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CURRICULUM VITAE

Peter Francis Hickey

PERSONAL DATA

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EDUCATION AND TRAINING

Degrees

2015	Ph.D. in Statistics Department of Mathematics and Statistics The University of Melbourne, Melbourne Advisors: **Terry Speed** and **Peter Hall**
2009	B. Sc. (First Class Honours) in Mathematics and Statistics University of Melbourne

Postdoctoral Training

2016–2018	Department of Biostatistics Johns Hopkins Bloomberg School of Public Health Advisor: **Kasper D. Hansen**

PROFESSIONAL EXPERIENCE

2018–Present	Senior Research Officer Advanced Technology and Biology Walter and Eliza Hall Institute of Medical Research
2016–2018	Postdoctoral Fellow Department of Biostatistics Johns Hopkins Bloomberg School of Public Health

2010–2015 Research Assistant
Bioinformatics Division
Walter and Eliza Hall Institute of Medical Research

PROFESSIONAL ACTIVITIES

Professional Memberships

Member, Statistical Society of Australia
Member, Australian Bioinformatics And Computational Biology Society
Member, Australasian Genomic Technologies Association

EDITORIAL ACTIVITIES

Served as *referee* for

Bioinformatics
Biostatistics
F1000Research
Genetic Epidemiology
Genome Biology
Heredity
Nature Methods
PLoS Computational Biology
PLoS Genetics

HONORS AND AWARDS

2019 Bioconductor Travel Award (To present at BioC in New York, USA)
2018 AGTA Travel Award (To present at the AGTA meeting in Adelaide, Australia)
2018 Bioconductor Travel Award (To present at BioC in Toronto, Canada)
2015 Bioconductor Travel Award (To present at BioC in Seattle, USA)
2015 Edith Moffat Travel Award (To interview for international for postdoctoral positions)
2013 Prize for best lightning talk at the Australian Epigenetics Conference
2013 Third prize for best lightning talk at the Young Statisticians Conference

PUBLICATIONS

Journal Articles (peer reviewed)

* indicates equal contributions
† indicates corresponding author(s) (if not the senior author)

[1] M. I. Love*†, C. Soneson, **P. F. Hickey**, L. K. Johnson, N. T. Pierce, L. Shepherd, M. Morgan, and R. Patro. "Tximeta: Reference sequence checksums for provenance identification in RNA-seq". *PLoS Computational Biology* (2020). DOI: 10.1371/journal.pcbi.1007664.

[2] 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. E. Ritchie, and G. T. Belz†. "The neuropeptide VIP confers anticipatory mucosal immunity by regulating ILC3 activity". *Nature Immunology* (2020). DOI: 10.1038/s41590-019-0567-y.

[3] S. Su*†, L. Tian, X. Dong, **P. F. Hickey**, S. Freytag, and M. E. Ritchie†. "CellBench: R/Bioconductor software for comparing single-cell RNA-seq analysis methods". *Bioinformatics* (2020). DOI: 10.1093/bioinformatics/btz889.

[4] G. M. Verstappen*†, J. A. Ice, H. Bootsma, S. Pringle, E. A. Haacke, K. de Lange, G. B. van der Vries, **P. F. Hickey**, A. Vissink, F. K. L. Spijkervet, C. J. Lessard†, and F. G. M. Kroese†. "Gene expression profiling of epithelium-associated FcRL4+ B cells in primary Sjögren's syndrome reveals a pathogenic signature". *Journal of Autoimmunity* (2020). DOI: 10.1016/j.jaut.2020.102439.

[5] 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". *Genome Research* (2019). DOI: 10.1101/gr.239442.118.

[6] 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". *The Journal of Orthopaedic and Sports Physical Therapy* (2019). DOI: 10.2519/jospt.2019.8895.

[7] H.-F. Koay*, S. Su, D. Amann-Zalcenstein, S. R. Daley, I. Comerford, L. Miosge, C. E. Whyte, I. E. Konstantinov, Y. d'Udekem, T. Baldwin, **P. F. Hickey**, S. P. Berzins, J. Y. W. Mak, Y. Sontani, C. M. Roots, T. Sidwell, A. Kallies, Z. Chen, S. Nüssing, K. Kedzierska, L. K. Mackay, S. R. McColl, E. K. Deenick, D. P. Fairlie, J. McCluskey, C. C. Goodnow, M. E. Ritchie, G. T. Belz, S. H. Naik, D. G. Pellicci†, and D. I. Godfrey†. "A divergent transcriptional landscape underpins the development and functional branching of MAIT cells". *Science Immunology* (2019). DOI: 10.1126/sciimmunol.aay6039.

[8] 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". *Nature Neuroscience* (2019). DOI: 10.1038/s41593-018-0297-8.

[9] J. T. Hickey*, **P. F. Hickey**, N. Maniar, R. G. Timmins, M. D. Williams, C. A. Pitcher, and D. A. Opar†. "A Novel Apparatus to Measure Knee Flexor Strength During Various Hamstring Exercises: A Reliability and Retrospective Injury Study". *The Journal of Orthopaedic and Sports Physical Therapy* (2018). DOI: 10.2519/jospt.2018.7634.

