

## Caitlin Simopoulos, PhD

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Roger Guindon Hall, University of Ottawa  
451 Smyth Road, Ottawa, Ontario, K1H 8L1  
(647) 280-6247  
csimopou@uottawa.ca  
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<b>DISCIPLINES</b>	Bioinformatics, Computational Biology, Molecular Biology, -omics Technologies, Machine Learning	
<b>EDUCATION</b>	<b>Doctor of Philosophy</b> - Computational Biology	2019
	<i>McMaster University, Hamilton, ON</i> Supervisors: Elizabeth Weretilnyk and Brian Golding Thesis: Using machine learning to predict long non-coding RNAs and exploring their evolutionary patterns and prevalence in plant transcriptomes	
	<b>Master of Bioinformatics (MBinf)</b>	2014
	<i>University of Guelph, Guelph, ON</i> Supervisors: Paul McNicholas and Steven Rothstein Major Research Project: Weighted gene correlation network analysis of maize and rice undergoing nitrogen stress	
	<b>Bachelor of Science</b> , Molecular Biology and Genetics	2012
	<i>University of Guelph, Guelph, ON</i>	
<b>SOFTWARE</b>	<a href="#">MetaProClust-MS1</a>	
	<ul style="list-style-type: none"><li>• Tool for clustering metaproteomes using Rapid MS1 profiles</li><li>• Written using R and Python</li><li>• Approach to intentional and resource conscious metaproteomic research</li></ul>	
	<a href="#">pepFunk</a>	
	<ul style="list-style-type: none"><li>• R Shiny app built for metaproteomic functional analysis</li><li>• Written in R</li><li>• Part of iMetaLab suite</li></ul>	
	<a href="#">CREMA</a>	
	<ul style="list-style-type: none"><li>• Prediction of lncRNAs from transcript sequences</li><li>• Unix command line interface</li><li>• Written using Python and R</li></ul>	
<b>CONTINUING EDUCATION</b>	<b>From Lab 2 Fulfillment</b> Entrepreneur workshop	2020
	<b>WinSETT</b> Becoming Leaders, professional development	2019
	<b>TECHNOMISE-CREATE</b> Professional development bootcamp	2019
	<b>Canadian Bioinformatics Training</b> Metabolomics workshop	2013
<b>RELEVANT EXPERIENCE</b>	<b>TECHNOMISE-CREATE Postdoctoral Associate</b>	2019-present
	<i>University of Ottawa, Ottawa, ON</i> Supervisor: Daniel Figeys Co-supervisor: Mathieu Lavallée-Adam Research topic:	

- Identify effects of drugs on human gut microbiomes based on a machine learning framework
- Reclassify drugs according to their effects on the gut microbiota
- Contribute to computational methodology for metaproteomic data analysis including the creation of web applications written in R shiny
- Working on an interdisciplinary and collaborative research team

#### **Research Assistant**

January 2014-August 2014

*University of Guelph, Guelph, ON*

Responsibilities:

- Identified transcriptional responses to nitrogen stress in rice.
- Created an efficient R package for genetic network analysis.
- Collaborated with a multi-disciplinary team.

#### **MBinf Research Project**

May 2013-December 2013

*University of Guelph, Guelph, ON*

Responsibilities:

- Analyzed microarray data of important crops undergoing nitrogen stress.
- Used and further developed programming skills in R.

#### **Undergraduate Research Project**

September 2011-April 2012

*University of Guelph, Guelph, ON*

Research topic:

- The effects of stress on *S. mediterranea* after RNAi knock-down of *age-1*.

#### **USEL Position**

Summer 2011

*University of Guelph and OMAFRA, Guelph, ON*

Responsibilities:

- Created a viral infection identification protocol for Ontario strawberries.
- Established relationships to maintain communication between OMAFRA and Ontario farmers.

