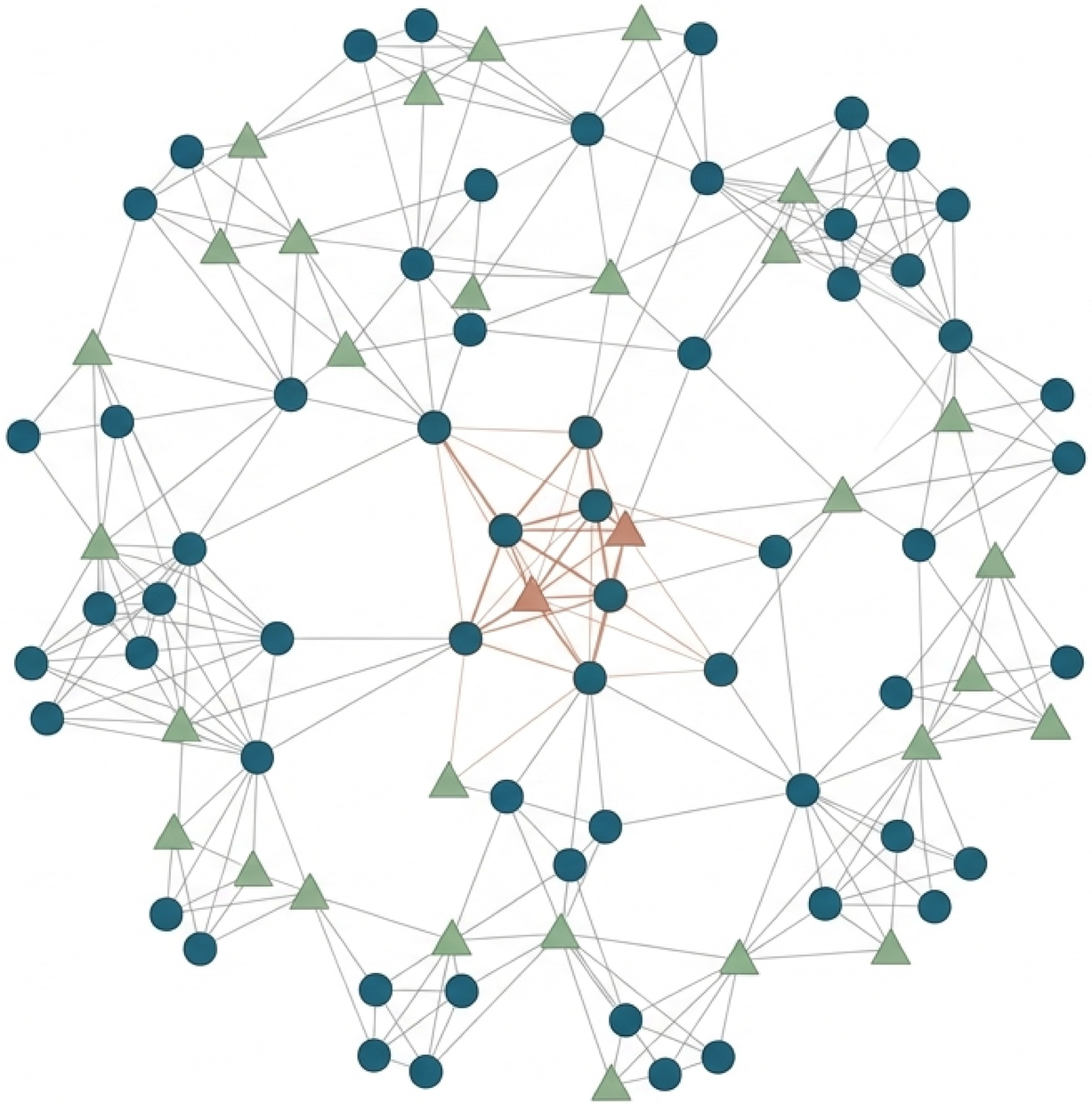
OmicsNet

Integrating Multi-Omics Data Through Feature-Level Networks

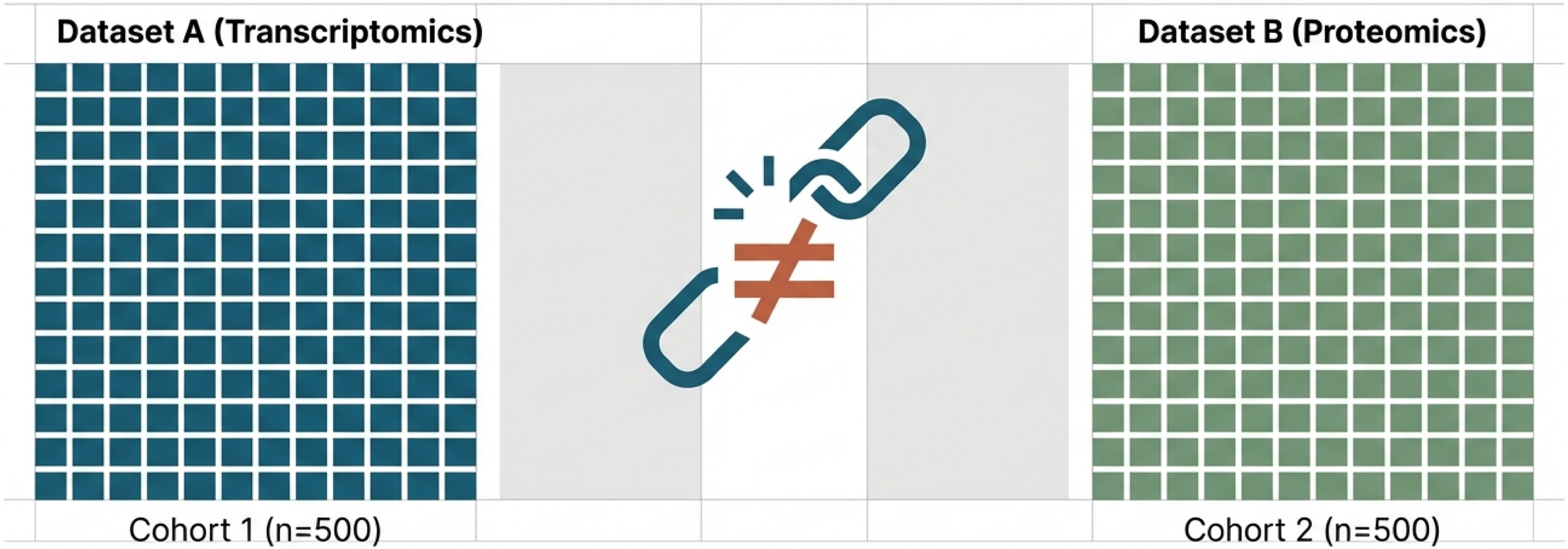
Unlocking functional associations across modalities without the need for sample overlap.



