

Miles C. Benton

Bioinformatics PhD and data scientist

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Currently

I am Postdoc Research Fellow at QUT working on the creation of methods to deal with, and analyse, large genomic data sets. These methods include the incorporation of multiple layers of both phenotypic and genomic data. I work on a range of complex human disorders, including: obesity and type-2 diabetes, multiple sclerosis, glaucoma, migraine, ovarian cancer and asthma. I am also leading the development of diagnostic and research pipelines for visualisation and translational interpretation of data from sequencing based approaches.

Professional Positions Held

2014-	Queensland University of Technology Postdoc Research Fellow, Bioinformatics
2013-	Environmental Science Research (ESR) Honorary Senior Scientist (Bioinformatics)
2011-	Victoria University of Wellington Lecturer CLNR580 (Clinical Research Preparation)
2010-	Victoria University of Wellington Lecturer BMSC406 (Science and Ethics)

Education

2010-14	Griffith University, Australia Bioinformatics PhD (supervisors: Lyn Griffiths, Rod Lea, Donia Macartney-Coxson and Geoff Chambers) Thesis: "Identification of Susceptibility Genes for Metabolic Syndrome in the Isolated Population of Norfolk Island"
2007-09	Victoria University of Wellington, NZ MSc Cell and Molecular Biology (HONS) Thesis: "Mitochondrial Genome Variation and Metabolic Traits in a Maori Community"
2004-07	Victoria University of Wellington, NZ BBMedSc Biomedical Science (Majors: Human Genetics, Molecular Pathology)

Technical skills

R	Git / GitHub	Data visualisation
Shiny	UNIX	Cluster computing
Statistics	Machine learning	HTML and CSS
LaTeX	Bash	
Markdown	Inkscape	

Distinctions and Memberships

Research Grants	2015	Pl. Wellington Medical Research Foundation: "Validation of Blood Cell Lineage Specific DNA methylation markers."
Professional Memberships	2015 - 2015 - 2014 -	Ad hoc reviewer, Gene Reviewer National Health and Medical Research Council, Australia Member Australasian Genomic Technologies Association (AGTA).
Honours and Distinctions	2017 2016 2015 2014 2012 2010-13 2007-10	QUT School of Biomedical Sciences Travel Grant QUT Carla Patterson Award – Best Paper, Early Career Researcher ESR Vision Best Paper Award (August 2015) Best Poster Presentation, Genemappers Conference 2014, Novotel Barossa Valley Resort, SA, Australia, 11th – 14th May 2014. Richard Stewart Memorial Prize (2nd place best presentation), Wellington Health and Biomedical Research Society Inaugural Grasshopper prize for Scientific Innovation. Wellington Health and Biomedical Research Society annual students and early researchers meeting, Victoria University of Wellington, Wellington, New Zealand, 19th November 2012. Best Student Presenter. 2nd Biomarker Discovery Conference, Shoal Bay Resort and Spa, NSW, Australia, 5th December 2012. Griffith University Higher Degree Research Scholarship ESR Masters Research Scholarship
Supervision	2016	Completed QUT Effective Supervisory Practices Level 1 A course designed to walk Research Supervisors through the frameworks and pragmatic issues associated with supervising in today's research environment; ultimately to provide them with effective and essential tools for their supervisory tool kit.

Publication Metrics

Journal articles: **26** H-index: **10** Citations: **315**

Publications

2017	Matovinovic E, Kho PF, Lea RA, Benton MC , Eccles DA, Haupt LM, Hewitt AW, Sherwin JC, Mackey DA, and Griffiths LR. (2017) Genome-wide linkage and association analysis of primary open-angle glaucoma endophenotypes in the Norfolk Island isolate. <i>Molecular Vision</i> (preliminary acceptance 4th July, awaiting publication) Jones A, Danielson KM, Benton MC , Ziegler O, Shah R, Stubbs RS, Das S, and Macartney-Coxson D. (2017) miRNA signatures of insulin resistance in obesity. <i>Obesity</i> (accepted, DOI: 10.1002/oby.21950)
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White NM, **Benton MC**, Kennedy D, Fox A, Griffiths LR, Lea RA, and Mengersen KL. (2017) Accounting for cell lineage and sex effects in the identification of cell-specific DNA methylation using a Bayesian model selection algorithm. *PLoS One* (accepted)

