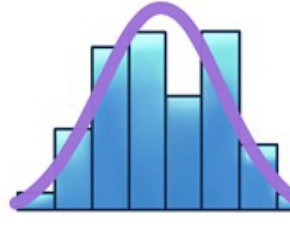
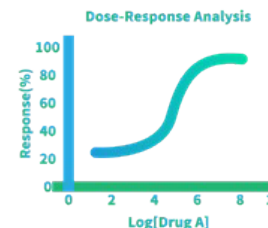
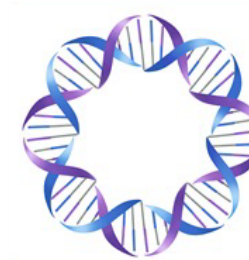
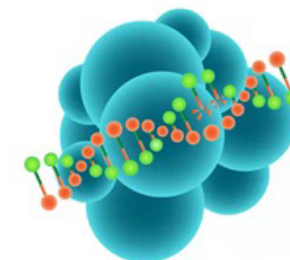


Transform data into therapeutic solutions

A cloud-based collaborative bioinformatics platform for drug hunters

Meritudio Bioinformatics Product Manual



Contact us to schedule a demo and obtain a free trial

E-mail: bd@meritudio.com
Website: www.meritudio.com



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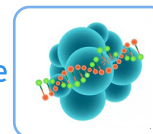
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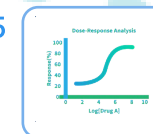
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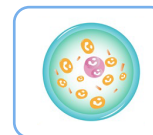
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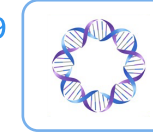
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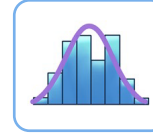
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About Us



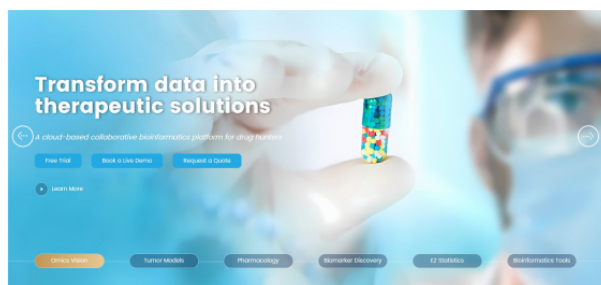
COMPANY PROFILE

About Us

Meritudio is a bioinformatics solutions company

We are your partner in pioneering bioinformatics solutions that propel drug discovery forward. Our mission is simple: we transform complex data into tangible therapeutic solutions that make a difference in patient care.

Meritudio Bioinformatics Services, our bespoke solutions, is tailored to your research needs covering biomarker discovery, target identification, omics analysis, statistics, and more. Partnering with pharmaceutical, biotech, and academic leaders, our interdisciplinary team of biologists, data scientists, and statisticians accelerates healthcare innovation.



Meritudio Bioinformatics Cloud, our flagship cloud platform, simplifies data analysis with six powerful modules: Tumor Models, Pharmacology, Biomarker Discovery, Omics Vision, EZ Statistics, and Bioinformatics Tools. Available as a SaaS solution, it offers flexible subscription plans for industrial and academic users, ensuring scalability, security, and dedicated resources for teams of all sizes.



Tumor Models



Pharmacology



Biomarker Discovery



Omics Vision



EZ Statistics



Bioinformatics Tools

4 Billion

Data points in database

200,000

Omics datasets

2,000

Cell lines

500+

Analytical functions

90%

Tasks completed within 1 minute

10-100X

Productivity boost

600+

Graphs

100+

Statistical tests

02 | Module 1

Tumor Models Database

A premier tumor model database to empower cancer research

Meritudio's Tumor Models module provides access to genomic and pharmacological data from **2,000** cancer cell lines and **1,800** oncology drugs. With intuitive search and advanced analytics, it's a powerful tool for cancer research. Licensing available for internal or commercial use, including custom solutions.



