

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

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## 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

<a href="#">CoRAL</a>	Tool for reconstructing focal amplifications using long-read sequencing data.
<a href="#">Cassiopeia</a>	Analysis tools for single-cell lineage tracing data.
<a href="#">VISION</a>	Functional annotation of scRNA-seq data.
<a href="#">SELAM</a>	Simulation framework for large-scale population admixture.

## References

Available on request.