Matthew G. Jones, PhD

NCI Early-Career K99/R00 Postdoctoral Fellow

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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**, NCI Early-Career K99/R00 Postdoctoral Fellow
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

Preprints

(1) Zhu K*, **Jones MG***, Luebeck J, Bu X, Yi H, Hung KL, Wong ITL, Zhang S, Mischel PS, Chang HY, Banfa V. CoRAL accurately resolves extrachromosomal DNA genome structures with long-read sequencing. *BioRxiv*. 2024

(2) Rose JC, Wong ITL, Daniel B, **Jones MG**, Hung KL, Curtis EJ, Mischel PS, Chang HY. Disparate pathways for extrachromosomal DNA biogenesis and genomic DNA repair. *BioRxiv*. 2023

(3) Sinha S, …, **Jones MG**, …Ruppin E. Predicting patient treatment response and resistance via single-cell transcriptomics of their tumors. *Submitted*. 2022

(4) Hung K*, **Jones MG***, Wong I*, Curtis EJ*, …, Mischel PS, Chang HY. Coordinated inheritance of extrachromosomal DNA species in human cancer cells. *BioRxiv*. 2023

*** denotes equal contribution**

Journal Articles

(1) Weng C, Yu F, Yang D, Poeschla M, Liggett LA, **Jones MG**, …, Weissman JS, Sankaran VG. Deciphering cell states and genealogies of human hematopoiesis. *Accepted, Nature*. 2023

(2) Heumos L*, Schaar A*, …, **Best Practice Writing Team**, Theis F. New best practices for single cell analysis across modalities. *Nature Reviews Genetics*. 2023

(3) **Jones MG***, Yang D, Weissman JS. New Tools for Lineage Tracing in Cancer In vivo. *Annual Reviews Cancer Biology (In press)*. 2023

(4) Yang D*, **Jones MG***, …, Yosef N, Jacks T, Weissman JS. Lineage tracing reveals the phylodynamics, plasticity, and paths of tumor evolution. *Cell*. 2022

(5) **Jones MG***, Rosen Y*, Yosef N. Interactive, integrated analysis of single-cell transcriptomic and phylogenetic data with PhyloVision. *Cell Reports Methods*. 2022.

(6) 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.

(7) 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

(8) **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

(9) Newberry RW, ..., **Jones MG**, ..., DeGrado WF, Kampmann M. Robust Sequence Determinants of α-Synuclein Toxicity in Yeast Implicate Membrane Binding. *ACS Chem. Biol.*. 2020

(10) DeTomaso D*, **Jones MG***, Subramaniam M, Ashuach T, Ye JC, Yosef N. Functional Interpretation of Single-Cell Similarity Maps. *Nature Communications*. 2019

(11) 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

(12) 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.

*** denotes equal contribution**

Book Chapters

(1) **Jones MG***, Piran Z*. Lineage tracing. *Multimodal single-cell analysis.* 2022

Teaching

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

Funding, Awards & Honors

2024-2028	NCI Pathway to Independence Award for Early-Stage Postdoctoral Researchers (K99/R00)
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

2023 Stanford Medicine EpiBio, seminar

2023 Cell Circuits and Epigenomics @ Broad Institute, seminar

2023 Department of Molecular and Cellular Biology @ UC Berkeley, seminar

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

2023 eDyNAmiC Cancer Grand Challenge Annual Symposium, seminar

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

2023 Mechanisms and Models of Cancer

2023 UCLA Computational Genomics Summer Institute (CGSI)

2019 Quantitative Biology Consortium Retreat

2019 Chan-Zuckerberg Biohub Confab

2019 Next Generation Genomics

2018 Quantitative Biology Consortium Retreat

Industry Experience

2022- Vevo Therapeutics, single-cell advisor and consultant

2020 Google Health Genomics, research intern

2016 United States Medical Affairs @ Genentech, intern

Professional Activities & Service

2023 Volunteer lecturer for Stanford Future Advances of Science and Technology (FAST) high school mentorship program

2022-2023 Volunteer lecturer at Berkeley High School, IB & AP Biology

2020-2021 UC Berkeley Computational Biology Skills Seminar, coordinator

2019 UC Berkeley Computational Biology Skills Seminar, volunteer module leader

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

Software

CoRAL	Tool for reconstructing focal amplifications using long-read sequencing data.
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.