HKU Med
LKS Faculty of Medicine
Centre for PanorOmic Sciences
香港大學泛組學科研中心

BIOINFORMATICS CORE

"Unlocking insights together:
We are your trusted Bioinformatics Partner."



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ABOUT US

At the CPOS Bioinformatics Core, our team of dedicated bioinformaticians specialises in delivering both standardised and customised data analysis solutions, along with user-friendly commercial software for self-analysis purposes. We offer comprehensive consultations on experimental design and analysis methodologies, specifically tailored to accommodate a diverse range of next-generation sequencing technologies across various omics applications, such as genomics, transcriptomics, methylation studies, and more. Furthermore, we are committed to empowering investigators by sharing our knowledge and expertise through hands-on training sessions and engaging workshops, ultimately enabling them to confidently conduct their own data analysis.



Standard Analysis Service



Custom Analysis Service



Self-Analysis Support (Single Cell)



Project Design and Analysis Consultation



Manuscript Preparation

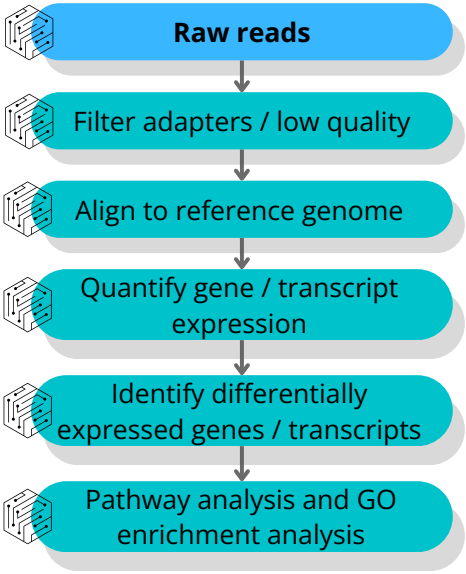
TRANSCRIPTOMICS ANALYSES

mRNA Sequencing

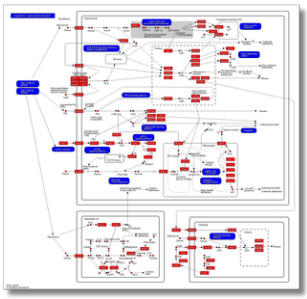
Overview

mRNA sequencing is a technique for quantifying gene and transcript expression levels, and identifying differentially expressed genes and transcripts. Our core provides commercial software for downstream KEGG pathway analysis and Gene Ontology enrichment analysis. Apart from human and mouse, we also have extensive experience in analysing with other species, such as golden hamster, zebrafish, bacteria, and more.

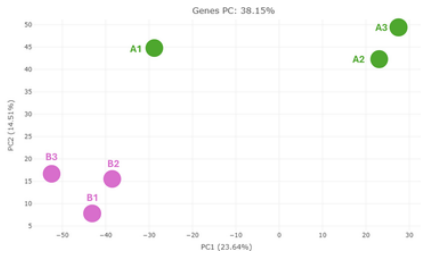
Workflow



Deliverables



Pathway analysis with KEGG database



PCA plot

<u>Standard deliverables</u>

- Gene / transcript expression level file
- List of differentially expressed genes / transcripts
- PCA plot

<u>Custom services</u>

- Custom references
- SNP / INDEL calling and annotation
- Alternative splicing analysis
- Fusion gene detection
- Novel exon prediction
- Visualisation plots such as volcano plot, heatmap and more

