

**Jarrett D. Phillips, PhD.**  
**Department of Integrative Biology, University of Guelph**

✉ [jphill01@uoguelph.ca](mailto:jphill01@uoguelph.ca)

[phillipsjarrett1@gmail.com](mailto:phillipsjarrett1@gmail.com)

 [jphill01](#)

 [Jarrett Phillips](#)

 [Jarrett D. Phillips](#)

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 [Jarrett Phillips](#)

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## **EDUCATION**

**PhD.** in Computational Sciences, University of Guelph 2016-2022  
Co-Advisors: Dr. Daniel Gillis and Dr. Robert Hanner

**Master of Bioinformatics (MBinf.)**, University of Guelph 2013-2014  
Co-Advisors: Dr. Robert Hanner and Dr. Daniel Ashlock

**BSc. (Hons.)** in Biological Science, University of Guelph 2009-2013

## **RELEVANT COURSEWORK**

**An Introduction to Interactive Programming in Python** 2014  
Rice University

- Online course through Coursera on the development of interactive applications in Python

**Introduction to DNA Barcoding** 2013  
University of Guelph

- Online course through Open Learning and Education Support (OpenEd)

## **RESEARCH EXPERIENCE**

**Postdoctoral Fellow** 2022  
University of Guelph  
Hanner Lab, Department of Integrative Biology  
Supervisor: Dr. Robert Hanner

- Mentored and supervised a Master of Bioinformatics (MBINF.) student on research project

**Summer Research Assistant**

2016

Algoma University

Plant and Soil Ecology Lab, Department of Biology

Invasive Species Research Institute (ISRI)

Supervisor: Dr. Pedro Antunes

- Offered bioinformatics and statistical analysis support in R
- Assisted Principal Investigator and undergraduate thesis student with initial drafting of a manuscript on invasive plant root lesion quantification

**Lab Assistant Volunteer**

2014-2016

Algoma University

Plant and Soil Ecology Lab, Department of Biology

Invasive Species Research Institute (ISRI)

Supervisor: Dr. Pedro Antunes

- Offered bioinformatics and statistical analysis support in R
- Assisted with collaborative and outreach initiatives for the Terrestrial Invasive Plant Species (TIPS) Network Project through drafting communication letters to public and private conservation agencies across Canada and the USA seeking volunteers to collect invasive plant species for root lesion quantification

**Undergraduate Research Assistant**

2013

University of Guelph

Vaccine Discovery Research Group

Supervisor: Dr. Mario Monteiro

- Performed various experimental techniques (gas chromatography-mass spectrometry (GC-MS) and Nuclear Magnetic Resonance (NMR)) on bacterial polysaccharide samples for vaccine synthesis and development under the supervision of qualified graduate students

**TEACHING EXPERIENCE****Graduate Teaching Assistant (GTA)**

2016-2020

University of Guelph

**CIS\*3130 – System Modelling and Simulation**

2020

~ 30 students · Python

**CIS\*1910 – Discrete Structures in Computing I**

2017

~ 300 students (~ 40 students per section)

**CIS\*2460 – Modelling of Computer Systems**

2016-2019

~ 60 students · R, Excel, Java

**STUDENT SUPERVISION AND MENTORSHIP**

I have directly supervised and mentored several undergraduate students in computer science and integrative biology, all of whom are, or will be, coauthors on my publications. My primary role has been to guide students through the entire scientific process (*i.e.*, formulating research questions, designing and setting up experiments to test hypotheses, collecting data and analyzing results and writing the manuscript drafts). Students completed research both as part of a course and as lab volunteers.