2000
Cell lines



30+
cancer types



2000
genes



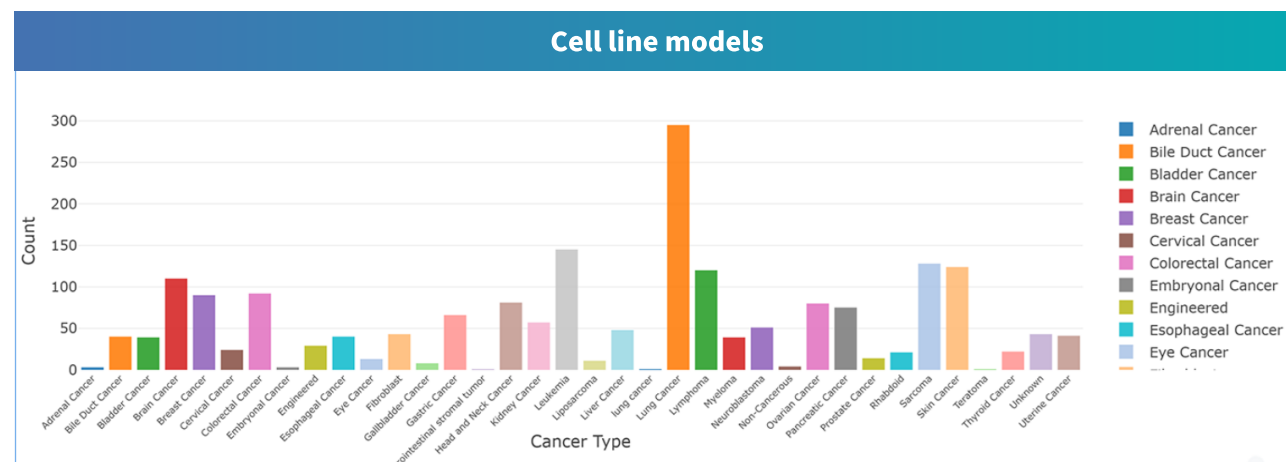
2300+
Pathways



2000
drugs

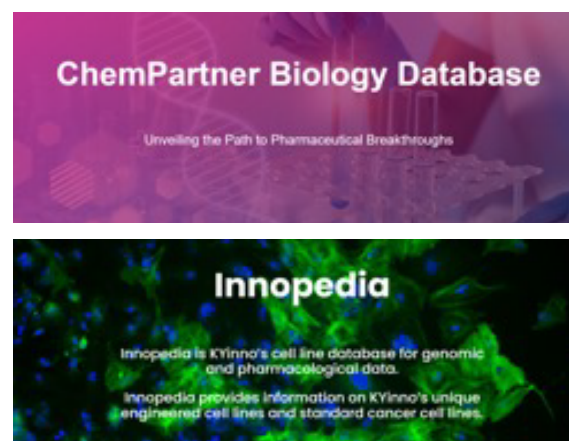


30+
analytic modules



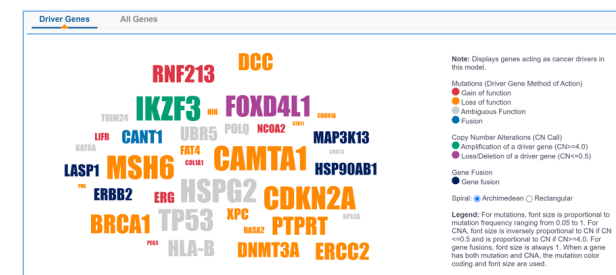
Available for Licensing

The Tumor Models Database is available for licensing with customizable options. Pharmaceutical companies use it for internal model management, while preclinical organizations showcase their services. Examples include ChemPartner's Biology Database and KYinno's Innopedia. Partner with us to enhance your research capabilities!

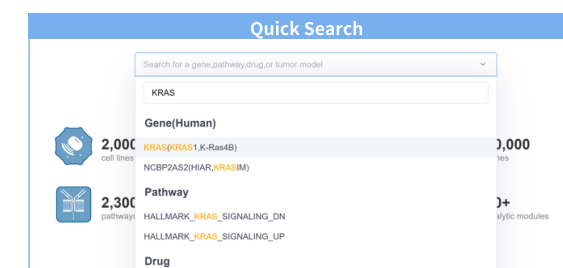


Intuitive Visualizations

Interactive figures, structured data, and real-time visualizations enable seamless comparisons of genes, pathways, drugs, and tumor models. Analyze dose-response curves with precision for actionable insights.



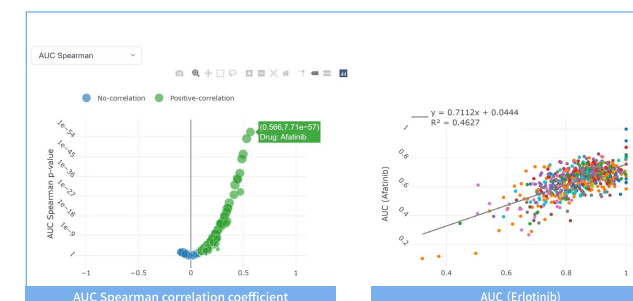
Smart Navigation



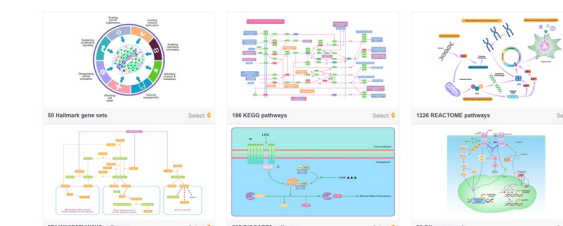
Navigate effortlessly with an intuitive interface designed for ease of use. Dedicated modules for Models, Genes, and Drugs, along with single-page summaries, simplify exploration. Advanced filters, search tools, and links to external databases like NCBI, Ensembl, OpenTargets, and OncoKB enhance usability.

Analysis Tools

Leverage normalized datasets for reliable cross-comparisons and advanced annotation tools like AlphaMissense for mutation classification. High-efficiency workflows deliver 90% of analyses in under 10 seconds, while biomarker discovery tools link drug response to genomic features for deeper insights.



