

James Cotton

Personal details

Full name: James Anthony Cotton

Date of Birth: 13 August 1976

Nationality: British

Employment

**RCUK Academic Fellow (permanent position, subject to probation), Queen Mary, University of London
August 2007-present**

**Postdoctoral Research Fellow, National University of Ireland Maynooth
February 2006-July 2007**

Research into phylogenomics and genome evolution, funded by Science Foundation Ireland and IRCSET postdoctoral fellowship

**Postdoctoral Research Assistant, The Natural History Museum, London
February 2003-February 2006**

Research into supertree theory and methods in collaboration with Dr Mark Wilkinson, funded by BBSRC grant

**Editor, Science Press Internet Services, London
June 1998-July 1999**

Writing on medical research and health policy, copy editing, proof reading

Education

Open University, UK — BSc (Hons) Mathematical Sciences, 2007

Open University, UK — Diploma in Mathematics, 2005

University of Glasgow, UK — PhD, 2003

University of Oxford, UK —BA (Hons) Biological Sciences (first class), 1997

Research grants awarded

BBSRC Co-Syst grant (06/2008-12/2008) £5,690

IRCSET Embark postdoctoral fellowship (10/2006-10/2008) €96,300

Irish Center for High-End computing, computer time grant (09/2006-09/2007) €2,395

Teaching experience

Extensive experience in teaching genetics, evolution, statistics and bioinformatics at undergraduate and masters level, Queen Mary, University of London

3rd-year Bioinformatics Programming, 1st-year molecular genetics NUI Maynooth, 2006

Intensive course on Molecular Systematics, University of Reading, 2004 and 2005

Guest lecture, EMBO bioinformatics course, NUI Maynooth, 2003

Level 1 biology demonstrator, University of Glasgow, 1999-2001, 80+ hours over 3 years.

Computing skills

Programming: Extensive experience in C++, R and Perl, experience in Python, SQL, BASIC, Pascal. Experience developing bioinformatics, phylogenetics and database tools. **Environments:** Considerable expertise with Mac OS, Linux, Windows, other UNIX. **Applications:** Microsoft Office, MySQL, Mathematica, R, Adobe and many others. **Bioinformatics:** BLAST, FASTA, SRS, EMBOSS, GCG, Clustal, Muscle, PHYLIP, PAUP, PAML, HyPhy, MrBayes, BEAST, most other molecular evolution and phylogenetics packages. **Internet:** HTML, PHP, Javascript, graphics preparation, some experience with FLASH.

Professional Service

Member of the Society of Systematic Biologists, Society for Molecular Biology and Evolution, International Society for Computational Biology. Council member and officer (Programme Secretary), Systematics Association 2009-present
Reviewer for *Systematic Biology*, *Bioinformatics*, *Molecular Biology and Evolution*, *Journal of Molecular Evolution*, *Systematics and Biodiversity*, *Evolutionary Bioinformatics Online*, *Cell and Molecular Biology Letters*, *Journal of Theoretical Biology*, *Algorithms for Molecular Biology*, *BMC Evolutionary Biology*

Publications

Chapters in Books

Wilkinson, M. and **J.A. Cotton**. 2006. Supertree methods for building the tree of life: divide-and-conquer approaches to large phylogenetic problems, *in* Towards the tree of life: taxonomy and systematics of large and species-rich taxa (Hodkinson, T., J. Parnell and S. Waldron, eds.). CRC Press.

Cotton, J.A. and R.D.M. Page. 2004. Tangled tales from multiple markers: reconciling conflict between phylogenies to build molecular supertrees, *in* Phylogenetic supertrees: combining information to reveal the tree of life (Bininda-Emonds, O.R.P., ed.) Kluwer Academic, Dordrecht, The Netherlands.

Page, R.D.M. and **J.A. Cotton**. 2000. GeneTree: A tool for exploring gene family evolution, *in* Comparative genomics: empirical and analytical approaches to gene order dynamics, map alignment and the evolution of gene families (Sankoff, D. and J.H. Nadeau, eds). Kluwer Academic Press, Dordrecht, The Netherlands.

