В

### **Data Processing**

Missing value handling
Biological replicate aggregation
Normalization & scaling
Clustering
Significant feature detection

### Causality

Convergent Cross Mapping Granger Causality Test

#### Correlation

 $\rightarrow$ 

Canonical Correlation Analysis

Dynamic-Time-Warping

Cross-Correlation Function

Spearman Correlation Coefficient

Pearson Correlation Coefficient

#### Visualization

Heatmap Similarity network Expression trend Dimensionality reduction Volcano plot Importance of features

## **Heuristic Ranking**

Potential gene-metabolite pairs

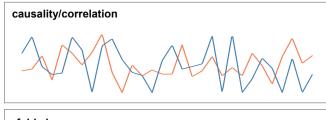
# Al Agent

 $\rightarrow$ 

GPT 3.5 from OpenAl API

each gene in transcriptome

(causality/correlation, fold change)
to represent gene- metabolite pair





peak decline

Use peak point and decline point of the target to calculate fold change of each gene