

5. CURRICULUM VITAE, PUBLICATIONS AND OTHER PUBLISHED WORKS

PART 1

1a. Personal details					
Full name	Title	First name	Second name(s)	Family name	
	Dr	Miles	C.	Benton	
Present position	Senior Scientist Bioinformatics / Computational Genomics				
Organisation/Employer	Institute of Environmental Science and Research, NZ				
Contact Address	Health, Biomarkers Team				
	Kenepuru Science Centre, 34 Kenepuru Drive, Kenepuru, Porirua				
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Personal website	http://sirselim.github.io/				

1b. Academic qualifications			
2014	PhD	"Identification of Susceptibility Genes for Metabolic Syndrome in the Isolated Population of Norfolk Island"	School of Medical Sciences, Griffith University, QLD, AUS
2009	MSc	Biomedical Science / Bioinformatics "Mitochondrial Genome Variation and Metabolic Traits in a Maori Community"	Victoria University of Wellington, NZ
2007	BBMedSc	Biomedical Science (Human Genetics, Molecular Pathology)	Victoria University of Wellington, NZ

1c. Professional positions held	
2019 – present	Genomics Aotearoa, Bioinformatics Leadership Team (Health)
2018 – present	Senior Scientist (Data Science / Bioinformatics), Institute of Environmental Science and Research (ESR), Porirua, NZ
2014 – June 2018	Postdoctoral Research Fellow, Queensland University of Technology, Brisbane, AUS
2011 – present	Part-time Lecturer for Research Preparation Course (CLNR-580), School of Biological Sciences, Victoria University of Wellington, NZ
2010 – present	Part-time Lecturer for Science and Ethics Course (BMSC 406), School of Biological Sciences, Victoria University of Wellington, NZ

1d. 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 recently completed a PostDoc position 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-generation 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-generation sequencing approach from Roche-Nimblegen.

1e. Total years research experience	5 years (post PhD)
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1f. Professional distinctions and memberships (including honours, prizes, scholarships, boards or governance roles, etc)

Research Grants

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

Professional Memberships and Related Experience

2019 – present Member Human Genomics Society of Australasia
 2015 – present Ad hoc reviewer, Gene, BMC Medical Genetics, Frontiers in Immunology, Frontiers in Genetics, Scientific Reports
 2015 – present Reviewer National Health and Medical Research Council, Australia and Australian Research Council, Australia
 2014 – present Member Australasian Genomic Technologies Association (AGTA)

Honours and Distinctions

2017 QUT Travel Award
 2016 QUT Carla Patterson Award – Best Paper, Early Career Researcher
 2015 ESR Vision Best Paper Award
 2014 Best Poster Presentation, Genemappers Conference, Barossa Valley Australia
 2012 Inaugural Grasshopper prize for Scientific Innovation. Wellington Health and Biomedical Research Society annual students and early researchers meeting, Victoria University of Wellington,
 2012 Best Student Presenter. 2nd Biomarker Discovery Conference, Shoal Bay NSW, Australia
 2010 - 2013 Griffith University Higher Degree Research Scholarship 2010-2013.
 2007 - 2010 ESR Masters Research Scholarship

Publication Metrics

Google Scholar h-index of 15, i10-index of 18 (from 715 citations)
 Scopus h-index of 13 (cited 480 times, based on 34 citable items)

Supervision

February 2018 Co-supervisor - Bioinformatics PhD student (Otago University/ESR)
 Secondary Supervisor – Bioinformatics Honors Student (QUT)
 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.

1g. Total number of peer reviewed publications and patents	Journal articles	Books	Book chapters, books edited	Conference proceedings	Patents
	39			38	

PART 2

2a. Research publications and dissemination

Peer-reviewed journal articles

Osborne AJ, Pearson JF, Noble AJ, Gemmell NJ, Horwood LJ, Boden JM, **Benton MC**, Macartney-Coxson D, and Kennedy MA. (2019) *Genome-wide DNA methylation analysis of heavy cannabis exposure in a New Zealand longitudinal cohort*. [bioRxiv](#)

