Q-omics

https://qomics.io

Smart Platform for Cancer Research

Data mining through ontology derived gene network modelling

Sukjoon Yoon, Professor
Dept of Biological Sciences,
Sookmyung women's university
& CBiS Inc., Seoul, Korea
Contact : yoonsj@sookmyung.ac.kr

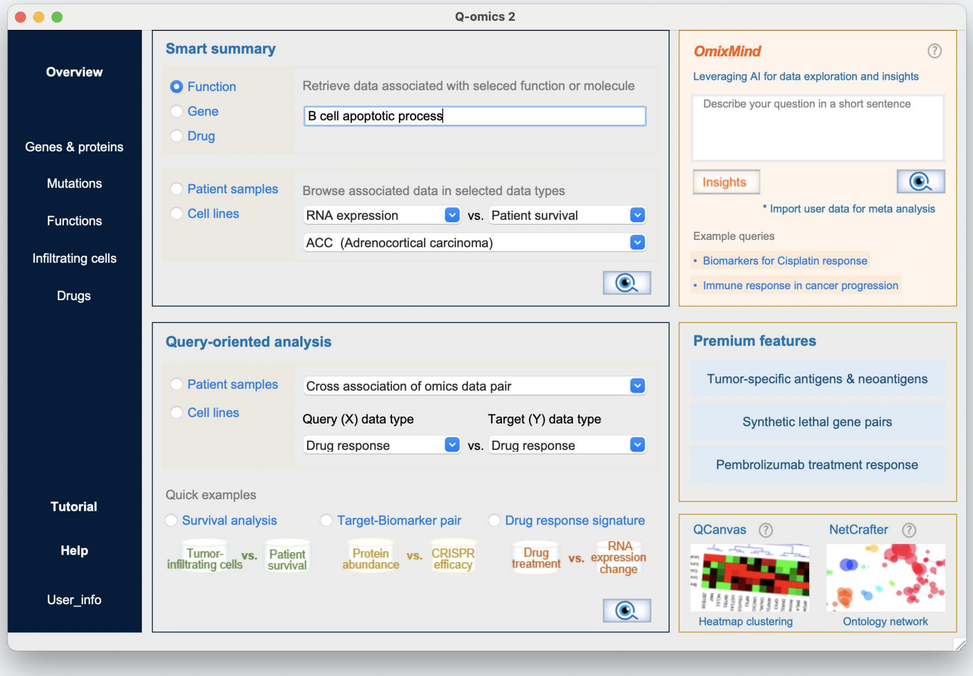
Q-omics is an AI-powered omics data mining platform that helps cancer researchers identify tumor-specific targets, prognostic biomarkers and underlying mechanisms - without requiring bioinformatics expertise.

The platform integrates over 1 billion multi-modal omics data points and computes 30 billion cross-associations reinforced by pan-cancer consensus scores. These associations are stored in **MetaDBs**, forming a foundational resource for robust target-biomarker discovery and mechanism studies.

At its core, the **NetCrafter** module builds ontology-derived gene networks to reveal functional gene modules and mechanistic hotspots across cancer types.

The **OmixMind** assistant enables "text-to-data mining" automatically generating research trends, Q-omics workflows and interpretations from natural-language queries.

Q-omics is evolving into **Bio-LDM**, a foundation model for autonomous omics data interpretation and novel hypothesis generation.