### **SCIENTIFIC OUTREACH**

#### **TECHNOMISE Special Seminar Organizing Committee**

2020-present

*Member*

- Invite respected researchers in the field of microbiomes to speak to TECHNOMISE-CREATE trainees
- Co-host monthly seminar series

#### **Early Career Scientist Committee**

2019-present

*Communication and Outreach, Member, Genetics Society of America*

- Work within a diverse team of early career scientists who are dedicated to science communication
- Communicate novel scientific discoveries by writing pieces published in online blogs or articles accessible to both scientists and the general public

#### **Pint of Science**

2019-present

*Local organizer*

- In charge of three day event that brings scientists into cafes and pubs
- Organize event logistics
- Invite speakers to the events
- Host the three day speaker series
- Lead other local volunteers

<b>TEACHING EXPERIENCE</b>	<b>Pulsar Collective</b>	2019-present
	<i>Mentor</i>	
	<ul style="list-style-type: none"> <li>• Visit highschoools virtually</li> <li>• Highlight underrepresented genders in STEM</li> <li>• Communicate that STEM is accessible to all genders</li> </ul>	
	<b>Skype a Scientist</b>	2020-present
	<i>Scientist volunteer</i>	
	<ul style="list-style-type: none"> <li>• Visit classrooms virtually</li> <li>• Answer student questions about science and research</li> </ul>	
	<b>Plant Molecular Workshop</b>	2013-2019
	<i>McMaster University, Hamilton, ON</i>	
	<ul style="list-style-type: none"> <li>• Lead high school students though typical plant molecular biology experiments</li> <li>• Develop young people's interest in biology</li> </ul>	
	<b>Researcher's Night Hamilton</b>	2018
	<i>Presenter</i>	
	<ul style="list-style-type: none"> <li>• Combined art and science for fun and approachable science outreach</li> <li>• Presented computational work in a visual manner to the public</li> </ul>	
	<b>Software Carpentry</b>	2017
	<i>Workshop Assistant</i>	
	<ul style="list-style-type: none"> <li>• Offer hands-on assistance to workshop attendees</li> <li>• Promote inclusivity in computer and data science</li> </ul>	
	<b>Student Mentoring</b>	2020 - present
	<i>University of Ottawa</i>	
	Isaac Kuk, Translational and Molecular Medicine	
	Expanding pepFunk to support eggNOG and GO annotations	
	<b>Teaching Assistant</b>	2014-2018
	<i>McMaster University, Hamilton, ON</i>	
	Biology 1M03: Biodiversity, Evolution & Humanity	
	<i>Tutorial TA (2014, 2017-2018)</i>	
	<ul style="list-style-type: none"> <li>• Lead an engaging, hands-on and discussion friendly tutorial</li> <li>• Mark weekly assignment and final group project</li> <li>• Answer online discussion board questions</li> </ul>	
	<i>Lead lecture TA (2015-2017)</i>	
	<ul style="list-style-type: none"> <li>• Act as first contact for all first year undergraduate life sciences students</li> <li>• Hold office hours to discuss lecture material</li> <li>• Answer online discussion board questions</li> </ul>	
	Biology 1A03: Cellular & Molecular Biology	
	<i>Lead lecture TA (2015-2017)</i>	
	<ul style="list-style-type: none"> <li>• Act as first contact for all first year undergraduate life sciences students</li> <li>• Hold office hours to discuss lecture material</li> <li>• Answer online discussion board questions</li> </ul>	
	Biology 4BB3: Plant Metabolism and Molecular Biology	
	<i>Lecture TA (2017)</i>	
	<ul style="list-style-type: none"> <li>• Develop and present lectures throughout the semester on appropriate material</li> <li>• Curate data for bioinformatics-focused final project</li> </ul>	

