
http://www.openbookproject.net/thinkcs/python/english2e/ch02.html

Assignment:

Python programming assignment #1

3. 1/11 (Th) Computational Topic: Intro to Python II

Flow control: if, elif, else, loops.
Data structures: lists and tuples, and list comprehensions.
Mutable vs immutable variables

Reading:

How to Think Like a Computer Scientist: Learning with Python.

Chapter 4: Conditionals
Chapter 6: Iteration
Chapter 7: Strings
Chapter 9: Lists
http://www.openbookproject.net/thinkcs/python/english2e/

Optionally also see:
Python Tutorial sections 3.1.4, 4.1-4.4, 5.1-5.3
https://docs.python.org/2/tutorial/

Assignment: Python exercise

4. 1/16 (Tu)

Genomics Topic: Storing genomics coordinate data
coordinate intervals, 0-based vs 1-based, UCSC-bed format, bedtools

Computational Topic: Introduction to Unix computing

Reading:

Introduction to UNIX commands
https://swcarpentry.github.io/shell-novice/01-intro/
https://swcarpentry.github.io/shell-novice/02-filedir/
https://swcarpentry.github.io/shell-novice/03-create/
https://swcarpentry.github.io/shell-novice/04-pipefilter/

Additional Unix tutorial (with built-in interface):
http://rik.smith-unna.com/command_line_bootcamp

Unix quick reference sheet:
https://www.rain.org/~mkummel/unix.html

Portions of Bedtools PDF manual (particularly Chapter 5, posted on Canvas)

Assignment:

Unix and bedtools exercise

5. 1/18 (Th)

Genomics Topic: *-seq
Assays for variation and function using sequencing as a read-out

Computational Topic: Intro to Python III
loops, iterables, methods, reading and writing files

Reading:

Shendure and Ji, *Nat Biotech,* 2008
http://www.nature.com/nbt/journal/v26/n10/pdf/nbt1486.pdf

Shendure and Lieberman Aiden, *Nat Biotech*, 2012
http://www.nature.com/nbt/journal/v30/n11/pdf/nbt.2421.pdf

Python file I/O
http://www.tutorialspoint.com/python/python_files_io.htm

Assignment: Python programming assignment - file and string manipulation

6. 1/23 (Tu)

Genomics Topic: Illumina Fastq Files
Sequence representation and quality scores, storing of paired-end reads

Computational Topic: Intro to Python IV
Functions, classes, dictionaries and sets
Reading:

FASTQ Format (Wikipedia)
https://en.wikipedia.org/wiki/FASTQ_format

Python:
How to Think Like a Computer Scientist: Learning with Python.
Chapter 3: Functions
http://www.openbookproject.net/thinkcs/python/english2e/ch03.html
Chapter 5: Fruitful functions
http://www.openbookproject.net/thinkcs/python/english2e/ch05.html
Chapter 12: Dictionaries
http://www.openbookproject.net/thinkcs/python/english2e/ch12.html

See also dictionaries documentation
https://docs.python.org/2/tutorial/datastructures.html#dictionaries

Assignment:

fastq file analysis exercise

7. 1/25 (Th)

Genomics Topic: Sequence alignment and Dynamic Programming
Local vs global alignments, Burrows-Wheeler transform

Reading:

Eddy, *Nat Biotech*, 2014
http://www.nature.com/nbt/journal/v22/n7/full/nbt0704-909.html

Assignment:

No assignment

8. 1/30 (Tu)

Genomics Topic: Significance of sequence matches
Dynamic programming, continued. Local vs global alignments.

Computational Topic: Intro to Python V
Basic python file I/O with tabular data
Reading in a matrix to a dictionary

Assignment
Dynamic programming and sequence alignment (by hand)

9. 2/1 (Th)

Genomics Topic: Assessing Significance
Basic parametric and nonparameteric statistical tests

Computational Topic: Statistics in Python I
Array manipulation and numeric computing with numpy/scipy. Random number generation for simulations, and statistical testing in python.

Reading:
Points of Significance series from *Nature Methods*:
Importance of being uncertain
http://www.nature.com/nmeth/journal/v10/n9/full/nmeth.2613.html
and
Non-parametric tests
http://www.nature.com/nmeth/journal/v11/n5/full/nmeth.2937.html

The rest of this excellent series is at:
http://www.nature.com/collections/qghhqm/pointsofsignificance

More lengthy: *A biologist's guide to statistical thinking and analysis*
http://www.ncbi.nlm.nih.gov/books/NBK153593/

10. 2/6 (Tu)

Computational Topic I: Statistics in Python (continued)

Computational Topic II: Python data visualization I
Matplotlib – basic plot construction

Assignment:
Python statistics and plotting assignment

11. 2/8 (Th)

Introduction to Cluster Computing
FLUX, process management, qsub

Assignment:
Cluster computing exercise

12. 2/13 (Tu) Genomics Topic: The multiple testing problem
p-values, False discovery rate, q-values.

