Patrick Kosuke Kimes, Ph.D.

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CURRENT APPOINTMENT

Postdoctoral Research Fellow	**June 2017 - Present**
Biostatistics and Computational Biology, Dana-Farber Cancer Institute	*Boston, MA*
Biostatistics, Harvard T. H. Chan School of Public Health	
Mentor: Rafael Irizarry	

EDUCATION

Ph.D. in Statistics, Certificate in Bioinformatics	**August 2015**
University of North Carolina at Chapel Hill	*Chapel Hill, NC*
Advisors: Yufeng Liu, J. S. Marron, D. Neil Hayes	
B.S. in Mathematics	**May 2009**
Pomona College	*Claremont, CA*
Advisor: Jo Hardin	

PROFESSIONAL EXPERIENCE

Postdoctoral Research Fellow	**June 2017 – Present**
Bioinformatics and Computational Biology, Dana-Farber Cancer Institute	*Boston, MA*
Biostatistics, Harvard T. H. Chan School of Public Health	
Principal Scientist I, Bioinformatics	**June 2015 – April 2017**
Roche Sequencing Solutions	*Pleasanton, CA*
Network Pharmacology Intern	**June 2014 – August 2014**
Janssen R&D (Johnson & Johnson)	*Spring House, PA*
Graduate Research Assistant	**January 2012 – May 2015**
Lineberger Comprehensive Cancer Center	*Chapel Hill, NC*

PUBLICATIONS

1 **Kimes PK**, Liu Y, Hayes DN, and Marron JS. (2017). Statistical significance for hierarchical clustering. **Biometrics**.

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.

PRESENTATIONS

· "Statistical Significance for Hierarchical Clustering," International Biometrics Society Journal Club (web-based), June 2017. **[invited talk]**

· "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*), Matlab (*formerly*)
Computing Tools	Git, GitHub, Emacs, Snakemake, Nextflow
Natural Languages	English, Japanese