Comprehensive Data



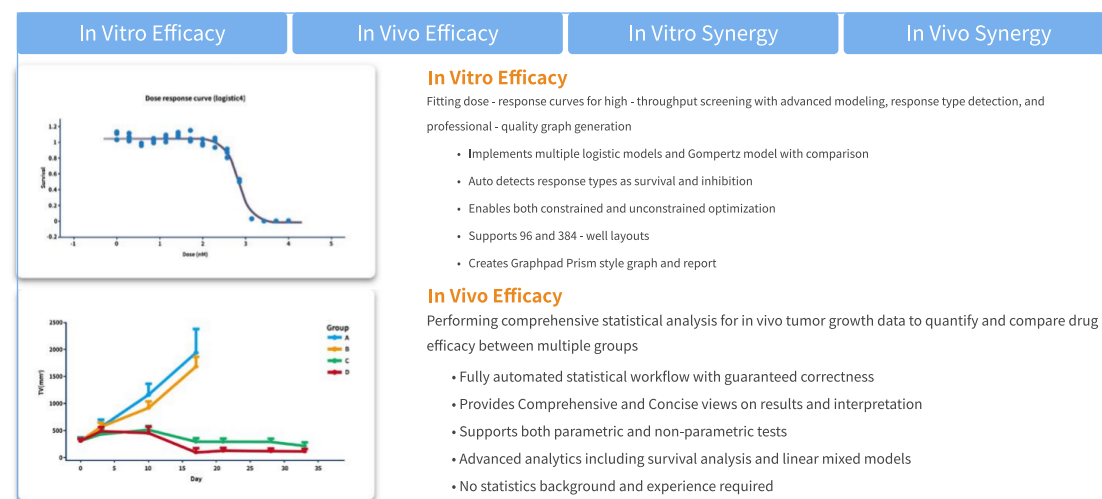
Explore 2,000 cancer cell lines with gene expression, mutations, CNV, and pathway data, plus 1,800 oncology drugs categorized by targets and mechanisms of action. Access 1M+ dose-response curves, 2,300+ signaling pathways, and 120M genomic and pharmacological data points.

02 | Module 2

Pharmacology

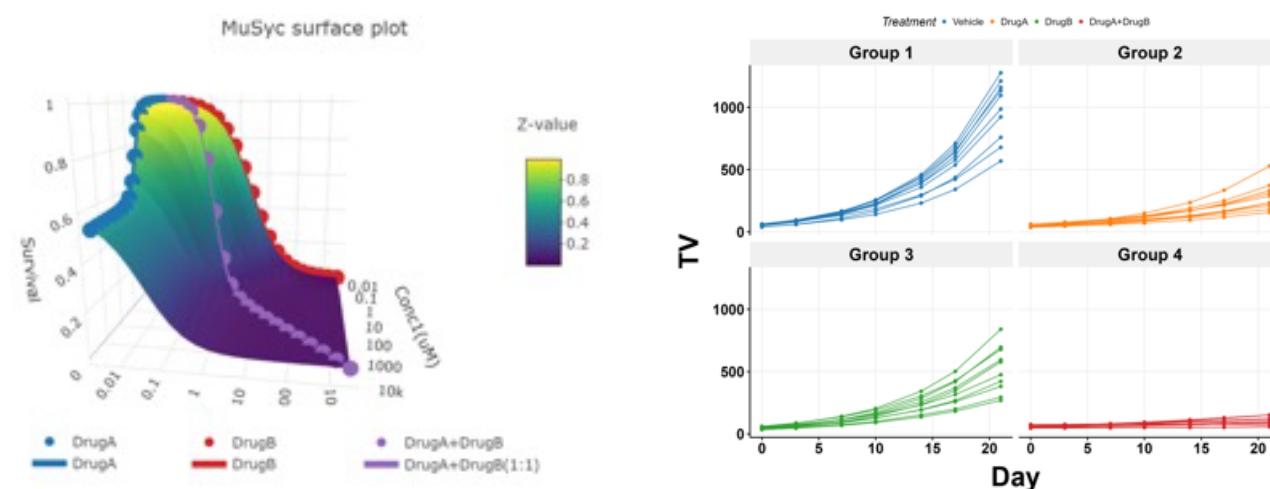
A convenient hub for evaluating drug efficacy and synergy

Meritudio's Pharmacology module uses cutting-edge methods to calculate **in vitro** and **in vivo efficacy** and **synergy**. With powerful analytics and interactive visuals, it simplifies result interpretation and drug assessment. Optimized defaults and flexible customization enable one-click, publication-ready reports—no stats expertise needed.



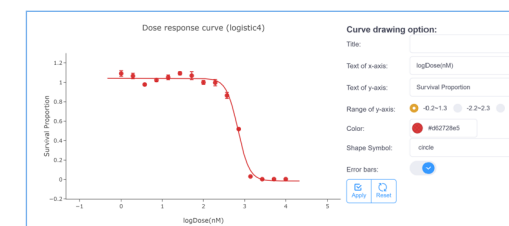
Unique Advantages of Pharmacology Module

Meritudio's Pharmacology Module offers enhanced synergy tools (MuSyC for in vitro, invivoSyn for in vivo), in vitro analysis with AUC for biomarker insights, and simplified in vivo synergy analysis for biologists. One-click reporting makes it intuitive and powerful.



