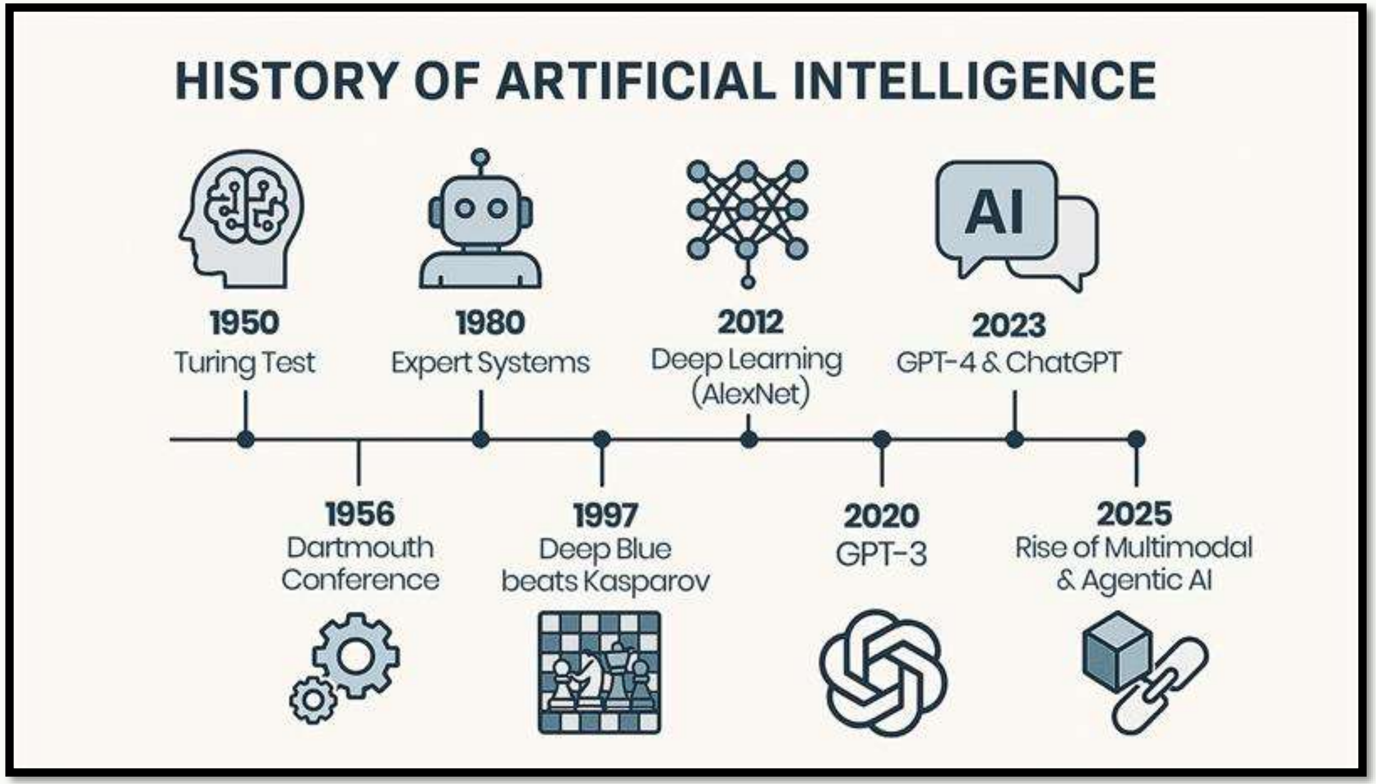
Enrich AI

Κουμαδωράκης Δημήτριος
Υποψήφιος Διδάκτορας Τμήμα Πληροφορικής
Ιονίου Πανεπιστημίου
Υπεύθυνος Καθηγητής: Αριστείδης Βραχάτης



