Peter Francis Hickey

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Research interests

I am interested in the development of statistical methods to analyse large scale genetics and genomics data sets. In my PhD research I am developing statistical methods and software for analysing whole genome studies of DNA methylation, such as from the methylC-seq and BS-seq technologies. I have also worked on several projects to identify pathogenic mutations causing Mendelian diseases via linkage mapping with microarrays and with whole exome sequencing, and on the analysis of genome-wide association studies.

Research experience

2010-current **Research Assistant**, Bioinformatics Division, WEHI, Melbourne, Australia.

2008-2009 **Summer Vacation Scholar**, Bioinformatics Division, WEHI, Melbourne, Australia.

2008 **Undergraduate Research Opportunities Program Scholar**, Bioinformatics Division, WEHI, Melbourne, Australia.

2007-2008 **Summer Vacation Scholar**, The Department of Mathematics and Statistics, The University of Melbourne, Melbourne, Australia.

Publications

Journal articles

Hickey P.F., Bahlo M. *X chromosome association testing in genome wide association studies*, Genetic Epidemiology, 2011; 35:664-670) `http://www.ncbi.nlm.nih.gov/pubmed/21818774`

Riley L.G., Cooper S., **Hickey P.F.**, Rudinger-Thirion J., McKenzie M., Compton A., Lim S.C., Thorburn D., Ryan M.T., Giegé R., Bahlo M., Christodoulou J. *Mutation of the mitochondrial tyrosyl-tRNA synthetase gene, YARS2, causes myopathy, lactic acidosis, and sideroblastic anemia-MLASA syndrome,*

American Journal of Human Genetics, 2010 Jul 9;87(1):52-9. `http://www.ncbi.nlm.nih.gov/pubmed/20598274`

Bahlo M., Stankovich J., Danoy P., **Hickey P.F.**, Taylor B.V., Browning S.R.; Australian and New Zealand Multiple Sclerosis Genetics Consortium (ANZgene), Brown M.A., Rubio J.P. *Saliva-derived DNA performs well in large-scale, high-density single-nucleotide polymorphism microarray studies*, Cancer Epidemiology, Biomarkers and Prevention, 2010 Mar;19(3):794-8. Epub 2010 Mar 3. `http://www.ncbi.nlm.nih.gov/pubmed/20200434`

Commentaries and meeting reports

Hickey P.F., Robinson M.D. *Genomics by the beach*, Genome Biology, 2014; 15:304. `http://genomebiology.com/2014/15/4/304`

Scholarships and awards

2015 Edith Moffat Travel Award.

2013 Prize for best lightning talk, Australian Epigenetics Conference 2013.

2013 EMBL Australia Travel Grant.

2013 Victorian Life Sciences Computation Initiative PhD Top-Up Scholarship.

2013 Prize for third best oral presentation, Young Statisticians Conference 2013.

2012 Statistical Society of Australia (Victoria Branch) scholarship to attend the Young Statisticians Conference (2013).

2011-2014 Australian Postgraduate Award.

2010 Best presentation (Statistics), 2010 Victorian Mathematics and Students' Conference.

2009 Maurice Belz scholarship, The University of Melbourne (competitive scholarship awarded to complete Honours degree in statistics, stochastic processes or operations research).

2009 Alan W Harris Honours scholarship, The Walter and Eliza Hall Institute of Medical Research.

Presentations

2015 **Genomic tuples and DNA methylation patterns**. Contributed talk, European Bioconductor Developers' Meeting, Heidelberg, Germany (12/01)

2014 **Simulating whole-genome DNA methylation data**. Contributed talk, Australian Statistical Conference/International Mathematical Statistics Annual Meeting, Sydney, Australia (10/07)

2014 **Simulating whole-genome bisulfite-sequencing data**. Poster, Lorne Genome, Lorne, Australia (17/01)

2013 **Simulating whole-genome bisulfite-sequencing data**. Poster, Epigenetics 2013, Shoal Bay, Australia (03/12)

2013 **Simulating whole-genome bisulfite-sequencing data**. Poster, Epigenomics of Common Diseases Meeting 2013, Cambridge, England (09/10)

