

**CURRICULUM VITAE (UPDATED: 24 JULY 2017)**

**BRUCE RANNALA**

**Mailing Address:**

Department of Evolution and Ecology  
University of California Davis  
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<http://rannala.org>

**Academic Degrees:**

Ph.D., 1995, Biology, Yale University  
M.Sc., 1991, Zoology, University of Toronto  
B.Sc. (1st Class Hons), 1989, Zoology, Univ. Brit. Columbia

**Positions Held:**

2013-2016  
Chair  
Graduate Group in Biostatistics  
University of California Davis

2004-present  
Professor  
Department of Evolution & Ecology  
University of California Davis

2004-2014  
Professor  
Genome Center  
University of California Davis

2006-2008  
Associate Director of Bioinformatics  
Genome Center  
University of California Davis

2002-2004  
Associate Professor

2000-2002  
Assistant Professor  
Department of Medical Genetics  
University of Alberta

1998-2000  
Assistant Professor  
Department of Ecology and Evolution  
SUNY Stony Brook

## 2. CV. Bruce Rannala

1995-1998  
Postdoctoral Researcher  
Department of Integrative Biology  
University of California Berkeley

### **Honors and Awards:**

2016-present, Guest Professor, Sun Yat-sen University, Guangzhou, China.  
2013-2016, Guest Professor, Center for Computational Molecular Evolution, Beijing Institute of Genomics, Beijing, China.  
2009, Miller Professor, UC Berkeley (1 semester appointment).  
2007-2012, Guest Professor, Center for Computational Molecular Evolution, Institute of Zoology, Chinese Academy of Sciences, Beijing, China.  
2006, Visiting Fellow, Newton Institute for Mathematical Sciences, Cambridge University, UK (2 month appointment).  
2002, Associate, Canadian Institute for Advanced Research, Program in Evolutionary Biology (5 year appointment).  
2001, CIHR/Peter Lougheed Scholar (5 year salary award and operating grant; national award to top-ranked CIHR new investigator).  
2001, Scholar, Canadian Genetic Diseases Network (5 year appointment).  
2001, Scholar, Alberta Heritage Foundation for Medical Research (5 year salary award and operating grant).  
1997 Visiting Professor, Ecole Normale Superieure, Paris France.  
1995-1997, Natural Sciences and Engineering Research Council (NSERC) of Canada Postdoctoral Fellowship (PDF 1), awarded for tenure abroad.  
1986-1995, Natural Sciences and Engineering Research Council (NSERC) of Canada Postgraduate Scholarships (PGS2, PGS3); University of Toronto Open Master's Fellowship; British Columbia Provincial Post-secondary Scholarships.

### **Selected Recent Invited Symposia and Workshops (2012-2017):**

2017: Instructor, Wellcome Trust Course on Molecular Evolution, Hinxton UK.  
2017: Instructor, Course on Molecular Evolution, Beijing Normal University, Beijing, China.  
2016: Keynote Speaker, Mathematical and Computational Biology Meeting, Montpellier, France.  
2016: Invited Speaker, Department of Botany, University of Delhi, New Delhi, India.  
2016: Instructor, EMBO Course on Molecular Evolution, Crete, Greece.  
2015: Seminar Speaker, Department of Biology, University of Tulsa, Tulsa, OK.  
2015: Invited Speaker, Royal Society, London, UK.  
2015: Seminar Speaker, Biostatistics Seminar, UC Davis.  
2015: Instructor, Wellcome Trust Course on Molecular Evolution, Hinxton UK.  
2015: Seminar Speaker, Department of Biology, University of Florida, Gainesville, FL.  
2014: Invited Speaker, Big Data Workshop, Field Museum, Chicago IL.  
2014: Seminar Speaker, Department of Biology and Evolution, University of Ferrara, Ferrara, Italy.  
2014: Seminar Speaker, Institute of Population Genetics, Vetmeduni Vienna.  
2014: Instructor, EMBO Course on Molecular Evolution, Crete, Greece.  
2013: Invited Speaker, CIHR STAGE, Dalla Lana School of Public Health, University of Toronto.  
2013: Seminar Speaker, Beijing Institute of Genomics, Beijing, China.  
2013: Instructor, Wellcome Trust Course on Molecular Evolution, Hinxton UK.  
2012: Seminar Speaker, Natural History Museum, Stockholm, Sweden.  
2012: Seminar Speaker, Laboratoire d'Ecologie Alpine, Joseph Fourier University, France.  
2012: Seminar Speaker, Department of Biology and Evolution, University of Ferrara, Italy.

