

CURRICULUM VITAE

Simon TAVARÉ

BIOGRAPHICAL

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Research Interests

Statistics and probability, with particular emphasis on statistical inference in molecular biology, human genetics, population genetics, molecular evolution, paleontology, cancer biology and bioinformatics. Microarray and resequencing data analysis. Fly tracking and behavior. Stochastic computation techniques, coalescent theory, probabilistic combinatorics. Experimental approaches to detecting methylation.

Education

University of Sheffield, UK Probability and Statistics BSc 1974
University of Sheffield, UK Probability and Statistics MSc 1975
University of Sheffield, UK Probability and Statistics PhD 1979

Professional Experience

2006 – Senior Group Leader, CR UK Cambridge Research Institute
2003 – Professor of Cancer Research (Bioinformatics)
 Department of Oncology, University of Cambridge
2003 – Professor, Department of Applied Mathematics
 and Theoretical Physics, University of Cambridge
2006 – Research Professor, Department of Biological Sciences, USC
2000 – 2006 Professor-at-Large, Keck Graduate Institute of Applied
 Life Sciences, Claremont CA
1989 – 2006 Professor, Department of Biological Sciences, USC
1999 – 2006 Professor, Department of Preventive Medicine,
 Keck School of Medicine, USC
1989 – 2006 Professor, Department of Mathematics, USC
1984 – 1989 Associate Professor of Mathematics, University of Utah
1983 – 1985 Associate Professor of Statistics, Colorado State University
1981 – 1983 Assistant Professor of Statistics, Colorado State University
1978 – 1981 Instructor of Mathematics, University of Utah
1978 – 1979 Research Fellow, Medical Biophysics and Computing,
 University of Utah
1977 – 1978 Lecturer in Probability and Statistics, University of Sheffield.

Visiting Appointments

Chalmers Jubilee Professor, Chalmers University, Sweden. 8-10/10.
G. C. Steward Visiting Fellowship in Mathematics, Gonville and Caius College, Cambridge, England. 1-7/2003
SAMSI, North Carolina. 9-10/2002
Université Blaise Pascal, Clermont-Ferrand, France. 7/2001
Institute for Pure and Applied Mathematics, UCLA. 9-12/2000
Isaac Newton Institute, University of Cambridge, England. 9/1998
Department of Mathematical Statistics, Chalmers University of Technology and Gothenburg University, Sweden. 5/1998
Department of Applied Mathematics, University of Zürich, Switzerland. 5-6/1997, 4-7/1996 (Gastprofessor), 8/1993, 12/1992, 5-6/1992.
Department of Mathematics, Monash University, Australia. 7/1997, 7/1994, 3/1993, 4-5/1990, 7-12/1980.
Department of Mathematics, Queen Mary and Westfield College, London. 8/1989, 9-12/1988
Department of Statistical Science, University College, London. 7-8/1988
Department of Mathematics, University of Southern California. 8-12/1987, 10-11/1984.
Mathematics Department, Stanford University. 6-8/1982, 6-8/1981, 6-8/1979.

Honors and Awards

2009	Elected Fellow, Academy of Medical Sciences (FMedSci)
2004	Elected Fellow, American Statistical Association
2003 – 2008	Royal Society/Wolfson Research Merit Award
2001	Medallion Lecture, Institute of Mathematical Statistics
1998 –	George and Louise Kawamoto Chair in Biological Sciences, USC
1998	Elected Fellow, American Association for the Advancement of Science
1993	Medallion Lecture, Institute of Mathematical Statistics
1992	Elected Fellow, Institute of Mathematical Statistics

Professional Qualification

1993	C Stat
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PUBLICATIONS

Books

1. Deonier RC, Tavaré S & Waterman MS. *Computational Genome Analysis: An Introduction*, 2005. Springer Verlag, New York. 540pp. ISBN: 0-387-98785-1

2. Arratia R, Barbour AD & Tavaré S. *Logarithmic Combinatorial Structures: A Probabilistic Approach*. EMS Monographs in Mathematics, **1**, 2003. European Mathematical Society Publishing House, Zuerich. 352pp.
3. Donnelly P & Tavaré S. (eds) *Progress in Population Genetics and Human Evolution*. IMA Volumes in Mathematics and its Applications, **87**, 1997. Springer Verlag, Berlin. 330pp.

Submitted Articles

4. Daelemans C, Ritchie ME, Smits G, Abu-Amero S, Sudbery IM, Forrest MS, Susana Campino S, Stanier P, Kwiatkowski D, Deloukas P, Dermitzakis ET, Tavaré S, Moore GE & Dunham I. High-throughput analysis of candidate imprinted genes and allele-specific gene expression in the human term placenta. *BMC Genomics*.
5. Stirling EJ, Goldman TD, Grover D, Tavaré S & Arbeitman MN. Neurons in the pars intercerebralis regulate circadian rhythm and male courtship behaviors, affecting the timing of social interactions in *Drosophila*. *PLoS Biology*.
6. Clark AM, Goldstein LD, Tevlin M, Tavaré S, Shaham S & Miska EA. The microRNA miR-124 controls gene expression in the sensory nervous system of *Caenorhabditis elegans*. *Nucleic Acids Research*.

Journal Articles

Reviews are indicated by **

In Press

7. Sassen S, Goldstein L, Stingl J, Blenkiron C, Le Quesne J, Spiteri I, Karagavriilidou K, Watson CJ, Tavaré S, Miska EA & Caldas C. Characterization of microRNA expression in post-natal mouse mammary gland development. *BMC Genomics*.
8. Curtis C, Lynch AG, Dunning MJ, Spiteri I, Marioni JC, Hadfield J, Chin S-F, Brenton J, Tavaré S & Caldas C. The pitfalls of platform comparison: DNA copy number array technologies assessed. *BMC Genomics*.
9. Barbosa-Morais NL, Dunning MJ, Samarajiwa S, Darot JFJ, Ritchie ME, Lynch AG & Tavaré S. A reannotation pipeline for Illumina BeadArrays: improving the interpretation of gene expression data. *Nucleic Acids Research*.
10. Grover G & Tavaré S. Finding behavioral motifs in fly trajectories. *Communications in Information and Systems*.

