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## **Dr. Robert Beiko**

Correspondence language: English

Sex: Male

Date of Birth: 5/12

Canadian Residency Status: Canadian Citizen

Country of Citizenship: Canada

## **Contact Information**

The primary information is denoted by (\*)

### **Address**

#### Courier

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## Dr. Robert Beiko

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### Language Skills

Language	Read	Write	Speak	Understand	Peer Review
English	Yes	Yes	Yes	Yes	Yes
French	Yes	Yes	Yes	Yes	Yes

### Degrees

- 1998/9 - 2003/9      Doctorate, Ph.D. Biology, Bioinformatics, University of Ottawa  
Degree Status: Completed  
Supervisors: Dr. Robert L. Charlebois, 1998/9 - 2003/9
- 1994/9 - 1998/4      Bachelor's, B.Sc.(Hons) Biology, Genetics, Dalhousie University  
Degree Status: Completed  
Supervisors: Dr. Gerald C. Johnston, 1997/5 - 1998/8

### Recognitions

- 2010/6 - 2010/6      Teaching Award  
Dalhousie Student Union  
Prize / Award
- 2007/4 - 2017/3      Canada Research Chair  
Natural Sciences and Engineering Research Council of Canada (NSERC)  
Prize / Award  
Canada Research Chair in Bioinformatics

### User Profile

Researcher Status: Researcher  
Research Career Start Date: 1998/09/03  
Engaged in Clinical Research?: No

Key Theory / Methodology: Investigating microbial community structure and evolution using computational techniques.

Research Interests: (i) Development of new models and approaches to understand the structure and similarity of microbial communities (ii) Investigating microbial metagenomes in human and model systems to understand the relationship between microbial function and human health (iii) Understanding the evolutionary processes (especially lateral gene transfer) that give rise to microbe-microbe and host-microbe interactions

Fields of Application: Communication and Information Technologies, Environment, Pathogenesis and Treatment of Diseases

Disciplines Trained In: Genetics, Microbiology

Areas of Research: Bioinformatics, Microorganisms, Genotype and Phenotype

Research Specialization Keywords: Bioinformatics, Comparative Genomics, Computational Biology, Human Microbiome, Metagenomics, Phylogenetics, Phylogeography

Research Disciplines: Computer Science, Genetics, Microbiology

## Employment

2016/7	Professor Computer Science, Computer Science, Dalhousie University Full-time, Professor Tenure Status: Tenure
2017/7 - 2022/6	Associate Dean Research Computer Science, Computer Science, Dalhousie University Full-time Tenure Status: Tenure
2011/7 - 2016/6	Associate Professor Computer Science, Computer Science, Dalhousie University Full-time, Associate Professor Tenure Status: Tenure
2006/9 - 2011/6	Assistant Professor Computer Science, Computer Science, Dalhousie University Full-time, Assistant Professor Tenure Status: Tenure Track
2003/6 - 2006/8	Postdoctoral Fellow Institute for Molecular Bioscience, Institute for Molecular Bioscience, University of Queensland Full-time, Professor Tenure Status: Non Tenure Track
1992/12 - 1997/10	Cartographic Technician Seabed Exploration Associates

## Affiliations

The primary affiliation is denoted by (\*)

(\*) 2016/7                      Professor, Computer Science, Dalhousie University

## Research Funding History

### Awarded [n=12]

2024/4 - 2028/3                      Articulating Microbiome Stewardship: Definition, Guiding Principles, Framework, Grant, Operating  
Principal Applicant

#### Funding Sources:

Canadian Institutes of Health Research (CIHR)  
Project Grants  
Total Funding - 707,624  
Funding Competitive?: Yes

2017/4 - 2023/3                      Integrating time, function, phylogenetics and genome dynamics to redefine microbial diversity, Grant, Operating  
Principal Applicant

**Funding Sources:**

2017/4 - 2023/3 Natural Sciences and Engineering Research Council of Canada (NSERC)  
Discovery Grants  
Total Funding - 200,000  
Portion of Funding Received - 100  
Funding Competitive?: Yes

2022/4 - 2023/3 Tracking the emergence and spread of antimicrobial resistance, Grant, Operating  
Principal Applicant

**Funding Sources:**

2017/4 - 2023/3 Compute Canada  
Resources for Research Groups  
Total Funding - 31,922  
Portion of Funding Received - 100  
Funding Competitive?: Yes

2018/9 - 2022/12 Antimicrobial Resistance: Emergence, Transmission, and Ecology (ARETE), Grant,  
Principal Investigator Operating  
Clinical Research Project?: No

**Funding by Year:**

2018/9 - 2021/8 Total Funding - 1,400,000 (Canadian dollar)

**Funding Sources:**

2018/9 - 2021/8 Genome Canada  
Bioinformatics and Computational Biology competition  
Total Funding - 1,400,000 (Canadian dollar)  
Portion of Funding Received - 500,000  
Funding Competitive?: Yes

2016/10 - 2022/9 Managing Microbial Corrosion in Canadian Offshore & Onshore Oil Production, Grant,  
Co-applicant Operating  
Clinical Research Project?: No

Project Description: Corrosion is a global phenomenon that leads to the deterioration of infrastructure in any industry. Within this industry, corrosion that involves microbial activities, deemed Microbiologically Influenced Corrosion (MIC), is thought to account for at least 20% of all corrosion cases. There is a lack of information about how MIC occurs under most operating conditions in the oil and gas industry, and genomics approaches that allow for a deeper understanding of microbial processes are critical for achieving a step change towards understanding and managing MIC in this industry. Our project deliverables will allow corrosion managers in the oil and gas industry to better predict when, where, and why failures due to MIC occur and how to best mitigate MIC.

**Funding Sources:**

2016/10 - 2020/9 Genome Canada  
2015 LARGE-SCALE APPLIED RESEARCH PROJECT  
COMPETITION  
NATURAL RESOURCES AND THE ENVIRONMENT  
Total Funding - 7,000,000 (Canadian dollar)  
Portion of Funding Received - 8  
Funding Competitive?: Yes

2021/1 - 2021/12 Environmental DNA by design: software tools for automated and precise species  
Principal Applicant identification, Contract

**Funding Sources:**

2021/1 - 2021/12 InNOVAcorp (Nova Scotia)  
 Early Stage Commercialization Fund  
 Total Funding - 50,000  
 Portion of Funding Received - 100  
 Funding Competitive?: Yes

2019/6 - 2020/5 Development of bioinformatics tools for environmental DNA analysis and test deployment  
 Principal Investigator in the field., Grant

**Funding by Year:**

2019/6 - 2020/5 Total Funding - 28,625 (Canadian dollar)

**Funding Sources:**

2019/6 - 2020/5 Ocean Frontier Institute  
 OFI Seed Fund  
 Total Funding - 28,625 (Canadian dollar)  
 Portion of Funding Received - 60  
 Funding Competitive?: Yes

Co-applicant : Vincent Sieben

2008/9 - 2017/8 The Dalhousie Centre for Comparative Genomics and Evolutionary Bioinformatics, Grant  
 Co-investigator

**Funding Sources:**

2008/5 - 2017/4 Tula Foundation  
 N/A  
 Total Funding - 3,000,000 (Canadian dollar)  
 Portion of Funding Received - 300,000  
 Funding Competitive?: No

2013/9 - 2017/8 Genomics approaches to the management of mixed stock fisheries in Canada: developing  
 Co-applicant tools for promoting fishery stability and the protection of biodiversity, Grant

**Funding Sources:**

2013/9 - 2016/8 Natural Sciences and Engineering Research Council of Canada  
 (NSERC)  
 Strategic Project Grants  
 Total Funding - 593,809 (Canadian dollar)  
 Portion of Funding Received - 100,000  
 Funding Competitive?: Yes

Co-applicant : Ian Bradbury;

Principal Investigator : Paul Bentzen

2007/4 - 2017/3 Canada Research Chair in Bioinformatics, Research Chair  
 Principal Investigator

**Funding Sources:**

2007/4 - 2017/3 Canada Research Chairs (CRC)  
 Tier 2 Canada Research Chairs  
 Total Funding - 1,000,000 (Canadian dollar)  
 Portion of Funding Received - 1,000,000  
 Funding Competitive?: Yes

2012/4 - 2017/3 Untangling the complex geographic and evolutionary patterns of microbes, Grant,  
 Principal Investigator Operating  
 Project Description: The tiny size of microorganisms belies their extraordinary complexity.  
 In spite of their size, most microbes have several thousand genes that encode a wide

range of metabolic and cellular functions, some acquired from distant relatives through the process of lateral gene transfer (LGT). The spread of antibiotic resistance and adaptation to challenging environments such as polluted sites are particularly compelling examples of the impact of microbial LGT on society. One consequence of LGT is that building a Tree of Life to understand the evolution of microorganisms may be impossible or a meaningless exercise, since so much genetic information has been shared between distant lineages. The first part of my proposed research will address this question, by using new criteria to assemble trees that are more resistant to the effects of LGT, and by developing phylogenetic network approaches.

**Funding Sources:**

2012/4 - 2017/3      Natural Sciences and Engineering Research Council of Canada (NSERC)  
Discovery Grants  
Total Funding - 165,000 (Canadian dollar)  
Portion of Funding Received - 165,000  
Funding Competitive?: Yes

Principal Investigator : Robert Beiko

2013/7 - 2016/12  
Co-investigator

A Federated Bioinformatics Platform for Public Health Microbial Genomics, Grant

**Funding Sources:**

2013/5 - 2016/4      Genome Canada  
Bioinformatics and Computational Biology  
Total Funding - 1,576,791 (Canadian dollar)  
Portion of Funding Received - 50,000  
Funding Competitive?: Yes

Co-investigator : Gary van Domselaar; Will Hsiao

**Completed [n=21]**

2015/9 - 2020/8  
Co-applicant

CHONe II: Conservation Strategies for Canada's Changing Oceans, Grant, Operating  
Clinical Research Project?: No

**Funding Sources:**

2015/9 - 2020/8      Natural Sciences and Engineering Research Council of Canada (NSERC)  
Strategic Network Grant  
Total Funding - 4,980,000 (Canadian dollar)  
Portion of Funding Received - 45,000 (Canadian dollar)  
Funding Competitive?: Yes

2016/10 - 2018/9  
Principal Applicant

Rapid prediction of antimicrobial resistance from metagenomics samples: data, models, and methods, Grant, Operating  
Clinical Research Project?: No  
Project Description: This project aims to enhance the Comprehensive Antibiotic Resistance Database (CARD) by supporting rapid processing of clinical metagenomic data to identify antimicrobial resistance genes, and enable discovery of new resistance genes from environmental samples.

**Funding Sources:**

2016/10 - 2018/9      Genome Canada  
 2015 Bioinformatics and Computational Biology Competition  
 Total Funding - 250,000 (Canadian dollar)  
 Portion of Funding Received - 0 (Canadian dollar)  
 Funding Renewable?: No  
 Funding Competitive?: Yes

Co-applicant : Fiona Brinkman;

Principal Investigator : Andrew McArthur

2016/10 - 2018/9  
 Co-applicant

The maternal and neonatal microbiota correlates of premature labor and adverse neonatal outcomes, Grant, Operating  
 Clinical Research Project?: Yes  
 Project Description: Premature labor and delivery occurs in about 11% of pregnancies globally and is a common cause of neonatal morbidity and mortality. Within the last few years, there has been an increased appreciation of the complexity of the vaginal and fecal microbiota of pregnant women and its relationship to preterm labor and birth. Our project will be situated at the Aga Khan University Hospital in Nairobi, Kenya, with the following objectives: - Determine whether the vaginal microbiota at the time of presentation with labor correlates with premature labor - Determine whether fecal microbiota at birth in premature infants predicts the subsequent occurrence of necrotizing enterocolitis or sepsis.

