

## Curriculum Vitae

Ziheng Yang, FRS

### R.A. Fisher Chair of Statistical Genetics

Department of Genetics, Evolution and Environment  
University College London  
Darwin Building  
Gower Street  
London WC1E 6BT, England  
Phone: +44 (20) 7679 4379  
Fax: +44 (20) 7679 7096  
Email: [z.yang@ucl.ac.uk](mailto:z.yang@ucl.ac.uk)

URL: <http://abacus.gene.ucl.ac.uk/>

*Present post:* R.A. Fisher Chair of Statistical Genetics, since 2010

## Biographical

*Date of birth:* 1 November 1964.

*Place of Birth:* Gansu Province, P.R. China.

*Citizenship:* British

## Research Interests

Molecular evolution; molecular phylogenetics; theoretical population genetics; computational biology and bioinformatics; computational statistics.

## Education

- Ph. D., 1992, agricultural science (molecular evolution), Beijing Agricultural University, P.R. China
- M. Sc., 1987, agricultural science (quantitative genetics and animal breeding), Beijing Agricultural University, China
- B. Sc., 1984, agricultural science, Gansu Agricultural University, China

## Professional History

- 2010-date, Director, RA Fisher Centre for Computational Biology, UCL.
- 2010-date, RA Fisher Chair of Statistical Genetics, Department of Genetics, Evolution and Environment, University College London.
- 2001-2010, Professor of Statistical Genetics, Department of Biology, University College London.
- 2000-2001, Reader of Evolutionary Genetics, Department of Biology, University College London.
- 1997-2000, Lecturer, Department of Biology, University College London.
- 1995-1997, Postdoctoral research fellow, Department of Integrative Biology, University of California at Berkeley.
- 1994-1995, Postdoctoral research fellow, Institute of Molecular Evolutionary Genetics, The Pennsylvania State University.
- 1993-1994, Postdoctoral research fellow (independent researcher) at Department of Zoology, The Natural History Museum (London).
- 1992-1993, Postdoctoral research fellow at Department of Zoology, University of Cambridge.
- 1992-1997, Lecturer of Genetics at Department of Animal Science, Beijing Agricultural University.

## Other Appointments and Affiliations

- June 2013-2016, Visiting Professor, Centre for Computational Genomics, Beijing Institute of Genomics, Chinese Academy of Sciences, Beijing.
- February-August 2011, Visiting Professor, Computer Science, Swiss Institute of Technology (ETH), Zurich.
- November 2010-February 2011, Visiting Professor, Institute of Zoology, Chinese Academy of Sciences, Beijing.
- August-November 2010, Visiting Professor, College of Life Sciences, Peking University, Beijing, China.
- 2008-2011, Changjiang Chair Visiting Professor, Sun Yat-sen University, Guangdong, China.
- 2007-2012, Director, Centre for Computational and Evolutionary Biology, Institute of Zoology, Chinese Academy of Sciences, Beijing.
- Oct 2007-Mar 2008, Visiting Professor, University of Tokyo, Japan.
- Oct-Nov 2004, Visiting Professor, University of Montpellier.
- 1998-1999, Research Associate, Natural History Museum.
- Nov 1997-Feb 1998, Visiting Associate Professor, Institute of Statistical Mathematics, Tokyo, Japan.

## Awards and Other Honours

- 2010, Frink Medal for British Zoologists, The Zoological Society of London.
- 2009, Royal Society Wolfson Research Merit Award
- 2008, Presidents' Award for Lifetime Achievement, Society for Systematic Biology
- 2006, Fellow of the Royal Society, The Royal Society of London
- 1995, Young Investigator's Prize from American Society of Naturalists.
- 1992 - 1993, China-EEC exchange programme, awarded as a postdoctoral fellowship in England.

## Grants

### Project Grants

- 2016-2019 BB/N000609/1. *Improving Bayesian methods for estimating divergence times integrating genomic and trait data*, BBSRC (co-PI with Dr Philip Donoghue of U. Bristol), £480K.
- 2016-2018 *The Origin of Plants: Genomes, rocks, and biogeochemical cycles*, 366K, NERC (co-PI. Leading PI: Harald Schneider, Natural History Museum), £366K.
- 2015-2017 *Untangling the enigmatic origins of placental mammals with fossils and genomics*, BBSRC (co-Applicant with Dr Anjali Goswami of UCL), £85K.
- 2013 - 2016 *Statistical methods for genomic analysis of species divergences*, BBSRC, £416K.
- 2012 - 2015 *Bayesian estimation of species divergence times integrating fossil and molecular information*. BBSRC (co-PI with Dr Philip Donoghue of U. Bristol), £446K.
- 2009 - 2014 *Meeting the challenges of population genomics and phylogenomics*. Royal Society Wolfson Research Merit Awards, £75K.
- 2009 - 2012 *Representation and incorporation of fossil data in molecular dating of species divergences*, BBSRC (co-PI with Dr Philip Donoghue of U. Bristol), £444K.
- 2005 - 2009 *Development of codon-based substitution models for detecting natural selection in protein-coding genes*, BBSRC (PI), £225K.
- 2005 - 2008 *Statistical methods for estimating species divergence times combining heterogeneous genetic data sets*, NERC (PI), £234K.
- 2001 - 2005 *From molecular adaptation to protein function: New tools for genome analysis*, Human Frontier Science Programme (co-PI with Drs Rasmus Nielsen and Karl Schmid) US\$750K.
- 2001 - 2004 *Development, evaluation, and application of phylogenetic methods for detecting molecular adaptation*, BBSRC (PI, with Dr Joe Bielawski as named researcher), £178K.
- 2001-2004 *Statistical and computational improvements to molecular phylogenetic estimation*, BBSRC (PI), £149K.
- 2000-2003 *Molecular phylogenetics and evolution of actinopterygian fishes as inferred from mitochondrial protein coding sequences*, BBSRC (Co-Appl, with Drs Mark Thomas (PI) and Mike Coates), £157K.
- 1998 - 2001 *Bayesian estimation of molecular phylogenies*, BBSRC (PI), £133K.

- 1998 - 2001 *Models of codon substitution and detection of adaptive molecular evolution*, BBSRC (PI), £148K.
- 1994 - 1996, *Molecular evolution and systematics of mammals*. National Science Foundation of China (PI).
- 1993 - 1994, *Reliability of phylogenetic inference*. Natural History Museum (London), Interdisciplinary research project.

## Travel and Equipment Grants

- 2009 *Bayesian automatic clustering and its use in population genetics*, UCL CoMPLEX travel grant to collaborate with Professor Jukka Corander of Department of Mathematics, Åbo Akademi University, Finland. £1250.
- 2005-2008 *Phylogenetic analysis of large molecular data sets from multiple loci and estimation of divergence times and ancestral population sizes*. National Science Foundation of China Collaborative Grant, China (Collaborator: Professor De-Xing Zhang, Institute of Zoology, Beijing, China), RMB Yuan 250,000.
- 2000 *Combining structural and evolutionary approaches to understand protein evolution*, International Scientific Interchange Scheme (BBSRC) for collaboration with Dr Belinda Chang in Rockefeller University, BBSRC, £2,900.
- 1999 - 2001 *Estimation of nucleotide substitution rates to study the mechanisms of molecular evolution*, Royal Society Joint Project for collaboration with Prof. Masami Hasegawa of Institute of Statistical Mathematics, Tokyo, Japan, £11,400.
- 1999 Joint Research Equipment Initiative (Co-Appl, with Profs Linda Partridge (PI), David Goldstein, Drs. Stephen Wilson, and David Gems). £312K.

## Publications (total citations: 51K, $h = 83$ , according to google scholar)

### Books

1. Yang, Z. 2006, *Computational Molecular Evolution*, Oxford University Press. 376 pages (ISBN: 9780198567028).
2. Yang, Z. 2014, *Molecular Evolution: A Statistical Approach*, Oxford University Press. 512 pages (ISBN: 9780199602612).

### Refereed Journal Articles (\*Corresponding author)

3. Rannala, B. Yang, Z.\* 2016. Efficient Bayesian species tree inference under the multispecies coalescent. *Systematic Biology*
4. Yang, Z. and P.C. Donoghue, 2016. Dating species divergences using rocks and clocks: an introduction. *Phil. Trans. R. Soc. B: Biol. Sci.*, **371**: 20150126.
5. Donoghue, P.C. and Z. Yang, 2016. The evolution of methods for establishing evolutionary timescales. *Phil. Trans. R. Soc. B: Biol. Sci.*, **371**:20160020
6. Dalquen, D., Zhu, T., Yang, Z.\* 2016. Maximum likelihood implementation of an isolation-with-migration model for three species. *Systematic Biology*, DOI:10.1093/sysbio/syw063
7. dos Reis, M.\*, P.C.J. Donoghue and Z. Yang\*, 2016. Bayesian molecular clock dating of species divergences in the genomics era. *Nature Reviews Genetics* **17**: 71-80.
8. dos Reis, M., Y. Thawornwattana, K. Angelis, M. J. Telford, P. C. J. Donoghue\*, and Z. Yang\*. 2015. Uncertainty in the timing of origin of animals and the limits of precision in molecular timescales. *Current Biology* **25**:2939-2950.
9. Yang, Z.\* 2015. The BPP program for species tree estimation and species delimitation. *Current Zoology* **61**: 854-865.
10. Matsumoto T., Akashi H., Yang Z.\* 2015. Evaluation of ancestral sequence reconstruction methods to infer nonstationary patterns of nucleotide substitution. *Genetics* **200**: 873-890. [*Genetics* highlight]
11. Liu, J., Zhang, D.-X., Yang, Z.\* 2015. A discrete-beta model for testing gene flow after speciation, *Methods in Ecology and Evolution*, 10.1111/2041-210X.12356.

