

# Joseph P. Bielawski

Department of Biology (75%)

Department of Mathematics & Statistics (25%)

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## PERSONAL INFORMATION

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### EDUCATION AND TRAINING

B.Sc. (Marine Science / Biology)	Southampton College, USA	1985–1989
M.A. (Biology)	Hofstra University, USA	1990–1994
Ph.D. (Genetics)	Texas A&M University, USA	1994–1999
Post-Doctoral Research Fellow	Department of Biology, UCL, UK	1999–2003

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### POSITIONS AND APPOINTMENTS

Assistant Professor	Department of Biology (75%) Dalhousie University	2003 – 2008
Assistant Professor	Department of Mathematics & Statistics (25%) Dalhousie University	2003 – 2008
Associate Professor	Department of Biology (75%) Dalhousie University	2008 – 2016
Associate Professor	Department of Mathematics & Statistics (25%) Dalhousie University	2008 – 2016
Professor	Department of Biology (75%) Dalhousie University	2017
Professor	Department of Mathematics & Statistics (25%) Dalhousie University	2017

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### HONOURS AND RECOGNITIONS

Genome Atlantic Research Chair Department of Biology, Dalhousie University	2003 – 2006
Research highlighted in the “all-stars of science” section of annual report of the Canadian Institute for Advanced Research (CIFAR)	2006
Canadian Institute of Advanced Research (CIAR) Membership in Program in Evolutionary Biology	2006 – 2008
Killam prize Awarded for exceptional research and contributions to scientific knowledge	2008

Scholar, Centre for Genomics & Evolutionary Bioinformatics Dalhousie University	2009 – 2016
Co-director, North American Workshop on Molecular Evolution Marine Biological laboratory (MBL), MA, USA	2016 – 2017

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PROFESSIONAL ACTIVITIES AND SERVICE

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**DEPARTMENT**

Committee of the whole, Department of Biology	2003 – 2018
Curriculum planning group for (A) Ecology and Evolution stream, and (B) Cellular and Molecular Biology stream, Department of Biology	2003 – 2004
Honours thesis referee and Annual Cameron Conference judge, Department of Biology	2004 – 2018
Graduate thesis committees, reader Department of Biology and Department of Mathematics & Statistics	2004 – 2018
IT advisory group, Department of Biology	2004 – 2007
Curriculum committee, Department of Biology	2005 – 2011
Web-site working-group, Department of Mathematics & Statistics	2005
Search committee for a developmental geneticist, Department of Biology	2006
Graduate program module coordinator, Department of Biology	2007 – 2018
Graduate directorate, Department of Biology	2007 – 2018
Chair, IT committee, Department of Biology	2007 – 2018
Search committee for CRC Research chair in Proteomics Department of Biology	2013
Search committee for CRC Research chair in Marine Quantitative Ecology, Department of Biology	2016
Acting Chair, Department of Biology (6 months: Jan-June)	2017
Chair advisor council	2017-present

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**UNIVERSITY**

Extra-departmental thesis committees, examiner:	2003 – 2016
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*Dept. of Biochemistry & Molecular Biology, Dept. of Pharmacology, Interdisciplinary Graduate Program in Computational Biology & Bioinformatics, Interdisciplinary PhD program, and Faculty of Computer Science.*

Working group for development of a university-level M.S. degree program in Computational Biology & Bioinformatics	2003 – 2006
Executive Committee, Interdisciplinary Graduate Program in Computational Biology & Bioinformatics	2006 – 2018
Admission Committee, Interdisciplinary Graduate Program in Computational Biology & Bioinformatics	2006 – 2018

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## **EXTERNAL**

Editorial board, <i>Systematic Biology</i>	2001 – 2005
Grant application referee (8 countries) <i>ISF, Israel; NKFIH, Hungary; NSERC Canada, NRF South Africa; NSF, USA; SNF Switzerland; Wellcome Trust, UK.</i>	2003 – 2018
Manuscript peer reviewer (20 journals) <i>Bioinformatics, BMC Bioinformatics, BMC Evolutionary Biology, Briefings and Bioinformatics, Clinical Infectious Diseases, Copeia, Evolution, Genetics, Genome Biology &amp; Evolution, Italian journal of Zoology, Heredity, Journal of Fish Biology, Journal of Molecular Evolution, Molecular Biology and Evolution, Nature, PLoS Computational Biology, PLoS Genetics, PLoS One, PNAS and Systematic Biology.</i>	2003 – 2018
Organizing Committee, Annual meeting of the Society for Molecular Biology and Evolution	2007
Organizer and chair, special symposium on "The Principles and Practice of Phylogenomic Inference". Joint with Canadian Genetics Society and the Canadian Society for Ecology and Evolution annual meetings	2009
Organizing Committee, 52 <sup>nd</sup> annual meeting of the Canadian Genetics Society, and the 4 <sup>th</sup> annual meeting of the Canadian Society for Ecology and Evolution	2009
Steering committee, North American Workshop on Molecular Evolution Marine Biological laboratory (MBL), MA, USA	2010 – 2018
Advisory board, European Workshop on Molecular Evolution	2011 – 2013
Editorial Board, <i>Frontiers in Ecology and Evolution</i>	2013 – 2018
Editor, <i>BMC Evolutionary Biology</i>	2014 – 2018
Co-director, North American Workshop on Molecular Evolution Marine Biological laboratory (MBL), MA, USA	2016 – 2018

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## SCHOLARLY ACTIVITIES

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### PUBLICATION METRICS

Total publications: 80<sup>1</sup>  
Total citations: 4811 (citations since 2013: 2059)  
h-index: 33  
i10-index: 48  
Top 5 citation counts: 1396, 557, 441, 351, 326

<sup>1</sup> Total publication count includes 66 articles and book chapters, and 14 competitive clinical conference abstracts.

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### PUBLICATIONS

66. Jones C.T., Susko E., Bielawski J.P., 2018. **Looking for Darwin in genomic sequences: validity and success depends on the relationship between model and data.** In *Evolutionary Genomics: Statistical and Computational Methods*. Maria Anisimova (ed.) 2<sup>nd</sup> edition (*In Press*), Human press.
65. Youssef, N., Budd, A., and Bielawski, J.P., 2018. **Introduction to Genome Biology and Diversity.** In *Evolutionary Genomics: Statistical and Computational Methods*. Maria Anisimova (ed.) 2<sup>nd</sup> edition (*In Press*), Human press.
64. Dunn, K.A., Andrews, K., Bashwih, R.O. and Bielawski, J.P., 2018. **Bayesian Inference of Microbial Community Structure from Metagenomic data using BioMiCo.** In *Mircrobiome Analysis: Methods and Protocols*, Beiko, R., Hsiao, Willina, & Parkinson, J. (eds), (*In Press*), Humana Press, Totowa, NJ.
63. Jones C.T., Youssef N., Susko E., Bielawski J.P., 2018. **Phenomenological Load on Model Parameters Can Lead to False Biological Conclusions.** *Mol Biol Evol.* 35(6):1473-1488.
62. Douglas, G.M., Hansen, R., Jones, C.M.A., Dunn, K.A., Comeau, A.M., Bielawski, J.P., Tayler, R., El-Omar, E.M., Russell, R.K., Hold, G.L., Langille, M.G.I., Van Limbergen, J., 2017. **Multi-omics differentially classify disease state and treatment outcome in pediatric Crohn's disease.** *Microbiome.* 2018, 6(1):13.
61. Jones, C., Youssef, N., Susko, E. and Bielawski, J., 2017. **Shifting balance on a static mutation-selection landscape: a novel scenario of positive selection.** *Molecular Biology and Evolution*, 34(2):391-407.
60. Dunn, K.A., Moore-Connors, J., MacIntyre, B., Stadnyk, A., Thomas, N.A., Noble, A., Mahdi, G., Rashid, M. Otle, A.R., Bielawski, J.P. and Van Limbergen, J., 2016. **The gut microbiome of pediatric Crohn's disease patients differs from healthy controls in genes that can influence the balance between a healthy and dysregulated immune response.** *Inflammatory Bowel Diseases*, 2(11):2607-2618.
59. Mingrone, J., Susko, E. and Bielawski, J., 2016. **Smoothed bootstrap aggregation for assessing selection pressure at amino acid sites.** *Molecular Biology and Evolution*, 33(11):2976-2989.

