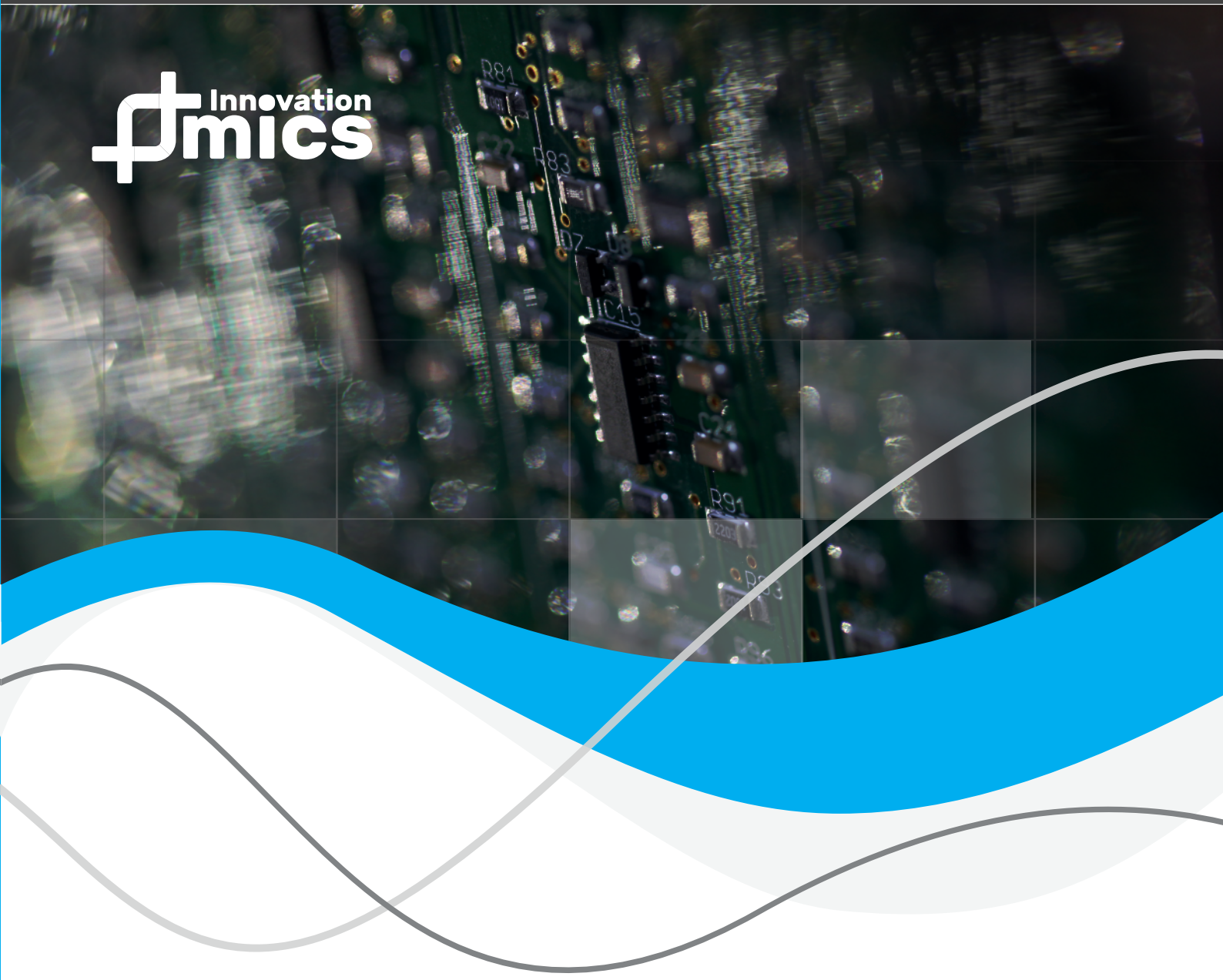


Dr. Tom

An Advanced and Multi-omics Data Visualisation System for Efficient Analysis and Discovery

Contents

Overview

Quick and Convenient Data Visualization Tools for Bulk RNA/Single-cell RNA Analysis

Use a wide range of interactive data visualization tools to visualize analysis results quickly and effectively, including differentially expressed gene statistics, heatmaps, enrichment charts, networks, cell clustering maps and more.