AI in Biology

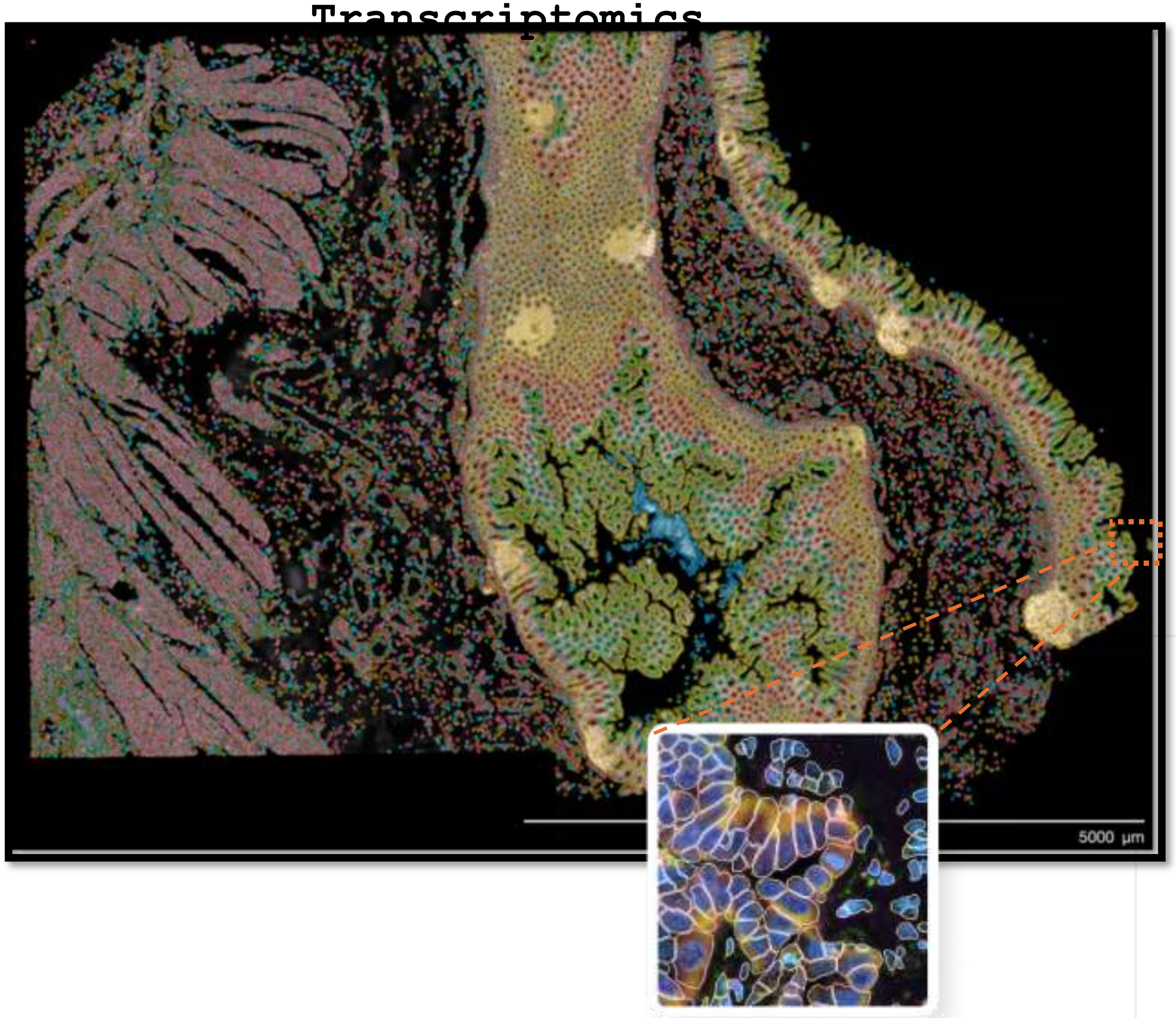
COMPLEXITY

DATA VOLUME

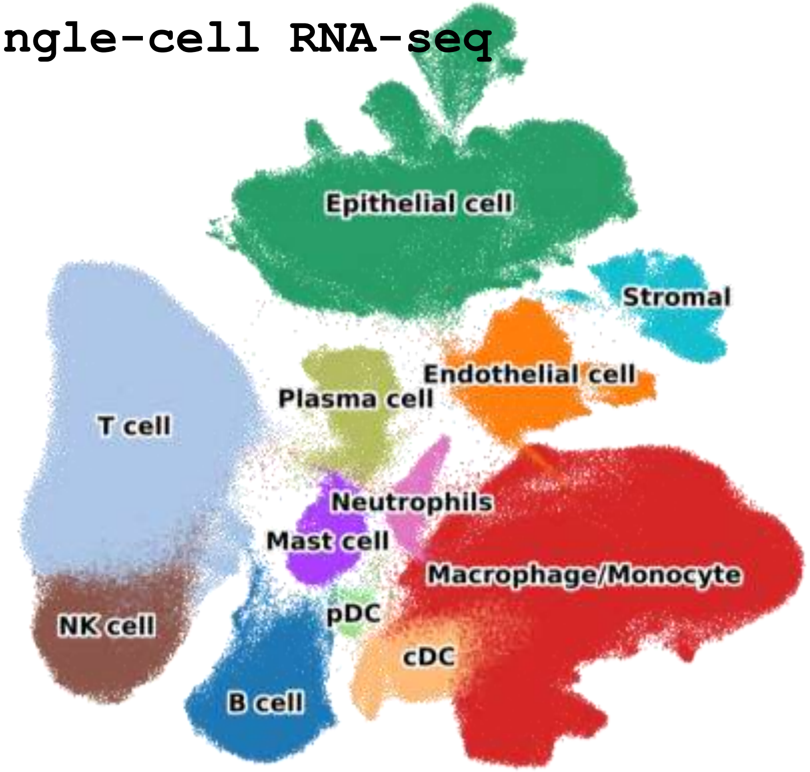
SPEED

INTEGRATION

Spatial Transcriptomics



Single-cell RNA-seq



Why genes matter:

- Cell typing
- Cell functions
- Disease mechanisms
- Differentiation
- Clinical relevance
- …