58. Dunn, K.A., Moore-Connors, J., MacIntyre, B., Stadnyk, A., Thomas, N.A., Noble, A., Mahdi, G., Rashid, M. Otley, A.R., Bielawski, J.P. and Van Limbergen, J., 2016. **Early changes in microbial community structure are associated with sustained remission following nutritional treatment of Pediatric Crohn's Disease.** *Inflammatory Bowel Diseases*, 22(12):2853-2862.
57. Bielawski, J.P., Baker, J.L. and Mingrone, J., 2016. **Inference of episodic changes in natural selection acting on protein coding sequences via CODEML.** *Current Protocols in Bioinformatics*, pp.6-15.
56. Moore-Connors, J., Dunn, K.A., Bielawski, J.P. and Van Limbergen, J., 2016. **Novel strategies for applied metagenomics.** *Inflammatory bowel diseases*, 22(3), pp.709-718.
55. Baker, J.L., Dunn, K.A., Mingrone, J., Wood, B.A., Karpinski, B.A., Sherwood, C.C., Wildman, D.E., Maynard, T.M. and Bielawski, J.P., 2016. **Functional divergence of the nuclear receptor NR2C1 as a modulator of pluripotentiality during Hominid evolution.** *Genetics*, 203(2), pp.905-922.
54. Bielawski, J.P., 2016. **Evolutionary models.** In: R. Kliman, ed. *Encyclopedia of Evolutionary Biology*. Elsevier. Volume 1, pp. 61-70.
53. Bielawski, J.P. and Jones., C.F., 2016. **Adaptive evolution: detection methods.** In: R. Kliman, ed. *Encyclopedia of Evolutionary Biology*. Elsevier. Volume 1, pp. 16-25.
52. Shafiei, M., Dunn, K.A., Boon, E., MacDonald, S.M., Walsh, D.A., Gu, H. and Bielawski, J.P., 2015. **BioMiCo: a supervised Bayesian model for inference of microbial community structure.** *Microbiome*, 3(1), p.1.
51. El-Swais, H., Dunn, K.A., Bielawski, J.P., Li, W.K. and Walsh, D.A., 2015. **Seasonal assemblages and short-lived blooms in coastal north-west Atlantic Ocean bacterioplankton.** *Environmental Microbiology*, 17(10), pp.3642-3661.
50. Garvin, M.R., Bielawski, J.P., Sazanov, L.A. and Gharrett, A.J., 2015. **Review and meta-analysis of natural selection in mitochondrial complex I in metazoans.** *Journal of Zoological Systematics and Evolutionary Research*, 53(1), pp.1-17.
49. Shafiei, M., Dunn, K.A., Chipman, H., Gu, H. and Bielawski, J.P., 2014. **BiomeNet: A Bayesian model for inference of metabolic divergence among microbial communities.** *PLoS Computational Biology*, 10(11), p.e1003918.
48. Yoder, A.D., Chan, L.M., dos Reis, M., Larsen, P.A., Campbell, C.R., Rasoloarison, R., Barrett, M., Roos, C., Kappeler, P., Bielawski, J. and Yang, Z., 2014. **Molecular evolutionary characterization of a V1R subfamily unique to strepsirrhine primates.** *Genome Biology and Evolution*, 6(1), pp.213-227.
47. Garvin, M.R., Bielawski, J.P., Sazanov, L.A. and A.J. Gharrett, 2014. **Positive Selection and Its Functional Implications in Metazoan Mitochondrial Genomes.** *Journal of Zoological Systematics and Evolutionary Research* 52(3). doi: 10.1111/jzs.12079
46. Bay R.A. and Bielawski J.P., 2013 **Inference of functional divergence among proteins when the evolutionary process is non-stationary.** *Journal of Molecular Evolution* 76(4):205-215.
45. Dunn K.A., Jiang W., Field C. and Bielawski J.P., 2013. **Improving evolutionary models for mitochondrial protein data with site-class specific amino acid exchangeability matrices.** *PLoS One*. 2013;8(1):e55816.

44. Bielawski J.P., 2013. **Detecting the signatures of adaptive evolution in protein-coding genes.** In: *Current Protocols in Bioinformatics*, John Wiley & Sons, Chapter 19:Unit 19.1.
43. Bay, R.A. and J.P. Bielawski, 2012. **Recombination Detection Under Evolutionary Scenarios Relevant to Functional Divergence.** *Journal of Molecular Evolution.* 73(5-6):273-286.
42. Garvin, M.R., J.P. Bielawski and A.J. Gharrett, 2011. **Positive Darwinian selection in the piston that powers proton pumps in complex I of the mitochondria of Pacific salmon.** *PLoS One.* 2011;6(9):e24127.
41. Bielawski, J.P., H. Gu, and K. A. Dunn. 2011. **Likelihood Based Clustering (LiBaC) for Codon Models.** In: *Codon Evolution: Mechanisms and Models*, Oxford University Press.
40. Dunn, K.A., J.P. Bielawski, T.J. Ward, C. Urquhart and H. Gu. 2009. **Reconciling ecological and genomic divergence among lineages of *Listeria*: the extended mosaic genome concept.** *Molecular Biology and Evolution* 68(5): 506-515.
39. Morine, M., H. Gu, R. Meyers, and J.P. Bielawski. 2009. **Niche breadth influences the functional cartography of metabolic networks.** *Journal of Molecular Evolution.* 68:506-515.
38. Ward, T.J., T.F. Ducey, T. Usgaard, K.A. Dunn, and J.P. Bielawski. 2008. **Multilocus genotyping assays for SNP-based subtyping of *Listeria monocytogenes*.** *Applied Environmental Microbiology*, 74: 7629-7642.
37. Bao, L., H. Gu, K.A. Dunn, and J.P. Bielawski. 2008. **Likelihood Based Clustering (LiBaC) for codon models, a method for grouping sites according to similarities in the underlying process of molecular evolution.** *Molecular Biology and Evolution* 25:1995-2007.
36. Sullivan, M.B., M.C. Coleman, V. Quinlivan, J.E. Rosenkrantz, A.S. DeFrancesco, G. Tan, R. Fu, J.A. Lee, J.B. Waterbury, J.P. Bielawski, S.W. Chisholm. 2008. **Portal protein diversity and phage ecology.** *Applied Environmental Microbiology*: 10:2810-2823.
35. Anisimova, M., J.P. Bielawski, K.A. Dunn, and Z. Yang. 2007. **Phylogenomic analysis of natural selection pressure in *Streptococcus*.** *BMC Evolutionary Biology*, 7:e154.
34. Bao, L., H. Gu, K.A. Dunn, and J.P. Bielawski. 2007. **Methods for selecting fixed-effect models for heterogeneous codon evolution, with comments on their application to gene and genome data.** *BMC Evolutionary Biology*, 7 Suppl 1:S5.
33. Aguileta, G., J.P. Bielawski, and Z. Yang. 2006a. **Rate variation and divergence dates among vertebrate  $\beta$ -globin genes.** *Gene*, 380:21-29.
32. Aguileta, G., J.P. Bielawski, and Z. Yang. 2006b. **Proposed standard nomenclature for the  $\beta$ -globin gene family.** *Genes and Genetic Systems*, 81:367-371.
31. Aris-Brosou, S. and J.P. Bielawski. 2006. **Large-scale analysis of synonymous substitution rates can be sensitive to assumptions about the process of mutation.** *Gene*, 378:58-64.
30. Field, S.F., M.Y. Bulina, I.V. Kelmanson, J.P. Bielawski, and M.V. Matz. 2006. **Adaptive evolution of color diversity and a putative binding site in fluorescent proteins from reef-building corals.** *Journal of Molecular Evolution*, 63:332-339.