Mine Your Data with Powerful and Intuitive Tools for Deeper Insight

Go beyond fundamental expression analysis with Dr. Tom's powerful and advanced algorithms, which combine with the table-chart interactive tools to provide new insight.

Quickly Reference World - Leading Public Databases for Cross Analysis

Supported with references from world-leading databases including KEGG, TCGA and NCBI.

AI-based Literature Retrieval and Big Data Interrogation

Convenient and effortless functionality to uncover relevant relationships between genes of interest and to explore pathways.

Introduction

Dr. Tom is a web-based solution for the convenient analysis, visualisation and interpretation of all types of RNA data, including small RNA, mRNA and lncRNA.

Designed by a team of expert RNA scientists and bioinformaticians with collective experience across thousands of RNA-based research projects, Dr. Tom provides a wide range of intuitive and interactive data visualisation tools specifically designed to save you time in your bulk-RNA/Single-cell RNA research.

In addition, powerful analysis tools and advanced algorithms allow you to mine your data to gain new insight and more value beyond standard available bulk-RNA/Single-cell RNA analysis services.

Data from many of the world's leading databases have been integrated into the Dr. Tom system allowing users to reference and cross-check all results and findings.

Dr. Tom is already relied upon by tens of thousands of scientists and researchers, and has shown itself to be a valuable and essential tool in addition to any institution's own internal data curation and analysis efforts.

https://biosys.innomics.com

Main Applications

Multiple gene-level and cell-level tools and table-chart visualization functionality for speeding up common RNA analysis work

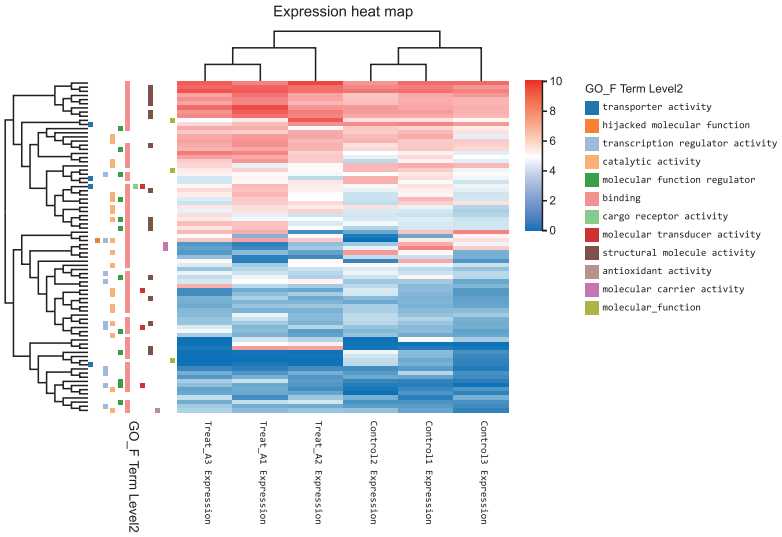
Multiple databases to enable new insight for data mining

User Profiles

Any scientist who needs ready-made data analysis tools and workflows to speed up their research work

