Bioinformatics and Biostatistical Analysis of Genetic and Clinical Data

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Background

The Genomics Research Centre undertakes molecular genomic and biological research aimed at identifying genes involved in disease, characterising gene structure and function, defining gene interactions and developing diagnostic and therapeutic applications. For these studies, GRC research team members utilise our well-characterised DNA populations as well as our tissue and cell model resources to examine a number of diseases and disorders. The Genomics Research Centre is a large and productive research group with interests and expertise in migraine, breast and skin cancer, mesenchymal stem cells, cardiovascular disorders, multiple sclerosis and lymphoma. The lab provides both infrastructure support through cutting-edge approaches and equipment along with research support through dedicated research staff, research collaborators (local, national and international) and postgraduate students.

Hypothesis

Novel mutations in genes causing complex diseases including cancers can be detected using Next Generation Sequencing (NGS) technology.

Aims

To date, we have identified specific gene loci and gene sets as being implicated in several disorders (including neurological, vascular and cancerous). This project will use advanced bioinformatics and biostatistical approaches to investigate the role of different genomic factors in predisposition to clinical symptoms and diseases. We are in the process of analysing this data from high-throughput array and next generation sequencing experiments to determine the role of genomics in disease pathology. Bioinformatics is applicable to all projects underway within the GRC and would be a highly valuable and interesting project.

Approaches

This project would suit students with good maths and computing skills and who are keen to apply these methods to our genomics projects. Students will have access to advanced computational and statistical expertise and tools. Successful students will learn about the new genomic technologies currently being implemented (e.g. whole genome sequence analyses).

Key Related Publications

1. Aquino, E. M., Benton, M. C., Haupt, L. M., Sutherland, H. G., **Griffiths, L. R.**, Lea, R. A. (2018). Current understanding of DNA methylation and age-related disease. *REVIEW OBM Genetics*, 2(2):016; doi:10.21926/obm.genet.1802016.
2. Dunn, P., Albury, C. L., Maksemous, N., Benton, M. C., Sutherland, H. G., Smith, R. A., Haupt, L. M., **Griffiths, L. R**. (2018). Next generation sequencing methods for diagnosis of epilepsy syndromes. [Review]. *Frontiers in Genetics, 9*(FEB). doi: 10.3389/fgene.2018.0002

3. Matovinovic, E., Ko, P.F., Lea, R.A., Benton, M., Haupt, L., Eccles, D., Hewitt, A., Sherwin, J., Mackey, D., & **Griffiths., L.R**., (2017) Genome-wide linkage and association analysis of primary open-angle glaucoma endophenotypes in the Norfolk Island isolate. *Molecular Vision* 23:660-665, Sept.2017.
4. Pollock, C.E., Sutherland, H.G., Naher, B.H., Lea, R.A., Haupt, L.M., Frith, A., MacGregor, A.E. and Griffiths L.R. (2018) The NRP1 migraine risk variant shows evidence of association with menstrual migraine. *J Headache Pain* Apr 18;19(1):31. doi: 10.1186/s10194-018-0857-z.
5. Kenenedy D.W., White, N.M., Benton, M.C., Fox, A., Scott, R.J., Griffiths, L.R., Mengersen, K. and Lea, R.A. (2018) Critical evaluation of linear regression models for cell-subtype specific methylation signal from mixed blood cell DNA. *PLoS One* 13(12):e0208915. doi: 10.1371/journal.pone.0208915.
6. Maksemous, N., Smith, R.A., Sutherland, H.G., Sampaio, H. and Griffiths, L.R. (2018) Whole-Exome Sequencing Implicates SCN2A in Episodic Ataxia, but Multiple Ion Channel Variants May Contribute to Pheotype Complexity. *Int J Mol Sci* 19(10) pii:E3113. doi: 10.3390/ijms19103113.