

Sara El-Shawa

✉ selshawa@uoguelph.ca • [linkedin.com/in/saraelshawa](https://www.linkedin.com/in/saraelshawa) • [saraelshawa](https://github.com/saraelshawa)

Education

University of Guelph

September 2020–September 2022

Master of Applied Science in Engineering

Collaborative Specialization in Artificial Intelligence

Vector Scholarship in Artificial Intelligence Recipient 2020-21 (CAD \$17 500)

Queen Elizabeth II Graduate Scholarship 2021-22 (CAD \$15 000)

GPA: 4.0/4.0

Supervisor: Dr. Graham Taylor

University of Toronto

September 2014–November 2018

Honours Bachelor of Science

Double major in Computer Science and Biology

GPA last two years of study: 3.88/4.0, **Dean's List**

Thesis Advisor: Dr. Rob W. Ness

Work Experience

Health AI Intern

January 2021–Present

Vector Institute

- Using mobility data to make COVID-19 forecasts in Ontario at the Public Health Unit level.

Data Manager & Web Programmer

May 2020–Present

Stanford University

- Updating MetaLab's website and conducting **meta-analyses** for cognitive development research using **R**.

Software Developer

April 2020–Present

University of Toronto

- Designing GUI and developing a data processing pipeline for analyzing videos of social interaction networks of flies.
- Developing tests to assess **information flow** between and among social interaction networks.

Teaching Assistant

January 2021–April 2021

University of Guelph

- Conducted tutorials, made videos, and explained linear algebra concepts to students in ENGG1500.

AI Researcher

November 2020–March 2021

Public Health Agency of Canada

- Predicted the severity of COVID-19 cases by investigating associations with clinical symptoms and comorbidities.

Data Science Research Intern

December 2018–February 2020

Harvard University

- Identified and analyzed **social networks** among groups of interacting animals using **MATLAB** and **Python**.
- Calculated and compared network measures such as **Bonacich power centrality** between female and male groups, and groups with and without early-life stress.
- Used Python packages **NetworkX**, **Pandas**, and **DeeplabCut** for animal tracking.

Robotics Research Intern

September 2019–February 2020

International Research Center for Neurointelligence, University of Tokyo

- Humanoid robot-infant** interaction to assess how a robot's contingent responsiveness contributes to infants' elicitation of gaze following.
- Designed and programmed GUI in Python for **Nao robot** to react contingently to a child through movements and vocalizations.

Genomics Research Assistant

May 2018–August 2018

University of Toronto

- Identified basic **graph theory** centrality measures in two biological networks using **Python** and **Bash**.
- Converted genetic network into **SQL** database for more efficient data retrieval using **python-sql** library.

Bioinformatics Research Assistant

May 2017–August 2017

University of Toronto

- Conducted analysis to study the effect of metabolic network topology using **Python**.
- Established and managed an analytical pipeline in **Bash** and created graphs in **R** for data analyses.

(Research experience continued)

Undergraduate Research Experience

Senior Thesis Project

September 2017–August 2018

University of Toronto

- Analyzed the influence of genetic network properties on selection by using divergence and diversity measures.
- Conducted analysis to find how the rate of adaptive evolution varies across the genetic network.
- Found that positive selection is more prevalent in genes that are highly connected and have a high betweenness centrality measure.
- Used Python packages such as **NumPy**, **Matplotlib**, and **Pandas** and R packages such as **dplyr** and **ggplot2**.
- Poster Presentation at SMBE 2018 in Japan, **Award**: Best Undergraduate Poster (USD \$500).
- **Manuscript in preparation**: **El-Shawa S.** and Ness, R. W. The effect of connectivity on the strength of selection in *Chlamydomonas reinhardtii*.

Computational Biophysics Undergraduate Researcher

May 2018–October 2018

University of Toronto

- Ran simulations in **C** and **Python** using fluctuation data to infer direction of molecular interactions within cells and presence of feedback in a multi-component system.
- Used stochastic processes by modifying the **Gillespie algorithm** to calculate covariance data between components to correctly identify positive and negative correlations.

Bioinformatics Undergraduate Researcher

January 2018–August 2018

University of Toronto

- Identified and used graph theory measures such as **clustering** and **connectivity** to analyze genetic mutations in a gene co-expression network using **Python** packages such as **NetworkX** and **Seaborn**.
- Compared network parameter distributions between salt-stress and de novo mutations in **R**.

Evolutionary Genomics Undergraduate Researcher

May 2017–August 2017

University of Toronto

- Conducted analysis to identify the full set of homologous genes between two model genomes.
- Worked with **Python** and **Bash**, and used Augustus, UBLAST, MUSCLE, Blast, and Standalone Blast.