29. Popescu, C.E., T. Borza, J.P. Bielawski, and R.W. Lee. 2006. **Synonymous and nonsynonymous substitution rate variation among nuclear genes in green algae: *Chlamydomonas reinhardtii* and *C. incerta*.** *Genetics*, 172:1567-1576.
28. Sullivan, M.B, D. Lindell, J.A. Lee, L.R. Thompson, J.P. Bielawski, and S.W. Chisholm. 2006. **Prevalence and evolution of core photosystem II genes in marine cyanobacterial viruses and their hosts.** *PLoS Biology*, 4:e234.
27. Bielawski, J.P. and Z. Yang. 2005. **Likelihood methods for detecting adaptive evolution.** In: *Statistical methods in Molecular Evolution*, Springer Verlag Series in Statistics in Health and Medicine. New York, New York.
26. Shi P., J.P. Bielawski, H. Yang, and Zhang Y.P. 2005. **Adaptive diversification of vomeronasal receptor 1 genes in rodents.** *Journal of Molecular Evolution*, 60:566-576.
25. Zeidner G., J.P. Bielawski., M. Shmoish, D.J. Scanlan, G. Sabehi, and O. Béjà. 2005. **Potential photosynthesis gene recombination between *Prochlorococcus* and *Synechococcus* via viral intermediates.** *Environmental Microbiology*, 10:1505-1513.
24. Aguilera G., J.P. Bielawski, and Z. Yang. 2004. **Gene conversion and functional divergence in the  $\beta$ -globin gene family.** *Journal of Molecular Evolution*, 59:177-189.
23. Bielawski J.P. and Z. Yang. 2004. **A maximum likelihood method for detecting functional divergence at individual codon sites, with application to gene family evolution.** *Journal of Molecular Evolution*, 59:121-132.
22. Bielawski J.P., K.A. Dunn, G. Sabehi, and O. Béjà. 2004. **Darwinian adaptation of proteorhodopsin to different light intensities in the marine environment.** *Proceedings of the National Academy of Sciences, USA*, 101:14824-14829.
21. Munad, L., J.P. Bielawski, R. Matyasek, A. Kovarik, R.A. Nichols, A.R. Leitch, and C.P. Lichtenstein. 2004. **The origin and evolution of geminivirus-related DNA sequences in *Nicotiana*.** *Heredity*, 92:352-358.
20. Bielawski, J.P. and Z. Yang. 2003a. **Maximum likelihood methods for detecting adaptive evolution in gene families.** In: *Gene and Genome Duplications and the Evolution of Novel Gene Functions*. A. Meyer and Y. Van De Peer (eds). Pp. 201-212.
19. Bielawski, J.P. and Z. Yang. 2003b. **Maximum likelihood methods for detecting adaptive evolution after gene duplication.** *Journal of Structural and Functional Genomics*, 3:201-212.
18. Sabehi, G., M. Ramon, J.P. Bielawski, M. Rosenber, E. F. Delong, and O. Béjà. 2003. **Novel proteorhodopsin variants from the Mediterranean and Red Seas.** *Environmental Microbiology*, 5:842-849.
17. Yang, W., J.P. Bielawski, and Z. Yang. 2003. **Widespread adaptive evolution in the human immunodeficiency virus type-1 genome.** *Journal of Molecular Evolution*, 57:212-221.
16. Anisimova, M., J.P. Bielawski, and Z. Yang. 2002. **Evaluation of the Bayesian approach to detecting codon sites under positive Darwinian selection.** *Molecular Biology and Evolution*, 19:950-958.
15. Bielawski, J.P. 2002. **Phylogenetic inference: an overview.** In: *Oxford Encyclopaedia of Evolution*. M. Pagel (eds) Oxford University Press, Oxford. Pp. 891-895.

14. Bielawski, J.P. and J.R Gold. 2002. **Mutation patterns of mitochondrial H- and L-strand DNA in closely related cyprinid fishes.** *Genetics*, 161:1589-1597.
13. Bielawski, J.P., A.C. Brault, and J.R Gold. 2002. **Phylogenetic relationships within genus *Pimephales* (Cyprinidae: Teleostei).** *Journal of Fish Biology*, 61: 293-297.
12. Ward, T.J., J.P. Bielawski, H.C. Corby-Kistler, E. Sullivan, and K. O'Donnell. 2002. **Ancient polymorphism and adaptive evolution in the trichothecene gene cluster of phytopathogenic *Fusarium*.** *Proceedings of the National Academy of Sciences, USA*, 99:9278-9283.
11. Anisimova, M., J.P. Bielawski, and Z. Yang. 2001. **The accuracy and power of the likelihood ratio test to detect adaptive molecular evolution.** *Molecular Biology and Evolution*, 18:1585-1592.
10. Bielawski, J.P. and J.R. Gold. 2001. **Phylogenetic relationships of cyprinid fishes in subgenus *Notropis* as inferred from nucleotide sequences of the mitochondrially encoded cytochrome b gene.** *Copeia*, 2001(3): 656-667.
9. Bielawski, J.P. and Z. Yang. 2001. **The role of selection in the evolution of the *DAZ* gene family.** *Molecular Biology and Evolution*, 18: 523-529.
8. Dunn, K.A., J.P. Bielawski, and Z. Yang. 2001. **Rates and patterns of synonymous substitutions in *Drosophila*: implications for translational selection.** *Genetics*, 157:295-305.
7. Bielawski, J.P., K.A. Dunn, and Z. Yang. 2000. **Rates of nucleotide substitution and mammalian nuclear gene evolution: approximate and maximum-likelihood methods lead to different conclusions.** *Genetics*, 156:1299-1308.
6. Yang, Z. and J.P. Bielawski. 2000. **Statistical tests of adaptive molecular evolution.** *Trends in Ecology and Evolution*, 15:496-502.
5. Ward, T.J., J.P. Bielawski, S.K. Davis, J. Templeton, and J.N. Derr. 1999. **Identification of domestic cattle hybrids in wild cattle and bison species: a general approach using mtDNA and the parametric bootstrap.** *Animal Conservation*, 2:51-57.
4. Schmidt, T.R., J.P. Bielawski, and J.R. Gold. 1998. **Molecular phylogenetics and evolution of the cytochrome b gene in the cyprinid genus *Lythrurus* (Actinoptergii: Cypriniformes).** *Copeia*, 1998(1): 14-22.
3. Bielawski, J.P. and J.R. Gold. 1996. **Unequal synonymous substitution rates within and between two protein-coding mitochondrial genes.** *Molecular Biology and Evolution*, 13:889-892.
2. Bielawski, J.P. and D.E. Pumo. 1996. **Randomly Amplified Polymorphic DNA (RAPD) analysis of Atlantic Coast striped bass populations.** *Heredity*, 78:32-40.
1. Bielawski, J.P., K. Noack, and D.E. Pumo. 1995. **Improving amplification of Randomly Amplified Polymorphic DNA Markers (RAPD) from vertebrate DNA.** *Biotechniques*, 18:856-859.

