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Smart Platform for Omics Data Mining and Precision Medicine



•	Q-omics 2	
Overview Function O Gene	Retrieve data associated with seleced function or molecule	Ad hoc analysis (2) Leveraging AI for data exploration and insights Describe your question in a short sentence
Nes & proteins Drug Mutations Patient s Functions Etrating cells Drugs	Browse associated data in selected data types (data-1) vs. (data-1) (Select lineage)	Examples • Biomarkers for Olaparbi response • Immune response in cancer progression • CRESPR targets associated with TPS3 mutations? • more
Query-orie		Premium features
Patient s Cell lines	Couery (X) data type Target (Y) data type (data-1) Street (data-2)	Synthetic lethal gene pairs

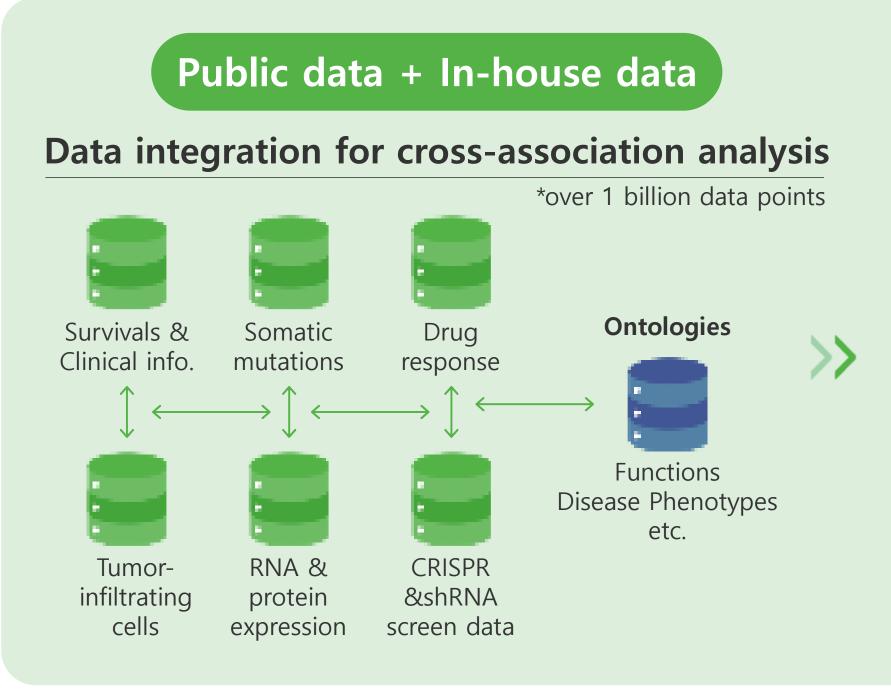
Q-omics integrates vast meta-data with LLMs and ontology-based deep learning, creating an unprecedented "Text-to-Omics Data Mining" smart platform. Researchers can effortlessly identify anticancer targets, biomarkers, and underlying mechanisms from complex multi-omics data—no computational skills required. With expanding omics datasets and advancing AI, Q-omics continuously evolves to enhance the analysis and interpretation of omics data, supporting biomedical research.



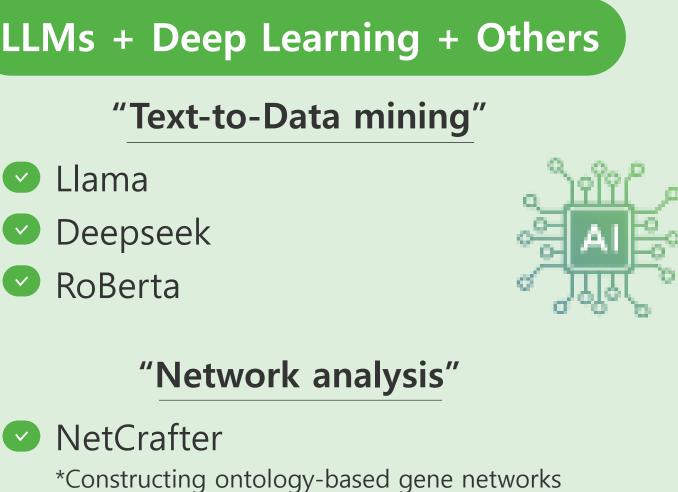
Tired of struggling with complex bioinformatics tools and outsourcing data analysis?

Q-omics can help!

Scalable platform for accelerating research and drug discovery



Q-omics p	olatform	LLMs + Deep Learning	
Meta DBs	Ad-hoc analysis	"Text-to-Data min	
Over 30 billion cross	Simple text queries	Llama	
-associated omics	V	Deepseek	
meta data pairs	Workflow generation	RoBerta	
	V		
-	Python coding	"Network analys	
	V		
Data consensus across pan-	Data mining and Analysis	VetCrafter	
cancer datasets	V	*Constructing ontology-based of	
Ontologies for data clustering and interpretation	Summary, Visualization & Prediction	GNN (Graph Neural N *Predicting anticancer botspots	



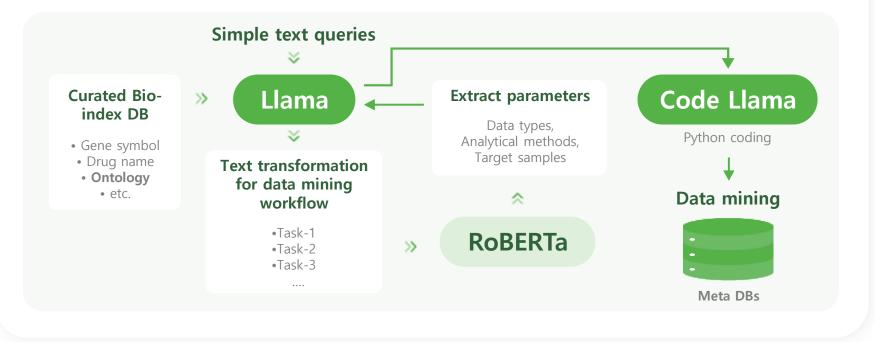
Network) *Predicting anticancer hotspots

Innovations in Q-omics.

