

CURRICULUM VITAE

Robert G. Beiko

Faculty of Computer Science, Dalhousie University, PO BOX 15000
Halifax, Nova Scotia, Canada, B3H 4R2

EDUCATION

Degrees

- Doctorate, Ph.D. Biology, Bioinformatics (Completed)** **Oct. 1998 - Oct. 2003**
University of Ottawa, Ontario, Canada, Academic
Supervisors: Dr. Robert L. Charlebois (1998/9 - 2003/9)
- Bachelor's, B.Sc.(Hons) Biology, Genetics (Completed)** **Oct. 1994 - May. 1998**
Dalhousie University, Nova Scotia, Canada, Academic
Supervisors: Dr. Gerald C. Johnston (1997/5 - 1998/8)

RECOGNITIONS

- Prize / Award, Teaching Award** **Jul. 2010 - Jul. 2010**
Dalhousie Student Union, Academic
- Prize / Award, Canada Research Chair** **May. 2007 - Mar. 2017**
Natural Sciences and Engineering Research Council of Canada (NSERC), Ontario, Canada, Federal Government
Canada Research Chair in Bioinformatics

EMPLOYMENT

Academic Work Experience

- Professor, Professor (Full-time)** **Jul. 2016**
Computer Science, Computer Science, Dalhousie University, Nova Scotia, Canada, Academic
(Jul. 2011)
- Associate Professor, Associate Professor (Full-time)** **Jul. 2011 - Jul. 2016**
Computer Science, Computer Science, Dalhousie University, Nova Scotia, Canada, Academic
- Assistant Professor (Full-time)** **Oct. 2006 - Jul. 2011**
Computer Science, Computer Science, Dalhousie University, Nova Scotia, Canada, Academic
- Postdoctoral Fellow (Full-time)** **Jul. 2003 - Aug. 2006**
Institute for Molecular Bioscience, Institute for Molecular Bioscience, University of Queensland, Australia, Academic
- Research Assistant (Full-time)** **Jan. 1997 - Aug. 1998**
Medicine, Faculty of, Biochemistry, Dalhousie University, Nova Scotia, Canada, Academic