12. Zhu T, dos Reis M, Yang Z.\* 2015. Characterization of the uncertainty of divergence time estimation under relaxed molecular clock models using multiple loci. *Systematic Biology* **64**: 267-280.
13. Yang, Z., and B. Rannala\*. 2014. Unguided species delimitation using DNA sequence data from multiple loci. *Mol. Biol. Evol.*: **31**: 3125-3135
14. Zhang C, Rannala B, Yang Z.\* 2014. Bayesian species delimitation can be robust to guide tree inference errors. *Systematic Biology* **63**: 993-1004
15. Angelis K, dos Reis M, Yang Z.\* 2014. Bayesian estimation of nonsynonymous/synonymous rate ratios for pairwise sequence comparisons. *Molecular Biology and Evolution* **31**(7): 1902-1913.
16. dos Reis, M., T. Zhu, and Z. Yang\*. 2014. The impact of the rate prior on Bayesian estimation of divergence times with multiple loci. *Systematic Biology* **63**(4): 555-565.
17. dos Reis, M.\*, M. J. Donoghue, and Z. Yang. 2014. Neither phylogenomic nor palaeontological data support a Paleogene origin of placental mammals. *Biological Letters* **10**: 20131003 [reported in *Discovery, The Scientist, Nature, and Times of India.*]
18. Yoder, A. D., L. M. Chan, M. dos Reis, P. A. Larsen, C. R. Campbell, R. Rasolarison, M. Barrett, C. Roos, P. Kappeler, J. P. Bielawski, and Z. Yang. 2014. Molecular evolutionary characterization of a V1R subfamily unique to Strepsirrhine primates. *Genome Biology and Evolution* **6**: 213-227.
19. Leaché, A. D.\*, R. B. Harris, B. Rannala, and Z. Yang. 2014. The influence of gene flow on Bayesian species tree estimation: A simulation study. *Systematic Biology* **63**: 17-30.
20. Yang Z.\*, Rodríguez C.E. 2013. Searching for efficient Markov chain Monte Carlo proposal kernels. *Proc Natl Acad Sci USA* **110**: 19307-19312.
21. Xu B, Yang Z.\* 2013. PamIX: A graphical user interface for PAML. *Molecular Biology and Evolution* **30**: 2723-2724.
22. dos Reis, M., and Z. Yang\*. 2013. Why do more divergent sequences produce smaller nonsynonymous/synonymous rate ratios in pairwise sequence comparisons? *Genetics* **195**:195-204.
23. Stadler T, Yang Z\* 2013. Dating phylogenies with sequentially sampled tips. *Systematic Biology* **62**: 674-688.
24. Zou X-H, Yang Z, Doyle JJ & Ge S.\* 2013. Multilocus estimation of divergence times and ancestral effective population sizes of *Oryza* species and implications for the rapid diversification of the genus. *New Phytologist* **198**: 1155-1164.
25. Rannala, B., and Yang Z.\* 2013. Improved reversible jump algorithms for Bayesian species delimitation. *Genetics* **194**: 245-253.
26. dos Reis M, and Yang Z.\* 2013. The unbearable uncertainty of Bayesian divergence time estimation. *Journal of Systematics and Evolution* **51**: 30-43.
27. Schabauer H, Valley M, Pacher C, Stockinger H, Stamatakis A, Robinson-Rechavi M, Yang Z, Salamin N. 2012. SlimCodeML: An optimized version of CodeML for the branch-site model. Pp. 700-708. 11th International Workshop on High Performance Computational Biology (HiCOMB). IEEE.
28. dos Reis M., Inoue J., Hasegawa M., Asher R., Donoghue P.C.\*, Yang Z.\* 2012. Phylogenomic data sets provide both precision and accuracy in estimating the timescale of placental mammal evolution. *Proc. R. Soc. Lond. B.* **279**: 3491-3500.
29. Zhai W, Nielsen R, Goldman N, Yang Z.\* 2012. Looking for Darwin in genomic sequences - validity and success of statistical methods. *Molecular Biology and Evolution* **29**: 2889-2893.
30. Zhu T, Yang Z.\* 2012. Maximum likelihood implementation of an isolation-with-migration model with three species for testing speciation with gene flow. *Molecular Biology and Evolution* **29**: 3131-3142.
31. Zhang C, Rannala B, Yang Z.\* 2012. Robustness of compound Dirichlet priors for Bayesian inference of branch lengths. *Systematic Biology* **61**: 779-784.
32. Yang Z.\*, Rannala B. 2012. Molecular phylogenetics: principles and practice. *Nature Review Genetics* **13**: 303-314.
33. Parham, J.\*, Donoghue, P, Bell, C, Calway, T, Head, J, Holroyd, P, Inoue, J, Irmis, R, Joyce, W, Ksepka, D, Patane, J, Smith, N, Tarver, J, van Tuinen, M, Yang, Z, Angielczyk, K, Greenwood, J, Hipsley, C, Louis, J, Makovicky, P, Mueller, J, Smith, K, Theodor, J, Warnock, R and Benton, M, 2012. Best practices for applying paleontological data to molecular divergence dating analyses. *Systematic Biology* **61**: 346-359.
34. Warnock, R.C.M., Z. Yang, and P.C.J. Donoghue\*. 2012. Exploring uncertainty in the calibration of the molecular clock. *Biological Letters* **8**: 156-159.

35. Rannala B., Zhu T., Yang Z.\* 2012. Tail paradox, partial identifiability and influential priors in Bayesian branch length inference. *Molecular Biology and Evolution* **29**: 325-335.
36. Zhang C., Zhang D.-X., Yang Z.\* 2011. Evaluation of a Bayesian coalescent method of species delimitation. *Systematic Biology* **60**: 747-761.
37. Brown RP, Yang Z. 2011. Rate variation and estimation of divergence times using strict and relaxed clocks. *BMC Evolutionary Biology* **11**: 271.
38. Zang, L.-L., X.-H. Zou, F.-M. Zhang, Z. Yang, S. Ge\*, 2011 Phylogeny and species delimitation of the C-genome diploid species in *Oryza*. *Journal of Systematics and Evolution* **49**: 386-395.
39. Groussin M., Pawlowski J., Yang Z.\* 2011. Bayesian relaxed clock estimation of divergence times in Foraminifera. *Molecular Phylogenetics and Evolution*, **61**: 157-166.
40. Yoshida I., Sugiura W., Shibata J., Ren F.\*, Yang Z., Tanaka H. 2011. Change of positive selection pressure on HIV-1 envelope gene inferred by early and recent samples. *PLOS One* **6**: e18630.
41. dos Reis M, Yang Z.\* 2011. Approximate likelihood calculation for Bayesian estimation of divergence times. *Molecular Biology and Evolution* **28**: 2161–2172.
42. Zhu T., Hu, Y., Ma, Z., Zhang, D.-X., Li, T. and Yang, Z.\* 2011. Efficient simulation under a population genetics model of carcinogenesis. *Bioinformatics* **27**: 837-843.
43. Yang Z.\* , dos Reis M. 2011. Statistical properties of the branch-site test of positive selection. *Molecular Biology and Evolution*, **28**: 1217-1228.
44. Wilkinson R.D.\* , M.E. Steiper, C. Soligo, R.D. Martin, Z. Yang, S. Tavaré. 2011. Dating primate divergences through an integrated analysis of palaeontological and molecular data. *Systematic Biology*, **60**: 16-31.
45. Chen M.-S.\* , X. Liu, Z. Yang, H. Zhao, R. Shukle, J. Stuart, S. Hulbert. 2010. Unusual conservation among genes encoding small secreted salivary gland proteins from a gall midge. *BMC Evolutionary Biology* **10**: 296.
46. Fletcher W. and Z. Yang\* 2010. The effect of insertions, deletions and alignment errors on the branch-site test of positive selection. *Molecular Biology and Evolution* **27**: 2257-2267.
47. Yang Z. and B. Rannala \*. 2010. Bayesian species delineation using multilocus sequence data. *Proc. Natl. Acad. Sci. USA*. **107**: 9264-9269.
48. Yang Z.\* 2010. A likelihood ratio test of parapatric speciation using genomic data from three species. *Genome Biology and Evolution* **2**: 200-211.
49. Beaumont, M.\* , R. Nielsen, C. Robert, J. Hey, O. Gaggiotti, L. Knowles, A. Estoup, M. Panchal, J. Corander, M. Hickerson, S. Sisson, N. Fagundes, L. Chikhi, P. Beerli, R. Vitalis, J.-M. Cornuet, J. Huelsenbeck, J. Novembre, M. Foll, Z. Yang, F. Rousset, D. Balding And L. Excoffier. 2010. In defence of model-based inference in phylogeography. *Molecular Ecology* **19**: 436-446.
50. Brown, R.P.\* and Z. Yang. 2010. Bayesian dating of shallow phylogenies with a relaxed clock. *Systematic Biology* **59**: 119-131.
51. Inoue, J., P. C. H. Donoghue, and Z. Yang\*. 2010. The impact of the representation of fossil calibrations on Bayesian estimation of species divergence times. *Systematic Biology* **59**: 74-89.
52. Yang, Z.\* , R. Nielsen, and N. Goldman, 2009 In defense of statistical methods for detecting positive selection. *Proceedings of the National Academy of Sciences of U.S.A.* **106**: E95-E95.
53. Fletcher W. and Z. Yang\*. 2009. INDELible: A flexible simulator of biological sequence evolution. *Molecular Biology and Evolution* **26**: 1879-1888.
54. Ren F., Tanaka, H., and Yang, Z.\*. 2009. A likelihood look at the supermatrix-supertree controversy. *Gene* **441**: 119-125.
55. Rota-Stabelli, O., Yang, Z. and Telford, M. \*. 2009. MtZoa: a general mitochondrial amino acid substitutions model for animal evolutionary studies. *Molecular Phylogenetics and Evolution* **52**: 268-272.
56. Schmid, K.J. and Yang, Z.\* 2008. The trouble with sliding windows. *PLoS One*, **3**: e3746
57. Goldman, N.\* and Yang, Z. 2008. Statistical and computational challenges in molecular phylogenetics and evolution, Introduction. *Philosophical Transactions of the Royal Society of London B*. **363**: 3889-3892.
58. Yang, Z.\* 2008. Empirical evaluation of a prior for Bayesian phylogenetic inference. *Philosophical Transaction of the Royal Society of London B: Biological Sciences*. **363**: 4031-4039.