How to start data mining?

Ad-hoc : Al-assisted workflows

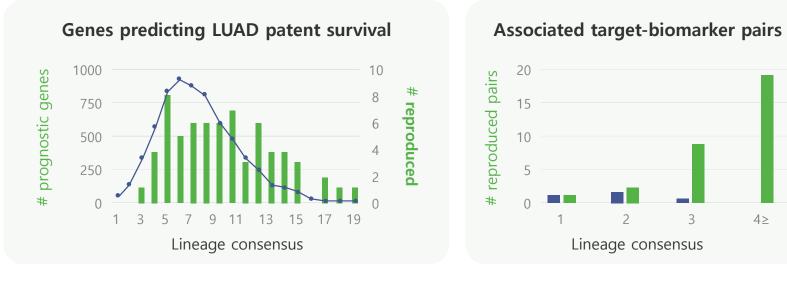
 \rightarrow No need of bioinformatics skills



Reliable & reproducible data mining?

Meta DBs : >30 billion associated data pairs

 \rightarrow Consensus targets and biomarkers across lineages and subtypes

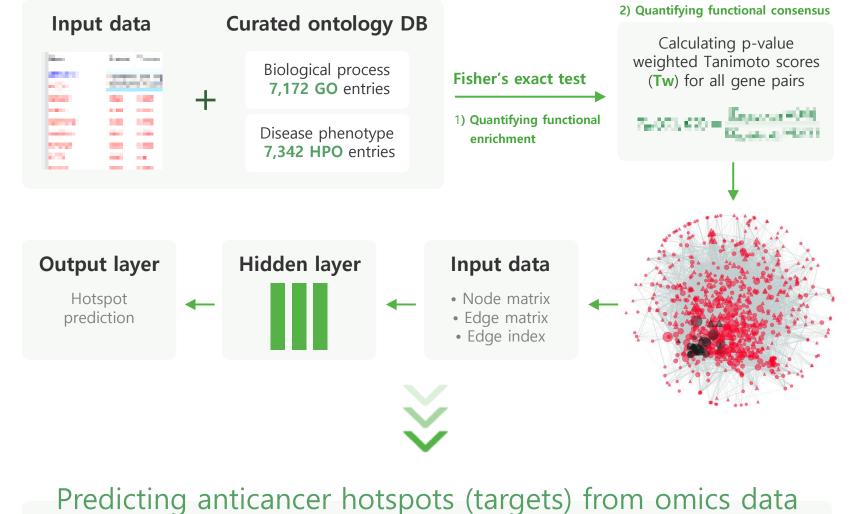


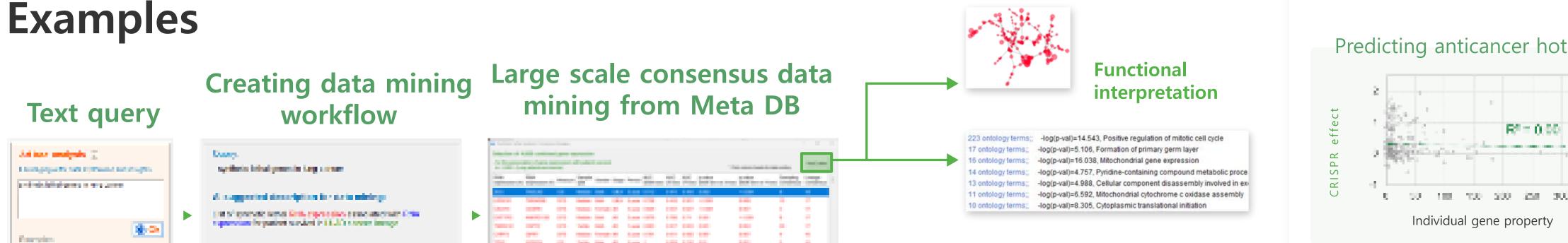
How to interpret results?

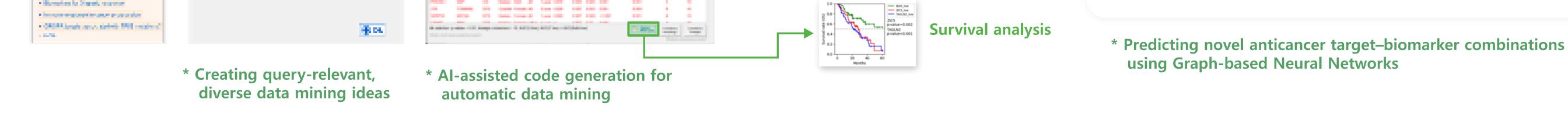
Ontology-based network analysis

 $R^{0} = 0.00$

 \rightarrow Create N2 connections with N gene data and machine learning







Allows for various application scenarios

- Consensus data for drug, target and biomarker discovery
- Gene-to-Function interpretation for underlying mechanisms and disease phenotypes
- Biomarkers in immunotherapy response
- Analysis of synthetic lethal gene pairs
- And many more ...

• Tumor-specific antigens and neo-antigens

The second second

- Pan-cancer agnostic target discovery
- Visualization and integrated analysis of user data
- Undruggable targets and new modalities in drug discovery

Availability & Collaboration

* Q-omics standard edition is free to use

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- * Customized editions are available to suit your needs
- * Partner with us on data-driven discovery projects

Explore Q-omics today https://qomics.io

 $R^{2} = 0.31$

Gene connections (Tw)