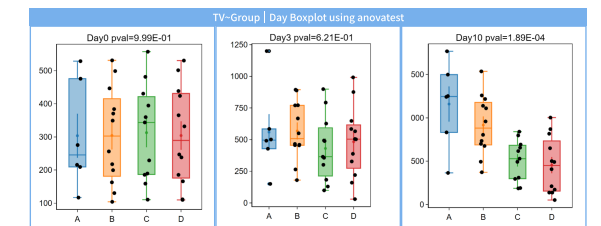
In Vitro Efficacy

Implements multiple logistic and Gompertz models with comparisons, auto-detects response types (survival, inhibition), and supports 96 and 384-well layouts. Generates GraphPad Prism-style graphs and reports for clear, actionable insights.



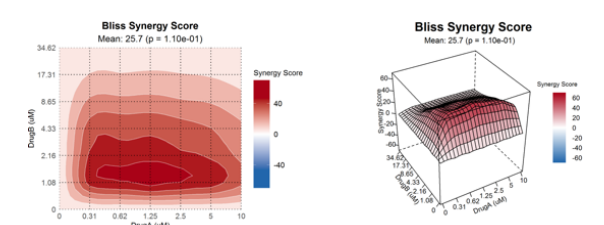
In Vivo Efficacy

Features a fully automated statistical workflow with guaranteed correctness, supporting both parametric and non-parametric tests. Provides comprehensive and concise result views, including advanced analytics like survival analysis and linear mixed models.



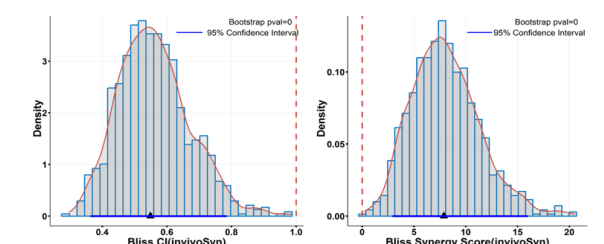
In Vitro Synergy

Supports matrix design, fixed ratio design, and single or multi-dose combinations. Evaluates synergy with Bliss, Loewe, and MuSyC models, detecting synergy, additivity, or antagonism. Results are visualized with heatmaps and surface plots for intuitive interpretation.



In Vivo Synergy

The first method to validate in vitro synergy in animal studies, implementing Bliss and HSA models for two or more drug combinations. Calculates combination index and synergy score with statistical assessment, ensuring high power and low false positive rates.

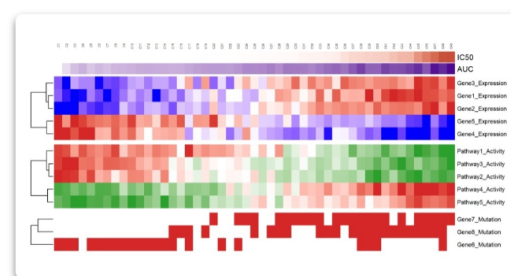


02 | Module 3

Biomarker Discovery

A powerful platform for performing multi-omics biomarker development

Meritudio's Biomarker Discovery module integrates **multi-omics** data to identify single or **multi-gene** biomarkers with precision. Advanced algorithms and intuitive workflows simplify complex tasks, enabling biologists to generate publication-ready reports and focus on driving innovation and translational research.

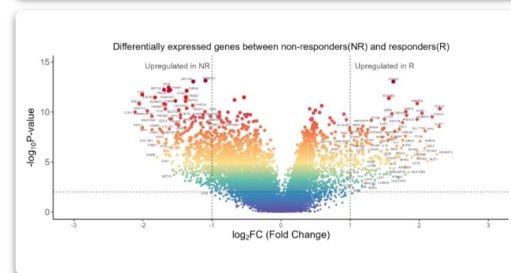


Cell Line Biomarker Discovery

Investigate mechanism of action and discover predictive biomarkers for oncology drugs from large-panel cell line screening assays

- Integrate public and in-house generated omics data for 2000 cancer cell lines
- Access over 2000 curated datasets for immediate analysis
- Upload efficacy data to combine with stored omics data for fast analysis
- Use advanced algorithms to create robust multi-gene, multi-omics biomarkers
- Predict drug response for un-assayed cell lines

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General Biomarker Discovery

Uncover biological insights and develop biomarkers using uploaded omics data and platform-curated biological context databases

- Streamlined upload for all omics data types and annotation files
- Specialized workflows for diverse omics and phenotypical data
- Advanced algorithms for constructing multi-gene, multi-omics biomarkers
- Customizable workflows to fit research or clinical requirements
- Generate publication-ready reports with high-quality figures

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Biomarker Discovery Module Powers Our Bespoke Service

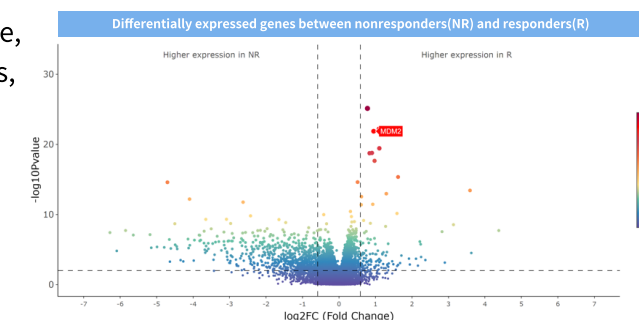
Meritudio leverages the Biomarker Discovery Module to deliver bespoke biomarker discovery services for clients, spanning preclinical (cell line, PDX, organoid) and clinical projects. Powered by our proprietary algorithm, the module can complete biomarker discovery in hours—compared to weeks or months with conventional methods—while identifying multi-gene, multi-omics biomarkers. Now trusted by many institutes, this module powers our bespoke biomarker discovery services, transforming the speed and precision of biomarker research.