Maltby V, Lea RA, Sanders K, White NM, **Benton MC**, Scott R, and Lechner-Scott J. (2017) Differential Methylation at MHC in CD4+ T cells is associated with multiple sclerosis independently of HLA-DRB1. *Clinical Epigenetics* 9(71)

Macartney-Coxson D, **Benton MC**, Blick R, Stubbs RS, Hagan RD, and Langston MA. (2017) Genome-wide DNA methylation analysis reveals loci that distinguish different types of adipose tissue in obese individuals. *Clinical Epigenetics* 9(48)

Benton MC, Sutherland HG, Macartney-Coxson D, Haupt LM, Lea RA, and Griffiths LR. (2017) Methylome-wide association study of whole blood DNA in the Norfolk Island isolate identifies robust loci associated with age. *Aging* 9(3)

Stuart S, **Benton MC**, Eccles D, Sutherland H, Haupt LM, Lea RA and Griffiths LR. (2017) Gene-Centric Analysis Implicates Nuclear Encoded Mitochondrial Protein Gene Variants in Migraine Susceptibility. *Molecular Genetics & Genomic Medicine*

2016 Sanders KA, **Benton MC**, Lea RA, Maltby VE, Agland S, Griffin N, Scott RJ, Tajouri L and Lechner-Scott J. (2016) Next-generation sequencing reveals broad down-regulation of microRNAs in secondary progressive multiple sclerosis CD4+ T-cells. *Clinical Epigenetics* 8(87)

2015 Fernando S, Speicher DJ, Bakr MM, **Benton MC**, Lea RA, Scuffham PA and Johnson NW. (2015) A Protocol for assessing maternal, environmental and epigenetic risk factors for dental caries in children. *BMC Oral Health* 15(167)

Benton MC, Lea RA, Macartney-Coxson D, Carless MA, Bellis C, Hanna M, Eccles D, Chambers GK, Curran JE, Blangero J and Griffiths LR. (2015) Serum bilirubin concentration is modified by UGT1A1 Haplotypes and Influences Risk of Type-2 Diabetes in the Norfolk Island Genetic Isolate. *BMC Genetics* 16(1)

Maltby VE, Graves MC, Lea RA, **Benton MC**, Sanders KA, Tajouri L, Scott RJ and Lechner-Scott J. (2015) Genome-wide DNA methylation profiling of CD8+ T cells shows a distinct epigenetic signature to CD4+ T cells in Multiple Sclerosis patients. *Clinical Epigenetics* 7(118)

Benton MC, Lea RA, Macartney-Coxson D, Carless MA, Göring HH, Bellis C, Hanna M, Eccles D, Chambers GK, Curran JE, Harper JL, Blangero J and Griffiths LR. (2015) A phenomic scan of the Norfolk Island genetic isolate identifies a major pleiotropic effect locus associated with renal disorder markers. *PLoS Genetics* 11(10)

Benton MC, Stuart S, Bellis C, Macartney-Coxson D, Eccles D, Curran JE, Chambers G, Blangero J, Lea RA and Griffiths LR. (2015) 'Mutiny on the Bounty': The Genetic History of Norfolk Island reveals extreme gender biased admixture. *Investigative Genetics* 6(11)

Rodriguez-Acevedo AJ, Ferreira MA, **Benton MC**, Carless MA, Göring HH, Curran JE, Blangero J, Lea RA and Griffiths LR. (2015) Common Polygenic Variation Contributes to Risk of Migraine in the Norfolk Island Population. *Human Genetics* (published online July 29th)