59. Vamathevan, J, S. Hasan, R. Emes, H. Amrine-Madsen, D. Rajagopalan, S. Topp, V. Kumar, M. Word, M. Simmons, S. Foord, P. Sanseau, Z. Yang, and J. Holbrook\*. 2008. The role of positive selection in determining the molecular cause of species differences in disease. *BMC Evolutionary Biology* **8**: 273.
60. Burgess, R. and Z. Yang\*. 2008. Estimation of hominoid ancestral population sizes under Bayesian coalescent models incorporating mutation rate variation and sequencing errors. *Molecular Biology and Evolution* **25**: 1979-1994.
61. Rannala B, and Z. Yang\*. 2008. Phylogenetic inference using whole genomes. *Annual Review of Genomics and Human Genetics* **9**: 217-231.
62. Emes, R. D.\* and Z. Yang. 2008. Duplicated paralogous genes subject to positive selection in the genome of *Trypanosoma brucei*. *PLoS One* **3**: e2295.
63. Furlong, R. F., and Z. Yang\*. 2008. Diversifying and purifying selection in the peptide binding region of DRB in mammals. *Journal of Molecular Evolution* **66**: 384-394.
64. Yang Z\*, and R. Nielsen. 2008. Mutation-selection models of codon substitution and their use to estimate selective strengths on codon usage. *Molecular Biology and Evolution* **25**: 568-579.
65. Zhou R., K. Zeng, W. Wu, X. Chen, Z. Yang, S. Shi, C.-I. Wu\*. 2007. Population genetics of speciation in nonmodel organisms: I. ancestral polymorphism in mangroves. *Molecular Biology and Evolution* **24**:2746-2754.
66. Anisimova, M.\* , J. P. Bielawski, K. Dunn, and Z. Yang. 2007. Phylogenomic analysis of natural selection pressure in *Streptococcus* genomes. *BMC Evolutionary Biology* **7**:154.
67. Yang, Z.\* 2007. Fair-balance paradox, star-tree paradox and bayesian phylogenetics. *Molecular Biology and Evolution* **24**: 1639-1655.
68. Yang, Z.\* 2007. PAML 4: Phylogenetic analysis by maximum likelihood. *Molecular Biology and Evolution* **24**: 1586-1591.
69. Rannala, B., and Z. Yang\*. 2007. Bayesian estimation of species divergence times from multiple loci using multiple calibrations. *Systematic Biology*, **56**: 453-466.
70. Anisimova, M., and Z. Yang\*. 2007. Multiple hypothesis testing to detect lineages under positive selection that affects only a few sites. *Molecular Biology and Evolution* **20**: 1219-1228.
71. Hurley, I.A., R.L. Mueller, K.A. Dunn, E.J. Schmidt, M. Friedman, R.K. Ho, V.E. Prince, Z. Yang, M.G. Thomas, M.I. Coates\*. 2007. A new time-scale for ray-finned fish evolution. *Proc. R. Soc. Lond. B. Biol. Sci.* **274**: 489-498.
72. Yang, Z.\* 2006. On the varied pattern of evolution of two fungal genomes: a critique of Hughes and Friedman. *Molecular Biology and Evolution* **23**:2279-2282.
73. Ren, F.\* , A. Tsubota, T. Hirokawa, H. Kumada, Z. Yang, and H. Tanaka. 2006. A unique amino acid substitution, T126I, in human genotype C of hepatitis B virus S gene and its possible influence on antigenic structural change. *Gene* **383**: 43-51.
74. Aguileta, G.\* , J. P. Bielawski, Z. Yang. 2006. Proposed standard nomenclature for the a- and b-globin gene families. *Genes and Genetic Systems*. **81**:367-371
75. Aguileta, G., J. P. Bielawski\*, and Z. Yang. 2006. Evolutionary rate variation among vertebrate beta globin genes: implications for dating gene family duplication events. *Gene* **380**: 21-29.
76. Yang, Z., and B. Rannala\*. 2006. Bayesian estimation of species divergence times under a molecular clock using multiple fossil calibrations with soft bounds. *Molecular Biology and Evolution* **23**: 212-226.
77. Zhang, J., R. Nielsen, and Z. Yang\*. 2005. Evaluation of an improved branch-site likelihood method for detecting positive selection at the molecular level. *Molecular Biology and Evolution* **22**: 2472-2479.
78. Ren, F., H. Tanaka, and Z. Yang\*. 2005. An empirical examination of the utility of codon-substitution models in phylogeny reconstruction. *Systematic Biology* **54**: 808-818.
79. Yang, Z.\* , and B. Rannala. 2005. Branch-length prior influences Bayesian posterior probability of phylogeny. *Systematic Biology* **54**: 455-470.
80. Sainudiin, R.\* , W.S.W. Wong, K. Yogeewaran, J. Nasrallah, Z. Yang, and R. Nielsen. 2005. Detecting site-specific physicochemical selective pressures: applications to the class-I HLA of the human major histocompatibility complex and the SRK of the plant sporophytic self-incompatibility system. *Journal of Molecular Evolution* **60**: 315-326.
81. Yang, Z., W.S.W. Wong, and R. Nielsen\*. 2005. Bayes empirical Bayes inference of amino acid sites under positive selection. *Molecular Biology and Evolution* **22**: 1107-1118.

82. Wong, W.S.W.\* , Z. Yang, N. Goldman, and R. Nielsen. 2004. Accuracy and power of statistical methods for detecting adaptive evolution in protein coding sequences and for identifying positively selected sites. *Genetics* **168**: 1041-1051.
83. Anisimova, A.\* and Z. Yang. 2004. Molecular evolution of hepatitis delta virus antigen gene: recombination or positive selection? *Journal of Molecular Evolution* **59**: 815-826.
84. 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.
85. Yang, Z.\* 2004. A heuristic rate smoothing procedure for maximum likelihood estimation of species divergence times. *Acta Zoologica Sinica* **50**:645-656.
86. 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.
87. Yoder, A.D.\* , and Z. Yang. 2004. Divergence dates for Malagasy lemurs estimated from multiple gene loci: fit with climatological events and speciation models. *Molecular Ecology* **13**:757-773.
88. Schein, M., Z. Yang, T. Mitchell-Olds, and K. J. Schmid\*. 2004. Rapid evolution of a pollen-specific oleosin-like gene family from *Arabidopsis thaliana* and closely related species. *Molecular Biology and Evolution* **21**: 659-669.
89. Yang, J., H. Gu and Z. Yang\*. 2004. Likelihood analysis of the chalcone synthase genes suggests the role of positive selection in the morning glories (*Ipomoea*). *Journal of Molecular Evolution* **58**: 54-63.
90. Aris-Brosou, S., and Z. Yang\*. 2003. Bayesian models of episodic evolution support a late pre-cambrian explosive diversification of the Metazoa. *Molecular Biology and Evolution* **20**: 1947-1954.
91. Yang Z., S. Ro, and B. Rannala\*. 2003. Likelihood models of somatic mutation and codon substitution in cancer genes. *Genetics* **165**: 695-705.
92. Yang, Z.\* and A. D. Yoder. 2003. Comparison of likelihood and bayesian methods for estimating divergence times using multiple gene loci and calibration points, with application to a radiation of cute-looking mouse lemur species. *Systematic Biology* **52**: 705-716.
93. 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.
94. 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
95. Nielsen, R.\* , and Z. Yang. 2003. Estimating the distribution of selection coefficients from phylogenetic data with applications to mtDNA. *Molecular Biology and Evolution* **20**:1231-1239.
96. Anisimova, M.\* , R. Nielsen and Z. Yang. 2003. Effect of recombination on the accuracy of the likelihood method for detecting positive selection at amino acid sites. *Genetics* **164**:1229-1236.
97. Yang, Z.\* , Stephens, D., Dawson, K. J., Drummond, A., Nicholls, G., Griffiths, R. C., Wilkinson-Herbots, H. M., Beaumont, M. A., Baird, S. J. E., Lascoux, M., Leblois, R., Estoup, A., Nielsen, R., Hey, J., Stumpf, M. P. H. & Wilkinson-Herbots, H. M. 2003. Inference from DNA data: population histories, evolutionary processes and forensic match probabilities: Discussion, *Journal of Royal Statistical Society A*. **166**: 188-201.
98. Bielawski, J.P.\* , and Z. Yang. 2003. Maximum likelihood methods for detecting adaptive evolution after gene duplication. *Journal of Structural and Functional Genomics* **3**: 201-212.
99. Yang, Z.\* 2002. Likelihood and Bayes estimation of ancestral population sizes in Hominoids using data from multiple loci. *Genetics* **162**: 1811-1823
100. Yang, Z.\* 2002 Inference of selection from multiple species alignments. *Current Opinion in Genetics and Development* **12**: 688-694.
101. Yang, J., J. Huang, H. Gu, Y. Zhong and Z. Yang\*. 2002. Duplication and adaptive evolution of chalcone synthase genes in the genus *Dendranthema* (Asteraceae). *Molecular Biology and Evolution* **19**: 1752-1759.
102. Jiggins, F.M.\* , G.D.D. Hurst, and Z. Yang. 2002. Host-symbiont conflicts: positive selection on the outer membrane protein of parasite but not mutualistic Rickettsiaceae. *Molecular Biology and Evolution* **19**: 1341-1349.
103. Anisimova, M., J. P. Bielawski and Z. Yang\*. 2002. Accuracy and power of Bayes prediction of amino acid sites under positive selection. *Molecular Biology and Evolution* **19**: 950-958.
104. Aris-Brosou, S., and Z. Yang\*. 2002. The effects of models of rate evolution on estimation of divergence dates with a special reference to the metazoan 18S rRNA phylogeny. *Syst. Biol.* **51**: 703-714.

105. Yang, Z.\*, and R. Nielsen. 2002. Codon-substitution models for detecting molecular adaptation at individual sites along specific lineages. *Molecular Biology and Evolution* **19**: 908-917.
106. Yang, Z.\*, and W. J. Swanson. 2002. Codon-substitution models to detect adaptive evolution that account for heterogeneous selective pressures among site classes. *Molecular Biology and Evolution* **19**: 49-57.
107. Jiggins, C.D., M. Linares, R.E. Naisbit, C. Salazar, Z. Yang, J. Mallet\*. 2001. Sex-linked hybrid sterility in a butterfly. *Evolution*. **55**:1631-1638.
108. Anisimova, M., J. P. Bielawski and Z. Yang\*. 2001. The accuracy and power of likelihood ratio tests to detect positive selection at amino acid sites. *Molecular Biology and Evolution* **18**: 1585-1592.
109. Bielawski, J.P. and Z. Yang\*. 2001. Positive and negative selection in the DAZ gene family. *Molecular Biology and Evolution* **18**: 523-529.
110. Swanson, W. J.\*, Z. Yang, M. F. Wolfner and C. F. Aquadro. 2001. Positive Darwinian selection in the evolution of mammalian female reproductive proteins. *Proceedings of the National Academy of Sciences of U.S.A.* **98**:2509-2514. (Featured in *New York Times* 27 February 2001, and *Cornell Chronical*)
111. Dunn, K. A.\*, J. P. Bielawski and Z. Yang. 2001. Substitution rates in Drosophila nuclear genes: implications for translational selection. *Genetics* **157**: 295-305.
112. Yang, Z.\* 2001. Maximum likelihood analysis of adaptive evolution in HIV-1 gp120 env gene. *Pacific Symposium on BioComputing* 2001 pages 226-237.
113. Thomas, M.G., E. Hagelberg, H. B. Jones, Z. Yang, and A. Lister\*. 2000. Molecular and morphological evidence on the phylogeny of the *Elephantidae*. *Proceedings of Royal Society of London B: Biological Sciences* **267**:2493-2500.
114. Yang, Z.\* 2000. Maximum likelihood estimation on large phylogenies and analysis of adaptive evolution in human influenza virus A. *Journal of Molecular Evolution* **51**: 423-432.
115. Yang, Z.\*, and J.P. Bielawski. 2000. Statistical methods for detecting molecular adaptation. *Trends in Ecology and Evolution* **15**: 496-503. (Our work on codon models featured in an article in the American Magazine *Natural History*, vol. 110 pp. 16-20, September 2001).
116. Bielawski, J.\*, K. 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.
117. Yang, Z.\*, W.J. Swanson, and V.D. Vacquier. 2000. Maximum likelihood analysis of molecular adaptation in abalone sperm lysin reveals variable selective pressures among lineages and sites. *Molecular Biology and Evolution* **17**: 1446-1455.
118. Yoder, A. D.\*, and Z. Yang. 2000. Estimation of primate speciation dates using local molecular clocks. *Molecular Biology and Evolution* **17**: 1081-1090.
119. Yang, Z.\*, R. Nielsen, N. Goldman, A.-M. K. Pedersen. 2000. Codon-substitution models for heterogeneous selection pressure at amino acid sites. *Genetics* **155**: 431-449.
120. Holbrook, J. D., G. M. Birdsey, Z. Yang, M. W. Bruford, and C. J. Danpure\*. 2000. Molecular adaptation of alanine:glyoxylate aminotransferase targeting in primates. *Molecular Biology and Evolution* **17**: 387-400.
121. Yang, Z.\* 2000. Complexity of the simplest phylogenetic estimation problem. *Proceedings of the Royal Society B: Biological Sciences* **267**: 109-116.
122. Yang, Z.\* 2000. Relating physicochemical properties of amino acids to variable nucleotide substitution patterns among sites. *Pacific Symposium on BioComputing* 2000: 81-92.
123. Yang, Z.\*, and R. Nielsen. 2000. Estimating synonymous and nonsynonymous substitution rates under realistic evolutionary models. *Molecular Biology and Evolution* **17**: 32-43.
124. Excoffier, L., and Z. Yang\*. 1999. Substitution rate variation among sites in the mitochondrial hypervariable region I of humans and chimpanzees. *Molecular Biology and Evolution* **16**: 1357-1368.
125. Yang, Z.\*, and A. Yoder. 1999. Estimation of the transition/transversion rate bias and species sampling. *Journal of Molecular Evolution* **48**: 274-283.
126. Rannala, B.\*, J. P. Huelsenbeck, Z. Yang, and R. Nielsen. 1998. Taxon sampling and the accuracy of large phylogenies. *Systematic Biology* **47**: 702-709.
127. Yang, Z.\*, R. Nielsen, and M. Hasegawa. 1998. Models of amino acid substitution and applications to mitochondrial protein evolution. *Molecular Biology and Evolution* **15**:1600-1611.