Enrichment Analysis

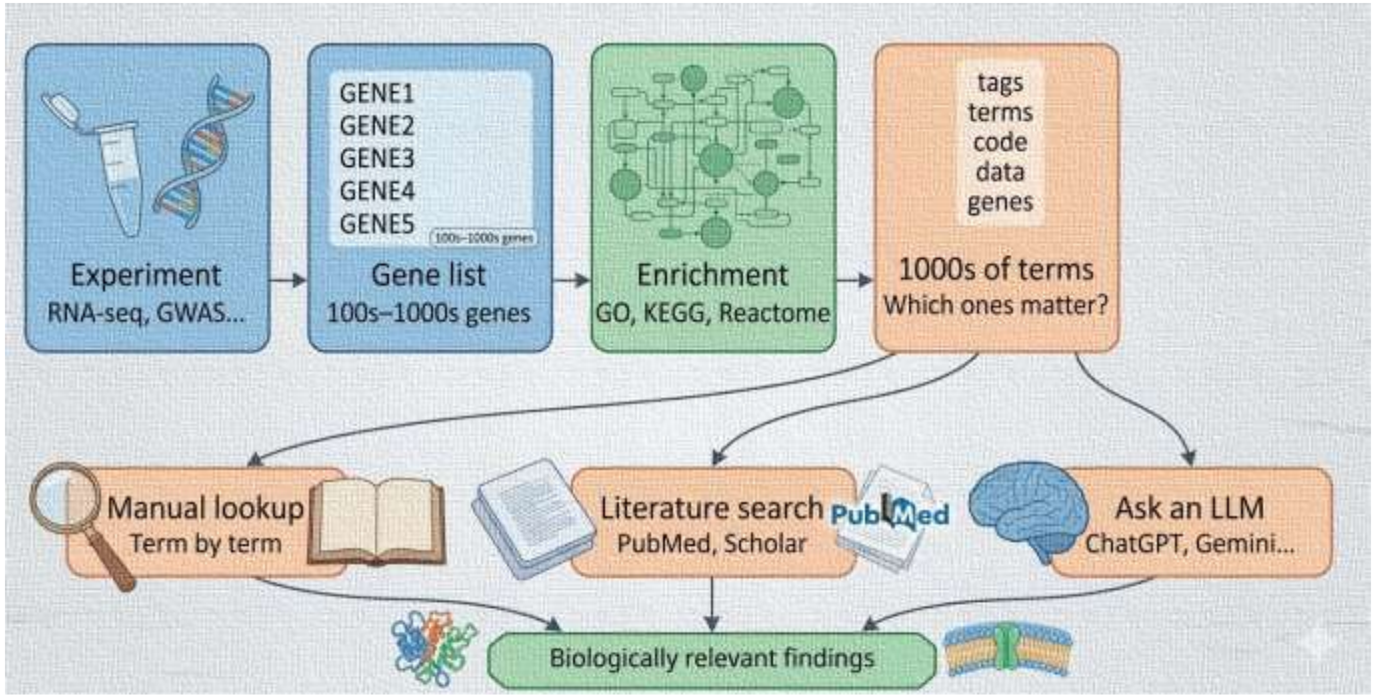
A statistical way to find enriched biologi l pathways . a t

