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EXECUTIVE SUMMARY

My academic work and research interests can best be described as **computational, mathematical,** and **statistical molecular biodiversity science**. Biodiversity is under threat in a rapidly changing world, where **mitigation** requires **innovative** and **collaborative solutions** from **multiple disciplines**, **particularly bioinformatics**. DNA-based specimen identification and species discovery, through techniques like **DNA barcoding** and **environmental DNA (eDNA),** offer promising ways forward, yet produce **overwhelming amounts of data** in need of navigation. I leverage **AI/ML/Data Science/Big Data** methods to help researchers find meaningful signal in a vast sea of noise.

ACADEMIC APPOINTMENTS

In my role as **Adjunct Professor**, much of my time is spent **connecting** and **interacting** with undergraduate and graduate students, with faculty in the **Department of Integrative Biology** and the **School of Computer Science** interested in working with me, as well as with other units on campus, such as the **Department of Population Medicine**.

Adjunct Professor, School of Computer Science   2023–Present
University of Guelph

EDUCATION

I am many things to many people: **a biologist**, **a molecular biodiversity scientist**, a computer scientist, **a bioinformatician**, a data scientist, a statistician, and a software engineer, among other titles. However, I am foremost **an interdisciplinary** and **collaborative researcher** and **teacher**, and my diverse educational background in a **cross-disciplinary field** clearly demonstrates this, particularly through the lens of **biodiversity informatics** and **genetic diversity assessment**.

Ph.D. in Computational Sciences, University of Guelph   2022
Co-Advisors: Dr. Daniel Gillis and Dr. Robert Hanner
Advisory Committee Members: Dr. Deborah Stacey and Dr. Graham Taylor
Dissertation: A Novel Statistical Framework for Assessment of Intraspecific Haplotype Sampling
Completeness: Implications for DNA Barcode Gap Estimation

Master of Bioinformatics, University of Guelph   2014
Co-Advisors: Dr. Robert Hanner and Dr. Daniel Ashlock
Major Paper: Assessing DNA Barcode Haplotype Sampling Diversity in the Ray-finned Fishes (Chordata: Actinopterygii)

BSc. in Biological Science, University of Guelph   2013
Coursework in bioinformatics, ecology, evolutionary biology, comparative animal physiology, genetics, mathematics, and statistics

RESEARCH EXPERIENCE

My research experience is highly varied, yet well-rounded and reflects my extensive **interdisciplinary and collaborative background** at the **intersection of the biological and computational sciences**. I have conducted work at **all scales of biological organization**, from microorganisms to animals and from **genomes to entire ecosystems**, involving both wild and domesticated (livestock) species.

Postdoctoral Fellow   2023–Present
University of Guelph
GBADs Informatics Team
Stacey Lab, School of Computer Science
Supervisor: Dr. Deborah Stacey

- Currently developing an R package to run a compartmentalized equation-based model called the Dynamic Population Model (DPM) for the Global Burden of Animal Diseases (GBADs) initiative to calculate the Animal Health Loss Envelope (AHLE) in livestock species as part of a larger team of computer scientists, software engineers, data scientists, epidemiologists, veterinarians, and economists.
- Co-developed and ran a week-long data workshop at the University of Liverpool alongside other members of the GBADs Informatics Working Group and international colleagues.

Postdoctoral Fellow   2023–Present
University of Guelph
Gillis Lab, School of Computer Science
Hanner Lab, Department of Integrative Biology
Supervisors: Drs. Daniel Gillis and Robert Hanner

- Mentored and supervised CIS*4900/4910, STAT*4600, IBIO*6070, and URA students in projects on seafood fraud and environmental DNA sampling using computational and statistical methods.
- Participated in conceptualization and drafting of various manuscripts for both academic and non-academic audiences, where I was lead author on most.

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

- Mentored and supervised a Master of Bioinformatics (MBINF.) BINF*6999 student on research project examining DNA barcoding in Canadian pests and disease vectors.
- Participated in conceptualization and drafting of various manuscripts and invited book chapters, many as primary author.