128. Hasegawa, M.\*, Y. Cao, and Z. Yang. 1998. Preponderance of slightly deleterious polymorphism in mitochondrial DNA: replacement/synonymous rate ratio is much higher within species than between species. *Molecular Biology and Evolution* **15**:1499–1505.
129. Nielsen, R.\* and Z. Yang. 1998. Likelihood models for detecting positively selected amino acid sites and applications to the HIV-1 envelope gene. *Genetics* **148**: 929–936.
130. Yang, Z.\*, and R. Nielsen. 1998. Synonymous and nonsynonymous rate variation in nuclear genes of mammals. *Journal of Molecular Evolution* **46**: 409–418.
131. Yang, Z.\* 1998. On the best evolutionary rate for phylogenetic analysis. *Systematic Biology* **47**:125–133.
132. Yang, Z.\* 1998. Likelihood ratio tests for detecting positive selection and application to primate lysozyme evolution. *Molecular Biology and Evolution* **15**: 568–573.
133. Yang, Z., and B. Rannala\*. 1997. Bayesian phylogenetic inference using DNA sequences: Markov chain Monte Carlo methods. *Molecular Biology and Evolution* **14**: 717–724.
134. Yang, Z.\*, and N. Goldman\*. 1997. Are big trees indeed easy? *Trends in Ecology and Evolution* **12**:357.
135. Yang, Z.\* 1997. PAML: a program package for phylogenetic analysis by maximum likelihood. *CABIOS* **13**: 555–556.
136. Yang, Z.\* 1997. On the estimation of ancestral population sizes. *Genetical Research* **69**: 111–116.
137. Huelsenbeck, J. P.\*, B. Rannala, and Z. Yang. 1997. Statistical tests of host–parasite coevolution. *Evolution* **51**:410–419.
138. Yang, Z.\* 1997. How often do wrong models produce better phylogenies? *Molecular Biology and Evolution* **14**:105–108.
139. Yang, Z.\* 1996. Statistical properties of a DNA sample under the finite-sites model. *Genetics* **144**:1941–1950.
140. Rannala, B., and Z. Yang\*. 1996. Probability distribution of molecular evolutionary trees: a new method of phylogenetic inference. *Journal of Molecular Evolution* **43**:304–311.
141. Yang, Z.\* 1996. Among-site rate variation and its impact on phylogenetic analyses. *Trends in Ecology and Evolution* **11**:367–372.
142. Yang, Z.\* 1996. Maximum likelihood models for combined analyses of multiple sequence data. *Journal of Molecular Evolution* **42**:587–596.
143. Yang, Z.\*, and S. Kumar. 1996. Approximate methods for estimating the pattern of nucleotide substitution and the variation of substitution rates among sites. *Molecular Biology and Evolution* **13**:650–659.
144. Yang, Z.\* 1996. Phylogenetic analysis using parsimony and likelihood methods. *Journal of Molecular Evolution* **42**:294–307.
145. Yang, Z.\*, S. Kumar, and M. Nei. 1995. A new method of inference of ancestral nucleotide and amino acid sequences. *Genetics* **141**:1641–1650.
146. Yang, Z.\*, I. J. Lauder, and H. J. Lin. 1995. Molecular evolution of the hepatitis B virus genome. *Journal of Molecular Evolution* **41**:587–596.
147. Yang, Z., N. Goldman\*, and A. E. Friday. 1995. Maximum likelihood trees from DNA sequences: a peculiar statistical estimation problem. *Systematic Biology* **44**:384–399.
148. Yang, Z.\*, and T. Wang. 1995. Mixed model analysis of DNA sequence evolution. *Biometrics* **51**:552–561.
149. Yang, Z.\*, and D. Roberts. 1995. On the use of nucleic acid sequences to infer early branchings in the tree of life. *Molecular Biology and Evolution* **12**:451–458.
150. Yang, Z.\* 1995. On the general reversible Markov-process model of nucleotide substitution: a reply to Saccone *et al.* *Journal of Molecular Evolution* **41**:254–255.
151. Yang, Z.\* 1995. Evaluation of several methods for estimating phylogenetic trees when substitution rates differ over nucleotide sites. *Journal of Molecular Evolution* **40**:689–697.
152. Yang, Z.\* 1995. A space-time process model for the evolution of DNA sequences. *Genetics* **139**:993–1005.

153. Yang, Z.\* , N. Goldman, and A. E. Friday. 1994. Comparison of models for nucleotide substitution used in maximum likelihood phylogenetic estimation. *Molecular Biology and Evolution* **11**:316–324.
154. Goldman, N.\* , and Z. Yang. 1994. A codon-based model of nucleotide substitution for protein-coding DNA sequences. *Molecular Biology and Evolution* **11**:725–736.
155. Yang, Z.\* 1994. Maximum likelihood phylogenetic estimation from DNA sequences with variable rates over sites: approximate methods. *Journal of Molecular Evolution* **39**:306–314.
156. Yang, Z.\* 1994. Statistical properties of the maximum likelihood method of phylogenetic estimation and comparison with distance matrix methods. *Systematic Biology* **43**:329–342.
157. Yang, Z.\* 1994. Estimating the pattern of nucleotide substitution. *Journal of Molecular Evolution* **39**:105–111.
158. Yang, Z.\* 1993. Maximum likelihood estimation of phylogeny from DNA sequences when substitution rates differ over sites. *Molecular Biology and Evolution* **10**:1396–1401.

## Book Chapters

159. Yang, Z. 2016. AWF Edwards and the origin of Bayesian phylogenetics, in AWF Edwards (R. G. Winther, ed.) Cambridge University Press, Cambridge, England.
160. Yang, Z. 2016. Bayesian phylogenetic inference in Encyclopaedia of Evolutionary Biology (Kliman, R.M. ed.), Volume 1, pp. 137-140, Elsevier
161. Wang Y, Yang Z. 2014. Priors in Bayesian Phylogenetics, pp.5-23 in *Bayesian Phylogenetics: Methods, Algorithms, and Applications* (M.-H. Chen, L. Kuo, and P. Lewis, eds). Chapman & Hall/CRC, London.
162. Rannala B, Yang Z. 2013. Molecular clock dating. Pp. 68-74 in Losos JB, Baum DB, Futuyma DJ, Hoekstra HE, Lenski RE, Moore AJ, Peichel CL, Schluter D, and Whitlock MC, eds. *The Princeton Guide to Evolution*. Princeton University Press, New York.
163. Goldman, N., and Yang, Z. 2012. Foreword for *Codon Evolution - Mechanisms and Models*, pp. ix-x in *Codon Evolution - Mechanisms and Models* (ed. Gina M. Cannarozzi and Adrian Schneider), Oxford University Press, Oxford.
164. Yang, Z. 2007. Adaptive molecular evolution, Chapter 12 in *Handbook of statistical genetics*, 3<sup>rd</sup> Edition, eds. by D. Balding, M. Bishop, and C. Cannings. Wiley, New York.
165. Bielawski, J. P., and Z. Yang. 2005. Maximum likelihood methods for detecting adaptive protein evolution. pp. 103-124, in *Statistical Methods in Molecular Evolution* (R. Nielsen ed.), Springer-Verlag, New York.
166. Yang, Z. 2005. Bayesian inference in molecular phylogenetics, pp. 63-90 in (Olivier Gascuel ed.) *Mathematics of Evolution and Phylogeny*, Oxford University Press, England.
167. Yang, Z. 2003. Adaptive molecular evolution, Chapter 9 (pp. 229-254) in *Handbook of statistical genetics*, 3<sup>rd</sup> Edition, eds. by D. Balding, M. Bishop, and C. Cannings. Wiley, New York.
168. Bielawski, J. P., and Z. Yang. 2003. Maximum likelihood methods for detecting adaptive evolution after gene duplication. Pp. 201-212, A. Meyer, and Y. Van De Peer (eds). *Genome Evolution: Gene and Genome Duplications and the Origin of Novel Gene Functions*. Kluwer Academic Publishers, Dordrecht.
169. Yang, Z. 2002. Molecular clock. pp.747-750 in M. Pagel et al. (eds). *Oxford Encyclopaedia of Evolution*. Oxford University Press, Oxford.
170. Yang, Z. 2001. Adaptive molecular evolution, Chapter 12 (pp. 327-350) in *Handbook of statistical genetics*, eds. D. Balding, M. Bishop, and C. Cannings. Wiley, New York.

## Refereed Journal Articles in Chinese

171. Yang, Z. 1995. Statistical estimation of molecular evolutionary trees. *Hereditas (Beijing)* **17**(suppl.):92–96.
172. Yang, Z., and N. Goldman. 1994. Evaluation and extension of Markov process models of nucleotide substitution. *Acta Genetica Sinica* **21**:17–23.
173. Yang, Z. 1994. Estimation of evolutionary distances between protein sequences. *Acta Genetica Sinica* **21**:193–200.
174. Yang, Z. 1993. Nonlinear models. In *Biostatistics*. Wu, Z. and Q. Zhang (eds.). Beijing Agricultural University Press, Beijing.
175. Yang, Z., and Y. Zhang. 1993. Amino–acid distances and a model for protein evolution. *Acta Agriculturae Universitatis Pekinensis* **19**:66–71.

