Computational Biology Facility

Specialist computing expertise to help organisations make sense of large datasets produced by omics technology and gain new insights into complex biological systems.

Analytical technologies in life science research increasingly produce large and complex datasets that are used to shed light on the most pressing biological questions and find solutions to medical and industrial challenges.

Interpreting and manipulating large datasets is an extremely specialised task, which often can’t be handled by individual researchers or in-house computational resources.

Our scientists, analysts and engineers have extensive experience of working with large datasets within a multi-omics environment, and offer a range of standard and bespoke consultancy services to help organisations make the most of emerging omics techniques.

We provide the computational expertise needed to analyse and interpret large datasets, as well as flexible and cost-effective access to IT resources, and commercial and open source software pipelines. We can also train your investigators to carry out a range of computational biology techniques, enhancing your in-house knowledge base and adding extra value to our consultancy services.

Our services

- Study design and power analysis
- Identification and analysis of suitable public domain omics datasets
- Data processing
- Data analysis
- Advanced statistical modelling for pathway analysis and biomarker discovery
- Advanced multi-omics dataset integration
- Custom bioinformatics pipelines, databases and software development
- Training in Computational and Systems Biology.
Case study

Novel software approach improves understanding of genomes

Challenge: Next generation sequencing technology has revolutionised the field of genomics by significantly speeding up the process of reading the sequence of DNA bases in a genome. However, while sequencing DNA has become much quicker, identifying the parts of the genome sequence (the genes) that code for proteins, the workhorse molecules of the cell that determine its nature and function, is still a relatively slow process and a significant bottleneck to discovery.

Solution: A team from the Computational Biology Facility, headed by Professor Andy Jones, developed a novel software package called ProteoAnnotator to address this issue. By combining a number of existing software modules, along with some new ones developed by the group, they use algorithms to predict sites of potential coding DNA sequence and then identify those that code for proteins using data directly observed in proteomics experiments. This allows faster and more confident identification of protein-coding DNA and, once incorporated into a genome sequence database, helps to produce an annotated DNA sequence that can be used in a wide variety of research contexts.

Impact: The group validated ProteoAnnotator by using it to refine the annotation of the genome from the parasite *Toxoplasma gondii*. They showed that by applying ProteoAnnotator they could demonstrate strong evidence for a large number of genes to be protein-coded, and could refine a number of genes that had been incorrectly annotated in the genome database, thus providing an improved resource for research scientists working on this important parasite.

Contact Us

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Why work with us?

• **Proven track record:** Highly experienced Computational Biologists with the expertise to analyse, interpret and predict large datasets.

• **Integrated multi-omics approach:** As part of the Technology Directorate, we are skilled at developing mathematical and computational approaches that draw on metabolomics, genomics, transcriptomics and proteomics to provide a broader understanding of biological systems.

• **Wide-ranging applications:** Experience across a range of techniques applicable to pharma and biotechs, toxicology, agriculture, personal care and many other sectors.

• **Flexible consultancy:** we can manage a project for you from study design to data interpretation, or train your investigators to use our facilities.

The Computational Biology Facility is a Shared Research Facility, managed by the University of Liverpool’s Technology Directorate, which aims to give the wider scientific community access to enabling technology and the academic expertise that supports it.

www.liverpool.ac.uk/technology-directorate