Non-academic Work Experience

Cartographic Technician

Seabed Exploration Associates, Private Sector

Dec. 1992 - Oct. 1997

Affiliations

Professor

Computer Science, Dalhousie University, Nova Scotia, Canada, Academic

Jul. 2016

PEER-REVIEWED PUBLICATIONS SINCE 2011

1. Nicholas W. Jeffery, Claudio DiBacco, Mallory Van Wyngaarden, Lorraine C. Hamilton, Ryan R.E. Stanley, C. McKenzie, Praveen Nadukkalam Ravindran, Robert Beiko, Ian R. Bradbury. (2017). RAD-sequencing reveals genome wide divergence between independent invasions of the European green crab (*Carcinus maenas*) in the Northwest Atlantic. *Ecology and Evolution*, epub ahead of print.
2. Aaron Petkau, Philip Mabon, Cameron Sieffert, Natalie Knox, Jennifer Cabral, Kelly Weedmark, Rahat Zaheer, Lee S. Katz, Celine Nadon, Aleisha Reimer, Eduardo Taboada, Robert G. Beiko, William Hsiao, Fiona Brinkman, Morag Graham, the IRIDA Consortium, and Gary Van Domselaar. (2017). SNVPhyl: A Single Nucleotide Variant Phylogenomics pipeline for microbial genomic epidemiology. *Microbial Genomics*. (Revision Requested)
3. Michael W. Hall, Jonathan Perrie, Robin R. Rohwer, Katherine D. McMahon, and Robert G. Beiko. (2017). Ananke: Ecological dynamics of microbial communities revealed by temporal clustering. *PeerJ*. (Submitted)
4. Michael W. Hall, Natasha Singh, Kester F. Ng, David K. Lam, Michael B. Goldberg, Howard C. Tenenbaum, Josh D. Neufeld, Robert G. Beiko & Dilani B. Senadheera. (2017). Inter-personal diversity and temporal dynamics of dental, tongue, and salivary microbiota in the healthy oral cavity. *npj Biofilms and Microbiomes*, 3, epub ahead of print.
5. Emma VA Sylvester, Paul Bentzen, Ian R Bradbury, Marie Clement, Jon Pearce, John Horne, and Robert G Beiko. (2017). Applications of Random Forest for SNP selection in individual assignment of Atlantic Salmon (*Salmo salar*). *Evolutionary Applications*. (Revision Requested)
6. Alexander Keddy and Robert G. Beiko. (2017). Investigating biogeographic patterns using point-based cartograms and the Geographically Coupled Phylogenetic Distance. *Global Ecology and Biogeography*. (Revision Requested)
7. Nadukkalam Ravindran P, Bentzen P, Bradbury I, Beiko RG. (2016). Computational filtering of paralogous sequences from RAD-seq data. *Molecular Ecology Resources*. (Revision Requested)
8. Rutherford K, Meehan C J, Langille M G I, Tyack S G, McKay J C, McLean N L, Benkel K, Beiko R G, Benkel B. (2016). Discovery of an expanded set of avian leukosis subgroup E proviruses in chickens using Vermillion, a novel sequence capture and analysis pipeline. *Poultry science*, 95, 2250-2258.
9. Zhan Luyao, Paterson Ian G, Fraser Bonnie A, Watson Beth, Bradbury Ian R, Nadukkalam Ravindran Praveen, Reznick David, Beiko Robert G, Bentzen Paul. (2016). MEGASAT: automated inference of microsatellite genotypes from sequence data. *Molecular ecology resources*, epub ahead of print, NA.
10. van Wyngaarden M, Snelgrove PVR, DiBacco C, Hamilton LC, Rodriguez-Ezpeleta, Zhan L, Beiko RG, Bradbury IR. (2016). Oceanographic variation influences spatial genomic structure in the sea scallop, *Placopecten magellanicus*. *Molecular Ecology*. (Submitted)
11. Dhanani Akhilesh S, Block Glenn, Dewar Ken, Forgetta Vincenzo, Topp Edward, Beiko Robert G, Diarra Moussa S. (2016). Correction: Genomic Comparison of Non-Typhoidal Salmonella enterica Serovars Typhimurium, Enteritidis, Heidelberg, Hadar and Kentucky Isolates from Broiler Chickens. *PloS one*, 11(2), e0148706.

