

Robert Beiko

Professor and Associate Dean Research
Faculty of Computer Science, Dalhousie University

Degrees:

Ph.D. Biology Bioinformatics, University of Ottawa, Canada, Ontario, 2003
B.Sc.(Hons) Biology Genetics, Dalhousie University, Canada, Nova Scotia, 1998

EMPLOYMENT HISTORY:

2016 – Professor, Computer Science, Dalhousie University, Canada, Nova Scotia
2011 – 2016 Associate Professor, Computer Science, Dalhousie University, Canada, Nova Scotia
2006 – 2011 Computer Science, Dalhousie University, Canada, Nova Scotia
2003 – 2006 Institute for Molecular Bioscience, University of Queensland, Australia
1997 – 1998 Medicine, Faculty of, Dalhousie University, Canada, Nova Scotia

HONOURS:

2010 Teaching Award, Dalhousie Student Union
2007 Canada Research Chair, Canada Research Chair in Bioinformatics, Natural Sciences and Engineering Research Council of Canada (NSERC), Canada, Ontario

SCHOLARLY and PROFESSIONAL ACTIVITIES:**Event Administration**

2011 – 2012 Organizing Committee member, iEvoBio 2012, iEvoBio meeting, Ottawa, Ontario, Canada
2015- Organizing Committee member, Canadian Bioinformatics Workshop in Metagenomics
2016- Organizing Committee member, Canadian Bioinformatics Workshop in Genomic Epidemiology

Editorial Activities

2016 – Associate Editor, mSystems
2012 – Associate Editor, BMC Genomics

Journal Review Activities

Reviewer, Over 30 journals

Conference Review Activities

Program Committee member, Over 15 conferences

Community and Volunteer Activities

2007 – Advisory Board member for SuperNOVA, an organization that organizes science camps and other activities for students aged 5-16

MEMBERSHIPS**Committee Memberships**

2014 – Committee Member, Canadian Bioinformatics and Computational Biology National Strategy Committee, CIHR / Genome Canada
2012 – 2018 Committee Member, Senate Honourary Degrees, Dalhousie University, Canada, Nova Scotia

University of Lethbridge

2016 – 2017 Chair, Curriculum Committee, Dalhousie University, Canada, Nova Scotia
2014 – 2016 Chair, Co-op Management Committee, Dalhousie University, Canada, Nova Scotia
2014 – 2017 Committee Member, Employee Benefits Committee, Dalhousie University, Canada, Nova Scotia

Other Memberships

2015 – Director, Master's of Science in Computational Biology and Bioinformatics program, Dalhousie University, Canada, Nova Scotia
2007 – 2011 Co-op Advisor, Dalhousie University, Canada, Nova Scotia

SUPERVISIONS:**Summary:****Completed**

Principal Supervisor 3 Bachelor's
1 Bachelor's Honours
1 Doctorate
9 Master's Thesis
6 Post-doctorate
4 Research Associate

Co-Supervisor 2 Bachelor's
1 Doctorate
3 Master's Thesis

In Progress

Principal Supervisor 1 Bachelor's
4 Doctorate
1 Master's Thesis
1 Post-doctorate

Co-Supervisor 1 Doctorate
1 Post-doctorate

EXTERNAL RESEARCH FUNDING:

Year(s)	Source	Type	Investigator	Amount
2018 - 2021	Genome Canada <u>Title:</u> Antimicrobial Resistance: Emergence, Transmission, and Ecology (ARETE) <u>Program:</u> Bioinformatics and Computational Biology competition	<u>Type:</u> Grant <u>Purpose:</u> Operating	<u>My Role:</u> Principal Investigator	<u>Funding Total:</u> \$1,400,000.00
2016 - 2020	Genome Canada <u>Title:</u> Managing Microbial Corrosion in Canadian Offshore & Onshore Oil Production <u>Program:</u> 2015 LARGE-SCALE APPLIED RESEARCH PROJECT COMPETITION NATURAL RESOURCES AND THE ENVIRONMENT	<u>Type:</u> Grant <u>Purpose:</u> Operating	<u>My Role:</u> Co-applicant	<u>Funding Total:</u> \$7,000,000.00
2016 - 2018	Genome Canada <u>Title:</u> Rapid prediction of antimicrobial resistance from metagenomics samples: data, models, and methods <u>Program:</u> 2015 Bioinformatics and Computational Biology Competition	<u>Type:</u> Grant <u>Purpose:</u> Operating	<u>My Role:</u> Principal Applicant	<u>Funding Total:</u> \$250,000.00
2016 - 2017	Springboard Atlantic <u>Title:</u> Novel Chlamydia vaccine antigen development by computational algorithms <u>Program:</u> Springboard	<u>Type:</u> Contract	<u>My Role:</u> Co-applicant	<u>Funding Total:</u> \$20,000.00
2015 - 2020	Natural Sciences and Engineering Research Council of Canada (NSERC) <u>Title:</u> CHONe II: Conservation Strategies for Canada's Changing Oceans <u>Program:</u> Strategic Network Grant	<u>Type:</u> Grant <u>Purpose:</u> Operating	<u>My Role:</u> Co-applicant	<u>Funding Total:</u> \$4,980,000.00

2015 - 2016	<p>Nova Scotia Health Research Foundation (NSHRF)</p> <p><u>Title:</u> Assessing microbial signatures of periodontitis in an aging population</p> <p><u>Program:</u> Development / Innovative Grants</p>	<p><u>Type:</u> Grant</p> <p><u>Purpose:</u> Operating</p>	<p><u>My Role:</u> Principal Applicant</p>	<p><u>Funding Total:</u> \$14,300.00</p>
2015 - 2016	<p>Mathematics of Information Technology and Complex Systems (MITACS)</p> <p><u>Title:</u> Genetic control of Reproductive Longevity in Mouse and Validation of a genetic marker panel to predict Fertility and Longevity traits in Holstein Dairy Cattle</p> <p><u>Program:</u> Accelerate</p>	<p><u>Type:</u> Grant</p> <p><u>Purpose:</u> Operating</p>	<p><u>My Role:</u> Principal Investigator</p>	<p><u>Funding Total:</u> \$90,000.00</p>
2014 - 2016	<p>National Research Council Canada (NRC) (Ottawa, ON)</p> <p><u>Title:</u> Development of a genetic marker panel to predict Fertility and Longevity traits in Holstein Dairy Cattle</p> <p><u>Program:</u> IRAP</p>	<p><u>Type:</u> Contract</p>	<p><u>My Role:</u> Principal Investigator</p>	<p><u>Funding Total:</u> \$165,000.00</p>
2014 - 2014	<p>EW Group GmbH</p> <p><u>Title:</u> Rapid Identification of Insertion Sites for Retroviral Elements in Complex Genomes</p> <p><u>Program:</u> N/A</p>	<p><u>Type:</u> Contract</p>	<p><u>My Role:</u> Principal Investigator</p>	<p><u>Funding Total:</u> \$32,000.00</p>
2013 - 2016	<p>Natural Sciences and Engineering Research Council of Canada (NSERC)</p> <p><u>Title:</u> Genomics approaches to the management of mixed stock fisheries in Canada: developing tools for promoting fishery stability and the protection of biodiversity</p> <p><u>Program:</u></p>	<p><u>Type:</u> Grant</p>	<p><u>My Role:</u> Co-applicant</p>	<p><u>Funding Total:</u> \$593,809.00</p>

