

# 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, computational biology: chromatin structure, gene regulation, epigenomics.  
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

Languages (fluent)	Python, R	Software tools	Git, SVN, Nose, Docker
Languages (familiar)	Java, C++	Numerical tools	Numpy/Scipy
GPGPU tools	Theano, Lasagne, CUDA, Torch		

## Research Experience

- Apr 2015 - present **Post Doctoral Research Scholar**, *Memorial Sloan Kettering Cancer Center*, New York, NY.
- Working on multi-task deep learning models for regulatory genomics (in development)
  - Working in several teams of post-docs and PhD students across different labs
  - Developed statistical model for calling significant interactions in HiC data
    - Paper published in Nature Communications
    - Contributed half of the manuscript figures
  - Mentoring students on several projects
  - Co-developed and taught quantitative biology course (<https://github.com/qbio-gsk/qbio-gsk>)
- Sept 2007 - **Research Assistant**, *Plant Sciences Department*, Montreal, QC, Canada.
- July 2008
  - Updated and enhanced web tools for online soybean transcriptome database.
  - Developed statistical significance test for differential gene expression.
- May 2006 - **Research Assistant**, *Department of Biology, Concordia University*, Montreal, QC, Canada.
- May 2007
  - Assembled a MySQL database for fungi phylogeny.
  - Helped to develop DNA barcoding web application.

*Memorial Sloan Kettering Cancer Center – New York, NY*

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## Industry Experience

- July 2013 - **Researcher**, *Chematria*, Toronto, ON, Canada, (*internship*).  
Jan 2014    ◦ Developed machine learning models for protein-ligand docking.  
              ◦ Supported by Mitacs Enterprise Award
- 2004-2005 **Technical Developer**, *The Jonah Group*, Toronto, ON, Canada, (*contract*).  
              ◦ Developed JSP and Apache Struts web applications for a variety of clients.

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## Publications

- Bioinformatics **GuideScan: a comprehensive and customizable guide RNA design tool**, Alexander Reinaldo-Perez, Yuri Pritykin, Joanna Alves Dos Campos Vidigal, Sagar Chhangawalla, Lee Zamparo, Christina S. Leslie, Andrea Ventura, *Nature Biotechnology*, 35, 347–349 (2017) doi:10.1038/nbt.3804.
- Bioinformatics **An integrated model for detecting significant chromatin interactions from high-resolution Hi-C data**, Mark Carty, Lee Zamparo, Alvaro González, Raphael Pelossof, Olivier Elemento, Christina S. Leslie, *Nature Communications*, Volume 8, Article number: 15454 (2017), doi:10.1038/ncomms15454.
- Bioinformatics **Exploring quantitative yeast phenomics with single cell analysis of DNA damage foci**, Erin B. Styles, Karen J. Founk, Lee Zamparo, et al., *Cell Systems*, Volume 3, Issue 3, p264–277.e10, September 2016.
- 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.

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## Talks and Posters

- Lightning talk, poster **HiC-DC: a model for detecting significant interactions via Hi-C**, M. Carty, L. Zamparo\*, A. González, R. Pelossof, O. Elemento, C. Leslie, ICML MLCB workshop, 2016, New York, NY.
- Lightning talk, poster **Dimensionality Reduction for High Content Screening Data**, L. Zamparo\*, Z. Zhang, NIPS MLCB workshop, 2014, Montreal, QC.
- Conference talk **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.
- Poster **Genome-wide methods to identify phenotypes**, L. Zamparo\*, E. Styles\*, B. Andrews, Z. Zhang, CSHL: Automated Imaging and High Throughput Phenotyping, 2012.
- Poster **Estimating protein copy number based on fluctuations in intensity**, L. Zamparo\*, T. Perkins, ISMB, 2008.