

DAVID VENUTO

<https://dvvenuto.github.io/>
(438) · 351 · 3432 ◇ dv.venuto@gmail.com

EDUCATION

McGill University

B.Sc. in Computer Science & Biology

Expected (May 2018)

Montreal, Quebec

- Relevant Coursework: Machine Learning, Data Structures and Algorithms, Software Systems, Statistics, Probability Theory, Functional Programming, and Computational Biology.
- Starting Ph.D. in Computer Science in September 2018. School TBD.

EXPERIENCE

McGill/Genome Quebec Innovation Center

Research Assistant

October 2015 - Present

Montreal, Quebec

- Researching convex optimization methods for kernel machines and convolutional neural networks.
- Developed SVMcompare, a novel learning to rank method supporting equality pairs that was casted as a maximum margin problem solvable using quadratic programming. Performance was shown to be superior to state of the art ELO rankings for chess match outcome predictions.
- Studied comparative epigenomics methods for mining next generation sequencing data.

The University of Hong Kong

Research Assistant

June - August 2016

Hong Kong, China

- Developed PathwayLearn, an R application for performing pathway analysis on gene expression data using heavily regularized models.
- Extracted, cleaned and visualized millions of lines of sequencing data. Identified optimal machine learning algorithms for pathway data.

RIKEN

Research Intern

May - August 2015

Yokohama, Japan

- Developed Python scripts for mining bioinformatics databases and prioritizing features.
- Optimized algorithms for 2D structure prediction of genetic sequences using convex strategies.

Blue Care Network

Informatics Intern

June - August 2014

Southfield, Michigan

- Performed Statistical analysis on patient data to identify strategies that could lower total claims cost.

RESEARCH PUBLICATIONS

D Venuto, TD Hocking, L Sphanurattana, M Sugiyama. Support vector comparison machines. Preprint arXiv:1401.8008. *Under Review at JMLR*. 2017.

D Venuto, G Bourque. Identifying co-opted transposable elements using comparative epigenomics. *Development, Growth and Differentiation*. 2018.

C Kanagaratham, V Chiwara, B Ho, S Moussette, M Youssef, **D Venuto**, L Jeannotte, G Bourque, JB de Sanctis, D Radzioch, A Naumova. Loss of the zona pellucida binding protein 2 (Zpbp2) gene in mice impacts airway hypersensitivity and lung lipid metabolism in a sex-dependent fashion. *Accepted to Mammalian Genome*. 2018.

Select Conference Presentations

D Venuto, *et al.*, Comparative epigenomics in primate immune cells reveals putatively exapted transposable element families. *FASEB Meeting* 2017, Big Sky. (Short Talk)

D Venuto, *et al.*, Mapping functional non-coding transcripts in primate immune cells using comparative epigenomics. *IHEC* 2016, Brussels. (Poster)

MAJOR AWARDS

The Hong Kong PhD Fellowship Scheme (Declined Offer)

~130,000 USD over 4 years. (~1% Acceptance Rate)

Computer Languages	Python (scikit-learn, numpy, scipy, pandas), R, Java, UNIX, SQL, C, OCaml.
Machine Learning Skills	Classification, Regression, Clustering, Feature Engineering, Computer Vision, Neural Networks, Convex Optimization.
Statistical Methods	Time Series, Hypothesis Testing, Dimensionality Reduction.
Technical Skills	Git, Hadoop, RNA/DNA/ChIP sequencing analysis, L ^A T _E X.
Employment Authorization	USA, Canada, EU.