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**CLINICAL CONFERENCE ABSTRACTS (COMPETITIVE, PUBLISHED)**

17. Dunn KA, Sigall-Boneh R, Bielawski JP, Turner D, Van Limbergen J, Levine A. 2017. **Crohn's disease exclusion diet and partial enteral nutrition (CED+PEN) vs exclusive enteral nutrition (EEN). Microbiome changes of a randomized clinical trial (RCT) in pediatric CD:**



- remission is associated with similar structural & functional profiles.** (talk) *Digestive Disease Week Chicago*.
16. Dunn KA, Sigall-Boneh R, Bielawski JP, Turner D, Van Limbergen J, Levine A. 2017 **Microbiome community structure and prediction of response to nutritional therapy in Pediatric Crohn's disease.** (talk) *Microbiome Human Nutrition*. Boston MA
  15. MacLellan A, Connors J, MacIntyre B, Douglas G, Dunn KA, Bielawski JP, Noble A, Mahdi G, Rashid M, Otley A, Cahill L, Langille M, Van Limbergen J. 2017. **Fibre intake is associated with microbiome changes in pediatric Crohn's disease patients following induction of remission induction with exclusive enteral nutrition (EEN).** (Poster) *Digestive Disease Week Chicago*
  14. Dunn KA, Sigall-Boneh R, Bielawski JP, Turner D, Van Limbergen J, Levine A. 2017. **Crohn's disease exclusion diet and partial enteral nutrition (CDED+PEN) vs exclusive enteral nutrition (EEN). Microbiome changes of a randomized clinical trial (RCT) in pediatric CD: remission is associated with similar structural + functional profiles.** (talk) *Journal of Crohn's and Colitis* 11(suppl\_1):S29-S29. (digital oral presentation)
  13. MacLellan A., Connors J., MacIntyre B., Douglas G., Dunn K.A., Bielawski J.P., Noble A., Mahdi G., Rashid M., Otley A.R., Cahill L., Langille M.G., Van Limbergen. 2017. **Fibre Intake is Associated with Microbiome Changes in Pediatric Crohn's Disease Patients Following Remission Induction with Exclusive Enteral Nutrition (EEN).** (talk) *J. European Crohn's and Colitis Organization, Inflammatory Bowel Disease*, February 15-18 2017 Barcelona Spain
  12. Dunn KA, Sigall Boneh R, Bielawski JP, Turner D, Van Limbergen J, Levine A. 2017. **Enteral nutrition induces changes in the functional repertoire of the human gut microbiome.** (poster) *International Symposium on Pediatric Inflammatory Bowel Disease (PIBD 2017)* September 13-16 2017 Barcelona Spain \*awarded a *PIBD Best Communication*.
  11. Hansen R, Douglas GM, Jones C, Dunn KA, Comeau AM, Bielawski JP, Tayler R, El-Omar EM, Russell RK, Hold GL, Langille MGI, Van Limbergen J. 2017. **Shotgun Metagenomics, 16S rRNA Gene Sequencing, and Human Genetics Differentially Classify Pediatric Crohn's Disease State and Treatment Outcome.** (poster) *International Symposium on Pediatric Inflammatory Bowel Disease (PIBD 2017)* September 13-16 2017 Barcelona Spain.
  10. Dunn KA, Moore-Connors J, MacIntyre B, Stadnyk A, Thomas NA, Noble A, Mahdi G, Rashid M, Otley AR, Bielawski JP, Van Limbergen J. (2016) **Early changes in microbial community structure are associated with sustained remission following nutritional treatment of Pediatric Crohn's Disease.** (talk) *World Congress of Pediatric Gastroenterology, Hepatology and Nutrition* .
  9. Dunn KA, Connors-Moore J, MacIntyre B, Mahdi G, Noble A, Rashid M, Thomas N, Stadnyk A, Otley AR, Bielawski JP, Van Limbergen J. (2016) **EEN induces significant changes in the metabolic capacity of gut microbiomes in pediatric CD patients.** (poster) *World Congress of Pediatric Gastroenterology, Hepatology and Nutrition* .
  8. Dunn, K.A., J. Connors, B. MacIntyre, A. Stadnyk, J. P. Bielawski, N. Thomas, A. R. Otley, J. Van Limbergen, 2015. **The dysbiosis index does not distinguish children with Crohn's disease from healthy siblings.** (talk) *United European Gastroenterology Journal* 2015;3(5S):A133 (OP412).
  7. Connors J, Hansen R, Dunn KA, Langille MG, Russell R, Otley AR, MacIntyre B, El-Omar E, Bielawski JP, Hold GL, Van Limbergen J. (2015). **Assessment of community structure and predictive functional profiling of the mucosa-associated microbiome implicates alterations in benzoate**

**metabolism in 'de novo' IBD after pouch-surgery and in treatment-naïve pediatric IBD.**

Digestive Disease Week, *Gastroenterology*.

6. Dunn, K.A., J. Connors, B. MacIntyre, A. Stadnyk, J. P. Bielawski, N. Thomas, A. R. Otle, J. Van Limbergen, 2015. **Clinical remission induced by exclusive enteral nutrition (EEN) in pediatric Crohn's disease is associated with microbiome metabolic changes toward increased xenobiotic biodegradation and metabolism.** (poster) *United European Gastroenterology Journal* 2015;3(5S):A441 (P1005) [This poster was featured as 'poster in the spotlight', and won best e-poster in the session on 'New insights into the management of paediatric and adolescent IBD.].
5. Connors, J., K.A. Dunn, J.P. Bielawski, A. Stadnyk, N. Thomas, A.R. Otle, J. Van Limbergen, 2015. **Clinical remission induced by exclusive enteral nutrition (EEN) in pediatric Crohn's disease is associated with microbiome metabolic changes toward altered xenobiotic biodegradation and metabolism.** (poster) *Digestive Disease Week*, Washington DC May 2015
4. Connors, J., R. Hansen, K.A. Dunn, M.G. Langille, R.K. Russell, A.R. Otle, B. MacIntyre, E. El-Omar, J.P. Bielawski, G.L. Hold, J. Van Limbergen, 2015. (poster) **Assessment of community structure and predictive functional profiling of the mucosa-associated microbiome implicates alterations in benzoate metabolism in 'de novo' IBD after pouch-surgery and in treatment-naïve pediatric IBD.** (poster) *10th Congress of European Crohn's and Colitis Organization*, Barcelona, Spain.
3. Connors, J., K.A. Dunn, J.P. Bielawski, A. Stadnyk, N. Thomas, A.R. Otle, J. Van Limbergen, 2015. (poster) **Clinical remission induced by exclusive enteral nutrition (EEN) in pediatric Crohn's disease is associated with microbiome metabolic changes toward altered xenobiotic biodegradation and metabolism.** (poster) *10th Congress of European Crohn's and Colitis Organization*, Barcelona, Spain.
2. Dunn, K.A., J. Moore-Connors, B. MacIntyre, A. Stadnyk, N.A. Thomas, A. Noble, G. Mahdi, M. Rashid, A. R. Otle, J. P Bielawski, J. Van Limbergen, 2016. **Early changes in microbial community structure are associated with sustained remission following nutritional treatment of pediatric Crohn's disease.** (talk) *World Congress of Pediatric Gastroenterology, Hepatology and Nutrition*, Montreal Quebec
1. Dunn, K.A., J. Moore-Connors, B. MacIntyre, A. Stadnyk, N.A. Thomas, A. Noble, G. Mahdi, M. Rashid, A.R. Otle, J.P. Bielawski, J. Van Limbergen, 2016. **EEN induces significant changes in the metabolic capacity of gut microbiomes in pediatric CD patients.** (poster) *World Congress of Pediatric Gastroenterology, Hepatology and Nutrition*, Montreal Quebec

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**MANUSCRIPTS SUMMITTED AND IN PREPARATION**

1. Mingrone, J., Susko, E. and Bielawski, J., Modified Likelihood Ratio Tests for Positive Selection. *Submitted to the Journal Bioinformatics*.
2. Bielawski, J.P., H. Gu, T. Kenney, and K. A. Dunn. Improved inference of site-specific selection pressure under a generalized parametric model of codon evolution. *Submitted to BMC Evolutionary Biology*.
3. Finlayson-Trick, E., Dunn, K.A., Connors, J., Bielawski, J.P., Stadnyk, A., Van Limbergen, J. Beyond taxonomy: metagenomics of bacterial heat shock protein in Crohn's disease inform translational research. *In preparation*.