12. Pesaranghader Ahmad, Matwin Stan, Sokolova Marina, Beiko Robert G. (2015). simDEF: definition-based semantic similarity measure of gene ontology terms for functional similarity analysis of genes. *Bioinformatics (Oxford, England)*, 32(9), 1380-7.
13. Ning Jie, Beiko Robert G. (2015). Phylogenetic approaches to microbial community classification. *Microbiome*, 3, 47.
14. Beiko Robert G. (2015). Microbial malaise: how can we classify the microbiome?. *Trends in microbiology*, 23(11), 671-9.
15. Dhanani Akhilesh S, Block Glenn, Dewar Ken, Forgetta Vincenzo, Topp Edward, Beiko Robert G, Diarra Moussa S. (2015). Correction: Genomic Comparison of Non-Typhoidal Salmonella enterica Serovars Typhimurium, Enteritidis, Heidelberg, Hadar and Kentucky Isolates from Broiler Chickens. *PloS one*, 10(9), e0137697.
16. Wong Dennis H-J, Beiko Robert G. (2015). Transfer of energy pathway genes in microbial enhanced biological phosphorus removal communities. *BMC genomics*, 16, 526.
17. Akhilesh S. Dhanani, Glenn Block, Ken Dewar, Vincenzo Forgetta, Edward Topp, Robert G. Beiko, and Moussa S. Diarra. (2015). Genomic Comparison of Non-typhoidal Salmonella enterica Serovars Typhimurium, Enteritidis, Heidelberg, Hadar and Kentucky isolates from Broiler Chickens. *PLoS ONE*, 10, e0128773.
18. 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.
19. 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.
20. Whidden Christopher, Zeh Norbert, Beiko Robert G. (2014). Supertrees Based on the Subtree Prune-and-Regraft Distance. *Systematic biology*, 63(4), 566-81.
21. 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.
22. O'Doherty KC, Neufeld JD, Brinkman FS, Gardner H, Guttman DS, Beiko RG. (2014). Opinion: Conservation and stewardship of the human microbiome. *Proceedings of the National Academy of Science*, 111(40), 14312-14313.
23. Boon Eva, Meehan Conor J, Whidden Chris, Wong Dennis H-J, Langille Morgan G I, Beiko Robert G. (2013). Interactions in the microbiome: communities of organisms and communities of genes. *FEMS microbiology reviews*, 38(1), 90-118.
24. Langille Morgan G I, Zaneveld Jesse, Caporaso J Gregory, McDonald Daniel, Knights Dan, Reyes Joshua A, Clemente Jose C, Burkepille Deron E, Vega Thurber Rebecca L, Knight Rob, Beiko Robert G, Huttenhower Curtis. (2013). Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. *Nature biotechnology*, 31(9), 814-21.
25. Parks Donovan H, Mankowski Timothy, Zangoeei Somayyeh, Porter Michael S, Armanini David G, Baird Donald J, Langille Morgan G I, Beiko Robert G. (2013). GenGIS 2: geospatial analysis of traditional and genetic biodiversity, with new gradient algorithms and an extensible plugin framework. *PloS one*, 8(7), e69885.
26. Porter MS, Beiko RG. (2013). SPANNER: taxonomic assignment of sequences using pyramid matching of similarity profiles. *Bioinformatics (Oxford, England)*, 29(15), 1858-64.
27. Eveleigh RJ, Meehan CJ, Archibald JM, Beiko RG. (2013). Being Aquifex aeolicus: Untangling a hyperthermophile's checkered past. *Genome biology and evolution*, 5(12), 2478-97.
28. Whidden C, Beiko RG, Zeh N. (2013). Fixed-Parameter Algorithms for Maximum Agreement Forests. *SIAM Journal on Computing*, 42(4), 1431-1466.
29. Curtis BA et al. (26th of 72 authors). (2012). Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. *Nature*, 492(7427), 59-65.

Beiko, Robert

30. Smith Silvia E, Showers-Corneli Patrice, Dardenne Caitlin N, Harpending Henry H, Martin Darren P, Beiko Robert G. (2012). Comparative genomic and phylogenetic approaches to characterize the role of genetic recombination in mycobacterial evolution. *PloS one*, 7(11), e50070.
31. Meehan Conor J, Beiko Robert G. (2012). Lateral gene transfer of an ABC transporter complex between major constituents of the human gut microbiome. *BMC microbiology*, 12, 248.
32. Parks Donovan H, Beiko Robert G. (2012). Measuring community similarity with phylogenetic networks. *Molecular biology and evolution*, 29(12), 3947-58.
33. Parks Donovan H, Beiko Robert G. (2012). Measures of phylogenetic differentiation provide robust and complementary insights into microbial communities. *The ISME journal*, 7(1), 173-83.
34. 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. (2012). Genome and low-iron response of an oceanic diatom adapted to chronic iron limitation. *Genome biology*, 13(7), R66.
35. Hug Laura A, Beiko Robert G, Rowe Annette R, Richardson Ruth E, Edwards Elizabeth A. (2012). Comparative metagenomics of three Dehalococcoides-containing enrichment cultures: the role of the non-dechlorinating community. *BMC genomics*, 13, 327.
36. MacDonald Norman J, Parks Donovan H, Beiko Robert G. (2012). Rapid identification of high-confidence taxonomic assignments for metagenomic data. *Nucleic acids research*, 40(14), e111.
37. Langille MG, Meehan CJ, Beiko RG. (2012). Human microbiome: a genetic bazaar for microbes?. *Current Biology*, 22(1), R20-R22.
38. Parks Donovan H, MacDonald Norman J, Beiko Robert G. (2011). Classifying short genomic fragments from novel lineages using composition and homology. *BMC bioinformatics*, 12, 328.
39. Chan Cheong Xin, Beiko Robert G, Ragan Mark A. (2011). Lateral transfer of genes and gene fragments in *Staphylococcus* extends beyond mobile elements. *Journal of bacteriology*, 193(15), 3964-77.
40. Beiko RG. (2011). Telling the whole story in a 10, 000-genome world. *Biology direct*, 6, 34.

