SERVICES

We provide computational analyses, tailored solutions and support for all aspects of biomedical data. Whether you are interested in biomarker discovery, looking for a way to manage and share your data more efficiently or preparing your next research proposal or manuscript..

Data analysis

We process and analyze data from various Omics domains and technologies (microarrays, sequencing) for humans and most common model organisms. All our analyses include quality control, read alignment (sequencing) or signal transformation (microarrays) and data preprocessing (filtering, normalization).

Genomics

The analysis of the genome (DNA) enables the identification of mutations and genetic variations associated to disease and is important, for example, for personalized treatments. For cancer research this is crucial to identify driver mutations (mutated genes that accelerate tumor genesis) and understand tumor evolution (clonality analysis).

We analyze data from Whole Genome and Exome sequencing (WGS/WES), targeted sequencing, SNP panels and genotyping microarrays.

Our analyses:

* Variant analysis (SNP, indels, copy number variation, structural variations)
* Variant annotation (predict effect on gene expression or protein function, clinical relevance)

Transcriptomics

Studying the ‘read out of the genome’, the cell’s transcriptome (RNA) allows to identify genes and pathways that are involved in specific diseases, conditions or responses to treatments. At the single cell level that can provide insight into rare cell populations and cellular trajectories. At the transcript level it allows insight into RNA diversity and cellular processes/mechanisms that in turn may vary across cell types and individuals.

We analyze data from expression microarrays (miRNA, mRNA) and various types of RNA sequencing protocols (small RNAseq, mRNA seq and single cell RNA-seq).

Our analysis:

* Gene quantification and annotation (RNA types and abundance)
* Target prediction (miRNA)
* Cluster analysis and dimensional reduction (k-means, PCA, MDS, tSNE )
* Differential expression analysis
* Pathway analysis of differentially expressed genes (up/downregulated)
* Alternative splicing, transcriptomic diversity
* Detection of fusion genes
* Variant calling (RNA editing)
* Cell type deconvolution (bulk mRNA-seq)

Epigenomics

Epigenomic modifications are modifications that affect the genome without modifying the underlying DNA sequence. These can be chemical modifications such as DNA methylation (= addition of a methyl group the 5th C of the cytosine base) or proteins (and their modifications) binding to the DNA that affect the DNA structural properties (packaging, 3D structure), for example. Ultimately, epigenomic modifications are thought to affect the DNA’s transcriptional potential (chromatin state), or in other words, regulate gene expression.

Epigenomic modifcations are used as biomarkers and provide insight into biological mechansim and processed.

DNA methylation

We analyse DNA methylation mainly from the Illumina Infinium beadchip microarray (human, mouse), but also from sequenced based technologies such as whole genome bisulfite sequencing, reduced representation bisulfite sequencing and bisulfite free tequnologies such as enzymatic Methyl-seq.

Our analysis:

* Differential methylation analysis
* Functional annotation of differential methylated CpGs and differentially methylated regions (associated genes, overlapping regulatory elements, CGI context)
* Identification of different types of methylation regions: unmethylated regions (UMRs), hypermethylated regions (UMRs), partially methylated domains (PMDs)
* Cell type deconvolution
* Age prediction
* CNV prediction

Chromatin

We process mainly sequencing data from Chromatin Immunopreciptation (CHIP-seq) to study protein binding (histones, transcription factors) and Assay for Transposase-Accessible Chromatin (ATAC-seq) to identify open chromatin regions.

Our analysis:

* Peak calling
* Functional annotation peaks (genes, regulatory)
* Motif analysis
* Differential analysis

Epitranscritomics

Similarly to epigenomic modifications, epitranscriptomic modification are modifications to the transcriptome that do not alter the underlying RNA sequence. Studying these modification allows insight into RNA bioilogy, cellular processes and mechanism the can be important in disease.

We mainly process data from .. (iCLIP) for the study RNA binding proteins

Our analysis:

* Peak calling
* Functional annotation peaks (RNA biotype, genes, gene region)
* Motif analysis
* Differential analysis

Tailored solutions

* Bioinformatic pipeline development/ workflow design
* Custom data management solutions (data bases, dashboards, web application)
* Data mining public databases -> hypothesis generation (or validation)

Support

* Consultancy, trainings, workflow design, visualization, manuscript preperation

Questions

Marker discovery (mechanisms) -> drug targets

Patient classification (cancer subtypes, demographics, personalized, treatments, treatment response) -> treatment impoval

Functional annotation