### 3. CV. Bruce Rannala

2012: Seminar Speaker, Biostatistics Seminar, UC Davis.

2012: Instructor, EMBO Course on Molecular Evolution, Crete, Greece.

2006-2017: Lecturer, Bodega Bay Applied Phylogenetics Workshop, Bodega Bay Marine Lab.

Invited Talks (pre-2012): approximately 4 per year.

#### Grants Received:

1998-2013 National Institutes of Health (NHGRI), "Disequilibrium Mapping of Complex Genetic Diseases" (R01 Operating Grant; 2 Competitive Renewals)

2001-2009, Canadian Institutes of Health Research, "Novel Statistical Approaches for Studying Complex Genetic Diseases" (MOP Operating Grant; 1 Competitive Renewal)

2002-2007, Quebec Genome Canada, "A Haplotype Map of the Human Genome and Biomedical Tool for Genetic Research in Canada" (PI: Tom Hudson, Collaborator)

2002, Canadian Foundation for Innovation/ISRIP "Centre of Excellence for Viral Hepatitis Research" (PI: Lorne Tyrrell, one of 10 Co-PIs)

2001-2006, Canadian Institutes of Health Research, "Novel Statistical Approaches for Studying Complex Genetic Diseases" (Peter Loughheed Research Award and Salary)

2001-2006, Alberta Heritage Foundation for Medical Research, "Novel Statistical Approaches for Studying Complex Genetic Diseases" (Equipment Grant and Salary)

2001-2006, Atlantic Genome Canada, "A Comparative Understanding of Prokaryotic Genome Evolution and Diversity" (PI: Ford Doolittle, one of 6 Co-PIs)

2000-2003, National Science Foundation, "Bayesian Estimation of Host-Parasite Cospeciation" (PI: J. Huelsenbeck, Co-PIs B. Larget and B. Rannala)

1993, National Science Foundation, "Genetic Effects of Extinction and Recolonization in a Host-Parasite System" (Dissertation Improvement Grant with Gunter P. Wagner)

1992-93: Numerous small grants (Frank M. Chapman Fund, American Museum of Natural History; Animal Behavior Society; National Geographic Society; Sigma Xi; John F. Enders Research Grant, Yale University)

#### Publications:

Journal Articles (PhD student and postdoc coauthors underlined):

1. B. Rannala and Z. Yang. 2017. Efficient Bayesian species tree inference under the multispecies coalescent. *Systematic Biology*. [syw119](#).
2. Z. Yang and B. Rannala. 2017. Bayesian species identification under the multispecies coalescent provides significant improvements to DNA barcoding analyses. *Mol. Ecol.* 26: 3028-3036.
3. B.R. Moore, S. Höhna, M.R. May, B. Rannala, J.P. Huelsenbeck. 2016. Critically evaluating the theory and performance of Bayesian analysis of macroevolutionary mixtures. *Proc. Natl. Acad. Sci. USA* 113: 9569-9574.
4. B. Rannala. 2016. Conceptual issues in Bayesian divergence time estimation. *Phil. Trans. R. Soc. B* 371: 2015.0134.
5. H. Alhaddad, C. Zhang, B. Rannala and L.A. Lyons. 2016. A glance at recombination hotspots in the domestic cat. *PLoS one* 11: e0148710.
6. B. Rannala. 2015. The art and science of species delimitation. *Current Zoology* 61: 846-853.
7. Z. Yang and B. Rannala. 2014. Unguided species delimitation using DNA sequence data from multiple loci. [Mol Biol Evol \(early online\)](#).
8. C. Zhang, B. Rannala, and Z. Yang. 2014. Bayesian species delimitation can be robust to guide tree inference errors. [Systematic Biology](#) 63: 993-1004.