"After evaluating several platforms and services, we found Meritudio's biomarker discovery service to be unparalleled in speed, predictive power, and innovation. Unlike others, Meritudio was the only provider capable of identifying composite biomarkers integrating multiple genes, leveraging gene expression, mutation data, and pathway activity—all from cell line-based assays. The biomarker exercise has been instrumental in guiding our drug development strategies. We highly recommend their services to any organization seeking cutting-edge solutions."

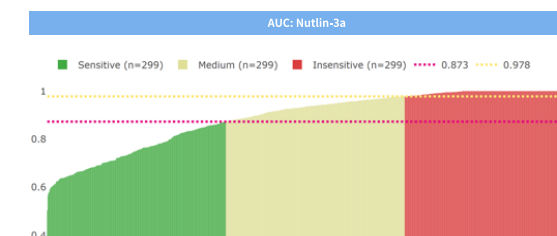
—CSO of a biotech

Biological Insights

Perform tailored analyses for each omics type, differential expression for genes and proteins, and enrichment/network analyses for pathways and modules. Access real-time activity data for 2,300+ pathways to uncover drug mechanisms and identify drugs with similar response profiles.



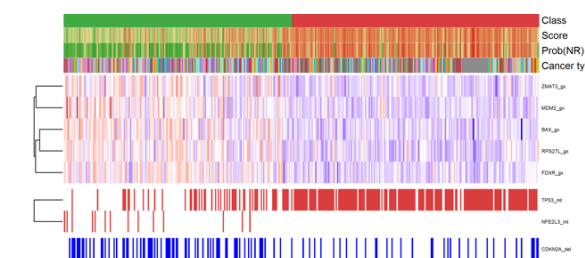
Customizable Solutions



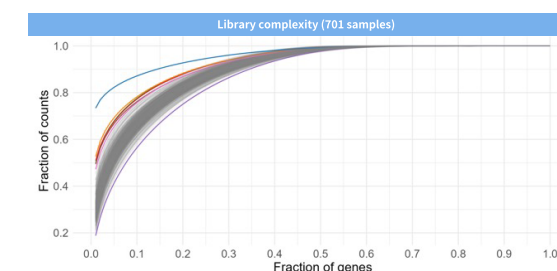
Streamline uploads of omics data and annotation files, explore results interactively, and customize graphs. Use flexible sample classification (e.g., IC50, AUC) and tailored workflows to bridge discovery research and clinical biomarker validation seamlessly.

Multi-omics Biomarkers

Integrate gene expression, mutations, CNV, and protein expression to develop multi-gene biomarkers. Leverage advanced algorithms and dedicated workflows for Cell Line and General Biomarker Discovery. Access 2,000+ curated datasets and generate high-quality, publication-ready reports.



Fast and Robust



Reduce analysis time from weeks to minutes with proprietary algorithms for biomarker ranking and model optimization. Ensure rigorous data quality control and process large-scale data with exceptional speed, accuracy, and stability.

02

Module 4

Omics Vision

An integrated workspace to visualize, analyze, and enable discovery from omics data

Meritudio's Omics Vision module features **Omics Visualizer** for code-free exploration of curated studies (GEO, TCGA) and **Omics Analyzer** for tailored analysis of RNAseq, proteomics, and more. Both tools simplify omics research, enabling efficient insights and publication-ready reports.



Omics Visualizer for Stored Omics Studies

Explore, analyze, and visualize curated omics studies with a code-free, interactive interface

- Access a vast repository of curated omics studies from trusted sources like GEO and TCGA.
- Browse and select projects effortlessly for detailed, in-depth analysis
- Utilize an interactive interface to explore data with customizable visualizations
- Generate publication-quality figures and reports for seamless integration into research
- Stay updated with a continually growing collection of rigorously curated datasets.

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Omics Analyzer for User-Uploaded Omics Studies

Analyze uploaded omics data with advanced, code-free tools for RNAseq, proteomics, and more

- Enjoy all features of Omics Visualizer, plus enhanced tools for user-uploaded data
- Perform rigorous data QC and batch effect detection and removal for reliable results
- Analyze multiple groups of samples, whether paired or unpaired
- Conduct diverse analyses: compare gene/protein expression, identify differentially expressed genes/proteins, and evaluate pathway activity, etc.
- Explore a single dataset with multiple analysis types, each customizable with various parameters

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Comprehensive Omics Data Analysis and Profiling Services

Meritudio's Omics Vision module, combined with offline tools, offers a complete suite for analyzing diverse omics data types—RNAseq, proteomics, single-cell transcriptomics, spatial transcriptomics, metagenomics, and more. Advanced functionalities include peak calling, pathway enrichment, variant detection, and multi-omics integration, streamlining workflows from raw data to publication-ready insights.