2009

11. Waskar M, Landis GN, Shen J, Curtis CN, Abdueva D, Skvortsov D, Tavaré S & Tower J. *Drosophila melanogaster* p53 has developmental stage-specific and sex-specific effects on adult life span indicative of sexual antagonistic pleiotropy. *Aging*, **1**, 1-31, 2009.
12. Grover D, Ford D, Brown C, Hoe N, Erdem E, Tavaré S & Tower J. Hydrogen peroxide stimulates activity and alters behavior in *Drosophila melanogaster*. *PLoS ONE*, **4**: e7580, 2009.
13. Knott S, Viggiani CJ, Aparicio OM & Tavaré S. Strategies for analyzing highly enriched IP-chip datasets. *BMC Bioinformatics*, **10**: 305, 2009.
14. Spyrou C, Stark R, Lynch AG & Tavaré S. BayesPeak: Bayesian analysis of ChIP-seq data. *BMC Bioinformatics*, **10**: 299, 2009.
15. Fernando H, Sewitz S, Darot J, Tavaré S, Huppert JL & Balasubramanian S. Genome-wide analysis of a G-quadruplex-specific single-chain antibody that regulates gene expression. *Nucleic Acids Research*, doi: 10.1093/nar/gkp740, 2009.
16. Ritchie ME, Carvalho BS, Hetrick KN, Tavaré S & Irizarry RA. R/Bioconductor software for Illumina's Infinium whole-genome genotyping BeadChips. *Bioinformatics*, **25**, 2621-2623, 2009.
17. ** Siegmund KD, Marjoram P, Tavaré S & Shibata D. Many colorectal cancers are "flat" clonal expansions. *Cell Cycle*, **8**, 2187–2193, 2009.
18. Tiemann-Boege I, Curtis CN, Shinde DN, Goodman DB, Tavaré S & Arnheim N. Product length, dye choice, and detection chemistry in the bead-emulsion amplification of millions of single DNA molecules in parallel. *Analytical Chemistry*, **81**, 5770–5776, 2009.
19. Knott S, Viggiani CJ, Tavaré S & Aparicio OM. Genome-wide replication profiles indicate an expansive role for Rpd3L in regulating replication initiation timing or efficiency, and reveal genomic loci of Rpd3 function in *Saccharomyces cerevisiae*. *Genes & Dev*, **23**, 1077–1090, 2009.
20. Grover D, Yang J, Ford D, Tavaré S & Tower J. Simultaneous tracking of movement and gene expression in multiple *Drosophila melanogaster* flies using GFP and DsRED fluorescent reporter transgenes. *BMC Research Notes*, **2**: 58, 2009.
21. Wilkinson RD & Tavaré S. Estimating the primate divergence time using conditioned birth-and-death processes. *Theoret Popul Biol*, **75**, 278–285, 2009.
22. Young ARJ, Narita M, Ferreira M, Kirschner K, Sadaie M, Darot JFJ, Tavaré S, Arakawa S, Shimizu S, Watt, FM & Narita M. Autophagy mediates the mitotic-senescence transition. *Genes & Dev*, **23**, 798–803, 2009.

23. Siegmund KD, Marjoram P, Woo Y-J, Tavaré S & Shibata D. Inferring clonal expansion and cancer stem cell dynamics from DNA methylation patterns in colorectal cancers. *Proc Natl Acad Sci USA*, **106**, 4828–4833, 2009.
 24. Shen J, Curtis C, Tavaré S & Tower J. A screen of apoptosis and senescence regulatory genes for life span effects when over-expressed in *Drosophila*. *Aging*, **1**, 191–211, 2009.
 25. Woo Y-J, Siegmund KD, Tavaré S & Shibata D. Mitotically older colorectal cancers in older individuals. *J Pathol*, **217**, 483–488, 2009.
 26. Jiang R, Tavaré S & Marjoram P. Population genetic inference from resequencing data. *Genetics*, **181**, 187–197, 2009.
- 2008
27. Grover D, Yang J, Tavaré S & Tower J. Simultaneous tracking of fly movement and expression using GFP. *BMC Biotechnology*, **8**: 93, 2008. (With press release)
 28. Dimas AS, Stranger BE, Beazley C, Finn RD, Ingle CE, Forrest MS, Ritchie ME, Deloukas P, Tavaré S & Dermitzakis ET. Modifier effects between regulatory and protein-coding variation. *PLoS Genetics*, **4** (10): e1000244, 2008.
 29. Wilson MD, Barbosa-Morais NL, Schmidt D, Conboy CM, Vanes L, Tybulewicz VLJ, Fisher EMC, Tavaré S & Odom DT. Species-specific transcription in mice carrying human chromosome 21. *Science*, **322**, 434–438, 2008.
 30. Hull ML, Rangel Escareno C, Godsland J, Doig J, Johnson C, Butt RP, Phillips S, Smith SK, Tavaré S, Print CG & Charnock-Jones DS. Endometrial-peritoneal interactions during endometriotic lesion establishment. *Am J Pathol*, **173**, 700–715, 2008.
 31. Marioni JC, White M, Tavaré S & Lynch AG. Hidden copy number variation in the HapMap trios. *Proc Natl Acad Sci USA*, **105**, 10067–10072, 2008.
 32. Szyjka SJ, Aparicio JG, Viggiani CJ, Knott S, Xu W, Tavaré S & Aparicio OM. Rad53 regulates replication fork restart after DNA damage in *Saccharomyces cerevisiae*. *Genes & Dev*, **22**, 1902–1920, 2008.
 33. Rakyán VK, Down TA, Thorne NP, Flicek P, Kulesha E, Gräf S, Tomazou EM, Bäckdahl L, Johnson N, Herberth M, Howe KL, Jackson DK, Miretti MM, Fiegler H, Marioni JC, Birney E, Hubbard TJP, Carter NP, Tavaré S & Beck S. mPod, an integrated resource for genome-wide identification and analysis of human tissue-specific differentially methylated regions (tDMRs). *Genome Res*, **18**, 1518–1829, 2008.
 34. Das PP, Bagijn MP, Goldstein LD, Woolford JR, Lehrbach NJ, Sapetschnig A, Buhecha HR, Gilchrist MJ, Howe KL, Stark R, Matthews N, Berezikov E, Ketting RF, Tavaré S & Miska EA. Piwi and piRNAs act upstream of an endogenous siRNA pathway to

