

Kelly Street, Ph.D.

Curriculum Vitae

Assistant Professor of Population and Public Health Sciences

Division of Biostatistics

Keck School of Medicine of USC

EDUCATION

2022 - Present	Keck School of Medicine of USC Assistant Professor of Population and Public Health Sciences Division of Biostatistics
2019 - 2022	Dana-Farber Cancer Institute Harvard T.H. Chan School of Public Health Postdoctoral Research Fellow in Data Science Advisor: Rafael Irizarry
2014 - 2018	University of California, Berkeley Doctor of Philosophy in Biostatistics Designated Emphasis in Computational Biology Advisor: Sandrine Dudoit
2012 - 2014	University of California, Berkeley Master of Arts in Biostatistics
2008 - 2012	University of Chicago Bachelor of Sciences in Mathematics

RESEARCH INTERESTS

- Development and evaluation of computational methods for high-dimensional genomic data, particularly single-cell RNA sequencing, immune profiling, and mass cytometry.
- Multi-omics integration for leveraging information from disparate genomic assays in the same experiment.
- Applied statistics education and communication, for both statisticians and non-statisticians.
- Genomic data visualization strategies.
- Reliable, open-source software development.

HONORS AND AWARDS

2017	Best Poster, Northern California Computational Biology Student Symposium
2017	Outstanding Graduate Student Instructor, U.C. Berkeley

2016 Best Poster, U.C. Berkeley Computational Biology Retreat
2015 Best Talk Runner-up, U.C. Berkeley Computational Biology Retreat
2015 Genomics Training Grant, NIH

RESEARCH EXPERIENCE

2019 - 2022 Dana-Farber Cancer Institute
Developed novel methods for integrating single-cell RNA sequencing data with paired T cell receptor sequencing data. Analyzed data from genome-wide assays measuring DNA methylation and chromatin accessibility. Designed strategies for quality control and classification of mass cytometry data. Developed R packages implementing GLM-PCA and condition-specific trajectory inference.

2015 - 2018 University of California, Berkeley
Dissertation: *Trajectory Inference and Analysis in Single-Cell Genomics*
Developed methods for trajectory inference and downstream differential expression analysis in single-cell RNA sequencing (scRNAseq). Performed statistical analysis for multiple scRNAseq projects with collaborators in Molecular and Cell Biology. Developed R packages for Bioconductor implementing novel analysis methods.

Summer 2015 Thermo Fisher Scientific
Ion Torrent R&D Internship
Assessed the efficacy of different sequencing strategies in accurately quantifying transcript usage in RNAseq.

2014 - 2015 University of California, Berkeley
Nina Holland Children's Environmental Health Lab
Served as data analyst and statistician on multiple projects. Studied microbial communities via 16S ribosomal RNA-Seq. Quantified miRNA levels and relationships to gene expression and protein abundances.

2013 - 2014 University of California, Berkeley
Master's Thesis in Biostatistics
Utilized publicly available single-cell RNA-Seq data to assess the impact of various normalization strategies and the effectiveness of various clustering methods at identifying specific cell types.

Summer 2011 University of Iowa
John Manak Biology Lab
Provided bioinformatics support, establishing an analysis pipeline for RNAseq data, including alignment, de novo transcriptome assembly, and expression quantification.

TEACHING EXPERIENCE

Course Facilitator

University of California, Berkeley

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| Fall 2018 | Foundations of Biostatistical Practice, U.C. Berkeley
Molecular and Cell Biology (MCB 293S) |
| Spring 2017,
2016 | Special Topics in Applied Biostatistical Practice
Public Health (PH 298) |

Graduate Student Instructor

University of California, Berkeley

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| Fall 2016 | Computational Statistics with Applications in Biology and Medicine II
Statistics (STAT 245D) |
| Spring 2016 | Statistical Genomics
Statistics (STAT 245F) |
| Fall 2015 | Computational Statistics with Applications in Biology and Medicine I
Statistics (STAT 245C) |
| Fall 2013,
2012 | Introduction to Probability and Statistics in Biology and Public Health
Public Health (PH 142) |
| Summer 2016,
2014, 2013 | Introduction to Biostatistics
Public Health (PH 141) |
| Spring 2013 | Statistical Analysis of Categorical Data
Public Health (PH 241) |

Teaching Assistant

University of Chicago

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| Spring 2012 | Mathematical Modeling for Pre-Med Students
Biological Sciences (BIOS 20172) |
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PUBLICATIONS

Peer-reviewed publications

BRAIN Initiative Cell Census Network (BICCN). "A multimodal cell census and atlas of the mammalian primary motor cortex." *Nature*, 2021.

Z Yao*, H Liu*, F Xie*, S Fischer*, et al. "An integrated transcriptomic and epigenomic atlas of mouse primary motor cortex cell types." *Nature*, 2021.

DA Braun*, **K Street***, KP Burke, DL Cookmeyer, T Denize, CB Pedersen, SH Gohil, N Schindler, L Pomerance, L Hirsch, Z Bakouny, Y Hou, J Forman, T Huang, S Li, A Cui, DB Keskin, J Steinharter, G Bouchard, M Sun, EM Pimenta, W Xu, KM Mahoney, BA McGregor, MS Hirsch, SL Chang, KJ Livak, DF McDermott, SA Shukla, LR Olsen, S Signoretti, AH Sharpe, RA Irizarry, TK Choueiri**, CJ Wu**. “Progressive immune dysfunction with advancing disease stage in renal cell carcinoma.” *Cancer Cell*, 2021.

