

# DAVID VENUTO

<https://github.com/dvVenuto>  
(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.

**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)

---

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