2013 **Bioinformatics for bisulfite sequencing**. Invited talk, La Trobe University Sequencing Users Group, Melbourne, Australia (28/08)

2013 **Exploiting local dependencies in genome-wide studies of DNA methylation**. Contributed talk, Young Statisticians Conference, Melbourne, Australia (07/02)

2012 **Spatial dependence of CpG-methylation from whole genome bisulfite sequencing**. Contributed talk, Epigenomics of Common Diseases Meeting, Baltimore, USA (15/10)

2012 **Spatial dependence of DNA methylation**. Contributed talk, Australian Statistical Conference, Adelaide, Australia (15/07).

2011 **Analysis of mouse exome sequencing: filtering institute specific single nucleotide variants (SNVs)**. Poster, GeneMappers - 8th Australian Human Gene Mapping Conference, Hobart, Australia (04/04).

2010 **X chromosome association testing in genome wide association studies**. Poster, The International Genetic Epidemiology Society Conference, Boston, USA (12/10).

2010 **X chromosome association testing in genome wide association studies**. Poster, The Australasian Microarray and Associated Technologies Association Conference, Hobart, Australia (16/09).

2010 **X chromosome association testing in genome wide association studies**. Invited talk, Statistical Society of Australia - Victorian branch meeting, Melbourne, Australia (24/08).

2010 **Bioinformatics - Applied statistics in modern molecular biology**. Contributed talk (with Davis McCarthy), 2010 Victorian Mathematics and Statistics Students' Conference, Melbourne, Australia (02/07).

2009 **Homozygosity by state analysis in highly inbred pedigrees**. Poster, GeneMappers - 7th Australian Human Gene Mapping Conference, Sydney, Australia (15/06)

Education

2011- **PhD candidate (Statistics)**. The University of Melbourne, Melbourne, Australia.
Supervisors: Professor Terry Speed and Professor Peter Hall.

2006-2009 **Bachelor of Science (Mathematics and Statistics) with First Class Honours**.
The University of Melbourne, Melbourne, Australia.
Honours Thesis: "X Chromosome Association Testing in Genome Wide Association Studies"
Supervisors: Dr Melanie Bahlo and Professor Richard Huggins.
Subjects studied include: Statistical Inference, Probability for Inference, Consulting and Applied Statistics, Data Mining, Stochastic Processes, Linear Models, Time Series and Forecasting

Teaching experience

Tutoring

2011 **Volunteer classroom assistant** Assisting in mathematics classes for final year high school students.

2006- **Private tutoring** One-on-one tutoring for students studying Masters-level biostatistics, third-year university level statistics and first-year university level engineering mathematics. Tutoring senior high school students in elementary, intermediate and advanced mathematics subjects and physics.

Consulting

2011- Analysis of mouse whole-exome and whole-genome sequencing for researchers at the Walter and Eliza Hall Institute of Medical Research.

2010- Analysis of human whole-exome and whole-genome sequencing data for researchers from the Murdoch Childrens Research Institute and the Collaborative Autism Study research group.

2008- Analysis of SNP chip data for researchers from the Murdoch Childrens Research Institute (Royal Children's Hospital, Melbourne), Children's Hospital at Westmead (Sydney), and Epilepsy Research Centre (Brain Research Institute, Melbourne).

Professional activities

Memberships

I am a member of the Statistical Society of Australia Inc. (SSAI), Australasian Microarray and Associated Technologies Association (AMATA), Institute of Mathematical Statistics (IMS) and the Bernoulli Society (BS).

Reviewing

Reviewed papers for *Genetic Epidemiology,* PLoS Genetics, *PLoS Computational Biology and* Heredity.

Software and computing skills

Please see my GitHub page for projects I have developed: https://github.com/PeteHaitch/

Programming languages: R, Python, shell scripting and Unix command line tools, C++

Operating systems: Unix, Mac OS X, Windows

Other: Various statistical genetics and next-generation sequencing analysis packages, LaTeX, MS Office

Referees

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