

Miles C Benton

PERSONAL DETAILS

Name: Miles C Benton

Organisation: Institute of Health and Biomedical Innovation, Queensland University of Technology

Address: Genomics Research Centre, Institute of Health and Biomedical Innovation, Queensland University of Technology, 60 Musk Avenue, Kelvin Grove Urban Village, Kelvin Grove, 4059 QLD, Australia.

Mobile: +64 21 247 222 9

Email: m.benton@qut.edu.au or miles.benton84@gmail.com

Website: <http://sirselim.github.io/>

GitHub: <https://github.com/sirselim>

PROFESSIONAL POSITIONS HELD

2010 (ongoing) Lecturer BMSC-406	Victoria University of Wellington
2011 (ongoing) Lecturer CLNR-580	Victoria University of Wellington
2013 (ongoing) Senior Scientist (Bioinformatics)	Environmental Science Research (ESR)
2014 (ongoing) PostDoc (Feb-)	Queensland University of Technology

EDUCATION

2010-2014: PhD School of Medical Sciences, Griffith University, Queensland, Australia.
Thesis: *"Identification of Susceptibility Genes for Metabolic Syndrome in the Isolated Population of Norfolk Island"*

2009: MSc (HONS) Cell and Molecular Biology, Victoria University of Wellington.
Thesis: *"Mitochondrial Genome Variation and Metabolic Traits in a Maori Community"*

2007: BBMedSc. Biomedical Science, Majors: Human Genetics, Molecular Pathology, Victoria University of Wellington.

PRESENT RESEARCH/PROFESSIONAL SPECIALITY

I completed my PhD exploring the underlying genetic susceptibility to obesity and metabolic disorders in the Norfolk Island population isolate. My main areas of research are Bioinformatics and Computational Genetics. I am currently in a PostDoc position at QUT working on the creation of methods to deal with, and analyse, large genomic data sets, including 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. Over the last 5 years I have been working closely with genome-wide methylation arrays and, more recently, next-gen sequencing approaches to DNA methylation and epigenetics. This involves the ongoing development of custom QC and analysis routines for Illumina 450K methylation arrays as well as a new next-gen sequencing approach from Roche-Nimblegen.

PROFESSIONAL DISTINCTIONS AND MEMBERSHIPS

Research Grants

2015 PI. Wellington Medical Research Foundation Validation of Blood Cell Lineage Specific DNA methylation markers

Professional Memberships and Related Experience

2015 – present Ad hoc reviewer, Gene

2015 – present Reviewer National Health and Medical Research Council, Australia

2014 – present Member Australasian Genomic Technologies Association (AGTA).

Honours and Distinctions

2017 QUT School of Biomedical Sciences Travel Grant

2016 QUT Carla Patterson Award – Best Paper, Early Career Researcher

2015 ESR Vision Best Paper Award (August 2015)

2014 Best Poster Presentation, Genemappers Conference 2014, Novotel Barossa Valley Resort, SA, Australia, 11th – 14th May 2014.

2012 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.

2012 Best Student Presenter. 2nd Biomarker Discovery Conference, Shoal Bay Resort and Spa, NSW, Australia, 5th December 2012.

2010-2013 Griffith University Higher Degree Research Scholarship 2010-2013.

2007-2010 ESR Masters Research Scholarship

Supervision

April 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.

TOTAL NUMBER OF PEER REVIEWED PUBLICATIONS

Journal articles: 26 Conference proceedings: 36 H-index: 10 Citations: 303

LIST OF PUBLICATIONS

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, awaiting publication)

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 (accepted 11th July, awaiting publication)

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*. Molecular Vision (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*. Obesity (accepted 3rd July, awaiting publication)

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 (accepted 11 April 2017)

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 5(2)

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)

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

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, 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)

ROHgen Consortium (2015) *Directional dominance on stature and cognition in diverse human populations.* Nature 523, 459–462

Benton MC, Johnstone A, Eccles D, Harmon B, Hayes MT, Lea RA, Griffiths LR, Hoffman E, Stubbs RS, 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)

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, Baines, KJ. (2014) *Characteristic DNA methylation profiles in peripheral blood monocytes are associated with inflammatory phenotypes of asthma.* Epigenetics 9(9)

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. *Mapping eQTLs in the Norfolk Island Genetic Isolate Identifies Candidate Genes for CVD-risk Traits.* (2013) American Journal of Human Genetics 93(6): 1087-99

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

Aya-Bonilla C, Green MR, Camilleri E, **Benton MC**, Keane C, Marlton P, Lea RA, Gandhi MK, 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**, 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, Griffiths LR. (2013) *Genetic Variation in Cytokine-Related Genes and Migraine Susceptibility*. *Twin Res Hum Genet* 20:1-8

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, 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

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

REFEREED CONFERENCE PROCEEDINGS

Oral Presentations

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

Benton MC. *Identification of allelic-specific methylation profiles in a genetic isolate*. AB³ACBS 2016, QUT, Brisbane, Australia, November 1st-2nd.

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

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.

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.

Benton MC, Sutherland H, Haupt L, Donia Macartney-Coxson, 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.

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.

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. *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

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

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.

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, 3rd - 6th December 2012.

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.

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.

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.

Poster Presentations

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.

White N, **Benton MC**, Lea RA and Mengersen K. *Baysian 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.

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.

Benton MC, Hagan RD, Johnstone A, Stubbs R, Langston MA, Macartney-Coxson D. *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.

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.

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.

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*. American Society of Human Genetics 2012.

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.

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.

Other forms of 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 Novemember 2015.

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.