



BIOINFORMATICS AND BIOSTATISTICS UNIT

DESCRIPTION OF THE UNIT

"Our mission is to promote and execute high quality translational research offering both methodological and analytical support".

The unit is mainly dedicated to analysing data from omics experiments, but also actively collaborates in different research projects, providing advice and support to researchers in the design, workflow implementation and analysis of experiments.

RESEARCH AND DEVELOPMENT SERVICES

Bioinformatics services:

- Analysis of gene panels, exomes and genomes ((SNVs, indels, CNVs) in both germline and somatic samples.
- Design and validation of gene panels.
- "De novo" assembly of small genomes.
- "De novo" assembly of transcriptiomes.
- RNA-Seq data analysis (gene and isoform quantification.
- RNA-Seq data analysis (gene and isoform quantification, differential expression analysis, variant identification, fusion genes).
- Functional enrichment analysis (identification of biological functions, cellular components or molecular functions with gene ontology terms, identification of altered metabolic pathways or related diseases).
- Microarray data analysis (both expression and methylation arrays).
- Complex network data integration, analysis and visualization.

innovacion@incliva.esBiostatistics services:

- Design of clinical and epidemiological studies
- Sample size estimation
- Simulation techniques
- Supervised and unsupervised analysis techniques
- Predictive modelling

Computing and storage services:

- Access to high performance computing (HPC) infrastructure.
- Data storage.
- Deployment, management and maintenance of computing infrastructure owned by our research groups in our data centre.

Additional Services:

- Advice and methodological support to write protocols, research project proposals, articles, doctoral/MSc/BSc thesis.
- Data mining and exploratory analysis of public databases
- Graphical representation of research results.
- Curation and analysis of databases.
- Training on demand and consulting.

UNIT RESOURCES

- Computing facility with 240 cores.
- 1TB of RAM memory, 100TB of redundant network storage and 20TB of fast non redundant storage local to the nodes for high I/O processes like short read alignments or variant calling from BAM files.

COLABORATION SOUGHT

Scientific services by contract research.

CONTACT

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