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 staining 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 (*e.g.*, herbivory, decay).

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 guidance and supervision of qualified graduate students.

TEACHING EXPERIENCE

Having completed my degree in **Computational Sciences** within the School of Computer Science, as opposed to biology, my teaching experience has been in the former space. Despite this, **learned skills** are **highly transferrable**.

Within CIS*1910 (Discrete Structures in Computing I, 400 students), a required course in the B.Comp. (Bachelor of Computing) program, which I am currently teaching, I am actively **managing eight teaching assistants** (seven undergraduate and one graduate) across eight lab sections. To ensure effective communication and consistency in feedback to students, TAs are required to complete lab activities on their own before we meet as a group to discuss solutions. TAs are also encouraged to develop teaching support materials such as YouTube videos. These have proven quite popular with the students, especially the channel [@JaskiratSinghSohal](#), having over 30 videos, 2500 total views, and 150 hours of watch time.

To better support the large class size of CIS*1910, I have set up a **course email account** (cis1910@socs.uoguelph.ca) through Redmine (an online ticketing management system) which allows seamless monitoring (and diverting from my own @uoguelph.ca account) of incoming student emails. Redmine is checked at the start and end of each weekday. Ticketing support systems such as Redmine would likely **benefit the teaching mission of the Department of Integrative Biology**, and the College of Biological Science (CBS) more broadly, and could **easily be set up**.

Additionally, I regularly post course announcements on D2L and make **extensive use of CourseLink's discussion board and survey tools** to encourage students to ask questions when they are struggling with course content and to provide me with feedback. If one student has a particular question, chances are other students have the exact same question.

Classes and labs have been designed to provide students with **experiential** and **hands-on learning** experiences such as completing questions on the whiteboard in front of the class. Students are assessed via midterm tests and exams. These have been developed to support not only conceptual understanding, but also procedural knowledge through a mix of **multiple choice**, **true/false**, and **short/long answer** questions. For instance, regarding true/false questions, if a statement is false, students must succinctly **explain why** in a few words or one short sentence.

I try to make my lectures as **accessible** and **engaging** as possible, especially using technology in the classroom. For example, during lectures, I employ a Logitech Spotlight Presentation Remote™ to magnify and highlight important parts of my slides. This also allows me to move around the room as I click through slides. Further, when requested, I have provided problem solutions to students registered with Student Accessibility Services (SAS) in advance so that they are able to more easily follow along during labs.

Observations from the delivery of CIS*1910 (Fall 2025) will be used to **support further pedagogical enhancement**. This includes redesigning assessments to incorporate answer-until correct (AUC) multiple choice integrated testlets (Dawkins *et al.*, 2020). These have been shown to improve comprehension of core course topics.

Within the Department, at the undergraduate level, I am confident in teaching core courses related to my area of expertise, such as Discovering Biodiversity (BIOL*1070), Ecology (BIOL*2060), Biostatistics for Integrative Biology (STAT*2230), Evolution (BIOL*2400), Population Genetics (BIOL*3020), Populations, Communities, and Ecosystems (BIOL*3060), and Evolutionary Ecology (BIOL*4120), among others having a quantitative eco-evolutionary flavour. At the graduate level, I am excited to teach **Bioinformatics Software Tools for Biological Data Analysis and Organization (BINF*6210)** and **Topics in Bioinformatics (BINF*6890)**, as well as Special Topics in Evolutionary Biology (IBIO*6020), among others offered by the Department.

I am also keen on **developing graduate experiential learning courses** that focus on the use of **AI/ML/Data Science/Big Data for biodiversity conservation and restoration**. This is best done in the context of my future involvement with Land'escapes, a 63000-acre privately-owned property located in Hastings County near Bancroft, ON. At present, we aim to **offer hands-on training modules** on acoustic surveys, camera trapping/thermal imaging, eDNA sampling, and hydrological and soil modelling using GIS **available** to **Bioinformatics MSc.** and **PhD.** and **coursework students** (*e.g.*, those in the MBINF and MDS (Master of Data Science) programs) likely during the summer semester. Space permitting, interested undergraduates may enroll as well. These team-taught modules will be facilitated by faculty

across the CBS and the College of Computational, Mathematical, and Physical Sciences (CCMPS), including Dr. Hanner, Dr. Jacobs, Dr. Dan Gillis, and Dr. Graham Taylor (College of Engineering, COE), and myself among many others.

