

Ontology-driven omics data mining

Bio-LDM (Biological Large Data Model)

Core ontology-grounded intelligence engine for discovering context-specific gene relationships, functional modules and disease mechanisms.

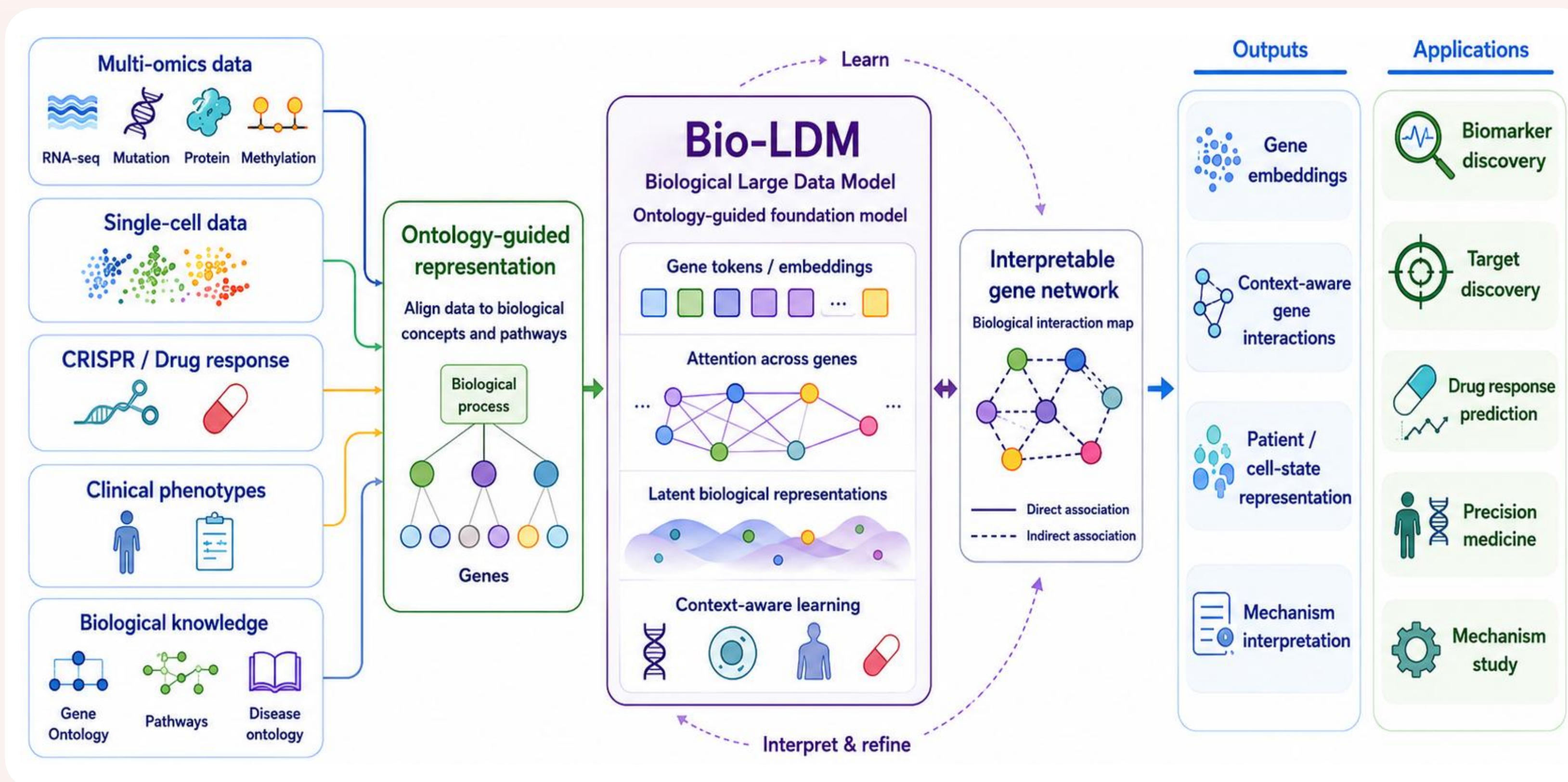
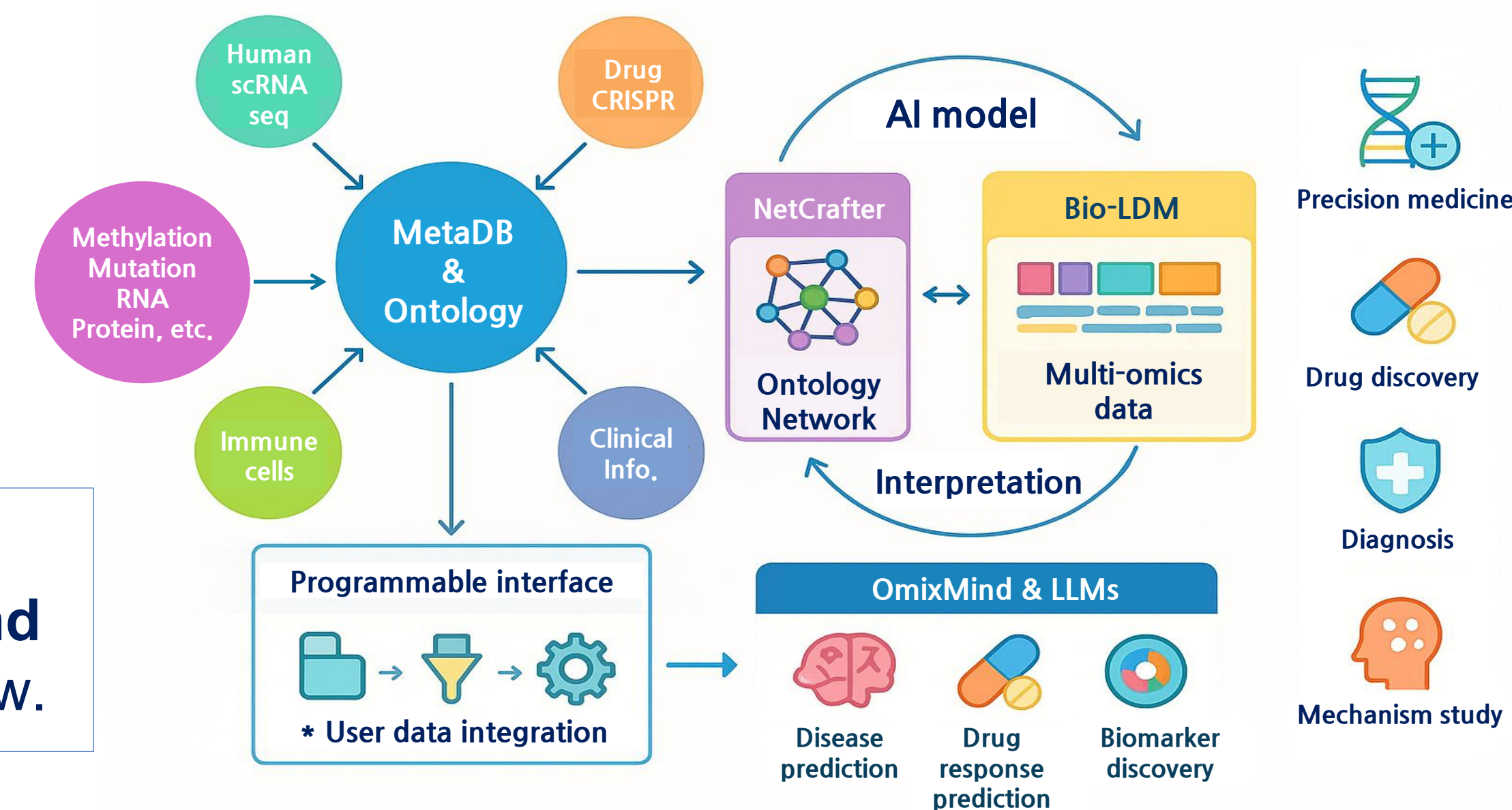
OmixMind & LLMs