**Funding Sources:**

2016/8 - 2019/8      Aga Khan University  
 Internal funding  
 Total Funding - 25,000 (United States dollar)  
 Portion of Funding Received - 20  
 Funding Competitive?: Yes

2016/8 - 2017/1  
 Co-applicant

Novel Chlamydia vaccine antigen development by computational algorithms, Contract  
 Clinical Research Project?: Yes  
 Project Description: This project will validate Chlamydia antigens that were predicted by a novel computational algorithm.

**Funding Sources:**

2016/7 - 2017/1      Springboard Atlantic  
 Springboard  
 Total Funding - 20,000 (Canadian dollar)  
 Portion of Funding Received - 0  
 Funding Renewable?: No  
 Funding Competitive?: Yes

Co-applicant : Jun Wang; Mat Kallada

2015/9 - 2016/9  
 Principal Applicant

Assessing microbial signatures of periodontitis in an aging population, Grant, Operating

**Funding Sources:**

2015/9 - 2016/9      Nova Scotia Health Research Foundation (NSHRF)  
 Development / Innovative Grants  
 Total Funding - 14,300 (Canadian dollar)  
 Portion of Funding Received - 14,300 (Canadian dollar)  
 Funding Competitive?: Yes

2013/9 - 2016/8  
 Principal Investigator

Scotia Support Grant, Grant, Operating  
 Clinical Research Project?: Yes

Project Description: This ongoing project aims to establish connections between frailty of human patients and the makeup of their microbiome. The project includes bioinformatics, model organism studies, and human trials.

**Funding Sources:**

2013/9 - 2015/8 Nova Scotia Health Research Foundation (NSHRF)  
 Scotia Support Grants  
 Total Funding - 48,000 (Canadian dollar)  
 Portion of Funding Received - 48,000  
 Funding Competitive?: Yes

Co-applicant : Kenneth Rockwood; Susan Howlett

2013/9 - 2016/5 A Pilot Project to Assess the Gut Microbes of Patients in an Assisted Living Facility, Grant  
 Principal Investigator

**Funding Sources:**

2013/9 - 2016/5 Nova Scotia Health Research Foundation (NSHRF)  
 Discovery / Innovative Grants  
 Total Funding - 15,000 (Canadian dollar)  
 Portion of Funding Received - 15,000  
 Funding Competitive?: Yes

Co-applicant : Kenneth Rockwood; Robert Rose; Susan Howlett

2014/11 - 2016/3 Development of a genetic marker panel to predict Fertility and Longevity traits in Holstein  
 Principal Investigator Dairy Cattle, Contract  
 Clinical Research Project?: No

**Funding Sources:**

2014/11 - 2016/3 National Research Council Canada (NRC) (Ottawa, ON)  
 IRAP  
 Total Funding - 165,000  
 Portion of Funding Received - 165,000 (Canadian dollar)  
 Funding Competitive?: No

2015/3 - 2016/3 Genetic control of Reproductive Longevity in Mouse and Validation of a genetic marker  
 Principal Investigator panel to predict Fertility and Longevity traits in Holstein Dairy Cattle, Grant, Operating  
 Clinical Research Project?: No

**Funding Sources:**

2015/3 - 2016/3 Mathematics of Information Technology and Complex Systems  
 (MITACS)  
 Accelerate  
 Total Funding - 90,000  
 Portion of Funding Received - 90,000 (Canadian dollar)  
 Funding Competitive?: Yes

2014/5 - 2015/3 Comparative Genomics to Identify Genes and Pathways Controlling Reproductive  
 Principal Investigator Longevity of Mammals, Contract  
 Clinical Research Project?: No

**Funding Sources:**

2013/3 - 2015/3 National Research Council Canada (NRC) (Ottawa, ON)  
 IRAP  
 Total Funding - 80,000  
 Portion of Funding Received - 80,000 (Canadian dollar)  
 Funding Competitive?: No



2013/9 - 2014/8  
Co-applicant

The role of the complement system in post-colitis colonization and recovery from injury,  
Grant, Operating  
Clinical Research Project?: No

**Funding Sources:**

2013/9 - 2014/8 Nova Scotia Health Research Foundation (NSHRF)  
Discovery / Innovative Grants  
Total Funding - 15,000 (Canadian dollar)  
Portion of Funding Received - 15,000  
Funding Competitive?: Yes

Principal Applicant : Andrew Stadnyk

2014/3 - 2014/8  
Principal Investigator

Rapid Identification of Insertion Sites for Retroviral Elements in Complex Genomes, Contract  
Clinical Research Project?: No

**Funding Sources:**

2014/3 - 2014/8 EW Group GmbH  
N/A  
Total Funding - 32,000  
Portion of Funding Received - 32,000 (Canadian dollar)  
Funding Competitive?: No

2013/9 - 2014/8  
Principal Investigator

Comparative Genomics, Grant, Operating  
Clinical Research Project?: No  
Project Description: Mapping fertility and reproductive longevity in a selectively bred mouse population

**Funding Sources:**

2013/9 - 2014/8 Mathematics of Information Technology and Complex Systems (MITACS)  
MITACS Accelerate  
Total Funding - 45,000 (Canadian dollar)  
Portion of Funding Received - 45,000  
Funding Competitive?: Yes

2011/7 - 2014/6  
Co-investigator

Biomonitoring 2.0, Grant, Operating  
Project Description: In partnership with Environment Canada, and building on a recently completed Genome Canada Technology Development project, we have developed high-throughput next generation sequencing tools for genomic analysis of biomonitoring samples used to assess the health of Canada's diverse ecosystems. This proposal will promote rapid uptake and integration of these technologies, through a real-world demonstration of their applicability in environmental monitoring. Our unique team with world-class experience in large-scale biodiversity genomics projects, will allow an amalgamation of next-generation sequencing, biodiversity science and advanced informatics, to produce a revolutionary biomonitoring approach built on data gathered from comprehensive habitats/biota for the Canadian resource/environmental management sector, including Environment Canada and Parks Canada, who are both fully engaged in this project.

**Funding Sources:**

2011/7 - 2014/6 Genome Canada  
Large-scale applied research projects  
Total Funding - 3,000,000 (Canadian dollar)  
Portion of Funding Received - 100,000  
Funding Competitive?: Yes

Principal Investigator : Hajibabaei, Mehrdad

2010/9 - 2013/8  
Co-investigator

Modeling and Mapping Microbial Diversity and Function with Marker Genes, Genomes and Metagenomes, Grant, Operating

Project Description: Microbiomics is a new science, born of molecular ecology and metagenomics. Molecular ecology uses specific marker genes amplified from environmental DNA samples to tell the microbiologist "Who is there?" -- what species occupy a particular site on or in the human body, for instance. Metagenomics looks at all the genes in an environmental DNA sample, thus providing a wealth of information about metabolic process (and disease processes) that might be under way there -- an answer to "What can they do?" Most large microbiomic projects will generate both kinds of information but our models for understanding one in terms of the other are as yet limited, and our ability to go from either to solid predictive knowledge -- "What will they do?" -- is limiting. Our project seeks to improve predictive ability through computational modeling and the bioinformatic analysis of available metagenomic data sets.

**Funding Sources:**

2010/9 - 2013/8 Canadian Institutes of Health Research (CIHR)  
Emerging Team Grant (Human Microbiome)  
Total Funding - 623,000 (Canadian dollar)  
Portion of Funding Received - 200,000  
Funding Competitive?: Yes

Principal Investigator : Doolittle, Ford

2012/6 - 2012/12  
Principal Investigator

Machine-learning classification of genomic polymorphism data relating to fertility and reproductive longevity, Grant

**Funding Sources:**

2012/5 - 2012/12 Natural Sciences and Engineering Research Council of Canada (NSERC)  
Engage  
Total Funding - 25,000 (Canadian dollar)  
Portion of Funding Received - 25,000  
Funding Competitive?: Yes

2009/9 - 2012/8  
Co-investigator

BEEM: Bioproducts and Enzymes from Environmental Metagenomes, Grant, Operating  
Project Description: Canadian citizens support a transition to a bioeconomy for two reasons: to reduce the net contribution of carbon into the atmosphere and to develop cheaper alternatives to fossil fuels. The biofuels idea is captivating: carbon is burned and released into the atmosphere as CO<sub>2</sub>, which is then breathed by plants to fuel their growth only to be cycled again. But of course plants are not only carbon. They also contain components that cannot be easily recycled, such as phosphorus, nitrogen and sulphur, and chemicals that are harmful to humans, such as the plant hormones that can disrupt our own hormonal systems. These chemicals & by-products of the bioeconomy processes & pose serious environmental concerns. Of course, the appreciation environmental issues associated with the processing of plants is not new; Canada's pulp and paper industry has been dealing with it for decades, and in doing so has developed processes that pollute minimally.

**Funding Sources:**

2009/9 - 2012/8 Genome Canada  
COMPETITION IN APPLIED GENOMICS RESEARCH IN BIOPRODUCTS OR C  
Total Funding - 5,000,000 (Canadian dollar)  
Portion of Funding Received - 100,000  
Funding Competitive?: Yes

Principal Investigator : Edwards, Elizabeth

2007/4 - 2012/3

Principal Investigator

New Computational Methods for Metagenomics, Grant, Operating

Project Description: Microbial life is responsible for an immense number of medical and environmental processes. The role of microbes in infectious disease is well known, but bacteria also provide essential services to us, including extracting important nutrients from our food. In the environment, microbes are essential in the turnover of nutrients, breaking down and building up important molecules in a cycle that is global in scope. By sequencing microbial genomes, we can learn a great deal about the roles they play and the myriad complex ways in which they interact. But the sheer amount of data is overwhelming, and the rate of increase in computer speed is being overtaken by the flood of sequence data. We need new and better computational methods to be able to take a random sampling of DNA from the environment and assess its function and its history.

**Funding Sources:**

2007/4 - 2012/3

Natural Sciences and Engineering Research Council of Canada (NSERC)

Discovery Grant

Total Funding - 115,000 (Canadian dollar)

Portion of Funding Received - 115,000

Funding Competitive?: Yes

Principal Investigator : Robert Beiko

2007/1 - 2010/12

Co-investigator

Metagenomics and the genetic basis of ecology and evolution of communities - complex

microbial communities in industrial processes as excellent paradigms, Grant, Operating

Project Description: Genome-level analysis has transformed understanding of biological diversity, but only now are we poised to marshal new technologies to address vital questions linking genetics with ecology and evolution. Using metagenomics as a key enabling technology, we will use novel experiments and computational analysis to address two pivotal questions in ecology and evolution, namely, the extent to which community-level phenomena are influenced by the genes of individuals, and how community-level properties influence the evolution of component species. In using phosphorus absorbing microbial communities in wastewater treatment as our model system, the work will provide key insights into an important industrial process.

