Josep Carreras LEUKAEMIA Research Institute

Bioinformatics Unit: Analysis Services

The unit provides data processing and analysis for genomic, epigenomic and transcriptomic data from microarrays and high-throughput sequencing

Microarrays

Genome

SNV panels
- QC, Variant calling
- Custom genotype clustering

Epigenome

DNA methylation (450K, EPIC)
- QC, Normalization
- Methylation calling (beta/M values)
- Clustering
- Differential methylation (DM/DMR)
- Gene + regulatory elements association

Transcriptome

Gene expression arrays
- QC, Normalization
- Quantification
- Clustering
- Differential expression
- Gene set enrichment analysis

microRNA arrays
- QC, Normalization
- Quantification
- Clustering
- Differential expression
- Target prediction
- Correlation miRNA-gene expression

High-throughput sequencing

Genome

Whole Genome Sequencing (WGS)
- Exome sequencing
- QC, Alignment
- Variant calling

Epigenome

ChIP-seq, ATAC-seq, DNAse-seq
- QC, Alignment
- Peak calling
- Differential binding
- Functional analysis

Whole Genome Bisulfite Sequencing (WGBS), Reduced Representation Analysis Bisulfite sequencing (RRBS)
- QC, Mapping
- Methylation calling
- Variant calling
- Differential analysis (DMR/ methylome segmentation)
- Functional annotation

Transcriptome

RNAseq (poly +/-, total)
- QC, mapping
- Quantification
- Alternative splicing
- Clustering
- Differential expression
- Gene set enrichment analysis

Other services:

- ❑ Consultancy
  - Experimental Design
  - Statistical advice
  - Recommendation analysis workflows and tools
- ❑ Training
  - Internships
  - Seminars
  - Workshops

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