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9. [Y. Wang](#) and B. Rannala. 2014. Bayesian inference of shared recombination hotspots between humans and chimpanzees. [Genetics \(early online\)](#).
10. H. Lockwood, [A. Guan](#), A. S. Yu; [C. Zhang](#), A. Zykovich, I. Korf, B. Rannala, and D. J. Segal. 2014. The Functional Significance of Common Polymorphisms in Zinc Finger Transcription Factors. [G3: Genes| Genomes| Genetics 4: 1647-1655](#).
11. [A. D. Leaché](#), R. B. Harris, B. Rannala, and Z. Yang. 2013. The Influence of Gene Flow on Species Tree Estimation: A Simulation Study. *Systematic Biology* 63: 17-30.
12. B. Rannala and Z. Yang. 2013. Improved reversible jump algorithms for Bayesian species delimitation. *Genetics* 195: 245-253.
13. [B. Padhukasahasram](#) and B. Rannala. 2013. Meiotic gene-conversion rate and tract length variation in the human genome. *Eur. J. Hum. Genet.* (early edition).
14. Z. Yang and B. Rannala. 2012. Molecular phylogenetics: Principles and practice. *Nat. Rev. Genet.* 13: 303-314.
15. [C. Zhang](#), B. Rannala and Z. Yang. 2012. Robustness of compound Dirichlet priors for Bayesian inference of branch lengths. *Syst. Biol.* 61: 779-784.
16. B. Rannala, [T. Zhu](#), Z. Yang. 2012. Tail paradox, partial identifiability and influential priors in Bayesian branch length inference. *Mol. Biol. Evol.* 29: 325-35.
17. [B. Padhukasahasram](#) and B. Rannala. 2011. Bayesian population genomic inference of crossing-over and gene-conversion. *Genetics* 189: 607-619.
18. [A. D. Leaché](#) and B. Rannala. 2011. The accuracy of species tree estimation under simulation: A comparison of methods. *Syst. Biol.* 60: 126-137.
19. Z. Yang and B. Rannala. 2010. Bayesian species delimitation using multilocus sequence data. *Proc. Natl. Acad. Sci. USA* 107: 9264-9269.
20. [Y. Wang](#) and B. Rannala. 2009. Population genomic inference of recombination rates and hotspots. *Proc. Natl. Acad. Sci. USA* 106: 6210-6214.
21. [Y. Wang](#) and B. Rannala. 2008. Bayesian inference of fine-scale recombination rates using population genomic data. *Phil. Trans. Roy. Soc. B* 363: 3921-3930.
22. [C. D. Fetterman](#), B. Rannala and M. A. Walter. 2008. Identification and analysis of evolutionary selection pressures acting at the molecular level in five forkhead subfamilies. *BMC Evol. Biol.* 8: 261.
23. B. Rannala and Z. Yang. 2008. Phylogenetic inference using whole genomes. *Ann. Rev. Genomics Hum. Genet.* 9: 217-231.
24. [K. Bumroongkit](#), B. Rannala, P. Traisathit, M. Srikummool, Y. Wongchai, and D. Kangwanpong. 2008. TP53 gene mutations of lung cancer patients in upper northern Thailand and environmental risk factors. *Cancer Genet. Cytogenet.* 185: 20-27.
25. [L. Mateiu](#) and B. Rannala. 2008. Bayesian inference of errors in ancient DNA caused by postmortem degradation. *Mol. Biol. Evol.* 25: 1503-1511.
26. [Cranston, K.](#), and B. Rannala. 2007. Summarizing a posterior distribution of trees using agreement subtrees. *Syst. Biol.* 56: 578-590.
27. Rannala, B., and Z. Yang. 2007. Inferring speciation times under an episodic molecular clock. *Syst. Biol.* 56: 453-466.
28. [Ro, S.](#), and B. Rannala. 2007. Inferring somatic mutation rates using the stop-EGFP mouse. *Genetics* 177: 9-16.
29. [Mateiu, L.](#), and B. Rannala. 2006. Inferring Complex DNA Substitution Processes on Phylogenies Using Uniformization and Data Augmentation. *Syst. Biol.* 55: 259-269.
30. Yang, Z., and B. Rannala. 2006. Bayesian estimation of species divergence times under a molecular clock using fossil calibrations with soft bounds. *Mol. Biol. Evol.* 23: 212-226.
31. [Ro, S.](#), and B. Rannala. 2005. Evidence from the stop-EGFP mouse supports a niche-sharing model of epidermal proliferative units. *Exp. Dermatology* 14: 1-6.

