Curriculum Vitae

Peter Hickey

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- Address: Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, 615 N. Wolfe St, E3527, Baltimore, MD 21202, USA

Education and research experience

- *2016-present*: **Postdoctoral Fellow** Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, USA.
  - Advisor: Assistant Professor Kasper Hansen
- *2011-2015*: **PhD (Statistics)** Department of Mathematics and Statistics, The University of Melbourne, Australia.
  - Thesis: The statistical analysis of high-throughput assays for studying DNA methylation
  - Advisors: Professor Terry Speed and Professor Peter Hall
- *2009-2015*: **Research Assistant** Bioinformatics Division, Walter and Eliza Hall Institute, Melbourne, Australia.
  - Advisor: Professor Melanie Bahlo
- *2008-2009*: **Undergraduate Research Opportunities Program scholar** Bioinformatics Division, Walter and Eliza Hall Institute, Melbourne, Australia.
  - Advisor: Professor Melanie Bahlo
- *2006-2009*: **Bachelor of Science (Mathematics and Statistics) with First Class Honours** The University of Melbourne, Australia.
  - Thesis: X chromosome association testing in genome-wide association studies
  - Advisors: Professor Melanie Bahlo and Professor Richard Huggins

Publications

*Indicates equal contributions

Journal articles

[1] J. T. Hickey, **P. F. Hickey**, N. Maniar, R. G. Timmins, M. D. Williams, C. A. Pitcher and D. A. Opar. "A novel apparatus measuring knee flexor strength during various hamstring exercises: A reliability and retrospective study". In: *Journal of Orthopaedic & Sports Physical Therapy* in press ().

[2] **P. F. Hickey**. "Representation and manipulation of genomic tuples in R". In: *The Journal of Open Source Software* 1.1 (May. 2016). DOI: 10.21105/joss.00020. URL: https://doi.org/10.21105/joss.00020.

[3] A. Keniry, L. J. Gearing, N. Jansz, J. Liu, A. Z. Holik, **P. F. Hickey**, S. A. Kinkel, D. L. Moore, K. Breslin, K. Chen, R. Liu, C. Phillips, M. Pakusch, C. Biben, J. M. Sheridan, B. T. Kile, C. Carmichael, M. E. Ritchie, D. J. Hilton and M. E. Blewitt. "Setdb1-mediated H3K9 methylation is enriched on the inactive X and plays a role in its epigenetic silencing". In: *Epigenetics & Chromatin* 9 (May. 18, 2016), p. 16. ISSN: 1756-8935. DOI: 10.1186/s13072-016-0064-6. URL: http://dx.doi.org/10.1186/s13072-016-0064-6.

[4] D. G. Phelan, D. J. Anderson, S. E. Howden, R. C. B. Wong, **P. F. Hickey**, K. Pope, G. R. Wilson, A. Pébay, A. M. Davis, S. Petrou, A. G. Elefanty, E. G. Stanley, P. A. James, I. Macciocca, M. Bahlo, M. M. Cheung, D. J. Amor, D. A. Elliott and P. J. Lockhart. "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". In: *European Heart Journal* 37.33 (Sep. 01, 2016), pp. 2586-2590. ISSN: 0195-668X, 1522-9645. DOI: 10.1093/eurheartj/ehw160. URL: http://dx.doi.org/10.1093/eurheartj/ehw160.

[5] D. Lacey, **P. F. Hickey**, B. D. Arhatari, L. A. O'Reilly, L. Rohrbeck, H. Kiriazis, X. Du and P. Bouillet. "Spontaneous retrotransposon insertion into TNF 3'UTR causes heart valve disease and chronic polyarthritis". In: *Proceedings of the National Academy of Sciences of the United States of America* 112.31 (Aug. 04, 2015), pp. 9698-9703. ISSN: 0027-8424, 1091-6490. DOI: 10.1073/pnas.1508399112. URL: http://dx.doi.org/10.1073/pnas.1508399112.

[6] H. Oey, L. Isbel, **P. F. Hickey**, B. Ebaid and E. Whitelaw. "Genetic and epigenetic variation among inbred mouse littermates: identification of inter-individual differentially methylated regions". In: *Epigenetics & Chromatin* 8 (Dec. 12, 2015), p. 54. ISSN: 1756-8935. DOI: 10.1186/s13072-015-0047-z. URL: http://dx.doi.org/10.1186/s13072-015-0047-z.