Course Instructor   2025
University of Guelph
CIS*1910 – Discrete Structures in Computing I
- Course content in deductive logic, set theory, and mathematical proof techniques.
- Managed 400 students along with eight undergraduate and graduate Teaching Assistants over eight lab sections.

Graduate Teaching Assistant (GTA)   2016–2020
University of Guelph
CIS*3130 – System Modelling and Simulation   2020
- Taught statistical and Monte Carlo methods in Python to approximately 30 students
CIS*1910 – Discrete Structures in Computing I   2017
- Taught deductive logic, set theory, and mathematical proof techniques to approximately 40 students
CIS*2460 – Modelling of Computer Systems   2016–2019
- Taught statistical and Monte Carlo methods in R, Excel, and Java to approximately 60 students

STUDENT SUPERVISION AND MENTORSHIP

My **overarching philosophy** and **pedagogy** when it comes to student supervision and mentorship is one **encompassing humility**, **kindness**, and **understanding**. From an **equity, diversity,** and **inclusion (EDI) standpoint**, having these ideals is important. While my research program is strongly focused on the **analysis** of **DNA sequence data** for **assessment** of **intraspecific** and **interspecific genetic variation**, it is important to be **open** and **flexible** to new perspectives and to recognize students' strengths and weaknesses, as well as opposing views.

* Indicates students under my direct mentorship/supervision
** Indicates students under my co-mentorship/co-supervision

Undergraduate

*Richard Cui   2025
Summer Undergraduate Research Assistant (URA) · Dynamical modelling of seafood fraud in the supply chain
*Nikolett Toth   2024-2025
CIS*4900/4910 · Mining association rules for eDNA spatiotemporal sampling
*Nikolett Toth   2024
Summer Undergraduate Research Assistant (URA) · Mining association rules for eDNA spatiotemporal sampling
*Fynn De Vuono-Fraser   2024
CIS*4900/4910 · Bayesian modelling of seafood fraud in the Canadian supply chain

*Zaid Al-Gayyali   2023
Summer Undergraduate Research Assistant (URA) · Seafood Fraud Visualization Tool Shiny app
*Fynn De Vuono-Fraser   2023
STAT*4600 · Bayesian modelling of seafood fraud in the Canadian supply chain
*Navdeep Singh   2021
CIS*4900 · HACSim R Shiny web application
*Scarlett Bootsma   2020–2021
CIS*4900/4910 · HACSim simulation study
**Maya Persram   2020
Hanner Lab volunteer · R reporting ecological meta-analysis
**Ashley Chen   2020
Hanner Lab volunteer · R reporting ecological meta-analysis
**Olivia Friesen Kroeker   2020
Hanner Lab volunteer · R reporting ecological meta-analysis
*Steven French   2018
CIS*4900/4910 · HACSim R package
**Julia Harvie   2018–2019
MCB*4500/4510 · Data mining GenBank and BOLD

Graduate

**Nathan Zeinstra   2024
IBIO*6070 · Bayesian habitat occupancy modelling of sea lamprey using eDNA
**Amina Asif   2022
BINF*6999 · DNA barcode gap analysis of Canadian disease vectors and agricultural pests
**Danielle St. Jean (*withdrawn*)   2018–2019
MSc. thesis (Mathematics) · DNA barcode sequence classification with machine learning
**Christina Fragel   2018–2019
BINF*6999 · DNA barcode sequence classification with machine learning
**Jiaojia (Paula) Yu   2018–2019
BINF*6999 · MDMAPR R Shiny app
**Ankita Bhanderi   2018
BINF*6999 · Data mining GenBank and BOLD

