fios
GENOMICS
ANALYSE - INTERPRET - INTEGRATE

At Fios Genomics we can process and statistically analyse data to pathway level following our proprietary analysis approaches, FGEz and FGEx.

FGEz and FGEx are differential expression and pathway enrichment analyses and are applicable to different areas:

- Genomics
- Transcriptomics
- Epigenetics
- Proteomics & metabolomics
- NGS and mass spectometry data

Data QC as a single dataset, to identify and remove any poor or outlier samples as this may impact negatively on the outcome of the hypothesis testing. Includes analysis of confounding within experimental design.

Assessment of genes, proteins, metabolites, or sites of interest within the dataset for finding significance or profiling across the sample groups.

Gene Ontology (GO) term/Reactome pathway enrichment analyses which involves the identification of over-presented GO terms/Reactome pathways in the chosen subset of significant genes. This approach is useful in that it provides a general insight into perturbed pathways or processes in the comparisons of interest.

Pathway/Network analyses which facilitate the identification of coordinated gene expression. When this approach is combined with statistics, it can identify groups of genes exhibiting similar expression profiles in the various sample groups.

OUR WORKFLOW

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