Jesse Eaton

Machine Learning Scientist

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EDUCATION

Carnegie Mellon University M.S. Computational Biology, School of Computer Science, GPA: 3.91 Tufts University B.S. Biomedical Engineering, GPA: 3.45

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

- Initiated development of a topic classifier from 0→1 in 1 month to unlock \$1.5M daily spend from Temu
- Led the development of a creator classifier, now used as the goaling metric in an org of 200 members. Reduced labeling budget by 90% and simplified architecture to reduce work from 10 FTE to 0.5 FTE
- Built inspiration hub signals to increase content production, receiving positive feedback from creators panel

Senior Machine Learning Scientist, Freenome

- 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

Machine Learning Research Engineer, Qeexo

- Generated multiple experimental company products by fusing sensor data with efficient machine learning classifiers <u>https://www.youtube.com/watch?v=1S6irWy8G20</u>
- 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

• 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

September 2019 - October 2023

October 2023 - Present y spend from Temu

rastructure

February 2018 - April 2019

September 2015 - August 2016

May 2015

December 2017