

Miriam Shiffman

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EDUCATION

MIT — 2016-present
Ph.D. candidate (GPA 5.0)
Computational & Systems Biology

RELEVANT COURSES:

Machine Learning
Bayesian Modeling & Inference
Fundamentals of Probability
Algorithms for Machine Learning
Picturing Science & Engineering
Advanced Computational Biology
Machine Learning for Healthcare
Deep Learning for Life Sciences
Frontiers in Health & Disease
Molecular Biology

Pomona College — 2009-2013
B.A., *Magna cum laude*
Molecular Biology

RELEVANT COURSES:

Linear Algebra • Probability
Deterministic Operations Research
Monte Carlo Methods • Statistics
Computation & Cognition
Foundations of Digital Design

EXPERIENCE

Ph.D. student, MIT CSAIL & Broad Institute
Cambridge, MA — 2016-present

- ⊆ Bayesian methods for learning from single-cell studies
- ⊆ Advised by [Tamara Broderick](#) and [Aviv Regev](#)

Research engineer intern, Fast Forward Labs
New York City — 2016

- ⊆ Published [series of whitepapers](#) for the FFL blog exploring the theory and applications of Variational Autoencoders (VAEs)
- ⊆ Developed open-source TensorFlow implementation: [vae-tf](#)

Programmer, Recurse Center
New York City — 2015

- ⊆ Received grant to pursue projects in machine learning, data visualization, and image processing

Fulbright scholar, Australian Centre for Ecogenomics,
University of Queensland
Brisbane, Australia — 2014-2015

- ⊆ Computational microbiology research, using next-generation DNA sequencing to study marsupial gut microbiomes, from community-level to individual population genomes
- ⊆ Led project to collect and analyze large-scale (10-100 Gb) metagenomic data using Python, command-line tools, and R
- ⊆ First-author publication, 2017

Cheese microbiologist, Cellars at Jasper Hill
Greensboro, VT — 2013

- ⊆ Inaugural microbiologist for an award-winning cheesemaker

Researcher, Pomona College
Claremont, CA — 2010-2013

- ⊆ Molecular genetics research, studying the evolution of selfish DNA (homing endonucleases) through bioinformatics and experiment
- ⊆ Senior research thesis; first-author manuscript

Intern, Harvard FAS Center for Systems Biology
Cambridge, MA — 2012

- ⊆ Studying cheese rind microbes as model microbial ecosystems
- ⊆ Poster presented at microbiology conference (ISME) in Seoul, 2014

PUBLICATIONS & MANUSCRIPTS

[Shiffman ME](#), WT Stephenson, G Schiebinger, J Huggins, T Campbell, A Regev, and T Broderick (2018) Reconstructing probabilistic trees of cellular differentiation from single-cell RNA-seq data. [arXiv: 1811.11790](#).

[Shiffman ME](#), RM Soo, PG Dennis, M Morrison, GW Tyson, and P Hugenholtz (2017) Gene and genome-centric analyses of koala and wombat fecal microbiomes point to metabolic specialization for Eucalyptus digestion. *PeerJ* 5(e4075).

[Shiffman ME](#) and BM Charalambous (2012) The search for archaeal pathogens. *Reviews in Medical Microbiology* 23(3): 45-51.

HONORS

NSF Graduate Research Fellowship
U.S. Fulbright Scholarship (Australia)

Bertsch Prize in Molecular Biology
Distinction in the Senior Thesis

Phi Beta Kappa

Sigma Xi

Jaeger Mathematics Prize

Shiffman ME and LM Seligman (manuscript) Evolutionary dynamics of homing endonucleases: Characterizing related inteins in functionally distinct host genes in hyperthermophilic archaea. In prep.

RECENT PRESENTATIONS

Reconstructing probabilistic trees of cellular differentiation (work with: A Regev, T Broderick, et al)

[Talks]

- † Spotlight, *Learning Meaningful Representations of Life* workshop @ NeurIPS (2019) Vancouver.
- † Contributed, *Women in Computational Biology* (2019) HHMI Janelia, Ashburn, VA.
- † Contributed, *BNP12* (2019) Oxford. [ISBA travel award]
- † Invited, *Phyloseminar.org*: series on nontraditional data (2019).
- † Contributed, *Bayesian Nonparametrics* workshop @ NeurIPS (2018) Montréal.
- † Invited primer, *Models, Inference, and Algorithms* (2018) Broad Institute, Cambridge, MA.

[Poster #1]: *initial description of the model.*

- † *Approximate Bayesian Inference* and *Machine Learning in Computational Biology* workshops @ NeurIPS (2017) Long Beach, CA.
- † *Machine Learning Summer School* (2018) Universidad Torcuato Di Tella, Buenos Aires.
- † *Women in Data Science* conference (2018) Microsoft Research New England, Cambridge, MA.
- † Broad Institute annual retreat (2017) Boston, MA.
- † MIT Computational & Systems Biology retreat (2018) Kennebunkport, ME.

[Poster #2]: *development of inference, simulation experiments showing recovery of latent trajectories.*

- † *Bayesian Nonparametrics* workshop @ NeurIPS (2018) Montréal. [Google travel award]
- † *Women in Machine Learning* workshop (2018) Montréal.
- † MIT College of Computing launch (2019) Cambridge, MA.
- † Broad Institute annual retreat (2018) Boston, MA.

[Poster #3]: *creative probabilistic programming for biology.*

- † *Learning Meaningful Representations of Life* workshop @ NeurIPS (2019) Vancouver. [NIH travel award]

OTHER PROJECTS

lda2vec-tf: simultaneous inference of document, topic, and word embeddings via *lda2vec*, a hybrid of **latent Dirichlet allocation** and **word2vec**

- ↔ Ported the **original model** (in Chainer) to the first published version in TensorFlow
- ↔ Adapted to analyze 25,000 microbial genomes (80 million genes) to learn **microbial gene and genome embeddings**, and predict the function of non-annotated genes

k-meanz: image segmentation (TensorFlow)

- ↔ **Visualization** of clustering dynamics

Set solver: team project to solve the card game “Set”

- ↔ **Computer vision** algorithms to detect winning sets in photos of dealt cards
- ↔ Interactive Twitter bot: **@ProfessorSet**

Pangea3: interactive map (D3) of global continental drift and fossil paleolocation over geologic time (230 million years)

- ↔ Team hackathon at the American Museum of Natural History (covered by **NY Observer**)

cinematic / lsbeer / mit-lunch: command-line tools for everyday life

TEACHING EXPERIENCE

Teaching Assistant, MIT 7.03 (undergraduate genetics), with Profs. Aviv Regev & Peter Reddien — 2018