ASSISTANTSHIPS, AWARDS, SCHOLARSHIPS, AND GRANTS[1]

Throughout my academic career, I have been successful in receiving many internal university assistantships, awards, scholarships, and grants to support my students and me on projects related to my research program, such as **Food From Thought**. I have also written two successfully funded Advancing Research Impact Fund (ARIF) grant applications, along with three successful **Undergraduate Research Assistantship (URA)** proposals. Additionally, I am currently **co-applicant/collaborator** on **several large externally funded grant applications** with an AI/ML/Data Science/Big Data focus, particularly **NSERC** and **NFRF**. Unsuccessful grant applications have served as learning experiences.

Completed

Food From Thought Advancing Research Impact (ARIF) Fund – Livestock Innovation Grant   2024
University of Guelph $40000.00 CAD
- 1-year postdoctoral funding to develop and refine the Dynamic Population Model (DPM) to assess global disease burden in livestock.

Food From Thought Advancing Research Impact (ARIF) Fund   2022
University of Guelph $30000.00 CAD
- 1-year postdoctoral funding to develop a Bayesian hierarchical binary logistic time-series regression model of seafood fraud in the Canadian supply chain.

SoCS Travel Grant   2019
University of Guelph $1000.00 CAD
- Supported travel to the 8th International Barcode of Life Conference in Trondheim, Norway to present doctoral research.

Arthur D. Latornell Graduate Travel Grant   2019
University of Guelph $500.00 CAD
- Awarded for first-class academic standing in Ph.D. coursework.
- Supported travel to the 8th International Barcode of Life Conference in Trondheim, Norway to present work related to resource management and conservation.

Graduate Teaching Assistantships   2017–2020
University of Guelph $34506.00-35148.00 CAD

Graduate Research Assistantships   2017–2019
University of Guelph $11000.00 CAD

CPES Graduate Dean's Scholarship   2017
University of Guelph $3500.00 CAD
- Awarded in recognition of achieving over 85% in Master's coursework.

CPES Graduate Excellence Entrance (GEE) Scholarship   2016
University of Guelph $30000.00 CAD
- Awarded in recognition of achieving over 85% in Master's coursework.

To be Submitted

Advancing Research Impact Fund: "Quick Wins" Knowledge Mobilization Fund   2025
University of Guelph $20000 CAD
- Knowledge mobilization of the GBADs Dynamic Population Model (DPM) in the Cloud as "Build Your Own" dashboards to visualize and summarize model output for end users in the form of tutorial and webinars.

NSERC Alliance Society Grant   2025
University of Guelph $5 million CAD
AI-Driven Biodiversity Restoration: Scalable Solutions for Ecosystem Monitoring and Conservation
- Research in collaboration with over 10 University of Guelph faculty across multiple colleges and departments, as well as diverse community partners like environmental consulting agencies and Indigenous communities, incorporating acoustic surveys, camera trapping and thermal imaging, environmental DNA (eDNA) sampling, and hydrological, GIS, and soil modelling.

NSERC CREATE Grant 2025
University of Guelph $9.9 million CAD
AI-Driven Training of Next-Generation Conservation Scientists
- Development of HQP training programs in collaboration with multiple members from the University of Guelph, Trent University, and the University of British Columbia across diverse departments, as well as diverse community partners like environmental consulting agencies and Indigenous communities, incorporating acoustic surveys, camera trapping and thermal imaging, environmental DNA (eDNA) sampling, and hydrological, GIS, and soil modelling.

To be Targeted

New Frontiers in Research Fund (NFRF) Transformation 2026
University of Guelph $24 million CAD
AI-Driven Biodiversity Monitoring: Scalable Solutions for Ecosystem Restoration through Interdisciplinary Innovation
- Research in collaboration with over 10 University of Guelph faculty and other institutions across multiple departments, as well as diverse community partners like environmental consulting agencies and Indigenous communities, incorporating acoustic surveys, camera trapping and thermal imaging, environmental DNA (eDNA) sampling, and hydrological and soil modelling.