- suppress Tc3 transposon mobility in the *Caenorhabditis elegans* germline. *Molecular Cell*, **31**, 79–90, 2008.
35. Down TA, Rakyan VK, Turner DJ, Flicek P, Li H, Kulesha E, Gräf S, Johnson N, Herrero J, Tomazou EM, Thorne NP, Bäckdahl L, Herberth M, Howe KL, Jackson DK, Miretti MM, Marioni JC, Birney E, Hubbard TJP, Durbin R, Tavaré S & Beck S. A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. *Nature Biotechnology*, **26**, 779–785, 2008.
 36. Dunning MJ, Ritchie ME, Barbosa-Morais NL, Tavaré S & Lynch AG. Spike-in validation of an Illumina-specific variance-stabilizing transformation. *BMC Research Notes*, **1**: 18, 2008.
 37. Palmer RD, Barbosa-Morais NL, Gooding EL, Muralidhar B, Thornton CM, Pett MR, Roberts I, Schneider DT, Thorne N, Tavaré S, Nicholson JC & Coleman N; On behalf of The Childrens Cancer and Leukaemia Group (CCLG). Pediatric malignant germ cell tumours show characteristic transcriptome profiles. *Cancer Research*, **68**: 4239–4247, 2008.
 38. Chu M, Siegmund KD, Hao Q-L, Crooks GM, Tavaré S & Shibata D. Inferring relative numbers of human leukocyte genome replications. *British Journal of Haematology*, **141**: 862–871, 2008.
 39. Grover D, Tower J & Tavaré S. O fly, where art thou? *J R Soc Interface*, **5**: 1181–1191, 2008.
 40. Dunning MJ, Barbosa-Morais NL, Lynch AG, Tavaré S & Ritchie ME. Statistical issues in the analysis of Illumina data. *BMC Bioinformatics*, **9**: 85, 2008.
- [2007](#)
41. Curtis C, Landis GN, Folk D, Wehr NB, Hoe N, Waskar M, Abdueva D, Skvortsov D, Ford D, Luu A, Badrinath A, Levine RL, Bradley TJ, Tavaré S & Tower J. Transcriptional profiling of MnSOD-mediated lifespan extension in *Drosophila* reveals a species-general network of aging and metabolic genes. *Genome Biology*, **8(12)**: R262, 2007.
 42. Marioni JC, Thorne NP, Valsesia A, Fitzgerald T, Redon R, Fiegler H, Andrews DT, Stranger BE, Lynch AG, Dermitzakis ET, Carter NP, Tavaré S & Hurles ME. Breaking the waves: improved detection of copy number variation from microarray-based comparative genomic hybridization. *Genome Biology*, **8(10)**: R228, 2007.
 43. Conboy CM, Spyrou C, Thorne NP, Wade EJ, Barbosa-Morais N, Bhattacharjee A, Young RA, Tavaré S, Lees JA & Odom DT. Cell cycle genes are the evolutionarily conserved targets of mammalian DREAM member E2F4. *PLoS ONE*, **2**: e1061, 2007.

44. Chin SF, Teschendorff AE, Marioni JC, Wang Y, Barbosa-Morais NL, Thorne NP, Costa J, Pinder SE, van de Wiel MA, Green AR, Ellis IO, Porter PL, Tavaré S, Brenton JD, Ylstra B & Caldas C. High-resolution array-CGH and expression profiling identifies a novel genomic subtype of ER negative breast cancer. *Genome Biology*, **8 (10)**: R215, 2007.
45. Blenkiron C, Goldstein LD, Thorne NP, Spiteri MI, Chin SF, Dunning M, Barbosa-Morais NL, Tavaré S, Caldas C & Miska EA. MicroRNA expression profiling of human breast cancer identifies new markers of tumour subtype. *Genome Biology*, **8 (10)**: R214, 2007.
46. Stranger BE, Nica AC, Forrest MS, Dimas A, Bird CP, Beazley C, Ingle C, Dunning M, Flicek P, Koller D, Montgomery S, Tavaré S, Deloukas P & Dermitzakis ET. Population genomics of human gene expression. *Nat Genet*, **39**, 1217–1224, 2007.
47. ** Shibata D & Tavaré S. Stem cell chronicles: Autobiographies within genomes. *Stem Cell Reviews*, **3**, 94–103, 2007.
48. Martin RD, Soligo C & Tavaré S. Primate origins: Implications of a Cretaceous ancestry. *Folia Primatol*, **78**, 277–296, 2007.
49. Chu MW, Siegmund KD, Eckstam CL, Kim JY, Yang AS, Kanel GC, Tavaré S & Shibata D. Lack of increases in methylation at three CpG-rich genomic loci in non-mitotic adult tissues during aging. *BMC Medical Genetics*, **8**:50, 2007.
50. Lynch AG, Marioni JC & Tavaré S. Numbers of CNVs and false negative rates will be underestimated if we do not account for the dependence between repeated experiments. *Amer J Hum Genet*, **81**, 418–420, 2007.
51. Dunning MJ, Smith ML, Ritchie ME & Tavaré S. *beadarray*: R classes and methods for Illumina bead-based data. *Bioinformatics*, **23**, 2183–2184, 2007.
52. Skvortsov D, Abdueva D, Curtis CN, Schaub B & Tavaré S. Explaining differences in saturation levels for Affymetrix GeneChip arrays. *Nucleic Acids Research*, **35**, 4154–4163, 2007.
53. Skvortsov D, Abdueva D, Stitzer M, Finkel SA & Tavaré S. Using expression arrays for copy number detection: an example from *E. coli*. *BMC Bioinformatics*, **8**:203, 2007.
54. Chin S-F, Wang Y, Thorne NP, Teschendorff AE, Pinder SE, Vias M, Naderi A, Roberts I, Barbosa-Morais NL, Garcia M, Iyer NG, Kranjac T, Robertson J, Ruffalo T, Aparicio SFR, Tavaré S, Ellis I, Brenton JD, Caldas C. Using array-comparative genomic hybridization to define molecular portraits of primary breast cancers. *Oncogene*, **26**, 1959–1970, 2007.