Harvey NR, Albury CL, Stuart S, **Benton MC**, Eccles DA, Connell J, Sutherland HG, Allcock RJ, Lea RA, Haupt LM, and Griffiths LR. (2019) *Ion torrent high throughput mitochondrial genome sequencing (HTMGS)*. [PLoS ONE](#) (accepted Nov 2nd 2019)

Macartney-Coxson D, Danielson K, Clapham J, **Benton MC**, Johnstone A, Jones A, Shaw O, Hagan RD, Hoffman EP, Hayes M, Harper J, Langston MA, and Stubbs RS. (2019) *MicroRNA profiling in adipose before and after weight-loss highlights the role of miR-223-3p and the NLRP3 inflammasome*. [Obesity](#) (accepted 30th Oct 2019)

Benton MC, Lea RA, Macartney-Coxson D, Sutherland HG, White NM, Kennedy DW, Mengersen K, Haupt LM, and Griffiths LR. (2019) *Genome-wide allele-specific methylation is enriched at gene regulatory regions in a multi-generation pedigree from the Norfolk Island isolate*. [Epigenetics and Chromatin](#) (accepted 16th Sept 2019)

Benton MC, Smith RA, Haupt LM, Albury CL, Maksemous N, Lea RA, and Griffiths LR. (2019) *Variant Call Format (VCF)-Diagnostic Annotation and Reporting Tool (VCF-DART) A Customizable Analysis Pipeline for Identification of Clinically Relevant Genetic Variants in Next-Generation Sequencing Data*. [Journal of Molecular Diagnostics](#) (In Press, Journal Pre-proof, Available online 20 August 2019)

Kennedy DW, White NM, **Benton MC**, Lea RL and Mengersen K . 2019 *Cell-type specific analysis of heterogeneous methylation signal using a Bayesian model-based approach*. [bioRxiv](#) (doi: <https://doi.org/10.1101/682070>)

Kennedy D, White NM, **Benton MC**, Fox A, Scott R, Griffiths LR, Mengersen KL and Lea RA. 2018 *Critical evaluation of linear regression models for cell-subtype specific methylation signal from mixed blood cell DNA*. [PLoS ONE](#) (accepted 27th Nov 2018)

MaltbyV, Lea RA, Graves M, Sanders K, **Benton MC**, Tajouri L, Scott R, and Lechner-Scott J. (2018) *Genome-wide DNA methylation changes in CD19+ B cells from relapsing-remitting multiple sclerosis patients*. [Scientific Reports](#)

Aquino EM, **Benton MC**, Haupt LM, Sutherland HG, Griffiths LR, and Lea RA. (2018) *Current understanding of DNA methylation and age-related disease*. [OBM Genetics](#) 2

Bradshaw G, Lualhati RL, Albury CL, Maksemous N, Roos-Araujo D, Smith RA, **Benton MC**, Eccles DA, Lea RA, Sutherland HG, Haupt LM and Griffiths LR. (2018) *Exome sequencing diagnoses X-linked moesin-associated immunodeficiency in a primary immunodeficiency case*. [Frontiers in Immunology](#) 9

Dunn P, Albury CL, Maksemous N, **Benton MC**, Sutherland HG, Smith RA, Haupt LM, and Griffiths LR. (2018) *Next Generation Sequencing Methods for Diagnosis of Epilepsy Syndromes*. [Frontiers in Genetics](#) 9

Kho PF, Lea RA, **Benton MC**, Eccles DA, Haupt LM, Hewitt AW, Sherwin JC, Mackey DA, Griffiths LR. (2018) *Expression QTL analysis of glaucoma endophenotypes in the Norfolk Island isolate provides evidence that immune-related genes are associated with optic disc size*. [Journal of Human Genetics](#) 63

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](#) 23

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 25(10)

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 12(9)

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

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

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. (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 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

Select Refereed conference proceedings

Oral Presentations

Benton MC. The 'omic coal face: classifying human genomic and epigenomic inheritance. IHBI Inspires, Brisbane, Australia, August 23rd-25th 2017.

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

Benton MC. Insights from a Genetic Isolate. AGTA 2016, Auckland, NZ, October 9th-12th. (Invited speaker and session chair)