ACADEMIC SERVICE

In addition to my research and teaching, I have had opportunities to gain experience in several **interdisciplinary** service roles that emphasize **collaborative** work.

GBADs Informatics Technical Workshop 2023
University of Liverpool
- Organized and participated in international workshop hosted by the GBADs programme.
- Tasks, duties, and responsibilities included arranging and facilitating talks for the Informatics working group.

Pathways to Increase Standards and Competency in eDNA Surveys (PISCeS) Conference 2023
University of Guelph
- Organized and participated in international eDNA conference hosted by the Hanner Lab.
- Tasks, duties, and responsibilities included registration, upload, and audiovisual support.

School of Computer Science (SoCS) Search Committee 2018
University of Guelph
- Associate Professor position in cybersecurity.
- Tasks, duties, and responsibilities included reviewing and ranking received applications, shortlisting strong candidates to be invited for formal interviews, participating in interview questioning, and attending organized events with candidates and other SoCS faculty.

School of Computer Science (SoCS) Search Committee 2017–2018
University of Guelph
- Two-year contractually limited Assistant Professor position in cybersecurity.
- Tasks, duties, and responsibilities included reviewing and ranking received applications, shortlisting strong candidates to be invited for formal interviews, participating in interview questioning, and attending organized events with candidates and other SoCS faculty.

ACADEMIC PEER REVIEW SERVICE

I have served as a peer reviewer for **several top journals** that regularly publish in **biodiversity informatics**, most notably *Molecular Ecology Resources*.

Ecology and Evolution, *F1000 Research*, *Frontiers in Ecology and Evolution*, *Lifestyle Genomics*, *Mitochondrial DNA Part A*, *Molecular Ecology Resources*, *Molecular Biology Reports*, *Methods in Ecology and Evolution*

PROCEEDINGS

Over the years, my students and I have contributed to, and participated in, several **national** and **international academic conferences**, **workshops**, and **symposia.** This has allowed me to broaden my network of interdisciplinary collaborators significantly.

SoCS Undergraduate Summer Project Show and Tell (student oral presentation)   2025
Richard Cui · The Importance in Design as a Computer Scientist
CEPS Undergraduate Student Poster Day (student poster presentation)   2024
Nikolett Toth · Association Rule Mining of eDNA Datasets
University of Guelph, Canada
CBS Undergraduate Poster Session (student poster presentation)   2024
Nikolett Toth · Association Rule Mining of eDNA Datasets
University of Guelph, Canada
9th International Barcode of Life Conference (poster presentation)   2024
Estação das Docas, Brazil · A Measure of the DNA Barcode Gap for Applied and Basic Research
(*not attended*)
GBADs Informatics Technical Workshop (oral presentation)   2023
University of Liverpool, England · The GBADs R Package (and Why We Need It!)
CEPS Student Research Day (student poster presentation)   2023
Fynn De Vuono-Fraser · Estimating Seafood Mislabelling Rates in Canada Using Bayesian Modelling
University of Guelph, Canada
Pathway to Increase Standards and Competency of eDNA Surveys (PICSeS)   2023
International Conference (poster presentation)
University of Guelph, Canada
8th International Barcode of Life Conference (oral presentation)   2019
NTNU University Museum and Norwegian Biodiversity Information Centre, Norway
Guelph BioMathematics and Statistics (BioM&S) Symposium
Artificial Intelligence and Machine Learning in Biology (attended)   2019
University of Guelph, Canada
CEPS Undergraduate Student Poster Day (student poster presentation)   2018
Steven French · Estimating Sampling Size Using Haplotype Accumulation Curves and Semiparametric Models
University of Guelph, Canada
7th International Barcode of Life Conference (oral presentation)   2017
University of Johannesburg, South Africa

SOFTWARE DEVELOPMENT

As a **biodiversity informatics researcher** whose work lies at the crossroads of multiple complementary disciplines, I feel **software** and **software development** unifies them all. I have created and contributed to many **open-source computational tools**, particularly **R packages** and **Shiny web applications** hosted on GitHub, the Comprehensive R Archive Network (CRAN), and the Shiny Server, several of which have been heavily used and cited.

