Clinical and Research Genomics
Spring 2014 Course
Weill Cornell Medical College / Memorial Sloan-Kettering Cancer Center | Rockefeller University
Tri-Institutional MD/PhD Program, and Graduate Program for Physiology, Biophysics, & Systems Biology

Wednesdays @ 2:30-4:00PM, 1305 York Ave., Y13-01 (13th floor conference room)
http://physiology.med.cornell.edu/faculty/mason/lab/clinicalgenomics/index.html

Professor:
Christopher E. Mason, Ph.D., Weill Cornell Medical College
TAs:
Sheng Li, Weill Cornell Medical College

The rapid advancement of Next-Generation Sequencing (NGS) has opened a wealth of opportunities for research in many fields: cancer biology, epigenetics, tumor evolution, microbiome and infectious disease dynamics, neuro-degeneration, personalized medicine, and improved diagnosis and risk assessment for patients. Moreover, there are emerging, faster NGS technologies that promise comprehensive molecular portraits of disease and actionable clinical results for doctors within a single day. Scientists and physicians will be better equipped to design studies and help patients if they possess an intricate knowledge of these molecular-profiling methods, their biological context, and their applicability to specific cases and diseases. Finally, a rich understanding of the complexity of the human genome is essential for the proper annotation of characterization of any new mutations/modifications found, since large-scale efforts at tumor and normal genome sequencing have dramatically altered our view of the "normal" genome and epigenome.

Thus, in this 10-week course, students will build a strong foundation of knowledge of high-throughput and NGS technologies (both existing and emerging), learn the applications of these technologies for basic and clinical research, and finally learn the essential tools for the analysis, integration, and application of these data relative to other public databases and phenotype repositories. We have a broad range of expertise being contributed from many leaders in the field, including:

Constantin Aliferis, M.D., Ph.D., New York University School of Medicine
Joel Dudley, Ph.D., Mount Sinai School of Medicine
Olivier Elemento, Ph.D., Weill Cornell Medical College
Christina Leslie, Ph.D., Memorial Sloan-Kettering Cancer Center
Ross Levine, M.D., Ph.D., Memorial Sloan-Kettering Cancer Center
Gholson Lyon, M.D., Ph.D., Cold Spring Harbor Laboratory
Christopher Mason, Ph.D., Weill Cornell Medical College
Ari Melnick, M.D., Weill Cornell Medical College
Craig Thompson, M.D., Memorial Sloan-Kettering Cancer Center
Shijia Zhu, Ph.D., Mount Sinai School of Medicine

Classes:

I. Sequencing Methods and Molecular Detection Techniques (March 19th)
1. Sequencing technologies: 454, Illumina, LifeTech, IonTorrent, Sanger, Nanopore and PacBio (Mason)
2. Current human genome variation and annotation: 1000g, TCGA, ICGC, RefSeq, AceView (Mason)

II. Chromatin Dynamics and Gene Regulation (March 26th)
3. Nuclear organization and methods for their detection (Mason)
4. Chromatin changes and methods: ChIP-Seq, Hi-C, CCC (Elemento)

III. Epigenomes and DNA Modifications (April 2nd)
5. DNA modifications and their detection, Pacbio, RRBS, MeDIP, mC, hmC (Zhu)
6. DNA methylation and Cancer: (Li)

IV. RNA-Sequencing, Epitranscriptomes, and Gene Fusions (April 9th)
9. RNA-Seq methods and gene fusions: libraries, case reports, and algorithms (Mason)
10. HITS-CLIP, miRNA, ncRNAs, and widespread disease relevance of RNA changes (Mason)

V. Clinical Genomics (April 16th)
7. Considerations for clinical sequencing: ClinSeq, Exome-Seq, WGS (Mason)
8. Genetic variation and whole genome sequencing (Mason)

VI. Bioinformatic and Statistical Methods For Clinical Genomics (April 23rd)
13. Targeted resequencing and personalized and disease genomics (Lyon)
14. Variant-calling method for genomics: SAMtools, GATK, Bayes-SNP, Pindel, MrFAST (Lyon)

VII. Proteomics, Metabolomics, and Onco-metabolites (April 30th)
11. 3'-Seq, CLIP-Seq and machine-learning methods for genome-wide integrated analysis (Leslie)
12. Metabolomic methods and onco-metabolites: Mass-Spec, MALDI-TOF (Thompson)

VII. Microbiome Characterizations and Cross-Species Analysis (May 7th)
15. Cloud-based resources: Aspera, Galaxy, MG-RAST, GobyWeb, HMP, Pathomap (Mason)
16. Visualization and modeling: IGV, UCSC, Genesifter, MD-simulations (Mason)

IX. Systems Biology, Integrative Genomics, and Disease Classification (May 14th)
17: Personalized medicine, Tumor sub-classification methods: PCA, machine learning (Mason)
18. Molecular signature de-convolution: Random Forest, Markov Blankets (Aliferis)

X. Pharmacogenomics, Genome Engineering, Synthetic Biology, & Personalized Medicine (May 21st)
19. Systems Biology, PharmKGb and Causal Network Inference: Integrative Genomics and drivers (Levine)
20. Genetic intellectual property and ethics, iGEM, CRISPR-Cas9, and synthetic biology (Mason)

Homework:
Each week there will be a few questions and/or one problem set, based on the lectures.
Homework from the prior week is due at the beginning of class.
Homework sets are expected to take, on average, 90-120 minutes to complete, depending on your prior computational skills and familiarity with the material. Help from faculty and the TA will be available during the week, and students are encouraged to ask for help, be critical, or include datasets and databases from external sources in their analysis.
The class is pass/fail for 3 credits.