RESEARCH FUNDING HISTORY

Co-applicant, Operating Grant, Managing Microbial Corrosion in Canadian Offshore & Onshore Oil Production (Awarded)

Oct. 2016 - Oct. 2020

Genome Canada: 2015 LARGE-SCALE APPLIED RESEARCH PROJECT COMPETITION NATURAL RESOURCES AND THE ENVIRONMENT (2016/10 - 2020/9) Total: \$7,000,000

Co-applicant, Operating Grant, CHONe II: Conservation Strategies for Canada's Changing Oceans (Awarded)

Oct. 2015 - Aug. 2020

Natural Sciences and Engineering Research Council of Canada (NSERC): Strategic Network Grant (2015/9 - 2020/8) Total: \$4,980,000 Received: \$45,000

Principal Applicant, Operating Grant, Rapid prediction of antimicrobial resistance from metagenomics samples: data, models, and methods (Awarded)

Oct. 2016 - Oct. 2018

Genome Canada: 2015 Bioinformatics and Computational Biology Competition (2016/10 - 2018/9) Total: \$250,000

Co-applicant, Operating Grant, The maternal and neonatal microbiota correlates of premature labor and adverse neonatal outcomes (Awarded)

Oct. 2016 - Oct. 2018

Aga Khan University, Total: \$25,000

Co-applicant, Grant, Genomics approaches to the management of mixed stock fisheries in Canada: developing tools for promoting fishery stability and the protection of biodiversity (Awarded)

Oct. 2013 - Aug. 2017

Beiko, Robert

Natural Sciences and Engineering Research Council of Canada (NSERC): Strategic Project Grants (2013/9 - 2016/8)
Total: \$593,809

Co-investigator, Grant, The Dalhousie Centre for Comparative Genomics and Evolutionary Bioinformatics (Awarded) Oct. 2008 - Aug. 2017

Tula Foundation: N/A (2008/5 - 2017/4) Total: \$3,000,000

Principal Investigator, Operating Grant, Untangling the complex geographic and evolutionary patterns of microbes (Awarded) May. 2012 - Mar. 2017

Natural Sciences and Engineering Research Council of Canada (NSERC): Discovery Grants (2012/4 - 2017/3) Total: \$165,000

Principal Investigator, Research Chair, Canada Research Chair in Bioinformatics (Awarded) May. 2007 - Mar. 2017

Canada Research Chairs (CRC): Tier 2 Canada Research Chairs (2007/4 - 2017/3) Total: \$1,000,000

Co-applicant, Contract, Novel Chlamydia vaccine antigen development by computational algorithms (Awarded) Aug. 2016 - Jan. 2017

Springboard Atlantic (2016/7 - 2017/1) Total: \$20,000

Co-investigator, Grant, A Federated Bioinformatics Platform for Public Health Microbial Genomics (Awarded) Jul. 2013 - Dec. 2016

Genome Canada: Bioinformatics and Computational Biology (2013/5 - 2016/4) Total: \$1,576,791

Principal Applicant, Operating Grant, Assessing microbial signatures of periodontitis in an aging population (Awarded) Oct. 2015 - Oct. 2016

Nova Scotia Health Research Foundation (NSHRF): Development / Innovative Grants (2015/9 - 2016/9) Total: \$14,300

Principal Investigator, Operating Grant, Scotia Support Grant (Completed) Oct. 2013 - Aug. 2016

