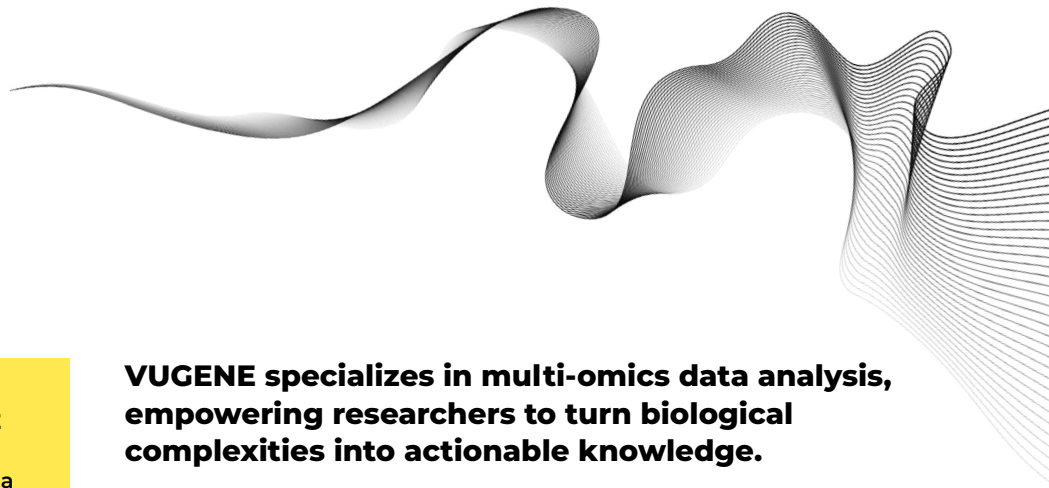




COMPREHENSIVE MULTI-OMICS EXPERTISE

Our team is experienced across the full spectrum of multi-omics research, ensuring a holistic understanding of biological systems.

EPIGENOMICS

Investigation of DNA and chromatin modifications

TRANSCRIPTOMICS

Single-cell, spatial, and bulk tissue analysis

PROTEOMICS

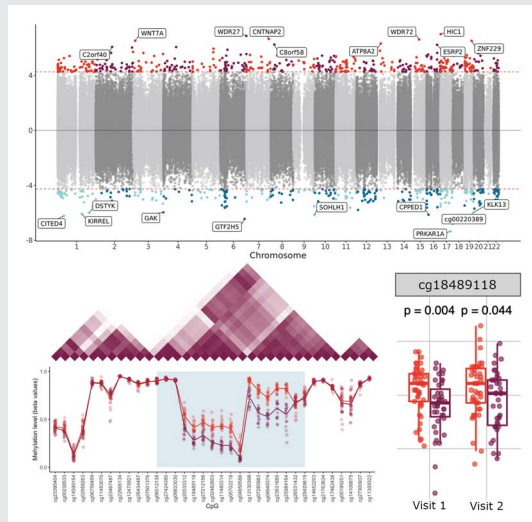
Comprehensive protein profiling

METABOLOMICS

Targeted and untargeted analysis

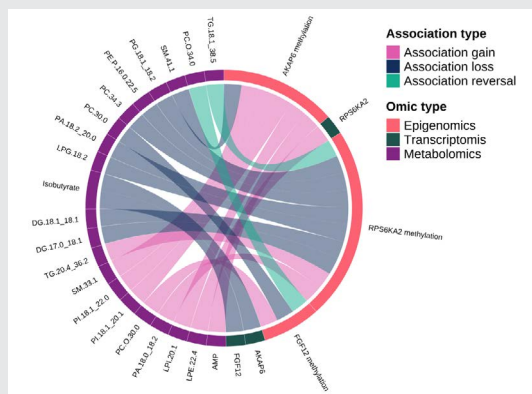
HOLISTIC VIEW

From genome-wide landscapes, to point-level changes, we ensure a holistic and thorough understanding of biological systems.



MULTI-OMICS INTEGRATION

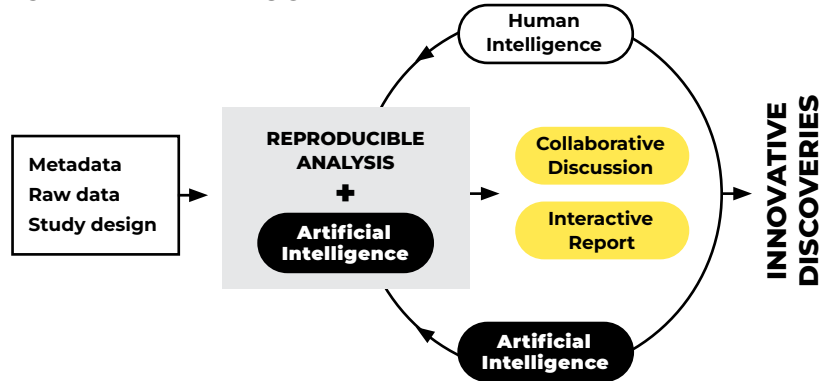
We provide deep biological insights by analyzing and integrating your data across multiple omics layers. Our intuitive visualizations translate this complexity into clear, actionable findings.



VUGENE specializes in multi-omics data analysis, empowering researchers to turn biological complexities into actionable knowledge.

CLIENT

VUGENE



Fast, Reproducible, and Reliable Results

Our standardized workflows accelerate data analysis, delivering scalable and reliable results to move your research forward.

The Power of Human and Artificial Intelligence

We combine the best of both worlds. After initial AI-powered analysis, our team of experts personally reviews the results, adjusts parameters, and refines the output. This iterative process distills the most valuable findings and uncovers truly novel insights.

