CURRICULUM VITAE

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## **EMPLOYMENT**

## 2015 - presentProfessor of Mathematical Genomics, Department of Statistics and Wellcome Trust Centre for Human Genetics, University of Oxford. Supernumerary Fellow of St John’s College.

## October 2007 - 2015Associate professor of Bioinformatics, Department of Statistics and Wellcome Trust Centre for Human Genetics, University of Oxford. Supernumerary Fellow of St John’s College.

October 2005 - October 2007 Broad Fellow, Broad Institute of MIT and Harvard.

October 2002 – October 2005 Nuffield Trust Fellow in Medical Mathematics, Department of Statistics, University of Oxford and Green College.

## October 2001 – October 2002 Retained Lecturer, Trinity College Oxford.

**EDUCATION AND TRAINING**

## October 1999 to October 2002 D.Phil in Statistics, Jesus College, Oxford.

Thesis title: ‘The detection of recombination events using DNA sequence data’. EPSRC funding and University Graduate Scholarship, Jesus College.

October 1995 to June 1999M.Math, Mathematics, Worcester College, Oxford.

Selected example invited external talks:

Meeting on polygenic risk scores (Columbia, 2019)

ESHG special session (Gothenberg, Sweden, 2019)

Ancient DNA meeting plenary talk (Copenhagen, Denmark, 2019)

Meiosis workshop (Montpellier, 2018)

University of Bath external seminar series (Bath, 2017)

BIOCEV seminar series (Prague, 2017)

Meeting on crossover control (Les Treilles, France 2017)

Oxford Brookes Biological and Medical Sciences seminar series (Oxford, 2016)

Plenary speaker, “Popgroup” meeting (Sheffield, 2015)

 “EMBO Meiosis” meeting on reproductive biology (UK, 2015)

 “Aliens, Foreigners & Strangers in Medieval England c.AD 500-1500” meeting with historians, archaeologists and geneticists (British Academy, 2015)

“Beyond the 1000 Genomes” meeting on human genetic variation (Cambridge, 2014)

“ESHG”: European Society for Human Genetics’ annual meeting (Milan, 2014)

“Biological Sequence Analysis and Probabilistic Models” meeting on methods and applications for DNA sequence analysis (Merton College Oxford, 2014)

“Coalescent Theory: Developments and Applications” workshop meeting on new methods in modelling ancestral relationships (Montreal, 2013)

“Royal Society meeting on Genetics” (Royal Society, London 2013)

 “The Biology of Genomes” meeting (Cold Spring Harbor, NY, 2012; session chair for “Computational Genomics”)

 “Cambridge Computational Biology Institute Annual Symposium” (Cambridge, 2011)

“SMBE” Society for Molecular Biology and Evolution’s annual meeting (Lyon, 2010)

“EMBO Meiosis” meeting on reproductive biology (Isle sur la Sorgue, France, 2009)

Seminars at many external departments and workshops include in recent years the University of Chicago, Harvard Medical School, MIT, Cornell University, the University of Washington, OIST Okinawa, KITP Santa Barbara, the University of Montreal, the University of Aarhus, the Newton Research Institute Cambridge, the University of Manchester, the University of Leicester.

**GRANTS HELD**

**The Wellcome Trust. Leveraging genetic variation to understand chromosome pairing, meiosis and the evolution of human disease risk.** Investigator award to Simon Myers. For the (i) development of approaches to analyse single-cell data and application to the study of meiosis and chromosome-pairing, (ii) the evolution of human phenotypes in health and disease, and the impact of natural selection on these.

2018-2024 £1,511,321

**The Wellcome Trust. Building a platform for genetic inference.** Collaborative award to Jonathan Marchini, Simon Myers and Garrett Hellenthal. Grant 200186/Z/15/Z. This grant is for analyses of the Genomics England sequencing data for 75,000 individuals, within a wider GeCIP collaboration.

2016-2020 £583,184

**The Wellcome Trust. Development of statistical and experimental approaches to understand the roles of recombination and migration in human biology and disease risk.** Investigator award to Simon Myers. Experimental materials, breeding costs and sequencing costs etc. at the WTCHG and analytical work at the department of statistics.

20/01/13-01/07/18 £1,026,000

**The NIH. Methods for genome-wide association studies in admixed populations (R01, collaborator, with Alkes Price (PI), David Reich, Nick Patterson).** Developing and applying statistical models to identify DNA stretches corresponding to different ancestry in “admixed” populations carrying a mixture of ancestries.

15/06/11-30/04/16 $515,000 per annum

**The Wellcome Trust. 1000 genomes project data analysis (co-investigator, with Gil McVean and Jonathan Marchini).** This work analysed dense resequencing data produced by the 1000 genomes project to understand human genetic variation.

