

Matthew G. Jones, PhD

NCI Early-Career K99/R00 Postdoctoral Fellow

2145 CCSR

Stanford University

Stanford, CA

Email: mgjones@stanford.edu

Home: mattjones315.github.io

ORCID iD: orcid.org/0000-0002-0363-4493

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) 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
- (2) Sinha S, ..., **Jones MG**, ...Ruppin E. [Predicting patient treatment response and resistance via single-cell transcriptomics of their tumors](#). *Submitted*. 2022
- (3) Hung K*, **Jones MG***, Wong I*, ..., Mischel PS, Chang HY. [Coordinated inheritance of extra-chromosomal 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 In Principle, 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 phylogenomics, 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 \$\alpha\$ -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) Zhu K*, **Jones MG***, Luebeck J, Bu X, Yi H, Hung KL, Wong ITL, Zhang S, Mischel PS, Chang HY, Bafna V. CoRAL accurately resolves extrachromosomal DNA genome structures with long-read sequencing. *Research in Computational Molecular Biology (RECOMB)*. 2024
- (2) 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**

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

Supervision & Mentorship

2022	Shiyi Yang, Graduate Student	UC Berkeley
2021-2022	Kevin An, Undergraduate	UC Berkeley
2021-2022	Ivan Kristanto, Undergraduate	UC Berkeley
2020-2022	Sohit Miglani, Junior Specialist	UC San Francisco
2020-2022	Joseph Min, Graduate Student	MIT
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
2019-2020	Suhas Rao, 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.