RulesTools · R package
- Streamlined tools to facilitate association rule mining and visualization using various discretization and imputation methods, along with heatmaps and Euler diagrams.
- R package available for download through the CRAN package repository.
- Has been downloaded over 1200 times since publication in January 2025.
- Currently being applied to assess invasive brook trout (*Salvelinus fontinalis*) eDNA detection and occupancy based on water samples collected from Hanlon Creek (Guelph, ON.), along with physicochemical metadata like temperature, pH, conductivity, and dissolved oxygen levels.

GBADsDPM (**G**lobal **B**urden of **A**nimal **D**isease**s** **D**ynamic **P**opulation **M**odel) · R package
- A novel stochastic age- and sex-structured compartmentalized equation-based model to assess the burden of animal diseases in livestock such as cattle, small ruminants, equids, swine, and poultry within developing countries like Ethiopia through calculation of the Animal Health Loss Envelope (AHLE)—the difference between monetary losses under current (disease) and ideal (no disease) conditions.
- This work has wide ranging implications, from animal physiology to animal welfare
- R package currently under active development.

HACSim (**H**aplotype **A**ccumulation **C**urve **Sim**ulator) · 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 CRAN or interactive use 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 40000 times and cited frequently since being published in May 2019.
- Has been applied to assess sampling sufficiency via sample size estimation in important species of mammals, reptiles, fishes, insects, and arachnids, such as monk seals (Monachini), Kemp's ridley sea turtles (*Lepidochelys kempii*), lake whitefish (*Coregonus clupeaformis*), sharks (Chondrichthyes), mosquitoes (Culicidae), aphids (Aphidoidea), and ticks (Ixodoidea), among other taxa of conservation and invasive concern.

VLF (**V**ery **L**ow **F**requency) · R package
- A novel tool to assess PCR errors, sequencing errors, chimeras/heteroplasmies, insertions/deletions (INDELS), nuclear-mitochondrial inserts (NUMTs), *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.*
- Has been downloaded over 40000 times since publication in 2013.
- Has been applied to assess the distribution of PCR, sequencing errors, and other artifacts, along with their rates in DNA barcode and amino acid sequence alignments of birds (Aves) and aquatic taxa in the context of seafood fraud.

Frequentist/Bayesian DNA barcode gap coalescent-informed estimators · R scripts
- A novel set of nonparametric Maximum Likelihood metrics to quantify the extent of overlap/separation of genetic distances computed from DNA sequence alignments. Useful in assessing the presence/absence of DNA barcode gaps–the difference between within-species genetic variation and among-species genetic divergence–for specimen identification and species delimitation, as well as applications like qPCR primer/probe design for seafood fraud and eDNA detection.
- Applied to assess DNA barcode gaps in species of predatory *Agabus* diving beetles in a book chapter on DNA barcoding protocols (Phillips *et al.*, 2024). Data/code are currently available on GitHub here.
- A Bayesian implementation available here written in the Stan probabilistic programming language has been conditionally accepted to *Molecular Ecology Resources* (article revisions currently under review).
- Will soon be converted to an easy-to-use R package and an R Shiny web application for global dissemination.

REFEREED WORK

I am very active when it comes to academic publishing in a wide variety of forms including **journal articles**, **book chapters**, and **conference abstracts**, as well as **building strong alliances** with researchers from a wide range of disciplines through **networking**. Most of my published work has been as **primary** and **senior author**. Many publications involve my students as either **first**, **co-first**, or **second author**.