01/01/09-01/01/12 £371,353

**The Wellcome Trust. Genetic characterization of commercially available outbred and wild mice (co-investigator, with Jonathan Flint and Richard Mott).** Genetic variation and its causes in wild *mus musculus*, the progenitor species of all mouse lab strains today.

01/10/09-01/10/12 £438,848

**PUBLICATIONS, with brief comments below selected papers**

In some cases, first or last authorship is joint (marked by \*).

1. Mahajan A, Spracklen CN,….,**Myers SR**,….,McCarthy MI, Morris AM. Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics (May 2022). https://doi.org/10.1038/s41588-022-01058-3
2. Davies B, Hinch AG, Cebrian-Serrano A, Alghadban S, Becker PW, Biggs D, Hernandez-Pliego P, Preece C, Moralli D, Zhang G,  **Myers S**, Donnelly P. Altering the binding properties of PRDM9 partially restores fertility across the species boundary. Molecular Biology and Evolution (2021).

In this experimental paper we show it is possible to partially restore fertility in hybrid males (in terms of ability to produce offspring) to two rodent species – Mus musculus and Mus spretus – that normally generate sterile male hybrid offspring, by changing a small part of a single gene, PRDM9. We also identify details of the underlying biological mechanism. These species have more diverged genomes than humans and chimpanzees.

1. Speidel L, Cassidy L, Davies RW, Hellenthal G, Skoglund P, **Myers S R**. Inferring population histories for ancient genomes using genome-wide genealogies.Molecular Biology and Evolution (2021). bioRxiv, https://doi.org/[10.1093/molbev/msab174](https://doi.org/10.1093/molbev/msab174)
2. Davies RW, Kucka M, Su D, Shi S, Flanagan M, Cunniff CM, Frank Chan Y, **Myers S R**. Rapid genotype imputation from sequence with reference panels. Nature Genetics (2021). https://doi.org/[10.1038/s41588-021-00877-0](https://doi.org/10.1038/s41588-021-00877-0)

This paper, following on from a study we also published in Nature Genetics, in 2016, develops a method allowing association mapping to be efficiently performed using ultra-cheap, very low coverage (e.g. 0.1x) sequencing data, in non-human and human settings, and for the first time fully exploiting information in individual sequencing “reads”, making this approach especially powerful for modern “long-read” sequencing technologies.

1. Wells D, Bitoun E, Moralli D, Zhang G, Hinch A, Jankowska J, Donnelly P, Green C, **Myers S R**. ZCWPW1 is recruited to recombination hotspots by PRDM9, and is essential for meiotic double strand break repair. eLife (2020). bioRxiv, https://doi.org/[10.7554/eLife.53392](https://doi.org/10.7554/eLife.53392)

In this experimental paper we identify a gene, ZCWPW1, to be responsible for working together with a gene we previously discovered, PRDM9, to help repair double strand breaks. This is a key step towards understanding how PRDM9 both positions almost all recombination events in mammals, and is also critical in directing “homology search” between chromosomes: ZCWPW1 is involved in the second process, but not the first, implying they have separate mechanisms.

1. Speidel S, Forest M, Shi S, **Myers S**. A method for genome-wide genealogy estimation for thousands of samples. Nature Genetics, September 2019. biorXiv, <https://doi.org/10.1101/550558>.

This paper develops and applies the first approach able to build genealogies, genome-wide, for tens of thousands of individuals in different populations. These genealogies are fundamental in population genetics, because all our genetic variation is inherited through the ancestral relationships they describe. (This paper was published back-to-back with another approach, developed independently, tsinfer). It was cited 117 times in 2021 (Google scholar), and has received 179 citations in total since publication.