Programmable LLM interface orchestrating Bio-LDM, MetaDB and NetCrafter for fully customized, project-specific analyses.

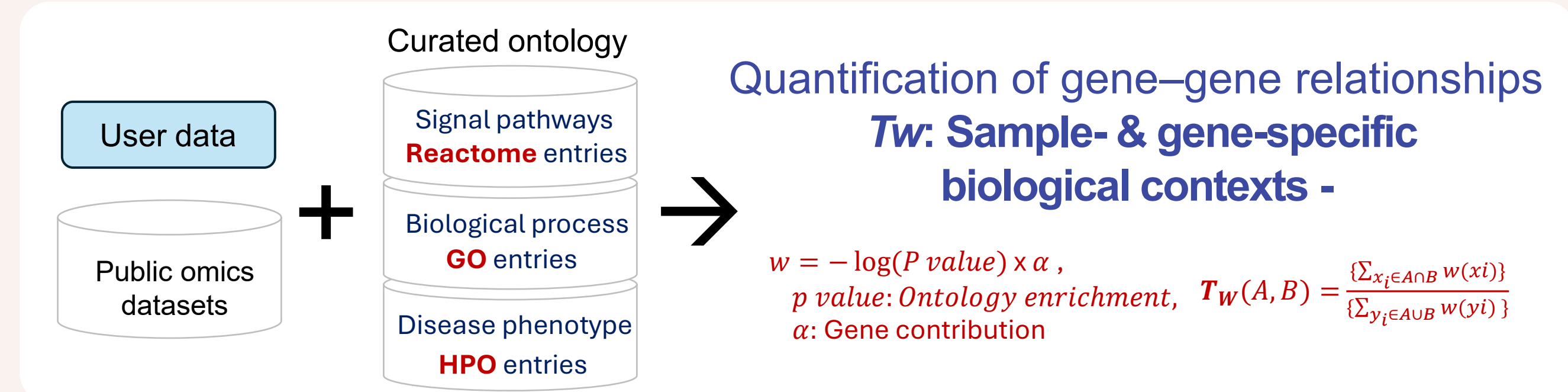
MetaDB

Over 1 billion multi-omics data point
30 billion cross-associations reinforced by consensus scores.

Bio-LDM discovers the hidden biology; **MetaDB** validates it, **NetCrafter** explains it and **OmixMind** turns it into a fully customized discovery workflow.



NetCrafter: Ontology-derived quantitative gene network modeling

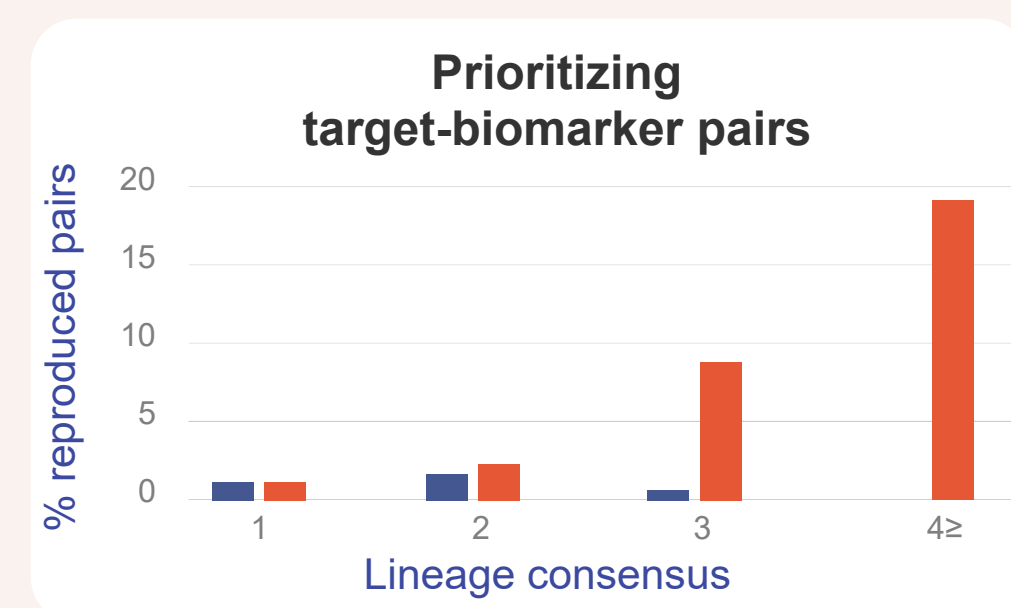


Meta DB prioritizes reproducible targets and biomarkers

- Consensus scoring on >30 billion associated data pairs in MetaDB
→ Reliable targets and biomarkers across lineages and subtypes