<b>Amina Asif</b> (with Bob Hanner)	2022
University of Guelph	
BINF*6999 · DNA barcode gap analysis	
<b>Navdeep Singh</b> (with Dan Gillis)	2021
University of Guelph	
CIS*4900 · HACSim RShiny web application	
<b>Maya Persram</b> (with Bob Hanner)	2020-present
University of Guelph	
Hanner Lab volunteer	
<b>Ashley Chen</b> (with Bob Hanner)	2020-present
University of Guelph	
Hanner Lab volunteer	
<b>Olivia Friesen Kroeker</b> (with Bob Hanner)	2020-present
University of Guelph	
Hanner Lab volunteer	
<b>Scarlett Bootsma</b> (with Dan Gillis)	2020-2021
University of Guelph	
CIS*4900/4910 · HACSim simulation study	
<b>Christina Fragel</b> (with Bob Hanner)	2018-2019
University of Guelph	
BINF*6999 · DNA barcode sequence classification with machine learning	
<b>Jiaojia (Paula) Yu</b> (with Bob Hanner)	2018-2019
University of Guelph	
BINF*6999 · MDMAPR qPCR R Shiny app	
<b>Steven French</b> (with Dan Gillis)	2018
University of Guelph	
CIS*4900/4910 · HACSim R package	
<b>Julia Harvie</b> (with Bob Hanner)	2018-2019
University of Guelph	
MCB*4500/4510 · Data mining GenBank and BOLD	
<b>Ankita Bhandari</b> (with Bob Hanner)	2018
University of Guelph	
BINF*6999 · Data mining GenBank and BOLD	

**ASSISTANTSHIPS, SCHOLARSHIPS AND GRANTS**

<b>Graduate Teaching Assistantships</b>	2017-2020
University of Guelph	\$34,506.00-35,148.00 CAD
<b>Graduate Research Assistantships</b>	2017-2019
University of Guelph	\$11,000.00 CAD
<b>CPES Graduate Dean's Scholarship</b>	2017
University of Guelph	\$3500.00 CAD
<ul style="list-style-type: none"> <li>Awarded in recognition of achieving over 85% in Master's coursework</li> </ul>	
<b>CPES Graduate Excellence Entrance (GEE) Scholarship</b>	2016
University of Guelph	\$30000.00 CAD
<ul style="list-style-type: none"> <li>Awarded in recognition of achieving over 85% in Master's coursework</li> </ul>	
<b>Arthur D. Latornell Graduate Travel Grant</b>	2019
University of Guelph	\$500.00 CAD
<ul style="list-style-type: none"> <li>Awarded for first-class academic standing in PhD. coursework</li> <li>Supported travel to the 8<sup>th</sup> International Barcode of Life Conference in Trondheim, Norway to present work related to resource management and conservation</li> </ul>	
<b>SoCS Travel Grant</b>	2019
University of Guelph	\$1000.00 CAD
<ul style="list-style-type: none"> <li>Supported travel to the 8<sup>th</sup> International Barcode of Life Conference in Trondheim, Norway</li> </ul>	

**ACADEMIC SERVICE**

<b>School of Computer Science (SoCS) Search Committee</b>	2018
University of Guelph	
<ul style="list-style-type: none"> <li>Associate Professor position in cybersecurity</li> </ul>	
<b>School of Computer Science (SoCS) Search Committee</b>	2017-2018
University of Guelph	
<ul style="list-style-type: none"> <li>Two-year contractually-limited Assistant Professor position in cybersecurity</li> </ul>	

**ACADEMIC PEER REVIEW SERVICE**

I have served as a reviewer for 9 manuscripts in 4 different journals, both alone or under the guidance of my PhD. supervisors.

<i>Ecology and Evolution</i> (2)	2021-2022
<i>Lifestyle Genomics</i> (1)	2022
<i>Molecular Ecology Resources</i> (5)	2019-2022
<i>Molecular Biology Reports</i> (1)	2020
<i>Methods in Ecology and Evolution</i> (1)	2020

**PROCEEDINGS**

I have presented graduate research at 3 international conferences, including both oral presentations and posters.

<b>8<sup>th</sup> International Barcode of Life Conference</b>	2019
NTNU University Museum and Norwegian Biodiversity Information Centre	
<b>7<sup>th</sup> International Barcode of Life Conference</b>	2017
University of Johannesburg	
<b>6<sup>th</sup> International Barcode of Life Conference</b>	2015
University of Guelph	

**RELEVANT SKILLS****Programming Languages and IDEs**

Google Colab · Julia · Python · PyCharm · R · RStudio · TeX

**Document Preparation Software, Spreadsheet Applications, Software Management and Version Control**

Excel · Git · GitHub · HTML · LaTeX · RMarkdown

**Other**

JAGS · R Shiny · Stan

**SOFTWARE DEVELOPMENT**

HACSim (**H**aplotype **A**ccumulation **C**urve **S**imulator) · R package · R Shiny web app