Enrichr

clusterProfiler

NIH National Institutes of Health
DAVID Bioinformatics

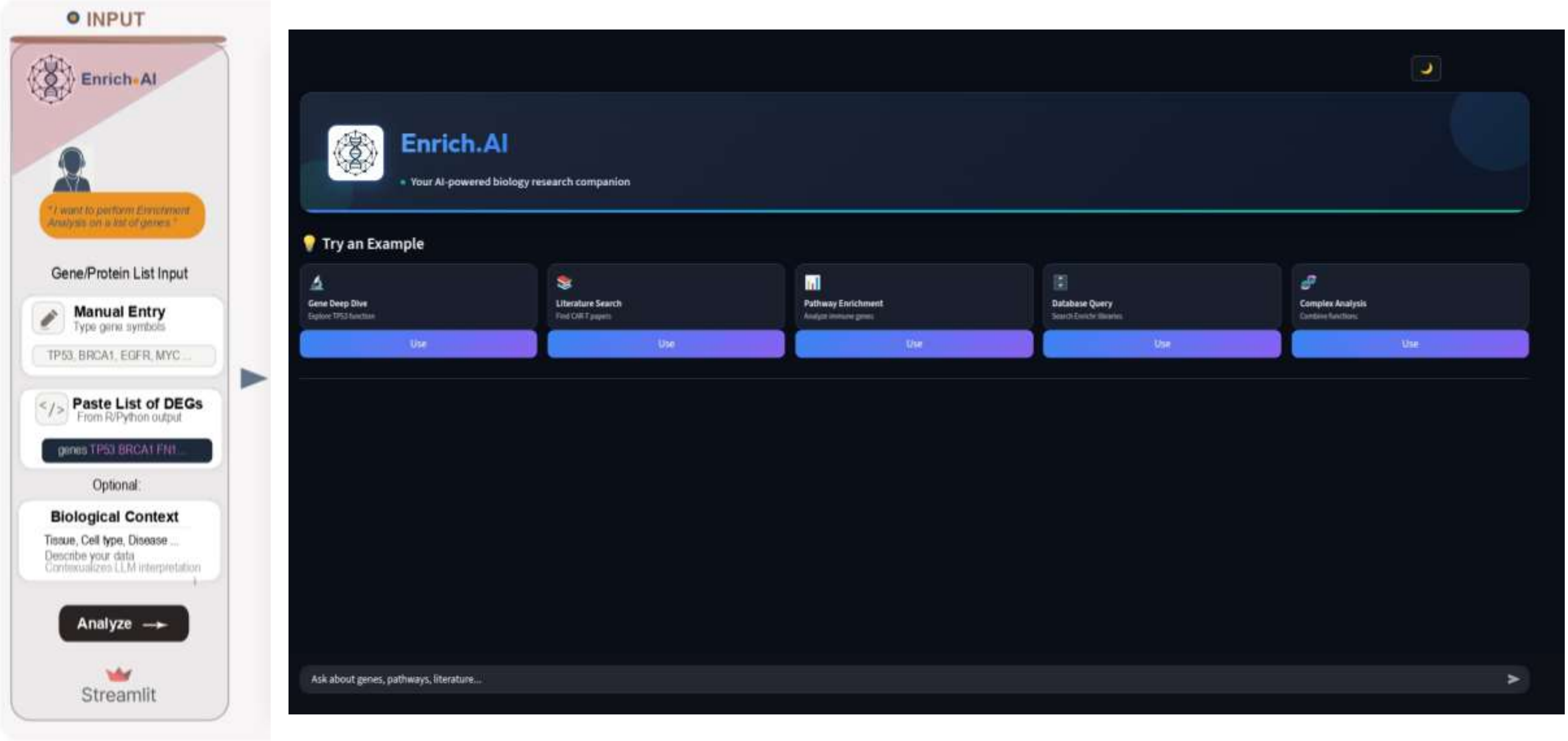
Current Workflow for a biologist:



Result:
Multiple hours spent without even visualizing them!