1. Li R\*, Bitoun E\*, Altemose N\*, Davies R W, Davies B, **Myers SR**. A high-resolution map of mammalian non-crossover events reveals impacts of genetic diversity on meiotic recombination. Nature Communications, August 2019. bioRxiv https://www.biorxiv.org/content/10.1101/428987v2.
2. Jung M\*, Wells D\*, Rusch J, Ahmed S, Marchini J, **Myers S\***, Conrad D\*. Unified single-cell analysis of testis gene regulation and pathology in 5 mouse strains. eLife, 2019. bioRxiv 393769, doi: <https://doi.org/10.1101/393769.>
3. Salter-Townshend M, **Myers S**. Fine-scale inference of ancestry segments without prior knowledge of admixing groups. Genetics, 2019; bioRxiv 376137; doi: https://doi.org/10.1101/376137.
4. Bycroft C, Fernandez-Rozadilla C, Ruiz-Ponte C, Quintela-García I, Carracedo A, Donnelly P\*, **Myers S R\***. Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula. Nature Communications, Jan 2019 **10**: 551. bioRxiv 250191, doi: <https://doi.org/10.1101/250191>.
5. A. Raveane, S. Aneli, F. Montinaro,…., **S. Myers**, …., A. Achilli, A. Olivieri, C. Capelli. Population structure of modern-day Italians reveals patterns of ancient and archaic ancestries in Southern Europe. Science Advances, 2018. bioRxiv https://www.biorxiv.org/content/10.1101/494898v1
6. Altemose N, Noor N, Bitoun E, Tumian A, Imbeault M, Chapman JR, Aricescu R, **Myers S R**. A map of human PRDM9 binding provides evidence for novel behaviors of PRDM9 and other zinc-finger proteins in meiosis. eLife 2017 (Oct); 6:e28383 DOI:[10.7554/eLife.28383](https://doi.org/10.7554/eLife.28383)
7. [Davies RW](https://www.ncbi.nlm.nih.gov/pubmed/?term=Davies%20RW%5BAuthor%5D&cauthor=true&cauthor_uid=27376236), [Flint J](https://www.ncbi.nlm.nih.gov/pubmed/?term=Flint%20J%5BAuthor%5D&cauthor=true&cauthor_uid=27376236), [**Myers S**](https://www.ncbi.nlm.nih.gov/pubmed/?term=Myers%20S%5BAuthor%5D&cauthor=true&cauthor_uid=27376236)**\***, [Mott R](https://www.ncbi.nlm.nih.gov/pubmed/?term=Mott%20R%5BAuthor%5D&cauthor=true&cauthor_uid=27376236)\*. Rapid genotype imputation from sequence without reference panels. Nat Genet. 2016 Aug;48(8):965-9. doi: 10.1038/ng.3594. Epub 2016 Jul 4.

This paper describes part of the thesis work of Robert Davies, a student in my group. It introduces a method allowing association mapping to be efficiently performed using cheap, very low coverage (e.g. 0.1x) sequencing data, in non-human and human settings. Unlike in published existing methods, no “panel” of previously gathered high quality data from the same species or population is required for its use, overcoming an important drawback of previous statistical approaches. The method allows powerful phenotype mapping, at a fraction of the experimental cost of more complete sequencing.

1. Davies B\*, Hatton EW\*, Altemose N, Hussin JG, Pratto F, Zhang G, Hinch AG, Moralli D, Biggs D, Diaz R, Preece C, Li R, Bitoun E, Brick K, Green C, Camerini-Otero RD, **Myers SR**\*, Donnelly P\*. Re-engineering the zinc fingers of PRDM9 reverses hybrid sterility in mice. Nature (2016), Advanced Online Publication 3rd February.

This is a key output of our experimental work at the WCHG, and is a close collaboration with the Donnelly and Davies groups. By humanizing a mouse at a gene we identified (ref. 16), we have discovered through breeding experiments that we can reverse sterility of hybrid (male) mice. The work moves towards an understanding of the as yet mysterious links between separation of subpopulations into distinct species, and recombination. Recombination is the defining feature of sexual reproduction, and is an essential process in mammals, with erroneous recombination leading to a range of human diseases.

1. van Dorp L, Balding D, **Myers S**, Pagani L, Tyler-Smith C, et al. (2015) [Evidence for a Common Origin of Blacksmiths and Cultivators in the Ethiopian Ari within the Last 4500 Years: Lessons for Clustering-Based Inference.](http://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1005397) PLoS Genet 11(8): e1005397.
2. George B.J. Busby, Garrett Hellenthal, Francesco Montinaro, Sergio Tofanelli, Kazima Bulayeva, Igor Rudan, Tatijana Zemunik, Caroline Hayward, Draga Toncheva, Sena Karachanak-Yankova, Desislava Nesheva, Paolo Anagnostou, Francesco Cali, Francesca Brisighelli, Valentino Romano, Gerard Lefranc, Catherine Buresi, Jemni Ben Chibani, Amel Haj-Khelil, Sabri Denden, Rafal Ploski, Pawel Krajewski, Tor Hervig, Torolf Moen, Rene J. Herrera, James F. Wilson, **Simon Myers**, Cristian Capelli, [The Role of Recent Admixture in Forming the Contemporary West Eurasian Genomic Landscape](http://www.sciencedirect.com/science/article/pii/S0960982215009495), Current Biology. 2015; 25(19), 2518-2526
3. Francesco Montinaro, George BJ Busby, Vincenzo L Pascali, **Simon Myers**, Garrett Hellenthal, Cristian Capelli [Unravelling the hidden ancestry of American admixed populations](http://www.nature.com/ncomms/2015/150324/ncomms7596/full/ncomms7596.html?WT.ec_id=NCOMMS-20150325). Nature communications 2015.
4. Williams AL, Genovese G, Dyer T, Altemose N, Truax K, Jun G, Patterson N, **Myers SR**, Curran JE, Duggirala R, Blangero J, Reich D, Przeworski M, for the T2D-GENES Consortium. Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. eLife, 2015;4. doi: 10.7554/eLife.04637
5. Leslie S\*, Winney B\*, Hellenthal G\*, Davison D, Boumertit A, Day T, Hutnik K, Royrvik EC, Cunliffe B, Wellcome Trust Case Control Consortium, International Multiple Sclerosis Genetics Consortium, Lawson DJ, Falush D, Freeman C, Pirinen M, **Myers S**, Robinson M, Donnelly P†, Bodmer W†. The fine scale genetic structure of the British population. Nature, 2015; 519, 309–314.DOI:

This paper is (we think) a groundbreaking study of the genetics of people from the UK, and its findings were widely reported throughout the UK national media. The key findings in the paper are based on applying and further developing the statistical approaches we published in references 10 and 15 below. The study uses data gathered (by the two senior authors) to understand genetic differences among the British, finding that people from different UK counties can be genetically distinguished, and estimating the contribution of Vikings and Anglo-Saxons to the British gene pool, in each case the first study to do so.

1. Hinch AG, Altemose N, Noor N, Donnelly P, **Myers SR**, Recombination in the Human Pseudoautosomal Region PAR1. PLoS Genet, 2014 10(7): e1004503. doi:10.1371/journal.pgen.1004503
2. Identifying recombination hotspots using population genetic data. [Auton](http://arxiv.org/find/q-bio/1/au%3A%2BAuton_A/0/1/0/all/0/1) A, [**Myers**](http://arxiv.org/find/q-bio/1/au%3A%2BMyers_S/0/1/0/all/0/1) **S**, [McVean](file:///C%3A%5CDocuments%20and%20Settings%5Cmyers%5CDesktop%5CMcVean) G. Bioinformatics, under revision. http://arxiv.org/abs/1403.4264
3. Hellenthal G, Busby GBJ, Band G, Wilson JF, Capelli C, Falush D\*, **Myers S**\*. A genetic atlas of human admixture history. Science. 2014; 343, (6172): 747-751.

In this study, which attracted considerable press attention, we developed and applied to a large dataset of 1500 individuals from 94 populations, a model-based approach to identify, and date, mixing events among human populations. The work is the first to describe, in detail, how the DNA of most humans is affected by such events, and discovers impacts on our DNA of recorded historical events, e.g. the Mongol empire.

1. Prado-Martinez, Javier, Sudmant, Peter H., Kidd, Jeffrey M.,…, **Myers S**,…., Hammer, Michael F.,Eichler, Evan E.,Marques-Bonet, Tomas. Great ape genetic diversity and population history. Nature. 2013; 499 (7459) 471-475.
2. Wellcome Trust Case Control Consortium, Maller JB, McVean G, Byrnes J, Vukcevic D, Palin K, Su Z, Howson JM, Auton A, **Myers S**, Morris A, Pirinen M, Brown MA, Burton PR, Caulfield MJ, Compston A, Farrall M, Hall AS, Hattersley AT,Hill AV, Mathew CG, Pembrey M, Satsangi J, Stratton MR, Worthington J, Craddock N, Hurles M, Ouwehand W, Parkes M, Rahman N, Duncanson A, Todd JA, Kwiatkowski DP, Samani NJ, Gough SC, McCarthy MI, Deloukas P, Donnelly P. Bayesian refinement of association signals for 14 loci in 3 common diseases. Nat Genet. 2012. Dec;44(12):1294-301. doi: 10.1038/ng.2435. Epub 2012 Oct 28.
3. Auton A, Fledel-Alon A, Pfeifer S, Venn O, Ségurel L, Street T, Leffler EM, Bowden R, Aneas I, Broxholme J, Humburg P, Iqbal Z, Lunter G, Maller J, Hernandez RD, Melton C, Venkat A, Nobrega MA, Bontrop R, **Myers S**, Donnelly P, Przeworski M, McVean G. [A fine-scale chimpanzee genetic map from population sequencing.](http://www.ncbi.nlm.nih.gov/pubmed/22422862) Science. 2012 Apr 13;336(6078):193-8. Epub 2012 Mar 15.
4. Bowden R, MacFie TS, **Myers S**, Hellenthal G, Nerrienet E, Bontrop RE, Freeman C, Donnelly P, Mundy NI. [Genomic tools for evolution and conservation in the chimpanzee: Pan troglodytes ellioti is a genetically distinct population.](http://www.ncbi.nlm.nih.gov/pubmed/22396655) PLoS Genet. 2012 Mar;8(3):e1002504. Epub 2012 Mar 1.
5. Lawson DJ, Hellenthal G, **Myers S**\*, Falush D\*. Inference of population structure using dense genotype data. PLoS Genet. 2012, PLoS Genet. 2012 Jan;8(1):e1002453. Epub 2012 Jan 26.