[10] 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". *Nature Structural & Molecular Biology* (2018). DOI: 10.1038/s41594-018-0111-z.

[11] 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". *Cell Reports* (2018). DOI: 10.1016/j.celrep.2018.10.044.

[12] **P. F. Hickey***†. "Representation and Manipulation of Genomic Tuples in R". *The Journal of Open Source Software* (2016). DOI: 10.21105/joss.00020.

[13] 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". *Epigenetics & Chromatin* (2016). DOI: 10.1186/s13072-016-0064-6.

[14] 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". *European Heart Journal* (2016). DOI: 10.1093/eurheartj/ehw160.

[15] D. Lacey*, **P. F. Hickey**, B. D. Arhatari, L. A. O'Reilly, L. Rohrbeck, H. Kiriazis, X.-J. Du, and P. Bouillet†. "Spontaneous retrotransposon insertion into TNF 3'UTR causes heart valve disease and chronic polyarthritis". *Proceedings of the National Academy of Sciences of the United States of America* (2015). DOI: 10.1073/pnas.1508399112.

[16] 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". *Epigenetics & Chromatin* (2015). DOI: 10.1186/s13072-015-0047-z.

[17] **P. F. Hickey***† and M. Bahlo. "X chromosome association testing in genome wide association studies". *Genetic Epidemiology* (2011). DOI: 10.1002/gepi.20616.

[18] 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". *Cancer Epidemiology, Biomarkers & Prevention* (2010). DOI: 10.1158/1055-9965.EPI-09-0812.

[19] 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". *American Journal of Human Genetics* (2010). DOI: 10.1016/j.ajhg.2010.06.001.

Journal Articles, Consortia member (peer reviewed)

[20] L. Jiang, M. Wang, S. Lin, R. Jian, X. Li, J. Chan, G. Dong, H. Fang, A. E. Robinson, F. Aguet, et al. "A quantitative proteome map of the human body". *Cell* (2020). DOI: 10.1016/j.cell.2020.08.036.

[21] GTEx Consortium, Laboratory, Data Analysis & Coordinating Center (LDACC)—Analysis Working Group, Statistical Methods groups—Analysis Working Group, Enhancing GTEx (eGTEx) groups, NIH Common Fund, NIH/NCI, NIH/NHGRI, NIH/NIMH, NIH/NIDA, Biospecimen Collection Source Site—NDRI, Biospecimen Collection Source Site—RPCI, Biospecimen Core Resource—VARI, Brain Bank Repository—University of Miami Brain Endowment Bank, Leidos Biomedical—Project Management, ELSI Study, Genome Browser Data Integration & Visualization—EBI, Genome Browser Data Integration & Visualization—UCSC Genomics Institute, University of California Santa Cruz, Lead analysts: Laboratory, Data Analysis & Coordinating Center (LDACC): NIH program management: Biospecimen collection: Pathology: eQTL manuscript working group: A. Battle, C. D. Brown, B. E. Engelhardt, and S. B. Montgomery. "Genetic effects on gene expression across human tissues". *Nature* (2017). DOI: 10.1038/nature24277.

[22] X. Li, Y. Kim, E. K. Tsang, J. R. Davis, F. N. Damani, C. Chiang, G. T. Hess, Z. Zappala, B. J. Strober, A. J. Scott, A. Li, A. Ganna, M. C. Bassik, J. D. Merker, GTEx Consortium, Laboratory, Data Analysis & Coordinating Center (LDACC)—Analysis Working Group, Statistical Methods groups—Analysis Working Group, Enhancing GTEx (eGTEx) groups, NIH Common Fund, NIH/NCI, NIH/NHGRI, NIH/NIMH, NIH/NIDA, Biospecimen Collection Source Site—NDRI, Biospecimen Collection Source Site—RPCI, Biospecimen Core Resource—VARI, Brain Bank Repository—University of Miami Brain Endowment Bank, Leidos Biomedical—Project Management, ELSI Study, Genome Browser Data Integration & Visualization—EBI, Genome Browser Data Integration & Visualization—UCSC Genomics Institute, University of California Santa Cruz, I. M. Hall, A. Battle, and S. B. Montgomery. "The impact of rare variation on gene expression across tissues". *Nature* (2017). DOI: 10.1038/nature24267.

[23] eGTEx Project. "Enhancing GTEx by bridging the gaps between genotype, gene expression, and disease". *Nature Genetics* (2017). DOI: 10.1038/ng.3969.

[24] A. Saha, Y. Kim, A. D. H. Gewirtz, B. Jo, C. Gao, I. C. McDowell, GTEx Consortium, B. E. Engelhardt, and A. Battle. "Co-expression networks reveal the tissue-specific regulation of transcription and splicing". *Genome Research* (2017). DOI: 10.1101/gr.216721.116.