Bosch P, **Benton MC**, Macartney-Coxson D and Kivell B. (2015) mRNA and microRNA analysis reveals modulation of biochemical pathways related to addiction in the ventral tegmental area of methamphetamine self-administering rats. *BMC Neuroscience* 16(1)

Joshi PK, ... **Benton MC**, Lea RA, Griffiths LR, ... and Wislon JF. (2015) Directional dominance on stature and cognition in diverse human populations. *Nature* 523(7561)

Benton MC, Johnstone A, Eccles D, Harmon B, Hayes MT, Lea RA, Griffiths LR, Hoffman E, Stubbs RS and Macartney-Coxson D. (2015) An analysis of DNA methylation in human adipose tissue reveals differential modification of obesity genes before and after gastric bypass and weight-loss. *Genome Biology* 16(1)

2014 Aya-Bonilla C, Camilleri E, **Benton MC**, Haupt LM, Marlton P, Lea RA, Gandhi MK and Griffiths LR. (2014) Fine mapping of the 15q21 region implicate TP53BP1 and B2M in the lymphomagenesis of Follicular and Diffuse Large B-Cell lymphomas. *Carcinogenesis & Mutagenesis* 5(6)

Gunawardhana LP, Gibson PG, Simpson JL, **Benton MC**, Lea RA and Baines, KJ. (2014) Characteristic DNA methylation profiles in peripheral blood monocytes are associated with inflammatory phenotypes of asthma. *Epigenetics* 9(9)

2013 **Benton MC**, Lea RA, Macartney-Coxson D, Carless MA, Göring HH, Bellis C, Hanna M, Eccles D, Chambers GK, Curran JE, Harper JL, Blangero J and Griffiths LR. (2013) Mapping eQTLs in the Norfolk Island Genetic Isolate Identifies Candidate Genes for CVD-risk Traits. *American Journal of Human Genetics* 93(6): 1087-99

Graves M, **Benton MC**, Lea R, Boyle M, Tajouri L, Macartney-Coxson D, Scott R and Lechner-Scott J. (2013) Methylation differences at the HLA-DRB1 locus in CD4+ T-Cells are associated with multiple sclerosis. *Multiple Sclerosis* 20(8):1033-1041

Aya-Bonilla C, Green MR, Camilleri E, **Benton MC**, Keane C, Marlton P, Lea RA, Gandhi MK and Griffiths LR. (2013) High resolution loss of heterozygosity screening implicates PTPRJ as a potential tumor suppressor gene that affects susceptibility to non-Hodgkin's lymphoma. *Genes, Chromosomes and Cancer* 52(5):467-79

Rodriguez-Acevedo AJ, Maher BH, Lea RA, **Benton MC**, and Griffiths LR. (2013) Association of oestrogen-receptor gene (ESR1) polymorphisms with migraine in the large Norfolk Island pedigree. *Cephalalgia* 33(14):1139-1147

Stuart S, Maher BH, Sutherland H, **Benton MC**, Rodriguez A, Lea RA, Haupt LM and Griffiths LR. (2013) Genetic Variation in Cytokine-Related Genes and Migraine Susceptibility. *Twin Res Hum Genet* 20:1-8

2012 **Benton MC**, Macartney-Coxson D, Eccles DA, Griffiths LR, Chambers GK and Lea, RA. (2012) Complete Mitochondrial Genome Sequencing Reveals Novel Haplotypes in a Polynesian Population. *PLoS ONE* 7(4): e35026

Maher BH, Lea RA, **Benton MC**, Cox HC, Bellis C, Carless M, Dyer TD, Curran J, Charlesworth JC, Buring JE, Kurth T, Chasman DI, Ridker PM, Schürks M, Blangero J and Griffiths LR. (2012) An X Chromosome Association Scan of the Norfolk Island Genetic Isolate Provides Evidence for a Novel Migraine Susceptibility Locus at Xq12. *PLoS ONE* 7(5): e37903

Presentations

Conference Talks

2017 **Benton MC**. Identification of allelic-specific methylation profiles in a genetic isolate. GeneMappers 2017 - Novotel Geelong, Victoria, Australia, April 26th-28th.