Articles in Journals

Yang Liu, **J.A. Cotton**, Bin Shen, Xiuqun Han, Stephen J. Rossiter and Shuyi Zhang. 2010. Convergent sequence evolution between echolocating bats and dolphins. *Current Biology* 20:53-54.

San Mauro, D., Gower, D., Massingham, T., Wilkinson, M., Zardoya, R. and **J.A. Cotton**. 2009. Experimental design in Caecilian systematics: phylogenetic information of mitochondrial genomes and nuclear rag1. *Systematic Biology* 58(4):425-438.

Zhao, H., Rossiter, S.J., Teeling E.C., Li, C., **Cotton, J.A.** and S. Zhang. 2009. The evolution of color vision in nocturnal mammals. *Proceedings of the National Academy of Sciences of the USA* 106:8980-8985.

Gold, K., **Cotton, J.A.** and A. Stollewerk. 2009. The role of Notch signalling and numb function in mechanosensory organ formation in the spider *Cupiennis salei*. *Developmental Biology* 327:121-131.

Cotton, J.A. and M. Wilkinson. 2009. Supertrees enter the mainstream of phylogenetics. *Trends in Ecology and Evolution* 24:1-3.

McCann, A., **Cotton, J.A.** and J.O. McInerney. 2008. The Tree of Genomes: An Empirical Comparison of Genome Phylogeny Reconstruction Methods. *BMC Evolutionary Biology* 8:312.

Li, G., Wang, J., Rossiter, S.J., Jones, G., **Cotton, J.A.** and S. Zhang. 2008. The hearing gene Prestin reunites echolocating bats. *Proceedings of the National Academy of Sciences of the USA* 37:13959-13964.

McInerney, J.O., **J.A. Cotton** and D. Pisani. 2008. The Tree of Life: Past, present...and future? *Trends in Ecology and Evolution* 23:276-281.

Peterson, K.J., **J.A. Cotton**, J.G. Gehling and D. Pisani. 2008. The Ediacaran emergence of bilaterians: congruence between the genetic and geologic fossil records. *Philosophical Transactions of the Royal Society Series B* 363:1435-1443.

Day, J.J., **J.A. Cotton** and T.G. Barraclough. 2008. Tempo and mode of diversification in Lake Tanganyika cichlid fishes. *PLoS One* 3:e1730.

Cotton, J.A. and M. Wilkinson. 2008. Quantifying the potential utility of phylogenetic characters. *Taxon* 57:131-136.

