New Zealand RS&T Curriculum Vitae Template

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/about https://github.com/sirselim		

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 a mentor on ESR's data science accelerator programme.

1e. Total years research experience	6 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*

Honours and Distinctions

2019	Mentor – Royal Society Powering Potential
2019	Data Carpentries Instructor
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 17, i10-index of 19 (from 901 citations)
Scopus	h-index of 13 (cited 590 times)

Supervision

2018 - present	Co-supervisor – 2 PhD students (Otago University/ESR)
	Co-supervisor – Masters student (University of Canterbury)
	Supervisor – Bioinformatics Honours Student (QUT) - completed
2016	Completed QUT Effective Supervisory Practices Level 1

Professional Memberships and Related Experience

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

1g. Total number of *peer reviewed* publications and patents	Journal articles	Books	Book chapters, books edited	Conference proceedings	Patents
	41			38	

PART 2

2a.   Research publications and dissemination
Peer-reviewed journal articles (**last 5 years**)

Harvey NR, Voisin S, Lea RA, Yan X, **Benton MC**, Papadimitriou ID, Jacques M, Haupt LM, Ashton KJ, Eynon N, and Griffiths LR. (**2020**) *Investigating the influence of mtDNA and nuclear encoded mitochondrial variants on high intensity interval training outcomes*. Scientific Reports 10, 11089.

Osborne AJ, Pearson JF, Noble AJ, Gemmell NJ, Horwood LJ, Boden JM, **Benton MC**, Macartney-Coxson D, and Kennedy MA. (**2020**) *Genome-wide DNA methylation analysis of heavy cannabis exposure in a New Zealand longitudinal cohort*. Translational Psychiatry 10(114)

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. (**2020**) *MicroRNA profiling in adipose before and after weight-loss highlights the role of miR-223-3p and the NLRP3 inflammasome*. Obesity *28*(3)

Dunn PJ, Maher BH, Albury CL, Stuart S, Sutherland HG, Maksemous N, **Benton MC**, Smith, RA, Haupt LM, and Griffiths LR. (**2020**) *Tiered analysis of whole-exome sequencing for epilepsy diagnosis*. Molecular Genetics and Genomics https://doi.org/10.1007/s00438-020-01657-x

Harvey NR, Voisin S, Lea RA, Yan X, **MC Benton**, Papadimitriou ID, Jacques M, Haupt LM, Ashton KJ, Eynon N, Griffiths and LR. (**2020**) *Identification of novel mitochondrial and mitochondrial related genetic loci associated with exercise response in the Gene SMART study*. biorxiv (DOI: https://doi.org/10.1101/2020.02.20.957340)

Harvey NR, Albury CL, Stuart S, **Benton MC**, Ecccles 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 14(11):e0224847

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 12(60)

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 21(6)

Macartney-Coxson D, Cameron A, Clapham J, and **Benton MC.** (**2019**) *DNA methylation in blood - potential to provide new insights in immune cell biology*. PREPRINT (Version 1) available at Research Square [DOI: https://doi.org/10.21203/rs.2.13274/v1]

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. <u>Frontiers in Immunology</u> 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.* <u>Frontiers in Genetics</u> 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.* <u>Obesity</u> 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.* <u>PLoS One</u> 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.* <u>Clinical Epigenetics</u> 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.* <u>Clinical Epigenetics</u> 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.* <u>Aging</u>

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.* <u>Molecular Genetics & Genomic Medicine</u>

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.* <u>Clinical Epigenetics</u> 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.* <u>BMC Oral Health</u> 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.* <u>BMC Genetics</u> 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.* <u>Clinical Epigenetics</u>

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.* <u>PLoS Genetics</u> 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.* <u>Investigative Genetics</u> 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.* <u>BMC Neuroscience</u> 16(1)

ROHgen Consortium (**2015**) *Directional dominance on stature and cognition in diverse human populations.* <u>Nature</u> 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.* <u>Genome Biology</u> 16(1)

Other forms of dissemination

I recently gave a 2 hour seminar for the University of Otago Genetics department around the use of Next Generation Sequencing technologies and pipelines for Clinical Genetics in NZ:

- **Benton MC.** Clinical Genomics: Customisable Analysis Workflows for Identification of Clinically Relevant Genetic Variants - An Update. Otago Genetics Seminar, University of Otago, Dunedin, NZ, August 24th **2020**.

I gave several presentations at NZ universities around the projects and initiatives that we have been working on at ESR since I started in July 2018:

- **Benton MC**. Genomics and Data Science at ESR ...something a little different... University of Otago, Dunedin, NZ, October 17th **2019**.
- **Benton MC**. Genomics and Data Science at ESR ...something a little different... University of Otago, Dunedin, NZ, August 20th **2019**.

I was invited to give a plenary at a Victoria University of Wellington clinical research symposium:

- **Benton MC**. My journey through genetics - wetlab to cafe. CLNR580 Plenary, Wellington, NZ, August 4th. **2018**

I was invited to talk at the Wellington Hospital about how clinicians can embrace and utilise effective data recording and management tools:

- **Benton MC**. *Online Resources, Databases and Clinical Data Management*. Wellington Hospital, Wellington, New Zealand, July 12th. **2017**

I gave a lunch time seminar at the Victoria University of Wellington Cell and Molecular Biology seminar series:

- **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**.

All of my presentations are available online (http://sirselim.github.io/presentations/).

I also host a series of open-access workshops/tutorials on my personal website and GitHub (http://sirselim.github.io/workshops-tutorials/). These are available and accessed by the general public, and several are used in university courses I teach.