

## 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.

**Katie Cox, Ph.D.** is a post-doctoral fellow in the Biology Department at Johns Hopkins University. Her graduate training was through the Cell, Molecular, Developmental Biology, and Biophysics program at Johns Hopkins, where she received pedagogical training through the Preparing Future Faculty Teaching Academy. She is currently a Dean's Postdoctoral Teaching Fellow, developing a laboratory course on bacterial evolution.

**Luigi Marchionni, MD, PhD**, is an assistant 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.

**Paul Schaughency, PhD**, is a post-doctoral fellow in the Cancer Biology Program at the SKCCC at Johns Hopkins. His graduate training was through the Biochemistry, Cellular, and Molecular Biology program at Johns Hopkins. He is also the Genomics Coordinator for the Experimental and Computational Genomics Core at the SKCCC 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

**Michael Considine**

**Jacob Heng**

**Paul Schaughency**

**Tyler Creamer**

**Eddie Imada**

**Alyza Skaist**

**Wikum Dinalankara**

**Alexis Norris**

**Heather Wick**

**Anuj Gupta**

# Practical GENOMICS



From Biology to Biostatistics

Workshop: August 14-17, 2017

# Agenda



CARNEGIE  
SCIENCE

Embryology



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Monday, August 14th

8:30 AM Breakfast / Registration  
9:00 AM Welcome & Introduction  
9:15 AM VirtualBox  
9:30 AM Journal Club  
10:00AM Introduction to the Command Line  
10:45 AM Break  
11:00 AM Build commands, pipe, redirect stdout  
11:30 AM R Refresher  
12:15 PM Lunch  
1:00 PM Basic subsetting  
1:45 PM Logical subset, order  
2:30 PM Break  
2:45 PM Basic \*apply  
3:30 PM Advanced \*apply  
4:00 PM Reproducible Research  
4:30 PM RMarkdown, factors  
5:00 PM Happy Hour

Tuesday, August 15th

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

Wednesday, August 16th

4:15 PM Identify H3K27me3 Peaks  
5:00 PM Happy Hour

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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  
10:45 AM Plot and explore RNAseq results  
11:30 AM PCA  
12:15 PM Lunch  
1:00 PM PCA Breakout Session  
2:00 PM Significance of Overlaps  
2:30 PM Break  
2:45 PM Gene Set Analysis  
3:15 PM Gene Set Analysis Hands On  
4:00 PM Gene Set Analysis Breakout Session  
5:00 PM Happy Hour

Thursday, August 17th

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 GRanges  
1:30 PM GRanges: Breakout Session  
2:30 PM Break  
2:45 PM Big Picture  
3:15 PM Big Picture: Hands On  
3:45 PM Big Picture: Breakout Session