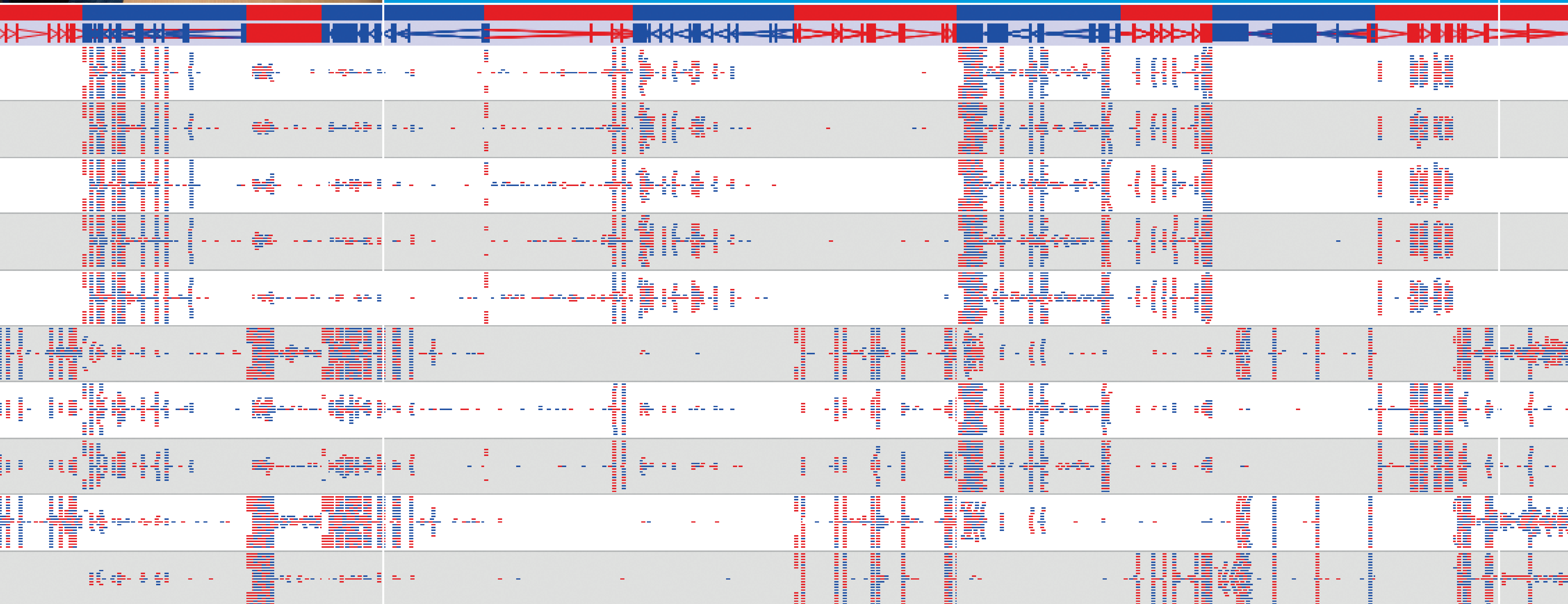


Bioinformatics Facility



The Babraham Bioinformatics Facility can support all your computational biology requirements. The team is composed of experienced bioinformaticians and statisticians, all of whom have a biological background. The Facility is happy to provide advice or practical assistance on how to apply computational methods to extract biological meaning from your data.



Bioinformatics Services

- Our experienced bioinformaticians can offer advice or practical assistance in the processing and analysis of a wide variety of different types of biological data.
- We have extensive experience of analysing high-throughput sequencing data including RNA-Seq, ChIP-Seq, Hi-C and many epigenetic sequencing techniques, both on bulk and single cell data.
- We can develop custom applications or pipelines to meet your specific requirements. Our range of publicly available software is used by bioinformaticians worldwide and we can bring our experience to your projects.

Training

- We offer a wide variety of practical bioinformatics and statistics training courses taught by experienced bioinformaticians.
- Our modular courses can be tailored to your needs at a convenient venue, alternatively delegates may attend the series of courses run at the Babraham Institute.

Statistics

- We can provide the assistance of an experienced bio-statistician to help with experimental design, data analysis or grant applications.

Infrastructure

- We can provide access to a large bioinformatics compute cluster to allow you to run large computationally demanding workflows.
- We can assist with the design and implementation of data management and processing infrastructure for your own pipelines.