K Van den Berge, H Roux de Bézieux, **K Street**, W Saelens, R Cannoodt, Y Saeys, S Dudoit, L Clement. “Trajectory-based differential expression analysis for single-cell sequencing data.” *Nature Communications*, 2020.

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

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

F Perraudeau, D Risso, **K Street**, E Purdom, S Dudoit. “Bioconductor workflow for single-cell RNA sequencing: Normalization, dimensionality reduction, clustering, and lineage inference.” *F1000 Research*, 2017.

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

Preprints

P Weiler, K Van den Berge, **K Street***, S Tiberi*. “A guide to trajectory inference and RNA velocity.” Book chapter. *bioRxiv*, 2021.

H Roux de Bézieux, K Van den Berge, **K Street***, S Dudoit*. “Trajectory inference across multiple conditions with condiments: differential topology, progression, differentiation, and expression.” *bioRxiv*, 2021.

K Van den Berge, H-J Chou, H Roux de Bézieux, **K Street**, D Risso, J Ngai, S Dudoit. “Normalization benchmark of ATAC-seq datasets shows the importance of accounting for GC-content effects.” *bioRxiv*, 2021.

H Roux de Bézieux, **K Street**, S Fischer, K Van den Berge, R Chance, D Risso, J Gillis, J Ngai, E Purdom, S Dudoit. “Improving replicability in single-cell RNA-Seq cell type discovery with Dune.” *bioRxiv*, 2020.

*/** Contributed equally

SOFTWARE

H Roux de Bézieux, **K Street**, K Van den Berge*. “traviz: Trajectory Functions for Visualization and Interpretation.” Bioconductor R package.

A Lun*, **K Street**. “TrajectoryUtils: Single-Cell Trajectory Analysis Utilities.” Bioconductor R package.

K Street*, FW Townes, D Risso, S Hicks. “scry: Small-Count Analysis Methods for High-Dimensional Data.” Bioconductor R package.

H Roux de Bézieux*, **K Street**. “Dune: Improving replicability in single-cell RNA-Seq cell type discovery.” Bioconductor R package.

FW Townes*, **K Street**, J Yeung. “glmpca: Feature Selection and Dimension Reduction based on a Multinomial Model.” CRAN R package.

K Van den Berge, H Roux de Bézieux*, **K Street**, L Clement, S Dudoit. “tradeSeq: trajectory-based differential expression analysis for sequencing data.” Bioconductor R package.

K Street*, D Risso, D Das, S Dudoit, K Van den Berge, R Cannoodt. “slingshot: Tools for ordering single-cell sequencing.” Bioconductor R package.

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PRESENTATIONS AND INVITED TALKS

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| 2022 | MD Anderson Cancer Center, Brain Tumor Program
Invited talk: “Single-Cell Trajectory Analysis” |
| 2021 | Harvard Chan Bioinformatics Core, Current Topics in Bioinformatics, virtual
Workshop: “A better way to clean CyTOF data using cytofQC” |
| 2021 | Northwestern University, Feinberg School of Medicine, Division of Pulmonary and Critical Care, Research in Progress seminar, virtual
Invited talk: “Differential Expression and Differential Topology in Single-Cell Trajectories” |
| 2021 | Dana-Farber Cancer Institute, NeoVax Scientific Seminar
Talk: “TCRseq Data Analysis” |
| 2021 | BioC 2021, virtual
Workshop: “Trajectory Inference Across Conditions: differential expression and differential progression” |
| 2021 | Interdisciplinary and Quantitative Biology Summer REU, virtual
Workshop: “Healthcare Innovation Replicathon” |
| 2020 | EuroBic 2020, virtual
Workshop: “Trajectory Inference Across Conditions” |
| 2020 | BioC 2020, virtual
Workshop: “Trajectory Inference Across Conditions” |
| 2020 | Broad Institute Single-Cell Meeting, virtual
Talk: “Single Cell Immune Profiling of Renal Cell Carcinoma” |
| 2020 | Interdisciplinary and Quantitative Biology Summer REU, virtual
Workshop: “Healthcare Innovation Replicathon” |

- 2019 Interdisciplinary and Quantitative Biology Summer REU, Río Piedras, Puerto Rico
Workshop: “Healthcare Innovation Replicathon”
- 2018 Statistical and Computational Challenges in High-Throughput Genomics with Application to Precision Medicine, Oaxaca, Mexico
Invited Talk: “Statistical Methods and Software for the Study of Stem Cell Differentiation Using Single-Cell Transcriptome Sequencing”
- 2018 BioC 2018, Toronto, Canada
Workshop: “Analysis of single-cell RNA-seq data: Dimensionality reduction, clustering, and lineage inference”
- 2017 BioC 2017, Boston, MA
Workshop: “Bioconductor workflow for single-cell RNA-seq data analysis: dimensionality reduction, clustering, and pseudotime ordering”
- 2016 BioC 2016, Stanford, CA
Workshop: “Analysis of Single-Cell RNA-Seq Data with R and Bioconductor”
- 2016 Computational Genomics Research Lab, Berkeley, CA
Workshop: “RNA-Seq Data Analysis”

REFERENCES

References are available upon request.