A Python package for bioinformatics integration.

The 'Sample Overlap' Bottleneck

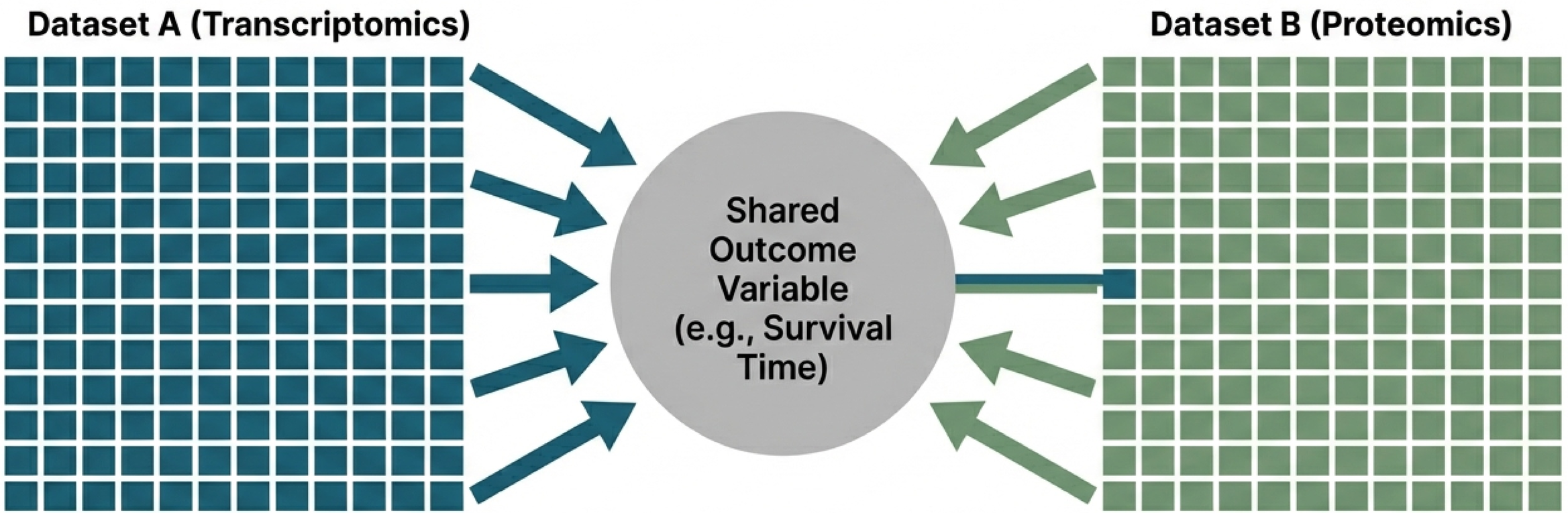
Traditional integration strategies require a perfect match: the same patient samples across all datasets. In large-scale public repositories, this is rare.