Any research scientist who needs easy access to multiple database references

Core Capabilities

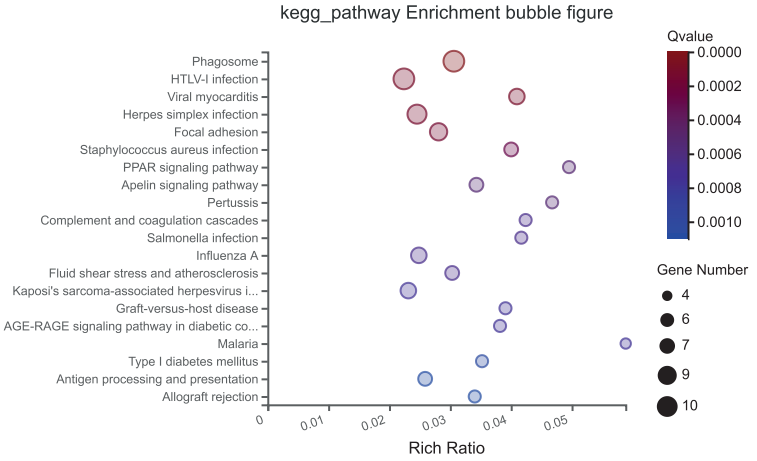


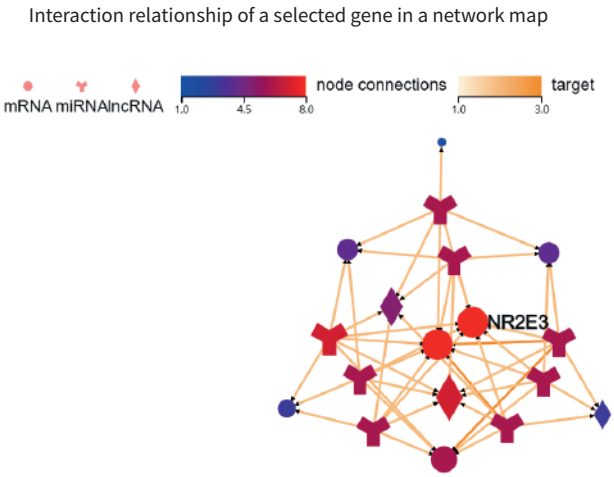
Expression Analysis

Dr. Tom's detailed, interactive heatmap functionality can be used to quickly identify genes that are commonly regulated. With simple point-and-click action, data can be selected and manipulated to show clusters under different pathways.

Enrichment Analysis

Dr. Tom accesses both free and licensed KEGG databases to allow users to conveniently and quickly find statistically significant trends in the extensive lists of genes generated by many functional genomics techniques and bioinformatics analysis approaches.



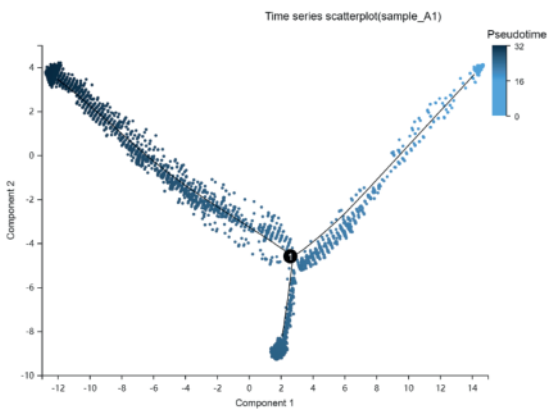


Association Analysis

With a simple click Dr. Tom shows RNA association with target genes, based on their interaction relationship (PPI, Target, ceRNA, and RNAplex), or based on the position relationship (upstream and downstream position).

Pseudo-time Analysis

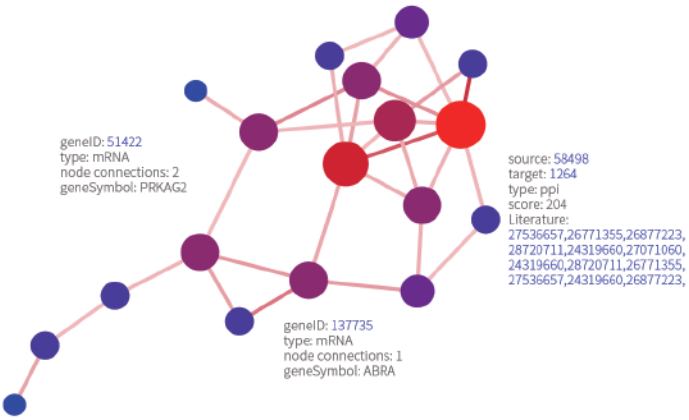
Dr. Tom provides pseudo-time analysis tools to estimate the cell differentiation status, and help researchers to discover the possible evolutional relationship between cells.

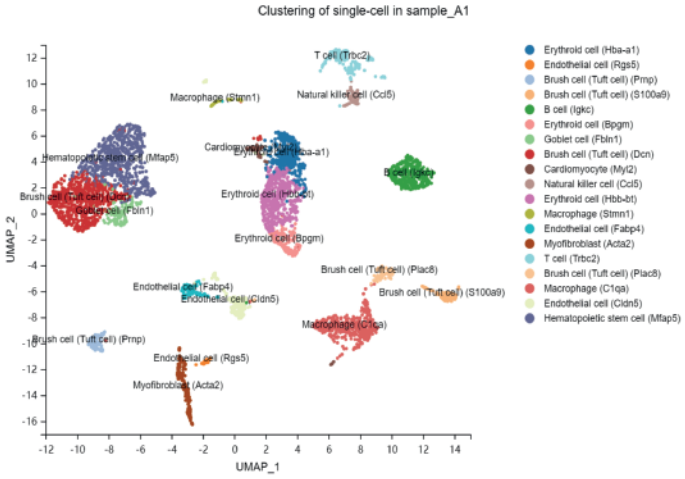


Reference Ontological Information Across Multiple Databases

Dr. Tom is able to reference multiple-databases for association analysis, including TCGA, NCBI and many more. This allows a user to quickly and conveniently view comprehensive ontological information for any gene of interest, including annotation, sequences, expression level, and a list of relevant published papers.