Strategic Project Grants				
2013 - 2016	Nova Scotia Health Research Foundation (NSHRF) <u>Title:</u> A Pilot Project to Assess the Gut Microbes of Patients in an Assisted Living Facility <u>Program:</u> Discovery / Innovative Grants	<u>Type:</u> Grant	<u>My Role:</u> Principal Investigator	<u>Funding Total:</u> \$15,000.00
2013 - 2015	Nova Scotia Health Research Foundation (NSHRF) <u>Title:</u> Scotia Support Grant <u>Program:</u> Scotia Support Grants	<u>Type:</u> Grant <u>Purpose:</u> Operating	<u>My Role:</u> Principal Investigator	<u>Funding Total:</u> \$48,000.00
2013 - 2014	Mathematics of Information Technology and Complex Systems (MITACS) <u>Title:</u> Comparative Genomics <u>Program:</u> MITACS Accelerate	<u>Type:</u> Grant <u>Purpose:</u> Operating	<u>My Role:</u> Principal Investigator	<u>Funding Total:</u> \$45,000.00
2013 - 2014	Nova Scotia Health Research Foundation (NSHRF) <u>Title:</u> The role of the complement system in post-colitis colonization and recovery from injury <u>Program:</u> Discovery / Innovative Grants	<u>Type:</u> Grant <u>Purpose:</u> Operating	<u>My Role:</u> Co-applicant <u>Principal Applicant:</u> Andrew Stadnyk	<u>Funding Total:</u> \$15,000.00
2013 - 2016	Genome Canada <u>Title:</u> A Federated Bioinformatics Platform for Public Health Microbial Genomics <u>Program:</u> Bioinformatics and Computational Biology	<u>Type:</u> Grant	<u>My Role:</u> Co-investigator	<u>Funding Total:</u> \$1,576,791.00
2013 - 2015	National Research Council Canada (NRC) (Ottawa, ON) <u>Title:</u>	<u>Type:</u> Contract	<u>My Role:</u> Principal Investigator	<u>Funding Total:</u> \$80,000.00

	Comparative Genomics to Identify Genes and Pathways Controlling Reproductive Longevity of Mammals <u>Program:</u> IRAP			
2012 - 2012	Natural Sciences and Engineering Research Council of Canada (NSERC) <u>Title:</u> Machine-learning classification of genomic polymorphism data relating to fertility and reproductive longevity <u>Program:</u> Engage	<u>Type:</u> Grant	<u>My Role:</u> Principal Investigator	<u>Funding Total:</u> \$25,000.00
2012 - 2017	Natural Sciences and Engineering Research Council of Canada (NSERC) <u>Title:</u> Untangling the complex geographic and evolutionary patterns of microbes <u>Program:</u> Discovery Grants	<u>Type:</u> Grant <u>Purpose:</u> Operating	<u>My Role:</u> Principal Investigator	<u>Funding Total:</u> \$165,000.00
2011 - 2014	Genome Canada <u>Title:</u> Biomonitoring 2.0 <u>Program:</u> Large-scale applied research projects	<u>Type:</u> Grant <u>Purpose:</u> Operating	<u>My Role:</u> Co-investigator	<u>Funding Total:</u> \$3,000,000.00
2010 - 2013	Canadian Institutes of Health Research (CIHR) <u>Title:</u> Modeling and Mapping Microbial Diversity and Function with Marker Genes, Genomes and Metagenomes <u>Program:</u> Emerging Team Grant (Human Microbiome)	<u>Type:</u> Grant <u>Purpose:</u> Operating	<u>My Role:</u> Co-investigator	<u>Funding Total:</u> \$623,000.00
2009 - 2012	Genome Canada <u>Title:</u> BEEM: Bioproducts and Enzymes from Environmental Metagenomes <u>Program:</u> COMPETITION IN APPLIED	<u>Type:</u> Grant <u>Purpose:</u> Operating	<u>My Role:</u> Co-investigator	<u>Funding Total:</u> \$5,000,000.00

