

Jesse Eaton

Machine Learning Scientist

jesseantoneaton@gmail.com
(631) 880-0732
San Francisco, CA
New York, NY

Website: jaebird123.github.io
Github: github.com/jeatonsf
Linkedin: linkedin.com/in/jesseaton

EDUCATION

Carnegie Mellon University

M.S. Computational Biology, School of Computer Science, GPA: 3.91

December 2017

Tufts University

B.S. Biomedical Engineering, GPA: 3.45

May 2015

SKILLS

Languages: Python, C++, C, Golang

Machine Learning: PyTorch, Sklearn, XGBoost, Flyte

Math: Algorithms, Probability, Statistics, Regression

Other: Genomics, Gcloud

EXPERIENCE

Software Engineer, Machine Learning, Meta

October 2023 - Present

- Make Instagram the best destination for creators

Senior Machine Learning Scientist, Freenome

September 2019 - October 2023

- Developed core machine learning model increasing classification performance of colorectal cancer detection to industry high of 0.9 sensitivity at 0.9 specificity
- Designed important features with high signal to noise in genomics data
- Promoted iterations of important models by developing framework for model comparison
- Streamlined user model reports by redesigned reporting and model diagnostic infrastructure
- Managed ML science intern leading to development of robust kmer model pipeline

Machine Learning Research Engineer, Qeexo

February 2018 - April 2019

- Generated multiple experimental company products by fusing sensor data with efficient machine learning classifiers <https://www.youtube.com/watch?v=1S6irWy8G20>
- Compressed gradient boosting classifier to 20 kB size for highly time/space/energy constrained environments achieving < 5ms classification time
- Increased customer awareness by demoing projects at Consumer Electronics Show 2019

Software Systems Engineer, MITRE

September 2015 - August 2016

- Built web based electronic medical validation tool for Health Services Department as main engineer using Amazon Elastic Compute Cloud (AWS)

PUBLICATIONS

Jesse Eaton, Jingyi Wang, Russell Schwartz, "Deconvolution and phylogeny inference of structural variations in tumor genomic samples." *Bioinformatics*, Volume 34, Issue 13, 01 July 2018, Pages i357–i365

Yifeng Tao, Ashok Rajaraman, Xiaoyue Cui, Ziyi Cui, **Jesse Eaton**, Hannah Kim, Jian Ma, Russell Schwartz, "Improving personalized prediction of cancer prognoses with clonal evolution models." *bioRxiv* 761510