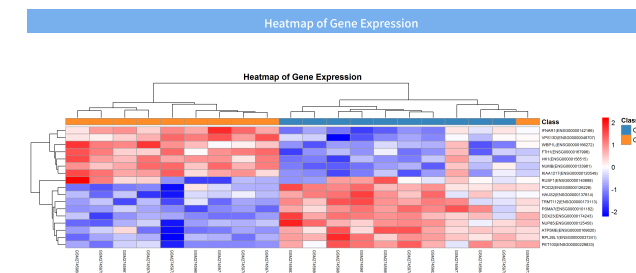
We collaborate with partners to provide high-quality omics profiling services (NGS, proteomics, single-cell RNAseq, etc.), enriching our platform with valuable data. Together, we deliver end-to-end solutions to accelerate biomedical discoveries. Contact us to learn how we can support your research.

Curated Studies

Explore curated omics studies from trusted sources like GEO and TCGA. Access a vast repository of rigorously curated datasets, continually updated, and seamlessly integrate external omics data for expanded analysis opportunities.

GSE_Series	Platform	Species	Groups	Sample_Size	Title	Summary
GSE128072	GPL15791	human	136	1231	Genetic and Epigenetic Fine Mapping of Complex Trait Associated Loci in the Human Liver	Deciphering the impact of genetic variation on gene regulation is fundamental to understanding common, complex human diseases. In this study, we obtained genome-wide RNA-Seq and ChIP-Seq for H3K4me3 and H3K27ac histone modifications data in the human liver. We mapped quantitative trait loci (QTLs) of gene expression levels and histone modification states. We integrated our findings with summary statistics of genome-wide association studies (GWAS) and identified candidate genes, gene regulatory regions, and variants in GWAS loci.
GSE155509	GPL15873	human	93	550	Acquired FGFR and FGFR alterations confer resistance to EGFR targeted therapy in ER+ metastatic breast cancer	Beyond acquired mutations in the estrogen receptor (ER), mechanisms of resistance to ER-directed therapies in ER+ breast cancer have not been clearly defined. We conducted a genome-scale functional screen spanning 10,138 genes to investigate genes whose overexpression confer resistance to selective estrogen receptor degraders. Pathway analysis of candidate resistance genes demonstrated that the FGFR, ERBB, insulin receptor, and MAPK pathways represented key modules of resistance. In parallel, we performed whole exome sequencing in paired pre-treatment and post-resistance biopsies from 60 patients with ER+ metastatic breast cancer who had developed resistance to ER-targeted therapy. The FGFR pathway was altered via FGFR1, FGFR2, or FGFR4 amplifications or FGFR2 mutations in 24 (40%) of the post-resistance biopsies. In 12 of the 24 post-resistance tumors exhibiting FGFR2/FGFR4 alterations, these alterations were not detected in the corresponding pre-treatment tumors, suggesting that they were acquired or enriched under the selective pressure of ER-directed therapy. In vitro experiments in ER+ breast cancer cells confirmed that FGFR2/FGFR4 alterations led to fulvestrant resistance as well as cross-resistance to the CDK4/6 inhibitor palbociclib, through activation of the MAPK pathway. The resistance phenotypes

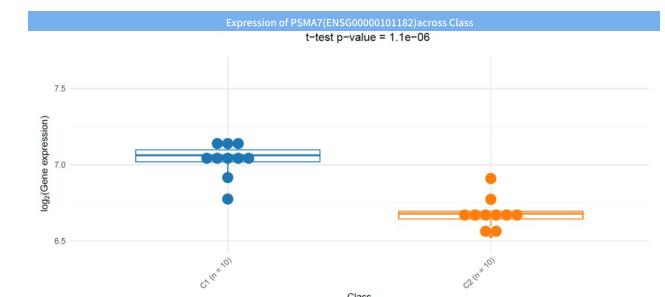
User Friendly



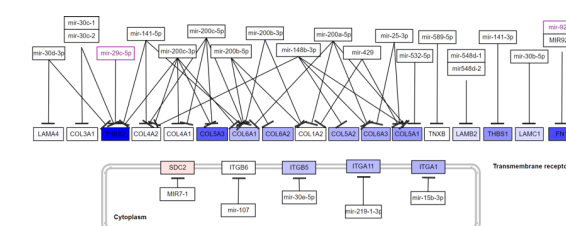
Designed for biologists and non-experts, the code-free interface offers step-by-step guidance, intuitive visualizations, and customizable workflows. Generate publication-ready reports with high-quality figures and tables effortlessly.

Advanced Analytics

Perform diverse analyses, including gene/protein expression comparison, pathway evaluation, and differential expression analysis. Automatically detect and correct batch effects for reliable results, with customizable parameters to fit specific research needs.



Biological Significance



Uncover key genes, proteins, and pathways driving phenotypic changes and disease processes. Link findings to functional annotations, interaction networks, and clinical outcomes for actionable therapeutic insights.

02 | Module 5

EZ Statistics

An intuitive statistics software to automate complex data analysis

Meritudio's EZ Statistics module revolutionizes statistical practice by **automating test selection** and **workflow design** based on user data. From two-group comparisons to predictive modeling, it ensures robust results with one-click solutions, an intuitive interface, and graphical reports. Designed for non-experts, it saves time and empowers confident, data-driven decisions.

Regression Analysis

This section focuses on performing regression analyses to examine relationships between predictor variables and a target variable. The target variable can be numeric, binary, or count data. Based on the target variable type, the appropriate regression method is applied: linear regression for numeric outcomes, logistic regression for binary outcomes, and Poisson regression for count outcomes.

