September 2, 2020

CURRICULUM VITAE

Peter Francis Hickey

PERSONAL DATA

Web Page:	http://www.peterhickey.org
Email:	hickey@wehi.edu.au
Mailing Address:	Walter and Eliza Hall Institute of Medical Research 1G, Royal Parade Parkville VIC, 3052

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

PROFESSIONAL ACTIVITIES

Professional Memberships

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

EDITORIAL ACTIVITIES

Served as *referee* for

Bioinformatics
Biostatistics
F1000Research
Genetic Epigemiology
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 and present the Eu
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. 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] 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.

[21] 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.

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

[23] 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.

[24] 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.

[25] 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.

[26] 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)

[27] 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.

[28] 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

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

[29] **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.

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

[31] **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.

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

GenomicTuples Representation and Manipulation of Genomic Tuples.

minfi Analyze Illumina Infinium DNA Methylation Arrays.

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.

CURRICULUM VITAE
Peter Francis Hickey

Part II

TEACHING

Ph.D. Supervision

Yue You (joint w/ Matt Ritchie), Medical Biology, WEHI, 2020–present.
Shian Su (joint w/ Matt Ritchie), Medical Biology, WEHI, 2020–present.

Undergraduate Supervision

Amelia Dunstone, Undergraduate Research Opportunities Program 2019–present.

Ph.D. Committee

Aravind Manda, Population Health and Immunity, 2020–present.
Megan Iminitoff, Epigenetics and Development Division, 2019–present.

Classroom Instruction - Invited Guest Lecturer

Introduction to Single-Cell 'Omics: University of Melbourne, 2019.
Analysis of ATAC-seq data: Johns Hopkins University, 2017.

Other significant teaching - Workshops and Short Courses

Hands on workshop on downstream analysis of 10X data.
Oz Single Cell 2019, Melbourne, Australia. 2019.

Effectively using the DelayedArray framework to support the analysis of large datasets.
BioC, New York, USA. 2019.

Data Organisation: Making Your Research Life Easier.
Australian Catholic University, Melbourne, Australia. 2019.

Analyzing 10X Chromium single-cell RNA-seq.
University of Melbourne, Melbourne, Australia. 2018.

Analyzing 10X Chromium single-cell RNA-seq.

Nanjing University, Nanjing, China. 2018.

Effectively using the DelayedArray framework to support the analysis of large datasets.
BioC, Toronto, Canada. 2018.

Analysing DNA methylation data with Bioconductor.
BioC, Palo Alto, USA. 2016.

PRESENTATIONS

Invited Talks (Seminars and Scientific Meetings)

1 Overview of single-cell bioinformatics. (2019) *Oz Single Cell* (Melbourne, Australia).

2 Bioinformatics for bisulfite sequencing. (2013) *La Trobe University* (Melbourne, Australia).

3 X chromosome association testing in genome wide association studies. (2010) *Statistical Society of Australia - Victorian branch meeting* (Melbourne, Australia).

Scientific Meetings (Contributions)

4 Getting help and helping others (including future you). (2018) *BioC Asia* (Melbourne, Australia).

5 Genome-wide analysis of DNA methylation in samples from the Genotype-Tissue Expression (GTEx) project. (2018) *AGTA* (Adelaide, Australia).

6 DelayedArray: A tibble for arrays. (2018) *useR!* (Brisbane, Australia).

7 Lessons from switching to on-disk storage using DelayedArray containers. (2018) *BioC* (Toronto, Canada).

8 Mapping the human brain epigenome and its links to disease. (2017) *Epigenetics Australia* (Brisbane, Australia).

9 Neuronal brain region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric disease heritability. (2017) *GTEx Project Community Meeting* (Rockville, USA).

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

11 DelayedMatrixStats: Porting the matrixStats API to work with DelayedMatrix objects. (2017) *BioC* (Boston, USA).

12 New features in 'bsseq' for analysing large whole genome bisulfite-sequencing datasets. (2016) *BioC* (Palo Alto, USA).

13 The 'GenomicTuples' package. (2015) *BioC* (Seattle, USA).

14 Genomic tuples and DNA methylation patterns. (2015) *BioC Europe* (Heidelberg, Germany).

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

16 Exploiting local dependencies in genome-wide studies of DNA methylation. (2013) *Young Statisticians Conference* (Melbourne, Australia).

17 Spatial dependence of CpG-methylation from whole genome bisulfite sequencing. (2012) *Epigenomics of Common Diseases Meeting* (Baltimore, USA).

18 Spatial dependence of DNA methylation. (2012) *Australian Statistical Conference* (Adelaide, Australia).

19 Bioinformatics - Applied statistics in modern molecular biology. (2010) *Victorian Mathematics and Statistics Students' Conference* (Melbourne, Australia).

Posters

20 Genome-wide analysis of DNA methylation in samples from the Genotype-Tissue Expression (GTEx) project. (2019) *Lorne Genome* (Lorne, Australia)

21 Developing 'standard' bioinformatics analyses for the Single Cell Open Research Endeavour (SCORE). (2018) *ABACBS* (Melbourne, Australia)

22 Simulating whole-genome bisulfite-sequencing data. (2014) *Lorne Genome* (Lorne, Australia)

23 Simulating whole-genome bisulfite-sequencing data. (2013) *Epigenetics Australia* (Shoal Bay, Australia)

24 Analysis of mouse exome sequencing: filtering institute-specific single nucleotide variants (SNVs). (2011) *GeneMappers* (Hobart, Australia)

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

26 X chromosome association testing in genome wide association studies. (2010) *The Australasian Microarray and Associated Technologies Association Conference* (Hobart, USA)

27 Homozygosity by state analysis in highly inbred pedigrees. (2009) *GeneMappers* (Sydney, USA)