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32. Yang, Z., and B. Rannala. 2005. Branch-length prior influences Bayesian posterior probability of phylogeny. *Syst. Biol.* 54: 455-470.
33. Cranston, K., and B. Rannala. 2005. Closing the gap between rocks and clocks. *Heredity* 94: 461-462.
34. Wang, Y., and B. Rannala. 2005. In silico analysis of disease-association mapping strategies using the coalescent process and incorporating ascertainment and selection. *Am. J. Hum. Genet.* 76: 1066-1073.
35. Wang, Y., and B. Rannala. 2004. A novel solution for the time-dependent probability of gene fixation or loss under natural selection. *Genetics* 168: 1081-1084.
36. Huelsenbeck, J.P., and B. Rannala. 2004. Frequentist properties of Bayesian posterior probabilities of phylogenetic trees under simple and complex substitution models. *Syst. Biol.* 53: 904-913. **(ISI Fast-breaking paper, Dec 2005; 34th of 50 most cited papers in Syst Biol)**
37. Ro, S., and B. Rannala. 2004. A stop-EGFP transgenic mouse to detect clonal cell lineages generated by mutation. *EMBO Reports* 5: 914-920.
38. Beaumont, M.A., and B. Rannala. 2004. The Bayesian revolution in genetics. *Nat. Rev. Genetics* 5: 251-261. **(April '04 Feature Article)**
39. Yang, Z., S. Ro, and B. Rannala. 2003. Likelihood models of somatic mutation and codon substitution in cancer genes. *Genetics* 165: 695-705.
40. Rannala, B., and Z. Yang. 2003. Bayes estimation of species divergence times and ancestral population sizes using DNA sequences from multiple loci. *Genetics* 164: 1645-1656.
41. Rannala, B. 2003. Stationary allele frequency distributions. *Encyclopedia of the Human Genome*, Nature Publishing.
42. Huelsenbeck, J.P., and B. Rannala. 2003. Detecting correlations between characters in a comparative analysis with uncertain phylogeny. *Evolution* 57: 1237-1247.
43. Wilson, G., and B. Rannala. 2003. Bayesian inference of recent migration rates using multilocus genotypes. *Genetics* 163: 1177-1191.
44. Rannala, B., and J.P. Reeve. 2003. Joint Bayesian estimation of mutation location and age using linkage disequilibrium. *Proc. Pac. Symp. Biocomput.* 8: 526-534.
45. Rannala, B. 2002. Identifiability of parameters in MCMC Bayesian inference of phylogeny. *Syst. Biol.* 51: 754-760.
46. Fisher, M.C., B. Rannala, V. Chaturvedi, and J.W. Taylor. 2002. Disease surveillance in recombining pathogens: Multilocus genotypes identify sources of human *Coccidioides* infections. *Proc. Natl. Acad. Sci. USA* 99: 9067-9071.
47. Reeve, J.P., and B. Rannala. 2002. DMLE+: Bayesian linkage disequilibrium gene mapping. *Bioinformatics* 18: 894-895.
48. Rannala, B. 2001. Finding genes influencing susceptibility to complex diseases in the post-genome era. *Am. J. Pharmacogenomics* 1: 203-221.
49. Ro, S., and B. Rannala. 2001. Commentary: Methylation patterns and mathematical models reveal dynamics of stem cell turnover in the human colon. *Proc. Natl. Acad. Sci. USA* 98: 10519-10521.
50. Rannala, B., and G. Bertorelle. 2001. Using linked genetic markers to infer the age of a mutation. *Human Mutation* 18: 87-100.
51. Rannala, B., and J.P. Reeve. 2001. High-resolution multipoint linkage disequilibrium mapping in the context of a human genome sequence. *Am. J. Hum. Genet.* 69: 159-178.
52. Slatkin, M., and B. Rannala. 2000. Estimating allele age. *Annu. Rev. Genomics Hum. Genet.* 1: 225-249.
53. Rannala, B., and M. Slatkin. 2000. Methods for multipoint disease mapping using linkage disequilibrium. *Genetic Epidemiology* 19: S71-S77.