This was a jointly led study (with Dr Falush) developing an MCMC-based approach using information not previously fully exploited, at combinations of DNA mutations, to identify population structure – genetic differences – among populations. This approach has proven to be very powerful and is the basis for references 3. and 6. above, as well as several of our other current projects, and those of other groups.

1. Bhatia G, Patterson N, Pasaniuc B, Zaitlen N, Genovese G, Pollack S, Mallick S, **Myers S**, Tandon A, Spencer C, Palmer CD, Adeyemo AA, Akylbekova EL, Cupples LA, Divers J, Fornage M, Kao WH, Lange L, Li M, Musani S, Mychaleckyj JC, Ogunniyi A, Papanicolaou G, Rotimi CN, Rotter JI, Ruczinski I, Salako B, Siscovick DS, Tayo BO, Yang Q, McCarroll S, Sabeti P, Lettre G, De Jager P, Hirschhorn J, Zhu X, Cooper R, Reich D, Wilson JG, Price AL. [Genome-wide comparison of African-ancestry populations from CARe and other cohorts reveals signals of natural selection.](http://www.ncbi.nlm.nih.gov/pubmed/21907010) Am J Hum Genet. 2011 Sep 9;89(3):368-81.
2. Gupta Hinch A, Tandon A, Patterson N, Song Y, Rohland N, Palmer CD, (72 additional authors not listed in full), Chanock SJ, Haiman CA, Wilson JG, Reich D\*, **Myers SR\***. The landscape of recombination in African Americans. Nature. 2011 Jul 20;476(7359):170-5.

In this paper we map recombination for the first time in a non-European group, by studying the genomes of over 30,000 African American people, as part of a large collaboration. We proved that recombination operates differently in some individuals with African ancestry relative to most Europeans, and these differences are driven by variation at the gene PRDM9.

1. Pasaniuc B, Zaitlen N, Lettre G, Chen GK, Tandon A, Kao WH, Ruczinski I, Fornage M, Siscovick DS, Zhu X, Larkin E, Lange LA, Cupples LA, Yang Q, Akylbekova EL, Musani SK, Divers J, Mychaleckyj J, Li M, Papanicolaou GJ, Millikan RC, Ambrosone CB, John EM, Bernstein L, Zheng W, Hu JJ, Ziegler RG, Nyante SJ, Bandera EV, Ingles SA, Press MF, Chanock SJ, Deming SL, Rodriguez-Gil JL, Palmer CD, Buxbaum S, Ekunwe L, Hirschhorn JN, Henderson BE, **Myers S**, Haiman CA, Reich D, Patterson N, Wilson JG, Price AL. Enhanced statistical tests for GWAS in admixed populations: assessment using African Americans from CARe and a Breast Cancer Consortium. PLoS Genet. 2011 Apr; 7(4):e1001371.
2. McVean G, **Myers S**. PRDM9 marks the spot. Nat Genet. 2010 Oct; 42(10); 821-2.
3. **Myers S**, Bowden R, Tumian A, Bontrop RE, Freeman C, MacFie TS, McVean G, Donnelly P. [Drive against hotspot motifs in primates implicates the PRDM9 gene in meiotic recombination.](http://www.ncbi.nlm.nih.gov/pubmed/20044541) Science. 2010 Feb 12; 327(5967):876-9. [Epub 2009 Dec 31.]

Using bioinformatic approaches and building on previous work (ref. 19) we found that a specific gene, PRDM9, controls the key meiotic process of recombination, by directing where recombination occurs in the genomes of mammals. (Other groups working independently in mice identified this gene independently and our papers were published back-to-back.) This discovery has transformed understanding of how recombination occurs in mammals, and has led to a large body of follow-up research, including in our own lab.