2016 **Benton MC**. Allelic-specific methylation: insights from a human genetic isolate. AB3ACBS 2016 - QUT, Brisbane, Australia, November 1st-2nd.

Benton MC. Insights from a Genetic Isolate. AGTA 2016, Auckland, NZ, October 9th-12th.

2015 **Benton MC**, Blick R, Lea RA and Griffiths LR. Reproducible Research, Big Data and Visualisation: is free software the solution? Big Biology and Bioinformatics Symposium (B3 2015), Queensland University of Technology, QLD, Australia, 23-25th November 2015.

White N, **Benton MC**, Lea RA, Griffiths LR, and Mengersen K. (2015) Cellular heterogeneity in DNA methylation: A new approach for the estimation of cellular proportions in whole blood. Big Biology and Bioinformatics Symposium (B3 2015), Queensland University of Technology, QLD, Australia, 23-25th November 2015.

2014	<p>Benton MC, Sutherland H, Haupt L, Donia Macartney-Coxson, Lea RA and Griffiths LR. As Time Goes By: Longitudinal profiling of DNA methylation. Wellington Health & Biomedical Research Society Young Investigators Meeting (80th meeting), Victoria University of Wellington, Wellington, New Zealand, 27th November 2014.</p> <p>Benton MC, Sutherland H, Haupt L, Lea RA and Griffiths LR. As Time Goes By: Longitudinal profiling of DNA methylation. Big Biology and Bioinformatics Symposium (B3 2014), Queensland University of Technology, QLD, Australia, 24-25th November 2014.</p> <p>Benton MC, Lea RA, Macartney-Coxson D, Carless MA, Göring HH, Bellis C, Hanna M, Eccles D, Chambers GK, Curran JE, Blangero J and Griffiths LR. A pedigree-based GWAS identifies UDP-glucuronosyltransferase (UDPGT) variants associated with serum bilirubin concentration and risk of Type-2 Diabetes in the Norfolk Island genetic isolate. Genemappers Conference 2014, Novotel Barossa Valley Resort, SA, Australia, 11-14th May 2014.</p>
2013	<p>Benton MC. Epigenetics – where the environment meets the genetics of disease: Interpreting high-throughput DNA Methylation data. QUT SBB symposium, Queensland University of Technology, Brisbane, Australia, 25-26th November 2013.</p> <p>Benton MC, Johnstone A, Eccles D, Harmon B, Hayes MT, Lea RA, Griffiths LR, Hoffman E, Stubbs RS, Macartney-Coxson D. Global DNA methylation profiling reveals significant differential methylation of subcutaneous and omental adipose tissue before and after weight loss. Queenstown Molecular Biology Meeting, Queenstown, New Zealand, August 2013 Epigenetics Satellite.</p> <p>Graves MC, Benton MC, Lea RA, Boyle M, Tajouri L, Macartney-Coxson D, Scott R, Lechner-Scott J. (2013) Epigenetic changes in CD4+ T cells isolated from relapsing-remitting multiple sclerosis patients.ECTRIMS Lecture: Multiple Sclerosis Journal 19: (S1) 18–73</p> <p>Benton MC, Eccles D, Macartney-Coxson D. What High-throughput ‘Omics’ and Bioinformatics can do for you! Malaghan Institute Seminar, Wellington, New Zealand, 24 th May 2013.</p>
2012	<p>Benton MC, Lea RA, Macartney-Coxson D, Carless MA, Göring HH, Bellis C, Hanna M, Eccles D, Chambers GK, Curran JE, Blangero J and Griffiths LR. Mapping eQTLs associated with CVD risk in the Norfolk Island genetic isolate. Biomarkers Discovery Conference 2012, Shoal Bay Resort and Spa, NSW, Australia, 3 rd - 6 th December 2012.</p> <p>Benton MC, Eccles D, Lea R, Sutherland H, Macartney-Coxson D, Griffiths L. Epigenetics – where the environment meets the genetics of disease: Interpreting high-throughput DNA Methylation data. WHBRS 2012, Victoria University of Wellington, Wellington, New Zealand.</p> <p>Benton MC, Lea RA, Macartney-Coxson D, Carless MA, Göring HH, Bellis C, Hanna M, Eccles D, Chambers GK, Curran JE, Blangero J and Griffiths LR. eQTL identification and mapping in the population isolate of Norfolk Island. Genemappers Conference. Port Douglas, Australia, 26-29th August 2012.</p>
2011	<p>Benton MC, Lea RA, Macartney-Coxson D, Cox H, Hanna M, Eccles D, Chambers GK, Griffiths L. A Phenome Scan for Metabolic Syndrome in the Norfolk Island Isolate. Goldcoast Health and Medical Research Council Conference 2011.</p>
