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Genomics Sequencing

The Capability

Genomics is a field of molecular biology that focusing on the function and interaction of genes (and proteins) within plant and animal cells.  The genome refers to the complete set of genetic material within an organism and where genetics focuses on the makeup and activity of a single gene, genomics is a genome-wide approach to studying these interactions.

Capillary-Electrophoresis (Sanger) sequencing is widely adopted in laboratories around the world as a standard for DNA analysis. Important advances in this field has led to the development of next generation sequencing (NGS) which extends the DNA analyses across millions of reactions in a massively parallel fashion. This enables rapid sequencing of large stretches of DNA spanning entire genomes in a single sequencing run. With unlimited dynamic range and high sensitivity, it is also used for quantitative applications such as gene expression analysis. The scope of data output resulting from these analyses requires bioinformatics tools and specialised software programs.

The University Platforms

[Melbourne Translational Genomics Platform](http://agd.path.unimelb.edu.au/electrophoresis-only/index.html) located at the Centre for Translational Pathology, leverages a number of different Sanger sequencing and NGS capabilities as well as bioinformatics access for clinical and basic research. The platform is NATA-accredited for Sanger sequencing, and is Australia’s first facility to be NATA-accredited for NGS.

The Platform also operates a PacBio RS II system, housed in the Department of Microbiology and Immunology. The sequencing system is a long-range sequencer based on single-molecule, real-time (SMRT) technology. It is designed for applications in de novo assembly, characterisation of genetic variation, methylation analysis and microbiology studies.

* **Sanger Sequencing**

MGTP has 16- and 48-capillary (pictured above) ABI genetic analysers and offers fee-for service sequencing and genotyping.

* **Next Generation Sequencing**

Illumina HiSeq2500 (pictured above) and MiSeq leverages massively parallel sequencing technology for whole genome, transcriptome and exome analysis.

Importantly, the Genomics Platform personnel have considerable expertise in genomic and genetic analysis, clinical and research sample processing and bioinformatics, and can provide training on all available technologies.

The Melbourne Translation Genomics Platform provides open access to all researchers on a fee-for-service basis.

Enquiries

Rachel Ramsdale

Phone

[+61 3 9035 3636](tel:0061390359602)

Email

[rachel.ramsdale@unimelb.edu.au](mailto:rachel.ramsdale@unimelb.edu.au?subject=Research%20Infrastructure%20Capabilities%20Enquiry)

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