1. [Pric](http://genetics.plosjms.org/cgi-bin/main.plex?form_type=get_simple_bio&ms_id=68322&ms_rev_no=2&ms_id_key=Yfi5z9opqa9ug0yVxDkTwg&j_id=83&auth_id=57039)e A , Tandon A, Patterson N, Barnes K, Rafaels N, Ruczinsk I, Beaty T, Mathias R, Reich D, **Myers S**. Sensitive Detection of Chromosomal Segments of Distinct Ancestry in Admixed Populations. PLoS Genet. 2009 Jun;5(6):e1000519

We developed an approach to identify segments of ancestry from different populations in “admixed” populations, e.g. African Americans, carrying a mixture of ancestries. The resulting software has been widely used, including in our own later research, and remains the most accurate tool available for such inference.

1. Price AL, Patterson N, Hancks DC, **Myers S**, Reich D, Cheung VG, Spielman RS. Effects of cis and trans ancestry on gene expression in African Americans. PLoS Genet. 2008 Dec;4(12):e1000294
2. **Myers S**, Freeman C, Auton A, Donnelly P, McVean G. A common sequence motif associated with recombination hot spots and genome instability in humans. Nat Genet. 2008 Aug 24. [Epub ahead of print]

In this paper we showed for the first time that the positions of normal human recombination, as well as the positions of disease-causing genome rearrangements, are both marked by a specific sequence motif, i.e. a genetic code, linking these events. This paper led on to subsequent work (ref. 16) showing this motif is bound by PRDM9, whose property of being a “zinc finger protein” we predicted using results of this study.

1. Price AL, Weale ME, Patterson N, **Myers SR**, Need AC, Shianna KV, Ge D, Rotter JI, Torres E, Taylor KD, Goldstein DB, Reich D. Long-range LD can confound genome scans in admixed populations. Am J Hum Genet. 2008 Jul;83(1):132-5
2. **Myers S**, [Fefferman C](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Fefferman%20C%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus), [Patterson N](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=Search&Term=%22Patterson%20N%22%5BAuthor%5D&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DiscoveryPanel.Pubmed_RVAbstractPlus). Can one learn history from the allelic spectrum? Theor Popul Biol. 2008 May;73(3):342-8.
3. [Gay J, **Myers S**, McVean G.](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=ShowDetailView&TermToSearch=17660532&ordinalpos=8&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVDocSum) Estimating meiotic gene conversion rates from population genetic data. Genetics. 2007 177(2):881-94
4. [Marchini J, Howie B, **Myers S**, McVean G, Donnelly P.](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=ShowDetailView&TermToSearch=17572673&ordinalpos=13&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVDocSum) A new multipoint method for genome-wide association studies by imputation of genotypes. Nat Genet. 2007 Jul;39(7):906-13.
5. [Haiman CA, Patterson N, Freedman ML, **Myers SR**, Pike MC, Waliszewska A, Neubauer J, Tandon A, Schirmer C, McDonald GJ, Greenway SC, Stram DO, Le Marchand L, Kolonel LN, Frasco M, Wong D, Pooler LC, Ardlie K, Oakley-Girvan I, Whittemore AS, Cooney KA, John EM, Ingles SA, Altshuler D, Henderson BE, Reich D.](http://www.ncbi.nlm.nih.gov/sites/entrez?Db=pubmed&Cmd=ShowDetailView&TermToSearch=17401364&ordinalpos=3&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_RVDocSum) Multiple regions within 8q24 independently affect risk for prostate cancer. Nat Genet. 2007 May;39(5):638-44.
6. Coop GM, **Myers SR**. [Live hot, die young: transmission distortion in recombination hotspots](http://genetics.plosjournals.org/perlserv/?request=get-document&doi=10.1371%2Fjournal.pgen.0030035.eor). PloS Genet. 2007. Early release: January 12, 2007.
7. Eyheramendy S, Marchini J, McVean G, **Myers S**, Donnelly P. A model-based approach to capture genetic variation for future association studies. Genome Research. 2007 Jan; 17(1):88-95.
8. **Myers SR**, McCarroll SA. [New insights into the biological basis of genomic disorders.](http://www.ncbi.nlm.nih.gov/pubmed/17133221) Nat Genet. 2006 Dec; 38(12):1363-4.
9. Spencer CCA, Deloukas P, Hunt S, Mullikin J, **Myers SR**, Silverman B, Donnelly P, Bentley D, McVean G. The influence of recombination on human genetic diversity. PLoS Genet. 2006 Sep 22;2(9).
10. **Myers S**, Spencer CC, Auton A, Bottolo L, Freeman C, Donnelly P, McVean G. The distribution and causes of meiotic recombination in the human genome. Biochem Soc Trans. 2006 Aug; 34 (Pt 4): 526-30.
11. **Myers SR**, Bottollo L, Freeman C, McVean G, Donnelly P. A fine-scale map of recombination rates and hotspots across the human genome. Science. 2005; Oct 14; 310 (5746): 321-4

In this paper, we published the first map of the positions, across the human genome, where recombination events take place. These were inferred by applying a statistical inference approach we developed to a large variation dataset. We made available a list of inferred hotspots, where these events cluster, and reported properties of these hotspots. This has been used and referred to in many subsequent studies of human genetic variation or disease mapping studies (over 700 citations).