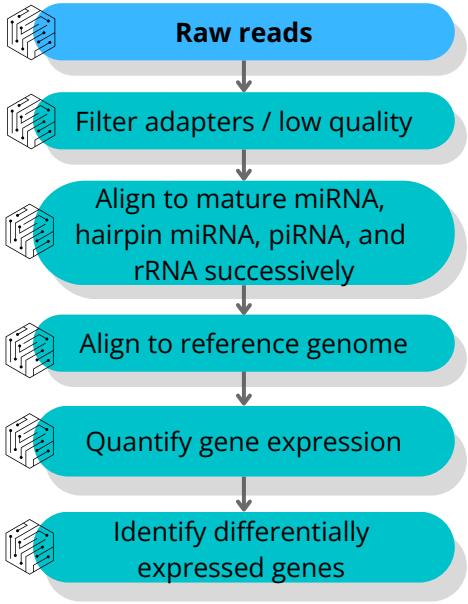
TRANSCRIPTOMICS ANALYSES

miRNA Sequencing

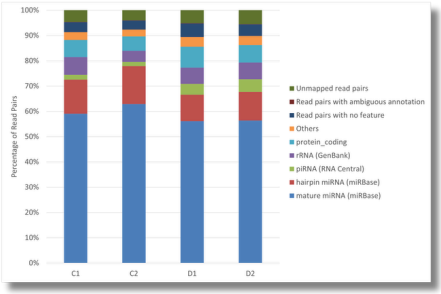
Overview

miRNA sequencing is a technique for identifying and profiling miRNAs, which are small non-coding RNA molecules and essential regulators of gene expression that interact with target mRNAs to inhibit translation or promote degradation. Our analysis service assists researchers in detecting miRNAs, quantifying expression levels, and comparing expression patterns across sample groups, thereby facilitating the investigation of miRNA functions in diverse biological processes. We support analysis for human and mouse.

Workflow



Deliverables



Distribution of reads for different gene biotypes

<u>Standard deliverables</u>

- miRNA expression level file
- List of differentially expressed miRNA

<u>Custom services</u>

- Target prediction
- Novel miRNA prediction
- Expression quantification of other known RNAs

GENOMICS ANALYSES

Human Whole Genome and Whole Exome Sequencing

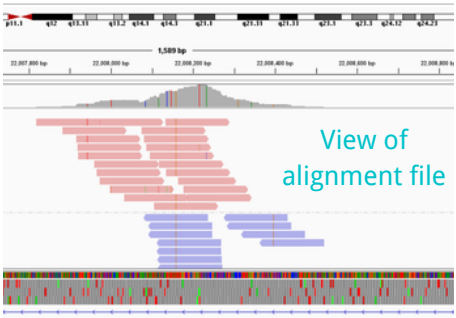
Overview

Human whole genome sequencing (WGS) and whole exome sequencing (WES) are two powerful genomic technologies that have revolutionised scientific and medical research. WGS captures an individual's complete genetic code, including both coding and non-coding regions, while WES selectively targets and sequences only the protein-coding regions of the genome. These techniques utilise high-throughput sequencing technologies to generate vast amounts of genetic data, providing valuable insights into the genetic basis of various phenotypes.

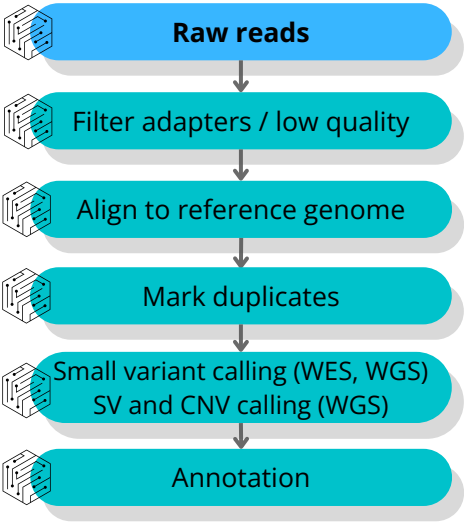
Bioinformatics Tool

Illumina DRAGEN Bio-IT Platform





Workflow



Deliverables

Standard deliverables

WGS & WES:

- Alignment files
- SNP / INDEL files
- List of annotated SNP / INDEL files

WGS Only:

- CNV / SV files
- List of annotated CNV / SV files

Custom services

WGS & WES:

- Somatic SNP / INDEL calling
- Somatic SNP / INDEL annotation

WES Only:

- Custom exome panels
- CNV analysis (with Panel of Normal)

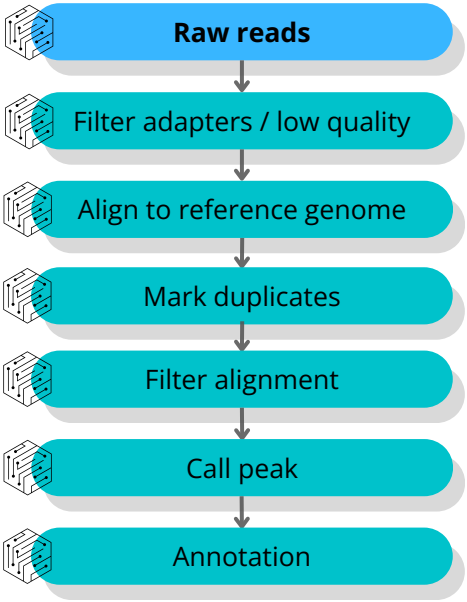
EPIGENOMICS ANALYSES

ChIP Sequencing

Overview

ChIP sequencing is a technique for identifying and profiling protein-DNA interactions, which play a crucial role in regulating gene expression and shaping cellular processes. Our analysis service assists researchers in detecting binding sites of transcription factors and histone modifications, quantifying enrichment levels, and comparing binding patterns across sample groups. This enables the investigation of protein-DNA interactions and their functions in various biological processes. We provide analysis support for human and mouse, as well as other species upon request.