Lineage and sampling consensus analysis of PD-1 expression associated with patient survival

• PD-1 expression was significantly associated with patient survival in 28 of 34 TCGA cancer types (p-values < 0.05). Each lineage's result is itself backed by many sampling conditions. • Higher PD-1 was favorable across these lineages, holding up best in SKCM (135 of 216 conditions), then UCEC at 92 and LVM at 88. Next step: Open the Consensus view to see where the signal holds, or draw a Kaplan-Meier plot for a specific gene.									
Lineage	Measure	Sample split	Gender	Stage	Period	AUC...	AUC...	p-value	Sampling consensus
SKCM	OS	Median	All	All	Extend...	0.433	0.260	< 0.001	135
UCEC	DFS	Median	All	All	Extend...	0.756	0.507	< 0.001	92
LVM	OS	Median	All	All	Extend...	0.424	0.759	< 0.001	88
HN5C	DFS	Median	Male	All	Extend...	0.464	0.261	< 0.001	74
KIRP	OS	Quartile	All	All	Extend...	0.591	0.836	0.001	61
STAD	OS	Quartile	All	II/IV	Extend...	0.609	0.203	0.007	58
LGG (B...	OS	Median	All	All	Extend...	0.380	0.508	< 0.001	51
LAML	DFS	Tertile	All	All	3-year	0.430	0.730	< 0.001	40
CESC	OS	Tertile	All	All	5-year	0.870	0.721	0.004	32
KIRC	DFS	Quartile	All	All	5-year	0.750	0.855	0.005	32



Lineage consensus of associations between CRISPR efficacy and RNA expression

→ Gene pairs with high consensus showed stronger reproducibility in independent shRNA screens.

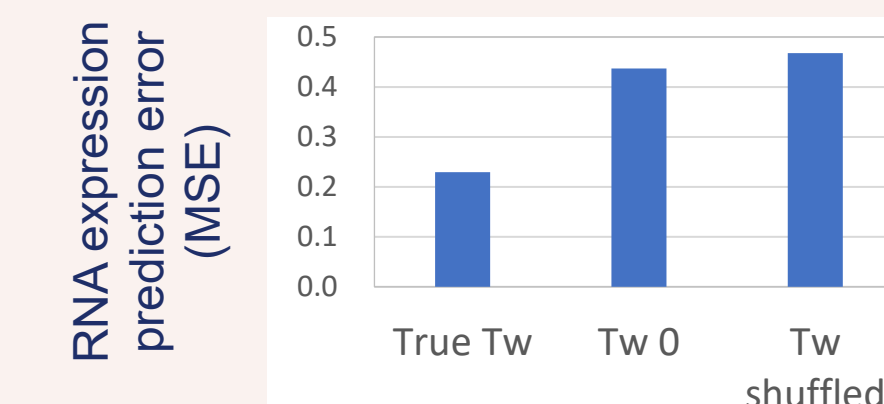
Bio-LDM: Ontology-guided Bio-AI architecture

Problem: Sparse omics data and incomplete ontology context limit conventional Bio-AI

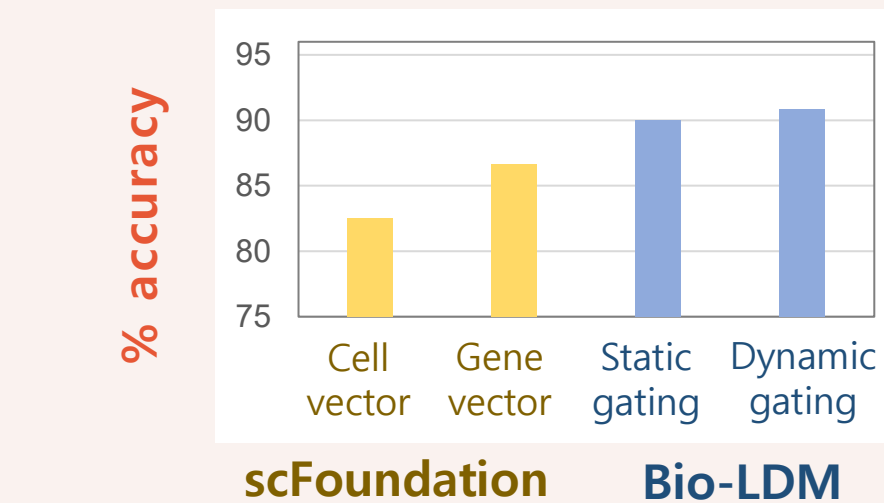
Solution: Bio-LDM™ learns structured biological context through NetCrafter-derived T_{w} -gated attention