Posters 2015	<p>Kennedy D, Lea RA, White N, Benton MC, Griffiths LR, and Mengersen K. (2015) Statistical deconvolution of DNA methylation data in mixed cell samples. Big Biology and Bioinformatics Symposium (B3 2015), Queensland University of Technology, QLD, Australia, 23-25th November 2015.</p> <p>Stuart S, Benton MC, Eccles DA, Sutherland H, Albury C, Haupt LM, Lea RA, and Griffiths LR. (2015) Full Mitochondrial Genome Sequencing Reveals that the 12S rRNA Mitochondrial subunit is Involved in Migraine Susceptibility in the Genetically Isolated Norfolk Island Population. Big Biology and Bioinformatics Symposium (B3 2015), Queensland University of Technology, QLD, Australia, 23-25th November 2015.</p> <p>Avgan N, Sutherland HG, Benton MC, Bellis C, Spriggins LG, Shum DHK, Lea RA, Haupt LM, and Griffiths, LR. (2015) A Genome-Wide Investigation of SNPs in Human Memory. Big Biology and Bioinformatics Symposium (B3 2015), Queensland University of Technology, QLD, Australia, 23-25th November 2015.</p> <p>Benton MC, Sutherland H, Haupt L, Lea RA and Griffiths LR. Longitudinal methylation changes in SGK1 are associated with blood glucose levels in healthy Norfolk Island females. Genemappers Conference 2015, Perth, WA, Australia, 10-12th November 2015.</p> <p>Sanders KA, Benton MC, Lea RA, Maltby VE, Agland S, Griffin N, Scott RJ, Tajouri L and Lechner-Scott J. (2015) MicroRNA sequencing identifies four down-regulated microRNAs in CD4+T-cells of secondary progressive multiple sclerosis patients. MS Research Australia Progress in MS Research Conference, Melbourne, AUSTRALIA, OCT 29-30, 2015</p> <p>Lea RA, Benton MC, Scott R. et al. (2015) Next Phase ANZGene Proposal - Epigenome-Wide Association Studies of Multiple Sclerosis. MS Research Australia Progress in MS Research Conference Melbourne, AUSTRALIA, OCT 29-30, 2015</p> <p>Maltby VE, Graves M, Lea RA, Benton MC, Scott RJ, Tajouri L and Lechner-Scott J. (2015) Minor methylation differences at various loci in CD8+T-Cells are associated with multiple sclerosis. MS Research Australia Progress in MS Research Conference Melbourne, AUSTRALIA, OCT 29-30, 2015</p> <p>Sanders KA, Benton MC, Lea RA, Maltby VE, Agland S, Griffin N, Scott RJ, Tajouri L and Lechner-Scott J. (2015) MicroRNA sequencing identifies down-regulated microRNA in CD4+T-cells of secondary progressive multiple sclerosis patients. 31st Congress of the European-Committee-for-Treatment-and-Research-in-Multiple-Sclerosis (ECTRIMS), Barcelona, SPAIN, OCT 07-10, 2015</p>
2014	<p>White N, Benton MC, Lea RA and Mengersen K. Bayesian hierarchical models for the analysis of DNA methylation. Big Biology and Bioinformatics Symposium (B3 2014), Queensland University of Technology, QLD, Australia, 24-25th November 2014.</p> <p>Hernández-Sánchez J, Lea RA, Benton MC, Sutherland H and Griffiths LR. Elastic Nets Haul in Obesity Markers: A Recipe to Analyze Big DNA Methylation Data Big Biology and Bioinformatics Symposium (B3 2014), Queensland University of Technology, QLD, Australia, 24-25th November 2014.</p> <p>Graves M, Benton MC, Lea R, Boyle M, Tajouri L, Macartney-Coxson D, Scott R and Lechner-Scott J. (2014) Epigenetic changes in CD8(+) T cells and CD19(+) B cells isolated from relapsing/remitting multiple sclerosis patients. Joint ACTRIMS-ECTRIMS, Boston, MA, SEP 10-13, 2014</p> <p>Miles C. Benton, Ronald D. Hagan, Alice Johnstone, Richard Stubbs, Michael A. Langston, Donia Macartney-Coxson. A tale of two [adipose] tissues: DNA methylation markers associated with weight-loss and tissue specificity. Genemappers Conference 2014, Novotel Barossa Valley Resort, SA, Australia, 11 th – 14 th May 2014. [PDF]</p>
2013	<p>Benton MC, Johnstone A, Eccles D, Harmon B, Hayes MT, Lea RA, Griffiths LR, Hoffman E, Stubbs RS, Macartney-Coxson D. Global DNA methylation profiling reveals significant differential methylation of subcutaneous and omental adipose tissue before and after weight loss. AMATA 2013, Surfers Paradise, Oct 13-16 – Australasian Microarray and Associated Technologies Association Conference.</p> <p>Jones A, Benton MC, Stubbs RS, Macartney-Coxson D. A comparison of plasma miRNA levels in insulin sensitive, insulin resistant and type 2 diabetic obese individuals versus lean controls: differential miRNA levels between groups. AMATA 2013, Surfers Paradise, Oct 13-16 – Australasian Microarray and Associated Technologies Association Conference.</p>