**Funding Sources:**

2007/1 - 2010/12

Australian Research Council

Discovery Project

Total Funding - 210,000 (Canadian dollar)

Portion of Funding Received - 0

Funding Competitive?: Yes

Principal Investigator : Blackall, Linda L

2006/9 - 2010/8

Principal Investigator

Computational Analysis of Genomic and Metagenomic Data, Grant, Establishment

Project Description: N/A - Startup funds, no summary available

**Funding Sources:**

2006/9 - 2010/8

Genome Atlantic

Startup Funds

Total Funding - 226,000 (Canadian dollar)

Portion of Funding Received - 226,000

Funding Competitive?: No

Principal Investigator : Robert Beiko

2007/4 - 2008/4

A Canadian platform for advanced comparative genomics, Grant

**Principal Investigator Funding Sources:**

2007/4 - 2008/4      Canada Foundation for Innovation (CFI)  
 Leaders Opportunity Fund  
 Total Funding - 322,000 (Canadian dollar)  
 Portion of Funding Received - 322,000  
 Funding Competitive?: Yes

Principal Investigator : Robert Beiko

**Under Review [n=1]**

2024/5 - 2025/4      Precise Species Identification for eDNA Sensing Applications

Principal Investigator

**Funding Sources:**

Dartmouth Ocean Technologies, Inc.  
 Industry Co-funding  
 Total Funding - 65,000  
 Funding Competitive?: No

Genome Atlantic  
 Environmental DNA Innovation Fund  
 Total Funding - 49,800  
 Funding Competitive?: Yes

**Courses Taught**

, Computer Science, Dalhousie University  
 Course Title: Informatics Structures  
 Course Code: INFX2600  
 Course Level: Undergraduate  
 Guest Lecture?: No

, Computer Science, Dalhousie University  
 Course Title: Introduction to Bioinformatics  
 Course Code: CSCI4180/CSCI6801  
 Course Level: Post Graduate  
 Guest Lecture?: No

, Computer Science, Dalhousie University  
 Course Title: Algorithms in Bioinformatics  
 Course Code: CSCI4181/CSCI6802  
 Course Level: Post Graduate  
 Guest Lecture?: No

**Student/Postdoctoral Supervision****Bachelor's [n=7]**

2019/5 - 2019/8      Jocelyn MacDonald (Completed) , Dalhousie University  
 Principal Supervisor      Student Degree Start Date: 2016/9  
    Thesis/Project Title: Phylogenetic analysis of antimicrobial resistance genes  
    Present Position: Associate Software Engineer, ResMed Canada

2018/5 - 2018/8  
Principal Supervisor Zhou Zhilei (Completed) , Dalhousie University  
Student Degree Start Date: 2016/9  
Student Canadian Residency Status: Student Work Permit  
Thesis/Project Title: Predicting antimicrobial resistance mutations in bacterial 16S sequences  
Present Position: Undergraduate student

2014/9 - 2014/12  
Co-Supervisor Michael Traynor (Completed) , Dalhousie University  
Student Degree Start Date: 2011/9  
Student Degree Received Date: 2015/5  
Thesis/Project Title: Machine-learning classification of oral microbial communities  
Present Position: Master's Student

2012/5 - 2012/8  
Co-Supervisor Joel Navarrete (Completed) , Dalhousie University  
Student Degree Start Date: 2010/9  
Student Degree Received Date: 2014/6  
Thesis/Project Title: Inferring phylogenetic supertrees based on the subtree prune-and-regraft distance  
Present Position: Bachelor's student

2012/5 - 2012/8  
Principal Supervisor Brett O'Donnell (Completed) , Dalhousie University  
Student Degree Start Date: 2010/9  
Student Degree Received Date: 2014/5  
Thesis/Project Title: Visual analysis of the relationship between biodiversity of taxonomy  
Present Position: Bachelor's student

2012/5 - 2012/10  
Principal Supervisor Nan Liu (Completed) , Dalhousie University  
Student Degree Start Date: 2007/9  
Student Degree Received Date: 2012/9  
Thesis/Project Title: Clustering of mouse single nucleotide polymorphism data  
Present Position: Unknown

2010/5 - 2011/8  
Principal Supervisor Catherine Holloway (Completed) , University of Waterloo  
Student Degree Start Date: 2006/9  
Student Degree Received Date: 2010/6  
Thesis/Project Title: Inferring networks of genomes using linear programming  
Present Position: PhD student

**Bachelor's Honours [n=6]**

2022/5 - 2023/4  
Principal Supervisor Shuting Xie (In Progress) , Dalhousie University  
Student Degree Start Date: 2022/5  
Student Degree Expected Date: 2022/8  
Thesis/Project Title: Feature selection in microbial community analysis  
Present Position: Master's student

2021/9 - 2022/4  
Principal Supervisor Julia Lewandowski (Completed) , Dalhousie University  
Student Degree Start Date: 2021/9  
Student Degree Received Date: 2022/5  
Thesis/Project Title: Distributed Gene Embeddings for the Analysis of Gene Neighborhoods and Classification of Candidate Antimicrobial Resistance Genes  
Present Position: Bioinformatics Software Developer, Dalhousie University

2021/5 - 2022/4  
Principal Supervisor Tanuj Fernando (Completed) , Dalhousie University  
Student Degree Start Date: 2021/5  
Student Degree Received Date: 2022/5  
Thesis/Project Title: Understanding behaviour of machine learning-based RNA secondary structure prediction software  
Present Position: Student

2021/5 - 2022/4  
Principal Supervisor Yuchan Zhong (Completed) , Dalhousie University  
Student Degree Start Date: 2021/5  
Student Degree Received Date: 2022/4  
Thesis/Project Title: Alignment of antimicrobial resistance genes in metagenomic assembly graphs  
Present Position: Graduate student

2018/9 - 2019/4  
Academic Advisor Alex Manuele (Completed) , Dalhousie University  
Student Degree Start Date: 2015/9  
Student Degree Received Date: 2019/5  
Thesis/Project Title: Comparing feature representation strategies in the classification of microbial community data  
Present Position: Database developer

2015/5 - 2016/8  
Principal Supervisor Jonathan Perrie (Completed) , Dalhousie University  
Student Degree Start Date: 2012/9  
Thesis/Project Title: Clustering methods for time-series analysis of microbial communities  
Present Position: Master's student, Waterloo University

**Master's Thesis [n=17]**

2022/9 - 2024/8  
Principal Supervisor Monica Alvaro Fuss (In Progress) , Dalhousie University  
Student Degree Start Date: 2022/9  
Student Degree Expected Date: 2024/8  
Thesis/Project Title: Changes in the microbiome during extended bedrest  
Present Position: Master's student, Dalhousie University

2020/1 - 2021/8  
Principal Supervisor Chandana Navanakere Rudrappa (Completed) , Dalhousie University  
Student Degree Start Date: 2020/1  
Student Degree Received Date: 2021/10  
Thesis/Project Title: Neighborhood clustering to analyse antimicrobial resistance in bacterial genomes  
Present Position: Data Engineer, Zenni Opticals

2020/1 - 2021/8  
Principal Supervisor Alex Manuele (Completed) , Dalhousie University  
Student Degree Start Date: 2020/1  
Student Degree Received Date: 2021/10  
Thesis/Project Title: Novel Approaches to Marker Gene Representation Learning Using Trained Tokenizers and Jointly Trained Transformer Models  
Present Position: Senior Bioinformatics Developer

2019/1 - 2022/10  
Co-Supervisor Jackie Purdue (Withdrawn) , Dalhousie University  
Student Degree Start Date: 2018/1  
Student Canadian Residency Status: Canadian Citizen  
Thesis/Project Title: Building aggregate representations of lateral gene transfer events  
Present Position: Master's Student

- 2017/9 - 2018/6  
Principal Supervisor Sayna Hajiloo (Withdrawn) , Dalhousie University  
Student Degree Start Date: 2017/9  
Student Canadian Residency Status: Study Permit  
Thesis/Project Title: Database and user interface development for microbially influenced pipeline corrosion  
Present Position: Unknown
- 2015/9 - 2017/8  
Principal Supervisor Emma Sylvester (Completed) , Dalhousie University  
Degree Name: Master's of Science (Computational Biology and Bioinformatics)  
Student Degree Start Date: 2015/9  
Student Degree Received Date: 2017/9  
Student Canadian Residency Status: Canadian Citizen  
Thesis/Project Title: Developing screening tools for genomic population structure in economically important species  
Present Position: Master's student
- 2014/9 - 2016/4  
Co-Supervisor Chaoyue Liu (Completed) , Dalhousie University  
Degree Name: Master's of Science (Statistics)  
Student Degree Start Date: 2014/9  
Student Degree Received Date: 2016/5  
Thesis/Project Title: Network-based approaches to identifying phylogenetically related sets of genes  
Project Description: Phylogenetic weighting of comparative genomic data  
Present Position: PhD Student
- 2014/9 - 2016/8  
Principal Supervisor Michael Hall (Completed) , Dalhousie University  
Degree Name: Master's of Science (Computational Biology and Bioinformatics)  
Student Degree Start Date: 2014/9  
Student Degree Received Date: 2016/10  
Student Canadian Residency Status: Canadian Citizen  
Thesis/Project Title: Time-series analysis of microbial communities  
Project Description: Microbial time-series analysis  
Present Position: Master's student
- 2014/9 - 2016/8  
Co-Supervisor Chang Chen (Completed) , Dalhousie University  
Student Degree Start Date: 2014/9  
Student Degree Received Date: 2016/10  
Thesis/Project Title: Statistical modeling of microbial community distributions  
Project Description: Modeling of phylogenetic beta diversity in microbial communities  
Present Position: Master's student
- 2014/5 - 2016/4  
Principal Supervisor Alex Keddy (Completed) , Dalhousie University  
Degree Name: Master's of Computer Science  
Student Degree Start Date: 2014/5  
Student Degree Received Date: 2016/5  
Thesis/Project Title: Cartographic techniques for molecular epidemiology  
Project Description: Geographic visualizations of genomic epidemiological data  
Present Position: Machine-learning developer