55. Nicolas P, Kim K-M, Shibata D & Tavaré S. The stem cell population of the human colon crypt: analysis via methylation patterns. *PLoS Computational Biology*, **3**, 364–374, 2007.
56. Stranger BE, Forrest MS, Dunning M, Thorne NP, Ingle CE, Beazley C, Redon R, Bird CP, de Grassi A, Lee C, Tyler-Smith C, Carter N, Scherer SW, Tavaré S, Deloukas P, Hurles ME & Dermitzakis ET. Relative impact of nucleotide and copy number variation on gene expression phenotypes. *Science*, **315**, 848–853, 2007.
- 2006
57. ** Dunning M, Smith M, Thorne NP, Tavaré S. beadarray: an R package to analyse Illumina BeadArrays. *R News*, **6**(5), 17–23, 2006.
58. Xu W, Aparicio JG, Aparicio OM & Tavaré S. Genome-wide mapping of ORC and Mcm2p binding sites on tiling arrays and precise identification of essential ARS consensus sequences in *S. cerevisiae*. *BMC Genomics*, **7**: 276, 2006.
59. Ibrahim AEK, Thorne NP, Baird K, Barbosa-Morais NL, Tavaré S, Collins VP, Wylie AH, Arends MJ & Brenton JD. Mmass: an optimised array-based method for assessing CpG island methylation. *Nucleic Acids Research*, **34**: e136, 2006.
60. Abdueva D, Skvortsov D & Tavaré S. Non-linear analysis of GeneChip arrays. *Nucleic Acids Research*, **34**, e105, 2006.
61. ** Marjoram P & Tavaré S. Modern computational approaches for analysing molecular-genetic variation data. *Nat Rev Genet*, **7**, 759–770, 2006.
62. Jiang R, Marjoram P, Borevitz JO & Tavaré S. Inferring population parameters from single-feature polymorphism data. *Genetics*, **173**, 2257–2267, 2006.
63. ** Shibata D & Tavaré S. Counting divisions in a human somatic cell tree: how, what and why. *Cell Cycle*, **5**, 610–614, 2006.
64. Millman K, Black CM, Stamm WE, Jones RB, Hook EW, Martin DH, Bolan G, Tavaré S & Dean D. Population-based genetic epidemiologic analysis of *Chlamydia trachomatis* serotypes and lack of associations between *ompA* polymorphisms and clinical phenotypes. *Microbes and Infection*, **8**, 604–611, 2006.
65. Jakobsson M, Hagenblad J, Tavaré S, Säll T, Halldén C, Lind-Halldén C & Nordborg M. A unique recent origin of the allotetraploid species *Arabidopsis suecica*: evidence from nuclear DNA markers. *Mol Biol Evol*, **23**, 1217–1231, 2006.
66. Marioni JC, Thorne NP & Tavaré S. BioHMM: a heterogeneous hidden Markov model for segmenting array CGH data. *Bioinformatics*, **22**, 1144–1146, 2006.

67. Dunning M, Thorne NP, Camilier I, Smith ML & Tavaré S. Quality control and low-level statistical analysis of Illumina BeadArrays. *REVSTAT*, **4**, 1–30, 2006.
68. Arratia R, Barbour AD & Tavaré S. A tale of three couplings: Poisson-Dirichlet and GEM approximations for random permutations. *Combin Probab Comput*, **15**, 31–62, 2006.
69. Kim JY, Tavaré S & Shibata D. Human hair genealogies and stem cell latency. *BMC Biology*, **4**:2, 2006.

2005

70. Stranger BE, Forrest MS, Clark AG, Minichiello M, Deutsch S, Lyle R, Hunt S, Kahl B, Antonarakis SE, Tavaré S, Deloukas P & Dermitzakis ET. Genome-wide associations of gene expression variation in humans. *PLoS Genet*, **1**, 695–704, 2005.
71. Kim JY, Tavaré S & Shibata D. Counting human somatic cell replications: Methylation mirrors human endometrial stem cell divisions. *Proc Natl Acad Sci USA*, **102**, 17739–17744, 2005.
72. Clark RM, Tavaré S & Doebley J. Estimating a nucleotide substitution rate for maize from polymorphism at a major domestication locus. *Mol Biol Evol*, **22**, 2304–2312, 2005.
73. Calabrese P, Mecklin JP, Järvinen HJ, Aaltonen LA, Tavaré S & Shibata D. Numbers of mutations to different types of colorectal cancer. *BMC Cancer*. **5**:126, 2005.
74. Kim JY, Siegmund KD, Tavaré S & Shibata D. Age-related human small intestine methylation: evidence for stem cell niches. *BMC Medicine*. **3**:10, 2005.
75. Arratia R, Barbour AD & Tavaré S. A probabilistic approach to analytic arithmetic on algebraic function fields. *Math Proc Camb Phil Soc*, **139**, 1–26, 2005.
76. Innan H, Zhang K, Marjoram P, Tavaré S & Rosenberg NA. Statistical tests of the coalescent model based on the haplotype frequency distribution and the number of segregating sites. *Genetics*, **169**, 1763–1777, 2005.