[7] **P. F. Hickey** and M. Bahlo. "X chromosome association testing in genome wide association studies". In: *Genetic Epidemiology* 35.7 (Nov. 2011), pp. 664-670. ISSN: 0741-0395, 1098-2272. DOI: 10.1002/gepi.20616. URL: http://dx.doi.org/10.1002/gepi.20616.

[8] M. Bahlo, J. Stankovich, P. Danoy, **P. F. Hickey**, B. V. Taylor, S. R. Browning, Australian, ew Zealand Multiple Sclerosis Genetics Consortium (ANZgene), M. A. Brown and J. P. Rubio. "Saliva-derived DNA performs well in large-scale, high-density single-nucleotide polymorphism microarray studies". In: *Cancer Epidemiology, Biomarkers & Prevention* 19.3 (Mar. 2010), pp. 794-798. ISSN: 1055-9965, 1538-7755. DOI: 10.1158/1055-9965.EPI-09-0812. URL: http://dx.doi.org/10.1158/1055-9965.EPI-09-0812.

[9] L. G. Riley, S. Cooper, **P. F. Hickey**, J. Rudinger-Thirion, M. McKenzie, A. Compton, S. C. Lim, D. Thorburn, M. T. Ryan, R. Giegé, M. Bahlo and J. Christodoulou. "Mutation of the mitochondrial tyrosyl-tRNA synthetase gene, YARS2, causes myopathy, lactic acidosis, and sideroblastic anemia-MLASA syndrome". In: *American Journal of Human Genetics* 87.1 (Jul. 09, 2010), pp. 52-59. ISSN: 0002-9297, 1537-6605. DOI: 10.1016/j.ajhg.2010.06.001. URL: http://dx.doi.org/10.1016/j.ajhg.2010.06.001.

Preprints

[1] L. F. Rizzardi*, **P. F. Hickey***, V. Rodriguez DiBlasi, R. Tryggvadóttir, C. M. Callahan, A. Idrizi, K. D. Hansen and A. P. Feinberg. "Neuronal brain region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric disease heritability". Mar. 24, 2017. DOI: 10.1101/120386. URL: http://biorxiv.org/content/early/2017/03/24/120386.

Theses

[1] **P. F. Hickey**. "The statistical analysis of high-throughput assays for studying DNA methylation". PhD thesis. Department of Mathematics and Statistics, The University of Melbourne, 2015. URL: https://minerva-access.unimelb.edu.au/handle/11343/55699.

[2] **P. F. Hickey**. "X chromosome association testing in genome-wide association studies". Honours Thesis. Department of Mathematics and Statistics, The University of Melbourne, Nov. 05, 2009.

Technical reports, conference papers and published abstracts

[1] I. Scheffer, K. Williams, C. Green, K. Pereira, N. Brown, **P. F. Hickey**, V. Lukic, G. Gillies, M. Delatycki, P. J. Lockhart, M. Bahlo and S. Wilson. "The Victorian Collaborative Autism Study: A family and community study of the genetics of autism spectrum disorder". In: *Journal of Intellectual Disability Research*. Ed. by J. of Intellectual Disability Research. Vol. 60. 7. 2016, p. 732. DOI: 10.1111/jir.12305.

[2] D. G. Phelan, G. R. Wilson, K. Pope, G. Gillies, J. Sim, M. Bahlo, **P. F. Hickey**, C. Bromhead, P. A. James, D. du Sart, M. Delatyki, R. Leventer, D. J. Amor and P. J. Lockhart. "Identification and characterisation of a novel hypertrophic cardiomyopathy gene". In: *Pathology: The Journal of the Royal College of Pathologists of Australasia*. Ed. by P. T. J. of the Royal College. Vol. 46. 2014, pp. S91-S92.

[3] D. G. Phelan, G. R. Wilson, J. Sim, M. Bahlo, **P. F. Hickey**, P. A. James, D. du Sart, M. Delatyki, D. J. Amor and P. J. Lockhart. "Identification and characterisation of a novel hypertrophic cardiomyopathy gene". In: *Global Heart*. Ed. by G. Heart. Vol. 9. 1. Elsevier, 2014, p. e316. DOI: http://dx.doi.org/10.1016/j.gheart.2014.03.2365.

Commentaries and meeting reports

[1] **P. F. Hickey** and M. D. Robinson. *Genomics by the beach*. Apr. 14, 2014. DOI: 10.1186/gb4171. URL: http://dx.doi.org/10.1186/gb4171.