1. Jeffreys AJ, Neumann R, Panayi M, **Myers S** & Donnelly P. Human recombination hot spots hidden in regions of strong marker association. Nature Genetics. 2005: 37, 601 - 606
2. Winckler W**\***, **Myers SR**\*, Richter DJ,5 Onofrio RC, McDonald GJ, Bontrop RE, McVean GAT, Gabriel SB, Reich D, Donnelly P, Altshuler D. Comparison of Fine-Scale Recombination Rates in Humans and Chimpanzees. Science. 2005 Apr 1; 308 (5718):107-11

This study, a collaboration with researchers at MIT, showed that, despite ~99% genetic similarity, recombination unexpectedly occurs at different positions in the genomes of humans and chimpanzees

1. Fearnhead P, Harding RM, Schneider JA, **Myers S**, Donnelly P. Application of coalescent methods to reveal fine-scale rate variation and recombination hotspots. Genetics. 2004 Aug;167 (4):2067-81.
2. [McVean GA\*, **Myers SR\***, Hunt S, Deloukas P, Bentley DR, Donnelly P.](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=pubmed&dopt=Abstract&list_uids=15105499) The fine-scale structure of recombination rate variation in the human genome. Science. 2004 Apr 23; 304 (5670): 581-4.
3. **Myers SR,** Griffiths RC**.** Bounds on the minimum number of recombination events in a sample history. Genetics. 2003 Jan; 163 (1): 375-94.

**With the International HapMap Consortium, WTCCC or 1000 Genomes project consortium (selected publications):**

I have been a member of the analysis group of the above major international consortia (each involving hundreds of researchers), contributing various analyses particularly regarding recombination and ancestry. The below are a selection of the resulting publications

1. The 1000 Genomes Project Consortium. [An integrated map of genetic variation from 1,092 human genomes.](https://www.researchgate.net/publication/260019462_An_integrated_map_of_genetic_variation_from_1092_human_genomes?ev=prf_pub) Nature 01/2012; 491(7422):56-65.
2. Gravel S, Henn BM, Gutenkunst RN, Indap AR, Marth GT, Clark AG, Yu F, Gibbs RA; 1000 Genomes Project, Bustamante CD. [Demographic history and rare allele sharing among human populations](http://www.ncbi.nlm.nih.gov/pubmed/21730125). Proc Natl Acad Sci U S A. 2011 Jul 19;108(29):11983-8. Epub 2011 Jul 5.
3. The 1000 Genomes Project Consortium. A map of human genome variation from population-scale sequencing. Nature. 2010 Oct 28;467(7319):1061-73.
4. The Wellcome Trust Case Control Consortium. [Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls.](http://www.ncbi.nlm.nih.gov/pubmed/20360734) Nature. 2010 Apr 1;464(7289):713-20.
5. The International HapMap Consortium. A second generation human haplotype map of over 3.1 million SNPs. Nature 2007:449(7164):851-61.
6. The International HapMap Consortium. A haplotype map of the human genome. Nature 2005 437(7063):1299-320.
7. The International HapMap Consortium. Integrating ethics and science in the International HapMap Project. Nature Reviews Genetics 2004: 5 467-475.
8. The International HapMap Consortium. The international HapMap project. Nature. 2003; 426 789-796.

**AWARDS**

2019 Professorial merit pay award (University of Oxford, recognition of distinction)

2017: Royal Society Francis Crick medal and lecture, given annually in any field in the biological sciences.

2015: Awarded title of full professor (University of Oxford, recognition of distinction)

2013: Genetics Society Balfour [award/lecture](http://www.genetics.org.uk/About/MedalsandLectures/BalfourLecture/BalfourLecture2013.aspx), an award “to mark the contributions to genetics of an outstanding investigator”

2010: Most cited paper in last 3 years published in Theoretical Population Biology, for the paper “Can one learn history from the allelic spectrum?” published in 2008

2006: Corcoran Memorial Prize for outstanding graduate work in Statistics, University of Oxford.

**UNDERGRADUATE AND GRADUATE TEACHING**

**Undergraduate lecture courses taught:**

MS2b fourth year (part C) course “Stochastic models in mathematical genetics” (2010-present, MT or HT, apart from one year while on sabbatical).