$$\text{Gene - Gene score}_{ij} = \frac{Q_i K_j^T}{\sqrt{d_k}} + f(T_{w_{ij}}), \text{ Ontology gating: } f_{ij} \approx T_{w_{ij}}(Q_i \cdot w_{Tw} + K_j \cdot w_{Tw})$$

Omics data prediction



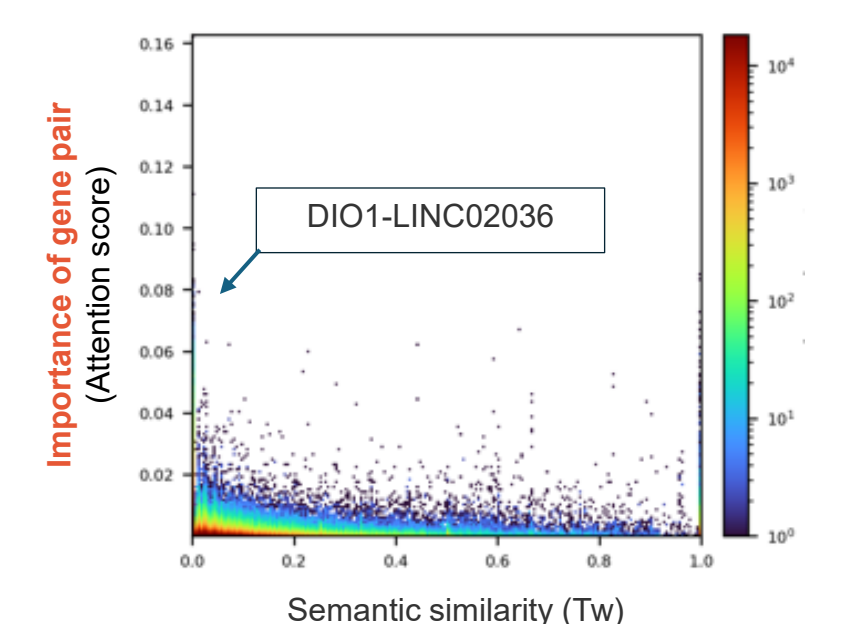
Sample type prediction



- Paper published (Briefings in Bioinformatics, 2026)
- Patent application filed in Korea, USA & China

Finding novel, tumor-specific gene-gene interaction

* Comparative analysis of attention score with T_w (functional association)