176. Yang, Z. 1993. Distributions of restriction endonuclease recognition sites in DNA sequences. *Hereditas (Beijing)* **15**(5):34–38.
177. Yang, Z. 1992. Nucleotide frequency analysis of the bacteriophage  $\Phi$ X174 genome. *Acta Genetica Sinica* **19**:475–480.
178. Yang, Z. 1992. How much information does the measure of information for DNA sequences reveal? *Hereditas (Beijing)* **14**(4):44–48.
179. Yang, Z., and Y. Zhang. 1991. The response to long-term selection. *Hereditas (Beijing)* **13**(1):44–48.
180. Yang, Z. 1991. Computer analysis of multiple homologous DNA sequences. *Hereditas (Beijing)* **13**(2):9–12.
181. Yang, Z. 1990. A collection of computer programs for the analysis of DNA sequences. *Hereditas (Beijing)* **12**(6):15–18.
182. Yang, Z. 1990. Associations of nucleotide substitutions during the evolution of DNA sequences. *Acta Genetica Sinica* **17**:354–359.
183. Yang, Z., Z. Wu, and Y. Zhang. 1989. The effect of long-term selection on the genetic structure of populations — a computer simulation study: II. the effect of long-term selection on genetic variances. *Acta Genetica Sinica* **16**:282–290.
184. Wu, Z., Y. Zhang, and Z. Yang. 1989. The effect of long-term selection on the genetic structure of populations — a computer simulation study: I. simulation model and selection response. *Acta Genetica Sinica* **16**:197–205.
185. Yang, Z. 1989. The branching process and its application in population genetics. *Mathematics in Practice and Theory* **1**:56–59.
186. Men, Z., C. Chen, Z. Yang, and J. Han. 1985. Study on the chromosomes of domestic pigs, *Sus Scrofa*. II. G-band karyotypes of the chromosomes. *J. Gansu Agricultural University* (3):37–43.
187. Men, Z., C. Chen, Z. Yang, and J. Han. 1985. Study on the chromosomes of domestic pigs, *Sus Scrofa*. I. The karyotypes and chromosome polymorphisms. *J. Gansu Agricultural University* (2):30–37.

### Papers in Conference Proceedings (Not Refereed)

188. Clote, P., G.J.P. Naylor, and Z. Yang. 2002. Proteins: structure, function and evolution. *Pacific Symposium on BioComputing 2002* pages 548-551.
189. Goldman, N., and Z. Yang. 1994. Models of DNA substitution and the discrimination of evolutionary parameters. In *Proceedings of the XVIIth International Biometrics Conference, Vol. I: Invited Papers*. International Biometrics Society, Hamilton, Ontario, Canada, pp. 407–420.

### Invited Book Reviews and Commentaries (Not Refereed)

190. Yang Z. 2010. Review of *The Timetree of Life* (by S. Blair Hedges and Sudhir Kumar). *Quart. Rev. Biol.* **85**:360-361.
191. Yang, Z. 2005. The power of phylogenetic comparison in revealing protein function. *Proceedings of the National Academy of Sciences of U.S.A.* **102**:3179-3180.
192. Yang, Z. 2004. A probabilist's account of modern molecular population genetics, Review of *Probability Models for DNA Sequence Evolution* (by Rick Durrett. Springer-Verlag, New York, 2002). *Heredity*, **92**:474-474.
193. Yang, Z. 2003. Phylogenetics as applied mathematics, Review of *Phylogenetics* (by Charles Semple and Mike Steel. Oxford University Press, 2003). *Trends in Ecology and Evolution* **18**:558-559.
194. Furlong, R. F., and Z. Yang. 2003. Comparative genomics coming of age. *Heredity* **91**: 533-534.

### Contributed Conference Abstracts (Incomplete)

195. Nielsen, R., Z. Yang, N. Goldman and A.-M. K. Pedersen 2001. *Detecting selection in the HIV-1 genome using the dn/ds ratio*. The 7th Annual International Discussion Meeting on HIV Dynamics and Evolution, 30 April 2001.
196. Yang, Z. 2000 *Use of local molecular clocks to date primate speciation dates*. American Evolution 2000 meeting. Bloomington, Indiana, 23-27 June 2000.

197. Yang, Z. 2000 *Maximum likelihood estimation on large phylogenies and analysis of adaptive evolution in human influenza virus A*. Society for Molecular Biology and Evolution Meeting, Yale University, 17-20 June, 2000.
198. Yang, Z. 1999 *Among-site rate variation in the mitochondrial D-loop in humans and chimpanzees*. The Evolution Meeting, University of Wisconsin, Madison, Wisconsin, June 22-26, 1999.
199. Yang, Z. 1999 *The effect of mutation and selection on amino acid substitution rates*. Workshop in Mathematical and Statistical Applications in Molecular Biology. Loughborough, April 7–8, 1999.
200. Yang, Z. 1998 *On the best evolutionary rate for phylogenetic analysis*. The Annual Meeting of Society of Systematic Biologists, Society for the Study of Evolution, American Society of Naturalists, and Numerical Taxonomy Group (the Evolution meeting), Vancouver, Canada, 20–24 June 1998.
201. Yang, Z. 1998 *Likelihood models of codon substitution and detection of positive selection*. The VIth Society for Molecular Biology and Evolution Meeting, Vancouver, Canada, 17–20 June 1998
202. Yang, Z. 1998 *Bayesian estimation of molecular evolutionary trees*. European Mathematical Genetics Meeting, Reading, England, April 2–4, 1998.
203. Yang, Z. 1996 *Among-site rate heterogeneity in phylogenetic analysis*. The 4th Annual meeting of the Society for Molecular Biology and Evolution. Tucson, Arizona, June 8–11, 1996.
204. Yang, Z. 1993 *Models of nucleotide substitution and maximum likelihood estimation of phylogeny*. Workshop on Mathematical and Statistical Aspects of Molecular Biology, University of Oxford, Oxford, January 4–5, 1993.

## Software Package

- *PAML (for Phylogenetic Analysis by Maximum Likelihood)*, 1993-date, is a package of phylogenetic programs for maximum likelihood analyses of nucleotide, amino acid and codon sequences. It has been widely used in a range of fields such as molecular evolution, phylogenetics, molecular biology, bacteriology, etc. It has attracted >6000 citations (June 2013).
- *BEAST (for Bayesian phylogenetics and phyllogeography)*, 2010-date, implements a Bayesian MCMC algorithm for species delimitation and inference under the multispecies coalescent model.

## Professional Service

### Society Memberships

- American Association for the Advancement of Sciences (1997-2008)
- International Society for Molecular Evolution (1997-2004)
- Society for Molecular Biology and Evolution (1997-date)
- Society for Systematic Biology (1998-date)

### Service on International Committees

- Member of Academic Board, Biology and Medicine Branch, National Centre for Mathematics and Interdisciplinary Sciences, Chinese Academy of Sciences, Beijing, 2011-2016
- Non-North American Vice President of the Society for the Study of Evolution, 2010-2011.
- Councillor of Society for Molecular Biology and Evolution, 2008-2010
- Member, Academic Board of State Key Laboratory of Systematic and Evolutionary Botany (LSEB), Beijing, The Chinese Academy of Sciences, since 2005
- Vice Chair, Academic Board, Institute of Zoology, Chinese Academy of Sciences, Beijing, 2008-date
- Member of the Academic Board, National Key Laboratory of Cellular and Molecular Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences. 2002-2007.
- Member of International Evaluation Committee for Kunming Institute of Zoology, Chinese Academy of Sciences. October 2003.
- Member of International Review Committee for the Molecular Evolution Group, Institute of Statistical Mathematics, Tokyo, Japan, November 1998

### Service on UCL Committees

- Biosciences MRes Stream Tutor, UCL, since 2008

- Computational Biology Steering Group, UCL.
- Member of Scientific Advisory Board, UCL Genetics Institute (UGI), since 2007
- Steering Committee Member of Bloomsbury Centre of Bioinformatics, London, since 2004.
- Board Member of London Bioinformatics Forum, since 2003
- Management Board Member for Centre for Computational Science, UCL, since 2003.
- Steering Committee Member, BSc/MSci programme in Mathematics with Biology, Mathematics, UCL, since 2003.
- Member of Bioinformatics Advisory Board, UCL, since 2001.
- Graduate adviser for the CoMPLEX Centre, UCL, since 1998.

## External Examination

External Examiner for Ph. D. thesis

- 2013 Carina Mugal, Evolutionary Biology Center, Uppsala University, Sweden.
- 2012 Jukka Sirén, Department of Mathematics, University of Helsinki, Finland.
- 2008 Boussau Bastien, devant L'Université Claude Bernard - Lyon 1, France
- 2005 Lachlan James Murray Coin, University of Cambridge.
- 2003 Howsun Jow, Department of Computer Science, University of Manchester.
- 2000 Simon Whelan, Department of Genetics, University of Cambridge.
- 1999 Anne-Mette Pedersen, Department of Ecology and Genetics, University of Århus, Denmark.

Committee member for Ph. D. students

- 2001-2007 Karen Cranston, University of Alberta (Supervisor: Professor Bruce Rannala);
- 2001-2007 Ligia M. Mateiu, University of Alberta (Supervisor: Professor Bruce Rannala).

## Editorial and Refereeing Service

- Editorial Board Member for
  - *Philosophical Transactions of the Royal Society B*, 2014-date.
  - *Biological Letters*, 2011-2013
- Associate Editor for
  - *Molecular Biology and Evolution*, 2006-2008
  - *Evolutionary Bioinformatics*, 2005-
  - *Genetics*, 2002-2007
  - *Systematic Biology*, 2001-2004
  - *Journal of Molecular Evolution*, 1998-2002
- Referee for funding agencies  
BBSRC, Human Frontier Science Program (HFSP), Israel Science Foundation, NERC, The Leverhulme Trust, National Science Foundation (USA), The Wellcome Trust.
- Referee for scientific journals  
*Annals of Human Genetics, Bioinformatics, Biological Reviews, Briefings in Bioinformatics, Computer Application in BioSciences, Current Biology, Genetical Research, Genetics, Genome Research, Genomics, Journal of American Statistical Association, Journal of Molecular Biology, Journal of Molecular Evolution, Journal of Theoretical Biology, Mathematical BioSciences, Molecular Biology and Evolution, Molecular Phylogenetics and Evolution, Nature, Nature Genetics, Nature Reviews Genetics, Proceedings of National Academy of Sciences U.S.A., Proceedings of the Royal Society Series B, Science, Systematic Biology, Trends in Biochemical Sciences, Trends in Genetics, Trends in Ecology and Evolution.*
- Faculty member of *FACULTY OF 1000*, a “revolutionary online service whose principal aim is to organize and evaluate the life sciences literature”.