- 2014/5 - 2016/8  
Principal Supervisor Luyao Zhan (Completed) , Dalhousie University  
Degree Name: Master's of Computer Science  
Student Degree Start Date: 2013/9  
Student Degree Received Date: 2016/9  
Thesis/Project Title: Inferring ecological population structure and environmental associations through automated analysis of repeat-containing and polymorphic DNA sequences  
Project Description: Algorithms for interpreting microsatellite data  
Present Position: Master's student
- 2013/9 - 2015/8  
Principal Supervisor Ning, Jie (Completed) , Dalhousie University  
Degree Name: Master's of Computer Science  
Student Degree Start Date: 2013/9  
Student Degree Received Date: 2015/8  
Thesis/Project Title: Phylogenetic approaches to microbial community classification  
Present Position: Master's student
- 2010/5 - 2012/12  
Principal Supervisor Michael Porter (Completed) , Dalhousie University  
Degree Name: Master's of Computer Science  
Student Degree Start Date: 2010/5  
Student Degree Received Date: 2012/12  
Thesis/Project Title: EVALUATING A MICROBIAL COMMUNITY THROUGH FEATURE MATCHING AND GRAPH TOPOLOGY  
Present Position: Developer / Research Associate
- 2009/9 - 2010/9  
Co-Supervisor Christopher Smith (Completed) , Dalhousie University  
Degree Name: Master's of Computer Science  
Student Degree Start Date: 2008/9  
Student Degree Received Date: 2010/9  
Thesis/Project Title: DATABURST: INTERACTIVE ANALYSIS OF HIERARCHICAL DATA USING RADIAL SPACE-FILLING DIAGRAMS  
Project Description: Radial visualization of viral genetic data  
Present Position: Web developer
- 2008/9 - 2012/5  
Principal Supervisor Robert Eveleigh (Completed) , McGill University / Genome Quebec  
Degree Name: Master's of Science (Computational Biology and Bioinformatics)  
Student Degree Start Date: 2008/9  
Student Degree Received Date: 2012/5  
Thesis/Project Title: BEING Aquifex aeolicus: UNTANGLING A HYPERTHERMOPHILE'S CHECKERED PAST  
Present Position: Bioinformatics Technician
- 2008/9 - 2010/8  
Principal Supervisor Sylvia Churcher (Completed) , Province of Nova Scotia  
Student Degree Start Date: 2008/9  
Student Degree Received Date: 2010/1  
Thesis/Project Title: Robustness of Phylogenetic Approaches to Microbial Diversity  
Present Position: Statistical Research Officer
- 2007/9 - 2009/10  
Principal Supervisor Scott Perry (Completed) , Dalhousie University  
Degree Name: Master's of Science (Computational Biology and Bioinformatics)  
Student Degree Start Date: 2007/9  
Student Degree Received Date: 2009/10  
Thesis/Project Title: CHARACTERIZING THE DISTINGUISHABILITY OF MICROBIAL GENOMES  
Present Position: Systems Architect



**Doctorate [n=12]**

- 2022/9 - 2027/8  
Principal Supervisor Sneha Murthy (In Progress) , Dalhousie University  
Student Degree Start Date: 2022/9  
Student Degree Expected Date: 2027/8  
Thesis/Project Title: Microbial Bioinformatics for Food Security  
Present Position: PhD student
- 2019/9 - 2023/12  
Principal Supervisor Jee In Kim (In Progress) , Dalhousie University  
Student Degree Start Date: 2019/9  
Thesis/Project Title: Prediction of antimicrobial resistance in enterococci  
Present Position: PhD student
- 2019/5 - 2023/8  
Principal Supervisor Diana Haider (In Progress) , Dalhousie University  
Student Degree Start Date: 2019/9  
Student Degree Expected Date: 2023/8  
Thesis/Project Title: Defining units in microbial ecology  
Present Position: PhD student
- 2017/1 - 2022/6  
Principal Supervisor Miriã Rafantes (In Progress) , Dalhousie University  
Student Degree Start Date: 2017/1  
Student Degree Expected Date: 2022/6  
Thesis/Project Title: Identification of transcriptional regulatory sequences in metagenomic data  
Present Position: PhD student
- 2016/9 - 2023/8  
Principal Supervisor Michael Hall (In Progress) , Dalhousie University  
Student Degree Start Date: 2016/9  
Student Degree Expected Date: 2023/8  
Thesis/Project Title: Temporal profiling of microbial communities  
Present Position: PhD student
- 2016/5 - 2022/9  
Co-Supervisor Chaoyue Liu (Completed) , Dalhousie University  
Student Degree Start Date: 2016/5  
Thesis/Project Title: Gene clustering based on co-occurrence with correction for common evolutionary history  
Present Position: Bioinformatics Software Developer  
Other Supervisors: Co-Supervisor - Gu, Hong
- 2015/1 - 2020/4  
Principal Supervisor Praveen Nadukkalam Ravindran (Completed) , Dalhousie University  
Degree Name: PhD (Computer Science)  
Student Degree Start Date: 2014/1  
Student Degree Received Date: 2020/4  
Thesis/Project Title: COMPUTATIONAL METHODS FOR EFFICIENT PROCESSING AND ANALYSIS OF SHORT-READ NEXT-GENERATION DNA SEQUENCING DATA  
Project Description: Computational methods for analysis of RADseq data  
Present Position: Staff Scientist, Illumina
- 2009/9 - 2013/8  
Co-Supervisor Christopher Whidden (Completed) , Dalhousie University  
Degree Name: PhD (Computer Science)  
Student Degree Start Date: 2009/9  
Student Degree Received Date: 2013/9  
Thesis/Project Title: EFFICIENT COMPUTATION AND APPLICATION OF MAXIMUM AGREEMENT FORESTS  
Present Position: Postdoctoral fellow

- 2008/9 - 2012/8  
Principal Supervisor Donovan Parks (Completed) , The University of Queensland  
Student Degree Start Date: 2008/9  
Student Degree Received Date: 2012/9  
Thesis/Project Title: GEOREFERENCED TREES AND THE PHYLOGENETIC SIMILARITY OF BIOLOGICAL COMMUNITIES  
Project Description: Linking phylogeny with geography and habitat  
Present Position: Postdoctoral Fellow
- 2008/9 - 2011/6  
Principal Supervisor Norman MacDonald (Withdrawn) , Dalhousie University  
Student Degree Start Date: 2008/9  
Thesis/Project Title: Machine-learning classification of genomic and metagenomic data  
Present Position: System administrator
- 2008/5 - 2018/4  
Principal Supervisor Dennis Wong (Completed) , Dalhousie University  
Degree Name: Interdisciplinary PhD  
Student Degree Start Date: 2008/5  
Student Degree Received Date: 2018/5  
Thesis/Project Title: Inferring orthology in lateral gene transfer in microbial genomes  
Project Description: Phylogenomics of metagenomic sequence data and inference of lateral gene transfer  
Present Position: Unknown
- 2007/9 - 2009/8  
Principal Supervisor Kathryn Duffy (Withdrawn) , Dalhousie University  
Student Degree Start Date: 2007/9  
Thesis/Project Title: Clustering of Biological Sequences  
Present Position: Consultant
- Post-doctorate [n=11]**
- 2020/6 - 2021/6  
Principal Supervisor Somayeh Kafaie (Completed) , Dalhousie University  
Student Degree Start Date: 2020/6  
Student Degree Received Date: 2021/6  
Thesis/Project Title: Network analysis of resistance determinants  
Present Position: Assistant Professor, Saint Mary's University
- 2020/5 - 2022/9  
Principal Supervisor Amjad Khan (In Progress) , Dalhousie University  
Student Degree Start Date: 2020/5  
Thesis/Project Title: Mathematical modelling of mobile element gene content  
Present Position: Postdoctoral Fellow, Western University
- 2019/9 - 2021/9  
Principal Supervisor Haley Sanderson (Completed) , Dalhousie University  
Student Degree Start Date: 2019/9  
Student Degree Received Date: 2021/8  
Thesis/Project Title: Genome-scale inference of mobile elements and transfer of antimicrobial resistance determinants  
Present Position: Bioinformatician, Agriculture/Agri-Food Canada
- 2017/6 - 2020/3  
Principal Supervisor Elvira Mitraka (Completed) , Dalhousie University  
Student Degree Start Date: 2017/6  
Student Degree Received Date: 2020/3  
Student Canadian Residency Status: Permanent Resident  
Thesis/Project Title: Ontology development for microbially influenced pipeline corrosion  
Present Position: Information Architect, Roche

- 2017/2 - 2021/12  
Principal Supervisor Finlay Maguire (Completed) , Dalhousie University  
Student Degree Start Date: 2017/2  
Student Degree Received Date: 2021/12  
Student Canadian Residency Status: Permanent Resident  
Thesis/Project Title: Identification of antimicrobial resistance genes in metagenomic data  
Present Position: Assistant Professor, Dalhousie University
- 2015/2 - 2016/3  
Principal Supervisor Jyoti Joshi (Completed) , Dalhousie University  
Student Degree Start Date: 2015/2  
Student Degree Received Date: 2016/3  
Thesis/Project Title: Transcriptomic analysis of reproductive longevity in cattle  
Project Description: SNP and transcript analysis in cattle  
Present Position: Research Associate, Dalhousie University
- 2014/11 - 2016/3  
Principal Supervisor Kacper Zukowski (Completed) , Dalhousie University  
Student Degree Start Date: 2014/11  
Student Degree Received Date: 2016/3  
Thesis/Project Title: Association of genomic variation with reproductive longevity in cattle  
Project Description: SNP analysis in mouse and cattle  
Present Position: Senior Bioinformatics Scientist, Ardigen
- 2014/4 - 2016/8  
Principal Supervisor Akhilesh Dhanani (Completed) , Dalhousie University  
Student Degree Start Date: 2014/4  
Student Degree Received Date: 2016/8  
Thesis/Project Title: Frailty and the Microbiome  
Project Description: Microbial community analysis in aging and frailty  
Present Position: Senior Scientist - NGS and Genomic Assays, Tessera Therapeutics
- 2013/9 - 2014/12  
Principal Supervisor Koenig, Jeremy (Completed) , Dalhousie University  
Student Degree Start Date: 2013/9  
Student Degree Received Date: 2014/12  
Thesis/Project Title: Inferring genotype-phenotype associations from mouse genomic data.  
Present Position: Postdoctoral fellow
- 2011/5 - 2013/12  
Principal Supervisor Morgan Langille (Completed) , Dalhousie University  
Student Degree Start Date: 2011/5  
Student Degree Received Date: 2013/12  
Thesis/Project Title: Mapping taxonomy to function in the human microbiome  
Present Position: Assistant Professor and Canada Research Chair (Pharmacology)
- 2011/3 - 2014/2  
Principal Supervisor Conor Meehan (Completed) , Dalhousie University  
Student Degree Start Date: 2011/3  
Student Degree Received Date: 2014/2  
Thesis/Project Title: Evolution of Lachnospiraceae, an important constituent of the human microbiome  
Project Description: Lateral gene transfer in the human microbiome  
Present Position: Postdoctoral fellow at the Institute of Tropical Medicine, Antwerp
- Research Associate [n=6]**
- 2022/5 - 2023/8  
Principal Supervisor Julia Lewandowski (In Progress) , Dalhousie University  
Student Degree Start Date: 2022/5  
Student Degree Expected Date: 2023/5  
Thesis/Project Title: Using gene order to inform antimicrobial resistance gene prediction  
Present Position: Bioinformatics Software Developer, Dalhousie University

2019/5 - 2022/7 Principal Supervisor	Alex Manuele (Completed) , Dalhousie University Student Degree Start Date: 2019/5 Student Degree Received Date: 2022/7 Thesis/Project Title: ARETE software development Present Position: Bioinformatics Software Developer, BenchSci Canada
2013/11 - 2015/9 Principal Supervisor	Nehil Jain (Completed) , Dalhousie University Student Degree Start Date: 2013/11 Thesis/Project Title: Statistical analysis of fertility data in Holstein cattle Present Position: Data and Infrastructure Engineer
2013/1 - 2014/12 Principal Supervisor	Rutherford, Katherine (Completed) , Dalhousie University Student Degree Start Date: 2013/1 Student Degree Received Date: 2014/12 Thesis/Project Title: Bioinformatic analysis of mouse and chicken genomic data Present Position: Research Associate
2012/12 - 2013/5 Principal Supervisor	Somayyeh Zangoeei (Completed) , Dalhousie University Student Degree Start Date: 2012/12 Student Degree Received Date: 2013/5 Thesis/Project Title: Geographic analysis of biomonitoring data from Wood Buffalo National Park Present Position: Technical position in San Francisco
2011/6 - 2012/9 Principal Supervisor	Timothy Mankowski (Completed) , Dalhousie University Student Degree Start Date: 2011/6 Thesis/Project Title: Geographic visualization systems for environmental genomic data Present Position: M.D.

