

# Clinical and Research Genomics

## Spring 2015 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

Thursdays @ 12:00PM-2:00PM

1305 York Ave., New York, NY 10065 (Y13-01, 13<sup>th</sup> 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:**

Ebrahim Afshinnekoo and Priyanka Vijay, 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, metagenomics, 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 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**

**Doron Betel, Ph.D., Weill Cornell Medical College**

**Joel Dudley, Ph.D., Mount Sinai School of Medicine**

**Olivier Elemento, Ph.D., Weill Cornell Medical College**

**Sheng Li, Ph.D., Weill Cornell Medical College**

**Ekta Khurana, 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**

**Andrea Sboner, Ph.D., Weill Cornell Medical College**

**Shijia Zhu, Ph.D., Mount Sinai School of Medicine**

## Classes:

### **I. Sequencing Methods and Molecular Detection Techniques (April 9<sup>th</sup>)**

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)
3. Nuclear organization and methods for their detection (Mason)

### **II. Epigenomes, DNA Modifications, and Chromatin Dynamics (April 16<sup>th</sup>)**

4. Chromatin changes and methods: ChIP-Seq, Hi-C, CCC (Elemento)
5. DNA modifications and their detection, Pacbio, RRBS, MeDIP, mC, hmC (Zhu)
6. DNA methylation and Cancer: (Li)

### **III. RNA-Sequencing, Epitranscriptomes, and Gene Fusions (April 23<sup>rd</sup>)**

7. RNA-Seq methods and gene fusions: libraries, case reports, and algorithms (Mason)
8. HITS-CLIP, miRNA, ncRNAs, and widespread disease relevance of RNA changes (Mason)
9. Epitranscriptome Dynamics and RNA regulation (Mason)

### **IV. Microbiome and Metagenome Characterizations and Cross-Species Analysis (April 30<sup>th</sup>)**

10. Cloud-based resources: Aspera, Galaxy, MG-RAST, GobyWeb, HMP, PathoMap (Mason)
11. Tools for large-scale data analysis and applications to personalized medicine (Dudley)

### **V. Proteomics, Metabolomics, and Statistical Methods For Clinical Genomics (May 7<sup>th</sup>)**

12. 3'-Seq, CLIP-Seq and machine-learning methods for genome-wide integrated analysis (Leslie)
13. Identification of gastric microbiome from endoscopic biopsy samples using WGS (Betel)
14. Systems Biology, PharmKGb and Causal Network Inference: Integrative Genomics and drivers (Levine)

### **VI. Clinical Genomics and Statistical Power (May 14<sup>th</sup>)**

15. Genetic variation and whole genome sequencing (Mason)
16. Targeted resequencing and personalized and disease genomics (Lyon)
17. Variant-calling method for genomics: SAMtools, GATK, Bayes-SNP, Pindel, MrFAST (Lyon)

### **VII. Systems Biology and Disease Classification (May 21<sup>st</sup>)**

- 18: Sub-classification methods: PCA, machine learning (Aliferis)
19. Molecular signature de-convolution: Random Forest, Markov Blankets (Aliferis)
20. Short-read alignments and gene expression (RNA-seq) (Sboner)

### **VIII. Pharmacogenomics, Genome Engineering, Synthetic Biology, & Personalized Medicine (May 28<sup>th</sup>)**

21. Cancer genomics and mutations across cancer types (Khurana)
22. 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 TAs 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.

## Contact:

Office hours are by appointment but all instructors are available by email: Christopher Mason ([chm2042@med.cornell.edu](mailto:chm2042@med.cornell.edu)), Ebrahim Afshinnekoo ([eba2001@med.cornell.edu](mailto:eba2001@med.cornell.edu)), and Priyanka Vijay ([prv2004@med.cornell.edu](mailto:prv2004@med.cornell.edu))