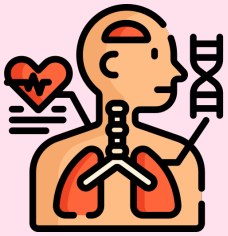
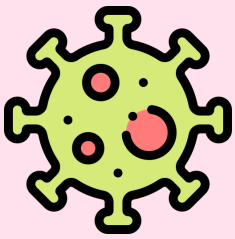
BioMavericks®

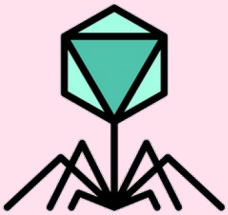
Data Solutions

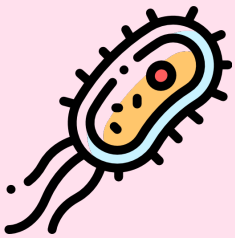
Diagnosis

Therapy









Research

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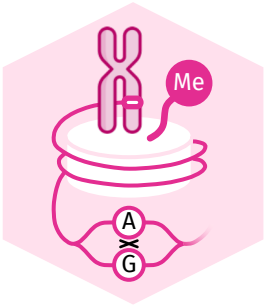
Linking Data to Insights

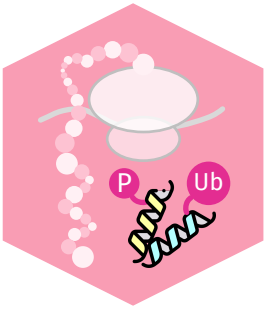


Genome: What could happen

Determining the genomic sequence provides functional clues of the numerous genes across different species. Generally, DNA elements in the genome works with other processes such as histone modification to keep an organism running. Therefore, decoding the DNA is the first step towards understanding the complex mechanism in humans.

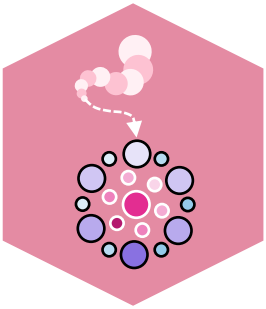
Transcriptome: What is happening

The complete set of RNA (aka. transcriptome) provides a snapshot of what appears to be happening in an organism. Upon splicing, mRNA carries information to the ribosome that gives rise to protein, and non-coding RNA regulates the process. Transcriptome analysis helps reveal gene expression & regulation in genetic variabilities.



Proteome: What makes it happen

Proteins change rapidly in response to environmental stimuli. It is vital to know what they modify and interact with, and how they contribute to life processes. Proteomics analysis helps address these questions by mapping protein networks and modifications involved in defence reactions.



Metabolome: What has happened

Metabolites are small molecules acting as substrates or end products of cellular metabolism. Comprehensive analysis of metabolites (aka. metabolomics) helps determine differences between a healthy and diseased organism, revealing key phenotypic information that other 'omics' approaches are not able to convey.

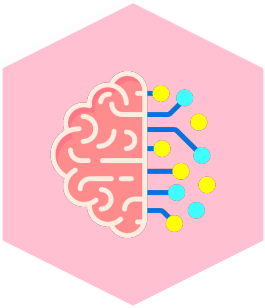
Our Solutions

Going beyond routine bioinformatic analysis

Our bespoke data solutions will help you address key questions of interest, from genomic mutations to cytotoxic metabolites. Through careful interpretation of your data, we will present you with in-depth analytical reports that help your project progress smoothly.

Leveraging the power of machine learning

Artificial intelligence (AI) is a powerful tool to help you achieve your goals efficiently; and it is crucial to have easy-to-understand AI outputs for scientists and clinicians. At BioMavericks, we leverage machine learning to not only classify your samples or predict traits but also highlight critical implications for your future projects.



Bringing your data to a whole new level

Following data analysis, we will guide you through each step of your experiments, filling in the gap between biomedical research and bioinformatics. Validation will provide extra information to your project, covering both proof-of-principle (e.g., IHC, etc.) & functional investigations (e.g., KO, etc.), depending on your specific needs.