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54. Huelsenbeck, J.P., B. Rannala, and J.P. Masly. 2000. Accommodating phylogenetic uncertainty in evolutionary studies. *Science* 88: 2349-2350.
55. Rannala, B., W-G. Qiu, and D.E. Dykhuizen. 2000. Methods for estimating gene frequencies and detecting selection in bacterial populations. *Genetics* 155: 499-508.
56. Huelsenbeck, J.P., B. Rannala, and B. Larget. 2000. A Bayesian framework for the analysis of cospeciation. *Evolution* 54: 352-364.
57. Knowles, L.L., D.J. Futuyma, W.F. Eanes, and B. Rannala. 1999. Insight into speciation from historical demography in the phytophagous beetle *Ophraella*. *Evolution* 53: 1846-1856.
58. Bertorelle, G., and B. Rannala. 1998. Using rare mutations to estimate population divergence times: a maximum likelihood approach. *Proc. Natl. Acad. Sci. USA* 95: 15452-15457.
59. Rannala, B., J. P. Huelsenbeck, Z. Yang, and R. Nielsen. 1998. Taxon sampling and the accuracy of large phylogenies. *Syst. Biol.* 47: 702-710.
60. Rannala, B., and M. Slatkin. 1998. Linkage disequilibrium mapping and Parkinson's disease. *Science* 280: 175a.
61. Rannala, B., and M. Slatkin. 1998. Likelihood analysis of disequilibrium mapping and related problems. *Am. J. Hum. Genet.* 62: 459-473.
62. Slatkin, M., and B. Rannala. 1997. The sampling distribution of disease-associated alleles. *Genetics* 147: 1855-1861.
63. Rannala, B. 1997. On the genealogy of a rare allele. *Theor. Popul. Biol.* 52: 216-223.
64. Rannala, B., and J.L. Mountain. 1997. Detecting immigrants by using multilocus genotypes. *Proc. Natl. Acad. Sci. USA* 94: 9197-9201.
65. Rannala, B. 1997. Gene genealogy in a population of variable size. *Heredity* 78: 417-423.
66. Yang, Z., and B. Rannala. 1997. Bayesian phylogenetic inference using DNA sequences: Markov Chain Monte Carlo methods. *Mol. Biol. Evol.* 14: 717-724.
67. Huelsenbeck, J.P., and B. Rannala. 1997. Phylogenetic methods come of age: testing hypotheses in an evolutionary context. *Science* 276: 227-232.
68. Huelsenbeck, J.P., and B. Rannala. 1997. Maximum likelihood estimation of phylogeny using stratigraphic data. *Paleobiology* 23: 174-180.
69. Huelsenbeck, J.P., B. Rannala, and Z. Yang. 1997. Statistical tests of host-parasite cospeciation. *Evolution* 51: 410-419.
70. Slatkin, M., and B. Rannala. 1997. Estimating the age of alleles using intraallelic variability. *Am. J. Hum. Genet.* 60: 447-458.
71. Rannala, B., and Z. Yang. 1996. Probability distribution of molecular evolutionary trees: a new method of phylogenetic inference. *J. Mol. Evol.* 43: 304-311.
72. Rannala, B. 1996. The sampling theory of neutral alleles in an island population of fluctuating size. *Theor. Popul. Biol.* 50: 91-104.
73. Rannala, B., and J.A. Hartigan. 1996. Estimating gene flow in island populations. *Genet. Res.* 67: 147-158.
74. Brown, C.R., M.B. Brown, and B. Rannala. 1995. Ectoparasites reduce long-term survival of their avian host. *Proc. Roy. Soc. Lond. B* 262: 313-319.
75. Rannala, B. 1995. Polymorphic characters and phylogenetic analysis: a statistical perspective. *Syst. Biol.* 44: 422-430.
76. Rannala, B., and J.A. Hartigan. 1995. Identity by descent in island-mainland populations. *Genetics* 139: 429-437.
77. Brown, C.R., and B. Rannala. 1995. Colony choice in birds: models based on temporally invariant site quality. *Behav. Ecol. Sociobiol.* 36: 221-228.
78. Rannala, B., and C.R. Brown. 1994. Relatedness and conflict over optimal group size. *Trends Ecol. Evol.* 9: 117-119.