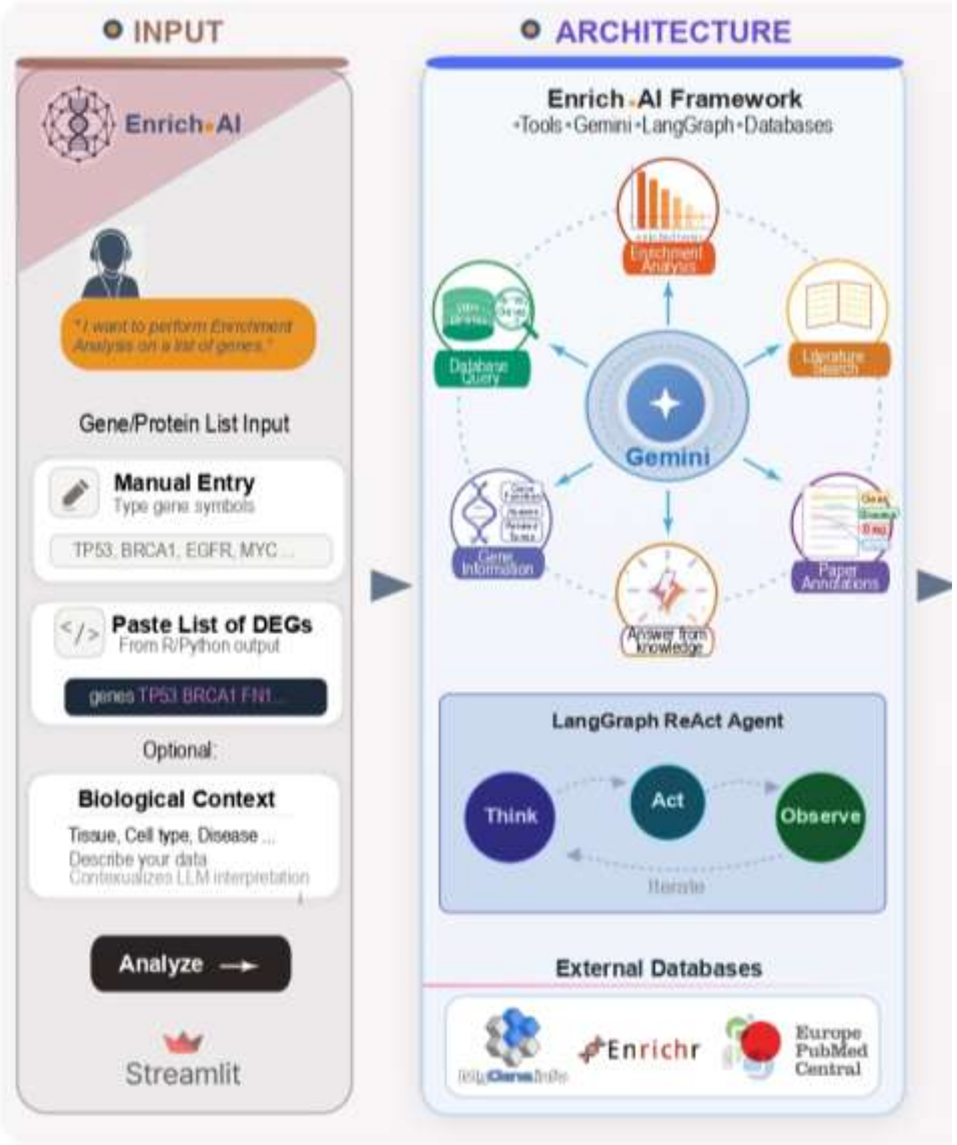
Enrich.AI

Autonomous LLM-Driven Enrichment Analysis Platform

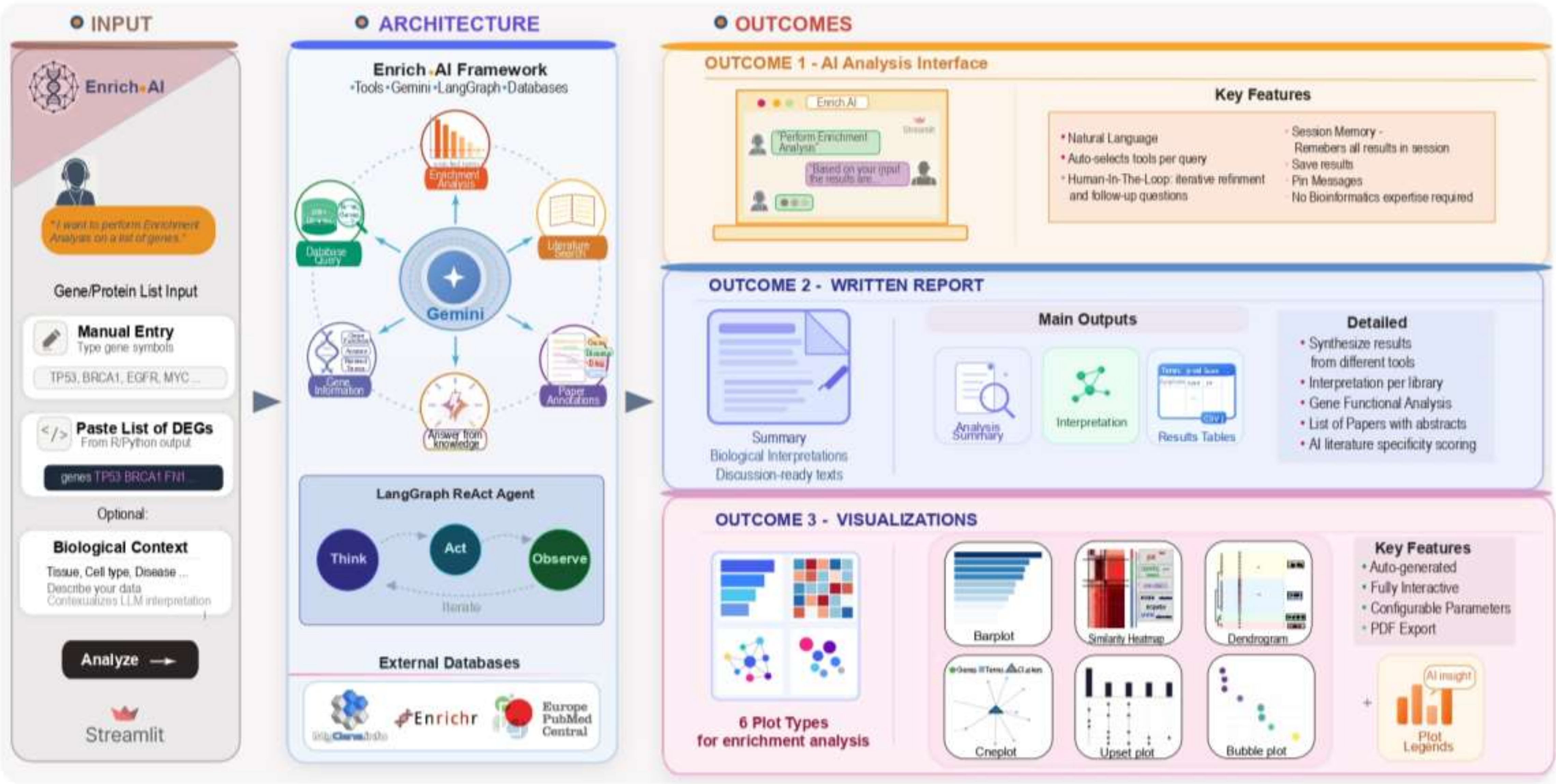


Enrich.AI

Autonomous LLM-Driven Enrichment Analysis Platform



Enrich.AI
Autonomous LLM-Driven Enrichment Analysis Platform



INPUT

Enrich.AI

"I want to perform Enrichment Analysis on a list of genes."

