

Kelly Street
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Education

University of California, Berkeley, Berkeley, CA
PhD Biostatistics **December 2018**
Adviser: Sandrine Dudoit
MA Biostatistics **May 2014**
University of Chicago, Chicago, IL
BS Mathematics **June 2012**
Iowa City West High School, Iowa City, IA **May 2008**

Research Experience

Single-Cell Analysis of Clear Cell Renal Cell Carcinoma **2019 - Present**
Dana-Farber Cancer Inst.

Led the statistical analysis of a large-scale, single-cell dataset

- Assessed methods and implemented full analysis pipeline for RNA-seq data
- Integrated expression data with paired T cell receptor sequence data

BRAIN Initiative Collaboration with Ngai Lab **2014 – Present**
University of California, Berkeley

Analyzed single-cell RNA-Seq data from multiple mouse brain regions

- Analyzed continuous cell-type transitions such as differentiation and regeneration
- Implemented and assessed a variety of clustering and dimensionality reduction methods

Slingshot Lineage Inference Method Development **2015 – 2018**

- Developed statistical tools for inferring continuous, branching trajectories in high-dimensional data
- Created and maintain the ‘slingshot’ R package, available via Bioconductor

Embryogenesis Collaboration with He Lab **2016 – 2018**

University of California, Berkeley

Used publicly available single-cell RNA-Seq data to model embryogenesis in mice

- Developed methods to combine datasets from disparate technologies to be jointly analyzed
- Modeled and clustered dynamic expression patterns

Holland Children’s Environmental Health Lab **2014 – 2015**

University of California, Berkeley

Served as data analyst and statistician on projects examining:

- Microbial communities in breast milk and saliva via 16S ribosomal RNA-Seq
- Quantification of miRNA levels and relationship to gene expression and protein abundances

Master’s Thesis in Biostatistics **Spring 2014**

University of California, Berkeley

Re-analyzed publicly available data from a single-cell RNA-Seq experiment

- Assessed impact of various normalization techniques
- Analyzed clustering patterns of high-quality samples to identify specific cell types

Manak Biology Lab **Summer 2011**

University of Iowa

Analyzed data from RNA-Seq experiments for comparison with microarray results

- Helped establish analysis pipeline from raw reads to gene expression quantification
- Performed de novo transcriptome assembly and differential expression testing

Honors and Awards

Invited Talk, Banff International Research Station for Mathematical Innovation and Discovery, Oaxaca, Mexico	Fall 2018
Best Poster, Northern California Computational Biology Symposium	Fall 2017
Outstanding Graduate Student Instructor	2016-17
Best Poster, UC Berkeley Computational Biology Retreat	Fall 2016
First Runner-up Best Talk, UC Berkeley Computational Biology Retreat	Fall 2015

Teaching Experience

Instructor

University of California, Berkeley:

- MCB 293S: Foundations of Biostatistical Practice
- PH 298: Special Topics in Applied Biostatistical Practice
- Computational Genomics Research Lab RNA-Seq Data Analysis Workshop
- Workshop at BioC 2016, 2017, 2018: Analysis of single-cell RNA-seq data with R and Bioconductor

TA/GSI

University of California, Berkeley:

- PH 240D: Computational Statistics with Applications in Biology and Medicine II, Sandrine Dudoit
- PH 240C: Computational Statistics with Applications in Biology and Medicine I, Sandrine Dudoit
- PH 240F: Statistical Genomics, Sandrine Dudoit
- PH 142: Introduction to Probability and Statistics in Biology and Public Health, Steve Selvin
- PH 241: Statistical Analysis of Categorical Data, Nicholas Jewell
- PH 141: Introduction to Biostatistics, Maureen Lahiff

University of Chicago:

- BIOS 20172: Mathematical Modeling for Pre-Med Students, Esmael Haddadian

Publications

Van den Berge K, Roux de Bézieux H, **Street K**, Saelens W, Cannoodt R, Saeys Y, Dudoit S, Clement L. "Trajectory-based differential expression analysis for single-cell sequencing data." *bioRxiv* (2019).

Street K, Risso D, Fletcher RB, Das D, Ngai J, Yosef N, Purdom E, Dudoit S. "Slingshot: cell lineage and pseudotime inference for single-cell transcriptomics." *BMC Genomics* 19, 477 (2018).

Gadye L, Das D, Sanchez MA, **Street K**, Baudhuin A, Wagner A, Cole MB, Choi YG, Yosef N, Purdom E, Dudoit S, Risso D, Ngai J, Fletcher RB. "Injury Activates Transient Olfactory Stem Cell States with Diverse Lineage Capacities." *Cell Stem Cell* 0, (2017).

Fletcher RB, Das D, Gadye L, **Street K**, Baudhuin A, Wagner A, Cole MB, Flores Q, Choi YG, Yosef N, Purdom E, Dudoit S, Risso D, and Ngai J. "Deconstructing Olfactory Stem Cell Trajectories at Single-Cell Resolution." *Cell Stem Cell* 0, (2017).

Davé V, **Street K**, Francis S, Bradman A, Riley L, Eskenazi B, Holland N. "Bacterial microbiome of breast milk and child saliva from low-income Mexican-American women and children." *Pediatr. Res.* 79, 846–854 (2016).

Holland N, Huen K, Tran V, **Street K**, Nguyen B, Bradman A, Eskenazi B. "Urinary Phthalate Metabolites and Biomarkers of Oxidative Stress in a Mexican-American Cohort: Variability in Early and Late Pregnancy." *Toxics* 4 (2016).

Huen K, Yousefi P, **Street K**, Eskenazi B, Holland N. "PON1 as a model for integration of genetic, epigenetic, and expression data on candidate susceptibility genes." *Environ Epigenet* 1 (2015).