

## Our Instructors

**Lauren Ciotti** is the communications associate for the Center for Computational Genomics and for the Experimental and Computational Genomics Core at the Sidney Kimmel Comprehensive Cancer Center (SKCCC) at Johns Hopkins.

**Michael Considine** is a Senior Biostatistician for the Division in the Department of Oncology, Johns Hopkins University School of Medicine. Mike performs genomic analyses for division collaborators, and developed an automated genomic analysis software tool.

**Melissa Keinath, Ph.D.** is a postdoctoral fellow at the Carnegie Institution of Washington, Department of Embryology. Her graduate training was through the Molecular, Cellular and Developmental Biology program at the University of Kentucky, where she worked on comparative genomics and evolutionary biology. She co-taught a graduate level bioinformatics course at the University of Kentucky for 3 years.

**Luigi Marchionni, MD, PhD**, is an associate professor in the Cancer Biology Program at the SKCCC at Johns Hopkins. He has extensive experience in the analysis and interpretation of genomic and genetic data and is a co-founding member of the Center for Computational Genomics at Johns Hopkins.

**Jonathan Pevsner, PhD**, is a professor in the Department of Neurology at the Kennedy Krieger Institute and the Department of Psychiatry and Behavioral Sciences at Johns Hopkins. His research expertise is in the genetic basis of childhood disease, including chromosomal disorders. He has taught bioinformatics at Johns Hopkins School of Medicine since 2000 and has published a textbook, *Bioinformatics and Functional Genomics*. He is a co-founding member of the Center for Computational Genomics at Johns Hopkins.

**Frederick Tan, PhD**, is a member of the bioinformatics research faculty at the Carnegie Institution of Washington, Department of Embryology. Dr. Tan manages the Carnegie bioinformatics and genomics resources and teaches hands-on workshops on topics such as Unix, Perl, RNAseq, and data management.

**Sarah Wheelan, MD, PhD**, is an associate professor in the Cancer Biology Program at the SKCCC at Johns Hopkins. She has worked on sequence analysis algorithms and applications to human disease since training at Johns Hopkins and NCBI. She is a co-founding member of the Center for Computational Genomics at Johns Hopkins and is co-director of the Experimental and Computational Genomics Core at the SKCCC at Johns Hopkins.

## Teaching Assistants

**Ike Adeshina**

**Melis Atalar**

**Sean Cho**

**Wikum Dinalankara**

**Anuj Gupta**

**Dorothy Hallberg**

**Jacob Heng**

**Alyza Skaist**

**Aleksei Stupnikov**

**Yuqi Tan**

# Practical GENOMICS



From Biology to Biostatistics

Workshop: June 25-28, 2018

## Agenda



CARNEGIE  
SCIENCE

Embryology





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Monday, June 25th

- 8:30 AM Breakfast / Registration
  - 9:00 AM Welcome & Introduction
  - 9:15 AM Web-based bioinformatics 
  - 9:45 AM Intro to Unix @MARCC
  - 10:00AM Navigate and Organize Files
  - 10:45 AM Break
  - 11:00 AM Explore Tabular Results in Unix
  - 11:30 AM R Refresher 
  - 12:15 PM Lunch
  - 1:00 PM Basic R Tasks
  - 2:30 PM Break
  - 2:45 PM Advanced R Tasks
  - 3:45 PM Reproducible research, Literate Programming, R Markdown
  - 5:00 PM Happy Hour
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Tuesday, June 26th

- 8:30 AM Breakfast
- 9:00 AM Q&A
- 9:30 AM Introduction to NGS & ChIP-seq 
- 10:00 AM First Things with FastQC and Bowtie
- 10:30 AM Break
- 10:45AM Wrangle Alignments with SAMtools
- 11:15 AM Visualize Data with IGV
- 11:45AM Summarize Coverage with deepTools
- 12:15PM Lunch
- 1:00 PM Call Peaks with MACS2
- 2:00 PM Trust, Faith, Sensitivity, Specificity 
- 2:30 PM Break
- 2:45 PM biomaRt for Annotation 
- 3:15 PM Annotate Peaks with annotatr
- 4:15 PM Identify H3K27me3 Peaks
- 5:00 PM Happy Hour

Wednesday, June 27th

- 8:30 AM Breakfast
  - 9:00 AM Q&A
  - 9:30 AM Introduction to RNAseq 
  - 10:00 AM Hands on with RSEM and EBSeq
  - 10:30 AM Break
  - 11:00 AM Plot and explore RNAseq results
  - 11:45 AM MARCC 
  - 12:15 PM Lunch
  - 1:00 PM PCA
  - 1:45 PM PCA Breakout Session
  - 2:30 PM Break
  - 2:45 PM Significance of Overlaps 
  - 3:15 PM GRanges 
  - 3:45 PM GRanges Hands On
  - 4:15 PM GRanges Breakout Session
  - 5:00 PM Happy Hour
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Thursday, June 28th

- 8:30AM Breakfast
- 9:00 AM Quiz Show: *concepts, code, prizes!*
- 10:30 AM Break
- 10:45 AM t-tests 
- 11:15 AM Multiple Test Correction 
- 11:45 AM Power Analysis with PROPER
- 12:15 PM Lunch
- 1:00 PM Gene Set Analysis 
- 1:30 PM Gene Set Analysis Hands On
- 2:00 PM Gene Set Analysis Breakout Session
- 2:15 PM Break
- 2:45 PM Big Picture 
- 3:15 PM Big Picture: Hands On
- 3:45 PM Big Picture: Breakout Session