Journal Articles

* Indicates students under my direct mentorship/supervision
** Indicates students under my co-mentorship/co-supervision

Published or Accepted

10. **Phillips, J.D.**, Hubert, N., and Hanner, R.H. A Bayesian-informed coalescent model of the DNA barcode gap. Conditionally accepted in *Molecular Ecology Resources*.
9. **Phillips, J.D.**, Hubert, N., and Hanner, R.H. A Bayesian coalescent model of the DNA barcode gap. Authorea. DOI: 10.22541/au.174073683.37707806/v1
8. Raymond, K., Sobkowich, K.E., **Phillips, J.D.**, Nguyen, L., McKechnie, I., Mohideen, R.N., Fitzjohn, W., Szurkowski, M., Davidson, J., Rushton, J., Stacey, D.A., and Bernardo T.M. (2024). GBADs informatics strategy: User-centric tools, data quality, and model interoperability. *WOAH Scientific and Technical Review*, **43**: 96-107. DOI: 10.20506/rst.43.3522.
7. **Phillips, J.D.** and *****De Vuono-Fraser, F.A. (2024). Statistical modelling of seafood fraud in the Canadian supply chain. bioRxiv. DOI: 10.1101/2024.02.05.578947.

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,* e96480*.* DOI: [10.3897/BDJ.11.e98480](10.3897/BDJ.11.e98480).

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. (2021). 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](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](10.1515/dna-2015-0008).

Submitted or Under Revision

2. **Phillips, J.D.** and *De Vuono-Fraser, F.A. Statistical modelling of seafood fraud highlights uncertainties in products from Metro Vancouver, British Columbia, Canada: Revisiting Hu *et al.* (2018). Submitted to *RSS Data Science and Artificial Intelligence.*

1. **Phillips, J.D.** and *De Vuono-Fraser, F.A. Swimming in uncertainty: How proper statistical modelling can help expose seafood product mislabeling. Submitted to *CHANCE*.

To Be Submitted

8. **Phillips, J.D.**, *Cui, R.C., and Yodzis, M.P. Seafood market product fraud erodes both consumer trust and resource sustainability within the global supply chain. Targeted to *Proceedings of the Royal Society B: Biological Sciences*.

7. *Toth, N., Antonie, M.L., Hanner, R.H., Gillis, D.J., and **Phillips, J.D.** Mining association rules for targeted spatiotemporal aquatic environmental DNA (eDNA) sampling. Targeted to *Aquatic Conservation: Marine and Freshwater Research*.

6. **Phillips, J.D.**, *Al-Gayyali, Z.B.**, *De Vuono-Fraser, F.A., Hanner, R.H. and Gillis, D.J. The Seafood Fraud Visualization Tool: An R Shiny web app to summarize, model, and visualize seafood mislabelling trends in the supply chain.

5. Morey, K.C., **Phillips, J.D.**, Loeza-Quintana, T., and Hanner, R.H. Haplotype diversity reveals challenges and opportunities for developing targeted detection assays for COI in Canadian freshwater fish. Targeted to *Environmental DNA.*

4. Young, R.G., **Persram, M., **Friesen, O., **Chen, A., **Yu, J., **Phillips, J.D.,** and Hanner, R.H. Incomplete and irregular reporting of the R statistical and computing environment highlights the need for citation guidelines to support scientific reproducibility.

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.

2. 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. Targeted to *PNAS.*
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 to *Methods in Ecology and Evolution.*

Book Chapters

Published or Accepted

2. **Phillips, J.D**., Griswold, C.K., Young, R.G., Hubert, N., and Hanner, R.H. (2024). A Measure of the DNA Barcode Gap for Applied and Basic Research. In: DeSalle, R. (eds) DNA Barcoding. Methods in Molecular Biology, vol 2744. Humana, New York, NY.
URL: https://link.springer.com/protocol/10.1007/978-1-0716-3581-0_24
1. Hubert, N., **Phillips, J.D.**, and Hanner, R.H. (2024). Delimiting Species with Single-Locus DNA Sequences. In: DeSalle, R. (eds) DNA Barcoding. Methods in Molecular Biology, vol 2744. Humana, New York, NY. URL: https://link.springer.com/protocol/10.1007/978-1-0716-3581-0_3

Conference Proceedings

4. Morey, K., Loeza-Quintana, T., **Phillips, J.**, and Hanner R. (2023). Haplotype diversity reveals challenges and opportunities for developing targeted detection assays for *COI* in Canadian freshwater fish. Pathways to Increase Standards and Competency in eDNA Surveys (PISCeS) Conference. Poster.
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. Oral presentation.
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. Oral presentation.
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. Poster.