Nova Scotia Health Research Foundation (NSHRF): Scotia Support Grants (2013/9 - 2015/8) Total: \$48,000

Principal Investigator, Grant, A Pilot Project to Assess the Gut Microbes of Patients in an Assisted Living Facility (Completed) Oct. 2013 - May. 2016

Nova Scotia Health Research Foundation (NSHRF): Discovery / Innovative Grants (2013/9 - 2016/5) Total: \$15,000

Principal Investigator, Operating Grant, Genetic control of Reproductive Longevity in Mouse and Validation of a genetic marker panel to predict Fertility and Longevity traits in Holstein Dairy Cattle (Completed) Mar. 2015 - Mar. 2016

Mathematics of Information Technology and Complex Systems (MITACS): Accelerate (2015/3 - 2016/3) Total: \$90,000

Principal Investigator, Contract, Development of a genetic marker panel to predict Fertility and Longevity traits in Holstein Dairy Cattle (Completed) Dec. 2014 - Mar. 2016

National Research Council Canada (NRC) (Ottawa, ON): IRAP (2014/11 - 2016/3) Total: \$165,000

Principal Investigator, Contract, Comparative Genomics to Identify Genes and Pathways Controlling Reproductive Longevity of Mammals (Completed) May. 2014 - Mar. 2015

National Research Council Canada (NRC) (Ottawa, ON): IRAP (2013/3 - 2015/3) Total: \$80,000

Beiko, Robert

Principal Investigator, Contract, Rapid Identification of Insertion Sites for Retroviral Elements in Complex Genomes (Completed) **Mar. 2014 - Aug. 2014**

EW Group GmbH: N/A (2014/3 - 2014/8) Total: \$32,000 Received: \$32,000

Co-applicant, Operating Grant, The role of the complement system in post-colitis colonization and recovery from injury (Completed) **Oct. 2013 - Aug. 2014**

Nova Scotia Health Research Foundation (NSHRF): Discovery / Innovative Grants (2013/9 - 2014/8) Total: \$15,000

Principal Investigator, Operating Grant, Comparative Genomics (Completed) **Oct. 2013 - Aug. 2014**

Mathematics of Information Technology and Complex Systems (MITACS): MITACS Accelerate (2013/9 - 2014/8) Total: \$45,000

Co-investigator, Operating Grant, Biomonitoring 2.0 (Completed) **Jul. 2011 - Jul. 2014**

Genome Canada: Large-scale applied research projects (2011/7 - 2014/6) Total: \$3,000,000

Co-investigator, Operating Grant, Modeling and Mapping Microbial Diversity and Function with Marker Genes, Genomes and Metagenomes (Completed) **Oct. 2010 - Aug. 2013**

Canadian Institutes of Health Research (CIHR): Emerging Team Grant (Human Microbiome) (2010/9 - 2013/8) Total: \$623,000

Principal Investigator, Grant, Machine-learning classification of genomic polymorphism data relating to fertility and reproductive longevity (Completed) **Jul. 2012 - Dec. 2012**

Natural Sciences and Engineering Research Council of Canada (NSERC): Engage (2012/5 - 2012/12) Total: \$25,000

Co-investigator, Operating Grant, BEEM: Bioproducts and Enzymes from Environmental Metagenomes (Completed) **Oct. 2009 - Aug. 2012**

Genome Canada: COMPETITION IN APPLIED GENOMICS RESEARCH IN BIOPRODUCTS OR C (2009/9 - 2012/8) Total: \$5,000,000

Principal Investigator, Operating Grant, New Computational Methods for Metagenomics (Completed) **May. 2007 - Mar. 2012**

Natural Sciences and Engineering Research Council of Canada (NSERC): Discovery Grant (2007/4 - 2012/3) Total: \$115,000

OTHER ACTIVITIES

Associate Editor, Journal, mSystems **Jan. 2016 - Dec. 2018**

Associate Editor, Journal, BMC Genomics **Jan. 2012 - Dec. 2018**

Peer reviewer for over 30 journals, >150 papers reviewed
15 conference program committee memberships since 2007