4. Jones, C., Susko, E. and Bielawski, J.P. A novel codon model for discriminating sites having temporally coherent shifts between selection regimes and those undergoing random shifts among regimes. For submission to *Molecular Biology and Evolution*.
5. Dunn, K.A., J.P. Bielawski, R. Sigall-Boneh, J. Van Limbergen, and A. Levine. Changes in structure and function of the gut microbiome over the course of alternative treatments for Crohn's disease; EEN and the exclusion diet yield similar results. For submission to *Inflammatory Bowel Diseases*.

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## INVITED PRESENTATIONS

- 2018 (i) *Opening remarks and workshop introduction. (ii) Dynamics of codon substitution on mutation-selection fitness landscapes, and (iii) computational tutorial on statistical method for detecting adaptive evolution in gene sequences*; North American Workshop on Molecular Evolution, Woods Hole, Massachusetts, USA
- 2017 *Seasonal dynamics of heterotrophic communities: from mixing to stratification*. Schulich Ocean Studies Initiative Conference, Eilat, Israel
- 2017 (i) *Dynamics of codon substitution on mutation-selection fitness landscapes, and (ii) computational tutorial on statistical method for detecting adaptive evolution in gene sequences*; North American Workshop on Molecular Evolution, Woods Hole, Massachusetts, USA
- 2017 (i) *Phylogenetic analysis of natural selection pressure, and (ii) detecting selection using codon models*. European Workshop on Phylogenomics, Český Krumlov, South Bohemia, Czech Republic
- 2016 *Modeling structure and function in metagenomes*; IMR Microbiome Research Symposium, Halifax, Nova Scotia, Canada
- 2016 (i) *Dynamics of codon substitution on mutation-selection fitness landscapes, and (ii) tutorial on analyzing gene sequences for presence of sites evolving under adaptive evolution*; North American Workshop on Molecular Evolution, Woods Hole, Massachusetts, USA
- 2015 (i) *Codon substitution models and phylogenetic analysis of protein coding sequences, and (ii) tutorial on analyzing gene sequences for presence of sites evolving under adaptive evolution*; North American Workshop on Molecular Evolution, Woods Hole, Massachusetts, USA
- 2015 *Phylogenetic methods for inferring functional divergence among proteins*; The 2015 European Workshop on Molecular Evolution, Český Krumlov, South Bohemia, Czech Republic
- 2014 (i) *Statistical modelling of protein coding sequence evolution, and (ii) tutorial on analyzing gene sequences for presence of sites evolving under adaptive evolution*; Workshop on Molecular Evolution, Woods Hole, Massachusetts, USA
- 2014 *"Bagging" and "smoothing" to improve empirical Bayes detection of site-specific positive selection*; Society for Molecular Biology and Evolution, San Juan, Puerto Rico, USA
- 2013 *Phylogenetic methods for inferring functional divergence among proteins*; The 2013 European Workshop on Molecular Evolution, Český Krumlov, South Bohemia, Czech Republic

- 2013 *Searching for functional divergence in genomes and metagenomes*; The 2013 European Genomics Workshop, Český Krumlov, South Bohemia, Czech Republic
- 2013 *The genomics and metagenomics of human aging*; Special symposium on the Biology of Aging, Conference on "Aging...from Cells to Society", Hosted by the Division of Geriatric Medicine, Dalhousie University, Canada
- 2013 *(i) Estimating the strength and direction of natural selection pressure acting on protein coding genes, and (ii) tutorial on analyzing gene sequences for presence of sites evolving under adaptive evolution*; Workshop on Molecular Evolution, Woods Hole, Massachusetts, USA
- 2012 *Bayesian inference of metabolic divergence among microbial communities*; Canadian Institute for Advance Research (CiFaR), Integrated Microbial Biodiversity (IMB) meeting, Canada
- 2012 *(i) Estimating the strength and direction of natural selection pressure acting on protein coding genes, and (ii) tutorial on analyzing gene sequences for presence of sites evolving under adaptive evolution*; Workshop on Molecular Evolution, Woods Hole, Massachusetts, USA
- 2011 *Bayesian methods for modelling and mapping human microbiome diversity and function*; Canadian Microbiome Initiative, Inaugural Team Meeting, Vancouver, British Columbia, Canada
- 2011 *Searching for functional divergence in genes, genomes and metagenomes*; Workshop on Modelling and mapping human microbiome diversity and function, sponsored by CGEB and the Canadian Microbiome Initiative Halifax, Canada
- 2011 *Implications of discrete versus fuzzy species definitions of groups represented by the tips of a phylogenetic tree*; TOLeration workshop, Dalhousie University, Canada
- (2009 – 2011) *Phylogenetic methods for inferring functional divergence among proteins*; The European Workshop on Molecular Evolution, Český Krumlov, South Bohemia, Czech Republic
- (2007 – 2011) *(i) Estimating the strength and direction of natural selection pressure acting on protein coding genes, and (ii) tutorial on analyzing gene sequences for presence of sites evolving under adaptive evolution*; Workshop on Molecular Evolution, Woods Hole, Massachusetts, USA, 2007-2014
- 2007 *Predictions on the future of molecular evolutionary biology in the coming decades*; Annual meeting of the CIFAR Program in Evolutionary Biology, Canada
- 2006 *(i) Phylogenetic analysis of protein coding genes, and (ii) tutorial on use of PAML package of computer programs to analyze gene sequences for presence of sites evolving under adaptive evolution*; Workshop on Molecular Evolution, Woods Hole, Massachusetts, USA
- 2006 *Phylogenomic analysis reveals divergent evolutionary dynamics among host and environment adapted lineages of *Listeria**; CIFAR workshop on Integrated Microbial Biodiversity, Banff, Alberta, Canada
- 2005 *(i) Codon substitution models and phylogenetic analysis of protein coding genes, and (ii) tutorial on use of PAML package of computer programs to analyze gene sequences for*

*presence of sites evolving under adaptive evolution*; Workshop on Molecular Evolution, Woods Hole, Massachusetts, USA