Workflow



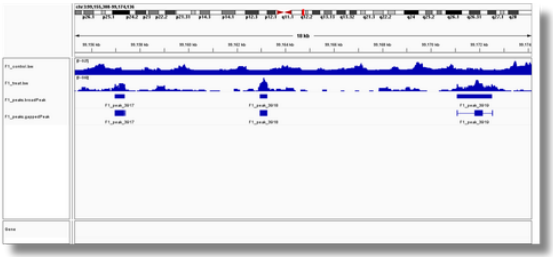
Deliverables

Standard deliverables

- Alignment files
- List of peaks
- List of annotated peaks
- BigWig files

Custom services

- Custom references
- Visualisation plots such as read signals



View of peak signals

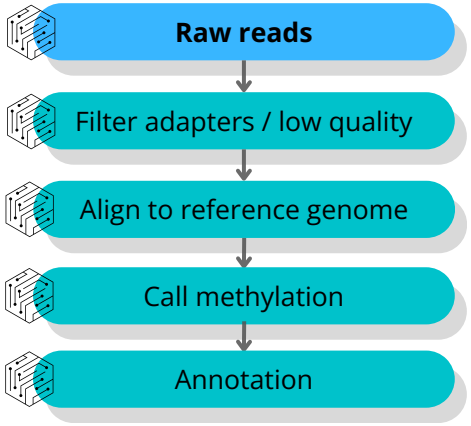
EPIGENOMICS ANALYSES

Bisulfite Sequencing

Overview

Bisulfite sequencing is a technique which provides researchers with the quantification of methylated cytosine in their samples. It is done by an additional bisulfite treatment step during library preparation. Our bisulfite sequencing analysis service includes analysing data from whole genome bisulfite sequencing (WGBS) and from reduced-representation bisulfite sequencing (RRBS). With our standard analysis, researchers can obtain the methylation landscape in their samples.

Workflow



Deliverables

Standard deliverables

- Alignment files
- List of annotated CpG methylation sites
- Bisulfite conversion rate of Lambda (if applicable)

Custom service

- Custom references

METAGENOMICS ANALYSIS

16S Amplicon

Overview

16S amplicon sequencing is a technique for identifying and profiling microbial communities by targeting the 16S ribosomal RNA gene, which is highly conserved among bacteria and archaea. Our analysis service aids researchers in detecting and characterising microbial populations, quantifying their relative abundance, and comparing community structures across sample groups. This facilitates the investigation of microbial diversity, ecology, and function in various biological and environmental contexts.

Deliverables

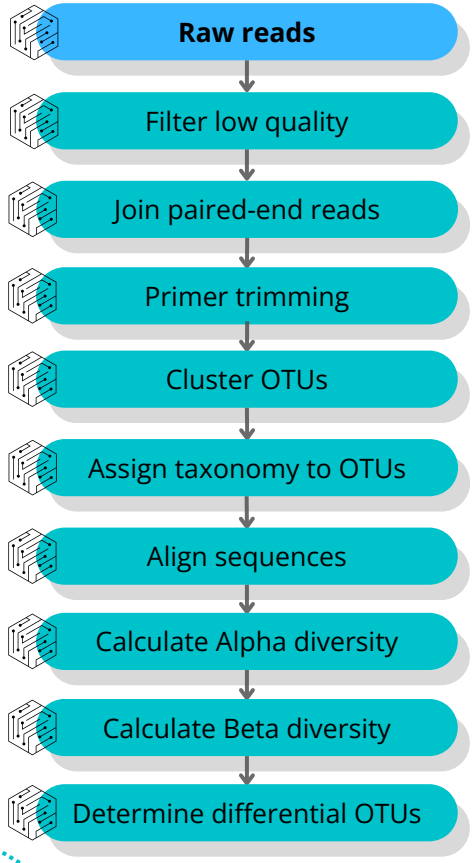
Standard deliverables

- OTU table
- Taxonomy summary
- Results of Alpha diversity
- Results of Beta diversity
- List of differential OTUs

Custom services

- Hierarchical clustering
- Linear discriminant analysis (LDA) effect size

Workflow



SELF-ANALYSIS SUPPORT

Partek Flow for single cell RNA analysis

Overview

Single cell RNA sequencing is a technique for identifying gene expression patterns at the single cell level. It can also engage with multiomic capabilities such as cell surface protein, and TCR / BCR sequencing.

Our core provides self-analysis option for single cell data with Partek Flow platform, which users can analyse single cell data without writing any codes.