- Grade final project

Biology 3B03: Plant Physiology  
*Lab TA (2018)*

- Lead plant physiology based wet labs
- Mark weekly lab reports

<b>HONOURS AND AWARDS</b>	<b>IAPB Travel Grant</b>	2018
	Awarded to present a seminar at IAPB Dublin, August 2018	
	<b>Catherine Jane Stevenson Memorial Bursary</b>	2016-2018
	Awarded for research supporting Northern Canada	
	<b>McMaster University Department of Biology Travel Scholarship</b>	2016
	Awarded for travel to attend CSPB-CSBV, 2016	
	<b>George H. Duff Student Travel Bursary</b>	2016
	Awarded for travel to attend CSPB-CSBV, 2016	
	<b>Outstanding Achievement as a Teaching Assistant</b>	2015
	Awarded to a graduate student in the Department of Biology for their outstanding achievement as a teaching assistant during the 2014/2015 school year.	
	<b>Graduate Scholarship</b>	2014
	McMaster University, Hamilton, Canada Total funding: \$1070/year	
	<b>Queen Elizabeth II Award in Science and Technology</b>	2013
	Awarded by nomination for academic merit, research strength, leadership, and communication skills. Total funding: \$5,000/semester	
	<b>University of Guelph Entrance Scholarship</b>	2008
	Awarded to students with a minimum 85% admission average. Total funding: \$1000	

<b>SELECT PUBLICATIONS</b>	<b>Simopoulos, CMA</b> , Ning, Z, Li, L, Khamis, MM, Zhang, X, Lavallée-Adam, M, Figeys, D. (2021). MetaProClust-MS1: A tool for clustering metaproteomes using rapid MS1 profiling. bioRxiv. <a href="https://doi.org/10.1101/2021.03.31.43786">https://doi.org/10.1101/2021.03.31.43786</a>	
	<b>Simopoulos, CMA*</b> , MacLeod, MJR*, Irani, S, Sung, WWL, Champigny, MJ, Summers, PS, Golding, GB, Weretilnyk, EA. (2020) Coding and long non-coding RNAs provide evidence of distinct transcriptional reprogramming for two ecotypes of the extremophile plant <i>Eutrema salsugineum</i> undergoing water deficit stress. BMC Genomics 21, 396 <a href="https://doi.org/10.1186/s12864-020-06793-7">https://doi.org/10.1186/s12864-020-06793-7</a>	
	<b>Simopoulos, CMA</b> , Ning, Z, Zhang, X, Li, L, Walker, K, Lavallée-Adam, M, Figeys, D. (2020). pepFunk, a tool for peptide-centric functional analysis in metaproteomic human gut microbiome studies. Bioinformatics, btaa289 <a href="https://doi.org/10.1093/bioinformatics/btaa289">https://doi.org/10.1093/bioinformatics/btaa289</a>	
	<b>Simopoulos, CMA</b> , Weretilnyk, EA, Golding, GB. (2019) Molecular traits of long non-protein coding RNAs from diverse plant species show little evidence of phyloge-	

netic relationships. (2019) G3. 9(8), 2511-2520 <https://doi.org/10.1534/g3.119.400201>

**Simopoulos CMA**, Weretilnyk, EA, Golding, GB. (2018). Prediction of plant lncRNA by ensemble machine learning classifiers. BMC Genomics. 19, 316 <https://doi.org/10.1186/s12864-018-4665-2>

Coneva, V\*, **Simopoulos, C\***, Casaretto, JA, El-kereamy, A, Guevara, D R, *et al.* (2014). Metabolic and co-expression network-based analyses associated with nitrate response in rice. BMC Genomics, 15, 1056 <http://www.biomedcentral.com/1471-2164/15/1056>

\* Shared first authorship

**OUTREACH PUBLICATIONS** Carla Bautista, Elisabeth Adkins Marnik, **Caitlin MA Simopoulos\***, Anna Drangowska-Way, Thomas James Smyth Merritt (2020) What is the new way scientists edit DNA? Frontiers for Young Minds. (*In press*).

**GSA Communications & Outreach Subcommittee\*** (November 26, 2020) Hurdles and advances to making science gender-neutral. ecrLife. <https://ecrlife.org/hurdles-and-advances-to-making-science-gender-neutral/>

**GSA Communications & Outreach Subcommittee\*** (October 8, 2020) Navigating fake news as a scientist. ecrLife. <https://ecrlife.org/navigating-fake-news-as-a-scientist/>

\* Written as a collaboration with the GSA Communications & Outreach Subcommittee.