- 2012 Griffiths LR, **Benton MC**, Cox H, Bellis C, Blangero J, Lea RA. Identification of a pleiotropic effect locus associated with a composite CVD risk trait in the genetic isolate of Norfolk Island. ASHG 2012. [PDF]
- 2011 **Benton MC**, Lea RA, Macartney-Coxson D, Cox H, Hanna M, Eccles D, Chambers GK, Griffiths L. A Phenome Scan for Metabolic Syndrome in the Norfolk Island Isolate. HGSA Conference, Seaworld, Queensland, Australia, 3-6th December 2011. [PDF]
- 2010 **Benton MC**, Macartney-Coxson D, Eccles D, Griffiths L, Chambers GK, Lea RA. A Mitochondrial Genome Scan for Thrifty Genes in Maori. WHBRS 2010, Wellington, New Zealand. [PDF]

Other dissemination

Benton MC. Online Resources, Databases and Clinical Data Management Wellington Hospital, Wellington, New Zealand, July 12th.

Benton MC. My journey - how bioinformatics changed my worldview: the many platforms, data types and analyses I've learnt along the way... and other general ramblings. Invited speaker, CMB Friday seminar series, Vitoria University of Wellington, Wellington, New Zealand, 6th November 2015.

Benton MC. A student's journey – how Bioinformatics changed my worldview: the many platforms, data types and analyses I've learnt along the way. ESR conference, Lincoln University, Christchurch, New Zealand, 3rd-5th December 2013.

Benton MC, Eccles D, Macartney-Coxson D. What High-throughput 'Omics' and Bioinformatics can do for you! Malaghan Institute Seminar, Wellington, New Zealand, 24th May 2013.

Links

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🔖 scholar

References

Available on request.