Lee Zamparo

Research Scholar, Memorial Sloan Kettering Cancer Center

▬▬ Education

2008–2015	**PhD, Computer Science**, *University of Toronto*, Toronto, ON, Canada.
	Research Interests: Machine learning, applications to problems in computational biology. Courses: Topics in Machine Learning, Machine Learning, Graph Theory, Machine learning for Computational Biology, Topics in Software Engineering
2012	**SciNet High Performance Computing Summer School**, *University of Toronto*, Toronto, ON, Canada.
2005–2008	**MSc, Computer Science**, *Concordia University*, Montreal, QC, Canada.
	Courses: Topics in Bioinformatics, Data-base systems, Readings in Evolutionary Algorithms, Mining Biological Sequences, Knowledge Representation in Bioinformatics
1999–2004	**BSc in Computer Science**, *University of Toronto*, Toronto, ON, Canada.
	Specialist in Computer Science and Statistics

▬▬ Technical skills

Programming	Python, R, Java, Matlab, C, Perl
Numerical Computing	Numpy, Scipy
Image Analysis	ImageJ, CellProfiler
Database	MySQL, SQLite
GPGPU	Theano, CUDA
Software Tools	Git, SVN, XML, Nose, JUnit, JSP
Operating Systems	Linux, Unix, Mac, Windows

▬▬ Experience in Research

Apr 2015 - present	**Post Doctoral Research Scholar**, *Memorial Sloan Kettering Cancer Center*, New York, NY.
	○ Joined the lab of Christina Leslie.
	○ Developing computational models of HiC data.
	○ Mentoring students on a variety of projects.
Sept 2007 - July 2008	**Research Assistant**, *Plant Sciences Department*, Montreal, QC, Canada.
	○ Updated and enhanced web tools for online soybean transcriptome database.
	○ Developed statistical significance test for differential gene expression.

May 2006 - May 2007	**Research Assistant**, *Department of Biology, Concordia University*, Montreal, QC, Canada. ○ Assembled a MySQL database for fungi phylogeny. ○ Helped to develop DNA barcoding web application.

Experience in Industry

July 2013 - Jan 2014	**Researcher**, *Chematria*, Toronto, ON, Canada, *(internship)*. Developed machine leaning models for chemical biology data. Supported by Mitacs Enterprise Award.
2004-2005	**Technical Developer**, *The Jonah Group*, Toronto, ON, Canada, *(contract)*. Developed JSP and Apache Struts web application as part of a team working for the Canadian Imperial Bank of Commerce.

Publications

Machine Learning	**Dimensionality Reduction for High-Content Screening Data**, *L. Zamparo*, Z. Zhang*, MLCB 2014, poster.
Machine Learning	**Dimensionality Reduction for High-Content Screening Data**, *L. Zamparo*, E. Styles*, B. Andrews, Z. Zhang*, MLSB 2013, poster.
Machine Learning	**Genome-wide methods to identify phenotypes**, *L. Zamparo*, E. Styles*, B. Andrews, Z. Zhang*, ICSB 2012, poster.
Machine Learning	**Genome-wide methods to identify phenotypes**, *L. Zamparo*, E. Styles*, B. Andrews, Z. Zhang*, CSHL: Automated Imaging and High Throughput Phenotyping, 2012.
Bioinformatics	**PhenoM: a database of morphological phenotypes caused by mutation of essential genes in Saccharomyces cerevisiae**, *K. Jin*, J. Li*, F.S. Vizeacoumar, Z. Li, R. Min, L. Zamparo, F. J. Vizeacoumar, A. Datti, B. Andrews, C. Boone, Z. Zhang*, NAR, vol. 40, No. D1, 2012.
Bioinformatics	**Statistical lower bounds on protein copy number from fluorescence expression images**, *L. Zamparo*, T. Perkins*, Bioinformatics, vol. 25, no. 20, 2009.
Bioinformatics	**Estimating protein copy number based on fluctuations in intensity**, *L. Zamparo*, T. Perkins*, ISMB, 2008.

Talks

Conference	**Dimensionality Reduction for High Content Screening Data**, *L. Zamparo*, Z. Zhang*, MLCB 2014, Montreal, QC.
Conference	**Dimensionality Reduction for High Content Screening Data**, *L. Zamparo*, Z. Zhang*, MASAMB 2014, Sheffield, UK.
Tech talk	**Dimensionality Reduction for High Content Screening Data**, *L. Zamparo*, Z. Zhang*, TorBUG 2014, Toronto, ON.