## Staff Supervision

## Event Administration

2022/1 - 2022/6	Lead organizer, ARETE All Hands Meeting, Workshop, 2022/5 - 2022/5
2018/9 - 2018/12	Co-organizer, Collaborative Health Data Workshop, Workshop, 2018/12 - 2018/12 Workshop and brainstorming session with over 40 participants from computer science, health, medicine, clinical practice, and health authorities.
2011/9 - 2012/7	Organizing Committee member, iEvoBio 2012, Conference, Hilmar Lapp, 2012/7 - 2012/7 iEvoBio meeting, Ottawa, Ontario, Canada

## Editorial Activities

2022/6 - 2027/6	Specialty Chief Editor, Frontiers in Microbiomes: Omics Approaches, Journal
2016/1 - 2026/12	Associate Editor, mSystems, Journal
2012/1 - 2022/12	Associate Editor, BMC Genomics, Journal

## Journal Review Activities

Reviewer, Over 30 journals  
Number of Works Reviewed / Refereed: 100

## Conference Review Activities

	Program Committee member, Over 15 conferences, Double Blind Number of Works Reviewed / Refereed: 50
2022/1 - 2022/4	Microbiome track co-chair, ISMB 2022, Blind

## Research Funding Application Assessment Activities

	External Reviewer, Various national and international Number of Applications Assessed: 30
2022/1	Chair, Bioinformatics Resource Allocation Committee, Compute Canada
2020/1	Committee Member, CIHR College of Reviewers, Canadian Institutes of Health Research
2017/1 - 2021/1	Committee Member, Bioinformatics Resource Allocation Committee, Compute Canada

## Promotion Tenure Assessment Activities

2012/1	Reviewer (internal and external) Number of Assessments: 5 Review of tenure and promotion for five external applicants, and periodic service on the Computer Science tenure and promotion committee as internal reviewer.
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## Community and Volunteer Activities

2007/9	Board member, SuperNOVA Advisory Board member for SuperNOVA, an organization that organizes science camps and other activities for students aged 5-16.
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## Committee Memberships

2022/7	Committee Member, Steering Committee, Institute for Comparative Genomics, Dalhousie University
2020/2	Co-chair, Scale AI Chair in AI for Marine Logistics
2019/11	Committee Member, CIHR IG Bioinformatics and Health Data Sciences Planning and Priority Committee, Canadian Institutes of Health Research
2012/1	Chair, Search Committees, Dalhousie University Chaired / participated in ~6 search committees including 2xCRC1, specialized Chair, Dean, Instructor, regular faculty positions
2012/9 - 2018/4	Committee Member, Senate Honourary Degrees, Dalhousie University
2016/9 - 2017/6	Chair, Curriculum Committee, Dalhousie University
2014/1 - 2017/6	Committee Member, Employee Benefits Committee, Dalhousie University
2014/9 - 2016/8	Chair, Co-op Management Committee, Dalhousie University
2006/9 - 2016/8	Committee Member, Undergraduate Committee, Dalhousie University
2014/8 - 2015/12	Committee Member, Canadian Bioinformatics and Computational Biology National Strategy Committee, CIHR / Genome Canada

## Other Memberships

- |                 |  |
|-----------------|--|
| 2015/9          | Director, Master's of Science in Computational Biology and Bioinformatics program,<br>Dalhousie University |
| 2007/1 - 2011/8 | Co-op Advisor, Dalhousie University  |

## Presentations

1. (2023). Stewardship, conservation, and evolution of the microbiome. Microbes and Social Equity Virtual Symposium 2023, United States of America  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
2. (2023). Our feature presentation: different strategies to predict antimicrobial resistance in Enterococcus. PHA4GE Seminar Series, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
3. (2023). Predicting resistance: accuracy is the beginning, not the end. Dalhousie Antimicrobial Resistance Conference 2023, Halifax, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
4. (2023). What (In)exactly Are We Trying to Steward?. University of Guelph Microbiomes, Health, and Environments workshop, Guelph, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
5. (2023). Are these the same plasmid? <?>Classifying the mobilome and resistome of Enterococcus faecium. ESCMID seminar series, Switzerland  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
6. (2023). Mobile Genetic Elements and Lateral Gene Transfer. VTEC 2023 Pre-symposium workshop, Canada  
Main Audience: Knowledge User  
Invited?: Yes, Keynote?: No
7. (2023). Deploying the DOT automated eDNA sampler in the marine environment. International Workshop in Environmental Genomics 2023, Canada  
Main Audience: Researcher  
Invited?: No, Keynote?: No
8. (2023). The sharp edges of mobilome prediction and phylogenomics. Invited seminar, Arctic University of Norway, Norway  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
9. (2023). Two Years in the Life of a Salmon. Fisheries and Oceans Canada Genomics Workshop, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: Yes
10. (2022). ARETE: Automating the inference and transmission of AMR. GRDI-AMR2 Seminar Series, Canada  
Main Audience: Decision Maker  
Invited?: Yes, Keynote?: No

11. (2022). Now you see it...Theory of Microbiome Analysis, Canada  
Main Audience: Knowledge User  
Invited?: Yes, Keynote?: Yes
12. (2022). Antimicrobial Resistance, Everywhere, All at Once. Invited seminar, Western University, London, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
13. (2022). Environmental DNA (eDNA) – What is it and what can it tell us?. H2O - Home to Oceans, Canada  
Main Audience: Knowledge User  
Invited?: Yes, Keynote?: No
14. (2022). Taxonomic analysis and statistics. IMPACTT / IMC Bioinformatics Workshop, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
15. (2022). ARETE: Automating the inference of transmission of AMR. ASM Conference on Rapid Applied Microbial Next-Generation Sequencing and Bioinformatic Pipelines, United States of America  
Main Audience: Researcher  
Invited?: No, Keynote?: No
16. (2021). Antimicrobial resistance on the move: so many genomes, so little time. Dalhousie Institute for Comparative Genomics seminar series, Canada  
Invited?: Yes, Keynote?: No
17. (2021). Searching for Antimicrobial Resistance in Metagenomic Data: Hits and Misses. Having IMPACTT: Advancing Microbiome Research, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
18. (2021). The HabHunter eDNA sampling and analysis pipeline. International Workshop in Environmental Genomics, Canada  
Main Audience: Knowledge User  
Invited?: Yes, Keynote?: No
19. (2021). Taxonomic analysis and statistics. Canadian Bioinformatics Workshop in Microbiome Analysis, Canada  
Main Audience: Researcher  
Invited?: No, Keynote?: No
20. (2021). No Safe Harbour: Finding the Genes that Cause Antimicrobial Resistance. University of Guelph bioinformatics seminar series, Canada  
Invited?: Yes, Keynote?: No
21. (2021). From Genomes to Transmission Maps in Ten Minutes or Less. UK - Canada One Health Workshop, United Kingdom  
Main Audience: Knowledge User  
Invited?: Yes, Keynote?: No
22. (2021). Research in the Faculty of Computer Science at Dalhousie (including, but not limited to, environmental DNA). Invited talk at Defence Research and Development Canada, Halifax, Canada  
Invited?: Yes, Keynote?: No
23. (2021). Phylogenomics and Genes on the Move. Canadian Bioinformatics Workshop in Genomic Epidemiology, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No

24. (2020). 23 and Flee: The promise and perils of machine learning in genomics. MLT Ai & Data Science Meetup, Moncton, Canada  
Main Audience: General Public  
Invited?: Yes, Keynote?: No, Competitive?: No
25. (2020). Mapping the shared evolutionary trajectories of resistance genes &c. BIRS 2020 Workshop, Oaxaca, Mexico  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
26. (2019). Has anyone seen my plasmid? Probing the dark corners of metagenome-assembled genomes. Emerging statistical challenges & methods for analysis of human microbiome data workshop, Banff, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
27. (2019). Les Réseaux Phylogénétiques. Phylogenetic Networks Summer School, Roscoff, France  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
28. (2018). Can a supercomputer understand love, DNA sequences, and microbial communities?. Invited seminar, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
29. (2018). Evolutionary and Temporal Views of Microbial Diversity. Canadian Society of Microbiologists annual meeting, Winnipeg, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: Yes, Competitive?: No
30. (2018). Antimicrobial resistance and the human microbiome. Invited presentation, Lisbon, Portugal  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No, Competitive?: No
31. (2018). Layers of diversity in microbial communities. The Reef Microbiome Workshop, Barbados  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No, Competitive?: No
32. (2018). The hunt for antimicrobial resistance in the human microbiome. International Microbiome Research Symposium, Vancouver, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
33. (2017). The aging and frail microbiome: diversity, time, and function. McMaster University - invited presentation, Hamilton, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No, Competitive?: No
34. (2017). Identifying key temporal and taxonomic bacterial clusters in the aging microbiome. Drexel University invited presentation, Philadelphia, United States of America  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No, Competitive?: No
35. (2017). Microbial Taxonomy: Abandon All Hope?. The Future of Systematics in Data- Centric Biology, Woods Hole, United States of America  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No, Competitive?: No



36. (2017). Predicting functional classes of genes from metagenomic data. 2017 International Workshop on Environmental Genomics, St. John's, Canada  
Main Audience: Knowledge User  
Invited?: Yes, Keynote?: No, Competitive?: No
- [37.](#) (2017). Phylogeographic Analysis. Canadian Bioinformatics Workshop in Infectious Disease Genomic Epidemiology, Vancouver, Canada  
Main Audience: Knowledge User  
Invited?: Yes, Keynote?: No, Competitive?: No  
Description / Contribution Value: Workshop presentation and practical session
- [38.](#) (2016). Aging, frailty and the microbiome: new methods, new insights. 5th Annual Canadian Human and Statistical Genetics Meeting, Halifax, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No, Competitive?: No
39. (2016). Lateral gene transfer: how many stories can a network tell?. EVOLUNET: PUBLIC LECTURES OF THE SUMMER SCHOOL ON NETWORKS, Roscoff, France  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No, Competitive?: No
40. (2016). What can the microbiome tell us about frailty?. Northwood Research Day 2016, Dartmouth, Canada  
Main Audience: Knowledge User  
Invited?: Yes, Keynote?: Yes
41. (2016). Common assumptions and pitfalls of microbiome analysis. Advancing Microbiome Research Symposium: Microbiome & Disease, Potomac, MD, United States of America  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No, Competitive?: No
- [42.](#) (2016). Metagenomics. Great Lakes Bioinformatics and the Canadian Computational Biology Conference 2016, Toronto, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No, Competitive?: No
- [43.](#) (2016). Phylogeography with GenGIS. VizBi 2016, Heidelberg, Germany  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No, Competitive?: No
44. (2016). Monitoring the microbiome in an assisted-care facility. IRIDA Annual General Meeting / public lecture, Vancouver, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No, Competitive?: No
- [45.](#) Morgan Langille, Michael Hall. (2016). Microbiome Analysis: 16S and Metagenomics. Great Lakes Bioinformatics and Canadian Computational Biology Conference, Toronto, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No, Competitive?: No
46. (2016). A Coevolution-Based Approach to the Identification of Genes with Similar Phylogenetic Distributions. Vancouver Bioinformatics Users' Group (VanBUG), Vancouver, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No, Competitive?: No
47. (2015). The microbiome and its impact on aging and frailty. Gerontological Society of America annual meeting, Orlando, United States of America  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No