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77. Tavaré S. Ancestral inference in population genetics. In *Lectures on Probability Theory and Statistics. Ecole d'Etés de Probabilité de Saint-Flour XXXI – 2001*. Ed. J. Picard. Lecture Notes in Mathematics, **1837**, 1–188, 2004. Springer Verlag, New York.
78. Landis GN, Abdueva D, Skvortsov D, Yang J, Rabin BE, Carrick J, Tavaré S & Tower J. Similar gene expression patterns characterize aging and oxidative stress in *Drosophila melanogaster*. *Proc Natl Acad Sci USA*, **101**, 7663–7668, 2004.

79. Millman KL, Black CM, Johnson R, Stamm W, Jones R, Hook E, Martin D, Bolan G, Tavaré S, & Dean D. Population-based genetic and evolutionary analysis of *Chlamydia trachomatis* urogenital strain variation in the United States. *J Bacteriol*, **186**, 2457–2465, 2004.
80. Calabrese P, Tavaré S & Shibata D. Pre-tumor progression: clonal evolution of human stem cell populations. *Am J Pathol*, **164**, 1337–1346, 2004.
81. Calabrese P, Tsao J-L, Yatabe Y, Salovaara R, Mecklin J-P, Järvinen HJ, Aaltonen LA, Tavaré S & Shibata D. Colorectal pre-tumor progression before and after loss of DNA mismatch repair. *Am. J. Pathol.*, **164**, 1447–1453, 2004.
82. Kim K-M, Calabrese P, Tavaré S & Shibata D. Enhanced stem cell survival in familial adenomatous polyposis. *Am. J. Pathol.*, **164**, 1369–1377, 2004.
- 2003
83. Marjoram P, Molitor J, Plagnol V & Tavaré S. Markov chain Monte Carlo without likelihoods. *Proc. Natl. Acad. Sci. USA*, **100**, 15324–15328, 2003.
- 2002
84. Tavaré S, Marshall CR, Will O, Soligo C & Martin RD. Using the fossil record to estimate the age of the last common ancestor of extant primates. *Nature*, **416**, 726–729, 2002.
85. ** Nordborg M & Tavaré S. Linkage disequilibrium: what history has to tell us. *Trends in Genetics*, **18**, 83–90, 2002.
- 2001
86. Millman KL, Tavaré S & Dean D. Recombination in the *ompA* gene but not the *omcB* gene of *Chlamydia* contributes to serovar-specific differences in tissue tropism, immune surveillance and persistence of the organism. *Journal of Bacteriology*, **183**, 5997–6008, 2001.
87. Yatabe Y, Tavaré S & Shibata D. Investigating stem cells in human colon by using methylation patterns. *Proc. Natl. Acad. Sci. USA*, **98**, 10839–10844, 2001. (With editorial.)
88. Markovtsova L, Marjoram P & Tavaré S. On a test of Depaulis and Veuille. *Mol. Biol. Evol.*, **18**, 1132–1133, 2001.
89. Tavaré S, Adams DC, Fedrigo O & Naylor GJP. A model for phylogenetic inference using structural and chemical covariates. *Pacific Symposium on Biocomputing*, **6**, 215–225, 2001.

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90. Arratia R, Barbour AD & Tavaré S. Limits of logarithmic combinatorial structures. *Ann. Probab.*, **28**, 1620–1644, 2000.
91. Markovtsova L, Marjoram P & Tavaré S. The effects of rate variation on ancestral inference in the coalescent. *Genetics*, **156**, 1427–1436, 2000.
92. Markovtsova L, Marjoram P & Tavaré S. The age of a unique event polymorphism. *Genetics*, **156**, 401–409, 2000.
93. Arratia R, Barbour AD & Tavaré S. The number of components in a logarithmic combinatorial structure. *Ann. Appl. Probab.*, **10**, 331–361, 2000.
94. Schbath S, Bossard N & Tavaré S. The effect of non-homogeneous clone length distribution on the progress of an STS mapping project. *J. Comp. Biol.*, **7**, 47–57, 2000.
95. Tsao JL, Yatabe Y, Salovaara R, Jarvinen HJ, Mecklin JP, Aaltonen LA, Tavaré S & Shibata D. Genetic reconstruction of individual colorectal tumor histories. *Proc. Natl. Acad. Sci. USA*, **97**, 1236–1241, 2000.

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97. Jaruzelska J, Zietkiewicz E, Batzer M, Cole D, Moisan J-P, Scozzari R, Tavaré S & Labuda D. Spatial and temporal distribution of the neutral polymorphisms in the last ZFX intron: analysis of the haplotype structure and genealogy. *Genetics*, **152**, 1091–1101, 1999.
98. Fan F, Liu C, Tavaré S & Arnheim N. Polymorphisms in the human DNA repair gene XPF. *Mutation Research Genomics*, **406**, 115–120, 1999.
99. Leeftang E, Tavaré S, Marjoram P, Neal COS, Srinidhi J, MacFarlane H, MacDonald ME, Gusella JF, de Young M, Wexler N & Arnheim N. Analysis of germline mutation spectra at the Huntington Disease locus supports a mitotic mutation mechanism. *Hum. Mol. Genet.*, **8**, 173–183, 1999.
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101. Griffiths RC & Tavaré S. The ages of mutations in gene trees. *Ann. Appl. Probab.*, **9**, 567–590, 1999.
102. Arratia R, Barbour AD & Tavaré S. The Poisson-Dirichlet distribution and the scale-invariant Poisson process. *Combin. Probab. Comput.*, **8**, 407–416, 1999.