Advisory Board member for SuperNOVA, an organization that organizes science camps and other activities for students aged 5-16

Committee Member, Canadian Bioinformatics and Computational Biology National Strategy Committee **Aug. 2014**
CIHR / Genome Canada, Federal Government

PRESENTATIONS SINCE 2011

1. Beiko, R. (2017). *The aging and frail microbiome: diversity, time, and function*. McMaster University - invited presentation, Hamilton, Canada.
2. Beiko, R. (2017). *Identifying key temporal and taxonomic bacterial clusters in the aging microbiome*. Drexel University invited presentation, Philadelphia, United States.
3. Beiko, R. (2016). *Monitoring the microbiome in an assisted-care facility*. IRIDA Annual General Meeting / public lecture, Vancouver, Canada.
4. Beiko, R. (2016). *A Coevolution-Based Approach to the Identification of Genes with Similar Phylogenetic Distributions*. Vancouver Bioinformatics Users' Group (VanBUG), Vancouver, Canada.
5. Beiko, R. (2016). *Common assumptions and pitfalls of microbiome analysis*. Advancing Microbiome Research Symposium: Microbiome & Disease, Potomac, MD, United States.
6. Beiko, R. (2016). *Lateral gene transfer: how many stories can a network tell?*. EVOLUNET: PUBLIC LECTURES OF THE SUMMER SCHOOL ON NETWORKS, Roscoff, France.
7. Beiko, R., Morgan Langille, Michael Hall. (2016). *Microbiome Analysis: 16S and Metagenomics*. Great Lakes Bioinformatics and Canadian Computational Biology Conference, Toronto, Canada. Retrieved from <https://www.iscb.org/glbioccbc2016-program/workshops>
8. Beiko, R. (2016). *Metagenomics*. Great Lakes Bioinformatics and the Canadian Computational Biology Conference 2016, Toronto, Canada. Retrieved from <https://www.iscb.org/glbioccbc2016-program/glbioccbc2016-full-agenda>
9. Beiko, R. (2016). *What can the microbiome tell us about frailty?*. Northwood Research Day 2016, Dartmouth, Canada.
10. Beiko, R. (2016). *Aging, frailty and the microbiome: new methods, new insights*. 5th Annual Canadian Human and Statistical Genetics Meeting, Halifax, Canada. Retrieved from <genetics16.mcgill-cihr-ig.ca>
11. Beiko, R. (2016). *Phylogeography with GenGIS*. VizBi 2016, Heidelberg, Germany. Retrieved from <https://vizbi.org/2016>
12. Beiko, R. (2015). *Soil, lateral gene transfer, and hybrid genomes*. Argonne National Laboratory 7th annual soil metagenomics meeting, Chicago, United States.
13. Beiko, R. (2015). *The microbiome and its impact on aging and frailty*. Gerontological Society of America annual meeting, Orlando, United States.
14. Beiko, R. (2015). *Upwardly mobile genes*. Invited seminar at Canadian National Microbiology Laboratory, Winnipeg, Canada.
15. Beiko, R. (2015). *Introduction to Metagenomics*. Canadian Bioinformatics Workshop - Analysis of Metagenomic Data, Halifax, Canada. Retrieved from <https://bioinformatics.ca/workshops/2015/analysis-metagenomic-data-2015>
Lead organizer and presenter at first Canadian Bioinformatics Workshop on Metagenomics
16. Beiko, R. (2014). *Microbiome analysis*. African perinatal probiotic study meeting, Athi River, Kenya.
17. Beiko, R. (2014). *Grand theft operon: lateral city*. IGERT symposium on Deep Genomics, Tucson, United States.
18. Beiko, R. (2014). *Biogeography of microorganisms. No borders. No limits. No fear*. Understanding biodiversity dynamics using diverse data sources, Canberra, Australia.
19. Beiko, R. (2014). *Gene sharing in microbes: good for the individual, good for the community?*. University of Waterloo Department of Biology seminar, Waterloo, Canada.
20. Beiko, R. (2014). *When trees can't agree*. Canadian Mathematical Society annual meeting, Hamilton, Canada.
21. Beiko, R. (2014). *Modeling and mapping microbial diversity and function with marker genes, genomes and metagenomes*. Canadian Microbiome Workshop 2014: from Research to Applications, Vancouver, Canada.
22. Beiko, R. (2014). *Computing the Microbial World*. Canadian High-Performance Computing Conference, Halifax, Canada.
23. Beiko, R. (2014). *The Human Microbiome (and friends)*. Genome Atlantic Human Genetics and Genomics Seminar series, Halifax, Canada.