OmixMind: Text-to-Data mining

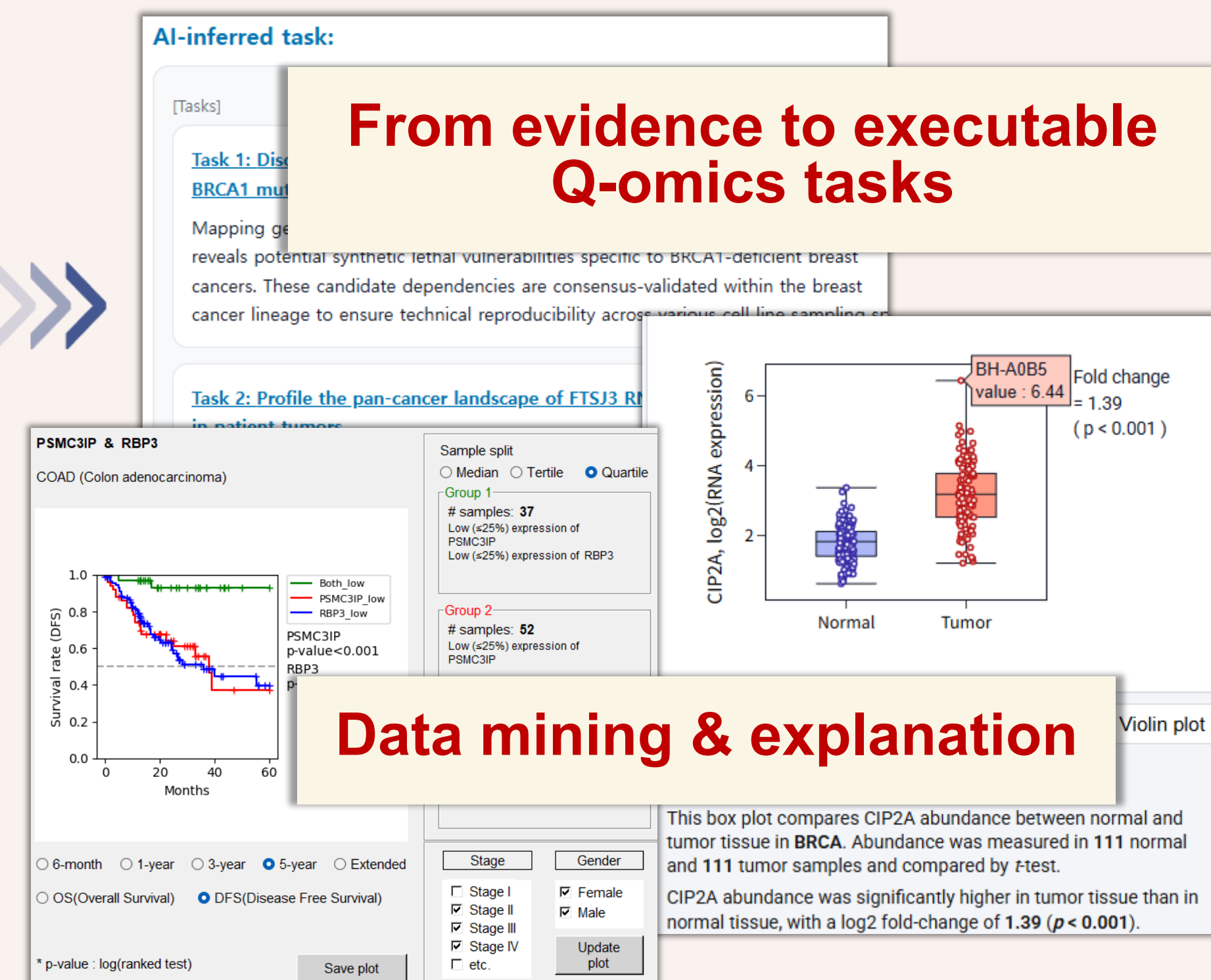
AI-assisted research synthesis

Research digest - Essential findings & trends from recent literature
50 papers from 159 results • 5 research clusters

Computational Prediction of Cancer Genetic Interactions (25 papers selected)
Keywords: Knowledge graphs, Graph neural networks, Transcriptomic buffering, Multi-omics integration, Genetic dependency
Summary: Advanced computational models, particularly knowledge graph-based neural networks and multimodal deep learning frameworks, are increasingly driving the prediction of novel synthetic lethal gene pairs for targeted cancer therapy. By integrating multi-omics profiles, transcriptomic buffering signatures, and high-order network structures, algorithms like BioPathNet and DigiBasil utilize path-based reasoning to capture complex molecular interactions and overcome the selection biases inherent in experimental CRISPR screens. These predictive frameworks enable the robust prioritization of context-specific genetic vulnerabilities, facilitating the discovery of reliable therapeutic targets across diverse cancer histotypes.

Multiplexed CRISPR Platforms for Genetic Interactions (12 papers selected)
Keywords: enAsCas12a, PROPER-seq, MARCH5, SLC25A28, Dual-guide CRISPR systems
Summary: Optimization of AsCas12a for combinatorial genetic screens in human cells. Nature biotechnology