48. (2015). Soil, lateral gene transfer, and hybrid genomes. Argonne National Laboratory 7th annual soil metagenomics meeting, Chicago, United States of America  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
49. (2015). Upwardly mobile genes. Invited seminar at Canadian National Microbiology Laboratory, Winnipeg, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
- [50.](#) (2015). Introduction to Metagenomics. Canadian Bioinformatics Workshop - Analysis of Metagenomic Data, Halifax, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No, Competitive?: No  
Description / Contribution Value: Lead organizer and presenter at first Canadian Bioinformatics Workshop on Metagenomics
51. (2014). Grand theft operon: lateral city. IGERT symposium on Deep Genomics, Tucson, United States of America  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
52. (2014). Computing the Microbial World. Canadian High-Performance Computing Conference, Halifax, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
53. (2014). Microbiome analysis. African perinatal probiotic study meeting, Athi River, Kenya  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
54. (2014). The Human Microbiome(and friends). Genome Atlantic Human Genetics and Genomics Seminar series, Halifax, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
55. (2014). Modeling and mapping microbial diversity and function with marker genes, genomes and metagenomes. Canadian Microbiome Workshop 2014: from Research to Applications, Vancouver, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
56. (2014). Biogeography of microorganisms. No borders. No limits. No fear. Understanding biodiversity dynamics using diverse data sources, Canberra, Australia  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
57. (2014). When trees can't agree. Canadian Mathematical Society annual meeting, Hamilton, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: Yes
58. (2014). Gene sharing in microbes: good for the individual, good for the community?. University of Waterloo Department of Biology seminar, Waterloo, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
59. (2013). Classifying DNA. Dalhousie In-House Computer Science Conference, Halifax, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: Yes

60. (2013). Biology's Big Data Revolution. Public lecture: Faculty of Computer Science, Halifax, Canada  
Main Audience: General Public  
Invited?: Yes, Keynote?: Yes
61. (2013). Visualizing species distributions and phylogeography using GenGIS. International Biogeography Society Special Meeting, Montreal, Canada  
Main Audience: Researcher  
Invited?: No, Keynote?: No
62. (2013). Evolution and ecology of GI-tract-associated Lachnospiraceae: Drop acid, lose your coat, leave in someone else's genes. SBE 2013, Chicago, United States of America  
Main Audience: Researcher  
Invited?: No, Keynote?: No
63. (2012). A network of everything??. Society for Molecular Biology and Evolution annual meeting, Dublin, Ireland  
Main Audience: Researcher  
Invited?: No, Keynote?: No
64. (2012). Genetic monitoring of H1N1 during the 2009 outbreak. Critical Infrastructure Protection Initiative, Halifax, Canada  
Main Audience: Decision Maker  
Invited?: Yes, Keynote?: No
65. (2012). GenGIS: a platform for visualization and analysis of genetic biodiversity data. Quebec biomonitoring meeting, Montreal, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
66. (2012). Major initiatives in microbiomics: industrial processes, environmental monitoring, human health. CAU-DAL joint workshops, Kiel, Germany  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
67. (2012). Biomonitoring 2.0: New approaches to biodiversity monitoring. iEvoBio 2012, Ottawa, Canada  
Main Audience: Researcher  
Invited?: No, Keynote?: No
68. (2012). GenGIS 2: New approaches to understand the geography of our microbial world. Canadian Society of Microbiologists annual meeting, Vancouver, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
69. (2012). Applying reference Condition Analysis using GenGIS. Canadian Aquatic Biomonitoring Network annual meeting, Fredericton, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
70. (2012). Microbes and communities: steps E, M, and V. Canadian Institute for Advanced Research (Integrated Microbial Biodiversity program) annual meeting 2012, Quebec, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
71. (2011). Who is doing what, and to whom: taxonomic assignments and network analysis in metagenome studies. SyMBIOTA Workshop, Toronto, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No

72. (2011). Bioinformatics of environmental samples: who is there, what are they doing, how will they respond. Next Generation DNA Sequencing in Environmental Risk Assessment and Monitoring: Future Challenges, Milan, Italy  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
73. (2011). GenGIS: Geospatial analysis and visualization of biodiversity. GIS Day, Halifax, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
74. (2011). Molecular and Functional Diagnostics. CIHR Microbiomics Grant workshop, Halifax, Canada  
Main Audience: Researcher  
Invited?: No, Keynote?: No
75. (2011). Modeling and mapping microbial diversity and function with marker genes, genomes and metagenomes, or MMMDFMGGM. CIHR Emerging Microbiome Teams, Vancouver, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
76. (2011). GenGIS: A 3D geospatial environment for the analysis of genetic data. iPlant collaborative workshop, Tucson, United States of America  
Main Audience: Researcher  
Invited?: No, Keynote?: No
77. (2011). Questions at the interface of evolution, ecology, space and time. Society for Molecular Biology and Evolution meeting, Kyoto, Japan  
Main Audience: Researcher  
Invited?: No, Keynote?: No
78. (2010). It's a Phylogenetic Network and Everyone's Invited!!. Questioning the Tree of Life meeting, London, United Kingdom  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
79. (2010). Geographic and temporal analysis of genomes and metagenomes. Canadian Institute for Advanced Research BigDATA meeting, Vancouver, Canada  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No
80. (2009). GenGIS:Geospatial analysis and visualization of microbial diversity. Canadian Institute for Advanced Research (Integrated Microbial Biodiversity program), Annual Meeting 2009, Asilomar, United States of America  
Main Audience: Researcher  
Invited?: Yes, Keynote?: No

## Broadcast Interviews

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|----------------------------|--|
| 2022/05/18 -<br>2022/05/18 | Data Through a Bioinformatics Lens, Data Crunch Podcast, Podcast |
| 2019/11/20 -<br>2019/11/20 | Antimicrobial Resistance, Global News, Global                    |

## Text Interviews

- |            |   |
|------------|---|
| 2016/09/15 | Metagenomes and antimicrobial resistance, FRAM DINSHAW, Halifax Chronicle Herald<br><a href="https://goo.gl/y8UCHp">https://goo.gl/y8UCHp</a> |
|------------|---|

## Publications

### Journal Articles

1. Donovan Parks, Macdonald Norman, Beiko Robert. Tracking the evolution and geographic spread of Influenza A. *PLoS currents*. 1: RRN1014.  
Published,  
Refereed?: Yes
2. Beiko Robert G, Keith Jonathan M, Harlow Timothy J, Ragan Mark A. Searching for convergence in phylogenetic Markov chain Monte Carlo. *Systematic biology*. 55(4): 553-65.  
Published,  
Refereed?: Yes
3. Baptiste Eric, O'Malley Maureen A, Beiko Robert G, Ereshefsky Marc, Gogarten J Peter, Franklin-Hall Laura, Lapointe François-Joseph, Dupré John, Dagan Tal, Boucher Yan, Martin William. Prokaryotic evolution and the tree of life are two different things. *Biology direct*. 4: 34.  
Published,  
Refereed?: Yes
4. Beiko Robert G, Harlow Timothy J, Ragan Mark A. Highways of gene sharing in prokaryotes. *Proceedings of the National Academy of Sciences of the United States of America*. 102(40): 14332-7.  
Published,  
Refereed?: Yes
5. Parks Donovan H, Beiko Robert G. Measuring community similarity with phylogenetic networks. *Molecular biology and evolution*. 29(12): 3947-58.  
Published,  
Refereed?: Yes
6. Beiko Robert G, Ragan Mark A. Detecting lateral genetic transfer : a phylogenetic approach. *Methods in molecular biology (Clifton, N.J.)*. 452: 457-69.  
Published,  
Refereed?: Yes
7. Charlebois Robert L, Beiko Robert G, Ragan Mark A. Microbial phylogenomics: Branching out. *Nature*. 421(6920): 217.  
Published,  
Refereed?: Yes
8. Charlebois Robert L, Clarke G D Paul, Beiko Robert G, St Jean Andrew. Characterization of species-specific genes using a flexible, web-based querying system. *FEMS microbiology letters*. 225(2): 213-20.  
Published,  
Refereed?: Yes
9. Langille Morgan G I, Meehan Conor J, Beiko Robert G. Human microbiome: a genetic bazaar for microbes?. *Current biology : CB*. 22(1): R20-2.  
Published,  
Refereed?: Yes
10. Beiko Robert G, Doolittle W Ford, Charlebois Robert L. The impact of reticulate evolution on genome phylogeny. *Systematic biology*. 57(6): 844-56.  
Published,  
Refereed?: Yes
11. Whalley Jacqueline, Brooks Stephen, Beiko Robert G. Radié: visualizing taxon properties and parsimonious mappings using a radial phylogenetic tree. *Bioinformatics (Oxford, England)*. 25(5): 672-3.  
Published,  
Refereed?: Yes

12. Ragan Mark A, Harlow Timothy J, Beiko Robert G. Do different surrogate methods detect lateral genetic transfer events of different relative ages?. *Trends in microbiology*. 14(1): 4-8.  
Published,  
Refereed?: Yes
13. McMillan David J, Beiko R G, Geffers R, Buer Jan, Schouls L M, Vlaminckx B J M, Wannet W J B, Sriprakash K S, Chhatwal G S. Genes for the majority of group a streptococcal virulence factors and extracellular surface proteins do not confer an increased propensity to cause invasive disease. *Clinical infectious diseases : an official publication of the Infectious Diseases Society of America*. 43(7): 884-91.  
Published,  
Refereed?: Yes
14. Perry Scott C, Beiko Robert G. Distinguishing microbial genome fragments based on their composition: evolutionary and comparative genomic perspectives. *Genome biology and evolution*. 2: 117-31.  
Published,  
Refereed?: Yes
15. Martin C Cristofre, Tsang Cemaine H, Beiko Robert G, Krone Patrick H. Expression and genomic organization of the zebrafish chaperonin gene complex. *Genome*. 45(5): 804-11.  
Published,  
Refereed?: Yes
16. Parks Donovan H, Porter Michael, Churcher Sylvia, Wang Suwen, Blouin Christian, Whalley Jacqueline, Brooks Stephen, Beiko Robert G. GenGIS: A geospatial information system for genomic data. *Genome research*. 19(10): 1896-904.  
Published,  
Refereed?: Yes
17. Holloway Catherine, Beiko Robert G. Assembling networks of microbial genomes using linear programming. *BMC evolutionary biology*. 10: 360.  
Published,  
Refereed?: Yes
18. Parks Donovan H, Beiko Robert G. Identifying biologically relevant differences between metagenomic communities. *Bioinformatics (Oxford, England)*. 26(6): 715-21.  
Published,  
Refereed?: Yes
19. Beiko Robert G, Ragan Mark A. Untangling hybrid phylogenetic signals: horizontal gene transfer and artifacts of phylogenetic reconstruction. *Methods in molecular biology (Clifton, N.J.)*. 532: 241-56.  
Published,  
Refereed?: Yes
20. Beiko Robert G, Charlebois Robert L. GANN: genetic algorithm neural networks for the detection of conserved combinations of features in DNA. *BMC bioinformatics*. 6: 36.  
Published,  
Refereed?: Yes
21. Parks Donovan H, Beiko Robert G. Measures of phylogenetic differentiation provide robust and complementary insights into microbial communities. *The ISME journal*. 7(1): 173-83.  
Published,  
Refereed?: Yes
22. MacDonald Norman J, Beiko Robert G. Efficient learning of microbial genotype-phenotype association rules. *Bioinformatics (Oxford, England)*. 26(15): 1834-40.  
Published,  
Refereed?: Yes