A Collaborative Process, Tailored to You

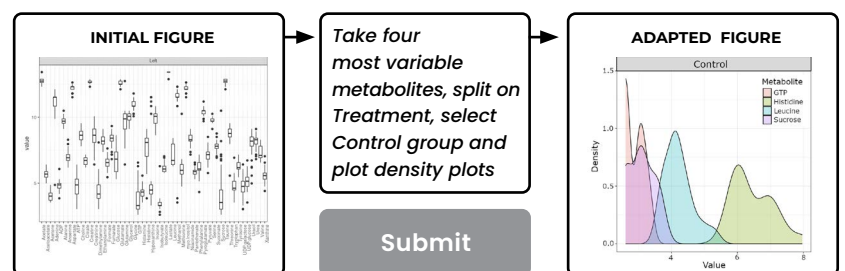
We believe in partnership. Throughout the project, we work closely with you, adapting our methods based on the discussions to ensure the results are perfectly tailored to your research goals.

Innovative Discoveries

Our multidisciplinary expertise, combined with AI-supported analysis, applies latest methods for rigorous screening of existing data and highlights truly novel findings within the results.

Interactive, AI-Assisted Service

Instantly customize figures, adjust parameters, and get help with interpretation using our bioinformatics agents – putting you in control of your data analysis.

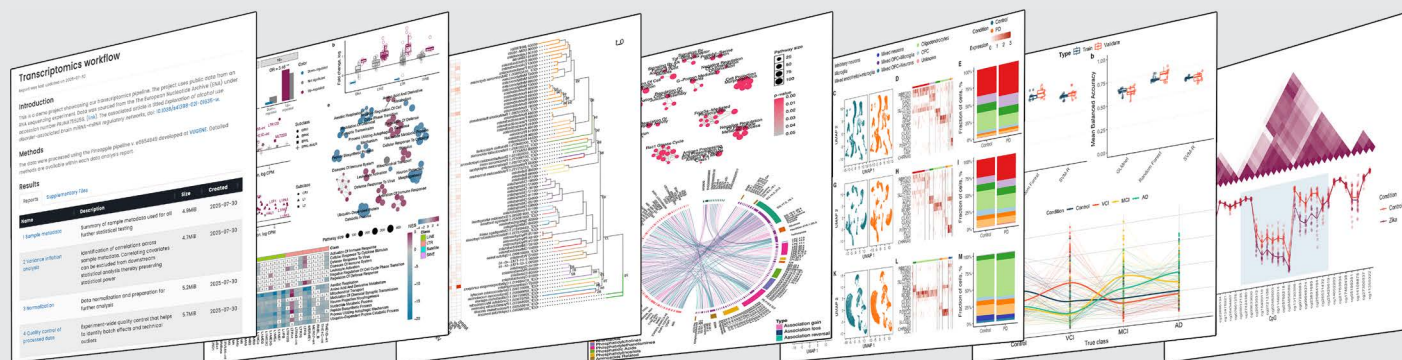


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**Clearer
Insights.
Better
Science.**



FROM DATA TO VALUE IN HOURS

Our AI-powered analysis automates each step, rapidly delivering results as an interactive web application that can be explored and shared across all stakeholders.

Identify Relevant Clinical Variables

Clinical information (e.g., age, sex, BMI, drug use) is used to identify the most relevant molecular changes. We compare AI-based predictions with supplied metadata to detect and correct labeling errors and select the minimal set of relevant clinical variables to preserve statistical power in subsequent steps.

Assess Quality

We perform quality control (QC) on each sample to identify library preparation problems and use a data-driven approach to detect samples that differ substantially from others in the experiment, ensuring more reliable downstream insights.

Normalize Across Samples and Call Peaks

To reveal true biological variation, we detect and reduce subtle technical noise that can arise during sample processing. We normalize DNA modification signals, filter out unreliable reads, adjust for known batch effects and call peaks when appropriate.

Find Differentially Modified Loci

Depending on your experimental design and research question, we select the most appropriate, statistically rigorous approach. We account for technical and biological variability, including cellular heterogeneity, and automatically fit an appropriate linear regression model to each gene.

Pinpoint Affected Pathways

We associate loci to genes, perform gene set enrichment analysis (GSEA) across all major pathway databases, clustering similar pathways to explore how groups of genes act together, even when individual genes are not statistically significant.

Build Diagnostic Classifiers

We identify the minimal set of biomarkers that best differentiate sample groups. By evaluating multiple machine learning algorithms and cross-validation strategies, we assess classifier accuracy for potential diagnostic, prognostic, or treatment applications.

ADDITIONAL VALUE OUT-OF-THE-BOX

Epigenomic data contains a wealth of valuable information that often goes unexplored. To ensure you do not miss key insights, these analyses are included as part of our standard workflow.

Differentially Methylated Windows

We perform data-driven detection of co-methylation regions and identify statistically differentially methylated regions (DMRs) using robust mixed effects linear regression models. These genomic locations contain epigenetic alterations that are the most relevant to a disease phenotype or environmental exposure.

Genomic Region Enrichment

We characterize canonical genomic regions, such as promoters, CpG islands, enhancers, chromatin accessibility regions that exhibit enrichment of differentially methylated loci or windows. This analysis allows us to infer potential gene expression changes resulting from epigenetic elements located at a distance from the regulated gene.

Ageing

We calculate carefully curated and validated epigenetic clock values by applying refined algorithms to DNA methylation data. This standardized measure of biological age acceleration provides a powerful tool for large-scale epidemiological studies, enabling the assessment of disease risk and lifespan prediction.

Get in touch to see how our intelligent analysis platform can redefine your multi-omics results

REQUEST A DEMO HERE



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