

# Bioinformatics Services

Bioinformatics addresses the challenges of analysing, storing and interpreting biological data with a range of computational and statistical techniques. This can involve analysing DNA and protein sequences, gene expression patterns, interaction and regulatory networks, protein structure prediction and a host of other applications.

## Hardware resources

Currently we have a 55-core high-performance Linux computing cluster with 136GB RAM and 10TB dedicated storage and using Platform LSF software for job management. This can facilitate a wide range of computationally intensive applications including sequence assembly and annotation and gene expression analysis.

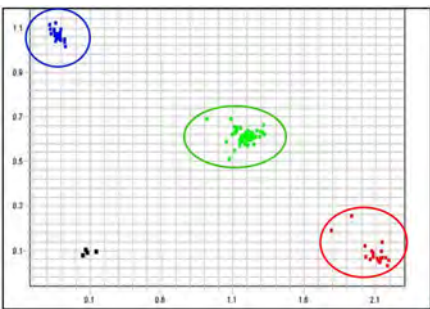
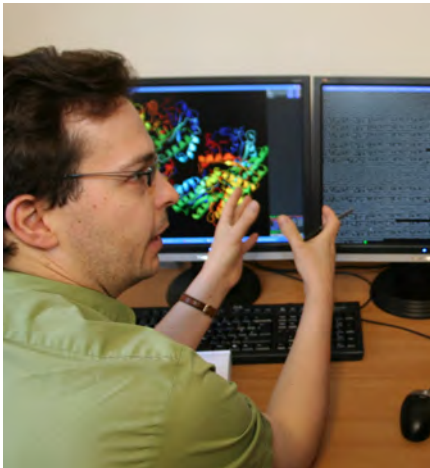
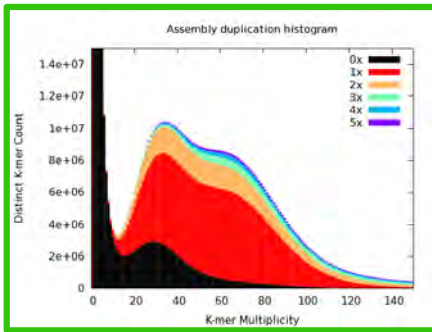
## Bioinformatics

Our main bioinformatics efforts are currently in sequencing, assembly and annotation of the rubber tree genome and in comparative studies of the rubber tree and related species.

## Main areas of expertise

- *De Novo* sequence assembly from next generation platforms and Sanger sequencing
- Functional annotation of genomic sequence
- Gene and protein sequence analysis
- Data curation
- RNA-seq and transcriptome analysis
- SNP marker selection
- Characterisation of target genes and gene families of interest

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