23. Chan Cheong Xin, Darling Aaron E, Beiko Robert G, Ragan Mark A. Are protein domains modules of lateral genetic transfer?. *PloS one*. 4(2): e4524.  
Published,  
Refereed?: Yes
24. Davies Mark R, McMillan David J, Beiko Robert G, Barroso Vanessa, Geffers Robert, Sriprakash Kadaba S, Chhatwal Gursharan S. Virulence profiling of *Streptococcus dysgalactiae* subspecies *equisimilis* isolated from infected humans reveals 2 distinct genetic lineages that do not segregate with their phenotypes or propensity to cause diseases. *Clinical infectious diseases : an official publication of the Infectious Diseases Society of America*. 44(11): 1442-54.  
Published,  
Refereed?: Yes
25. Beiko Robert G, Charlebois Robert L. A simulation test bed for hypotheses of genome evolution. *Bioinformatics (Oxford, England)*. 23(7): 825-31.  
Published,  
Refereed?: Yes
26. Chan Cheong Xin, Beiko Robert G, Ragan Mark A. Detecting recombination in evolving nucleotide sequences. *BMC bioinformatics*. 7: 412.  
Published,  
Refereed?: Yes
27. Hug Laura A, Beiko Robert G, Rowe Annette R, Richardson Ruth E, Edwards Elizabeth A. Comparative metagenomics of three *Dehalococcoides*-containing enrichment cultures: the role of the non-dechlorinating community. *BMC genomics*. 13: 327.  
Published,  
Refereed?: Yes
28. Parks Donovan H, MacDonald Norman J, Beiko Robert G. Classifying short genomic fragments from novel lineages using composition and homology. *BMC bioinformatics*. 12: 328.  
Published,  
Refereed?: Yes
29. Beiko Robert G. Telling the whole story in a 10,000-genome world. *Biology direct*. 6: 34.  
Published,  
Refereed?: Yes
30. Chan Cheong Xin, Beiko Robert G, Ragan Mark A. Lateral transfer of genes and gene fragments in *Staphylococcus* extends beyond mobile elements. *Journal of bacteriology*. 193(15): 3964-77.  
Published,  
Refereed?: Yes
31. Clarke G D Paul, Beiko Robert G, Ragan Mark A, Charlebois Robert L. Inferring genome trees by using a filter to eliminate phylogenetically discordant sequences and a distance matrix based on mean normalized BLASTP scores. *Journal of bacteriology*. 184(8): 2072-80.  
Published,  
Refereed?: Yes
32. Beiko Robert G, Chan Cheong Xin, Ragan Mark A. A word-oriented approach to alignment validation. *Bioinformatics (Oxford, England)*. 21(10): 2230-9.  
Published,  
Refereed?: Yes
33. Beiko Robert G, Hamilton Nicholas. Phylogenetic identification of lateral genetic transfer events. *BMC evolutionary biology*. 6: 15.  
Published,  
Refereed?: Yes

34. Slater F R, Johnson C R, Blackall L L, Beiko R G, Bond P L. Monitoring associations between clade-level variation, overall community structure and ecosystem function in enhanced biological phosphorus removal (EBPR) systems using terminal-restriction fragment length polymorphism (T-RFLP). *Water research*. 44(17): 4908-23.  
Published,  
Refereed?: Yes
35. Macdonald Norman, Parks Donovan, Beiko Robert. SeqMonitor: influenza analysis pipeline and visualization. *PLoS currents*. 1: RRN1040.  
Published,  
Refereed?: Yes
36. MacDonald Norman J, Parks Donovan H, Beiko Robert G. Rapid identification of high-confidence taxonomic assignments for metagenomic data. *Nucleic acids research*. 40(14): e111.  
Published,  
Refereed?: Yes
37. Chan Cheong Xin, Beiko Robert G, Darling Aaron E, Ragan Mark A. Lateral transfer of genes and gene fragments in prokaryotes. *Genome biology and evolution*. 1: 429-38.  
Published,  
Refereed?: Yes
38. Ragan Mark A, Beiko Robert G. Lateral genetic transfer: open issues. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*. 364(1527): 2241-51.  
Published,  
Refereed?: Yes
39. Meehan Conor J, Beiko Robert G. Lateral gene transfer of an ABC transporter complex between major constituents of the human gut microbiome. *BMC microbiology*. 12: 248.  
Published,  
Refereed?: Yes
40. Lommer Markus, Specht Michael, Roy Alexandra-Sophie, Kraemer Lars, Andreson Reidar, Gutowska Magdalena A, Wolf Juliane, Bergner Sonja V, Schilhabel Markus B, Klostermeier Ulrich C, Beiko Robert G, Rosenstiel Philip, Hippler Michael, LaRoche Julie. Genome and low-iron response of an oceanic diatom adapted to chronic iron limitation. *Genome biology*. 13(7): R66.  
Published,  
Refereed?: Yes
41. A Mane, H Sanderson, AP White, R Zaheer, RG Beiko, C Chauve. (2024). PlasEval: a framework for comparing and evaluating plasmid detection tools. *BMC Bioinformatics*.  
Submitted,  
Refereed?: Yes, Open Access?: Yes
42. Haider D, Hall MW, LaRoche J, Beiko RG. (2024). Mock microbial community meta-analysis using different trimming of amplicon read lengths. *Environmental Microbiology*. 26: e16566.  
Published,  
Refereed?: Yes
43. Tiffany Y Hsu, Etienne Nzabarushimana, Dennis Wong, Chengwei Luo, Robert G Beiko, Morgan Langille, Curtis Huttenhower, Long H Nguyen, Eric A Franzosa. (2024). Profiling novel lateral gene transfer events in the human microbiome. *Nature Microbiology*.  
Revision Requested,  
Refereed?: Yes



44. Kim JI, Manuele A, Maguire F, Zaheer R, McAllister TA, Beiko RG. (2024). Identification of key drivers of antimicrobial resistance in *Enterococcus* using machine learning. Canadian Journal of Microbiology. NA: NA.  
Submitted,  
Refereed?: Yes
45. Hendricks A, Mackie CM, Luy E, Sonnichsen C, Smith J, Grundke I, Tavasoli M, Furlong A, Beiko RG, LaRoche J, Sieben V. (2023). Compact and Automated eDNA Sampler for *in situ* Monitoring of Aquatic Environments. Scientific Reports. NA: NA.  
Published,  
Refereed?: Yes
46. Wilcox M, Jeffery N, DiBacco C, Bradbury I, Lowen B, Wang Z, Beiko RG, Stanley R. (2023). Integrating seascape resistances and gene flow to produce area-based metrics of functional connectivity for marineconservation planning. Landscape Ecology. NA: NA.  
Published,  
Refereed?: Yes
47. \*Hall MW, Wellappuli NC, Huang RC, Wu K, Lam DK, Glogauer M, Beiko RG, Senadheera DB. (2023). A search for “perio-probiotics” by longitudinal dissection of oral bacterial community shifts during the onset and resolution of gingivitis. ISME Communications. NA: NA.  
Published,  
Refereed?: Yes
48. Alcock BP, Huynh W, Chalil R, Smith KW, Raphenya AR, Wlodarski MA, Edalatmand A, Petkau A, Syed SA, Tsang KK, Baker SJC, Dave M, McCarthy MC, Mukiri KM, Nasir JA, Golbon B, Imtiaz H, Jiang X, Kaur K, Kwong M, Liang ZC, Niu KC, Shan P, Yang JYJ, Gray KL, Hoad GR, Jia B, Bhandu T, Carfrae LA, Farha MA, French S, Gordzevich R, Rachwalski K, Tu MM, Bordeleau E, Dooley D, Griffiths E, Zubyk HL, Brown ED, Maguire F, Beiko RG, Hsiao WWL, Brinkman FSL, Van Domselaar G, McArthur AG. (2023). CARD 2023: expanded curation, support for machine learning, and resistome prediction at the Comprehensive Antibiotic Resistance Database. Nucleic Acids Research. 51: D690-D699.  
Published,  
Refereed?: Yes, Open Access?: Yes
49. Gulavi E, Mwendwa F, Atandi DO, Okiro PO, \*Hall MW, Beiko RG, Adam RD. (2022). Vaginal microbiota in women with spontaneous preterm labor versus those with term labor in Kenya: A case control study. BMC Microbiology. NA: NA.  
Co-Author  
Accepted,  
Refereed?: Yes, Open Access?: Yes
50. \*Sanderson H, Gray K, \*Manuele A, Maguire F, \*Khan A, \*Liu C, \*Navanekere Rudrappa C, Nash JHE, Robertson J, Bessonov K, Oloni M, Alcock BP, Raphenya AR, McAllister TA, Peacock SJ; Gouliouris T, McArthur AG, Brinkman FSL, Fink RC, Zaheer R, Beiko RG. (2022). Exploring the mobilome and resistome of *Enterococcus faecium* in a One Health context across two continents. Microbial Genomics. 8: NA.  
Published,  
Refereed?: Yes, Open Access?: Yes
51. \*Bernardino M, Beiko RG. (2022). Genome-scale prediction of bacterial promoters. BioSystems. 221: 104771.  
Published,  
Refereed?: Yes

52. \*Liu C, Kenney T, Beiko RG, Gu H. (2022). The Community Coevolution Model with Application to the Study of Evolutionary Relationships between Genes based on Phylogenetic Profiles. *Systematic Biology*. NA: <https://doi.org/10.1093/sysbio/syac052>  
<http://dx.doi.org/https://doi.org/10.1093/sysbio/syac052>  
Published,  
Refereed?: Yes
53. Pesaranghader A, Matwin S, Sokolova M, Grenier J-C, Beiko RG, Hussin JG. (2022). deepSimDEF: deep neural embeddings of gene products and Gene Ontology terms for functional analysis of genes. *Bioinformatics*. 38: 3051-3061.  
Published,  
Refereed?: Yes, Open Access?: Yes
54. \*Kim JI, Maguire F, Tsang K, Gouliouris T, Peacock S, McAllister T, McArthur A, Beiko RG. (2022). Machine learning for antimicrobial resistance prediction: Current practice, limitations, and clinical perspective. *Clinical Microbiology Reviews*. NA: e0017921.  
Published,  
Refereed?: Yes, Synthesis?: Yes
55. Alcock BP, Raphenya AR, Wlodarski MA, Jia B, Gray KL, Hoad GR, Maguire F, Beiko RG, Brinkman FSL, van Domselaar G, McArthur AG. (2021). CARD-Resistomes: A pathogen-based collection of computationally predicted resistomes from the Comprehensive Antibiotic Resistance Database. *Microbial Genomics*. NA: NA.  
Submitted,  
Refereed?: Yes, Open Access?: Yes
56. Tsang KK, Maguire F, Zubyk HL, Chou S, Edalatmand A, Wright GD, Beiko RG, McArthur, AG. (2021). Identifying novel  $\beta$ -lactamase substrate activity through in silico prediction of antimicrobial resistance. *Microbial Genomics*. 7(1): NA.  
Published,  
Refereed?: Yes, Open Access?: Yes
57. Huang Y, Ragush CM, Johnston LH, \*Hall MW, Beiko RG, Jamieson RC, Hansen LT. (2021). Changes in bacterial communities during treatment of municipal wastewater in arctic wastewater stabilization ponds. *Frontiers in Water*. 3: 99.  
Published,  
Refereed?: Yes
58. Peabody MA, Lau WYV, Hoad GR, Jia B, Maguire F, Gray KL, Beiko RG, Brinkman FSL. (2020). PSORTm: a bacterial and archaeal protein subcellular localization prediction tool for metagenomics data. *Bioinformatics (Oxford, England)*. 36(10): 3043-3048.  
Published,  
Refereed?: Yes
59. Maguire F, Jia B, Gray KL, Lau WYV, Beiko RG, Brinkman FSL. (2020). Metagenome-assembled genome binning methods with short reads disproportionately fail for plasmids and genomic Islands. *Microbial genomics*. 6(10): NA.  
Published,  
Refereed?: Yes
60. Alcock BP, Raphenya AR, Lau TTY, Tsang KK, Bouchard M, Edalatmand A, Huynh W, Nguyen AV, Cheng AA, Liu S, Min SY, Miroshnichenko A, Tran HK, Werfalli RE, Nasir JA, Oloni M, Speicher DJ, Florescu A, Singh B, Faltyn M, Hernandez-Koutoucheva A, Sharma AN, Bordeleau E, Pawlowski AC, Zubyk HL, Dooley D, Griffiths E, \*Maguire F, Winsor GL, Beiko RG, Brinkman FSL, Hsiao WWL, Domselaar GV, McArthur AG. (2020). CARD 2020: antibiotic resistome surveillance with the comprehensive antibiotic resistance database. *Nucleic acids research*. 48(D1): D517-D525.  
Published,  
Refereed?: Yes

