

Jarrett D. Phillips, PhD.
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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**

2023

University of Guelph

Gillis Lab, School of Computer Science

Hanner Lab, Department of Integrative Biology

- Developed a Bayesian hierarchical binary logistic time-series regression model of seafood fraud in the Canadian supply chain

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
- Participated in conceptualization and drafting of various manuscripts

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 the School of Computer Science and the Department of 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.

Fynn de Vuono-Fraser (with Dan Gillis)

2023

University of Guelph

STAT*4600 · Bayesian modelling of seefood fraud in the Canadian supply Chain

Amina Asif (with Bob Hanner)

2022

University of Guelph

BINF*6999 · DNA barcode gap analysis of Canadian disease vectors and agricultural pests

Navdeep Singh (with Dan Gillis)

2021

University of Guelph

CIS*4900 · HACSim RShiny web application

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

ASSISTANTSHIPS, SCHOLARSHIPS AND GRANTS

Graduate Teaching Assistantships University of Guelph	2017-2020 \$34,506.00-35,148.00 CAD
Graduate Research Assistantships University of Guelph	2017-2019 \$11,000.00 CAD
CPES Graduate Dean's Scholarship University of Guelph	2017 \$3500.00 CAD
<ul style="list-style-type: none"> Awarded in recognition of achieving over 85% in Master's coursework 	
CPES Graduate Excellence Entrance (GEE) Scholarship University of Guelph	2016 \$30000.00 CAD
<ul style="list-style-type: none"> Awarded in recognition of achieving over 85% in Master's coursework 	

- Arthur D. Latornell Graduate Travel Grant** 2019
 University of Guelph \$500.00 CAD
- Awarded for first-class academic standing in PhD. coursework
 - Supported travel to the 8th International Barcode of Life Conference in Trondheim, Norway to present work related to resource management and conservation
- SoCS Travel Grant** 2019
 University of Guelph \$1000.00 CAD
- Supported travel to the 8th International Barcode of Life Conference in Trondheim, Norway
- Food from Thought Advancing Research Impact (ARIF) Fund** 2022
 University of Guelph \$30000.00 CAD
- Postdoctoral funding to develop a Bayesian hierarchical binary logistic time-series regression model of seafood fraud in the Canadian supply chain

ACADEMIC SERVICE

- School of Computer Science (SoCS) Search Committee** 2018
 University of Guelph
- Associate Professor position in cybersecurity
- School of Computer Science (SoCS) Search Committee** 2017-2018
 University of Guelph
- Two-year contractually-limited Assistant Professor position in cybersecurity

ACADEMIC PEER REVIEW SERVICE

I have served as a reviewer for 14 manuscripts in 7 different journals, both alone or under the guidance of my PhD. supervisors.

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|---|-----------|
| <i>Ecology and Evolution</i> (2) | 2021-2022 |
| <i>F1000 Research</i> (1) | 2022 |
| <i>Frontiers in Ecology and Evolution</i> (2) | 2022 |
| <i>Lifestyle Genomics</i> (2) | 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 |

I have served as Guest Editor on various journal special issues:

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| <i>International Journal of Environmental Research and Public Health</i> | 2022-2023 |
| Mobile Applications for Environment and Health Monitoring | |

PROCEEDINGS

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

8th International Barcode of Life Conference	2019
NTNU University Museum and Norwegian Biodiversity Information Centre	
7th International Barcode of Life Conference	2017
University of Johannesburg	
6th International Barcode of Life Conference	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
- 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 21000 times (c. 408 times per month) since being published in May 2019

VLF (Very Low Frequency) · R package

- A tool to assess PCR errors, sequencing errors, *etc.* in the form of very low frequency variants, within DNA sequences using a sliding window approach
- R package available for download through [CRAN](#)
- Manuscript published in the *Biodiversity Data Journal*

REFEREED WORK**Journal Articles**

Citations: 114 · H-index: 4 (According to Google Scholar, as of February 2023)

*Indicates students under my direct mentorship or supervision

Published or Accepted

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

Submitted or Under Revision

1. Young, R.G., *Persram, M., *Friesen, O., *Chen, A., *Yu, J. **Phillips, J.D.** and Hanner, R.H. (Under review). 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

3. 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.
2. **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*.
1. **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*.

Book Chapters*Submitted or Under Revision*

1. Hubert, N., **Phillips, J.D.**, and Hanner, R.H. Delimiting species with single-locus DNA sequences. *Methods in Molecular Biology*. Springer.

In Preparation or To Be Submitted

1. **Phillips, J.D.**, Griswold, C.K., Young, R.G., Hubert, N., and Hanner, R.H. A measure of the DNA barcode gap for applied and basic research. *Methods in Molecular Biology*. Springer.

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

6. **Phillips, J.D.** (2022) Mind the Gap — The DNA Barcode Gap, That is. Contributed CEPS Research Highlights article (<https://www.uoguelph.ca/ceps/news/2022/08/mind-gap—dna-barcode-gap>).
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

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| <ol style="list-style-type: none"> 1. Wireframing session volunteer
University of Guelph <ul style="list-style-type: none"> • 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 | 2021 |
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REFERENCES

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