- Loader, S.P., D. Pisani, **J.A. Cotton**, D.J. Gower, J.J. Day and M. Wilkinson. 2007. Relative timescales reveal multiple origins of parallel disjunct distributions of African caecilian amphibians. *Biology Letters* 3:505-508.
- Pisani, D., **J.A. Cotton** and J.O. McInerney. 2007. Supertrees disentangle the chimeric origin of eukaryotic genomes. *Molecular Biology and Evolution* 24:1752-1760.
- Cotton, J.A.** and M. Wilkinson. 2007. Majority-rule supertrees. *Systematic Biology* 56:445-452.
- Wilkinson, M., **J.A. Cotton**, F.-J. Lapointe and D. Pisani. 2007. Properties of supertree methods in the consensus setting. *Systematic Biology* 56:330-337.
- Cotton, J.A.** and R.D.M. Page. 2006. The shape of human gene family phylogenies. *BMC Evolutionary Biology* 6:66
- Cotton, J.A.**, C.S.C. Slater and M. Wilkinson. 2006. Discriminating supported and unsupported relationships in supertrees using triplets. *Systematic Biology* 55:345-350
- Pfister, K., P.R. Shah, H. Hummerich, A. Russ, **J.A. Cotton**, A.A. Annuar, S.M. King and E.M.C. Fisher. 2006. Genetic analysis of the cytoplasmic dynein subunit families. *PLoS Genetics* 2:1.
- Wilkinson, M., D. Pisani, **J.A. Cotton**, and I. Corfe. 2005. Measuring support and finding unsupported relationships in supertrees. *Systematic Biology* 54:419-431.
- Wilkinson, M., **J.A. Cotton**, C. Creevey, O. Eulenstein, S.R. Harris, F.-J. Lapointe, C. Levasseur, J.O. McInerney, D. Pisani and J.L. Thorley. 2005. The shape of supertrees to come: tree-shape related properties of fourteen supertree methods. *Systematic Biology* 54:419-431.
- Cotton, J.A.** and R.D.M. Page. 2005. Rates and patterns of gene duplication and loss in the human genome. *Proceedings of the Royal Society of London, Series B* 272:277-285.
- Cotton, J.A.** 2004. Analytical methods for detecting paralogy in molecular datasets. *Methods in Enzymology* 395:700-724
- Wilkinson, M., **J.A. Cotton** and J.L. Thorley. 2004. The information content of trees and their matrix representations. *Systematic Biology* 53:989-1001.
- Cotton, J.A.** and R.D.M. Page. 2003. Gene tree parsimony vs. uninode coding for phylogenetic reconstruction. *Molecular Phylogenetics and Evolution* 29:298-308.
- Cotton, J.A.** and R.D.M. Page. 2002. Going nuclear: vertebrate phylogeny and gene family evolution reconciled. *Proceedings of the Royal Society of London, Series B* 269:1555-1561.
- J.A. Cotton.** 2001. An unusual genetic system allows recombination to be recognized in an animal mitochondrial genome. *Genome Biology* 2(10):reports0034.
- J.A. Cotton.** 2001. Techniques commonly applied to the discovery of unknown prokaryotes have been used to identify new eukaryotic lineages within picoplankton. *Genome Biology* 2(7):reports0016.
- J.A. Cotton.** 2001. Invertebrate retroelements have borrowed diverse viral envelopes for infection. *Genome Biology* 2(2):reports0006.
- J.A. Cotton.** 2000. A new division of the Archaea could be the most ancient living lineage. *Genome Biology* 1(6):reports0076.
- J.A. Cotton.** 2000. Genome structure confirms the chastity of some ancient asexuals. *Genome Biology* 1(3):reports0068.
- J.A. Cotton.** 2000. DNA libraries from uncultured microbes reveal insights into the functional and genomic diversity of soil bacteria. *Genome Biology* 1(2):reports0060.

Conference Contributions

- Page, R.D.M. and **J.A. Cotton.** 2001. Vertebrate phylogenomics: reconciled trees and gene duplications, in *Proceedings of the pacific symposium on biocomputing 2002* (Altman, R.B., A.K. Dunker, L. Hunter, K. Lauderdale and T.E. Klein, eds). World Scientific Press, Singapore.

Major Presentations

- Society for Molecular Biology and Evolution, Tempe, AZ, June 2006: Understanding and evaluating the performance of supertree methods
- Virtual Institute of Bioinformatics Éire, Dublin, Ireland, April 2006: Will we ever have enough data to build the tree of life?
- Society for Molecular Biology and Evolution, Auckland NZ, June 2005: Inferring trees from trees: investigating properties of supertree methods

Invited, Bioinformatics seminar series, Trinity College, Dublin, Nov 2004: Models of gene duplication and loss: two links between pattern and process

4th Biennial of the Systematics Association, Trinity College, Dublin, August 2003: The shape of human gene family phylogenies

Evolution 2002, University of Illinois, Urbana-Champaign, IL, 28 June-2nd July 2002: A molecular timescale for vertebrate gene family evolution

Pacific Symposium on Biocomputing, Hawai'i, 3rd-7th January 2002: Vertebrate Phylogenomics: Reconciled Trees and Gene Duplications

3rd Young Systematists Forum, Natural History Museum, December 2001: The evolutionary dynamics of gene families: phylogenetic methods reveal the birth and death of gene lineages

Evolution 2001 University of Tennessee, Knoxville, TN, 26-30th June 2001: Nuclear gene duplications support a traditional view of vertebrate phylogeny

2nd Young Systematists Forum, Natural History Museum, November 2000: A phylogenetic approach to studying gene duplications, and what it tells us about vertebrate phylogeny

DCAF, Hotel Le Chantecler, St Adele, Quebec, 22-25th September 2000: GeneTree: A tool for exploring gene family evolution