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Education

- 2017–2022 **Ph.D., Bioinformatics, University of California, San Francisco**
Thesis Title: *Following tumor progression step-by-step with CRISPR/Cas9-based single-cell lineage tracing technologies and improved computational methods*
Research Advisors: Jonathan Weissman and Nir Yosef
Thesis Committee Members: Hani Goodarzi and Matthew Spitzer
- 2013–2017 **B.A., Computer Science, University of California, Berkeley**
Research Advisors: Rasmus Nielsen, Russ Corbett-Detig, & Nir Yosef

Academic Appointments

- 2022– **Stanford University**, Postdoctoral Scholar
Hosted by Howard Chang
- 2017–2022 **University of California, San Francisco**, Graduate Student Researcher
Advised by Jonathan Weissman and Nir Yosef
- 2020 **Weizmann Institute, Rehovot Israel**, Visiting Researcher Fellow
Hosted by Ido Amit

Publications

Journal Articles

- (1) Yang D*, **Jones MG***, ..., Yosef N, Jacks T, Weissman JS. [Lineage tracing reveals the phylogenetics, plasticity, and paths of tumor evolution](#). *Cell*. 2022
- (2) **Jones MG***, Rosen Y*, Yosef N. [Interactive, integrated analysis of single-cell transcriptomic and phylogenetic data with PhyloVision](#). *Cell Reports Methods*. 2022.
- (3) Gong W*, Granados A*, Hu J*, **Jones MG***, Raz O*, Salvador-Martinez I*, Zhang H*, ..., Meyer P. [Benchmarked approaches for cell lineage reconstructions of in vitro dividing cells and in silico models of Caenorhabditis elegans and Mus musculus developmental trees](#). *Cell Systems*. 2021.

- (4) Quinn JJQ*, **Jones MG***, Okimoto RA, Nanjo S, Chan MM, Yosef N, Bivona TG, Weissman JS. [Single-cell lineages reveal the rates, routes, and drivers of metastasis in cancer xenografts.](#) *Science*. 2021
- (5) **Jones MG***, Khodaverdian A*, Quinn JJ*, Chan MM, Hussmann JA, Wang R, Xu C, Weissman JS, Yosef N. [Inference of Single Cell Phylogenies from Lineage Tracing Data with Cassiopeia.](#) *Genome Biology*. 2020
- (6) Newberry RW, ..., **Jones MG**, ..., DeGrado WF, Kampmann M. [Robust Sequence Determinants of \$\alpha\$ -Synuclein Toxicity in Yeast Implicate Membrane Binding.](#) *ACS Chem. Biol.*. 2020
- (7) DeTomaso D*, **Jones MG***, Subramaniam M, Ashuach T, Ye JC, Yosef N. [Functional Interpretation of Single-Cell Similarity Maps.](#) *Nature Communications*. 2019
- (8) Chan MM*, Smith ZD*, Grosswendt S, Kretzmer H, Norman T, Adamson B, Jost M, Quinn JJ, Yang D, **Jones MG**, Khodaverdian A, Yosef N, Meissner A, Weissman JS. [Molecular recording of mammalian embryogenesis.](#) *Nature*. 2019
- (9) Corbett-Detig, R. and **Jones, M.** [SELAM: Simulation of Epistasis and Local adaptation during Admixture with Mate choice.](#) *Bioinformatics*. 2016

*** denotes equal contribution**

Refereed Workshop Papers

- (1) Ouardini K, Lopez R, **Jones MG**, Prillo S, Zhang R, Jordan MI, Yosef N. [Reconstructing unobserved cellular states from paired single-cell lineage tracing and transcriptomics data.](#) ICML Workshop in Computational Biology. 2021.

Teaching Assistant

2020	CS176: Algorithms for Computational Biology	University of California, Berkeley
2020	BP205B: Dynamical Systems Modeling	University of California, San Francisco
2019	BP205B: Dynamical Systems Modeling	University of California, San Francisco
2018	CS176: Algorithms for Computational Biology	University of California, Berkeley

Funding, Awards & Honors

2019-2022	UCSF Discovery Fellowship
2020	Allen Institute Cell Lineage Reconstruction DREAM Challenge Best Performer
2019	Quantitative Biology Consortium Retreat Best Poster
2018	Quantitative Biology Consortium Retreat Best Poster

Presentations

Invited Talks

2022	Stanford Biostatistics Workshop, seminar
2022	UCSF Single Cell Interest Group, seminar
2022	Cell Circuits and Epigenomics @ Broad Institute, seminar
2021	Greenleaf Lab @ Stanford, group meeting
2021	Cellular & Tissue Genomics @ Genentech, seminar
2021	Wysocka Lab @ Stanford, group meeting
2021	Chang Lab @ Stanford, group meeting
2021	Weinberg Lab @ MIT, journal club
2021	Royer Group @ Biohub & Wagner Group @ UCSF, group meeting
2021	AI/ML @ Genentech, seminar
2021	NIH Single Cell Users Group, seminar
2021	Yale Center for Biomedical Data Science, seminar
2020	UC Berkeley Computational Biology Skills Seminar, seminar
2019	UC Berkeley Computational Biology Skills Seminar, seminar

Contributed Talks

2021	NIH Centers of Excellence in Genomic Science (CEGS) Annual Meeting
2021	Society for Molecular Biology and Evolution (SMBE) Annual Meeting
2021	The Cancer Target Discovery and Development Alliance NIH Site Visit
2021	CZI Biohub Seed Networks Computational Biology Meeting
2020	Hindsight 2020 - The Allen Institute Developmental Recording Symposium
2020	CZI Seed Network 2020 Annual Meeting
2020	Center for Genomic Editing and Recording (CGER) Retreat
2019	UC Berkeley Computational and Genomic Biology Retreat
2019	Quantitative Biology Consortium Retreat

Posters

2019	Quantitative Biology Consortium Retreat
2019	Chan-Zuckerberg Biohub Confab
2019	Next Generation Genomics
2018	Quantitative Biology Consortium Retreat

Industry Experience

2020	Google Health Genomics, research intern
2016	United States Medical Affairs @ Genentech, intern

Professional Activities

2020-2021	UC Berkeley Computational Biology Skills Seminar, coordinator
2019	UC Berkeley Computational Biology Skills Seminar, participant
2018-2019	Northern California Computational Biology Student Symposium, coordinator
2019	UCSF Integrative Program in Quantitative Biology (IPQB) Bootcamp, coordinator
2018	UCSF Integrative Program in Quantitative Biology (IPQB) Bootcamp, Bioinformatics Module Leader

Supervision

2021-2022	Kevin An, Undergraduate	UC Berkeley
2021-2022	Ivan Kristanto, Undergraduate	UC Berkeley
2020-2022	Sohit Miglani, Junior Specialist	UC San Francisco
2019-2022	Richard Zhang, Research Engineer	UC Berkeley
2020-2021	Khalil Ouardini, MSc Student	ENS Cachan, MVA
2019-2021	Yanay Rosen, Undergraduate	UC Berkeley
2019-2021	Robert Wang, Undergraduate	UC Berkeley

Software

- [Cassiopeia](#) Analysis tools for single-cell lineage tracing data.
- [VISION](#) Functional annotation of scRNA-seq data.
- [SELAM](#) Simulation framework for large-scale population admixture.

References

Available on request.