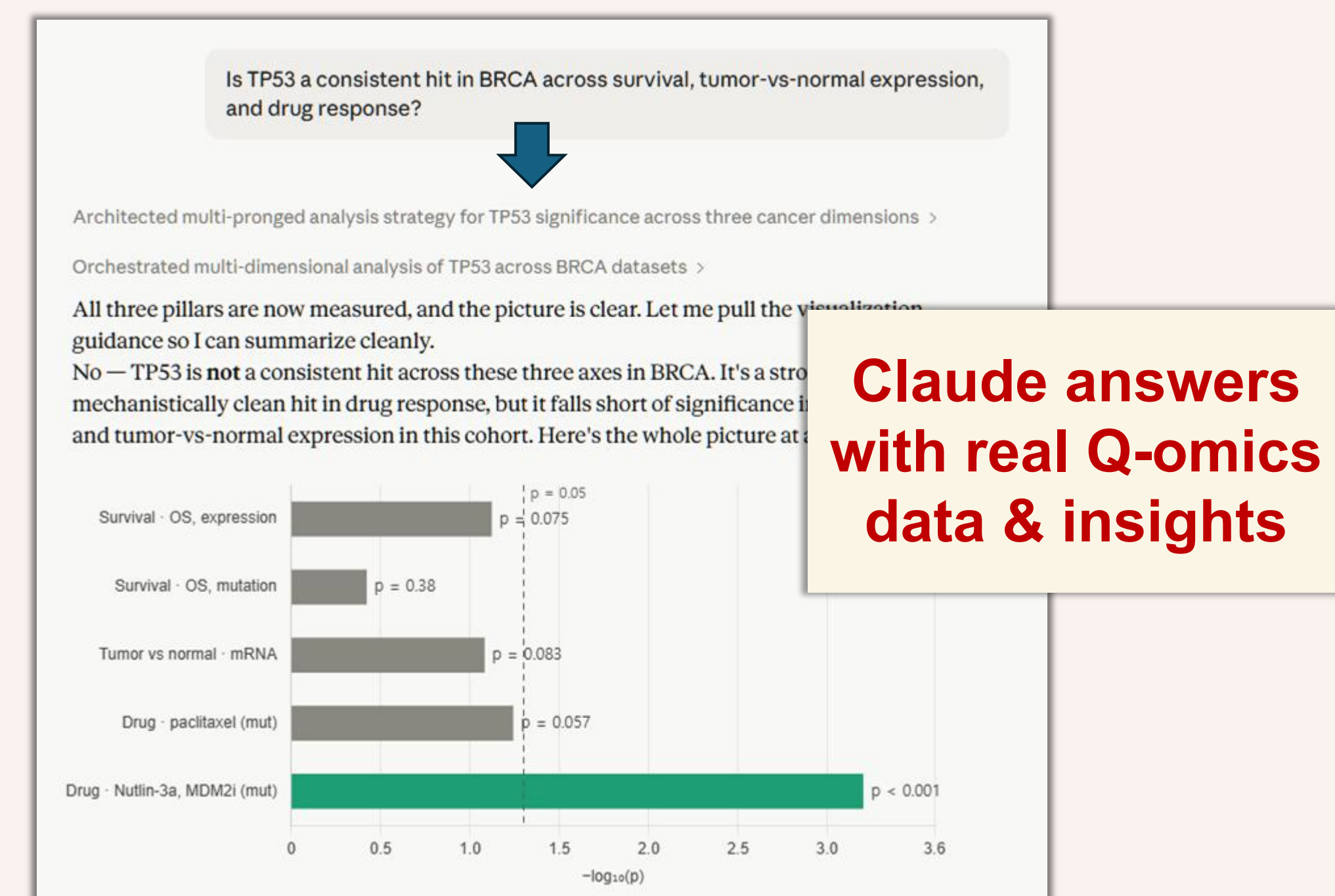
From evidence to executable Q-omics tasks



Data mining & explanation

Connect LLMs to Q-omics

AI agents for research & drug discovery pipelines



Claude answers with real Q-omics data & insights

Diverse applications including:

- Drug target and biomarker discovery
- Functional interpretation for underlying mechanisms and disease phenotypes
- Biomarkers in immunotherapy response
- Synthetic lethal gene pairs
- Tumor- antigen discovery
- Undruggable targets and new modalities in drug discovery
- AI-assisted analysis of user data

Availability & Collaboration

- Explore Q-omics **SaaS** at <https://qomics.ai>, AWS Cloud and via **MCP** on **Claude** and **ChatGPT**
- For collaboration, we offer partner-specific **Evidence Sprint**, **cloud/API integration** and confidential **PoC** options