103. Arratia R, Barbour AD & Tavaré S. On Poisson-Dirichlet limits for random decomposable combinatorial structures. *Combin. Probab. Comput.*, **8**, 193–208, 1999.
- [1998](#)
104. Griffiths RC & Tavaré S. The age of a mutation in a general coalescent tree. *Stochastic Models*, **14**, 273–295, 1998.
- [1997](#)
105. Arratia R, Barbour AD & Tavaré S. Random combinatorial structures and prime factorizations. *Notices of the American Mathematical Society*, **44**, 903–910, 1997.
106. Tavaré S, Balding DJ, Griffiths RC & Donnelly P. Inferring coalescence times for molecular sequence data. *Genetics*, **145**, 505–518, 1997.
- [1996](#)
107. Shenkar R, Navidi W, Tavaré S, Dang MH, Chomyn A, Attardi G, Cortopassi G & Arnheim N. The mutation rate of the human mitochondrial DNA deletion mtDNA⁴⁹⁷⁷. *Amer. J. Hum. Gen.*, **59**, 772–780, 1996. (With editorial.)
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- [1995](#)
110. Donnelly P & Tavaré S. Coalescents and genealogical structure under neutrality. *Annu. Rev. Genet.*, **29**, 401–421, 1995.
111. Leeflang EP, Zhang L, Tavaré S, Hubert R, Srinidhi J, MacDonald ME, Myers RM, de Young M, Wexler NS, Gusella JF & Arnheim N. Single sperm analysis of the trinucleotide repeats in the Huntington’s disease gene: quantification of the mutation frequency spectrum. *Hum. Molec. Genet.*, **4**, 1519–1526, 1995.
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ACTIVE GRANT SUPPORT

National Institutes of Health P50 HG02790, Center of Excellence in Genome Science. *Genomic analysis of the genotype-phenotype map*. PI. 9/09–8/14.

National Institutes of Health R01 MH084678. *Statistical methods for relating sequence data to phenotype*. Co-investigator (P. Marjoram PI). 9/08–6/11.

PROFESSIONAL SERVICE

Advisory Boards

Advisory Board, PUMPKIN (Membrane pumps in cells and disease, Aarhus University) (2007 –)

Advisory Board, Gene Ontology Consortium (2006 –)
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Advisory Board, Gothenburg Mathematical Modelling Centre, Sweden. (2006 –)
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Steering Committee for Statistics, Eurandom, Holland. (2004 –)
Senior Advisory Board, NESCent, North Carolina. (2004 – 2007)
Science Advisory Board, BioDiscovery, Inc. (2003 –)
Science Advisory Board, Institute for Pure and Applied Mathematics (IPAM), UCLA (2002 – 2008)
International Advisory Board, Swegene, Sweden (2001 – 2006)
Scientific Advisory Panel, The Allan Wilson Centre for Molecular Ecology and Evolution, Massey University, New Zealand. (2003 – 2005)
Science Advisory Board, Amersham plc. (2001 – 2004)
Scientific Advisory Board, Chalmers University of Technology Bioscience Initiative (1999 – 2001)
Scientific Advisory Board, GeneData AG (1997 – 2002)

Society Membership

American Association for the Advancement of Science (1991 –)
American Statistical Association (1992 –)
Institute of Mathematical Statistics (1978 –)
 Member, Committee on Fellows, 1996–99.
Royal Statistical Society (1974 –)
Genetics Society of America (1990 –)

Editorial and Refereeing Services

Member, Biological Sciences Funding Committee, CRUK. (2008 –)

Cancer Prevention Research (Editorial Board, 2008 –)

MathematicS In Action (Editorial Board, 2008 –)

Annals of Applied Statistics (Associate Editor, 2007 –)

Statistics Surveys (IMS Associate Editor, 2007 –)

Evolutionary Bioinformatics (Editorial Board, 2005 –)

Human Genomics (Editorial Board, 2003 –)

Annals of Human Genetics (Associate Editor, 2003 –)

Journal of Computational Biology (Associate Editor, 1997 –)

Journal of the Royal Society Interface (Editorial Board, 2003 – 2009)

Genetics (Associate Editor, 1997 – 2003)

Journal of Mathematical Biology (Editorial Board, 2000 – 2003)

Bernoulli (Associate Editor, 2000 – 2003)

Annals of Probability (Associate Editor, 2000 – 2002)

Combinatorics, Probability and Computing (Editorial Board, 1996 – 2001)

Annals of Applied Probability (Associate Editor, 1993 – 1999)

Stochastic Models (Editorial Board, 1991 – 2001)

Mathematical Biosciences (Editorial Board, 1990 – 2001)

Stochastic Processes and their Applications (Associate Editor, 1989 –1993)

Theoretical Population Biology (Associate Editor, 1985 –1987)

Referee for 30+ journals in statistics, probability, combinatorics and biology

Advisory Board, Kluwer Series in Computational Biology (1998 – present)

Referee for numerous grant proposals (e.g. CRUK, BBSRC, EPSRC, NSF, NIH, NSA, Wellcome Trust, Keck, Swiss Nationalfond)

Postdoctoral Fellows

- M.S. McPeck (1994–1995) Professor of Statistics, University of Chicago
- P. Marjoram (1995–1998) Research Associate Professor of Biostatistics, USC Keck School of Medicine
- J. K. Lee (1995–1997) Associate Professor, Biostatistics & Epidemiology, University of Virginia
- S. Schbath (1996) Unité Mathématique, Informatique et Génome (MIG), INRA, Jouy, France
- A. Pluzhnikov (1996–1998) Research Associate, Cox lab, University of Chicago
- S. Kruglyak (1998–2000) Illumina, Inc.
- D. Golinelli (2000–2002) Statistics Group, RAND Corporation, Santa Monica
- N. Rosenberg (2001–2004) Assistant Professor, Departments of Human Genetics, Biostatistics, and Ecology & Evolutionary Biology, University of Michigan
- P. Calabrese (2001–2004) Research Assistant Professor, Program in Molecular and Computational Biology, USC
- P. Nicolas (2004–2005) Unité Mathématique, Informatique et Génome (MIG), INRA, Jouy, France
- C. Rangel Escareño (2003–2006) Investigador Asociado, Instituto Nacional de Medicina Genómica (INMEGEN), Mexico City
- A. E. Teschendorff (Cambridge, 2005–2006) Heller Fellow, UCL Cancer Institute, London
- J. Aparicio (2004–2007) CHLA
- N. P. Thorne (Cambridge, 2004–2008) Bioinformatics Division, WEHI, Melbourne
- I. Tiemann-Boege (Cambridge, 2007–2008) Institute of Biophysics, Johannes Kepler University, Austria
- M. E. Ritchie (Cambridge, 2006–2008) Bioinformatics Division, WEHI, Melbourne
- N. Barbosa-Morais (Cambridge, 2006–present)
- A. G. Lynch (Cambridge, 2006–present)
- C. N. Curtis (Cambridge, 2007–present)