	GENOMICS RESEARCH IN BIOPRODUCTS OR C			
2008 - 2017	<p>Tula Foundation</p> <p><u>Title:</u> The Dalhousie Centre for Comparative Genomics and Evolutionary Bioinformatics</p> <p><u>Program:</u> N/A</p>	<u>Type:</u> Grant	<u>My Role:</u> Co-investigator	<u>Funding Total:</u> \$3,000,000.00
2007 - 2017	<p>Canada Research Chairs (CRC)</p> <p><u>Title:</u> Canada Research Chair in Bioinformatics</p> <p><u>Program:</u> Tier 2 Canada Research Chairs</p>	<u>Type:</u> Research Chair	<u>My Role:</u> Principal Investigator	<u>Funding Total:</u> \$1,000,000.00
2007 - 2012	<p>Natural Sciences and Engineering Research Council of Canada (NSERC)</p> <p><u>Title:</u> New Computational Methods for Metagenomics</p> <p><u>Program:</u> Discovery Grant</p>	<u>Type:</u> Grant	<u>My Role:</u> Principal Investigator	<u>Funding Total:</u> \$115,000.00
2007 - 2008	<p>Canada Foundation for Innovation (CFI)</p> <p><u>Title:</u> A Canadian platform for advanced comparative genomics</p> <p><u>Program:</u> Leaders Opportunity Fund</p>		<u>My Role:</u> Principal Investigator	<u>Funding Total:</u> \$322,000.00
2007 - 2010	<p>Australian Research Council</p> <p><u>Title:</u> Metagenomics and the genetic basis of ecology and evolution of communities - complex microbial communities in industrial processes as excellent paradigms</p> <p><u>Program:</u> Discovery Project</p>	<u>Type:</u> Grant	<u>My Role:</u> Co-investigator	<u>Funding Total:</u> \$210,000.00
2006 - 2010	<p>Genome Atlantic</p> <p><u>Title:</u></p>	<u>Type:</u> Grant	<u>My Role:</u> Principal Investigator	<u>Funding Total:</u> \$226,000.00

	Computational Analysis of Genomic and Metagenomic Data <u>Program:</u> Startup Funds	<u>Purpose:</u> Establishment		
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PUBLICATIONS:Books Edited

1. Beiko RG, Hsiao W, Parkinson J. (2018). *Microbiome Analysis: Methods and Protocols* (1 , Vol. 1849) (Beiko RG, Hsiao W, Parkinson J, Eds.), United States: Springer.

Refereed Chapters In Books

3. DP Martin, RG Beiko. (2010). Genetic Recombination and Bacterial Population Structure. In Robinson DA, Falush D, Feil E (Eds.), *Bacterial Population Genetics in Infectious Disease* (pp. 61-85). United States: Wiley.
2. Beiko RG, Ragan MA. (2009). Untangling hybrid phylogenetic signals - HGT and artifacts of phylogenetic reconstruction. In Gogarten MB, Gogarten JP, Olendzenski L (Eds.), *Horizontal Gene Transfer: Genomes in Flux* (pp. 241-256). United States: Humana Press.
1. Beiko RG, Ragan MA. (2008). Detecting lateral genetic transfer : a phylogenetic approach. In Keith JM (Ed.), *Bioinformatics* (pp. 457-469). United States: Humana Press.

Non-Refereed Chapters In Books

1. Meehan CJ, Langille MGI, Beiko RG. (2014). Frailty and the Microbiome. In Theou O, Rockwood K (Ed.), *Frailty in ageing: biological, clinical and social implications* (pp. 54-65). United Kingdom: Karger.

Refereed Journal Articles

68. Stanley RR, DiBacco C, Lowen B, Beiko RG, Jeffery NW, Van Wyngaarden M, Bentzen P, Brickman D, Benestan L, Bernatchez L, Johnson C. (2018). A climate-associated multispecies cryptic cline in the northwest Atlantic. *Science Advances*, 3, eaaq0929.
67. Nadukkalam Ravindran P, Bentzen P, Bradbury I, Beiko RG. (2018). Computational filtering of paralogous sequences from RAD-seq data. *Molecular Ecology Resources*, 8, 7002-7013.
66. van Wyngaarden M, Snelgrove PVR, DiBacco C, Hamilton LC, Rodriguez-Ezpeleta, Zhan L, Beiko RG, Bradbury IR. (2018). Oceanographic variation influences spatial genomic structure in the sea scallop, *Placopecten magellanicus*. *Ecology and Evolution*, 8, 2824-2841.
65. Alexander Keddy and Robert G. Beiko. (2018). Investigating biogeographic patterns using point-based cartograms and the Geographically Coupled Phylogenetic Distance. *Global Ecology and Biogeography*, 27, 330-338.
64. 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, 2255-2265. (Accepted)
63. Sylvester E, Beiko RG, Bentzen P, Paterson I; Horne J, Watson B, Lehnert S, Duffy S, Clément M, Robertson M, Bradbury I. (2018). Environmental extremes drive population structure at the northern range limit of Atlantic salmon in North America. *Molecular Ecology*, 27, 4026-4040. (Accepted)
62. Houfani AA, Větrovský T, Navarrete OU, Štursová M, Tláskal V, Beiko RG, Boucherba N, Baldrian P, Benallaoua S, Jorquera MA. (2018). Cellulase–hemicellulase activities and bacterial community composition of different soils from Algerian ecosystems. *Microbial Ecology*, tbd, epub. (Accepted)