- 2005 *(i) Tree-thinking, a gentle introduction to phylogenetics, (ii) Codon substitution models and phylogenetic analysis of protein-coding genes: Parts I & II and (iii) PAML demonstration: "PAML: phylogenetic analysis by maximum likelihood"*; Workshop on Bioinformatics: data gathering and application to molecular biology University of Puerto Rico, USA
- 2005 *Phylogenetic methods for detecting molecular adaptation*; Statistics Colloquium series, Dalhousie University, Canada
- 2005 *Using tree-thinking and ancestral reconstruction to study Darwinian evolution of molecules*; Department of Biology Colloquium Series, University of Puerto Rico, USA
- 2005 *Using tree-thinking to study the evolution of molecules*; Philosophy department Colloquium series on "Evolutionary explanation: cross-disciplinary approaches", Dalhousie University, Canada
- 2004 *(i) Codon substitution models and phylogenetic analysis of protein coding genes, and (ii) tutorial on use of PAML package of computer programs to analyze gene sequences for presence of sites evolving under adaptive evolution*; Workshop on Molecular Evolution, Woods Hole, Massachusetts, USA
- 2002 *(i) Codon substitution models and phylogenetic analysis of protein coding genes, (ii) Maximum likelihood methods for detecting functional divergence following gene duplication, and (iii) tutorial on use of PAML package of computer programs to analyze gene sequences for presence of sites evolving under adaptive evolution*; Workshop on Molecular Evolution, Woods Hole, Massachusetts, USA
- 2001 *Detecting adaptive molecular evolution after gene duplication*; Symposium on gene and genome duplications and the evolution of novel gene functions. Sponsored by *Conferences Jaques Monod* of the C.N.R.S., Aussois, France
- 2000 *Rates and patterns of synonymous substitutions in Drosophila: implications for translational selection*; Symposium on adaptive molecular evolution, co-sponsored by the Zoological Society of London and CEE, United Kingdom
- 2000 *Rates of nuclear gene evolution in mammals and Drosophila: approximate and maximum-likelihood methods lead to different conclusions*; Queen Mary and Westfield College Colloquium Series, University of London, United Kingdom

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#### **OTHER SCHOLARLY CONTRIBUTIONS: SOFTWARE**

- BiomeNet:** A Bayesian method for inferring the metabolic basis of functional divergence between microbial communities.  
Open source distribution: <https://sourceforge.net/projects/biomenet/>
- BioMiCo:** A hierarchical Bayesian mixture model for microbial community structure.  
Open source distribution: <https://sourceforge.net/projects/biomico/>
- CodemIFE:** Implements 11 new fixed effect models of codon evolution.  
Open source distribution: available on request

- LiBaC:** Implements a novel statistical technique to group sites according to similarities in the underlying process of molecular evolution.  
Open source distribution: available on request
- Codeml\_SBA:** Implements a novel method of statistical inference that combines the properties of bootstrapping, kernel smoothing and bagging.  
Open source distribution: [https://github.com/Jehops/codeml\\_sba](https://github.com/Jehops/codeml_sba)
- DendroCypher:** A tool for manipulating and labelling a bifurcating tree data structure.  
Open source distribution: <https://bitbucket.org/EvoWorks/dendrocypher>
- Proteus:** A large program under current development that implements a wide variety of Markov models for molecular data that can be applied to real data in either a maximum likelihood or Bayesian inference framework. (currently > 70,000 lines of code).  
Distribution: <https://bitbucket.org/EvoWorks> (private repository while under development; release expected in 2017 under an open source licence)

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## RESEARCH GRANTS AND AWARDS

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No.	ROLE	FUNDING SOURCE & TITLE	AMOUNT	PERIOD
21.	co-PI	Schulich Ocean Studies Centre Supplemental Support Grant: <i>Dynamics of complex microbial communities and metabolic potential during the spring bloom in the Gulf of Aqaba, Red Sea.</i>	\$30,000	2017-2018
20.	co-applicant	Genome Canada Large-Scale Applied Research Project: ATRAP - Algal Blooms, Treatment, Risk Assessment, Prediction and Prevention through Genomics (1 post doc to Dal)	~\$11 million	10/2016-09/ 2020
19.	co-applicant	NSHRF: <i>Role of fecal microbiome in optimizing aparaginase therapy in childhood acute lymphoblastic leukemia.</i>	\$149,833	2016-2018
18.	PI	NSERC Discovery Grant: <i>A general framework for modeling functional divergence at the molecular level, and investigating relationships to phenotype</i>	\$105,000	2015-2020
17.	co-PI	Schulich Ocean Studies Centre: <i>Dynamics of complex microbial communities and metabolic potential during the spring bloom in the Gulf of Aqaba, Red Sea.</i>	\$150,000	2015-2017
16.	co-applicant	Dalhousie Strategic Research Initiatives fund (SHRIF): An integrated resource for metagenomics and microbiomics in Atlantic Canada	\$200,000	2014
15.	co-applicant	NASPGHAN: <i>A metagneomic approach to diagnosis, induction and maintenance of deep remission following exclusive enteral nutrition in paediatric Crohn's Disease</i>	\$150,000	2013-2015

(CD)

14.	co-applicant	NSHRF Scotia Support Grant, Medical Category: <i>Scotia support for a pilot project to assess the gut microbiomes of patients in an assisted living facility.</i>	\$44,934	2013-2015
13.	co-applicant	NSHRF Development/Innovation Grant, Medical Category: <i>A pilot project to assess the gut microbiomes of patients in an assisted living facility.</i>	\$14,202	2013-2014
12.	PI	ACEnet/Sun Microsystems Research Fellowship: <i>Modeling ecologically relevant microbial phenotypes.</i>	\$20,000	2011-2012
11.	co-applicant	CIHR Emerging Team Grant, Canadian Microbiome Initiative: <i>Modeling and mapping microbial diversity and function with marker genes, genomes and metagenomes.</i>	\$675,000	2010-2014
10.	PI	NSERC Discovery Grant: <i>Evolutionary analysis of protein diversification: model improvement, assessment and application to real data.</i>	\$145,000	2009-2014
10.	PI	Tula Foundation Research Award: <i>The origins and evolution of microbial molecular diversity.</i>	\$250,000	2007-2012
9.	PI	NSHRF Research Award: <i>System-level analysis of metabolic network evolution in intracellular bacteria.</i>	\$17,824	2006-2007
8.	PI	CFI Infrastructure operating Fund: <i>Computer systems technician.</i>	\$26,396	2006-2007
7.	PI	CFI New opportunities grant: <i>A high performance computer cluster for microbial phylogenomics.</i>	\$219,813	2006
6.	PI	NSERC Individual Discovery Grant: <i>Microbial adaptive evolution: a phylogenomic approach.</i>	\$115,000	2004-2009
5.	co-applicant	NSERC Research Tools and Equipment Grant, 2004: <i>Upgrade of Sun computer system with new computer cluster.</i>	\$63,268	2004
4.	co-applicant	BBSRC research grant, UK: <i>Development, evaluation, and application of phylogenetic methods for detecting molecular adaptation.</i>	£96,161 (GBP)	2002-2004
3.	co-applicant	BBSRC research grant, UK: <i>Estimation of evolutionary rates in mammalian genomes to test theories of isochore origins and evolution.</i>	£25,000 (GBP)	2001-2003
2.	PI	Thomas R. Slick Research Fellowship, Texas A&M University, TX, USA: <i>Rates and patterns of mitochondrial genome evolution in Notropin Fishes.</i>	\$10,000 (USD)	1998-1999
1.	PI	NSF Doctoral Dissertation Improvement Grant, USA: <i>Molecular phylogenetics and evolution of Notropin fishes.</i>	\$12,000 (USD)	1997

RESEARCH COLLABORATIONS

As my group is working almost entirely in computational molecular evolution, genomics and metagenomics, my approach to research is intrinsically interdisciplinary. Being cross-appointed in Biology (75%) and Mathematics & Statistics (25%), and also being a member of the Center for Genomics and Evolutionary Bioinformatics (CGEB), has afforded me many opportunities for close collaboration with groups from other disciplines, and to pursue research unworkable from a single discipline. My current collaborations are listed below.