~1 billion public omics data

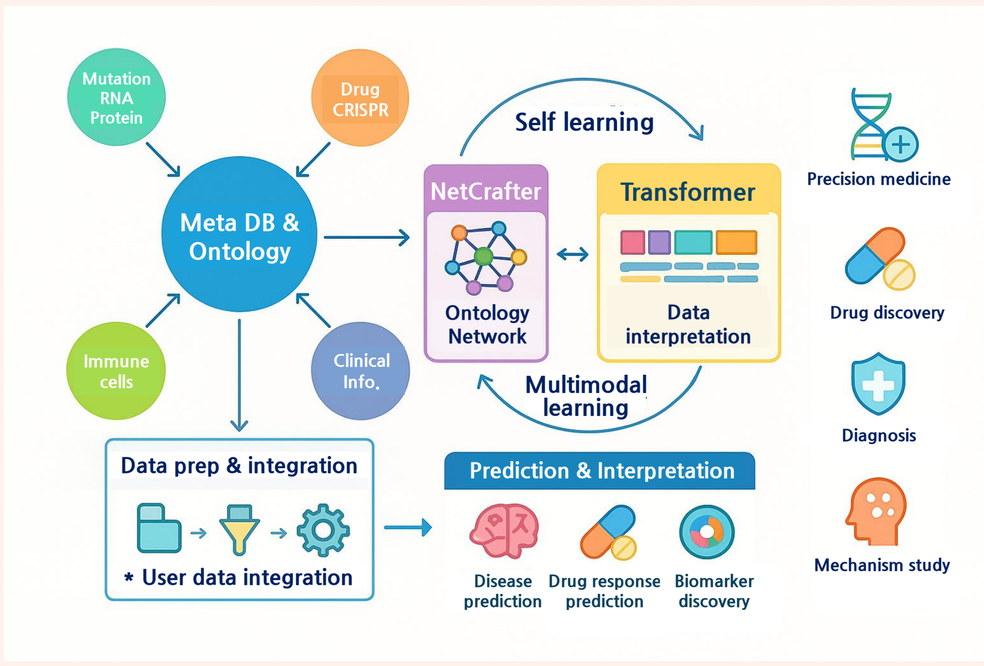
~30 billion proprietary meta data

+

Ontologies & Gene sets

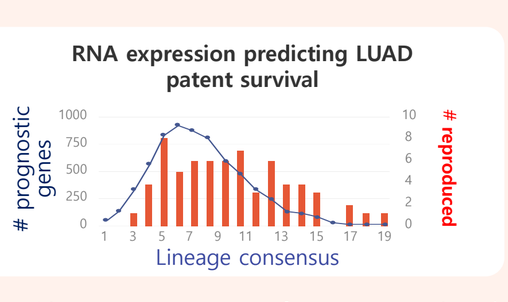
AI models: LLMs & Graph transformers

Biological Large Data Model (Bio-LDM)



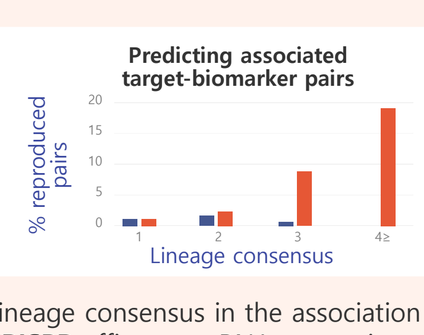
Consensus-driven reproducible data mining

- **Consensus scoring** on >30 billion associated data pairs in **Meta DBs**
  - → **Finding consensus targets and biomarkers across lineages and subtypes**



Blue: Lineage consensus of genes associated with patient survival in ~33 cancer lineages

Scarlet: Distribution of lineage consensus of prognostic LUAD-specific prognostic genes

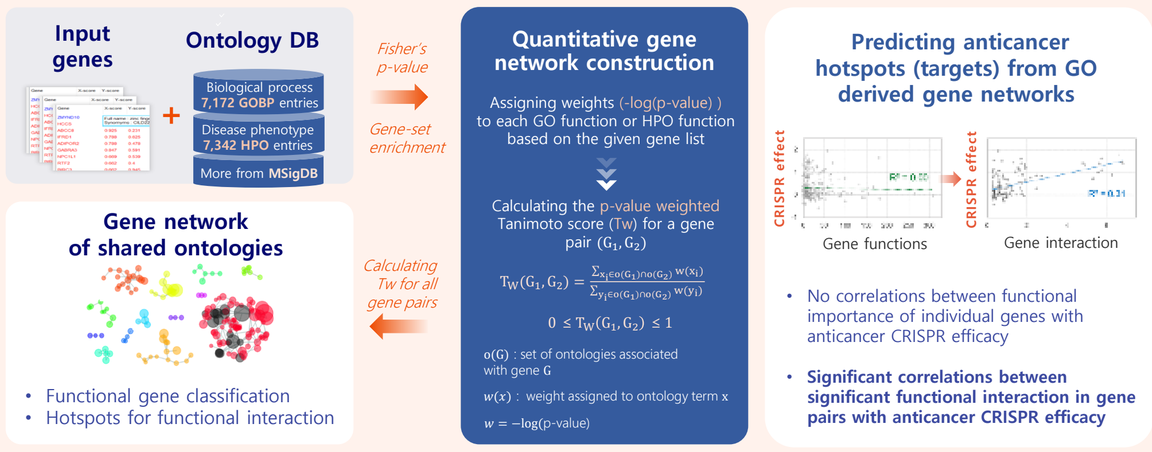


Lineage consensus in the association between **CRISPR** efficacy vs. RNA expression gene pairs

→ Gene pairs with high consensus showed stronger reproducibility in **shRNA** experiment.

