Life science is fast becoming a data science. We’re here to help.

EXPERT ADVICE
- high end computing – in-house or in the Cloud
- experimental design
- grant writing
- data analysis, management and curation
- project management and collaboration
- open science – where and how to publish your data for maximum exposure
- all life sciences: agricultural, health, ecological

TRAINING
- Hands-on workshops, interactive webinars, online tutorials including:
  - Unix for beginners
  - high performance computing for life scientists
  - using the Genomics Virtual Laboratory
  - variant calling
  - RNA-Seq data analysis
  - open source science with Git and GitHub
  - bioinformatics best practices

COLLABORATIONS
- partner with our platform development and research infrastructure experts
- connect with the international partners of the EMBL Australia Bioinformatics Resource that we host
- access Australia’s bioinformatics resources via the EMBL-ABR: Melbourne Bioinformatics Node
- communicate with 700+ subscribers to our mailing list

EMBL-ABR is hosted at Melbourne Bioinformatics through a funding agreement between the University of Melbourne and Bioplatforms Australia.

@MelBioInf
melbournebioinformatics.org.au
Our team of over 30 research scientists and bioinformaticians have published more than 200 papers and written numerous popular tools that are currently used around the world.

Microbial Genomics
Lead: Torsten Seemann

Torsten’s “Ten recommendations for creating usable bioinformatics command line software” was Gigascience’s most downloaded paper in 2016, Prokka, the rapid prokaryotic genome annotation tool, has been cited more than 800 times.

The Microbial Genomics Group is contributing to the worldwide implementation of next generation sequencing technologies as the new “gold standard” in public health. International partnerships are growing the demand to adopt the Australian-made Genomics Virtual Laboratory as a training and research tool.

Human Genomics
Leads: Bernard Pope & Daniel Park

Leading the Australian bioinformatics component of the Pan Prostate Cancer Consortium, the group is working to apply standardised analysis pipelines to the largest and highest-quality collection of prostate cancer samples ever assembled.

As part of the Australian Genomics Health Alliance, the group is curating the registry of clinical pipelines to develop a standard vocabulary for pipeline comparison and improvement. The newly developed clinical-grade variant calling pipeline and variant curation database for Melbourne Genomics has been deployed around Victoria.

“Our partnership with Melbourne Bioinformatics is a key driver behind our program to bring the full power of genomics to Australian public and clinical microbiology laboratories. Melbourne Bioinformatics is critical to our efforts by providing accessible software tools and analysis platforms to interrogate the genome data in a framework that can then be deployed across Australia, and potentially across the globe for the benefit of all.”

Prof Tim Stinear
Scientific Director, Doherty Applied Microbial Genomics
Doherty Institute, University of Melbourne