



PETER WILLS BIOINFORMATICS CENTRE

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The sequencing of the human and other genomes has spawned many technologies that use genome-sequence information to change the way biologists work. Where previously it was possible to only query factors like the expression level of a single gene in an experiment; genome-wide microarrays have made it possible to get the expression levels of all the genes in an organism. These advances have not been limited to expression. Neither have they been limited to microarrays, with high-throughput sequencing methods and microarrays allowing us to probe the genome to identify alternate splicing of genes, the identification of transcription-factor binding sites, miRNA expression, DNA modification and so on. This unprecedented genome information has challenged many well-established beliefs, and the pervasive expression of genomes has raised questions of how genomes are regulated, and even required us to change our definition of a gene.

The Peter Wills Bioinformatics Centre is interested in understanding fundamental biological questions such as these, and applies numerical and computational methods to large data-generating technologies such as microarrays and high-throughput sequencing. While some of our work can be regarded as purely bioinformatic – we are much more interested in setting up collaborations with experimental biologists and applying our expertise to a specific area of research.

Project: The application of bioinformatics methods to complex disease

In association with an experimental medical researcher in any of the Garvan's research programs we would like to jointly supervise a student. While the student may spend some time doing experimental work - primarily the student will be involved in the development and application of bioinformatics methods to the problem at hand.