Consequence: Multi-modal insights remain locked in silos.

The Solution: Feature-Level Integration

OmicsNet bypasses sample matching by building networks based on association patterns with a shared outcome.



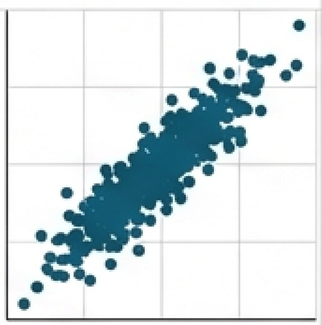
If **Gene X** and **Protein Y** correlate with the same outcome, they are functionally linked.

The Similarity Engine

How connections are mathematically formed.

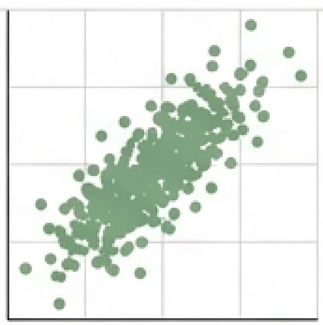
Step 1. Correlation → **Step 2. Calculation Block** → **Step 3. Network Edge**

Feature A vs. Outcome



Correlation = 0.8

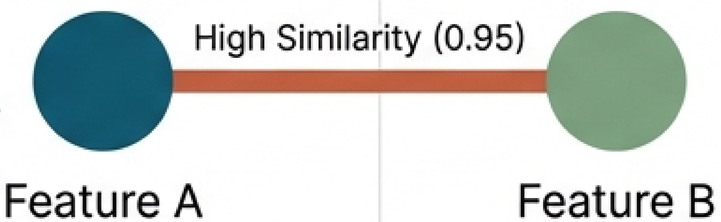
Feature B vs. Outcome



Correlation = 0.75

$$\text{Similarity} = 1 - |\text{corr}_1 - \text{corr}_2|$$

(e.g., 1 - |0.8 - 0.75| = 0.95)

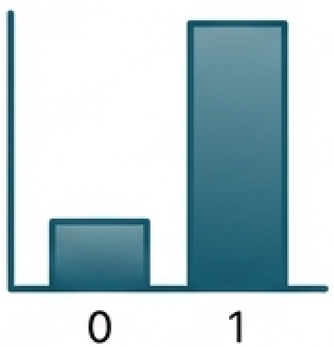


Features with similar predictive patterns are connected, regardless of sample origin.

Adaptable Architectures

Statistical methods automatically adjust to your experimental design.