- A novel nonparametric stochastic (Monte Carlo) local search optimization method of iteratively generating species' haplotype accumulation curves through extrapolation to assess within-species sampling completeness
- R package and Shiny app respectively available for download through the Comprehensive R Archive Network ([CRAN](https://cran.r-project.org/)) package repository or at [shinyappps.io](https://shinyappps.io)
- Publication in *PeerJ Computer Science* was one of the top five most viewed papers in the category *Optimization Theory and Computation*
- Has been downloaded over 15000 times (c. 290 times per month) since being published in May 2019

**REFEREED WORK****Journal Articles**

Citations: 86 · H-index: 4 (According to Google Scholar, as of May 2022)

\*Indicates students under my direct mentorship or supervision

**Published or Accepted**

5. **Phillips, J.D.**, Gillis, D.J. and Hanner, R.H. (2022). Lack of statistical rigor in DNA barcoding likely invalidates the presence of a true species' barcode gap. *Frontiers in Ecology and Evolution*, 10: 859099. DOI: [10.3389/fevo.2022.859099](https://doi.org/10.3389/fevo.2022.859099).
4. D'Ercole, J., Dincă, V., Opler, P.A., Kondla, N.G., Schmidt, C.B., **Phillips, J.D.**, Robbins, R., Burns, J.M., Miller, S.E., Grishin, N., Zakharov, E.V., deWaard, J.R., Ratnasingham, S. and Hebert, P.D.N. (2020). A DNA barcode library for the butterflies of North America. *PeerJ*, 9: e11157. DOI: [10.7717/peerj.11157](https://doi.org/10.7717/peerj.11157).
3. **Phillips, J.D.**, \*French, S.H., Hanner, R.H. and Gillis, D.J. (2020). HACSim: An R package to estimate intraspecific sample sizes for genetic diversity assessment using haplotype accumulation curves. *PeerJ Computer Science*, 6(192): 1-37. DOI: [10.7717/peerj-cs.243](https://doi.org/10.7717/peerj-cs.243).
2. **Phillips, J.D.**, Gillis, D.J. and Hanner, R.H. (2019). Incomplete estimates of genetic diversity within species: Implications for DNA barcoding. *Ecology and Evolution*, 9(5): 2996-3010. DOI: [10.1002/ece3.4757](https://doi.org/10.1002/ece3.4757).
1. **Phillips, J.D.**, Gwiazdowski, R.A., Ashlock, D. and Hanner, R. (2015). An exploration of sufficient sampling effort to describe intraspecific DNA barcode haplotype diversity: examples from the ray-finned fishes (Chordata: Actinopterygii). *DNA Barcodes*, 3: 66-73. DOI: [10.1515/dna-2015-0008](https://doi.org/10.1515/dna-2015-0008).

**Submitted or Under Revision**

1. Young, R.G., \*Persram, M., \*Friesen, O., \*Chen, A., \*Yu, J. **Phillips, J.D.** and Hanner, R.H. (Under Revision). Incomplete and irregular reporting of the R statistical and computing environment highlights the need for citation guidelines to support scientific reproducibility. *PeerJ Computer Science*.

**In Preparation or To Be Submitted**

4. D'Ercole, J., Dapporto, L., **Phillips, J.D.**, Dincă, V.E., Vila, R., Talavera, G. and Hebert, P.D.N. Macrogenetics of North American butterflies—The impact of Quaternary climatic fluctuations.
3. **Phillips, J.D.**, \*Singh, N., Hanner, R.H. and Gillis, D.J. The HACSim R Shiny app: A web interface to estimate specimen sampling sufficiency for species genetic diversity assessment with DNA sequence data. Targeted for *Bioinformatics*.
2. **Phillips, J.D.**, \*Bootsma, S.E., Hanner, R.H. and Gillis, D.J. Solving the genetic specimen sample size problem with a local search optimization algorithm. Targeted for *Methods in Ecology and Evolution*.

1. Athey, T.B.T., **Phillips, J.D.**, Hanner, R.H. and McNicholas, P.D. VLF: An R package for the analysis of very low frequency variants in DNA sequences. Targeted for *Biodiversity Data Journal*.

### Conference Proceedings

3. **Phillips, J.D.**, Gillis, D. and Hanner, R. (2019). HACSim: Iterative extrapolation of haplotype accumulation curves for assessment of intraspecific COI DNA barcode sampling completeness. Scientific abstracts from the 8th International Barcode of Life Conference, Trondheim, Norway (ed. Torbjørn Ekrem), *Genome*, 62(6): 349-453.