61. Michael W. Hall, Robin R. Rohwer, Jonathan Perrie, Katherine D. McMahon, and Robert G. Beiko. (2017). Ananke: Ecological dynamics of microbial communities revealed by temporal clustering. *PeerJ*, 5, e3812.
60. 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*, 11, 153-165.
59. 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*, 7, 2513–2524.
58. 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*, 3, e000116.
57. 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, 2.
56. 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.
55. 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.
54. 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.
53. 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.
52. Ning Jie, Beiko Robert G. (2015). Phylogenetic approaches to microbial community classification. *Microbiome*, 3, 47.
51. Beiko Robert G. (2015). Microbial malaise: how can we classify the microbiome?. *Trends in microbiology*, 23(11), 671-9.
50. 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.
49. Wong Dennis H-J, Beiko Robert G. (2015). Transfer of energy pathway genes in microbial enhanced biological phosphorus removal communities. *BMC genomics*, 16, 526.
48. 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.
47. 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.
46. 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.

45. Whidden Christopher, Zeh Norbert, Beiko Robert G. (2014). Supertrees Based on the Subtree Prune-and-Regraft Distance. *Systematic biology*, 63(4), 566-81.
44. 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.
43. 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.
42. Langille Morgan G I, Zaneveld Jesse, Caporaso J Gregory, McDonald Daniel, Knights Dan, Reyes Joshua A, Clemente Jose C, Burkepile 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.
41. 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.
40. Porter MS, Beiko RG. (2013). SPANNER: taxonomic assignment of sequences using pyramid matching of similarity profiles. *Bioinformatics (Oxford, England)*, 29(15), 1858-64.
39. 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.
38. Whidden C, Beiko RG, Zeh N. (2013). Fixed-Parameter Algorithms for Maximum Agreement Forests. *SIAM Journal on Computing*, 42(4), 1431-1466.
37. Curtis BA et al. (26th of 72 authors). (2012). Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. *Nature*, 492(7427), 59-65.
36. 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.
35. 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.
34. 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.
32. 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.
31. 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.
30. 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.
29. 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.
28. 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.
27. Beiko RG. (2011). Telling the whole story in a 10, 000-genome world. *Biology direct*, 6, 34.
26. Holloway Catherine, Beiko Robert G. (2010). Assembling networks of microbial genomes using linear programming. *BMC evolutionary biology*, 10, 360.