S. Samarajiwa (Cambridge, 2008–present)

Q. A. Fu (Cambridge, 2008–present)

Scientific Officer

I. Spiteri (Senior Scientific Officer; Cambridge, 2009 – present)

Postgraduate Students

Completed PhD

P. J. Joyce (PhD 1988) *Age-ordered distributions for population genetics models*. Professor, Departments of Mathematics and Statistics, University of Idaho.

R. S. Lundstrom (PhD 1990) *Stochastic models and statistical methods for DNA sequence data*. Idaho Technology Inc., Salt Lake City, Utah.

L. Markovtsova (PhD 2000) *Markov chain Monte Carlo methods in population genetics*. Bioinformatician, Roche Pharmaceuticals.

O. Will (PhD 2001) *Statistical inference in the fossil record*. OTX, Los Angeles, California.

J. Wu (PhD 2001) *Statistical inference for molecular data: man, motifs and microarrays*. Research Associate, Department of Statistics, Carnegie Mellon University.

K. Millman (PhD 2005) *Molecular and genetic epidemiology of Chlamydia trachomatis in the United States*. Postdoc, Dean Lab, CHORI.

D. Abdueva (PhD 2006) *Probe-target hybridization modeling and its application to the analysis of microarrays*. Affymetrix

D. Scvortsov (PhD 2006) *Detection of deleted and duplicated genomic DNA using HMM analysis of GeneChip data*. Illumina

W. Xu (PhD 2006) *Searching for and beyond replication origins*. Biostatistician, Stanford Genome Center.

O. Sargsyan (PhD 2006) *Analytical and simulation results for the general coalescent*. Postdoc, Wakeley Lab, Harvard.

V. Plagnol (PhD 2006) *Ancestral inference from molecular and paleontological data*. Postdoc, Todd Lab, Cambridge.

R. Jiang (PhD 2006) *Modeling and analyzing novel genetic data: single feature polymorphisms and polony sequences*. Postdoc, Wall Lab, UCSF.

R. Alaghband (PhD 2007) *Inference for stochastic models of molecular data*. Trading and Quantitative Research, JPMorgan.

C. Curtis (PhD 2007) *Analysis of high-density oligonucleotide gene expression data for dissecting aging pathways*. Postdoc, Tavaré lab, CRUK CRI.

J.-C. Marioni (PhD 2007) *Statistical methods for array CGH and copy number variation experiments*. Postdoc, Stephens Lab, University of Chicago.

R. Wilkinson (PhD 2007) *Bayesian inference of primate divergence times*. Lecturer, Statistics Department, University of Nottingham. (from Oct 2009)

M. Dunning (PhD 2008) *Genome-wide analyses using bead-based microarrays*. Bioinformatics Core, CRUK CRI.

T. Hardcastle (PhD 2009) *Model-driven analysis of high-throughput genomic data in late-stage ovarian cancer*. [Joint with J. Brenton] Postdoc, Baulcombe lab, Cambridge.

I. Manolopoulou (PhD 2009) *A Bayesian approach to Nested Clade Analysis*. Postdoc, SAMSI, North Carolina.

D. Grover (PhD 2009) *Real-time tracking and analysis of Drosophila behavior and gene expression*. Postdoc, Rubin lab, HHMI Janelia Farm.

L. Goldstein (PhD 2009; submitted) *Statistical analysis of microRNA expression and related data*.

C. Spyrou (PhD 2009; submitted) *Development and application of Bayesian methodology for some missing data problems in biology*.

Current PhD students

D. Speed (PhD 2006–2009)

S. Knott (PhD 2006–present) [Joint with O. Aparicio]

S. Ivakhno (PhD 2007–2010)

J. Woolford (PhD 2007–2010) [Joint with E. A. Miska]

A. Sottoriva (PhD 2008–2011)

M. L. Smith (PhD 2009–2011)

T. Nellimoottil (PhD 2007–present) [Joint with O. Aparicio]

Supervised 26 MS thesis students.

Conference Organization (since 2004)

Program Committee, RECOMB 2008.

Program Committee, RECOMB 2007.

Chair of Organizing Committee, Program on Stochastic Computation in the Biological Sciences. Isaac Newton Institute, Oct – Dec 2006.

Scientific Committee, 31st conference on Stochastic Processes and their Applications (Bernoulli Society). Paris, France, July 2006.

Organizer, session on Statistical Genetics. 25th European Meeting of Statisticians. Oslo, Norway, July 2005.

Organizing Committee, Workshop on Genome-wide Association Studies. USC, California. April 2005.

Invited Lecture Series (since 2005; from 14 since 1990)

Copy number variation in the genome: technologies, statistics and applications. Interface 2007: the 39th Symposium on the Interface of Statistics, Computing Science, and Applications. (4 1-hour lectures, with JC Marioni) Philadelphia, 5/23-26/07.

Ancestral inference. 2nd Cornell Probability Summer School on *Probability problems that arise from genetics.* (6 1.25-hour lectures) Cornell, NY. 6/26-7/7/06.

Invited Conference Lectures (since 2005; from 100 since 1990)

Statistical Methods for Very Large Data Sets. Baltimore, MD. 6/1–3/11.