Gene/Protein List Input

Manual Entry
Type gene symbols
TP53, BRCA1, EGFR, MYC ...

Paste List of DEGs
From R/Python output
genes TP53 BRCA1 FN1 ...

Optional:

Biological Context
Tissue, Cell type, Disease ...
Describe your data
Contexualizes LLM interpretation

Analyze →

Streamlit

ARCHITECTURE

Enrich.AI Framework
•Tools •Gemini •LangGraph •Databases

Gemini
Enrichment Analysis
Literature Search
Paper Annotations
Answer from knowledge
Gene Information
Database Query

LangGraph ReAct Agent
Think
Act
Observe
Iterate

External Databases
Enrichr
Europe PubMed Central

OUTCOMES

OUTCOME 1 - AI Analysis Interface

Enrich.AI
"Perform Enrichment Analysis"
"Based on your input the results are..."

Key Features
- Natural Language
- Auto-selects tools per query
- Human-In-The-Loop: iterative refinment and follow-up questions
- Session Memory - Remebers all results in session
- Save results
- Pin Messages
- No Bioinformatics expertise required

OUTCOME 2 - WRITTEN REPORT

Summary
Biological Interpretations
Discussion-ready texts

Main Outputs
Analysis Summary
Interpretation
Results Tables

Detailed
- Synthesize results from different tools
- Interpretation per library
- Gene Functional Analysis
- List of Papers with abstracts
- AI literature specificity scoring

OUTCOME 3 - VISUALIZATIONS

6 Plot Types for enrichment analysis

Barplot
Similarity Heatmap
Dendrogram
Cneplot
Upset plot
Bubble plot

Key Features
- Auto-generated
- Fully Interactive
- Configurable Parameters
- PDF Export

+

AI insight
Plot Legends

AI Analysis Summary

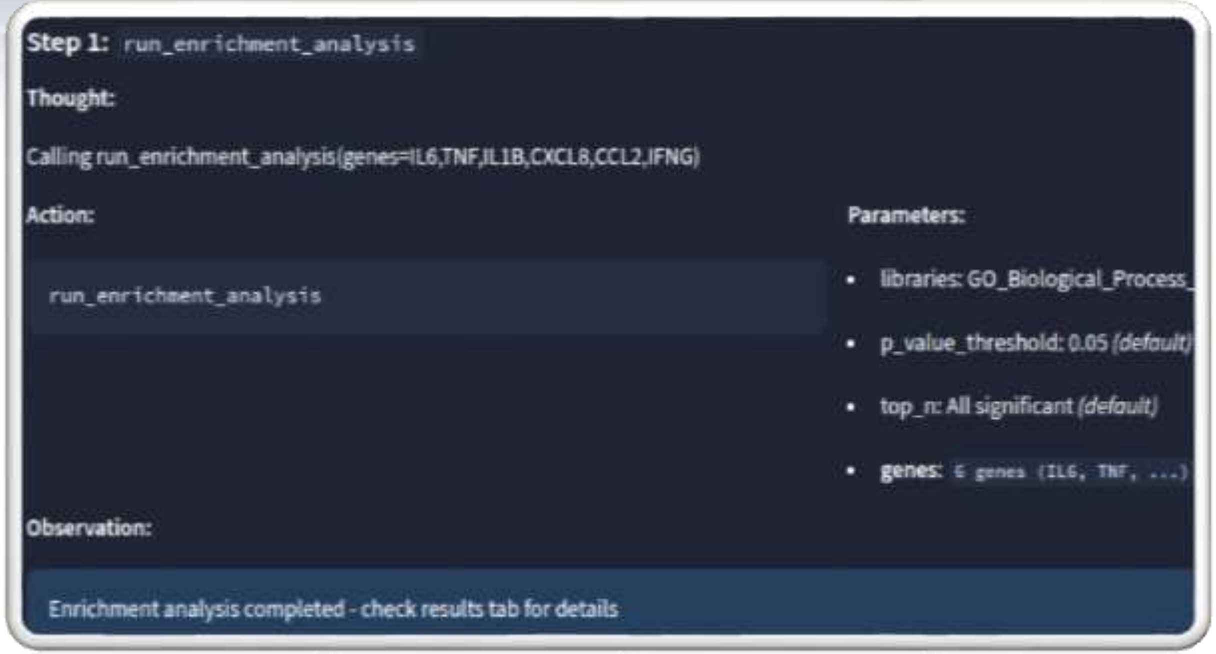
An enrichment analysis was conducted on a provided gene list comprising IL6, TNF, IL1B, CXCL8, CCL2, and IFNG using the `run_enrichment_analysis` tool, which leveraged several Enrichr libraries including GO Biological Process, GO Molecular Function, KEGG, Reactome, and MSigDB Hallmark. The objective was to identify significantly enriched biological themes, given that the input genes are established pro-inflammatory cytokines and chemokines.