25. Slater F R, Johnson C R, Blackall L L, Beiko R G, Bond P L. (2010). 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.
24. Parks Donovan H, Beiko Robert G. (2010). Identifying biologically relevant differences between metagenomic communities. *Bioinformatics (Oxford, England)*, 26(6), 715-21.
23. Perry Scott C, Beiko Robert G. (2010). Distinguishing microbial genome fragments based on their composition: evolutionary and comparative genomic perspectives. *Genome biology and evolution*, 2, 117-31.
22. MacDonald NJ, Beiko RG. (2010). Efficient learning of microbial genotype-phenotype association rules. *Bioinformatics (Oxford, England)*, 26(15), 1834-40.
21. Chan Cheong Xin, Beiko Robert G, Darling Aaron E, Ragan Mark A. (2009). Lateral transfer of genes and gene fragments in prokaryotes. *Genome biology and evolution*, 1, 429-38.
20. Bapteste 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. (2009). Prokaryotic evolution and the tree of life are two different things. *Biology direct*, 4, 34.
19. Ragan Mark A, Beiko Robert G. (2009). Lateral genetic transfer: open issues. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, 364(1527), 2241-51.
18. Parks Donovan H, Porter Michael, Churcher Sylvia, Wang Suwen, Blouin Christian, Whalley Jacqueline, Brooks Stephen, Beiko Robert G. (2009). GenGIS: A geospatial information system for genomic data. *Genome research*, 19(10), 1896-904.
17. Chan Cheong Xin, Darling Aaron E, Beiko Robert G, Ragan Mark A. (2009). Are protein domains modules of lateral genetic transfer?. *PloS one*, 4(2), e4524.
16. Whalley Jacqueline, Brooks Stephen, Beiko Robert G. (2009). Radié: visualizing taxon properties and parsimonious mappings using a radial phylogenetic tree. *Bioinformatics (Oxford, England)*, 25(5), 672-3.
15. Beiko Robert G, Doolittle W Ford, Charlebois Robert L. (2008). The impact of reticulate evolution on genome phylogeny. *Systematic biology*, 57(6), 844-56.
14. Davies Mark R, McMillan David J, Beiko Robert G, Barroso Vanessa, Geffers Robert, Sriprakash Kadaba S, Chhatwal Gursharan S. (2007). 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.
13. Beiko Robert G, Charlebois Robert L. (2007). A simulation test bed for hypotheses of genome evolution. *Bioinformatics (Oxford, England)*, 23(7), 825-31.
12. Chan Cheong Xin, Beiko Robert G, Ragan Mark A. (2006). Detecting recombination in evolving nucleotide sequences. *BMC bioinformatics*, 7, 412.
11. McMillan David J, Beiko R G, Geffers R, Buer Jan, Schouls L M, Vlamincx B J M, Wannet W J B, Sriprakash K S, Chhatwal G S. (2006). 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.
10. Beiko Robert G, Keith Jonathan M, Harlow Timothy J, Ragan Mark A. (2006). Searching for convergence in phylogenetic Markov chain Monte Carlo. *Systematic biology*, 55(4), 553-65.
9. Beiko Robert G, Hamilton Nicholas. (2006). Phylogenetic identification of lateral genetic transfer events. *BMC evolutionary biology*, 6, 15.
8. Ragan Mark A, Harlow Timothy J, Beiko Robert G. (2005). Do different surrogate methods detect lateral genetic transfer events of different relative ages?. *Trends in microbiology*, 14(1), 4-8.
7. Beiko Robert G, Harlow Timothy J, Ragan Mark A. (2005). Highways of gene sharing in prokaryotes. *Proceedings of the National Academy of Sciences of the United States of America*, 102(40), 14332-7.

6. Beiko Robert G, Chan Cheong Xin, Ragan Mark A. (2005). A word-oriented approach to alignment validation. *Bioinformatics (Oxford, England)*, 21(10), 2230-9.
5. Beiko Robert G, Charlebois Robert L. (2005). GANN: genetic algorithm neural networks for the detection of conserved combinations of features in DNA. *BMC bioinformatics*, 6, 36.
4. Charlebois Robert L, Clarke G D Paul, Beiko Robert G, St Jean Andrew. (2003). Characterization of species-specific genes using a flexible, web-based querying system. *FEMS microbiology letters*, 225(2), 213-20.
3. Charlebois Robert L, Beiko Robert G, Ragan Mark A. (2003). Microbial phylogenomics: Branching out. *Nature*, 421(6920), 217.
2. Martin C Cristofre, Tsang Cemaine H, Beiko Robert G, Krone Patrick H. (2002). Expression and genomic organization of the zebrafish chaperonin gene complex. *Genome / National Research Council Canada = Génome / Conseil national de recherches Canada*, 45(5), 804-11.
1. Clarke G D Paul, Beiko Robert G, Ragan Mark A, Charlebois Robert L. (2002). 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.

Non-Refereed Journal Articles

2. 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.
1. Langille MG, Meehan CJ, Beiko RG. (2012). Human microbiome: a genetic bazaar for microbes? *Current Biology*, 22(1), R20-R22.