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79. Rannala, B. 1992. Comparative evolutionary genetics of trematode parasites (Plagiorchiidae) and their anuran hosts. *Can. J. Zool.* 70: 993-1000.
80. Rannala, B. 1991. Evidence for host allozymes present on electrophoretic gels of trematode parasites (Digenea: Plagiorchiiformes). *J. Parasitol.* 77: 805-808.
81. Rannala, B. 1990. Genetic distance and parasite taxonomy. *J. Parasitol.* 76: 929-930.
82. Rannala, B. 1990. Electrophoretic evidence concerning the relationship between *Haplometrana* and Glythelminis (Digenea: Plagiorchiiformes). *J. Parasitol.* 76: 746-748.

### Book Chapters:

1. Rannala, B. and Z. Yang. (expected 2013). Molecular dating. In: *Princeton Guide to Evolution* (ed. J. Losos). Princeton University Press.
2. Wang, Y., and B. Rannala. 2004. Simulating a coalescent process with recombination and ascertainment. In: *Computational Methods for SNPs and Haplotype Inference* (eds. S. Istrail, M. Waterman and A. Clark). *Lecture Notes in Bioinformatics 2983*: 84-95. Springer-Verlag.
3. Huelsenbeck, J.P., Rannala, B., and B. Larget. 2002. A statistical perspective for reconstructing the history of host-parasite associations. In: *Tangled Trees: Phylogenies, Cospeciation and Coevolution* (ed. R.D.M. Page). University of Chicago Press.
4. Rannala, B., and Y. Michalakis. 2002. Population genetics and cospeciation. In: *Tangled Trees: Phylogenies, Cospeciation and Coevolution* (ed. R.D.M. Page). University of Chicago Press.
5. Rannala, B. 2002. Molecular phylogenies and virulence evolution. In: *Virulence Management: The Adaptive Dynamics of Pathogen-Host Interactions* (eds. U. Dieckmann, J.A.J. Metz, M.W. Sabelis and K. Sigmund). Cambridge University Press.
6. Huelsenbeck, J.P. and B. Rannala. 2000. Using stratigraphic data in phylogenetics. In *Morphological Evolution* (ed. J. Wiens). Smithsonian Institution Press.

### Selected graduate texts citing one or more papers by Bruce Rannala:

1. *Human Genetic Linkage Analysis* by J. Ott (John Hopkins Univ Press, 1999)
2. *Molecular Evolution and Phylogenetics* by M. Nei and S. Kumar (Oxford Univ Press, 2000)
3. *Biological Sequence Analysis* by R. Durbin, S. Eddy, A. Krogh, and G. Mitchison (Cambridge Univ Press, 1998)
4. *Statistical Methods in Bioinformatics: An Introduction* by W. Ewens and G. Grant (Springer, 2001)
5. *Phylogenetic Trees Made Easy: A How-to Manual for Molecular Biologists* by B.G. Hall (Sinauer Press, 2001)
6. *Bioinformatics: The Machine Learning Approach* by P. Baldi and S. Brunak (MIT Press, 2001)
7. *Phylogenetic Inference* by J. Felsenstein (Sinauer Press, 2003)
8. *Mathematical Population Genetics* by W. Ewens (Springer, 2003)
9. *Gene Genealogies, Variation and Evolution: A primer in coalescent theory* by J. Hein, M. Schierup, and C. Wiuf (Oxford Univ Press, 2004)
10. *Computational Molecular Evolution* by Z. Yang (Oxford Univ Press, 2006)
11. *Coalescent Theory* by J. Wakeley (Roberts and Company, 2009)

### **Reviewer for Journals:**

Reviewer for *Science*, *Nature*, *Nature Genetics*, *Nature Reviews Genetics*, *PLOS Biology*, *Proc. Natl. Acad. Sci. USA*, etc. Review 20-40 papers per year.

