Peter Francis Hickey

Curriculum Vitae

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- Address: Molecular Medicine Division, Walter and Eliza Hall Institute of Medical Research, 1G Royal Parade, Parkville Victoria 3052, Australia
- Australian Citizen

Education and research experience

- *2018 – present*: **Senior Research Officer** Molecular Medicine Division, Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia.
- *2016 – 2018*: **Postdoctoral Fellow** Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, USA.
  - Advisor: Assistant Professor Kasper Hansen
- *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
- *2010 – 2015*: **Research Assistant** Bioinformatics Division, Walter and Eliza Hall Institute of Medical Research, 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
- *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] L. Boukas, J. M. Havrilla, **P. F. Hickey**, A. R. Quinlan, H. T. Bjornsson, and K. D. Hansen. "Coexpression patterns define epigenetic regulators associated with neurological dysfunction". In: *Genome Research* 29 (Mar. 2019), pp. 532 - 542. DOI: 10.1101/gr.239442.118. URL: https://www.ncbi.nlm.nih.gov/pubmed/30858344.

[2] J. T. Hickey, R. G. Timmins, N. Maniar, E. Rio, **P. F. Hickey**, C. A. Pitcher, M. D. Williams, and D. A. Opar. "Pain-Free Versus Pain-Threshold Rehabilitation Following Acute Hamstring Strain Injury: A Randomized Controlled Trial". In: *The Journal of orthopaedic and sports physical therapy* (Jun. 2019), pp. 1-35. ISSN: 0190-6011, 1938-1344. DOI: 10.2519/jospt.2019.8895.

[3] 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 trait heritability". In: *Nature Neuroscience* 22.2 (Feb. 2019), pp. 307 - 316. DOI: 10.1038/s41593-018-0297-8. URL: https://www.ncbi.nlm.nih.gov/pubmed/30643296.

[4] 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* 48.2 (Feb. 2018), pp. 72 - 80. DOI: 10.2519/jospt.2018.7634. URL: https://www.ncbi.nlm.nih.gov/pubmed/29073840.

[5] N. Jansz, A. Keniry, M. Trussart, H. Bildsoe, T. Beck, I. D. Tonks, A. W. Mould, **P. F. Hickey**, K. Breslin, M. Iminitoff, M. E. Ritchie, E. McGlinn, G. F. Kay, J. M. Murphy, and M. E. Blewitt. "Smchd1 regulates long-range chromatin interactions on the inactive X chromosome and at Hox clusters". In: *Nature Structural & Molecular Biology* 25 (Aug. 2018), pp. 766 - 777. DOI: 10.1038/s41594-018-0111-z. URL: https://www.ncbi.nlm.nih.gov/pubmed/30127357.

[6] N. Jansz, T. Nesterova, A. Keniry, M. Iminitoff, **P. F. Hickey**, G. Pintacuda, O. Masui, S. Kobelke, N. Geoghegan, K. A. Breslin, T. A. Willson, K. Rogers, G. F. Kay, A. H. Fox, H. Koseki, N. Brockdorff, J. M. Murphy, and M. E. Blewitt. "Smchd1 Targeting to the Inactive X Is Dependent on the Xist-HnrnpK-PRC1 Pathway". In: *Cell Reports* 25.7 (Nov. 2018), pp. 1912 - 1923.e9. DOI: 10.1016/j.celrep.2018.10.044. URL: https://www.ncbi.nlm.nih.gov/pubmed/30428357.

[7] The eGTEx Project. "Enhancing GTEx: Bridging the gaps between genotype, gene expression, and disease". In: *Nature Genetics* 49.12 (Dec. 2017), pp. 1664 - 1670. DOI: 10.1038/ng.3969. URL: https://www.ncbi.nlm.nih.gov/pubmed/29019975.

[8] **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.

[9] 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. 2016), p. 16. DOI: 10.1186/s13072-016-0064-6. URL: https://www.ncbi.nlm.nih.gov/pubmed/27195021.

[10] 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. 2016), pp. 2586 - 2590. DOI: 10.1093/eurheartj/ehw160. URL: https://www.ncbi.nlm.nih.gov/pubmed/27106955.