Fig. of Reference Ontological Information Across Multiple Databases





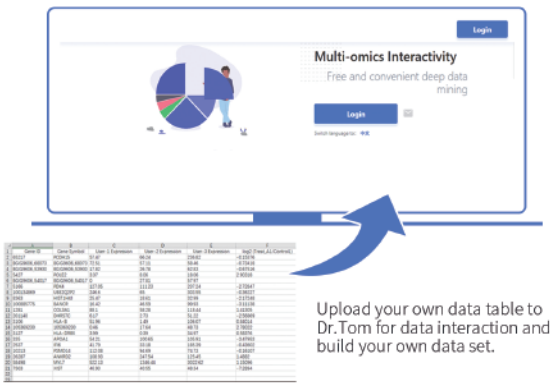
Cell Clustering and Cell Annotation Analysis

For single-cell RNA research, Dr. Tom let the users adjust the parameters and produce customized cell clustering plot. Besides, users can upload their own cell annotation database for custom cell annotation.

Custom Datasets

Customers can upload their own gene expression data, using tool boxes for data graphing and visualization.

Fig. of Custom Datasets



User Example

Ye et al. Clinical Epigenetics (2019) 11:137
https://doi.org/10.1186/s13148-019-0723-0

Clinical Epigenetics

RESEARCH Open Access

Co-inhibition of HDAC and MLL-menin interaction targets MLL-rearranged acute myeloid leukemia cells via disruption of DNA damage checkpoint and DNA repair

Jing Ye[1†], Jie Zha[1†], Yuanfei Shi[1†], Yin Li[2], Delin Yuan[1], Qinwei Chen[1], Fusheng Lin[1], Zhihong Fang[1], Yong Yu[3*], Yun Dai[4*] and Bing Xu[1*]

Publication: Clinical Epigenetics
Impact factor: 5.496
Posted: October 7, 2019
Original link:
https://clinicalepigeneticsjournal.biomedcentral.com/articles/10.1186/s13148-019-0723-0

Background:
The researchers wanted to study the mechanism of poor prognosis of chidamide and MI-3 (hereinafter referred to as C and M) inhibitors for the synergistic treatment of mixed leukemia (MLL) gene recombination.They utilized multiple Dr. Tom analysis functions to help answer several questions key to their paper. Some of these questions and how they were answered are listed below.

1. The researchers wanted to know what are the pathways for change after processing.
KEGG enrichment analysis showed that when C and M were combined, the most significant pathways were cell cycle, DNA replication, and repair pathways.

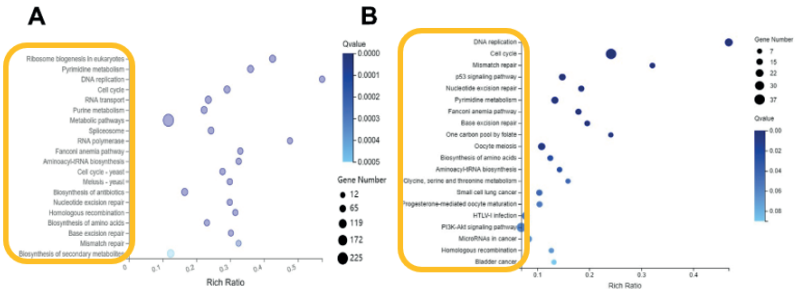


Figure 1 A and B are KEGG enrichment analyses after processing for 24 and 48 hours, respectively

2. The researchers wanted to know which treatment effect is more prominent and causes the above pathways change.
GSEA analysis further showed that the vast majority of these changes originated from C, not M (Figure 2B is processed by C).