## Conference and Workshop Organization

- *EMBO Practical Course on Computational Molecular Evolution*, Heraklion, Crete, 8-19 May 2016 (Co-Organizers: Drs Nick Goldman, Aidan Budd, & Alexandros Stamatakis).
- Royal Society Discussion Meeting *Dating species divergence using rocks and clocks*, 9-10 November 2015, The Royal Society, London (co-organizer Dr Phil Donoghue).

- *Mathematics in population genetics and evolution*, Mini-symposium at International Congress on Industrial and Applied Mathematics (ICIAM 2015), Beijing, 10-14 August 2015 (co-Organiser: Professor Zhi-Ming Ma).
- *Bayesian Methods to Estimate Species Divergence Times*, University of Bristol, 30 - 31 July 2015 (co-Organisers: Drs Mario dos Reis and Philip Donoghue).
- *Workshop on Molecular Evolution and Systematics*, Beijing Institute of Genomics, Chinese Academy of Sciences, Beijing, China, 17-23 August 2014 (Co-Organizer: Professor De-Xing Zhang).
- *EMBO Practical Course on Computational Molecular Evolution*, Heraklion, Crete, 4-15 May 2014 (Co-Organizers: Drs Nick Goldman, Aidan Budd, Alexandros Stamatakis, & Georgios Kotoulas).
- *Wellcome Trust Advanced Workshop on Computational Molecular Evolution*, Hinxton, 29 April-10 May 2013 (Co-Organizers: Drs Nick Goldman, Aidan Budd, & Alexandros Stamatakis).
- *EMBO Practical Course on Computational Molecular Evolution*, Heraklion, Crete, 29 April-10 May 2012 (Co-Organizers: Drs Nick Goldman, Aidan Budd, Alexandros Stamatakis, & Georgios Kotoulas).
- *Society for Molecular Biology and Evolution 2011 Annual Meeting*, 26-30 July 2011, Tokyo Japan, Global Organizing Committee Member.
- *Wellcome Trust Advanced Workshop on Computational Molecular Evolution*, Hinxton, 10-21 April 2011 (Co-Organizers: Drs Nick Goldman, Aidan Budd, & Alexandros Stamatakis).
- *Workshop on Molecular Evolution and Systematics*, Institute of Zoology, Chinese Academy of Sciences, Beijing, China, 12-17 June 2010 (Co-Organizer: Professor De-Xing Zhang).
- *EMBO Practical Course on Computational Molecular Evolution*, Heraklion, Crete, 3-12 May 2010 (Co-Organizers: Drs Nick Goldman, Aidan Budd, Alexandros Stamatakis, & Georgios Kotoulas).
- *Wellcome Trust Advanced Course on Molecular Evolution*, Hinxton, 30 March - 8 April 2009 (Co-Organizers: Drs Nick Goldman and Aidan Budd).
- *Workshop on Molecular Evolution and Systematics*, Institute of Zoology, Chinese Academy of Sciences, Beijing, China, 12-16 May 2008 (Co-Organizer: Professor De-Xing Zhang).
- Royal Society Discussion Meeting *Statistical and computational challenges in molecular phylogenetics and evolution*, 28-29 April 2008, The Royal Society, London (co-organizer Dr Nick Goldman).
- *PhyloGroup Meeting VII*, 28 September 2007, Cambridge (Co-Organizer Dr Nick Goldman)
- *PhyloGroup Meeting VI*, 12 January 2007, EBI, Hinxton (Co-Organizer Dr Nick Goldman)
- *PhyloGroup Meeting V*, 28 April 2006, UCL, London
- *PhyloGroup Meeting IV*, 21 October 2005, UCL, London
- *PhyloGroup Meeting III*, 5 October 2004, University College London, London
- *Workshop on Molecular Evolution and Systematics*, Institute of Zoology, Chinese Academy of Sciences, Beijing, China, 19-22 August 2004 (Co-Organizer: Professor De-Xing Zhang).
- Symposium on *Methodological advances in estimation of species divergence dates using molecular data*, International Congress of Zoology, 23-27 August 2004, Beijing, China (Co-Organizer: Dr Bruce Rannala).
- Symposium on "Exploring clade divergence age estimation: why are fossil and molecular data in conflict regarding the age of crown placental mammals?" (Co-Organizer: Dr Anne Yoder), Fort Collins, Colorado, 26-30 June 2004
- Organising Committee Member of the series *Mathematics of Evolution and Phylogeny*, Institut Henri Poincare, Paris, since 2004.
- *PhyloGroup Meeting II*, 18 February 2004, UCL, London
- *PhyloGroup Meeting I*, 16 September 2003, UCL, London
- *Proteins, Structure, Function and Evolution*. 3-8 January 2002 at Lihue, Kauai, Hawaii, (co-organizers: Drs Peter Clote and Gavin Naylor).
- *Adaptive molecular evolution*. 27 April 2000 at Zoology Society of London, London, Centre for Ecology and Evolution workshop (co-organizer Dr Bill Jordan).

## Academic Supervision and Hosting of Visitors

### Postdocs Supervised

- Dr Daniel Dalquen (RA1A), 2013-.
- Dr Mario dos Reis, BBSRC Research Fellow (RA1A), 2010-
- Dr Jun Inoue, BBSRC Research Fellow (RA1A), 2008-2010 (currently Lecturer, Okinawa Institute of Technology)



- Dr Maria Anisimova, BBSRC Research Fellow (RA1A), 2005-2008 (now Zurich U. Applied Sciences)
- Dr Rick Desper, NERC Research Fellow (RA1A), 2005-2007
- Dr Samit Kundu, BBSRC Research Fellow (RA1A), 2003-2004
- Dr Becky Furlong, BBSRC Research Fellow (RA1A), 2003-2004 (Editor, *Genome Medicine*)
- Dr Paul Michael-Agapow, BBSRC Research Fellow (RA1A), 2002-2004 (currently Dept Biology, Imperial College)
- Dr Lounes Chikhi, BBSRC Research Fellow (RA1A), 2001-2002 (currently Group Leader, Population and Conservation Genetics Group, Instituto Gulbenkian de Ciência in Oeiras, Portugal)
- Dr Paul Taylor, Wellcome Research Fellow, 2000-2002
- Dr Joe Bielawski, BBSRC Research Fellow (RA1A), 1999-2003 (currently Associate Professor, Dept Maths and Stats, Dalhousie University, Canada)
- Dr Kathy Dunn, BBSRC Research Fellow (RA1A), 1999-2003

## Ph. D. Students Supervised

- Rachel Warnock, Department of Earth Sciences, University of Bristol, joint supervision with Prof. Philip Donoghue (2009-date).
- John Ambrose, Royal Free Medical School (2010-, joint supervision with Anna Geretti)
- Will Fletcher (2006-2010), Quantitative Analyst, Smartodds Ltd.
- Yuval Itan (2005-2009, joint supervision with Dr Mark Thomas).
- Jessica Vamathevan (2005-2008), Senior Scientific Investigator, Computational Biology, GlaxoSmithKline, Stevenage, UK
- Dave Dale (2002-2006).
- Daniel White (2001-2004, joint supervision with Dr Andres Ruiz-Linares).
- Sarah Darwin (2001-2007, joint supervision with Professor Jim Mallet).
- Giselle Walker, Natural History Museum (2001-2004, joint supervision with Dr Martin Embley) "Eukaryote evolution and the systematics of amoeboid flagellates". (currently Lecturer, Dept Botany, University of Otago, New Zealand)
- Gabriela Estrada (2000-2004) "The evolution of the vertebrate beta-globin gene family". (currently postdoc in Comparative Genomics Group, CRG-Centre for Genomic Regulation, Barcelona, Spain)
- Maria Anisimova (2000-2003) "Detecting positive selection in protein-coding genes". (currently Junior Group Leader, Dept Computer Science, ETH Zurich)
- Wa Yang (1999-2003) "The evolution of human AIDs viruses".
- Stephane Aris-Brosou (1999-2002) "*Bayes molecular phylogenetics: estimation of divergence dates and hypothesis testing*". (currently Associate Professor, Director of Bioinformatics, Dept Biology, University of Ottawa, Canada)

## M.Sc. Students Supervised

- Rhiju Das (MRes. 2000) *Systematics of Phylogeny Reconstruction*
- Maria Anisimova (MRes. 2000) *The power of the likelihood ratio test to detect adaptive molecular evolution*
- Jonathan Wald (MRes. 2001) *A molecular genetic investigation into selection and gene flow in the *Heliconius melpemone* species complex*
- Christian Bottomley (MRes. 2002) *An investigation into the role of diversifying selection in the evolution of the merozoite surface protein (MSP1) of *Plasmodium falciparum**
- Chris Mullaley (MRes. 2002) *Molecular evolutionary analysis of a set of sequenced rhinovirus genes*

## Hosts to Collaborators (1 week or longer)

- (7 days in 2012) Professor Bruce Rannala, University of California Davis.
- (5 months in 2012) Professor Anne Yoder, Duke University
- (10 days in 2011) Professor Bruce Rannala, University of California Davis.
- (1.5 months in 2008) Dr Fengrong Ren, Associate Professor, Tokyo Medical and Dental University.
- (2 weeks in 2008) Dr Richard Brown, Reader, School of Biological & Earth Sciences, Liverpool John Moores University, Liverpool.

- (2 months in 2006) Dr Fengrong Ren, Associate Professor, Tokyo Medical and Dental University.
- (1 week in 2005) Professor Bruce Rannala, University of California, Davis, California.
- (2 weeks in 2005) Dr Fengrong Ren, Associate Professor, Tokyo Medical and Dental University.
- (2 weeks in 2004) Dr Fengrong Ren, Associate Professor, Tokyo Medical and Dental University.
- (6 months in 2004) Carlos Shrago, Universidade Federal Do Rio de Janeiro, Brazil.
- (2 months in 2004) Dr Ying Cao, Assistant Professor, Institute of Statistical Mathematics, Tokyo.
- (4 weeks in 2003) Dr Fengrong Ren, Assistant Professor, Tokyo Medical and Dental University.
- (2 weeks in 2003) Dr Bruce Rannala, Associate Professor, University of Alberta, Edmonton, Canada.
- (1 week in 2002) Dr Bruce Rannala, Assistant Professor, University of Alberta, Edmonton, Canada.
- (1 week in 2002) Dr Karl Schmid, Assistant Professor, Max-Planck Institute of Molecular Ecology, Jena, Germany.
- (8 weeks in 2001) Mr Raazesh Sainudiin, Graduate Student, Cornell University.
- (6 weeks in 2000) Dr Fengrong Ren, Assistant Professor, Tokyo Medical and Dental University.
- (2 weeks in 2000) Dr Hidetoshi Shimodaira, Assistant Professor, Institute of Statistical Mathematics, Tokyo.
- (1 week 1999) Dr Belinda Chang, Rockefeller University.
- (2 weeks in 1999) Dr Rasmus Nielsen, Harvard University
- (3 weeks in 1999) Dr Hidetoshi Shimodaira, Assistant Professor, Institute of Statistical Mathematics, Tokyo.

