BIOGRAPHICAL SKETCH
Bruce Rannala

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(a) Professional Preparation

Institution	Location	Major/Area	Degree	Year
University of British Columbia	Canada	Zoology	B.Sc.	1989
University of Toronto	Canada	Zoology	M.Sc.	1991
Yale University	U.S.A.	Biology	PhD	1995
University of Calif., Berkeley	U.S.A.	Population Genetics	Postdoc	95-98

(b) Appointments

2004-present	Professor, Dept. of Evolution and Ecology, UC Davis
2013-2016	Chair, Biostatistics Graduate Group, UC Davis
2012-2016	Guest Professor, Beijing Institute of Genomics, Beijing
2004-2014	Professor, Genome Center, UC Davis
2009	Miller Professor, UC Berkeley
2006-2008	Associate Director of Bioinformatics, Genome Center, UC Davis
2001-2007	CIHR Peter Lougheed Scholar
2001-2007	Scholar, Alberta Heritage Foundation for Medical Research
2006	Visiting Fellow, Newton Institute for Mathematical Sciences, Cambridge
2002-2004	Associate Professor, Dept. of Medical Genetics, University of Alberta, Edmonton
2000-2002	Assistant Professor, Dept. of Medical Genetics, University of Alberta, Edmonton
1998-2000	Assistant Professor, Dept. of Ecol. and Evol., SUNY Stony Brook

(c) Publications (selected from a total of 80 peer-reviewed publications)

Publications related to the proposed project
Y. Wang and B. Rannala. 2014. Bayesian inference of shared recombination hotspots between humans and chimpanzees. Genetics 198: 1621–1628.
B. Padhukasahasram and B. Rannala. 2013. Meiotic gene-conversion rate and tract length variation in the human genome. European Journal of Human Genetics doi: 10.1038/ejhg.2013.30.
B. Padhukasahasram and B. Rannala. 2011. Bayesian population genomic inference of crossing-over and gene-conversion. Genetics 189: 607-619.
Y. Wang and B. Rannala. 2009. Population genomic inference of recombination rates and hotspots. Proceedings of the National Academy of Sciences USA 106: 6210-6214.
Y. Wang and B. Rannala. 2008. Bayesian inference of fine-scale recombination rates using population genomic data. Philosophical Transactions of the Royal Society B 363: 3921-3930.

Other publications
H. Alhaddad, C. Zhang, B. Rannala, and L.A. Lyons. In Review. A glance at recombination hotspots in the domestic cat. PLoS One. doi: http://dx.doi.org/10.1101/028043.
S. 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.
Z. Yang and B. Rannala. 2014. Unguided species delimitation using DNA sequence data from multiple loci. Molecular Biology and Evolution 31: 3125–3135.
Z. Yang and B. Rannala. 2012. Molecular phylogenetics: principles and practice. Nature Reviews Genetics 13: 303-314.
M.A. Beaumont and B. Rannala. 2004. The Bayesian revolution in genetics. Nature Reviews Genetics 5: 251-261.

(d) Synergistic Activities
Dr. Rannala's research group has developed (and supports) several open source population genetics software packages including BayesAss, DMLE, Immanc and InferRho. Rannala also collaborated in the development of the BPP program for Bayesian phylogenetics (distributed by Ziheng Yang). Dr. Rannala has contributed to the diversity of the (predominantly male) community of theoretical population geneticists, with 4 of 5 students completing a Ph.D. under his supervision being female. Dr. Rannala has also co-supervised, or mentored, Ph.D. students from several developing countries including China and Thailand and regularly teaches in international phylogenetics workshops in China, Greece, Sweden, the UK and the US.