Peter Francis Hickey

Department of Biostatistics
Johns Hopkins Bloomberg School of Public Health
615 North Wolfe Street
Baltimore, MD 21205-2179, USA

Mob: +1-443-515-7937

Email: peter.hickey@gmail.com
GitHub: https://github.com/PeteHaitch/
Web: http://www.peterhickey.org
Google Scholar: http://scholar.google.com.au/citations?user=pQhJuagAAAAJ&hl=en

Research interests

I am a statistician who enjoys analysing data and making it easier for others to do the same. I am especially interested in analysing genomics data to better understand basic molecular biology and to improve human health. This ranges from understanding variation in chromatin accessibility between individual cells to comparing DNA methylation levels in neurons from different brain regions to identifying regions of the genome shared identical by descent in families with rare Mendellian disease.

Collaboration is essential to my research. Working with and learning from experts in other fields is one of the most enjoyable parts of my job. I also believe that this is one of the main ways in which my expertise in statistics and data analysis can make a valuable contribution to scientific research. In all my collaborations I have derived great pleasure from teaching and helping colleagues to improve their computational and bioinformatics skills.

I am also interested in developing new statistical methodology and adapting existing methods to new applications, as the need arises. I firmly believe that new statistical methodologies should be accompanied by a useful software implementation. Developing open source software and contributing to the open source software community is the other major way in which I can contribute my skills and expertise to scientific research.

Expertise

I have nine years' experience collaborating with molecular biologists, geneticists, and clinical researchers, as well as fellow statisticians and bioinformaticians. During this time I have developed expertise in analysing data from a broad range of genomic assays for measuring genetic variation, DNA methylation, chromatin accessibility, and gene expression. I have developed pipelines used by colleagues in my lab to automate routine bioinformatics analyses and data processing, such as performing data quality control, aligning sequencing reads from DNA/RNA/ATAC/bisulfite-sequencing, and counting reads mapped to features in preparation for downstream analysis.

During this time I've analysed data from and helped design experiments across a range of designs: from typical molecular biology experiments with small sample sizes and multifactorial designs, to complex human pedigrees with consanguinity from rare populations, to large genome-wide association studies with many thousands of samples.

I also have three years' experience collaborating with exercise and sports scientists, where I have helped design experiments, provided general advice on data collection and management, performed statistical analyses, and taught data analysis and visualisation using the R programming language.

I have more than a decade's experience with the statistical programming language, R, and several years' experience with Python, C++, and shell scripting. I not only use R for data analysis, but to create software packages that are available through the Bioconductor project. Recently, I have been helping in the design of core Bioconductor software for the analysis of single -cell genomics data, for working with data that are stored on disk because they are too large to store in RAM, and for making it easier to do integrative analyses on samples for which we have multiple types of assays.

Research experience

2016-current **Postdoctoral Fellow**, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, USA.

2009-2015 **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 J.T., **Hickey P.F.**, Maniar N., Williams M., Timmins R., Opar D. *A novel apparatus measuring knee flexor strength during various hamstring exercises: A reliability and retrospective study*, Journal of Orthopaedic & Sports Physical Therapy, 2017; (in press)

Hickey P.F. *Representation and Manipulation of Genomic Tuples in R*, Journal of Open Source Software, 2016. `http://dx.doi.org/10.21105/joss.00020`

Keniry A., Gearing L.J., Jansz N., Liu J., Holik A.Z., **Hickey P.F.**, Kinkel S.A., Moore D.L., Breslin K., Chen K., Liu R., Phillips C., Pakusch M., Biben C., Sheridan J.M., Kile B.T., Carmichael C., Ritchie M.E., Hilton D.J., Blewitt M.E. *Setdb1-mediated H3K9 methylation is enriched on the inactive X and plays a role in its epigenetic silencing*, Epigenetics & Chromatin, 2016; 18:9-16 `https://www.ncbi.nlm.nih.gov/pubmed/27195021`

Phelan D.G., Anderson D.J., Howden S.E., Wong R.C., **Hickey P.F.**, Pope K., Wilson G.R., PÃľbay A., Davis A.M., Petrou S., Elefanty A.G., Stanley E.G., James P.A., Macciocca I., Bahlo M., Cheung M.M.,

Amor D.J., Elliott D.A., Lockhart P.J. *ALPK3-deficient cardiomyocytes generated from patient-derived induced pluripotent stem cells and mutant human embryonic stem cells display abnormal calcium handling and establish that ALPK3 deficiency underlies familial cardiomyopathy*, European Heart Journal, 2016; 37(33):2586-90 https://www.ncbi.nlm.nih.gov/pubmed/27106955

