Patrick Kosuke Kimes, Ph.D.

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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. "Statistical significance for hierarchical clustering." **Revision under review**.

2 **Kimes PK**, Hayes DN, Marron JS, and Liu Y. "Binary large-margin classification with multiple decision rules." **Statistical Learning and Data Mining**, 2016.

3 Ko YH, Walter V, Catalano M, Yin X, **Kimes PK**, Xiao X and Hayes DN. "Integrative analysis of miRNAs classify two distinct stages of epithelial cell differentiation in head and neck squamous cell carcinoma (HNSCC)." **Cancer Research** (conference abstract), 2015.

4 **The Cancer Genome Atlas Research Network**, "Comprehensive genomic characterization of head and neck squamous cell carcinomas." **Nature**, 2015.

5 **Kimes PK***, Cabanski CR*, Wilkerson MD, Zhao N, Johnson AR, Perou CM, Makowski L, Maher CA, Liu Y, Marron JS, and Hayes DN. "SigFuge: single gene unsupervised clustering of RNA-seq reveals differential isoform usage among cancer samples." **Nucleic Acids Research**, 2014. *: *joint first authors*

6 **The Cancer Genome Atlas Research Network**, "Comprehensive molecular profiling of lung adenocarcinoma." **Nature**, 2014.

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 Postdoc/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 (*beginner*), C++ (*beginner*)
Computing Tools	Git, GitHub, Emacs, Snakemake, Nextflow
Natural Languages	English, Japanese

Last update: November 3, 2016