Paving your way to clinical applications

We will work in partnership with you and help you achieve a variety of clinical applications, ranging from early diagnosis of diseases to cell & gene therapies. Therefore, our data solutions shine not just in bioinformatic analysis but also in pre-clinical research.

DNA Analysis

Genomic DNA Sequencing

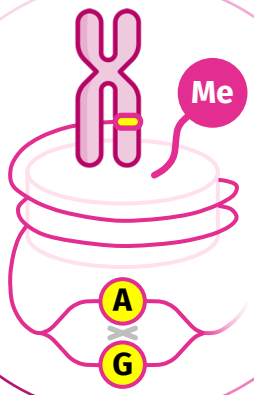
Analysing genomic sequence reveals not only polymorphism but driver mutations in both coding and non-coding regions. We will help you investigate all types of genomic alterations in your data that can be used as molecular signatures.

- **Germline/somatic mutations (e.g., new-born & paediatric diseases)**
- **Copy number variations & eQTLs (e.g., rare cancers)**
- **Gene/viral fusion discovery (e.g., carcinogenesis)**

Chromatin Accessibility

Mapping accessible chromatin via ATAC-seq provides a global view of regulatory regions critical for gene expression in different cell types. Upon peak calling, a variety of downstream analyses can be performed in a project-specific manner.

- **Differential accessibility, nucleosome positioning, motif enrichment, etc.**
- **Data integration and cross comparison with ChIP-Seq, Hi-C, and other methods.**



Methylome

Methylome analysis helps researchers identify aberrant DNA methylation that has been implicated in a number of diseases such as cancer. Comparative analysis of methylome and other omics such as transcriptome offers valuable insight into gene regulation & biomarker identification.

- **Differential methylation measured at bulk or single-cell resolution**
- **Identification of methylation-driven cancer-associated genes**

CRISPR-Screening

CRISPR-Cas9 is currently the simplest, most versatile & precise approach to explore gene functions. High-throughput screening results helps elucidate the relationship between genotype and phenotype, paving the way for targeted therapy for genetic diseases.

- **Assessment of guide RNA-mediated perturbation effect (on/off target)**
- **Identification and characterisation of gene targets across different conditions**

RNA Analysis

Microarray & Bulk RNA-seq

Transcriptome profiling provides a snap-shot of actively transcribed genes. These could either give rise to proteins or non-coding transcripts that regulate cellular activities.

- **Analysis of co-expressed modules, differentially expressed genes, dysregulated pathways, and regulatory networks**
- **Inference of carcinogenesis & other biological processes**

Single-cell RNA-seq

While bulk RNA-seq can reveal changes of an organism in detail, sequencing the transcripts at single-cell resolution will allow us to deconvolute complex tissues and discover novel markers from rare & unexpected cell types.

- **Analysis of cell type specific genes and pathways that can be modulated by small-molecule drugs**
- **Prediction of cell types and cell-cell interactions critical for diagnosis & therapy**

Non-coding RNA

Non-coding RNAs are regulatory molecules mediating development and cancer processes. Analysing ncRNAs will reveal their potentials in diagnosis & targeted therapy.

- **Analysis of alternative splicing that gives rise to non-coding RNAs such as lncRNA, miRNA, circRNA, and snRNA.**
- **Predicting novel non-coding transcripts & interactions using machine learning**
- **Profiling A-to-I editing in ncRNAs**

Spatial Transcriptome

Spatial transcriptomics brings together transcripts & their tissue locations, navigating researchers to investigate function as well as structure.

- **Spatial curation and distribution of cell types paired with their gene expression profiles**
- **Validation of the inferred cell-cell interactions from RNA-seq data by using spatial information**
- **Multi-sample integration (multi-omics)**

Protein Analysis

Proteome

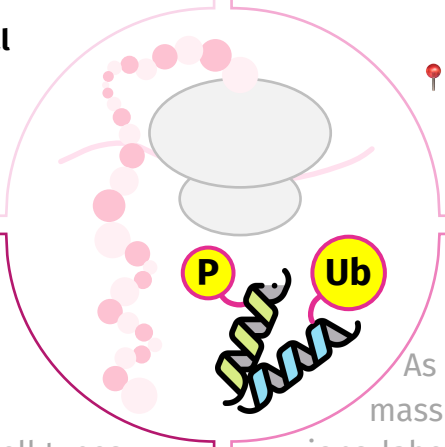
In contrast with the constant genome, the proteome changes in response to various factors from the organism & the environment. Proteomic data will help elucidate how proteins function and interact with one another.