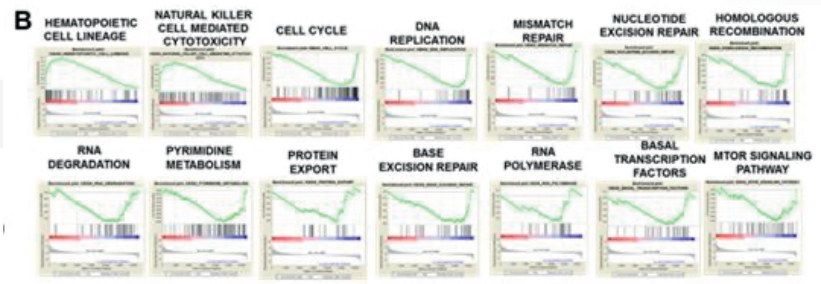


Figure 2 GSEA analysis under C treatment

3. The researchers wanted to know what is the intersection of differentially expressed genes under each treatment.
Venn diagrams of differential genes under different treatments, 635 genes were expressed under all three treatments (Figure 3C).
They also wanted to learn are these genes up / down regulated consistently across treatments.
Clicking on the center of the graph shows the gene set, and a heat map is shown. Fifty-nine genes showed different trends (shown in the box in Figure 3D). M treatment was down-regulated and C treatment or M + C treatment was up-regulated.
The researchers then wanted to screen out the genes with different trends, as above.
By selecting the box on the map, the relevant gene set is shown, and a heat map generated. The heat map (Figure 3E) corroborates the result of point 2.

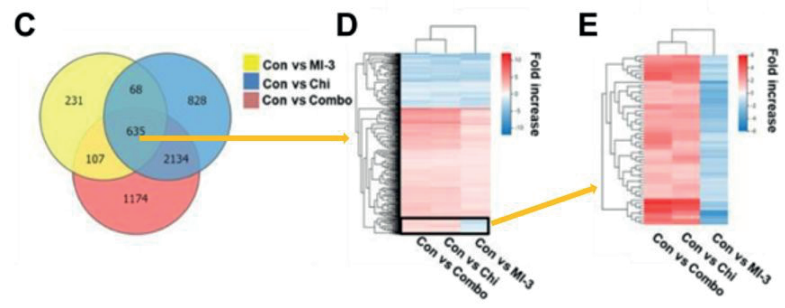


Figure 3 Venn diagrams of differential genes at three hours in three treatments of C. D, a heat map of gene clustering in common, and 59 heat maps of different genes with different expression trends in each treatment of E

4. The researchers wanted to know what is the function of the genes shown in the previous step.
GO and KEGG analysis (Figures 4D and E) found that these genes are involved in crucial survival signaling pathways and cytokine pathways necessary for inflammatory responses.

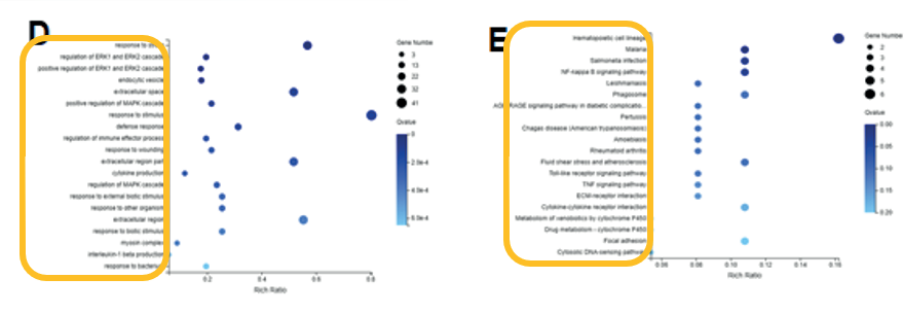


Figure 4 D and E are GO and KEGG analyses of 59 genes, respectively

5. The researchers wanted to continue to screen for other vital genes.
They selected different groups of expressions, adjusted the filtering conditions, and generated a heat map.

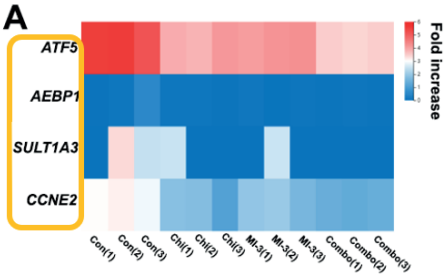


Figure 5 Heat map of clustering of four essential genes

About Us

Innomics Inc. offers cutting-edge next-generation sequencing (NGS) and mass spectrometry solutions to researchers and healthcare professionals. By leveraging advanced technologies and committing ourselves to continuous innovation, Innomics delivers cost-effective, high-quality solutions that help our clients achieve their research objectives swiftly and effectively.

