

# Matthew G. Jones, PhD

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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

### Preprints

- (1) Sinha S, ..., **Jones MG**, ...Ruppin E. [Predicting patient treatment response and resistance via single-cell transcriptomics of their tumors](#). *Submitted*. 2022
- (2) Hung K\*, **Jones MG\***, Wong I\*, ..., Mischel PS, Chang HY. [Coordinated inheritance of extra-chromosomal DNA species in human cancer cells](#). *BioRxiv*. 2023

### Journal Articles

- (1) Heumos L\*, Schaar A\*, ..., **Best Practice Writing Team**, Theis F. [New best practices for single cell analysis across modalities](#). *Nature Reviews Genetics*. 2023

- (2) **Jones MG\***, Yang D, Weissman JS. [New Tools for Lineage Tracing in Cancer In vivo](#). *Annual Reviews Cancer Biology (In press)*. 2023
- (3) Yang D\*, **Jones MG\***, ..., Yosef N, Jacks T, Weissman JS. [Lineage tracing reveals the phylogenomics, plasticity, and paths of tumor evolution](#). *Cell*. 2022
- (4) **Jones MG\***, Rosen Y\*, Yosef N. [Interactive, integrated analysis of single-cell transcriptomic and phylogenetic data with PhyloVision](#). *Cell Reports Methods*. 2022.
- (5) 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.
- (6) 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
- (7) **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
- (8) Newberry RW, ..., **Jones MG**, ..., DeGrado WF, Kampmann M. [Robust Sequence Determinants of  \$\alpha\$ -Synuclein Toxicity in Yeast Implicate Membrane Binding](#). *ACS Chem. Biol.*. 2020
- (9) DeTomaso D\*, **Jones MG\***, Subramaniam M, Ashuach T, Ye JC, Yosef N. [Functional Interpretation of Single-Cell Similarity Maps](#). *Nature Communications*. 2019
- (10) 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
- (11) 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.

### 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

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	Cell Circuits and Epigenomics @ Broad Institute, 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**

- 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, 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

<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.