Conference Publications

6. Norbert Zeh, Chris Whidden. (2010). Fast FPT Algorithms for Computing Rooted Agreement Forests: Theory and Experiments. In *Symposium on Experimental Algorithms*.
5. Parks DH, Beiko RG. (2009). Quantitative Visualizations of Hierarchically Organized Data in a Geographic Context. In *Geoinformatics*.
4. Beiko RG, Whalley J, Wang S, Clair H, Smolyn G, Churcher S, Porter M, Blouin C, Brooks S. (2008). Spatial Analysis and Visualization of Genetic Biodiversity. In *Free and Open Source Software for Geoinformatics 2008*.
3. Chan CX, Beiko RG, Ragan MA. (2007). A two-phase approach for detecting recombination in nucleotide sequences. In *South African Bioinformatics Workshop*.
2. Wang S, Beiko RG, Brooks S. (2007). Collapsible 3D Terrains for GIS Visualization. In *Geovisualization*.
1. Chan CX, Beiko RG, Ragan MA. (2007). Large-scale detection of recombination in nucleotide sequences. In *Proceedings of the International Conference on Mathematical Biology*.

PRESENTATIONS:

51. (2018). "Evolutionary and Temporal Views of Microbial Diversity". Canadian Society of Microbiologists annual meeting, Winnipeg, Canada.
50. (2018). "Antimicrobial resistance and the human microbiome". Invited presentation, Lisbon, Portugal.
49. (2018). "Layers of diversity in microbial communities". The Reef Microbiome Workshop, Barbados.
48. (2017). "Microbial Taxonomy: Abandon All Hope?". The Future of Systematics in Data- Centric Biology, Woods Hole, United States.
47. (2017). "Predicting functional classes of genes from metagenomic data". 2017 International Workshop on Environmental Genomics, St. John's, Canada.
46. (2017). "Phylogeographic Analysis". Canadian Bioinformatics Workshop in Infectious Disease Genomic Epidemiology, Vancouver, Canada. Retrieved from <https://bioinformatics.ca/workshops/2017/infectious-disease-genomic-epidemiology-2017>

Workshop presentation and practical session

45. (2017). "The aging and frail microbiome: diversity, time, and function". McMaster University - invited presentation, Hamilton, Canada.
44. (2017). "Identifying key temporal and taxonomic bacterial clusters in the aging microbiome". Drexel University invited presentation, Philadelphia, United States.
43. (2016). "Monitoring the microbiome in an assisted-care facility". IRIDA Annual General Meeting / public lecture, Vancouver, Canada.
42. (2016). "A Coevolution-Based Approach to the Identification of Genes with Similar Phylogenetic Distributions". Vancouver Bioinformatics Users' Group (VanBUG), Vancouver, Canada.
41. (2016). "Common assumptions and pitfalls of microbiome analysis". Advancing Microbiome Research Symposium: Microbiome & Disease, Potomac, MD, United States.
40. (2016). "Lateral gene transfer: how many stories can a network tell?". EVOLUNET: PUBLIC LECTURES OF THE SUMMER SCHOOL ON NETWORKS, Roscoff, France.
39. (2016). "What can the microbiome tell us about frailty?". Northwood Research Day 2016, Dartmouth, Canada.
38. 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/glbioccb2016-program/workshops>
37. (2016). "Metagenomics". Great Lakes Bioinformatics and the Canadian Computational Biology Conference 2016, Toronto, Canada. Retrieved from <https://www.iscb.org/glbioccb2016-program/glbioccb2016-full-agenda>
36. (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
35. (2016). "Phylogeography with GenGIS". VizBi 2016, Heidelberg, Germany. Retrieved from <https://vizbi.org/2016>
34. (2015). "Soil, lateral gene transfer, and hybrid genomes". Argonne National Laboratory 7th annual soil metagenomics meeting, Chicago, United States.
33. (2015). "The microbiome and its impact on aging and frailty". Gerontological Society of America annual meeting, Orlando, United States.
32. (2015). "Upwardly mobile genes". Invited seminar at Canadian National Microbiology Laboratory, Winnipeg, Canada.
31. (2015). "Introduction to Metagenomics". Canadian Bioinformatics Workshop - Analysis of Metagenomic Data, Halifax, Canada. Retrieved from <https://bioinformatics.ca/workshops/2015/analysis-metagenomic-data-2015>
30. (2014). "Gene sharing in microbes: good for the individual, good for the community?". University of Waterloo Department of Biology seminar, Waterloo, Canada.
29. (2014). "Grand theft operon: lateral city". IGERT symposium on Deep Genomics, Tucson, United States.
28. (2014). "Biogeography of microorganisms. No borders. No limits. No fear". Understanding biodiversity dynamics using diverse data sources, Canberra, Australia.
27. (2014). "Microbiome analysis". African perinatal probiotic study meeting, Athi River, Kenya.
26. (2014). "When trees can't agree". Canadian Mathematical Society annual meeting, Hamilton, Canada.
25. (2014). "Modeling and mapping microbial diversity and function with marker genes, genomes and metagenomes". Canadian Microbiome Workshop 2014: from Research to Applications, Vancouver, Canada.
24. (2014). "Computing the Microbial World". Canadian High-Performance Computing Conference, Halifax, Canada.
23. (2014). "The Human Microbiome(and friends)". Genome Atlantic Human Genetics and Genomics Seminar series, Halifax, Canada.