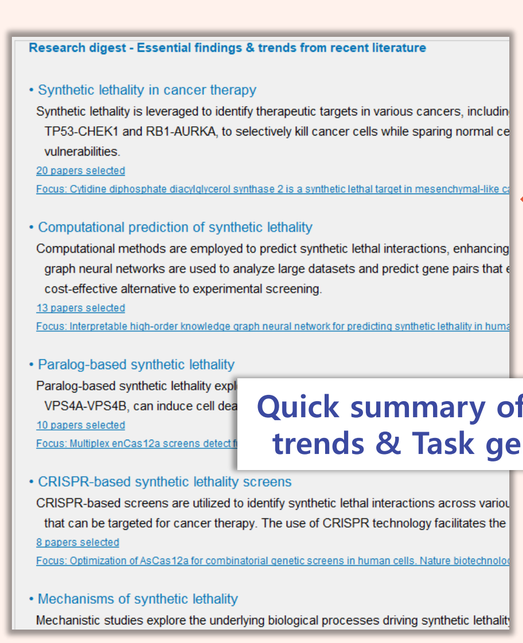
How to interpret results?

- **NetCrafter:** Ontology-derived gene network modeling and interpretation

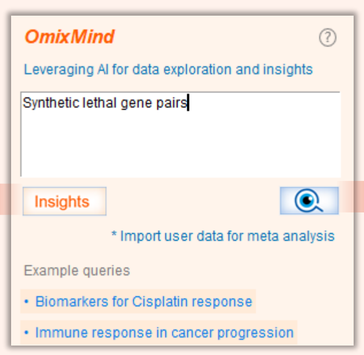


How to start data mining?

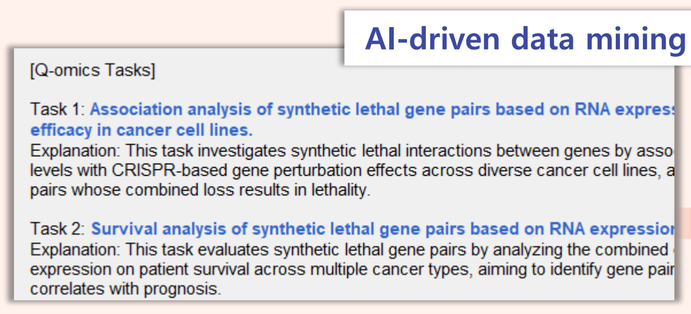
- **OmixMind : "Text-to-Data Mining" Assistant → No bioinformatics skills required**



Quick summary of research trends & Task generation

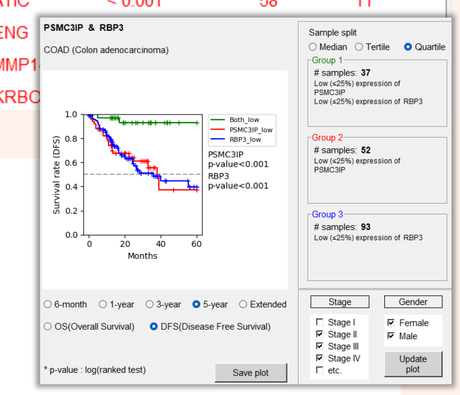


AI-driven data mining



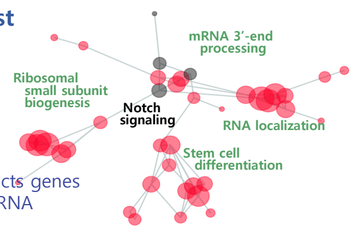
Gene pairs whose synergistic RNA expression is significant associated with patient survival

RNA expression (X)	RNA expression (Y)	p-value (Both low vs Y low)	Sampling consensus	Lineage consensus
PSMC3IP	RBP3	< 0.001	81	11
SULT2B1	SERF2	< 0.001	62	12
ALX1	ZDHHC9	< 0.001	61	12
ATP13A1	DPM2	< 0.001	61	11
KIAA1614	ATIC	< 0.001	58	11
CDK16	ENG			
PAXIP1	MMP1			
NGF	KRBC			



Functional interaction in most consensus gene pairs

Sampling consensus > 20,
Lineage consensus > 10



Genes in Notch signaling connects genes in stem cell differentiation and RNA metabolism

Survival analysis of synthetic lethal gene pairs

Co-low expression of RSMC3IP and RBP3 showed improves patient survival compared to individual low expression in 182 patients

Diverse applications including:

- Consensus drug, target and biomarker discovery
- Functional interpretation for underlying mechanisms and disease phenotypes
- Biomarkers in immunotherapy response
- Synthetic lethal gene pairs
- Tumor-specific antigens and neo-antigens
- Pan-cancer agnostic target discovery
- Visualization and integrated analysis of user data
- Undruggable targets and new modalities in drug discovery

References

NetCrafter: Ontology-based gene network construction and interpretation, (Submitted)

Current advances in comprehensive omics data mining for oncology and cancer research, Biochim Biophys Acta Rev Cancer, 2023 Nov.

Q-omics: Smart software for assisting oncology and cancer research, Mol Cells, 2021, 44(11):843-850

Availability & Collaboration

- Q-omics 2 standard edition is free to use → https://qomics.io
- The web-based, smarter and more convenient **Q-omics 3** will be available in Dec. 2025
- We are open to collaborative opportunities in data mining and drug discovery