The analysis identified 702 highly significant terms, robustly confirming the genes' established roles in immunity and inflammation across various biological contexts. Top GO Biological Process terms included "Inflammatory Response" (Adjusted P-value: 1.45e-09) and "Cellular Response To Lipopolysaccharide," while GO Molecular Function terms were led by "Cytokine Activity" (Adjusted P-value: 7.76e-12) and "Chemokine Activity." KEGG analysis revealed strong associations with numerous infectious diseases like "Malaria" (Adjusted P-value: 1.52e-14), "Chagas disease," and "Influenza A," alongside autoimmune conditions such as "Rheumatoid arthritis," and central pathways including "IL-17 signaling pathway" and "Cytokine-cytokine receptor interaction." Further reinforcing these findings, Reactome highlighted "Signaling By Interleukins" and "Cytokine Signaling In Immune System," while MSigDB Hallmark pointed to "Allograft Rejection," "TNF-alpha Signaling via NF-kB," and "IL-6/JAK/STAT3 Signaling."

These coherent findings unequivocally demonstrate that the provided gene list represents core inflammatory mediators critical for orchestrating innate and adaptive immune responses. Their consistent enrichment across diverse databases underscores their fundamental roles in recruiting immune cells, activating effector functions, and serving as key signaling hubs in complex immune networks. This comprehensive analysis confirms their direct involvement in host defense against a broad spectrum of infectious diseases and their significant contribution to autoimmune and chronic inflammatory pathologies, including roles in neuroinflammation, cellular stress responses, and metabolic inflammation, reflecting their central role in both acute and long-term immune regulation and disease progression.

Results Table

term	library
Inflammatory Response (GO:0006954)	GO_Biological_Process_2023
Cellular Response To Lipopolysaccharide (GO:0071222)	GO_Biological_Process_2023
Regulation Of Calcidiol 1-Monooxygenase Activity (GO:0060558)	GO_Biological_Process_2023
Positive Regulation Of Cellular Biosynthetic Process (GO:0031328)	GO_Biological_Process_2023
Regulation Of Peptide Hormone Secretion (GO:0090276)	GO_Biological_Process_2023
Positive Regulation Of Chemokine Production (GO:0032722)	GO_Biological_Process_2023
Regulation Of Glial Cell Proliferation (GO:0060251)	GO_Biological_Process_2023
Positive Regulation Of Phagocytosis (GO:0050766)	GO_Biological_Process_2023
Regulation Of Neurogenesis (GO:0050767)	GO_Biological_Process_2023
Cytokine-Mediated Signaling Pathway (GO:0019221)	GO_Biological_Process_2023



Step 1: `run_enrichment_analysis`

Thought:

Calling run_enrichment_analysis(genes=IL6,TNF,IL1B,CXCL8,CCL2,IFNG)

Action:

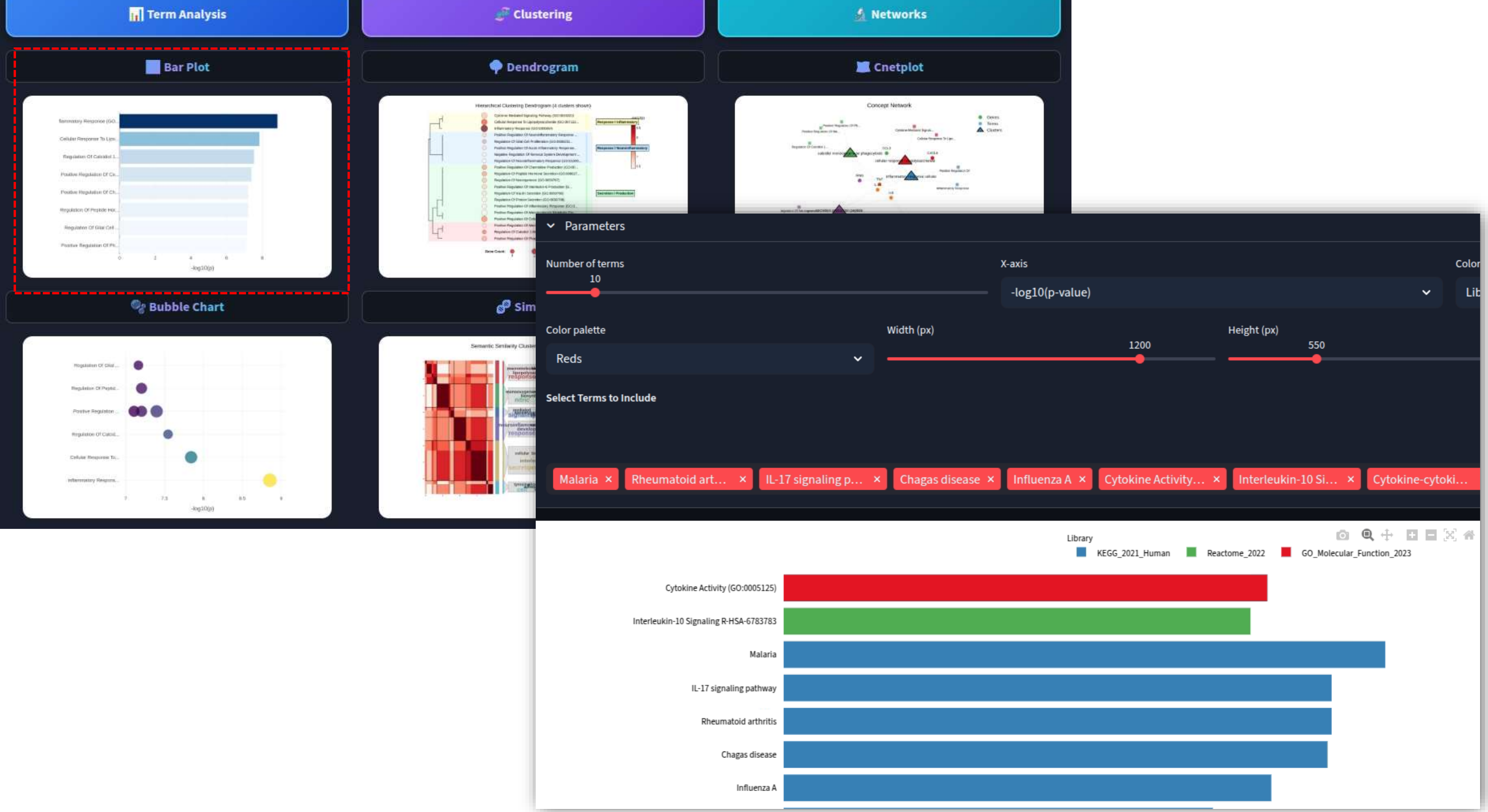
```
run_enrichment_analysis
```

Parameters:

- libraries: GO_Biological_Process_
- p_value_threshold: 0.05 *(default)*
- top_n: All significant *(default)*
- genes: `6 genes (IL6, TNF, ...)`

Observation:

Enrichment analysis completed - check results tab for details



Parameters

Number of terms 10

X-axis -log10(p-value)

Color palette Reds

Width (px) 1200

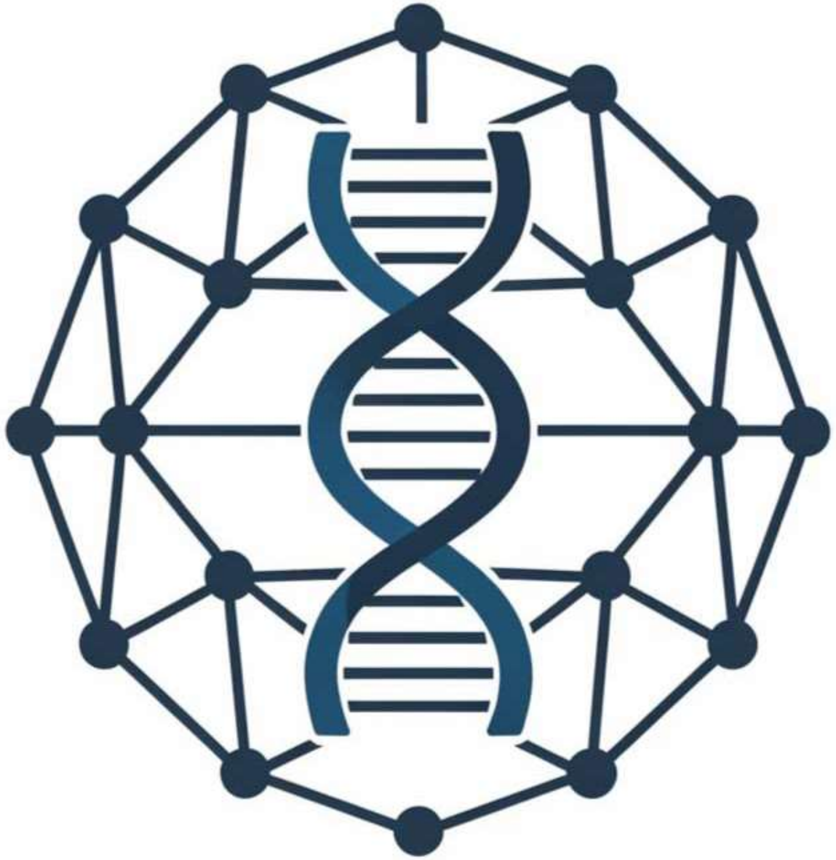
Height (px) 550

Select Terms to Include

Malaria × Rheumatoid art… × IL-17 signaling p… × Chagas disease × Influenza A × Cytokine Activity… × Interleukin-10 Si… × Cytokine-cytoki…

Conclusion

- Enrich.AI is the first AI tool for enrichment analysis
- Enrichment, Literature, gene lookup, and access to every pathway and database available
- New visualizations with full ability for optimization
- Free to use
- Code accessible



Questions?