24. Beiko, R. (2013). *Visualizing species distributions and phylogeography using GenGIS*. International Biogeography Society Special Meeting, Montreal, Canada.
25. Beiko, R. (2013). *Evolution and ecology of GI-tract-associated Lachnospiraceae: Drop acid, lose your coat, leave in someone else's genes*. SMBE 2013, Chicago, United States.
26. Beiko, R. (2013). *Biology's Big Data Revolution*. Public lecture: Faculty of Computer Science, Halifax, Canada.
27. Beiko, R. (2013). *Classifying DNA*. Dalhousie In-House Computer Science Conference, Halifax, Canada.
28. Beiko, R. (2012). *Genetic monitoring of H1N1 during the 2009 outbreak*. Critical Infrastructure Protection Initiative, Halifax, Canada.
29. Beiko, R. (2012). *GenGIS 2: New approaches to understand the geography of our microbial world*. Canadian Society of Microbiologists annual meeting, Vancouver, Canada.
30. Beiko, R. (2012). *GenGIS: a platform for visualization and analysis of genetic biodiversity data*. Quebec biomonitoring meeting, Montreal, Canada.
31. Beiko, R. (2012). *Applying reference Condition Analysis using GenGIS*. Canadian Aquatic Biomonitoring Network annual meeting, Fredericton, Canada.
32. Beiko, R. (2012). *Biomonitoring 2.0: New approaches to biodiversity monitoring*. iEvoBio 2012, Ottawa, Canada.
33. Beiko, R. (2012). *Major initiatives in microbiomics: industrial processes, environmental monitoring, human health*. CAU-DAL joint workshops, Kiel, Germany.
34. Beiko, R. (2012). *Microbes and communities: steps E, M, and V*. Canadian Institute for Advanced Research (Integrated Microbial Biodiversity program) annual meeting 2012, Quebec, Canada.
35. Beiko, R. (2012). *A network of everything??*. Society for Molecular Biology and Evolution annual meeting, Dublin, Ireland.
36. Beiko, R. (2011). *Who is doing what, and to whom: taxonomic assignments and network analysis in metagenome studies*. SyMBIOTA Workshop, Toronto, Canada.
37. Beiko, R. (2011). *Molecular and Functional Diagnostics*. CIHR Microbiomics Grant workshop, Halifax, Canada.
38. Beiko, R. (2011). *GenGIS: Geospatial analysis and visualization of biodiversity*. GIS Day, Halifax, Canada.
39. Beiko, R. (2011). *Modeling and mapping microbial diversity and function with marker genes, genomes and metagenomes, or MMMDFMGGM*. CIHR Emerging Microbiome Teams, Vancouver, Canada.
40. Beiko, R. (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.
41. Beiko, R. (2011). *Questions at the interface of evolution, ecology, space and time*. Society for Molecular Biology and Evolution meeting, Kyoto, Japan.
42. Beiko, R. (2011). *GenGIS: A 3D geospatial environment for the analysis of genetic data*. iPlant collaborative workshop, Tucson, United States.

Book Chapters

1. Meehan CJ, Langille MGI, Beiko RG. (2014). Frailty and the Microbiome. *Frailty in ageing: biological, clinical and social implications* (pp. 54-65). Karger.

Book Reviews

1. Beiko R. (2014). Bioinformatics: Hypothesis Free—Or Hypotheses Freed? *BioScience* 9:844-845.