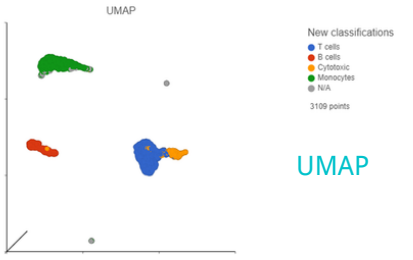
Featured Partek Flow functions:

- Single cell data QA/QC
- Expression normalisation
- Dimension Reduction: PCA, UMAP
- Biomarker detection
- Cell clustering
- Cell type annotation
- Differential expression
- Pathway enrichment

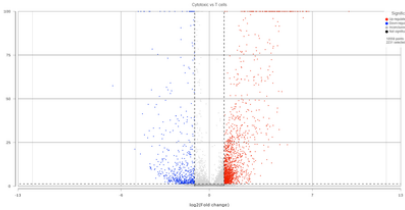
Supported 10X single cell data types:

- Gene Expression, VDJ, Feature Barcode, Flex, Visium, etc.

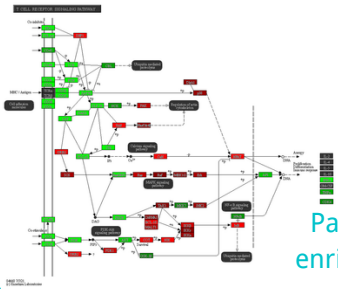
Interactive visualization



UMAP

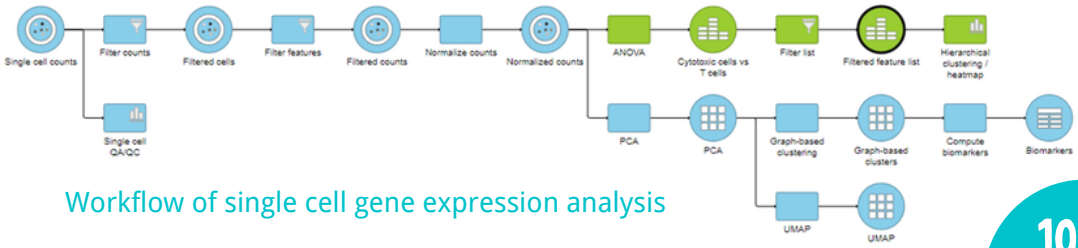


Volcano plot



Pathway enrichment

Point-and-click interface



Workflow of single cell gene expression analysis

EDUCATION & TRAINING

We are proud to present our interactive workshops, designed to empower researchers with the knowledge and skills needed to efficiently perform their own data analysis.



INTRODUCTION TO LINUX AND HPCF

HIGH PERFORMANCE COMPUTING FACILITY

COMMAND LINE INTERFACE

PORTABLE BATCH SYSTEM

SSH & SFTP

BASH SCRIPTING

INTRODUCTION TO PYTHON

LISTS, DICTIONARY AND LOOPS

FUNCTIONS AND METHODS

CONDITIONAL STATEMENTS

REGULAR EXPRESSION

PYTHON MODULES





INTRODUCTION TO R

GRAMMAR OF GRAPHICS

DATA MANIPULATION

RSTUDIO

VECTORS AND DATA FRAMES

GGPLOT2

HANDS-ON WORKSHOP SINGLE CELL DATA ANALYSIS

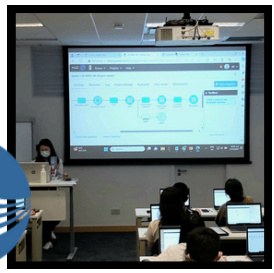
PARTEK FLOW

POINT-AND-CLICK

SINGLE-CELL DATA QC

CELL CLASSIFICATION

VISUALIZATION WITH INTERACTIVE DATA VIEWER



RESEARCH PUBLICATION SUPPORT

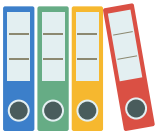
We offer research publication support exclusive for CPOS-analysed data, encompassing services such as, method description preparation, generation of high-quality publication-level plots and data submission to GEO. Our team ensures that your research is accurately and effectively communicated while making valuable contributions to the scientific community.











We appreciate your acknowledgement of CPOS in your publications with data and analysis generated at our Centre. Proper recognition documents the impact of our work and helps justify the continuation of subsidised services.

CONTACT US

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2185-5055



Please note that all analyses mentioned in this promotional material are applicable to specific sequencing platform only. Kindly contact us for details. Additionally, the listed analysis deliverables may be subject to updates, and we reserve the right to make the final decision.