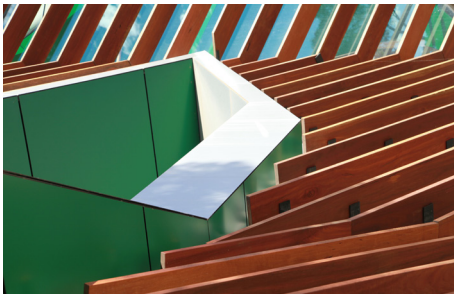




Bioinformatics for high throughput sequencing. The John Curtin School of Medical Research & Research School of Biology workshop

Monday 3 December 2012 12.45 - 5.30pm

The John Curtin School of Medical Research seminar rooms 1 & 2



This half day workshop is an introduction to bioinformatic analysis of high throughput sequencing. The various sequencing techniques, the type of data that they produce and mainstream applications will be described. The workshop will also include the areas of service offered by the ANU Genome Discovery Unit (GDU).

Audience All researchers aiming to write grants that include bioinformatics in 2013. Postdocs and lab leaders who would like to know more about high throughput sequencing techniques, their applications and the sequencing and bioinformatic services offered by the BRF and GDU respectively. Graduate and postgraduate students who are planning to use next generation sequencing in their research.

Schedule

	Speaker	Presentation
12.45pm	Gavin Huttley	Opening Remarks
1.00pm	Torsten Seemann	Introduction to next generation sequencing (NGS)
1.30pm	Aaron Chuah	Variant discovery
1.45pm	Justin Borevitz	Genotyping By Sequencing
2.00pm	Norman Warthmann	Current Generation Genetic Mapping
2.15pm	Jason Bragg	Population phylogenomics
2.30pm	Break	Courtyard discussion mediated by Gavin Huttley
3.00pm	Torsten Seemann	De novo assembly
3.15pm	Hardip Patel	RNA-Seq (transcriptome sequencing)
3.30pm	Cameron Jack	ChIP-Seq
3.45pm	Sylvain Forêt	Bisulfite sequencing
4.00pm	Peter Milburn	BRF library and sequencing services and outlook
4.15pm	Gavin Huttley	Closing remarks
4.30pm	End	Discussion / happy hour

Presented by

Research School of
Biology

The John Curtin School of
Medical Research

ANU College of

Medicine, Biology
& Environment