

**Jarrett D. Phillips, BSc. (Hons.), MBinf., PhD. ABD**✉ [jphill01@uoguelph.ca](mailto:jphill01@uoguelph.ca) [jphill01](#) [Jarrett Phillips](#) [Jarrett D. Phillips](#) [Jarrett Phillips](#) [Jarrett Phillips](#)**Professional Summary of Research Interests and Expertise**

A highly motivated and passionate bioinformatician, data scientist and researcher naturally driven by curiosity to use mathematical, statistical and computational methods to answer fundamental and applied research questions in biodiversity science, evolutionary biology, ecology, genomics and bioinformatics, particularly related to molecular species identification and discovery through DNA barcoding and other DNA-based approaches.

**Education****Doctor of Philosophy (PhD.), Computational Sciences**

2016-Present

University of Guelph

- Thesis title: A Novel Statistical Framework for Assessment of Intraspecific Haplotype Sampling Completeness
- Cumulative GPA: 90%

Advisor: Dr. Daniel J. Gillis, School of Computer Science

Co-Advisor: Dr. Robert H. Hanner, Department of Integrative Biology

**An Introduction to Interactive Programming in Python**

2014

Rice University

- Online course through Coursera on the development of interactive applications in Python
- Grade received: 98.4%

**Master of Bioinformatics (MBinf.)**

2013-2014

University of Guelph

- Primary coursework in bioinformatics, data science, statistics, and machine learning within the R Statistical Computing Environment
- Major research project title: Assessing haplotype sampling efficiency in Actinopterygii using DNA barcodes
- Cumulative GPA: 85.8%

Advisor: Dr. Robert H. Hanner, Department of Integrative Biology

Co-Advisor: Dr. Daniel A. Ashlock, Department of Mathematics and Statistics

**Introduction to DNA Barcoding**

2013

University of Guelph

- Online course through the Open Learning and Education Support (OpenEd)
- Grade received: 97.0%

**Honors Bachelor of Science (BSc. (Hons.)) Biological Science**

2009-2013

University of Guelph

- Primary coursework in bioinformatics, evolutionary biology, ecology, mathematics and statistics

**Research Experience****Summer Research Assistant**

2016

Algoma University

Antunes Plant and Soil Ecology Lab, Department of Biology

Invasive Species Research Institute (ISRI)

- 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

Antunes Plant and Soil Ecology Lab, Department of Biology

Invasive Species Research Institute (ISRI)

- 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

Monteiro Vaccine Discovery Research Group

- 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**

<b>Graduate Teaching Assistant (GTA)</b>	2016-2020
University of Guelph	
<b>CIS*3130 – System Modelling and Simulation</b>	2020
~ 30 students · Python	
<b>CIS*1910 – Discrete Structures in Computing I</b>	2017
~ 300 students (~ 40 students per section)	
<b>CIS*2460 – Modelling of Computer Systems</b>	2016-2019
~ 60 students · R, Excel, Java	

**Undergraduate Student Supervision**

<b>Navdeep Singh</b> (with Dan Gillis)	2021
University of Guelph	
CIS*4900 · HACSim RShiny web application	
<b>Scarlett Bootsma</b> (with Dan Gillis)	2020-2021
University of Guelph	
CIS*4900/4910 · HACSim simulation study	
<b>Steven French</b> (with Dan Gillis)	2018
CIS*4900/4910 · HACSim R package	

**Assistantships, Awards, Scholarships and Travel Grants**

<b>Graduate Teaching Assistantships</b>	2017-2020
University of Guelph	\$34,506.00-35,148.00
<b>Graduate Research Assistantships</b>	2017-2019
University of Guelph	\$11,000.00
<b>CPES Graduate Dean's Scholarship</b>	2017
University of Guelph	\$3500.00
<b>CPES Graduate Excellence Entrance (GEE) Scholarship</b>	2016
University of Guelph	\$30000.00
<b>Arthur D. Latornell Graduate Travel Grant</b>	2019
University of Guelph	\$500.00
<b>SoCS Travel Grant</b>	2019
University of Guelph	\$1000.00

**Academic Service**

<b>School of Computer Science (SoCS) Search Committee</b>	2018
University of Guelph	
• Associate Professor position in cybersecurity	
<b>School of Computer Science (SoCS) Search Committee</b>	2017-2018

University of Guelph

- Two-year contractually-limited Assistant Professor position in cybersecurity

### **Academic Peer Review Service**

<i>Molecular Ecology Resources</i>	2019-2020, 2021
<i>Molecular Biology Reports</i>	2020
<i>Methods in Ecology and Evolution</i>	2020

### **Proceedings**

<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	

### **Skills**

#### **Programming Languages and IDEs**

R · RStudio · TeX · Python · PyCharm

#### **Document Preparation, Spreadsheet Applications, Version Control and Continuous Integration**

LaTeX · RMarkdown · Excel · HTML · Git · GitHub · Travis CI

#### **Other**

R Shiny

### **Software Development**

HACSim (**H**aplotype **A**ccumulation **C**urve **S**imulator) · R package · RShiny 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
- Available for download through the Comprehensive R Archive Network (CRAN) package repository
- 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 12000 times (c. 290 times per month) since being published in May 2019.

## Refereed Work

### Journal Articles

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*.
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.
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.
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.

### 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

### 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).

### **Accepted**

N/A

### **Submitted**

1. Young, R.G., Persram, M., Friesen, O., Chen, A., Yu, J. **Phillips, J.D.** and Hanner, R.H. R you citing your use of the R statistical computing and graphics environment correctly? *Scientific Data*.

### **To Be Submitted**

3. **Phillips, J.D.**, Gillis, D.J. and Hanner, R.H. Lack of statistical rigor in DNA barcoding likely invalidates the presence of a true species' barcode gap. *Frontiers in Ecology and Evolution*.

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.

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.

### **References**

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