**CONFERENCE PRESENTATION** **Simopoulos, C**, Ning, Z, Zhang, X, Li, L, Walker, K, Lavallée-Adam, M, Figeys, D. pepFunk: peptide-centric functional enrichment for metaproteomic gut microbiome data. Video presentation at useR!2020. <https://youtu.be/UZtpi-Bg9i0>

**Simopoulos, C**, Ning, Z, Zhang, X, Li, L, Walker, K, Lavallée-Adam, M, Figeys, D. pepFunk: peptide-centric functional enrichment for metaproteomic gut microbiome data. Virtual oral presentation at ISMB2020.

**Simopoulos, C. Simopoulos, C**, Ning, Z, Zhang, X, Li, L, Walker, K, Lavallée-Adam, M, Figeys, D. pepFunk: peptide-centric functional enrichment for metaproteomic gut microbiome data. Poster at the 2020 meeting for the European Conference on Computational Biology. (*Poster presentations cancelled due to the COVID-19 pandemic.*)

**Simopoulos, C.**, Weretilnyk, E. A., Golding, G. B. (August 21, 2018) *Local adaptation in the extremophile Eutrema salsugineum: Exploring the roles of putative lncRNAs*  
Oral presentation at the 2018 meeting of the International Association for Plant Biotechnology, Dublin, Ireland.

**Simopoulos, C.**, Weretilnyk, E. A., Golding, G. B. (July 15, 2018) *Using machine learning to predict long non-protein coding RNAs from plant transcriptome*  
Poster presented at the joint meeting of ASPB and CSPB, Montreal, Quebec.

**Simopoulos, C.**, Golding, G. B., Weretilnyk, E. A. (Nov 19, 2016) *An improved method for long non-coding RNA prediction that includes small ORF coding probabilities*

Presented at the annual Biology Graduate Research Day at McMaster University in Hamilton, Ontario.

**Simopoulos, C.**, Golding, G. B., Weretilnyk, E. A. (Nov 19, 2016) *An improved method for long non-coding RNA prediction that includes small ORF coding probabilities*

Presented at the annual Eastern meeting of the Canadian Society of Plant Biologists at McMaster University, Hamilton, Ontario

**Simopoulos, C.** Golding, G. B., Weretilnyk, E. A. (June 16, 2016) *Insights into the abiotic stress response of *Eutrema salsugineum* by co-expression network analysis*

Poster presented at the annual national meeting of the Canadian Society of Plant Biologists at Queen's University, Kingston, Ontario.

Garvin, A.\*, **Simopoulos, C.\***, Sung, W., Golding, B., Weretilnyk, E. (Nov. 21, 2015) *A long non-coding RNA associated with nutrition in *Eutrema salsugineum*: An example of local adaptation?*

Poster presented at the annual Eastern meeting of the Canadian Society of Plant Biologists at the University of Toronto, Toronto, Ontario.

\* Shared first authorship

**Simopoulos, C.** Garvin, A., Sung, W., Golding, B., Weretilnyk, E. (Oct. 15, 2015) *How do outlier samples affect the results of a co-expression network?*

Poster presented annual Biology Graduate Research Day at McMaster University in Hamilton, Ontario.

**Simopoulos, C.**, Garvin, A., Sung, W., Golding, B., Weretilnyk, E. (Dec 4, 2014) *Does Yukon *Eutrema salsugineum* require elevated sulfur and, if so, why?*

Poster presented at annual Biology Graduate Research Day at McMaster University in Hamilton, Ontario.

<b>PROFESSIONAL AFFILIATIONS</b>	International Society for Computational Biology	2020-present
	Genetics Society of America	2019-present
	The Canadian Society for Plant Biologists	2014-2019
	Canadian Association for Plant Biotechnology	2018

**JOURNAL REVIEW ACTIVITIES**

- Molecular Omics
- Journal of Proteomics
- Nature Protocols
- Scientific Reports
- Interface Focus
- F1000 Research