Computer skills

Very proficient with statistical computing, particularly R, and standard tools for analysing genomics data such as Bioconductor, SAMtools, and BEDtools. Familiar with C++, C, Python, Unix shell tools, Sun Grid Engine, Slurm. Developed pipelines for analysing genomics data including whole-genome and whole-exome sequencing, ATAC-seq, RNA-seq, and whole-genome bisulfite-sequencing.

Software packages

Developer and contributor to several R packages through the Bioconductor project. Also developed and published Python software. Please see https://github.com/PeteHaitch for additional projects.

R packages

Download statistics from http://bioconductor.org/packages/stats/bioc for years since I have been a substantial author/contributor to the package.

Author

- GenomicTuples: Representation and Manipulation of Genomic Tuples
  - Number of downloads (2014-2017): 497, 2426, 2022, 870
- bsseq: Analyze, Manage and Store Bisulfite Sequencing Data
  - Number of downloads (2014-2017): 5049, 6631, 8419, 5069

Contributor

- minfi: Analysing Illumina Infinium DNA Methylation Arrays
  - Number of downloads (2017): 18539

Python packages

Author

- methtuple: A caller for DNA methylation events that co-occur on the same DNA fragment from high-throughput bisulfite sequencing data, such as methylC-seq

Funding

Grants

- *2015*: Bioconductor Travel Grant
  - To attend the Bioconductor meeting in Seattle, USA
- *2013*: EMBL Australia Travel Grant
  - To attend the EMBL PhD Symposium in Heidelberg, Germany

Scholarships

- *2013*: Victorian Life Sciences Computation Initiative PhD Top-Up Scholarship.
- *2012*: Statistical Society of Australia (Victoria Branch) scholarship to attend the Young Statisticians Conference (2013).
- *2011-2015*: Australian Postgraduate Award.
- *2009*: Maurice Belz scholarship, The University of Melbourne
  - A 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

Awards

- *2015*: Edith Moffat Travel Award
- To interview for international for postdoctoral positions and attend the European Bioconductor meeting
- *2013*: Prize for best lightning talk, Australian Epigenetics Conference 2013.
- *2013*: Prize for third best oral presentation, Young Statisticians Conference 2013.
- *2010*: Best presentation (Statistics), 2010 Victorian Mathematics and Students' Conference.

Presentations

Talks

Conferences

- *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 features in `bsseq` for analysing large whole genome bisulfite-sequencing datasets**. Lightning talk, BioC 2016, San Franciso, USA (24/06)
- *2016*: **`GenomicTuples`**. 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) [slides]
- *2014*: **Making sense of DNA methylation data**. PhD completion seminar, Melbourne, Australia (15/09) [video | pdf]
- *2014*: **Simulating whole-genome DNA methylation data**. Contributed talk, Australian Statistical Conference/International Mathematical Statistics Annual Meeting, Sydney, Australia (10/07) [slides]
- *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).
- *2010*: **Bioinformatics - Applied statistics in modern molecular biology**. Contributed talk (with Davis McCarthy), 2010 Victorian Mathematics and Statistics Students' Conference, Melbourne, Australia (02/07).

Other

- *2013*: **Bioinformatics for bisulfite sequencing**. Invited talk, La Trobe University Sequencing Users Group, Melbourne, Australia (28/08)
- *2010*: **X chromosome association testing in genome wide association studies**. Invited talk, Statistical Society of Australia - Victorian branch meeting, Melbourne, Australia (24/08).

Posters

- *2014*: **Simulating whole-genome bisulfite-sequencing data**. Poster, Lorne Genome, Lorne, Australia (17/01) [pdf]
- *2013*: **Simulating whole-genome bisulfite-sequencing data**. Poster, Epigenetics 2013, Shoal Bay, Australia (03/12) [pdf]
- *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) *2009*: **Homozygosity by state analysis in highly inbred pedigrees**. Poster, GeneMappers - 7th Australian Human Gene Mapping Conference, Sydney, Australia (15/06)

Teaching experience

Workshops

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

Tutoring

- *2006-2014*: Private tutoring
  - One-on-one and small-group 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.
- *2011*: Classroom assistant
  - Assisting in mathematics classes for final year high school students

Professional activities and service

Reviewing

Referee for *Nature Methods*, *PLoS Genetics*, *Genome Biology*, *Bioinformatics*, *PLoS Computational Biology*, *Genetic Epidemiology*, *Heredity*, and *F1000*.

Professional society memberships

- Member, Statistical Society of Australia
- Member, International Biometric Society (ENAR)

References

Professor Terry Speed

Bioinformatics Division

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

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Professor Melanie Bahlo

Population Health and Immunity Division

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