Reading:
Storey and Tibshirani, *PNAS*, 2003
http://www.pnas.org/content/100/16/9440.full
Online plotting reference

13. 2/15 (Th) Genomics Topic: Sequence Analysis I
Properties of Illumina data, introduction to mapping reads and the BAM format

Computational Topic: BWA and samtools
Manipulating BAM files using samtools and pysam

Reading:
Li et al *Bioinformatics*, 2009
http://bioinformatics.oxfordjournals.org/content/25/16/2078.long

SAM/BAM specification: http://samtools.github.io/hts-specs/SAMv1.pdf

14. 2/20 (Tu) Genomics Topic: Sequence Analysis II
Theory and implementation of short read alignment, including Burrows-Wheeler read mapping.

Computational Topic: Picard tools
Read mapping with bwa on FLUX

Reading:
Trapnell and Salzberg, *Nature Biotech,* 2009
http://www.nature.com/nbt/journal/v27/n5/abs/nbt0509-455.html

15. 2/22 (Th) Genomics Topic: Sequence Analysis III
Variant calling, statistical models for joint vs individual calling. Considering different scenarios, somatic vs germline

Computational Topic: GATK and samtools
Variant calling models

Reading:
Li, *Bioinformatics*, 2011
http://bioinformatics.oxfordjournals.org/content/27/21/2987.long

DePristo et al., Nature Genetics, 2011
http://www.nature.com/ng/journal/v43/n5/full/ng.806.html

2/27 (Tu) **No class – "Spring" Break**
3/1 (Th) **No class – "Spring" Break**

16. 3/6 (Tu)

Genomics Topic: Sequence Analysis IV
Selecting variants, hard filters vs variant quality calibration., VCF format.

Reading:

DePristo et al., Nature Genetics, 2011
http://www.nature.com/ng/journal/v43/n5/full/ng.806.html

Danecek et al. Bioinformatics, 2011
http://bioinformatics.oxfordjournals.org/content/27/15/2156

VCF format specification:
https://samtools.github.io/hts-specs/VCFv4.2.pdf

17. 3/8 (Th)

Genomics Topic: RNA-seq (I)
Experimental strategies for expression profiling using sequencing. Algorithmic aspects of RNA read mapping, isoform detection, and quantification at the gene, isoform, and exon levels. Normalization.

Computational Topic: RNA-seq read mapping
Alignment vs alignment-free methods.

Reading:

Oshlack et al., *Genome Biol*, 2010
https://genomebiology.biomedcentral.com/articles/10.1186/gb-2010-11-12-220

Conesa et al., *Genome Biol*, 2016
https://genomebiology.biomedcentral.com/articles/10.1186/s13059-016-0881-8

18. 3/13 (Tu)

Genomics Topic: RNA-Seq II
Measures of abundance (FPKM, TPM). Expression quantitative trait locus (QTL) statistical framework for studies of genetic variants' impact upon expression.

Computational Topic: Bowtie, STAR, and alignment-free methods

Reading:

Lior Pachter, "Estimating number of transcripts from RNA-Seq measurements (and why I believe in paywall)"
https://liorpachter.wordpress.com/2014/04/30/estimating-number-of-transcripts-from-rna-seq-measurements-and-why-i-believe-in-paywall/

Trapnell et al. *Nature Biotech*, 2013
http://www.nature.com/nbt/journal/v31/n1/full/nbt.2450.html

Assignment:

eQTL analysis exercise

19. 3/15 (Th) Python Data Visualization II - Advanced Topics (Final Project Teams Due)

Pandas and Advanced Plotting

Reading:
To be determined

20. 3/20 (Tu) Clustering (Ryan Mills, Ph.D, guest-lecture) (Final Project Ideas Due)
Algorithms and applications for grouping data based on similarity

21. 3/22 (Th) Genomics Topic: Functional Genomics I
Chromatin profiling data, chip-seq, Peak calling

Reading:
To be determined

22. 3/27 (Tu) Genomics Topic: Functional Genomics II
Chromatin conformation assays, concepts and processing

Reading:
To be determined

23. 3/29 (Th) HMMs and Segmentation

Reading:
To be determined
Assignment:
Work on final projects

24. 4/3 (Tu) Machine Learning and Statistical Inference
SVMs, Decision Tree/Random Forest, Neural Nets
ROC curves, Cross validation, and the "overfitting" problem
Reading:
To be determined
Assignment:
Work on final projects

25. 4/5 (Th) Version Control, gitHub, and Reproducible Analyses
Reading:
To be determined
Assignment:
Work on final projects

26. 4/10 (Tu) Final Project Lab

27. 4/12 (Th) Final Project Presentations

28. 4/17 (Tu) Final Project Presentations