Oey H., Isbel L., **Hickey P.F.**, Ebaid B., Whitelaw E. *Genetic and epigenetic variation among inbred mouse littermates: identification of inter-individual differentially methylated regions*, Epigenetics & Chromatin, 2015; 8:54 https://www.ncbi.nlm.nih.gov/pubmed/26692901

Lacey D., **Hickey P.F.**, Arhatari B.D., O'Reilly L.A., Rohrbeck L., Kiriazis H., Du X.J., Bouillet P. *Spontaneous retrotransposon insertion into TNF 3'UTR causes heart valve disease and chronic polyarthritis*, Proceedings of the National Academy of Sciences, 2015; 112(31):9698-9703 https://www.ncbi.nlm.nih.gov/pubmed/26195802

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

Preprints

Rizzardi L.[*], **Hickey P.F.**[*], Rodriguez V., Tryggvadottir R., Callahan C., Idrizi A., Hansen K.D., Feinberg A.P. *Neuronal brain region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric disease heritability*, bioRxiv, 2017. http://dx.doi.org/10.1101/120386

Technical reports, conference papers and published abstracts

Scheffer I., Williams K., Green C., Pereira K., Brown N, **Hickey P.F.**, Lukic V., Gillies G., Delatycki M., Lockhart P., Bahlo M., Wilson S. *The Victorian Collaborative Autism Study: A family and community study of the genetics of autism spectrum disorder*, Journal of Intellectual Disability Research, 2016:628-767 http://dx.doi.org/10.1111/jir.12305

Phelan D., Wilson G., Sim J., Bahlo M., **Hickey P.F.**, James P., du Sart D., Delatyki M., Amor D., Lockhart P. *PW283 Identification and characterisation of a novel hypertrophic cardiomyopathy gene*, Global Heart, 2014; 9(1), e316 http://dx.doi.org/10.1016/j.gheart.2014.03.2365

Phelan D., Wilson G., Pope K., Gillies G., Sim J., Bahlo M., **Hickey P.F.**, Bromhead C., James P, du Sart D., Delatyki M., Leventer R., Amor D., Lockhart P.J. *Identification and Characterisation of A Novel Gene for Cardiomyopathy*, Pathology: The Journal of the Royal College of Pathologists of Australasia, 2014; 46(S91-S92) http://dx.doi.org/10.1097/01.PAT.0000443656.23969.86

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`

Software and computing skills

I develop and maintain the GenomicTuples Bioconductor package for storing and manipulating genomic tuples. I am a co-maintainer of and contributer to the bsseq Bioconductor package for analysing bisulfite-sequencing data. I have also made contributions to core Bioconductor packages.

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

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

Operating systems: GNU/Linux, macOS, Windows

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

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).

2011-2015 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

2017 **Developing statistical methods for large epigenomic studies in the human brain**. Contributed talk, ENAR 2017 Spring Meeting, Washington D.C., USA (03/13)

2016 **New stuff in bsseq for analysing large whole genome bisulfite-sequencing datasets**. Lightning talk, BioC 2016, San Franciso, USA (24/06)

2016 **Genomic tuples**. Lightning talk, BioC 2015 Developers' Day, Seattle, USA (20/7)

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

2011-2015 **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

Workshops

2016 **Analysing DNA methylation data with Bioconductor**. BioC 2016, Palo Alto, USA (26/06)

Tutoring

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

2006-2014 **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

2011-2015 Analysis of mouse whole-exome and whole-genome sequencing for researchers at the Walter and Eliza Hall Institute of Medical Research.

2010-2015 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.

2008-2015 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

Reviewing

I have reviewed papers for *Nature Methods,* PLoS Genetics, *Genome Biology,* Bioinformatics, *PLoS Computational Biology,* Genetic Epidemiology, *Heredity, and* F1000.

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).

Referees

Professor Terry Speed
Bioinformatics Division
The Walter and Eliza Hall Institute of Medical Research
1G Royal Parade, Parkville, Victoria 3052, AUSTRALIA
Tel: +61 (0) 3 9345 2697
Fax: +61 (0) 3 9347 0852
Email: terry@wehi.edu.au

Assistant Professor Kasper Hansen
Department of Biostatistics
Johns Hopkins Bloomberg School of Public Health
615 North Wolfe Street
Baltimore, MD 21205-2179, USA
Tel: +1-410-955-3067
Fax: +1-410-955-0958
Email: khansen@jhsph.edu

Professor Melanie Bahlo
Population Health and Immunity Division
The Walter and Eliza Hall Institute of Medical Research
1G Royal Parade, Parkville, Victoria 3052, AUSTRALIA
Tel: +61 (0) 3 9345 2630
Fax: +61 (0) 3 9347 0852
Email: bahlo@wehi.edu.au

Last updated: May 18, 2017