[11] 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. 2015), pp. 9698 - 9703. DOI: 10.1073/pnas.1508399112. URL: https://www.ncbi.nlm.nih.gov/pubmed/26195802.

[12] 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. 2015), p. 54. DOI: 10.1186/s13072-015-0047-z. URL: https://www.ncbi.nlm.nih.gov/pubmed/26692901.

[13] **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. DOI: 10.1002/gepi.20616. URL: https://www.ncbi.nlm.nih.gov/pubmed/21818774.

[14] M. Bahlo, J. Stankovich, P. Danoy, **P. F. Hickey**, B. V. Taylor, S. R. Browning, Australian & New 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. DOI: 10.1158/1055-9965.EPI-09-0812. URL: https://www.ncbi.nlm.nih.gov/pubmed/20200434.

[15] 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. 2010), pp. 52 - 59. DOI: 10.1016/j.ajhg.2010.06.001. URL: https://www.ncbi.nlm.nih.gov/pubmed/20598274.

Preprints and under review

[1] C. Seillet, K. Luong, J. Tellier, N. Jacquelot, R. D. Shen, **P. F. Hickey**, V. C. Wimmer, L. Whitehead, K. Rogers, G. K. Smyth, A. L. Garnham, M. Ritchie, and G. T. Belz. "Vasoactive intestinal peptide confers anticipatory mucosal immunity by regulating ILC3 activity". Aug. 2019. DOI: 10.1101/729400.

[2] K. J. Trevis, N. J. Brown, C. Green, P. Lockhart, **P. F. Hickey**, M. Fanjul-Fernández, C. Bromhead, T. Desai, T. Vick, G. Gillies, H. Mountford, E. Fitzpatrick, L. Gordon, P. Hewson, V. Anderson, M. B. Delatycki, I. E. Scheffer, and S. J. Wilson. "Tracing Autism Traits in Large Multiplex Families to Identify Endophenotypes of the Broader Autism Phenotype". Jun. 2019. DOI: 10.1101/659722. URL: https://www.biorxiv.org/content/10.1101/659722v1.abstract.

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. 2009.

Technical reports, conference papers and published abstracts

[1] I. Scheffer, K. Williams, C. Green, K. Pereira, N. J. Brown, **P. F. Hickey**, V. Lukic, G. Gillies, M. Delatycki, P. J. Lockhart, M. Bahlo, and S. J. 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, 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. 2014, p. e316. DOI: 10.1016/j.gheart.2014.03.2365.

Commentaries and meeting reports

[1] **P. F. Hickey** and M. D. Robinson. *Genomics by the beach*. Apr. 2014. DOI: 10.1186/gb4171. URL: https://www.ncbi.nlm.nih.gov/pubmed/25001045.

Computer skills and software development

Very proficient with statistical computing, particularly R, and strategies for managing and analysing large (multi-gigabyte to terabtye size) datasets, especially genomics data. Familiar with C, C++, and various databases — both as standalone tools and as integrations with and extensions of R — as well as Python, Unix shell tools, and cluster job schedulers.

Developer and contributor to several R packages through the Bioconductor project. Also developed and published Python software. Additional projects are available from https://github.com/PeteHaitch.

R packages

Download statistics are reported for years since I have been a substantial author/contributor to the package (data from https://bioconductor.org/packages/stats/).

Author

- GenomicTuples: Representation and Manipulation of Genomic Tuples
  - Number of downloads (2014-2019): 496, 2426, 2029, 1825, 1606, 1143
- bsseq: Analyse, Manage and Store Bisulfite Sequencing Data
  - Number of downloads (2014-2019): 5045, 6631, 8439, 12373, 16206, 17705
- DelayedMatrixStats: Functions that Apply to Rows and Columns of 'DelayedMatrix' Objects
  - Number of downloads (2017-2019): 166, 27931, 47336

Contributor

- minfi: Analysing Illumina Infinium DNA Methylation Arrays
  - Number of downloads (2017-2019): 38632, 45666, 35143

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 whole-genome bisulfite-sequencing