## Invited Lectures and Seminars

### Plenary, Keynote or Named Lectures

1. *Estimation of species divergence times incorporating fossil and molecular information.* Keynote lecture at JOBIM 2015, Annual French Bioinformatics Meeting, Clermont-Ferrand, France, 6-9 June 2015.
2. *The limit of species divergence time estimation.* SAMSI Fall Course 2014-5 on *Statistical and Mathematical Challenges in Molecular Evolution*, North Carolina, 16 September 2014.
3. *MCMC: how would you propose?* Department of Statistics and Operations Research. University of North Carolina, Chapel Hill, 15 September 2014.
4. *Multispecies coalescent and its use in population genetics inference from genomic data.* Bioinformatics Opening Workshop for Program on Beyond Bioinformatics: Statistical and Mathematical Challenges, SAMSI, North Carolina, 8-12 September 2014.
5. *The impact of the prior on Bayesian molecular clock dating.* Workshop on Methods for Biodiversity Research, Fudan University, Shanghai, China, 10-12 March 2014.
6. *Bayesian delimitation of species using genomic sequence data.* Keynote lecture, Symposium on Computational Biology, Institute of Genomics, Chinese Academy of Sciences, Beijing, 27-28 November 2011.
7. *Bayesian estimation of species divergence times,* Plenary speech, Annual Congress of Brazilian Society of Genetics, 30 August - 3 September 2011, Aguas de Lindoia, Sao Paulo, Brazil.
8. *Bayesian estimation of species divergence times,* 2011 Journal of Systematics and Evolution Symposium, Linzhi, Tibet, China, 6-9 August 2011.
9. *Species delimitation using genomic sequence data.* Advanced Seminar Series, Institute of Biological Sciences, Chinese Academy of Sciences, Beijing, 26 November 2010.
10. *Over-confident Bayesian and molecular phylogenetics.* Keynote lecture, ComBi Symposium 18 December 2009, Turku Castle, Finland
11. *Detecting adaptive molecular evolution in protein-coding DNA sequences,* Centro de Ciencias Genomicas-UNAM, Cuernavaca, 20 October 2008.
12. *Bayesian estimation of hominoid ancestral population sizes,* Keynote speech at The 2008 LASR workshop "The Art and Science of Statistical Bioinformatics". University of Leeds, 16-17 July 2008.
13. *Detecting Darwinian selection in DNA sequences.* Keynote speech, The University of Tokyo 130<sup>th</sup> Anniversary International Symposium on "Frontier of Microbial and Plant Biotechnology in Environmental and Life Sciences". University of Toyo, Japan, 5-6 December 2007.
14. *Estimation of species divergence times.* Keynote speech, Asia-Africa Evolution Meeting, Chiba, Japan, 4-6 December 2007.
15. *Estimation of species divergence times by incorporating uncertainties in fossils,* Keynote speech, International symposium on "Evolutionary Biology in the 21st Century - Tracing Patterns of Evolution through the Tree of Life", 3-7 June 2007, Beijing



16. *Markov chain Monte Carlo in genetics*, Keynote lecture at Summer Symposium in Bioinformatics, International Centre of Excellence for Education in Mathematics (ICE-EM), Australian National University, 6-10 December 2004, Canberra, Australia
17. *Detecting adaptive protein evolution*, keynote lecture at Summer Symposium in Bioinformatics, International Centre of Excellence for Education in Mathematics (ICE-EM), Australian National University, 6-10 December 2004, Canberra, Australia
18. *Dating techniques*, Xiangshan Science Symposium on Genomics and Evolution, Beijing, 28-30 October 2003.
19. *Markov-process models of codon substitution and their use to detect adaptive molecular evolution*. Keynote lecture at Workshop on Computational Evolutionary Biology and Ecology, May 6–8, 1999. Tallahassee, Florida State University.

## Other invited lectures

20. *Statistical inference using genomic sequence data from multiple closely related species*, Kunming Institute of Zoology, 12 October 2016.
21. *Learning about population history using genomic sequence data*, Gansu Agricultural University, 10 October 2016.
22. *Bayesian inference under the multispecies coalescent model from genomic sequence data*. Dog10k conference, Beijing, 17-19 June 2016.
23. *Bayesian estimation of species trees under the multispecies coalescent*. 10-12 December 2015, University of California at Berkeley.
24. *Some species tree methods are more equal than others*. Mathematical Approaches to Evolutionary Trees, 16-18 September 2015, Imperial College, London.
25. *Multispecies coalescent model and its applications in analysis of genomic sequence data*. International Congress on Industrial and Applied Mathematics (ICIAM 2015), Beijing, 10-14 August 2015.
26. *Bayesian molecular clock dating*, Workshop on “Bayesian methods to estimate species divergence times”, University of Bristol, 30 - 31 July 2015.
27. *Estimation of species divergence times integrating molecules and fossils*. 28 May 2015, Imperial College, Silwood Park.
28. *Bayesian estimation of species divergence times*. 17 February 2014, University of Ferrara, Italy.
29. *Bayesian species delimitation using multilocus genomic sequence data*. Phylogenetics workshop, Swedish Natural History Museum, Stockholm, 14 June 2013.
30. *The uncertainty of Bayesian divergence time estimation*. Swedish Natural History Museum, Stockholm, 14 June 2013.
31. *The uncertainty of Bayesian divergence time estimation*. Institute of Zoology, Chinese Academy of Sciences, Beijing, 15 March 2013.
32. *Maximum likelihood implementation of an isolation with migration model for three species*, College of Life Sciences, Sun-Yatsen University, Guangzhou, China, 11 December 2012
33. *Species delimitation using genomic sequence data*, in Symposium on *Computational and Statistical Phylogenetics*, Vigo, Spain, 13-14 September 2012.
34. *The impact of prior on Bayesian estimation of branch lengths*, College of Life Sciences, Sun-Yatsen University, Guangzhou, China, 31 December 2011.
35. *Bayesian estimation of species divergence times*. Workshop on Molecular Evolution and Phylogenetics, Institute of Zoology, Chinese Academy of Sciences, Beijing, 26-29 December 2011.
36. *Bayesian estimation of species divergence times*, Segunda Escuela Latinoamericana de Evolution, 7-18 November 2011, Universidad Austral de Chile, Valdivia, Chile.
37. *Species delimitation using genomic sequence data*. National Institute of Genetics, Mishima, Japan, 28 January 2011.
38. *Species delimitation using genomic sequence data*. China Agricultural University, Beijing, 10 January 2011.
39. *Species delimitation using genomic sequence data*. College of Life Sciences, Sun Yat-sen University, Guangzhou, China, 8 December 2010.
40. *Detection of positive selection in protein-coding DNA sequences*. Workshop on Molecular Evolution and Phylogenetics, Institute of Zoology, Chinese Academy of Sciences, Beijing, 12-17 June 2010.
41. *Adaptive molecular evolution*. EMBO Practical Workshop on Molecular Evolution, 3-15 May 2010.

42. *Population genomics and human-chimpanzee speciation*, Symposium on comparative genomics, University of St. Andrews, 18 August 2009.
43. *Detection of Darwinian selection from genomic comparisons*, Bioinformatics and Comparative Genomics Summer School, University of St. Andrews, 15-17 August 2009.
44. *Coalescent and human-chimpanzee speciation*, Peking University, China, 5 May 2009.
45. Wellcome Trust Advanced Workshop on Molecular Evolution, 29 March-9 April 2009, Wellcome Trust Genome Campus, Hinxton, Cambridge, UK (co-organizer, with Drs Nick Goldman and Aidan Budd, and lecturer).
46. *Lecture 1: Comparison between two protein-coding gene sequences;*  
*Lecture 2: Codon models and positive selection in protein evolution;*  
*Lecture 3: PAML demo.*  
Graduate Course on Population Genetics, University of Helsinki, 10 November 2008.
47. *Estimation of hominoid ancestral population sizes*, Centro de Ciencias Genomicas-UNAM, Cuernavaca, 20 October 2008.
48. *Detecting adaptive evolution in protein-coding DNA sequences*, University of Nebraska at Lincoln, 15 October 2008.
49. *Estimation of hominoid ancestral population size and complex speciation of humans and chimpanzees*, Institut für Tierzucht und Genetik, Veterinärmedizinische Universität, Wien. 15 September 2008.
50. *Bayesian estimation of hominoid ancestral population*, Department of Integrative Biology, University of California at Berkeley. 12 September 2008.
51. *Coalescent and estimation of hominoid ancestral population*, College of Life Sciences, Sun Yat-sen University, Guangzhou, China. 18 August 2008.
52. *Estimation of hominoid ancestral population sizes*, Institut fuer Genetik, Universitaet zu Koeln, Germany, 9-11 June 2008.
53. *Detection of positive selection in protein-coding DNA sequences.* Workshop on Molecular Evolution and Phylogenetics, Institute of Zoology, Chinese Academy of Sciences, Beijing, 12-16 May 2008.
54. *Empirical evaluation of a prior for Bayesian phylogenetic inference*, Royal Society Discussion Meeting, London, 28-29 April 2008
55. *Estimation of hominoid ancestral population sizes*, 6 March 2008, Kyushu University, Fukuoka, Japan.
56. *Training Workshop on Computational Molecular Evolution*, four-day course including lectures and computer demonstrations at Taiwan National University, 29 December 2007 - 1 January 2008.
57. *Estimation of species divergence times by incorporating uncertainties in fossils.* Gordon Conference on Structural, Functional & Evolutionary Genomics, Hinxton, Cambridge, 30 July - 4 August 2007.
58. *Statistics in Genetics*, 15 June 2007, Institute of Applied Mathematics, Chinese Academy of Sciences, Beijing, China.
59. *Biodiversity and Conservation Biology in the Tibet Plateau*, keynote speech in "2007 International Workshop on Biodiversity", 8 June 2007, University of Tibet.
60. *Detecting selective pressures from comparative analysis of protein-coding sequences*, Institute of Zoology, Beijing, China, 30 April 2007.
61. *The star-tree paradox and Bayesian phylogenetics*, Institute of Statistical Mathematics, Tokyo, Japan, 27 March, 2007.
62. *The star-tree paradox and Bayesian phylogenetics*, Zhongshan University, Guangdong, China, 2 January, 2007.
63. *Lindley's paradox, star-tree paradox, and Bayesian phylogenetics*, Newton Institute of Mathematical Sciences, Cambridge, 15 December, 2006.
64. *Detecting adaptive protein evolution*, University of Groningen, Centre for Ecological and Evolutionary Studies, 26 October 2006.
65. *Training Course in Molecular Phylogenetics*, two-day course including lectures and computer demonstrations at Rothamsted Research Institute, 18-19 October 2006.
66. *Phylogenetic methods for detecting adaptive protein evolution*, University of Lausanne, 8 June 2006.
67. *Codon substitution models and adaptive protein evolution*, University of Bern, 9 June 2006.
68. *Phylogenetic methods for detecting adaptive protein evolution*, Workshop on "Statistical methods for identification of genes under natural selection", Helsinki, 15-19 May 2006.
69. *Detecting molecular adaptation from genomic sequences: near the horizon of unknowables*, Workshop on Chicken Genomics & Development, Cold Spring Harbor Laboratory. New York, 7-10 May 2006.
70. *Estimation of species divergence times*, Zhongshan University, Guangdong, China, 24 April 2006.
71. *Models in molecular evolution*, Fudan University, Shanghai, 19 April 2006.