### **Editorial Duties:**

2004-2006: Associate Editor, *American Journal of Human Genetics*  
2001-2004: Associate Editor, *Systematic Biology*

## 8. CV. Bruce Rannala

### **Graduate Group Memberships at UC Davis:**

Population Biology (2005-present), Genetics (2010-present), Biostatistics (2011-present).

### **Selected External Reviews For Granting (and Award) Agencies:**

Canadian Institutes of Health Research, CAN  
MacArthur Foundation, US  
Michael Smith Foundation, CAN  
National Environment Research Council, UK  
National Institutes of Health, USA  
National Science Foundation, USA  
Natural Sciences and Engineering Research Council, CAN  
Netherlands Organisation for Scientific Research  
Qatar National Research Fund  
United States-Israel Bi-National Science Foundation  
Wellcome Trust, UK

### **Recent Grant Review Panels (2009-present):**

2017: CIHR Project Grant Program, Final Assessment Stage (Ottawa)  
2015: Canadian Institutes of Health Research (CIHR) grant review panel, Genetics 2 (Ottawa)  
2013: NIH Genetic Variation and Evolution study section (online due to government closure)  
2012: NIH Genetic Variation and Evolution study section (Los Angeles, CA)  
2011: Canadian Institutes of Health Research (CIHR) grant review panel, Genetics (Ottawa)  
2011: NIH Genetic Variation and Evolution study section (Washington, DC)  
2010: NSF Systematics review panel (Arlington, VA)  
2010: Canadian Institutes of Health Research (CIHR) grant review panel, Genetics (teleconference)  
2009: NSERC of Canada site visit (Guelph University)  
2006-2009: National Evolutionary Synthesis Center, Durham NC, Science Board Member  
pre-2009: 1-2 panels per year.

### **Teaching Experience (Instructor):**

#### University of California Davis

MCB 010 (Undergraduate Level), Introduction to Human Heredity  
(Instructor: Wn '11, Wn '12, Sp '13, Sp '15, Sp'16)  
EVE 131 (Undergraduate Level), Human Genetic Variation and Evolution (developed new course)  
(Instructor: Wn '08, Sp '10, Wn '13 Wn '15)  
EVE 231 (Graduate Level), Principles of Biological Data Analysis (developed new course)  
(Instructor: Wn '06, Wn '07, Fa '10)

#### University of Alberta

MDGEN 604 (Graduate Level), Statistical Methods in Medical Genetics (developed new course)  
(Instructor: Fa '04)  
MDGEN 603 (Graduate Level), Seminars in Medical Genetics  
(Coordinator for 1/2 of course [with Alicia Chan]: Fa '02)  
MDGEN 602 (Graduate Level), Seminar (Journal Club) on Mapping Complex Diseases  
(Instructor: Wn '01)  
BIOL 520 (Graduate Level), Advanced Phylogenetic Analysis  
(Guest Lecturer: Fa '01)  
MDGEN 601 (Graduate Level), Selected Topics in Medical Genetics  
(Course Coordinator; 1/3 of lectures; Wn '02)



## 9. CV. Bruce Rannala

### University of Calgary

MDSC 755.40 (Graduate Level), Genomics  
(Guest Lecturer: Fa '01, Fa '02, Fa '03)

### SUNY Stony Brook

BEE 552 (Graduate Level), Biometry  
(Instructor for 1/2 of course [with F. J. Rohlf]: Sp '99)

BEE 565 (Graduate Level), Molecular Evolution  
(Guest Lecturer: Sp '99)

BEE 691, Graduate Seminar on Coalescent Theory  
(Instructor: Fa '99)