- 2003-present With **Dr. Hong Gu, Professor of Statistics at Dalhousie University** to develop of novel statistical methods for microbial metagenomics. *This collaboration involves co-supervision of graduate students in statistics.*
  
- 2009-present With **Dr. Edward Susko, Professor of Statistics at Dalhousie University**, to develop novel (i) Markovian models of codon evolution and (ii) methods for inference of positive selection. *We currently co-supervise two PhD students in statistics (Joseph Mingrone and Christopher Jones).*
  
- 2013-present With **Dr. Johan Van Limbergen, Clinician and Scientist in Pediatric Gastroenterology and Nutrition - Dalhousie University & IWK Health Centre**, to (i) investigate human gut microbiome structure and function in IBD patients, with a special emphasis on difference between those who maintain remission and those that do not, and (ii) to train and develop predictive models for clinical use in personalized treatment of IBD at the IWK Health Centre. *I am a co-applicant with Dr. Van Limbergen on grants No. 1, 4, and 5 above.*
  
- 2014-present With **Debbie Lindell and Oded Béjà at Technion Institute, Israel** to study the Dynamics of complex microbial communities and metabolic potential during the spring bloom in the Gulf of Aqaba, Red Sea via metagenomics. *I am co-applicant with Drs Lindell and Béjà on grant No. 3 above.*
  
- 2015-present With **Ketan Kulkarni, Clinician and Scientist in the Division of Hematology/Oncology IWK Health Centre**, to study gut microbiome profiling in optimizing asparaginase therapy in childhood acute lymphoblastic leukemia. *I am co-applicant with Dr. Kulkarni on Grant No. 1 above.*

TEACHING ACTIVITIES

**UNDERGRADUATE COURSES**

<b>Term</b>	<b>No.</b>	<b>Title</b>	<b>%</b>	<b>Sections</b>	<b>Students</b>
2018 W	STAT1060	Introductory Statistics for Sciences	50%	2x	419
2017 F	BIOL2030	Genetics & Molecular Biology	33%	1x	245
2017 F	BIOL3046	Molecular Evolution	100%	1x	35
2017 W	STAT1060	Introductory Statistics for Sciences	50%	2x	435



2016 F	BIOL2030	Genetics & Molecular Biology	33%	1x	258
2016 F	BIOL3046	Molecular Evolution	100%	1x	40
2016 W	STAT1060	Introductory Statistics for Sciences	50%	2x	406
2015 F	BIOL2030	Genetics & Molecular Biology	33%	1x	255
2015 F	BIOL3046	Molecular Evolution	100%	1x	37
2015 W	STAT1060	Introductory Statistics for Sciences	50%	2x	400
2014 F	STAT1060	Introductory Statistics for Sciences	20%	2x	435
2014 F	BIOL2030	Genetics & Molecular Biology	33%	1x	226
2014 F	BIOL3046	Molecular Evolution	100%	1x	38
2014 W	STAT1060	Introductory Statistics for Sciences	20%	3x	760
2014 W	DISP	Bioinformatics lecture & lab	n.a.	1x	57
2013 F	STAT1060	Introductory Statistics for Sciences	20%	2x	447
2013 F	BIOL2030	Genetics & Molecular Biology	33%	1x	245
2013 F	BIOL3046	Molecular Evolution	100%	1x	49
2013 W	STAT1060	Introductory Statistics for Sciences	20%	3x	718
2013 W	DISP	Bioinformatics lecture & lab	n.a.	1x	69
2012 F	STAT1060	Introductory Statistics for Sciences	20%	2x	475
2012 F	BIOL2030	Genetics & Molecular Biology	33%	1x	227
2012 F	BIOL3046	Molecular Evolution	100%	1x	46
2012 W	STAT1060	Introductory Statistics for Sciences	20%	3x	698
2012 W	DISP	Bioinformatics lecture & lab	n.a.	1x	67
2011 F	STAT1060	Introductory Statistics for Sciences	20%	2x	419
2011 F	BIOL2030	Genetics & Molecular Biology	33%	1x	214
2011 F	BIOL3046	Molecular Evolution	100%	1x	46
2011 W	STAT1060	Introductory Statistics for Sciences	20%	3x	602
2011 W	DISP	Bioinformatics lecture & lab	n.a.	1x	75
2010 W	STAT1060	Introductory Statistics for Sciences	20%	3x	602
2010 W	BIOL2030	Genetics & Molecular Biology	33%	1x	199
2010 W	DISP	Bioinformatics lecture & lab	n.a.	1x	68
2009 F	STAT1060	Introductory Statistics for Sciences	20%	2x	366
2009 F	BIOL2030	Genetics & Molecular Biology	33%	1x	209
2009 F	BIOL3046	Molecular Evolution	100%	1x	42
2009 W	STAT1060	Introductory Statistics for Sciences	20%	3x	572
2009 W	DISP	Bioinformatics lecture & lab	n.a.	1x	62
2008 F	STAT1060	Introductory Statistics for Sciences	20%	2x	340
2008 F	BIOL2030	Genetics & Molecular Biology	33%	1x	187
2008 F	BIOL3046	Molecular Evolution	100%	1x	41
2008 W	STAT1060	Introductory Statistics for Sciences	20%	2x	536
2008 W	DISP	Bioinformatics lecture & lab	n.a.	1x	69
2007 F	STAT1060	Introductory Statistics for Sciences	20%	2x	354
2007 F	BIOL2030	Genetics & Molecular Biology	33%	1x	164
2007 F	BIOL3046	Molecular Evolution	100%	1x	41
2007 W	DISP	Bioinformatics lecture & lab	n.a.	1x	68

2006 F	BIOL2030	Genetics & Molecular Biology	33%	1×	190
2006 F	BIOL3046	Molecular Evolution	100%	1×	30
2005 F	BIOL3046	Molecular Evolution	100%	1×	38
2004 F	BIOL3046	Molecular Evolution	100%	1×	34

Note: DISP indicates the Dalhousie Integrated Science Program

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### OTHER TEACHING

2007-2016 I have been the graduate modules coordinator (BIOL5705, BIOL5706 and BIOL5707) from 2007. In addition to organizing the modules, and coordinating the grading, I also serve as instructor of a graduate module as needed. Typically, between 10-15 graduate modules are taught each year in the Department of Biology.

2001-2002 While a postdoctoral research fellow at University College London, I contributed lectures to the Center for Mathematics and Physics in the Life Sciences and Experimental Biology (CoMPLEX) graduate program.

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### ADVANCED UNDERGRADUATE STUDENT SUPERVISION (Dalhousie, n=17; total, n=22)

- Principle supervisor **Thompson, Jordan**  
 Title: *Develop programming skills and use them to reconcile alternative functional annotations within a gene sequence database*  
 Program(s): Biology Experiential learning  
 Dates: 05/2018 – 09/2018
- Principle supervisor **Jennifer Allot**  
 Title: *The Relationship Between Bile Acids and Gut Community Structure in Pediatric Crohn's Disease*  
 Program(s): Biology Honours (completed)  
 Dates: 09/2017 – 05/2018
- Principle supervisor **Danielle Pyne**  
 Title: *Analysis of Asparaginase Gene Family (ans) Evolution and Divergence*  
 Program(s): Biology Honours (completed)  
 Dates: 09/2017 – 05/2018
- Principle supervisor **Lauren Runnalls**  
 Title: *Develop programming skills and use them to identify HtpG sequences and identify the bacterial species of origin.*  
 Program(s): Biology Experiential learning  
 Dates: 01/2017 – 04/2017
- Principle supervisor **Nguyen, Steven**  
 Title: *Powers and pitfalls of codon models inferred under a formal mutation selection model of adaptive evolution.*

