

Patrick Kosuke Kimes, Ph.D.

patrick.kimes@gmail.com

913-314-4511

San Francisco, CA 94123

EDUCATION

University of North Carolina at Chapel Hill

August 2015

Ph.D. in Statistics

Certificate in Bioinformatics/Computational Biology

Pomona College

May 2009

B.S. in Mathematics

PROFESSIONAL EXPERIENCE

Roche Sequencing

June 2015 – Present

Principal Scientist, Bioinformatics

Pleasanton, CA

- Developing/benchmarking algorithms for sequencing-based diagnostics
- Building Python pipelines and R packages for automating internal analyses
- Leading/organizing Bioinformatics Unit R Users Group
- Recruited and mentored PhD-level summer intern (June – August 2016)

Janssen R&D (Johnson & Johnson)

June 2014 – August 2014

Network Pharmacology Intern

Spring House, PA

- Explored network topology-based algorithms for gene coexpression analysis
- Delivered analysis pipeline as a complete R package for internal use

Lineberger Comprehensive Cancer Center

January 2012 – May 2015

Graduate Research Assistant

Chapel Hill, NC

- Developed visualization and clustering methods for RNA-seq data
- Contributed RNA-seq data analyses to The Cancer Genome Atlas (TCGA)

PUBLICATIONS

- 1 **Kimes PK**, Liu Y, Hayes DN, and Marron JS. (2017). Statistical significance for hierarchical clustering. **Biometrics**, to appear.
- 2 **Kimes PK**, Hayes DN, Marron JS, and Liu Y. (2016). Binary large-margin classification with multiple decision rules. **Statistical Analysis and Data Mining: The ASA Data Science Journal**, 9(2), 89–105.
- 3 Ko YH, Walter V, Catalano M, Yin X, **Kimes PK**, Xiao X, and Hayes DN. (2015). Integrative analysis of miRNAs classify two distinct stages of epithelial cell differentiation in head and neck squamous cell carcinoma (HNSCC). **Cancer Research**, 75(15 Supplement), 4007.
- 4 **The Cancer Genome Atlas Research Network**. (2015). Comprehensive genomic characterization of head and neck squamous cell carcinomas. **Nature**, 517(7536), 576–582.
- 5 **Kimes PK***, Cabanski CR*, Wilkerson MD, Zhao N, Johnson AR, Perou CM, Makowski L, Maher CA, Liu Y, Marron JS, and Hayes DN. (2014). SigFuge: single gene unsupervised clustering of RNA-seq reveals differential isoform usage among cancer samples. **Nucleic Acids Research**, 42(14), e113.

*: joint first authors

- 6 **The Cancer Genome Atlas Research Network.** (2014). Comprehensive molecular profiling of lung adenocarcinoma. *Nature*, 511(7511), 543–550.

IN PREPARATION

- 7 **Kimes PK, Liu Y.** "Approximate soft classification using parallel large-margin classifiers."

PRESENTATIONS

- "Large-Margin Classification with Multiple Decision Rules," Joint Statistical Meetings (Chicago, IL), August 2016. **[invited paper/talk]**
- "Methods and Applications of Statistical Significance in Clustering," USF Math Colloquium (San Francisco, CA), November 2015. **[invited talk]**
- "Statistical Significance for Hierarchical Clustering," Joint Statistical Meetings (Seattle, WA), August 2015. **[contributed talk]**
- "SigFuge: unsupervised discovery in RNA-seq data," The Cancer Genome Atlas' 3rd Annual Scientific Symposium (Bethesda, MD), May 2014. **[poster]**
- "SigFuge: unsupervised discovery in RNA-seq data," Lineberger Comprehensive Cancer Center Post-doc/Faculty Research Day (Chapel Hill, NC), September 2013. **[poster]**
- "Adaptive Nonparametric Tests for the Two-Sample Location Model with Applications to Microarray Data," Pomona College Summer Research Conference (Claremont, CA), September 2007. **[poster]**

HONORS

- **Travel Grant**, *UW Summer Institute in Statistical Genetics* **July 2012**
- **Cambanis-Hoeffding-Nicholson Prize**, *UNC Statistics* **December 2011**
- **Senior Service Award**, *Pomona College* **May 2009**
- **Pomona College Scholar**, *Pomona College* **Spring 2006 to Fall 2007**
- **Summer Research Grant (SURP)**, *Pomona College* **Summer 2007**

TEACHING EXPERIENCE

- **Instructor's Assistant**, *UNC, STOR 455 – Statistical Methods I* **Fall 2011**
- **Instructor's Assistant**, *UNC, STOR 155 – Introduction to Statistics* **Fall 2010, Spring 2011**

PUBLIC CODE

- [R/spliceclust](#): Visualization/exploratory analysis of splicing across RNA-seq samples.
- [R/sigclust2](#): Assessing the statistical significance in hierarchical clustering.
- [R/SigFuge](#): Clustering/visualization of RNA-seq read depth at per-base resolution.

SKILLS

Computer Languages	R, bash, Python (<i>beginner</i>), C++ (<i>beginner</i>)
Computing Tools	Git, GitHub, Emacs, Snakemake, Nextflow
Natural Languages	English, Japanese