BEE 554 (Graduate Level), Population Genetics  
(Instructor for 1/2 of course [with D. Dykhuizen]: Sp '00)

BIO 302 (Undergraduate Level), Human Genetics (developed new course)  
(Instructor: Sp '00)

### **Postdoctoral Researchers Supervised:**

4/99 to 7/01: Dr. Xue-jun Qin (supported by NIH grant). Project Title: "Statistical methods for transmission/disequilibrium mapping of disease loci: An information theory approach" (currently a Research Associate at Duke University)

9/00 to 10/05: Dr. Jeffrey Reeve (supported by Killam memorial postdoctoral fellowship). Project Title: "Bayesian multipoint disequilibrium mapping methods using Markov chain Monte Carlo" (currently a Staff Biostatistician at the University of Alberta)

9/01 to 9/03: Dr. Greg Wilson (supported by CIHR grant). Project Title: "Multilocus genetic methods of identifying admixed individuals and inferring recent rates of migration among populations" (currently a Wildlife Biologist at the Canadian Wildlife Service)

9/08 to 9/10: Dr. Adam Leache (supported by NSF postdoctoral fellowship). Project title: "Using simulation to evaluate the performance of species tree inference methods" (currently an Assistant Professor at the University of Washington)

01/09 to 7/12: Dr. Badri Padhukasahasram (supported by NIH grant). Project Title: "Improved methods for inferring recombination processes in humans that incorporate gene conversion" (currently a Research Scientist at Illumina)

08/11 to 7/13: Dr. Anna Guan (supported by NIH grant). Project Title: "Population genomic analysis of cancers" (currently a Research Team Leader at 23andMe)

### **Graduate Students Supervised:**

9/16 to present: Sneha Chakraborty (Ph.D. student). Biostatistics graduate group.

9/15 to 6/16: Huiyu Sun (M.S. student). Bioinformatics project. (currently a data analyst at Immune Tolerance Network [ITN])

6/08 to 6/14: Rattanasak Wongkomonched (Co-supervisor: Ph.D. Student). Project Title: "A genome-wide case-control association study of lung cancer patients in Northern Thailand"

9/10 to 9/12: Chi Zhang (PhD Exchange Student). Project Title: "Robustness of compound Dirichlet priors for Bayesian inference of branch lengths" (currently an Associate Professor at Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences, Beijing).

6/02 to 11/08: Ying Wang (Ph.D. student). Project Title: "A new method for constructing a fine-scale linkage map of the human genome" (currently an Associate Professor at the Beijing Institute of Genomics, Beijing)

6/03 to 6/08: Kanokkan Bumroonkit (Co-supervisor: Ph.D. Student). Project Title: "Somatic mutations of TP53 in lung cancer patients from Northern Thailand" (currently an Assistant Professor of Anatomy, Chiang Mai University, Thailand)

## 10. CV. Bruce Rannala

6/02 to 2/07: Karen Cranston (Ph.D. student). Project Title: "New methods for accelerating and assessing convergence of Bayesian phylogenetic inference algorithms" (currently lead PI of Open Tree of Life and Bioinformatics Project Manager, NESCent)

3/01 to 12/06: Ligia Mateiu (Ph.D. student). Project Title: "New methods for modeling among-site rate variation in phylogenetic inference" (currently a Bioinformatics Team Leader at Universiteit Antwerpen, Belgium)

8/99 to 9/05: Weon-sang (Simon) Ro (Ph.D. student). Project Title: "The stop-EGFP transgenic mouse as a novel system for estimating somatic mutation rates in vivo" (currently a Research Assistant Professor at Yonsei University Medical School, South Korea)

8/04 to 8/05: Christina Fetterman (M.Sc. student). Project Title: "Patterns of evolution and natural selection in the FOXC gene family" (Co-supervisor Dr. Michael Walter, at University of Alberta)

8/99 to 8/00: Bixia Ji (M.S. student). Project Title: "Evidence for overdominant selection on HLA loci: Modeling and DNA sequence analysis of the Finnish population" (currently a Senior Software Engineer, Declara)