

Matthew Jones, PhD Candidate

CONTACT

PHONE: (818) 300-8991
EMAIL: matthew.jones@ucsf.edu
GITHUB: [mattjones315](https://github.com/mattjones315)

EDUCATION & TRAINING

Current PhD BIOINFORMATICS, **University of California, San Francisco** (GPA: 4.0)

2017 B.A. COMPUTER SCIENCE, **University of California, Berkeley**

RESEARCH EXPERIENCE

CURRENT	PhD Student - UC San Francisco & UC Berkeley Advisors: Jonathan Weissman & Nir Yosef Development of computational tools and CRISPR/Cas9-based technologies to investigate cancer progression & innate immune system dynamics in the tumor microenvironment.
2020	Research Intern - Google Health Hosts: Babak Alipanahi & Babak Behsaz Deep learning models for predicting Chronic Obstructive Pulmonary Disease (COPD) risk from Electronic Health Record (EHR) and genomic data.
2017	Undergraduate Researcher - UC Berkeley Advisor: Nir Yosef Computational method development, statistical inference, and software deployment for the analysis of large single cell RNA-seq (scRNA-seq) datasets.
2015-2016	Undergraduate Researcher - UC Berkeley Advisors: Rasmus Nielsen & Russell Corbett-Detig Investigation in the influences of admixture & local adaptation on population structure through simulation & software development.

PUBLICATIONS

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. *BioRxiv*. 2020

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

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

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

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. CRISPR-based molecular recording of mammalian embryogenesis. *Nature*. 2019

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

*** denotes equal contribution**

TEACHING

CS176: Algorithms for Computational Biology, 2020 - **Graduate Student Instructor, UC Berkeley**

BP205B: Dynamical Systems Modeling, 2020 - **Graduate Teaching Assistant, UCSF**

BP205B: Dynamical Systems Modeling, 2019 - **Graduate Teaching Assistant, UCSF**

CS176: Algorithms for Computational Biology, 2018 - **Reader, UC Berkeley**

AWARDS & FELLOWSHIPS

UCSF Discovery Fellowship

Best Poster - Quantitative Biology Consortium Retreat, 2019

Best Poster - Quantitative Biology Consortium Retreat, 2018

COMMUNITY SERVICE & OTHER EXPERIENCE

UC Berkeley Computational Biology Skills Seminar Coordinator, 2020

UC Berkeley Computational Biology Skills Seminar Participant, 2019

Coordinator for Northern California Computational Biology Student Symposium, 2018-19

UCSF Integrative Program in Quantitative Biology (IPQB) Bootcamp Coordinator, 2019

UCSF Integrative Program in Quantitative Biology (IPQB) Bootcamp Bioinformatics Leader, 2018

TALKS

“Inference of single-cell lineage tracing phylogenies and applications in cancer biology”. Center for Genomic Editing and Recording (CGER) Retreat. 2020

“Getting started with Tensorflow”. UC Berkeley Computational Biology Skills Seminar. 2020

“Leveraging high-resolution single-cell lineage tracing to study metastasis in a lung cancer xenograft model”. UC Berkeley Computational and Genomic Biology Retreat. 2019

“Inference of Single-Cell Phylogenies from Lineage Tracing Data”. Quantitative Biology Consortium Retreat. 2019

“Building your first R package”. UC Berkeley Computational Biology Skills Seminar. 2019

POSTERS

“Inference of Single Cell Phylogenies from Lineage Tracing Data”. Quantitative Biology Consortium Retreat. 2019

“Inference of Single Cell Phylogenies from Lineage Tracing Data”. Chan-Zuckerberg Biohub Confab. 2019

“Functional Interpretation of Single-Cell Similarity Maps”. Next Generation Genomics. 2019

“Functional Interpretation of Single-Cell Similarity Maps”. Quantitative Biology Consortium Retreat. 2018