START

Single Sample Analysis

This section focuses on analyzing single-sample data, including tasks such as calculating descriptive statistics, testing for normality, and comparing the sample to a reference value using appropriate statistical tests.

START

Two Variables Analysis

This section focuses on analyzing relationships between two variables. If both variables are numeric, correlation analysis is performed. If both variables are categorical, a test of independence is conducted.

START

Two Group Comparison Analysis

This section focuses on comparing two groups to determine if there are significant differences between them. Parametric or non-parametric tests are applied based on the results of normality tests.

START

Multiple Group Comparison Analysis

This section focuses on comparing multiple groups to determine if there are significant differences among them. Parametric or non-parametric omnibus tests are applied based on normality test results. If significant differences are found, post-hoc tests are conducted to analyze pairwise differences between specific groups.

START

Survival Analysis

This section focuses on survival analysis, including non-parametric Kaplan-Meier curves and semi-parametric Cox regression models, to analyze time-to-event data.

START

Longitudinal Analysis

This section focuses on analyzing longitudinal data, including repeated measures ANOVA and mixed-effects models, to examine changes over time within subjects.

START

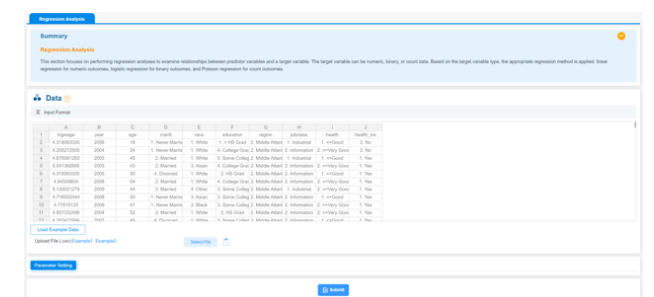
Dimension Reduction Analysis

This section is designed to conduct dimension reduction analyses, utilizing principal component analysis (PCA), t-distributed stochastic neighbor embedding (t-SNE) and uniform manifold approximation and projection (UMAP) to visualize high dimension data in 2D space, helping to identify patterns, clusters, or outliers in the data.

START

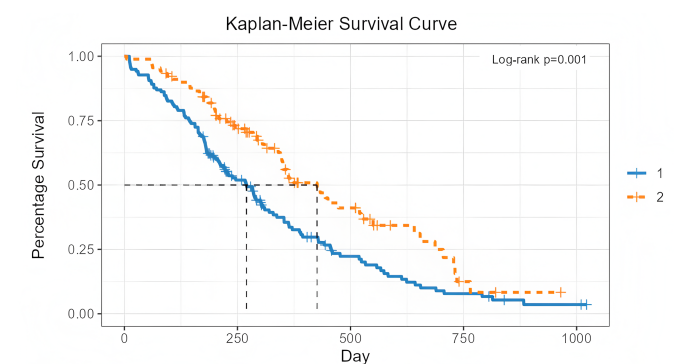
Easy to Use

Generate instant reports with one click after uploading or pasting data. Access seven intuitive categories of common statistical analyses, with automatic test selection and customizable workflows. Enjoy professional statistical self-service tools tailored to your needs.



Simple to Understand

Clear descriptions, default values, and summarized results make analysis accessible. Intuitive figures, tables, and step-by-step guidance simplify interpretation. Reports are available in interactive web and print-ready PDF form for seamless use.



Powerful Statistics

Access over 50 parametric and non-parametric tests, including linear models, mixed effects models, and survival analysis. Automatically design multi-step statistical procedures with best practices for small sample sizes and advanced machine learning tools for in-depth analysis.

Table of Statistical Tests

Category	Parametric Tests	Non-Parametric Tests
Comparison of Means	1. t-test (One-sample)	2. Wilcoxon Signed-Rank Test
	3. t-test (Independent)	4. Mann-Whitney U Test
	5. Paired t-test	6. Wilcoxon Matched-Pairs Test
	7. ANOVA (One-way)	8. Kruskal-Wallis Test
	9. ANOVA (Two-way)	10. Friedman Test
Comparison of Variances	11. F-test (Variance ratio test)	12. Levene's Test

02

Module 6

Bioinformatics Tools

A collection of tools for handling common bioinformatics tasks

Meritudio's Bioinformatics Tools module features **Data Visualization**, **Data Conversion**, and **Data Analysis**. Simplify complex data with customizable graphs, transform formats seamlessly, and perform robust bioinformatics tasks—all code-free and accessible for biologists and bioinformaticians.

Bar Plot
A bar plot visualizes the central tendency of a numeric variable using the height of each rectangle. It also includes error bars to indicate the uncertainty around the estimate.

SUBMIT

Box Plot
A box plot displays the distribution of a dataset, showing key statistics such as the median, quartiles, minimum, maximum, and outliers. It consists of a box with whiskers extending to the data points.

SUBMIT

Bubble Plot
A bubble plot is a type of scatter plot where a third dimension of data is represented by the size of the markers, adding an additional layer of information to the visualization.

SUBMIT

Clustergram
A clustergram combines a heatmap with a dendrogram, often used in gene expression analysis. It helps identify groups of genes with similar expression patterns through hierarchical clustering.