Funding

Awards

- *2019*: Bioconductor Travel Award
  - To attend the Bioconductor meeting in New York, USA
- *2018*: AGTA Travel Award
  - To attend the AGTA meeting in Adelaide, Australia
- *2018*: Bioconductor Travel Award
  - To attend the Bioconductor meeting in Toronto, Canada
- *2015*: Bioconductor Travel Award
  - To attend the Bioconductor meeting in Seattle, USA
- *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

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

Grants

- *2013*: EMBL Australia Travel Grant
  - To attend the EMBL PhD Symposium in Heidelberg, Germany

Presentations

Talks

Conferences

- *2019*: **Overview of single-cell bioinformatics**. Oz Single Cell 2019, Melbourne, Australia (21/7)
- *2018*: **Getting help and helping others (including future you)**. BioCAsia 2018, Mebourne, Australia (29/11)

- *2018*: **Genome-wide analysis of DNA methylation in samples from the Genotype-Tissue Expression (GTEx) project**. AGTA 2018, Adelaide, Australia (05/11)
- *2018*: **Lessons from switching to on-disk storage using DelayedArray containers.** Contributed talk, BioC 2018 Developers' Day, Toronto, Canada (25/7)
- *2018*: **DelayedArray: A tibble for arrays.** Contributed talk, useR! 2018, Brisbane, Australia (13/07)
- *2017*: **Mapping the human brain epigenome and its links to disease.** Contributed talk, Epigenetics 2017, Brisbane, Australia (31/10)
- *2017*: **Neuronal brain region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric disease heritability.**. Contributed talk, GTEx Project Community Meeting, Rockville, USA (28/06)
- *2017*: **Developing statistical methods for large epigenomic studies in the human brain**. Contributed talk, ENAR 2017 Spring Meeting, Washington D.C., USA (13/03)
- *2017*: **DelayedMatrixStats: Porting the matrixStats API to work with DelayedMatrix objects.** Lightning talk, BioC 2017, Boston, USA (26/07)
- *2016*: **New features in `bsseq` for analysing large whole genome bisulfite-sequencing datasets**. Lightning talk, BioC 2016, San Francisco, USA (24/06)
- *2016*: **The `GenomicTuples` package**. 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*: **Making sense of DNA methylation data**. PhD completion seminar, Melbourne, Australia (15/09)
- *2014*: **Simulating whole-genome DNA methylation data**). Contributed talk, Australian Statistical Conference/International Mathematical Statistics Annual Meeting, Sydney, Australia (10/07)
- *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

- *2019*: **Genome-wide analysis of DNA methylation in samples from the Genotype-Tissue Expression (GTEx) project**. Poster, Lorne Genome, Lorne, Australia (17/02)
- *2018*: **Developing 'standard' bioinformatics analyses for the Single Cell Open Research Endeavour (SCORE)**. Poster, ABACBS, Mebourne, Australia (27/11)
- *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)

- *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

- *2019*: **Hands on workshop on downstream analysisof 10X data**]. BioC 2019, New York, USA (25/6) Oz Single Cell 2019, Melbourne, Australia (21/7)
- *2019*: **Effectively using the DelayedArray framework to support the analysis of large datasets**. BioC 2019, New York, USA (25/6)
- *2019*: **Data Organisation: Making Your Research Life Easier**. Australian Catholic University, Melbourne, Australia (02/07)
- *2018*: **Analyzing 10X Chromium single-cell RNA-seq**. University of Melbourne, Melbourne, Australia (06/06)
- *2018*: **Analyzing 10X Chromium single-cell RNA-seq**. Nanjing University, Nanjing, China (11/12)
- *2018*: **Effectively using the DelayedArray framework to support the analysis of large datasets**. BioC 2018, Toronto, Canada (25/7)
- *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 teaching 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*, *Biostatistics*, *PLoS Computational Biology*, *Genetic Epidemiology*, *Heredity*, and *F1000*.

Professional society memberships

- Member, Statistical Society of Australia
- Member, Australasian Genomic Technologies Association

References

Associate Professor Kasper Hansen

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