- Program(s): Biology Honours (completed)  
Dates: 09/2015 – 05/2016
- Principle supervisor **Youssef, Noor**  
Title: *Analysis of the impact of non-stationary evolution on the inference of selection pressure.*  
Program(s): Biology Honours (completed)  
Dates: 09/2014 – 05/2015
- Principle supervisor **Khalak, Yuriy**  
Title: *A genetic algorithm for optimization of the likelihood function under a Markov model of codon sequence evolution.*  
Program(s): NSERC USRA  
Dates: 09/2009 – 05/2010
- Principle supervisor **MacDonald, Shelly**  
Title: *Use of a novel Bayesian supervised classifier for analysis of factors influencing the human vaginal microbiome.*  
Program(s): NSERC USRA & Biology Honours (completed)  
Dates: 06/2013 – 05/2014
- Principle supervisor **Astle, Jasmine**  
Title: *Evidence for selection switching and signal for positive selection in yeast and mammalian genomes.*  
Program(s): NSERC USRA & Biology Honours (completed)  
Dates: 06/2012 – 05/2013
- Principle supervisor **Byers-Heinlein, Alyssa**  
Title: *Effects of chromosome recombination on evolutionary rate.*  
Program(s): Biology Honours (completed)  
Dates: 09/2008 – 05/2009
- Principle supervisor **Mingrone, Joseph**  
Title: *Error assessment of codon models using cross validation.*  
Program(s): NSERC USRA & Biology Honours (completed)  
Dates: 05/2008 – 05/2009
- Principle supervisor **Carson, Kaitlyn**  
Title: *Phylogenomic analysis of positive selection in the genus Listeria.*  
Program(s): DISP research project  
Dates: 02/2008 – 05/2008
- Principle supervisor **Tredger, Emily**  
Title: *Phylogenomic analysis of positive selection in the genus Listeria.*  
Program(s): DISP research project  
Dates: 02/2008 – 05/2008
- Principle supervisor **Weber, Rachel**  
Title: *Selection on Pseudomonas genome and the relationship to metabolism.*  
Program(s): Biology Honours (completed)  
Dates: 09/2006 – 05/2007
- Principle supervisor **Johnson, Luke**  
Title: *Protein evolution in marine mammals.*

Program(s): NSERC USRA & Biology Honours (completed)  
Dates: 06/2006 – 05/2006

Principle supervisor **Kepkey, Rosie**  
Title: *Adaptive evolution of the Spike gene of SARS-CoV*  
Program(s): DISP research project  
Dates: 02/2004 – 07/2004

Principle supervisor **Smith, Josephine**  
Title: *Adaptive evolution of the Spike gene of SARS-CoV*  
Program(s): DISP research project  
Dates: 02/2004 – 07/2004

NOTE: I was on the research project advisory committee of five students in the CoMPLEX program at the University College London (UCL), UK: Dave Dale (2002), Christian Bottomley (2002), Christian Mullaly (2002), Thomas MacCarthy (2001), Christina Vogel (2001).

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#### **MASTERS STUDENT SUPERVISION (Dalhousie, n=9; total, n=10)**

Co-supervisor **Bjorndahl, Paul**  
Title: Modelling and analysis of complex microbial community dynamics and metabolic potential during the spring bloom in the Gulf of Aqaba, Red Sea.  
Program: MSc in Statistics  
Dates: 09/2017 – present

Principle supervisor **Bashwih, Rana**  
Title: *Inference and investigation of marine microbial community structures in the global oceans.*  
Program: Interdisciplinary MSc in Bioinformatics & Computational Biology (completed)  
Dates: 09/2013 – 08/2016 (completed)

Co-supervisor **Tang, Chongci**  
Title: *Statistical approaches for matching the components of complex microbial communities*  
Program: MSc in Statistics (completed)  
Dates: 09/2014 – 08/2016

Co-supervisor **Chen, Wei**  
Title: *The exploration of effect of model misspecification and development of an adequacy-test for substitution models in phylogenetics.*  
Program: MSc in Statistics (completed)  
Dates: 09/2010 – 08/2012

Principle supervisor **Bay, Rachael**  
Title: *Analysis of functional constraint and recombination in gene sequences of the cyanobacteria Prochlorococcus.*  
Program: MSc in Biology (completed)  
Dates: 09/2008 – 08/2010

Co-supervisor **Urquhart, Caroline**  
Title: *Analysis of prokaryotic metabolic networks*  
Program: MSc in Statistics (completed)

Dates: 09/2006 – 03/2011

- Principle supervisor **Morine, Melissa**  
Title: *Functional topology and evolution in prokaryotic metabolic networks*  
Program: MSc in Biology (completed)  
Dates: 09/2005 – 08/2007
- Co-supervisor **Li, Li**  
Title: *Development of spherical data analysis techniques for phylogenetics.*  
Program: MSc in Statistics (completed)  
Dates: 09/2005 – 08/2006
- Co-supervisor **Jiang, Wenyi**  
Title: *Analysis of the impact of physiochemical properties of amino acids on models of protein evolution.*  
Program: MSc in Statistics (completed)  
Dates: 09/2004 – 08/2006
- Co-supervisor **Bao, Le**  
Title: *Generalized fixed effects models and likelihood based clustering in codon substitution models.*  
Program: MSc in Statistics (completed)  
Dates: 09/2004 – 08/2005
- Co-supervisor **Anisimova, Maria**  
Title: *Evaluating likelihood ratio tests to detect positive selection.*  
Program: MS, Center for Mathematics and Physics in the Life Sciences and Experimental Biology (CoMPLEX), University College London, United Kingdom  
Dates: 1999 – 2000

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#### **PHD STUDENT SUPERVISION (Dalhousie, n=3)**

- Co-supervisor **Mingrone, Joseph**  
Title: *Novel statistical method for improving the inference of positively selected sites in protein coding sequences.*  
Program: PhD in Statistics  
Start date: 09/2009 – present
- Co-supervisor **Jones, Christopher**  
Title: *Development and assessment of Markovian codon models for the joint analyses of gene sequence and phenotypic evolution.*  
Program: PhD in Statistics  
Start date: 01/2014 – present
- Principle supervisor **Youssef, Noor**  
Title: *Extension of the mutation-selection (MutSel) modeling framework to include epistasis.*  
Program: PhD in Biology  
Dates: 09/2015 – present

## POST-DOCTORAL FELLOW & RESEARCH ASSOCIATE SUPERVISION (n=4)

- Principle supervisor **Wei, Zhou**  
Title: *Bayesian modeling and analysis of complex microbial communities*  
Program: Postdoctoral Research Scientist (Large-scale research initiative, ATRAPP, funded by Genome Canada)  
Dates: 08/2018– [2020]
- Principle supervisor **Baker, Jennifer**  
Title: *Evolutionary surveys for genes having functional divergence during Hominid evolution*  
Program: visiting Research Scientist  
Dates: 2014, 2015
- Principle supervisor **Dunn, Katherine**  
Title: *Inference of microbial community structure and function from metagenomic data*  
Program: Postdoctoral Research Scientist (CIHR, NASPGHAN & Schulich-funded)  
Dates: 2009 – 2016
- Principle supervisor **Boon, Eva**  
Title: *Modeling and analysis of human microbiome data and aging*  
Program: CIHR-funded Postdoctoral Research Scientist  
Dates: 08/2012 – 02/2014
- Co-supervisor **Shafiei, Mahdi**  
Title: *Bayesian inference of metabolic divergence among microbial communities.*  
Program: CIHR-funded & ACEnet-funded Postdoctoral Research Scientist  
Dates: 09/2011 – 07/2013
- Principle supervisor **Dunn, Katherine**  
Title: *The origins and evolution of microbial molecular diversity*  
Program: Tula-funded Postdoctoral Research Scientist  
Dates: 10/2007 – 09/2013