Moderations Statistics (2012, HT) (The statistics department’s first year undergraduate statistics course, for all first year mathematicians.)

Part A Statistics (2008-2010, HT) (The statistics department’s second year undergraduate statistics course, taken by all Maths and Statistics degree undergraduates and optional for other Mathematics undergraduates).

**Graduate teaching:**

Statistics representative for the Life Sciences Interface Doctoral Training Centre (LSI-DTC), 2009-2010, 2012-2014. Interviewing course applicants, co-ordinating scheduling, provision, assessment of two-week graduate-level modules, attending committee meetings, induction sessions and department project presentations, liaising between the LSI-DTC and the department and its members, etc.

I have also acted as module co-ordinator for the “Introductory Statistics”, “Statistics”, and “Bioinformatics”, modules on this course in different years, organising and teaching on the module in each case.

Dissertations, other supervisions etc.: I have supervised many fourth year dissertations and MSc dissertations. I have also regularly supervised projects for the LSI-DTC. I have acted as departmental supervisor for a number of students on the MSc in Applied Statistics. I have taught individual days on other graduate courses at the WCHG and elsewhere, and teach classes relating to the MS2b course to graduate students on the MSc in Applied statistics.

**GRADUATE TRAINING AND SUPERVISION**

Supervision of >20 graduate students and postdoctoral researchers. Current DPhil students (4): at the Department of Statistics and the WCHG in Headington. The Myers group also currently includes 3 postdoctoral researchers, based in the Department of Statistics and at the WCHG.

**OTHER MISCELLANEOUS DUTIES**

I am a member of St John’s College Governing Body. I also currently serve on the College’s Research committee. I have served and currently serve on committees within the statistics department, e.g. Research committee, Academic committee, Departmental committee, Committees Working Group (aiming to streamline the number of department committees).

**MSc in Applied Statistics examiner 2012-2014.** Checking examination questions, regulations and dates etc, invigilating, marking, moderating and finalising individual grades together with the other internal and external examiners.

**Chairman of examiners, MSc in Bioinformatics, 2009-2012.** Part-time MSc course (with regular full-time modules) providing higher-level training to students in full time employment.

**2009-2012.** Organised the “Mathgenbio” seminar series, a term-time series of up to 24 weekly seminars per year, run by the mathematical genetics and bioinformatics groups within the department, with regular international speakers.

I have acted as an undergraduate admissions interviewer for mathematics and statistics, for Mansfield College (1 year) and Worcester College (2 years).

I regularly (on average several times per term) act as an internal or external thesis examiner for DPhil/PhD students, either for the final thesis examination or for first/second year examinations.

I serve on the Wellcome Trust Genetics, Genomics and Population Research Expert Review Group (2019-present). Reviewer: Science, Nature Genetics, PLoS Genetics, Genome Research, ASHG, etc, grant applications for the Wellcome Trust. Co-organiser, ProbGen 2016.

**PRESENT AND FUTURE RESEARCH**

The Myers group’s research interests centre on the area of mathematical and statistical genetics, specifically the development and application of stochastic models to understand patterns of variation in samples drawn from a population. In addition, we have a lab-based research program based at the WCHG in Oxford.

One focus is on the fundamental biological processes involved in meiosis, and the regulation of meiotic gene expression. We are also particularly interested in meiotic recombination, which is essential for human reproduction, and together with mutation creates all genetic diversity in most species, and its evolution through time. Using a combination of statistical analysis approaches, and lab-based research, we are studying how a particular zinc-finger protein called PRDM9 binds target genomic sites and positions recombination hotspots in mammals. Prdm9 is also the only known mammalian speciation gene. We have identified unexpected links between PRDM9’s impacts on recombination, the pairing of homologous chromosomes during meiosis, hybrid fertility, and speciation.

The second key research strand for the group is the use of model-based approaches to study population genetics and ancestry: fine-scale population structure, admixture events, and population history. One direction is extending and applying techniques we have developed to identify and understand DNA differences and migrations between human populations at extremely fine geographic scales – e.g. between neighbouring regions within individual countries including the UK (see ref. 14), and Spain (ref. 5). A second is to extend these approaches to allow more precise inferences, and to new problems – e.g. the relationship between recent inter-individual relationships and measurable phenotypes including disease risk. In collaborative work with other groups, we are applying these approaches to the 500,000 UK BIOBANK samples, and to the 100,000 Genomics England sequenced genomes. Recently, we have developed a method for genealogical inferences genome wide (ref. 1) and this approach will be powerful for a range of questions, in particular evolution of human phenotypes through time and between populations.