[25] M. H. Tan, Q. Li, R. Shanmugam, R. Piskol, J. Kohler, A. N. Young, K. I. Liu, R. Zhang, G. Ramaswami, K. Ariyoshi, A. Gupte, L. P. Keegan, C. X. George, A. Ramu, N. Huang, E. A. Pollina, D. S. Leeman, A. Rustighi, Y. P. S. Goh, GTEx Consortium, Laboratory, Data Analysis & Coordinating Center (LDACC)—Analysis Working Group, Statistical Methods groups—

Analysis Working Group, Enhancing GTEx (eGTEx) groups, NIH Common Fund, NIH/NCI, NIH/NHGRI, NIH/NIMH, NIH/NIDA, Biospecimen Collection Source Site—NDRI, Biospecimen Collection Source Site—RPCI, Biospecimen Core Resource—VARI, Brain Bank Repository—University of Miami Brain Endowment Bank, Leidos Biomedical—Project Management, ELSI Study, Genome Browser Data Integration & Visualization—EBI, Genome Browser Data Integration & Visualization—UCSC Genomics Institute, University of California Santa Cruz, A. Chawla, G. Del Sal, G. Peltz, A. Brunet, D. F. Conrad, C. E. Samuel, M. A. O'Connell, C. R. Walkley, K. Nishikura, and J. B. Li. "Dynamic landscape and regulation of RNA editing in mammals". *Nature* (2017). DOI: 10.1038/nature24041.

[26] T. Tukiainen, A.-C. Villani, A. Yen, M. A. Rivas, J. L. Marshall, R. Satija, M. Aguirre, L. Gauthier, M. Fleharty, A. Kirby, B. B. Cummings, S. E. Castel, K. J. Karczewski, F. Aguet, A. Byrnes, GTEx Consortium, Laboratory, Data Analysis & Coordinating Center (LDACC)—Analysis Working Group, Statistical Methods groups—Analysis Working Group, Enhancing GTEx (eGTEx) groups, NIH Common Fund, NIH/NCI, NIH/NHGRI, NIH/NIMH, NIH/NIDA, Biospecimen Collection Source Site—NDRI, Biospecimen Collection Source Site—RPCI, Biospecimen Core Resource—VARI, Brain Bank Repository—University of Miami Brain Endowment Bank, Leidos Biomedical—Project Management, ELSI Study, Genome Browser Data Integration & Visualization—EBI, Genome Browser Data Integration & Visualization—UCSC Genomics Institute, University of California Santa Cruz, T. Lappalainen, A. Regev, K. G. Ardlie, N. Hacohen, and D. G. MacArthur. "Landscape of X chromosome inactivation across human tissues". *Nature* (2017). DOI: 10.1038/nature24265.

[27] F. Yang, J. Wang, GTEx Consortium, B. L. Pierce, and L. S. Chen. "Identifying cis-mediators for trans-eQTLs across many human tissues using genomic mediation analysis". *Genome Research* (2017). DOI: 10.1101/gr.216754.116.

Preprints (not peer reviewed)

* indicates equal contributions
† indicates corresponding author(s) (if not the senior author)

[28] L. M. Weber*, A. A. Hippen, **P. F. Hickey**, K. C. Berrett, J. Gertz, J. A. Doherty, C. S. Greene, and S. C. Hicks. "Genetic demultiplexing of pooled single-cell RNA-sequencing samples in cancer facilitates effective experimental design". *bioRxiv* (2020). Preprint. DOI: 10.1101/2020.11.06.371963.

[29] A. Keniry*, N. Jansz, L. J. Gearing, I. Wanigasuriya, J. Chen, C. M. Nefzger, **P. F. Hickey**, Q. Gouil, J. Liu, K. A. Breslin, M. Iminitoff, T. Beck, A. T. del Fierro, L. Whitehead, S. A. Kinkel, P. C. Taberlay, T. Willson, M. Pakusch, M. E. Ritchie, D. J. Hilton, J. M. Polo, and M. E. Blewitt†. "Xmas ESC: A new female embryonic stem cell system that reveals the BAF complex as a key regulator of the establishment of X chromosome inactivation". *bioRxiv* (2019). Preprint. DOI: 10.1101/768507.

[30] 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". *bioRxiv* (2019). Preprint. DOI: 10.1101/659722.

Theses, Editorials

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

[32] **P. F. Hickey** and M. D. Robinson. "Genomics by the beach". *Genome biology* (2014). DOI: 10.1186/gb4171.

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

Citation databases

Google Scholar: profile (link)
ORCID: 0000-0002-8153-6258 (link)
Europe PMC Citations: profile (link)

PRACTICE ACTIVITIES

Software - Bioconductor Project

bsseq Analyze, Manage and Store Bisulfite Sequencing Data.

CellBench Construct Benchmarks for Single Cell Analysis Methods.

DelayedMatrixStats Functions that Apply to Rows and Columns of 'DelayedMatrix' Objects.

GenomicTuples Representation and Manipulation of Genomic Tuples.

MatrixGenerics S4 Generic Summary Statistic Functions that Operate on Matrix-Like Objects.

minfi Analyze Illumina Infinium DNA Methylation Arrays.

tximeta Transcript Quantification Import with Automatic Metadata.

Software - Other

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.