22. (2013). "Visualizing species distributions and phylogeography using GenGIS". International Biogeography Society Special Meeting, Montreal, Canada.
21. (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.
20. (2013). "Biology's Big Data Revolution". Public lecture: Faculty of Computer Science, Halifax, Canada.
19. (2013). "Classifying DNA". Dalhousie In-House Computer Science Conference, Halifax, Canada.
18. (2012). "Genetic monitoring of H1N1 during the 2009 outbreak". Critical Infrastructure Protection Initiative, Halifax, Canada.
17. (2012). "GenGIS 2: New approaches to understand the geography of our microbial world". Canadian Society of Microbiologists annual meeting, Vancouver, Canada.
16. (2012). "GenGIS: a platform for visualization and analysis of genetic biodiversity data". Quebec biomonitoring meeting, Montreal, Canada.
15. (2012). "Applying reference Condition Analysis using GenGIS". Canadian Aquatic Biomonitoring Network annual meeting, Fredericton, Canada.
14. (2012). "Biomonitoring 2.0: New approaches to biodiversity monitoring". iEvoBio 2012, Ottawa, Canada.
13. (2012). "Major initiatives in microbiomics: industrial processes, environmental monitoring, human health". CAU-DAL joint workshops, Kiel, Germany.
12. (2012). "Microbes and communities: steps E, M, and V". Canadian Institute for Advanced Research (Integrated Microbial Biodiversity program) annual meeting 2012, Quebec, Canada.
11. (2012). "A network of everything??". Society for Molecular Biology and Evolution annual meeting, Dublin, Ireland.
10. (2011). "Who is doing what, and to whom: taxonomic assignments and network analysis in metagenome studies". SYMBIOTA Workshop, Toronto, Canada.
9. (2011). "Molecular and Functional Diagnostics". CIHR Microbiomics Grant workshop, Halifax, Canada.
8. (2011). "GenGIS: Geospatial analysis and visualization of biodiversity". GIS Day, Halifax, Canada.
7. (2011). "Modeling and mapping microbial diversity and function with marker genes, genomes and metagenomes, or MMMDFMGGM". CIHR Emerging Microbiome Teams, Vancouver, Canada.
6. (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.
5. (2011). "Questions at the interface of evolution, ecology, space and time". Society for Molecular Biology and Evolution meeting, Kyoto, Japan.
4. (2011). "GenGIS: A 3D geospatial environment for the analysis of genetic data". iPlant collaborative workshop, Tucson, United States.
3. (2010). "It's a Phylogenetic Network and Everyone's Invited!!". Questioning the Tree of Life meeting, London, United Kingdom.
2. (2010). "Geographic and temporal analysis of genomes and metagenomes". Canadian Institute for Advanced Research BigDATA meeting, Vancouver, Canada.
1. (2009). "GenGIS: Geospatial analysis and visualization of microbial diversity". Canadian Institute for Advanced Research (Integrated Microbial Biodiversity program), Annual Meeting 2009, Asilomar, United States.

Book Reviews

1. (2014). Bioinformatics: Hypothesis Free—Or Hypotheses Freed?.