72. *Bayesian methods in genetics*, Teaching course in Bioinformatics, Tokyo Dental and Medical University, 24 & 27 March 2006.
73. *Detecting molecular adaptation from genomic sequences*, Omix Informatics Symposium, Tokyo Dental and Medical University, 20 March 2006.
74. *Detection of molecular adaptation in protein-coding genes*, University of York, 9 February 2006.
75. *Phylogenetic methods to detect adaptive protein evolution*, Max Planck Institute of Chemical Ecology, Jena, Germany, 17 November 2005.
76. *Adaptive evolution in viral genomes*, Windeyer Institute of Medical Sciences, UCL, 28 June 2005.
77. *Introduction to molecular phylogenetics*, two-day course at Institute of Zoology, Chinese Academy of Sciences, Beijing, China, 2-3 May 2005.
78. *Detecting molecular adaptation through phylogenetic sequence comparison*, Fudan University, Shanghai, China, 27 April 2005.
79. *Phylogenetic analysis in the post-genomic age*, Novartis Foundation/Royal Society Discussion Meeting on *Insights into evolution from post-genomic data*. London, 6 April 2005.
80. *Workshop in Molecular Phylogenetics*, two-day course (lectures and computer demonstrations) at Rothamsted Research Institute, 17-18 March 2005.
81. *Markov chain Monte Carlo in genetics & phylogenetics: 3-hour lecture*, University of Montpellier II, 25 October 2004.
82. *Detecting adaptive protein evolution*, University of Montpellier II, 12 October 2004.
83. *Bayes empirical Bayes inference of sites under positive selection*. PhyloGroup meeting III, 5 October 2004, University College London.
84. *Adaptive protein evolution*, Workshop in Molecular Evolution and phylogenetics, Institute of Zoology, Beijing, China, 19-22 August 2004.
85. *The effects of prior models in Bayesian MCMC estimation of divergence times*, International Congress of Zoology, Beijing, 23-27 August 2004.
86. *Markov chain Monte Carlo methods for integrated analysis of heterogeneous genetic data sets*, University of California, San Diego 1 December 2003.
87. *Estimation of species divergence times from molecular sequence data*, Institute of Zoology, Chinese Academy of Sciences, Beijing, 31 October 2003.
88. *Detection of molecular adaptation from comparison of protein-coding DNA sequences*, Workshop on Mathematics of Evolution and Phylogeny", Paris, France, 15 – 19 June 2003.
89. *Statistical methods for detecting molecular adaptation*, Symposium on "Relating molecular evolution and protein function", Valencia, Spain, 13-14 June 2003.
90. *Phylogenetic analysis of protein coding DNA sequences*, Woods Hole Workshop on Molecular Evolution, 27 July – 9 August 2003, Woods Hole, MA (one 3-hour lecture and one computer demonstration).
91. *Phylogenetic methods for detecting adaptive molecular evolution*, Laboratoire d'Ecologie Alpine, Université Joseph Fourier, Grenoble, France, 16 May 2003.
92. *Evolutionary comparison of gene sequences to help understand protein function*. School of Biosciences, University of Birmingham, 13 November 2002.
93. *Phylogenetic methods for detecting adaptive molecular evolution*, Departmental of Ecology and Evolutionary Biology, Yale University, 20 March 2002.
94. *Phylogenetic methods for detecting adaptive molecular evolution*, Symposium on *Molecular Evolutionary Genetics*, Annual Meeting of American Genetics Association, 22-24 March 2002, Tempe, Arizona.
95. *Statistical methods for detecting molecular adaptation*, Symposium on *Molecular Evolution and Systematics*, 26-28 December 2001, Academia Sinica, Taipei, Taiwan (lecture and computer demonstration).
96. *Statistical methods for detecting molecular adaptation*, 31 December 2001, Department of Biology, National Tsinghua University, Taiwan.
97. *Use of phylogenies to detect adaptive molecular evolution*, Symposium on *Systematics: the foundation of biology?* 28 November 2001, Natural History Museum, London.
98. *Markov models of codon substitution for detecting adaptive molecular evolution*, 13 November, 2001, Department of Statistics, University of Oxford.
99. *Phylogenetic methods to detect adaptive molecular evolution*, 5th Anton Dohrn Workshop *Natural Selection and the Neutral Theory*, 24-27 October 2001, Ischia, Italy.
100. *Codon substitution models and phylogenetic analysis of protein coding genes*, Woods Hole Workshop on Molecular Evolution, 27 July – 10 August 2001, Woods Hole, MA (one lecture and one computer demonstration).

101. *Models of codon substitution to detect adaptive molecular evolution*, 16 July 2001, Department of Medical Genetics, University of Alberta, Edmonton, Canada.
102. *Estimation of synonymous and nonsynonymous substitution rates and the evolution of mammalian nuclear genes*, 3 July 2001, Department of Biometrics, Cornell University, USA.
103. *Detecting adaptive evolution in viral genes*, 27 – 29 April 2001, *VIIIth International Meeting on HIV Dynamics and Evolution*, Paris, France.
104. *Estimation of synonymous and nonsynonymous substitution rates and the evolution of mammalian and Drosophila genes*, *Workshop on Population Genetics at the Molecular Level*, Montreal, Canada, 8-11 March 2001.
105. *Maximum likelihood analysis of adaptive evolution in HIV-1 gp120 env gene*. *Pacific Symposium on BioComputing 2001*, Kona, Hawaii, 4-9 January 2001.
106. *Dating speciation events using local molecular clocks*. The 26<sup>th</sup> CIB Seminar, Center for Information Biology, National Institute of Genetics, Mishima, Japan. 6 December 2000.
107. *Molecular clocks*, Department of Systematics and Animal Biology, University of Geneva, 24 November 2000.
108. *Detecting molecular adaptation to study protein function*, Stockholm Bioinformatics Center, University of Stockholm, 9 November 2000.
109. *Maximum likelihood calculation on large phylogenies and analysis of adaptive evolution in human influenza virus A*, Department of Statistics, University of Reading. 6 July 2000.
110. *Phylogenetic methods for detecting adaptive molecular evolution*. University of Edinburgh, 31 May 2000.
111. *Statistical methods for detecting molecular adaptation*. College of Life Sciences, Peking University, 27 March 2000.
112. *Dating speciation events using local molecular clocks*. Institute of Statistical Mathematics, Tokyo, 9 March 2000.
113. *Statistical methods for detecting adaptive molecular evolution*. *Evolution 2000*, Tokyo, 5-7 March 2000.
114. *Relating physicochemical properties of amino acids to variable nucleotide substitution patterns among sites*. Pacific Symposium on Computational Biology 2000, Honolulu, Hawaii, 4-9 January 2000.
115. *Statistical methods for detecting molecular adaptation*. Department of Genetics, Queen's Medical School, University of Nottingham. November 24, 1999.
116. *Models of codon substitution and adaptive evolution in abalone sperm lysin*. School of Biological Sciences, University of Manchester. September 15, 1999.
117. *Models of codon substitution and their use to detect adaptive molecular evolution*. VIIth Conference of European Society of Evolutionary Biology, August 23-28, 1999, Barcelona, Spain.
118. *Detecting adaptive molecular evolution*. BBSRC Workshop on Molecular Evolution and Diversity, May 10–11, 1999, Warwick, England.
119. *Models of amino acid substitution*, Natural History Museum Systematics Discussion Group, October 1, 1998.
120. *On the estimation of ancestral population sizes*. Newton Institute Program on *Biomolecular structure and function in the context of genome projects*, Population genetics week organised by Profs Simon Tavare and Peter Donnelly, Cambridge (England), September 25, 1998.
121. *Statistical tests in molecular phylogenetics*. Prof Joe. Felsenstein's EC Summer School on *Phylogenetic Methods*, Cambridge, UK, August 13, 1998 (lecture and computer demonstration)
122. *Bayesian estimation of molecular evolutionary trees*, Department of Statistics, UCL, May 11, 1998.
123. *Bayesian estimation of molecular evolutionary trees*, CoMPLEX workshop on Population Biology, UCL, April 29, 1998.
124. *Bayesian estimation of molecular evolutionary trees*, Institute of Statistical Mathematics, Tokyo, Japan, February 25, 1998.
125. *Models of codon substitution and their use to understand the evolutionary process of protein-coding DNA sequences*, National Institute of Genetics, Mishima, Japan, February 11, 1998.
126. *Models of DNA sequence evolution and their use in phylogenetic analysis*. Department of Genetics, University of Cambridge, January 23, 1997.
127. *Models of DNA sequence evolution and their use in phylogenetic analysis*. Natural History Museum (London) Systematics Discussion Group, January 20, 1997.
128. *Modelling the variation of substitution rates among sites in a DNA sequence*. Departments of Statistics and Genetics, North Carolina State University, November 15, 1995.

129. *Reconstruction of ancestral nucleotide or amino acid sequences by the likelihood approach*. American Society of Naturalists Young Investigators Prize Symposium. McGill University, Montreal, Quebec, July 8–12, 1995.
130. *Evolutionary trees from DNA sequences: a peculiar statistical estimation problem*. International Biometrics Society British Region Meeting, February 14, 1994.
131. *Variation of substitution rates across nucleotide sites*. Computer Users Group Symposium at the 126th Meeting of the Society for General Microbiology. University of Exeter, Exeter, England, September 7–9, 1993.
132. *Maximum likelihood phylogenetic estimation with variable rates among sites*, Natural History Museum (London) Systematics Discussion Group. April 20, 1993.
133. *Statistical properties of maximum likelihood and distance-based methods of phylogenetic estimation*, Queen Mary and Westfield College, London, March 17, 1993.

## Courses Taught

- 2001-date. Molecular evolution, BSc, MSc and MSci course, UCL.
- 2011. Probability modelling in molecular evolution, graduate course, ETH Zurich, Zurich.
- 2010. Computational Molecular evolution, graduate course, Peking University, Beijing
- 1999-2008. Quantitative Biology, first-year undergraduate course at UCL.
- 1998-2007. Molecular Evolution and Systematics, MSc. course in CoMPLEX, UCL.
- 1992, Biostatistics, undergraduate course at Beijing Agricultural University, China
- 1988, Quantitative Genetics and Animal Breeding, undergraduate course at Gansu Agricultural University, China.
- 1987, Biostatistics, undergraduate course at Gansu Agricultural University, China.