Christopher Rohlicek

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Education

2020 - 2021 **Brown University** – ScM in Data Science (GPA: 4.0/4.0)
Relevant Coursework: Probability, Statistics, and Machine Learning; Data Engineering; Statistical Learning; Deep Learning and Special Topics in Data Science; Modern Applications of Probability and Statistics

2016 - 2020 **Harvard University** – AB in Applied Mathematics (GPA: 3.6/4.0)
Relevant Coursework: Matrix Methods in Data Analysis, Signal Processing, and Machine Learning; Decision Theory; Abstraction and Design in Computation; Computer Networks; Optimization; Honors Linear Algebra and Multivariable Calculus and Real Analysis; Theory of Groups and Vector Spaces; Vector Space Methods for Differential Equations

Work Experience

Broad Institute of MIT and Harvard September 2021 - present
Associate Computational Biologist – Popic Lab

- Researching applications of novel deep learning approaches to detecting genomic structural variation; Leading development of methods of complex variant detection and benchmarking
- Developed simulation engine for modeling context-aware complex genomic variation and creating synthetic genomes for method development and evaluation; Software package released with publication and benchmark datasets
- Leading investigations of generative adversarial network (GAN) applications to histology imaging, and dataset optimization techniques for bioinformatics applications
- Initiated and led interdisciplinary reading group exploring machine learning and applications in computational biology

Brown University – Carney Institute for Brain Science June 2020 - August 2021
Research Assistant to Prof. Jason Ritt

- Investigated dynamical dimensionality reduction of neurophysiological brain models
- Used recurrent neural networks to solve inverse problem posed by empirical neural spike data
- Developed method for dimensionality reduction of high-dimensional dynamical systems

MIT Lincoln Laboratory May 2019 - August 2019
Research Intern with Dr. Michael Brandstein

- Applied signal processing and speech recognition techniques to identify bird species from flight call data
- Combined CNNs and k-nearest neighbors to improve on best published accuracy from 94% to 99%

O&R Patent Law May 2018 – August 2018
Software Intern

- Developed Python-based productivity tools to save hundreds of person-hours
- Used Python and SQL to automate entity resolution and summarization of records for financial analysis

Publications and Presentations

Popic, V., **Rohlicek, C.**, Cunial, F., Garimella, K., Meleshko, D., Hajirasouliha, I. (2023) "A Deep Learning Framework for Structural Variant Discovery and Genotyping." *Nature Methods*.

Rohlicek, C., Jiang, N., Shlyakhter, I., Popic, V. (2023) "insilicoSV: a context-aware extensible structural variant simulator." *Bioinformatics (in review)*.

Rohlicek, C., Battistella, E., Popic, V. (2023) "Complex Structural Variant Discovery in Short Reads Using Deep Learning." (*in preparation*).

Lecture titled "Introduction to Neural Networks: Applications and Intuition" presented as part of a course taught by V. Popic at the *East European Bioinformatics and Computational Genomics School*; October 2022

Brendel, M. Honigsberg. R, Maharjan S., **Rohlicek, C.** "Weakly-supervised tumor purity prediction from H&E stained slides." Poster presented at 2022 Starr Cancer Consortium Retreat; April 2022; Cold Spring Harbor, NY.

"A deep learning approach to structural variant discovery" and "Cue: A framework for cross-platform structural variant calling and genotyping with deep learning," presented with V. Popic at Models, Inference& Algorithms Initiative interinstitutional seminar series, Broad Institute of MIT and Harvard, February 2022.

Select Academic Projects

Molecular Toxicity Prediction
Deep Learning and Special Topics in Data Science, Brown University
Completed research on the use of CNNs and BERT-inspired models for the processing of SMILES molecule representations; implemented a novel strategy for predicting toxicity.

Neural Network Parameter Reduction Using Pruning and Matrix Decomposition
Matrix Methods, MIT (cross-registered)
Conducted experiments in PyTorch comparing effects of magnitude-based pruning techniques to matrix decomposition methods of network size reduction.

Reviews

ISMB (Conference): 1 paper

Technical Skills

Programming Languages	Python, Java, OCaml, SQL, R, MATLAB, Julia, Bash
Libraries	PyTorch, Tensorflow, Keras, Pysam, Numpy, Pandas, Scikit-learn