SUBMIT

Density Heatmaps
A density heatmap, or 2D histogram, visualizes the distribution of data points across two dimensions. It uses color intensity to represent the frequency or aggregation of points within each bin.

SUBMIT

Dumbbell Plot
A dumbbell plot is used to highlight changes or differences between two sets of data points, making it ideal for comparing before-and-after scenarios.

SUBMIT

Histograms
A histogram represents the distribution of numerical data by dividing it into bins and displaying the count or frequency of data points within each bin.

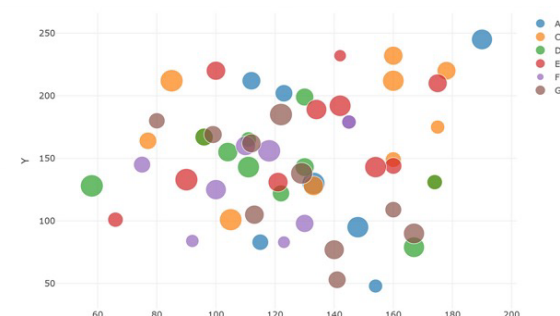
SUBMIT

Line Plot
A line plot displays data points connected by straight lines, making it ideal for visualizing trends, patterns, and relationships, especially in time series data.

SUBMIT

Data Visualization

Save time with ready-to-use templates and intuitive design tools. Create interactive, customizable visuals without coding, and export high-quality graphs in multiple formats for clear, insightful data representation.



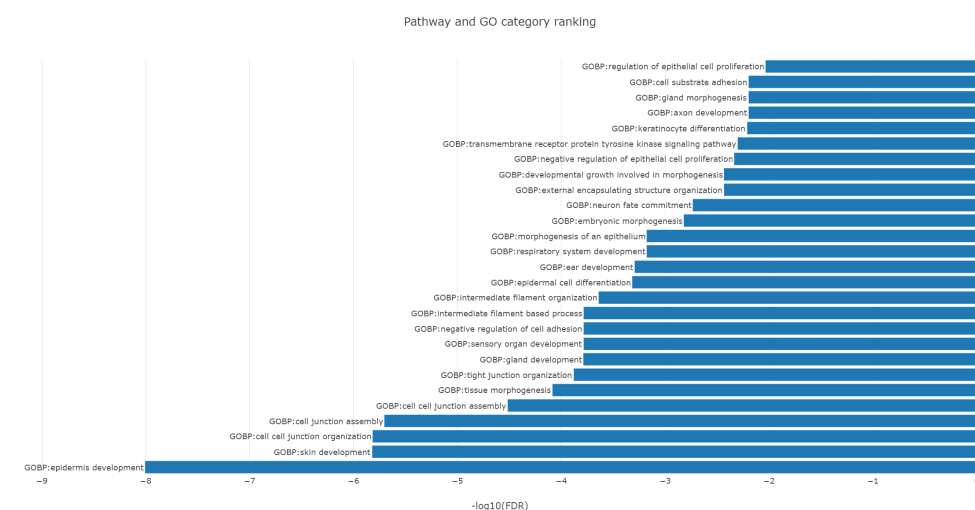
Data Conversion

Convert gene IDs and file formats seamlessly with batch processing for large datasets. Automatically integrate annotations and ensure compatibility with popular tools and databases, streamlining workflows in one platform.

Ensembl_ID	Gene_Symbol
ENSG00000000005	TNMD
ENSG00000000419	DPM1
ENSG00000000457	SCYL3
ENSG00000000460	C1orf112
ENSG00000000971	CFH
ENSG00000001036	FUCA2
ENSG00000001084	GCLC
ENSG00000001167	NFYA
ENSG00000001460	STPG1
ENSG00000001461	NIPAL3
ENSG00000001497	LAS1L

Data Analysis

Simplify common bioinformatics tasks with pre-built pipelines and advanced analyses—no programming needed. Identify functional insights with integrated annotation tools, assess data quality automatically, and query public databases directly.



03

Meritudio Bioinformatics Services

Your trusted partner for tailored bioinformatics solutions. Our powerhouse team of biologists, bioinformaticians, data scientists, and statisticians collaborate with you to achieve scientific excellence. From biomarker discovery and target identification to omics data analysis and custom database development, we uncover insights that drive innovation. Our advanced statistics services ensure robust, reliable outcomes. Contact us to explore how we can support your research goals!



Cutting-edge Analysis

Harness advanced algorithms and tools to uncover deep insights from complex biological data, driving breakthroughs in research and development.



Custom Solutions

Tailor-made approaches to address unique challenges, ensuring precise results that align with specific project goals.



Rapid Turnaround

Accelerate your discoveries with efficient pipelines, delivering timely results to support swift decision-making and innovation.



Data Security

Safeguarding sensitive information through robust cybersecurity measures, ensuring confidentiality and compliance with industry regulations.



Expert Team

Our interdisciplinary team of biologists, data scientists, and statisticians guarantees expert guidance and accurate interpretation of findings.



Collaborative Partnerships

Engage in a dynamic partnership to strategize, execute and refine analyses, fostering a seamless exchange of ideas and knowledge.



Biomarker Discovery



Drug Efficacy and Synergy Assessment



Bioinformatics Database & Software Development



Target Identification



Omics Data Analysis



Statistics Services



And more...