- **Identification and quantification of selected peptides (e.g., biomarkers)**
- **Analysis of post-translational modifications that modulate cell activities (e.g., signalling pathways)**

Complexome

Proteins can be labelled metabolically (e.g., SILAC) or chemically (e.g., iTRAQ or TMT) prior to mass spectrometry. This strategy significantly saves machine time & makes the results more comparable than the label-free proteomics.

- **Global profiling of secreted proteins and pathways (i.e., secretomics) in different cell populations**
- **Estimation of protein turnover, cell growth, isotope recycling through pulsed SILAC**



Interactome

Mapping the whole set of protein-protein interactions (i.e., interactome) in certain cell types will help reveal disease mechanisms that expedite drug development.

- **Inference of interactions between host and pathogen, drug and target, and among different cell types**
- **Analysis of genetic interactions in the context of drug development (e.g., > 2 mutated genes that lead to selective killing of cancer cells)**

Mass Cytometry

As a variation of flow cytometry, mass cytometry utilises rare metal ions-labelled antibodies to distinguish up to 100 unique protein characteristics at single-cell resolution.

- **Differential discovery analyses in high-dimensional cytometry data**
- **Identification of differentially abundant cell populations in response to different conditions (e.g., healthy vs. diseased, treated vs. untreated) using machine learning framework**

Metabolite Analysis

Metabolome

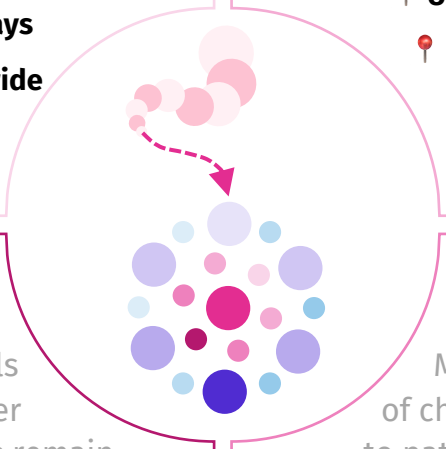
The whole set of metabolites reflects the final product of gene expression, giving rise to the phenotype of an organism. By analysing metabolomic profiles with LC-MS/NMR, researchers are able to identify new biomarkers for disease diagnosis.

- **MS peak profiling & annotation, isotope pattern decomposition, & enrichment analysis of metabolic pathways**
- **Modelling for metabolome-wide association studies (MWAS) using machine learning**

Multi-Omics

Integration of multi-omics data becomes a critical component of metabolomics research, aiming to gain holistic insights into the identification of new targets or intervention strategies.

- **Cross-data sets comparison, validation, and integration among omic modalities**
- **Unsupervised clustering analysis**
- **Phenotype association analysis**
- **Regulatory network analysis**
- **Biological pathway analysis**



Disease Diagnosis

In contrast to the weak signals of cfDNA or CTC in early cancer patients, specific metabolites remain detectable in the pathological process. These metabolites could be found in the urine & body fluids, making it accessible for non-invasive diagnosis.

- **Metabolite profiling through HPLC-MS, GC-MS, IMS-TOF-MS, NMR, etc.**

Drug Screening

Metabolites serve as readouts of chemical reactions in response to pathophysiological changes and environmental stimuli. Thus, measuring metabolites in patients will allow us to assess drug efficacy that navigates drug screening.

- **Drug efficacy and toxicity evaluation (e.g., hepatotoxicity, organ damage, etc.) using LC-MS-based metabolomics that leads to discovery of specific biomarkers**

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