

Yuliya Zubak

Email | GitHub | LinkedIn | Site

Education

Indiana University Bloomington

Cognitive Science PhD

Matriculating Sept 2025

University of Toronto, Scarborough Campus

Sept 2015 – Jun 2020

Honors BSc: Molecular Biology & Biotechnology (Specialist Double Major, Co-op), Neuroscience (Major, 3rd)

Thesis: Development and validation of a novel polygenic risk score for depression (2020) with Yuliya Nikolova

Awards & Grants

- CogSci Student Travel Grant 2024
- NSERC Research Grant 2019
- BioTalent Research Grant 2019, 2018

Languages & Tools

Javascript, React, Python, R (RMarkdown), SQLite, PHP, HTML5, BIOPAC (EEG), Freesurfer (fMRI), PrediXcan, Matlab, LaTeX, WebPPL

Papers

- **Zubak, Y.**, Dronavalli, P., Chuang, Y., & Hawkins, R. (2024). Distributed statistical inference in social interaction networks. Proceedings of the Annual Meeting of the Cognitive Science Society, 46.
<https://escholarship.org/uc/item/8km974x4>
- Lunardon, A. and Patena W., Warren-Williams M., Pacini C., **Zubak Y.**, Laudon M., Silflow C., Lefebvre P., Jonikas M. (2024). The *Chlamydomonas reinhardtii* CLiP2 mutant collection expands genome coverage with high-confidence disrupting alleles. BioRxiv
- Scipio, M. D., Tavares, E., Deshmukh, S., Audo, I., Green-Sanderson, K., **Zubak, Y.**, . . . Vincent, A. (2020). Phenotype Driven Analysis of Whole Genome Sequencing Identifies Deep Intronic Variants (...). IOVS <https://doi.org/10.1167/iovs.61.10.36>
- Bergey C.A., Lyu A., O’Keeffe M., Li B., **Zubak Y.**, Plum B., Yang S., Patil A., Zhou I., Hawkins R. (in prep). Examining Social Interaction from a Preschooler’s Point of View.
- Lunardon, A. and Patena W., Warren M., Pacini C., **Zubak Y.**, [...] Jonikas M. (in prep). An expanded Chlamydomonas mutant library enables placement of eukaryotic photosynthetic genes into pathways.

Posters

- Distributed statistical inference in epistemic networks **Zubak Y.**, Robert H. (2025) Society for Philosophy and Psychology 2025 Annual Meeting
- Chemical genetics of the newly expanded Chlamydomonas mutant library **Zubak Y.**, Lunardon A., Patena W., Pacini C., Jonikas M.C. (2023) Chlamy2023
- Inflammatory response to ethanol in neuroimmune cell culture models of FASD. **Zubak, Y.**, Torres-Perez, M., Tian, A., (...) Muffat, J. (2019) Sickkids Summer Undergraduate Research

Research Experience

Lab Manager/Research Coordinator

Sept 2023 – Present

Dr. Robert Hawkins, Linguistics, Stanford University

- Studied social learning and networking behaviors in epistemically difficult conditions, designing a web game, recruiting participants from Prolific, and analyzing the resulting data (Bayesian and mixed effect models), and modeling behavior with agents
- Trained and supervised ten undergraduate research assistants in ethical data collection, as well as pre-processing and analyzing multivariate datasets including text, audiovisual, and fMRI data
- Inaugural lab manager; established lab culture, dissolved lab silos, created and maintained lab resources such as the lab website and a lab database of best practices, established the lab’s experimental and data analysis pipelines, and maintained research protocols with the Institutional Review Board

Research Specialist

Nov 2021 – Oct 2023

Dr. Martin Jonikas, Department of Molecular Biology, Princeton University

- Generated and replicated a collection of random DNA insertion algal mutants (300k unique mutants) as part of the Chlamydomonas Library Project, towards the aim of creating a whole-genome library of Chlamydomonas reinhardtii as a global scientific resource
- Developed a list of systems-targeting compounds, then designed and tested a high-throughput pooled screen, with the intent of collecting high quality phenotypic data on each mutant by exposing them to hundreds of compounds targeting all major protein pathways. This ultimately created an atlas of the organism
- Modified statistical pipeline to identify mutants before and after compound exposure

Junior Research Analyst

Sept 2019 – Apr 2020

Dr. Yuliya Nikolova, Centre for Addiction and Mental Health (CAMH)

- Created and applied a prediction score for genetic risk factors between the sexes based on MDD-associated candidate regions and genes using linear regression models based on transcriptomic, polymorphism and MRI data from the Human Connectome Project
- Used R, Freesurfer, and prediXcan to process data and complete a large volume of data conversion and processing, keeping a detailed record of work using Rmarkdown

Research Summer Student

May 2019 – Aug 2019

Dr. Julien Muffat, Neurosciences and Mental Health, Hospital for Sick Children

- Opened a new project for the lab in examining the cellular origins of Fetal Alcohol Spectrum Disorder, conducting a literature search, designing and carrying out experiments, and processing resultant data
- Cultured and maintained human neuroimmune models in the form of iPSC derived astrocytes, neurons, phagocytes, and cancer cells using high resolution and immunofluorescence microscopy
- Gathered the data with RT-qPCR and created a data analysis pipeline for multi-gene expression that controlled for various variables (eg. primer annealing) and graphed the significant results

Research Assistant

Jan 2019 – Apr 2019

Dr. Karen Gordon, Department of Otolaryngology, Hospital for Sick Children

- Analyzed EEG brain scan data in MATLAB

Research Assistant

Sept 2018 – Dec 2018

Dr. Elise Heon, Genetics and Genome Biology, Hospital for Sick Children

- Employed bioinformatics to outline a backbone pipeline to filter whole genome BAM files

Extracurricular Activities

(2021) **Fellow** NATO Innovation Hub Thinktank

(2015-2021) **Director** on Board of Directors

(Elected, Two Terms) YCC No. 457

(2018-2020) **Moderator** University of Toronto
Scarborough Discord Server

(2017-2018) **First Year Representative**
Association of Philosophy Students