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
Advised 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 (* denotes equal contribution)

(1) **Jones MG***, Sun D*, ..., Chen F, Weissman JS, Yosef N, Yang D. Spatiotemporal lineage tracing reveals the dynamic spatial architecture of tumor growth and metastasis. *BioRxiv*. 2024.

(2) Kraft K*, Murphy SE*, **Jones MG***, ..., Chang HY. Enhancer potential of an ancient retrotransposable element when amplified on ecDNA. *BioRxiv*. 2024.

(3) Noorani I*, Haughey M*, ..., **Jones MG**, ..., Mischel PS, Swanton C, Werner B. Extrachromosomal DNA driven oncogene spatial heterogeneity and evolution in glioblastoma. *BioRxiv*. 2024.

(4) Prillo S, An K, Wu W, Kristanto I, **Jones MG**, Song YS, Yosef N. Tree reconstruction guarantees from CRISPR-Cas9 lineage tracing data using Neighbor-Joining. *BioRxiv*. 2024.

Journal Articles (* denotes equal contribution)

(1) Hung K*, **Jones MG***, Wong I*, Curtis EJ*, …, Mischel PS, Chang HY. Coordinated inheritance of extrachromosomal DNA species in human cancer cells. *Nature*. 2024

(2) 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. *Genome Research* (In Press). 2024

(3) Rose JC, Belk JA, …, **Jones MG**, …, Mischel PS, Chang HY. Disparate pathways for extrachromosomal DNA biogenesis and genomic DNA repair. *Cancer Discovery*. 2024

(4) Sinha S, …, **Jones MG**, …Ruppin E. PERCEPTION predicts patient response and resistance to treatment using single-cell transcriptomics of their tumors. *Nature Cancer*. 2024

(5) Weng C, Yu F, Yang D, Poeschla M, Liggett LA, **Jones MG**, …, Weissman JS, Sankaran VG. Deciphering cell states and genealogies of human hematopoiesis. *Nature*. 2024

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

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

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

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

(10) 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.

(11) 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

(12) **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

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

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

(15) 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

(16) Corbett-Detig, R. and **Jones, M**. SELAM: Simulation of Epistasis and Local adaptation during Admixture with Mate choice. *Bioinformatics*. 2016

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.

Submitted (* denotes equal contribution)

(1) Huang YH*, Belk JA*, ..., **Jones MG**, ..., Chang HY. A unified molecular approach for spatial epigenome, transcriptome, and cell lineages. 2024.

(2) Hung KL*, Sankar V*, Wong ITL, Kraft K, Shi Q, **Jones MG**, ..., Chang HY. Genetic elements retain extrachromosomal DNA in dividing cancer cells. 2024.

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) - R00: $250k/year for 3 years
2024	Cancer Grand Challenges Future Leaders Conference, Best Talk
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

2024	MD Anderson Systems Biology, seminar
2024	Stanford RNA Medicine Program (RAMP), seminar
2024	Stanford Medicine EpiBio, seminar
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

2024	Cancer Grand Challenges Future Leader Conference
2024	UCLA Computational Genomics Summer Institute (CGSI)
2024	Oxford Nanopore Technologies London Calling 2024
2024	RECOMB 2024, CoRAL team presentation
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

2024	Mechanisms and Models of Cancer
2024	Oxford Nanopore Technologies London Calling 2024
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

2024	Helen Wang, MSTP Student	Stanford
2024	William Khavari, High school student	Henry M Gunn High School
2024-	Valeh Valiollah Pour Amiri, Graduate Student	Stanford
2024-	Leena Satpathy, Undergraduate Researcher	UC Berkeley
2023	Lucy Zhang, Graduate Student	Stanford
2022	Jeremy D'Silva, Graduate Student	Stanford
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

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.