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

		Post code	5022
Work telephone	+64 21 247 222 9	**Mobile**	+64 21 247 222 9

Email	miles.benton84@gmail.com; miles.benton@esr.cri.nz
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	Postdoctural 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

My current role is as a Senior Scientist at ESR. I have extensive experience in computational genomics and bioinformatics, specialising in human health genomics. I completed a post doc at Queensland University of Technology (Brisbane, Australia) working on the development of methods to deal with ever expanding genomic data sets and their access and interpretation back to the people that matter (i.e. clients, clinicians, researchers, public, etc). Part of my role at ESR has been implementing deep learning techniques in several key genomic areas, including clinical variant calling/identification and base-calling of DNA sequence data. I am also leading the development of machine learning/AI technology on portable Nvidia modules for field/remote deployment and use. In May 2019 I was appointed to the Genomics Aoteoroa Bioinformatics Leadership Team, where I am responsible for overseeing bioinformatics support for health projects across New Zealand. I am also heavily involved in the Data Carpentries as an instructor and facilitator, and am also a mentor on ESR's data science accelerator programme.

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

Research Grants

2019	PI, ESR Strategic Science Investment Funding: *Clinically Relevant Human Genomics at ESR*
2019	PI, ESR Pioneer Funding: *Growing ESRs genomics reputation – compiling and refining a eukaryotic reference genome*
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
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 14, i10-index of 16 (from 639 citations)
Scopus	h-index of 13 (cited 413 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

1g. Total number of *peer reviewed* publications and patents	Journal articles	Books	Book chapters, books edited	Conference proceedings	Patents
	36			38	

PART 2

Peer-reviewed journal articles

Benton MC, Smith RA, Haupt LM, Albury CL, Maksemous N, Lea RA, and Griffiths LR. (2019) *A Customisable Analysis Pipeline for Identification of Clinically Relevant Genetic Variants in Next Generation Sequencing Data*. Journal of Molecular Diagnostics (accepted)

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

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)

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)

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

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

2b.   Previous research work

Research title: *DNA methylation in blood - potential to provide new insights in immune cell biology.* This project was funded by a grant in from the Wellington Medical Research Foundation
Principal outcome: Highlighted the use of previously established publicly available data to inform research questions and experimental design. The research outcome was a set of discriminatory markers which provide additional insights into immune cell biology and developmental processes. *(Paper under submission)*.
Principal end-user and contact: International research community

2c.   Describe the commercial, social or environmental impact of your previous research work

While still at the discovery end of the spectrum the DNA methylation biomarker work has identified compelling, putative methylation biomarkers predictive of immune cell population and function - these are of immediate research interest and may be of clinical utility further down the track. Taken together the results highlight the significant potential of such analyses and markers to uncover new facets of immunology.

2d.   Demonstration of relationships with end-users

With respect to my fundamental research I regularly engage with clinicians to ascertain what additional clinical tools would be most useful to them and how my research might aid in the development of such tools. I also present at International and National Conferences and seek to further establish International Collaborations (Professor Greg Gibson, Georgia University of Technology, USA, Professor Jim Wilson, Oxford University, UK and Professor Michael Langston, University of Tennessee, USA with whom I collaborate on the DNA methylation biomarker work).

In addition, I regularly contribute to training and up-skilling of: ESR staff, Hospital staff (doctors, nurses, researchers), University staff and students and people from various other institutes.