NON-REFEREED WORK

In addition to refereed work, I believe **scientific communication** to **broad non-technical audiences** using **plain**, **accessible** and **inclusive language** is a necessary skill to have in the biodiversity informatics toolbox. I have contributed several **blog posts**, **videos**, and **College Research Highlights articles** about my collaborative research projects over the years.

* Indicates students under my direct mentorship/supervision

13. *Cui, R.C. (2025). The Importance in Design as a Computer Scientist. Student-contributed SoCS Show and Tell video URL: https://github.com/RichaCui70/Dynamics-between-Seafood-Fraudsters-and-Buyers/blob/main/Summer%20Showcase%20-%20Richard%20Cui.mp4

12. **Phillips, J.D.**, *De Vuono-Fraser, F.A., Gillis, D.J., and Hanner, R.H. (2024). Statistical modelling of seafood fraud. Whiteboard explainer video. URL: https://www.moon-man.com/whiteboard-animation-production-company.

11. *****Toth, N. (2024). eDNA Collection Gets a Tech Update. Student-contributed CEPS Research Highlights article. URL: https://www.uoguelph.ca/ceps/news/2024/07/edna-collection-gets-tech-upgrade

10. *****Toth, N. (2024). Unravelling eDNA with Association Rule Mining. Contributed guest post to the Science Borealis-syndicated blog of Dr. Daniel Gillis. URL: https://danielgillis.wordpress.com/2024/08/15/unravelling-edna-with-association-rule-mining/

9. **Phillips, J.D.** (2024). Summer URA Position. Contributed guest post to the Science Borealis-syndicated blog of Dr. Daniel Gillis. URL: https://danielgillis.wordpress.com/2024/02/07/summer-ura-position-2/

8**. Phillips, J.D.** (2022). A Novel Statistical Framework for Assessment of Intraspecific Haplotype Sampling Completeness: Implications for DNA Barcode Gap Estimation. Ph.D. Thesis. URL: https://atrium.lib.uoguelph.ca/items/8addfcc5-f21c-4691-89b7-c4db051892eb

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

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

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

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

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

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

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

Aside from my research, teaching, and service responsibilities, I have also volunteered my time in several capacities on campus. Each of my volunteer roles involve **significant student interactions**.

Student Research Connections Networking Night   2025
University of Guelph
- Connected with motivated undergraduate students interested in conducting research projects under my supervision over the summer semester and beyond.

Wireframing session   2021-2025
University of Guelph
- Participated in student-led use case mobile app prototype demonstrations for CIS*3750 – System Analysis and Design in Applications.
- Involved several community partners such as The Grove Hubs, an NGO aimed at bringing awareness to youth mental health.
- Graded students based on several factors via Qualtrics surveys.

REFERENCES

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[1] Only includes received assistantships, awards, scholarships, and grants. Non-funded grants are below.

Food from Thought Advancing Research Impact (ARIF) Fund – Knowledge Mobilization Grant   2024
University of Guelph $30000 CAD
- 1-year postdoctoral funding to develop association rule classifiers for targeted aquatic eDNA species detection

NSERC Postdoctoral Fellowship   2021
University of Waterloo $90000.00 CAD
- 2-year postdoctoral funding to develop an ensemble machine learning model for taxonomic classification of regulated species in Canada

Guelph Institute for Environmental Research Small Grants Program (GIER SGP)   2020
University of Guelph $15000.00 CAD
- 1-year postdoctoral funding to develop a Bayesian hierarchical binary logistic time-series regression model of seafood fraud in the Canadian supply chain