We provide integrated multi-omics solutions to academic institutions, pharmaceutical companies, health care providers, and other organizations across a wide range of applications, including:

- Basic research on human, plant, animal and microbial species
- Clinical research in human health
- Genetic testing and screening
- Agriculture and biodiversity preservation and sustainability

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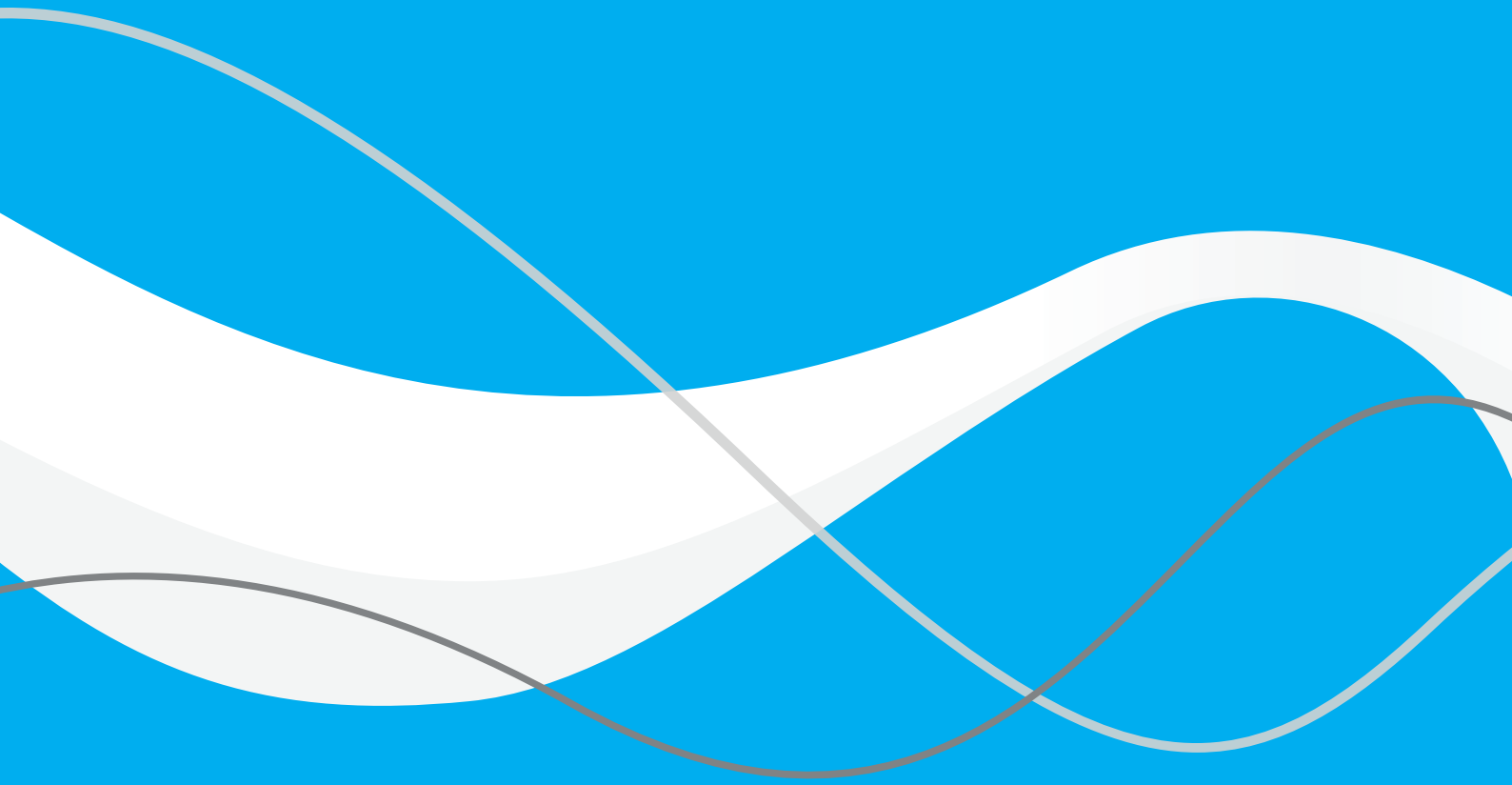
If you have any questions or would like to discuss how our services can help you with your research, please don't hesitate to contact us at P_contact@innomics.com. We look forward to hearing from you!



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