61. Houfani AA, Vetrovský T, Navarrete OU, Štursová M, Tláškal V, Beiko RG, Boucherba N, Baldrian P, Benallaoua S, Jorquera MA. (2019). Cellulase-Hemicellulase Activities and Bacterial Community Composition of Different Soils from Algerian Ecosystems. *Microbial ecology*. 77(3): 713-725.  
Published,  
Refereed?: Yes
62. \*Maguire F, Rehman MA, Carrillo C, Diarra MS, Beiko RG. (2019). Identification of Primary Antimicrobial Resistance Drivers in Agricultural Nontyphoidal *Salmonella enterica* Serovars by Using Machine Learning. *mSystems*. 4(4): e00211-19.  
Published,  
Refereed?: Yes
63. \*Nadukkalam Ravindran P, Bentzen P, Bradbury IR, Beiko RG. (2019). RADProc: A computationally efficient de novo locus assembler for population studies using RADseq data. *Molecular ecology resources*. 19(1): 272-282.  
Published,  
Refereed?: Yes
64. Stanley RRE, DiBacco C, Lowen B, Beiko RG, Jeffery NW, Van Wyngaarden M, Bentzen P, Brickman D, Benestan L, Bernatchez L, Johnson C, Snelgrove PVR, Wang Z, Wringe BF, Bradbury IR. (2018). A climate-associated multispecies cryptic cline in the northwest Atlantic. *Science advances*. 4(3): eaaq0929.  
Published,  
Refereed?: Yes
65. \*Liu C, \*Wright B, Allen-Vercoe E, Gu H, Beiko RG. (2018). Phylogenetic Clustering of Genes Reveals Shared Evolutionary Trajectories and Putative Gene Functions. *Genome biology and evolution*. 10(9): 2255-2265.  
Published,  
Refereed?: Yes
66. Bradbury IR, Wringe BF, Watson B, Paterson I, Horne J, Beiko RG, Lehnert SJ, Clément M, Anderson EC, Jeffery NW, Duffy S, \*Sylvester EVA, Robertson M, Bentzen P. (2018). Genotyping-by-sequencing of genome-wide microsatellite loci reveals fine-scale harvest composition in a coastal Atlantic salmon fishery. *Evolutionary applications*. 11(6): 918-930.  
Published,  
Refereed?: Yes
67. \*Sylvester EVA, Bentzen P, Bradbury IR, Clément M, Pearce J, Horne J, Beiko RG. (2018). Applications of random forest feature selection for fine-scale genetic population assignment. *Evolutionary applications*. 11(2): 153-165.  
Published,  
Refereed?: Yes
68. \*Nadukkalam Ravindran P, Bentzen P, Bradbury IR, Beiko RG. (2018). PMERGE: Computational filtering of paralogous sequences from RAD-seq data. *Ecology and evolution*. 8(14): 7002-7013.  
Published,  
Refereed?: Yes
69. \*Sylvester EVA, Beiko RG, Bentzen P, Paterson I, Horne JB, Watson B, Lehnert S, Duffy S, Clément M, Robertson MJ, Bradbury IR. (2018). Environmental extremes drive population structure at the northern range limit of Atlantic salmon in North America. *Molecular ecology*. 27(20): 4026-4040.  
Published,  
Refereed?: Yes
70. Van Wyngaarden M, Snelgrove PVR, DiBacco C, Hamilton LC, Rodríguez-Ezpeleta N, \*Zhan L, Beiko RG, Bradbury IR. (2018). Oceanographic variation influences spatial genomic structure in the sea scallop, *Placopecten magellanicus*. *Ecology and evolution*. 8(5): 2824-2841.  
Published,  
Refereed?: Yes

71. \*Hall MW, Rohwer RR, \*Perrie J, McMahon KD, Beiko RG. (2017). Ananke: temporal clustering reveals ecological dynamics of microbial communities. *PeerJ*. 5: e3812.  
Published,  
Refereed?: Yes
72. Jeffery NW, DiBacco C, Van Wyngaarden M, Hamilton LC, Stanley RRE, Bernier R, FitzGerald J, Matheson K, McKenzie CH, Nadukkalam Ravindran P, Beiko RG, Bradbury IR. (2017). RAD sequencing reveals genomewide divergence between independent invasions of the European green crab (*Carcinus maenas*) in the Northwest Atlantic. *Ecology and evolution*. 7(8): 2513-2524.  
Published,  
Refereed?: Yes
73. \*Zhan L, Paterson IG, Fraser BA, Watson B, Bradbury IR, \*Nadukkalam Ravindran P, Reznick D, Beiko RG, Bentzen P. (2017). megasat: automated inference of microsatellite genotypes from sequence data. *Molecular ecology resources*. 17(2): 247-256.  
Published,  
Refereed?: Yes
74. Jeffery NW, Stanley RRE, Wringe BF, Guijarro-Sabaniel J, Bourret V, Bernatchez L, Bentzen P, Beiko RG, Gilbey J, Clément M, Bradbury IR. (2017). Range-wide parallel climate-associated genomic clines in Atlantic salmon. *Royal Society open science*. 4(11): 171394.  
Published,  
Refereed?: Yes
75. \*Rutherford K, \*Meehan CJ, \*Langille MGI, Tyack SG, McKay JC, McLean NL, Benkel K, Beiko RG, Benkel B. (2017). Discovery of an expanded set of avian leucosis subgroup E proviruses in chickens using Vermillion, a novel sequence capture and analysis pipeline. *Poultry science*. 96(5): 1516.  
Published,  
Refereed?: Yes
76. Petkau A, Mabon P, Sieffert C, Knox NC, Cabral J, Iskander M, Iskander M, Weedmark , Zaheer R, Katz LS, Nadon C, Reimer A, Taboada E, Beiko RG, Hsiao W, Brinkman FSL, Graham M, Van Domselaar G. (2017). SNVPhyl: a single nucleotide variant phylogenomics pipeline for microbial genomic epidemiology. *Microbial genomics*. 3(6): e000116.  
Published,  
Refereed?: Yes
77. Pesaranghader A, Matwin S, Sokolova M, Beiko RG. (2016). simDEF: definition-based semantic similarity measure of gene ontology terms for functional similarity analysis of genes. *Bioinformatics (Oxford, England)*. 32(9): 1380-7.  
Published,  
Refereed?: Yes
78. Hajibabaei M, Baird DJ, Fahner NA, Beiko RG, Golding GB. (2016). A new way to contemplate Darwin's tangled bank: how DNA barcodes are reconnecting biodiversity science and biomonitoring. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*. 371(1702)  
Published,  
Refereed?: Yes
79. Dhanani Akhilesh S, Block Glenn, Dewar Ken, Forgetta Vincenzo, Topp Edward, Beiko Robert G, Diarra Moussa S. (2015). Genomic Comparison of Non-Typhoidal Salmonella enterica Serovars Typhimurium, Enteritidis, Heidelberg, Hadar and Kentucky Isolates from Broiler Chickens. *PloS one*. 10(6): e0128773.  
Published,  
Refereed?: Yes
80. Meehan Conor J, Langille Morgan G I, Beiko Robert G. (2015). Frailty and the Microbiome. *Interdisciplinary topics in gerontology and geriatrics*. 41: 54-65.  
Published,  
Refereed?: Yes

81. Beiko Robert G. (2015). Microbial malaise: how can we classify the microbiome?. *Trends in microbiology*. 23(11): 671-679.  
Published,  
Refereed?: Yes
82. Wong Dennis H-J, Beiko Robert G. (2015). Transfer of energy pathway genes in microbial enhanced biological phosphorus removal communities. *BMC genomics*. 16: 526.  
Published,  
Refereed?: Yes
83. Ning Jie, Beiko Robert G. (2015). Phylogenetic approaches to microbial community classification. *Microbiome*. 3: 47.  
Published,  
Refereed?: Yes
84. Langille Morgan Gi, Meehan Conor J, Koenig Jeremy E, Dhanani Akhilesh S, Rose Robert A, Howlett Susan E, Beiko Robert G. (2014). Microbial shifts in the aging mouse gut. *Microbiome*. 2(1): 50.  
Published,  
Refereed?: Yes
85. Meehan Conor J, Beiko Robert G. (2014). A phylogenomic view of ecological specialization in the Lachnospiraceae, a family of digestive tract-associated bacteria. *Genome biology and evolution*. 6(3): 703-13.  
Published,  
Refereed?: Yes
86. Whidden Christopher, Zeh Norbert, Beiko Robert G. (2014). Supertrees Based on the Subtree Prune-and-Regraft Distance. *Systematic biology*. 63(4): 566-81.  
Published,  
Refereed?: Yes
87. O'Doherty Kieran C, Neufeld Josh D, Brinkman Fiona S L, Gardner Humphrey, Guttman David S, Beiko Robert G. (2014). Opinion: Conservation and stewardship of the human microbiome. *Proceedings of the National Academy of Sciences of the United States of America*. 111(40): 14312-3.  
Published,  
Refereed?: No
88. Parks Donovan H, Tyson Gene W, Hugenholtz Philip, Beiko Robert G. (2014). STAMP: statistical analysis of taxonomic and functional profiles. *Bioinformatics (Oxford, England)*. 30(21): 3123-4.  
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## Intellectual Property

### Patents

1. MICROFLUIDIC CHIP, SYSTEMS, AND METHODS FOR CAPTURING OF ENVIRONMENTAL DNA. United States of America. PCT/CA2020/050738. 2020/09/01.  
Patent Status: Granted/Issued  
Inventors: Creelman JJ, Luy EA, Henderson Beland GC, Morgan SC, LaRoche MEJ, Tavasoli M, Beiko RG, Race RE, Furlong A