Invited session on ABC Methods for Genetic Data. 19th International Conference on Computational Statistics (COMPSTAT2010). Paris, France. 08/22–27/10.

Closing Lecture, European Meeting of Statisticians. Piraeus, Greece. 08/17-22/10.

Keynote Lecture, International Conference on Artificial Intelligence and Statistics (AISTATS 2010). Sardinia. 05/13–15/10.

Plenary Lecture, Conference on Genomics and Mathematics, Canberra, Australia. 05/07/10.

Approximate Bayesian Computation and the evolution of tumours. Conference at Department of Medical Epidemiology and Biostatistics (part of the 200th Anniversary celebration of the Karolinska Institutet). Stockholm, Sweden. 03/26/10.

Quantitative Biology and Bioinformatics in Modern Medicine. Queen's University Belfast. 3/2–3/10.

Evolutionary approaches to cancer. 26th Genes and Cancer Symposium, University of Warwick. 12/14–16/09.

Evolutionary approaches to cancer. Conference in honour of A. D. Barbour. Zurich, Switzerland. 12/4/09.

Evolutionary approaches for studying cancer stem cells. Symposium on Biostatistics and Statistical Genetics. University of Limerick. 9/18/09.

Some statistical issues in the analysis of Illumina sequencing experiments. EPSRC Symposium Workshop on Information extraction from complex data sets (INF). Warwick University. 9/14-18/09.

I spy with my little eye: tracking applications for Drosophila behavioural genetics. Invited session on Bioinformatics. RSS Conference, Edinburgh. 9/8–11/09.

Approximate Bayesian Computation: what, why and when? Invited session on Advanced Monte Carlo Methods. JSM, Washington DC. 8/1–6/09.

O fly where art thou? 5th CCBI Annual Meeting. University of Cambridge. 5/20/09.

O fly where art thou? Second Biennial Newcastle Workshop on Statistical Bioinformatics and Stochastic Systems Biology. Newcastle University. 5/18–19/09.

Random trees in biology and cancer. Tree workshop, Oberwolfach Mathematics Institute. 1/18–24/09.

Genes and flowering times. Beyond Boundaries: from Physics to Plant Sciences. A symposium to celebrate 150th anniversary of the birth of JC Bose. Christ's College, Cambridge. 12/6/08.

O stem cell, where art thou? Minisymposium on Mathematical Analysis of Biological Sequences, SIAM 2008. San Diego, CA. 7/7–11/08.

High-throughput analysis of methylation patterns for tracking cell lineages. Cambridge Cancer Centre Symposium, Cambridge UK. 6/27/08.

Computational molecular biology: an introduction for statisticians. RSS Medical Section Meeting “Introduction to Bioinformatics”. Royal Statistical Society. London. 6/26/08.

High-throughput detection of methylation patterns for tracking cell lineages. Keynote address. Emerging Statistical Challenges in Genome and Translational Research. Banff International Research Station, Banff, Canada. 6/1-6/08.

Using methylation tags to track stem cells. Stem Cells 2007. Punta Cana, Dominican Republic. 12/13-16/07.

Statistical issues in copy number detection. BioC2007. Seattle, WA. 8/6-7/07.

Stochastic models for the evolution of stem cells in colon crypts. 26th Leeds Annual Statistical Research (LASR) Workshop. Leeds, UK. 7/4-6/07.

Statistical issues when detecting copy number variation. Statistics for Biomolecular Data Integration and Modeling. Ascona, Switzerland. 6/10-15/07.

O stem cell, where art thou? CBMI Annual Symposium. University of Kent. 4/26/07.

Inferring the behaviour of colon crypts by exploiting methylation patterns. Workshop on Statistics in Genomics and Proteomics. Coimbra, Portugal. 3/9-10/07.

Oligo antics: array applications in cancer research. COGEME Interest Group Meeting. Manchester, UK. 11/7-8/06.

Now you know your ABCs: examples and problems. Workshop on Recent Advances in Monte Carlo based inference. Isaac Newton Institute, Cambridge UK. 10/30/06.

Some comments on approximate Bayesian computation XXIII International Biometric Conference. Montreal. 7/16-21/06.

Using methylation patterns to understand the stem cell population of the human colon. Bioinformatics 2006. Aarhus, Denmark. 6/15-18/06.

Whole genome scans: full employment for statisticians? East Kent Section, Royal Statistical Society. Canterbury, Kent. 4/05/06.

Genome-wide associations of gene expression variation in humans. Sequence Analysis Toward System Biology Workshop. IPAM, Los Angeles. 1/9-13/06.

Statistical issues for expression analysis of Illumina bead-based microarrays. Plenary Lecture, Workshop on Statistics in Genomics and Proteomics. Estoril, Portugal. 6-8/10/05.

Posterior inference on the stem cell population of the human colon through analysis of methylation patterns. Session on Bioinformatics, JSM2005. Minneapolis, MN. 7-11/8/05.

Using the fossil record to date splits in the primate tree. Stochastic Modelling of Complex Systems (SMOCS-05). Great Barrier Reef, Australia. 10-16/7/05.

Identifying expression variation with the Illumina platform. Keynote Speaker, International Workshop on Statistical Modelling (focus on statistical contributions to modern genomic research). Sydney, Australia. 10-15/7/05.

Some comments on approximate Bayesian computation. Keynote Speaker, Australian Mathematical Sciences Institute Symposium on Recent Advances in Biostatistics, Bioinformatics and Markov chain Monte Carlo. Sydney, Australia. 8-9/7/05.

Stem cell evolution in the colon. Symposium on Branching in Biology. Gothenburg University, Sweden. 5/22-25/05

Identifying expression variation on the Illumina platform. International HapMap Project conference on Genomic Studies and the HapMap. University of Oxford, UK. 3/15-18/05

Contributed Conference Lectures or Departmental Seminars

33 (since 2005; from 157 since 1990) in Australia, Canada, Denmark, France, Germany, Ireland, Sweden, Switzerland, UK, USA.

November 8, 2009