2. **Phillips, J.D.**, Gillis, D. and Hanner, R. (2017). Intraspecific sample size estimation for DNA barcoding: Are current sampling levels enough? Scientific abstracts from the 7th International Barcode of Life Conference, Johannesburg, South Africa (ed. M. van der Bank), *Genome*, 60(11): 881-1019.

1. **Phillips, J.D.**, Gwiazdowski, R.A., Ashlock, D. and Hanner, R. (2015). An exploration of sufficient sampling effort to describe intraspecific haplotype diversity in the ray-finned fishes (Chordata: Actinopterygii). Scientific abstracts from the 6th International Barcode of Life Conference, Guelph, ON., Canada (ed. S.J. Adamowicz), *Genome*, 58(5): 163-303.

### NON-REFEREED WORK

I have communicated aspects of my research to non-technical audiences through various online media.

### Blog posts

5. **Phillips, J.D.** (2020). Barcode Cracking. Contributed CEPS Research Highlights article (<https://www.uoguelph.ca/ceps/news/2020/02/barcode-cracking>)

4. **Phillips, J.D.** (2020). Protecting Biodiversity Through the Lens of Genetic Diversity. Contributed guest post to the blog of Dr. Daniel Gillis (<https://danielgillis.wordpress.com/2020/01/30/protecting-biodiversity-through-the-lens-of-genetic-diversity/>).

3. **Phillips, J.D.** (2019). IBOL8 and the Midnight Sun. Contributed guest post to the blog of Dr. Daniel Gillis (<https://danielgillis.wordpress.com/2019/07/02/reflections-ibol8-and-the-midnight-sun/>).

2. **Phillips, J.D.** (2017). The Big Five and IBOL7. Contributed guest post to the blog of Dr. Daniel Gillis (<https://danielgillis.wordpress.com/2017/12/06/reflections-the-big-five-and-ibol7/>).

1. **Phillips, J.D.** (2016). Sample size estimation for DNA barcoding: Are current sampling levels enough? Contributed guest post to the DNA Barcoding Blog (<http://dna-barcoding.blogspot.com/2016/01/guest-post-sample-size-estimation-for.html>).

### Newsletters

1. **Phillips, J.D.** (2016). Sample size estimation for DNA barcoding of ray-finned fishes: Are current sampling levels enough? Contributed newsletter article to the Barcode Bulletin, 7(1).

**VOLUNTEER EXPERIENCE**

1. Wireframing session volunteer  
University of Guelph

2021

- Participated in student-led use case app prototype demonstrations for CIS\*3750 – System Analysis and Design in Applications
- Graded students based on several factors via Qualtrics surveys

**References**

Dr. Daniel Gillis  
Associate Professor  
School of Computer Science  
University of Guelph  
50 Stone Road East  
Guelph, ON.  
N1G 2W1  
[dgillis@uoguelph.ca](mailto:dgillis@uoguelph.ca)

Dr. Robert Hanner  
Full Professor  
Department of Integrative Biology  
University of Guelph  
50 Stone Road East  
Guelph, ON.  
N1G 2W1  
(519) 824-4120 ext. 53479  
[rhanner@uoguelph.ca](mailto:rhanner@uoguelph.ca)

Dr. Rodger Gwiazdowski

Adjunct Professor  
Department of Environmental Conservation  
University of Massachusetts Amherst  
Amherst, MA, USA  
01003  
(413) 320-3755  
[rgwiazdowski@umass.edu](mailto:rgwiazdowski@umass.edu)

Owner  
Advanced BioConsulting LLC.  
139 Spring Street  
Shrewsbury, MA, USA  
01545  
(413) 320-3755  
[rodger.gwiazdowski@gmail.com](mailto:rodger.gwiazdowski@gmail.com)

Supervisory Fish and Wildlife Biologist  
Sucker Recovery Coordinator  
Klamath Falls Fish and Wildlife Office  
1936 California Ave  
Klamath Falls, OR, USA  
97601  
(541) 591-9905



Dr. Robert Young  
Postdoctoral Research Associate  
Department of Integrative Biology  
University of Guelph  
50 Stone Road East  
Guelph, ON.  
N1G 2W1  
(519) 824-4120  
[rgyoung6@gmail.com](mailto:rgyoung6@gmail.com)