Binary Outcome



Disease vs. Healthy,
Responder vs. Non-Responder

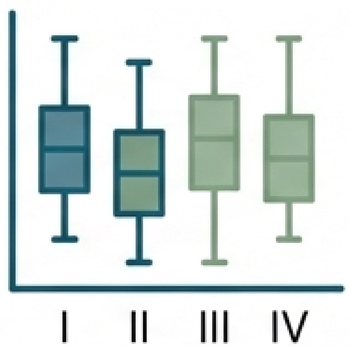
Method: **Point-biserial Correlation**

Continuous Outcome

Age, BMI, Survival Time,
Risk Scores

Method: **Pearson** or **Spearman Correlation**

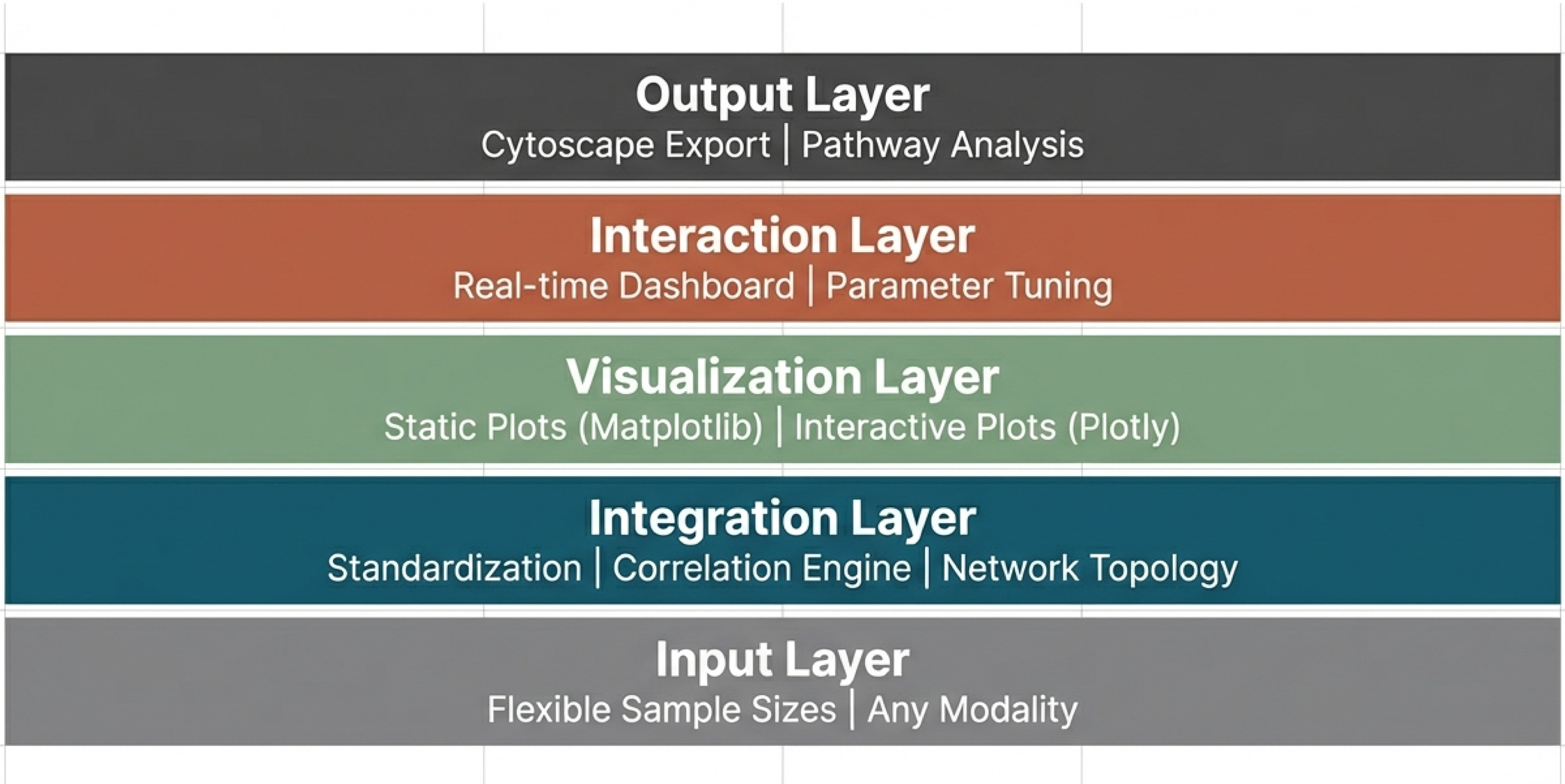
Multinomial Outcome



Subtypes, Stages (I-IV),
Cell Types

Method: **ANOVA** or **Kruskal-Wallis**

Modular System Architecture

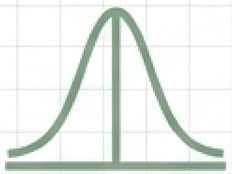


Smart Feature Selection

Prevent “hairball” networks by filtering for biological relevance using four strategies.

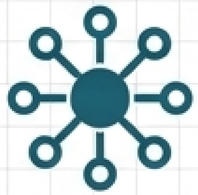
By Association

Prioritizes features with highest predictive power for the outcome.



By Variance

Selects features with the widest data spread.



By Centrality

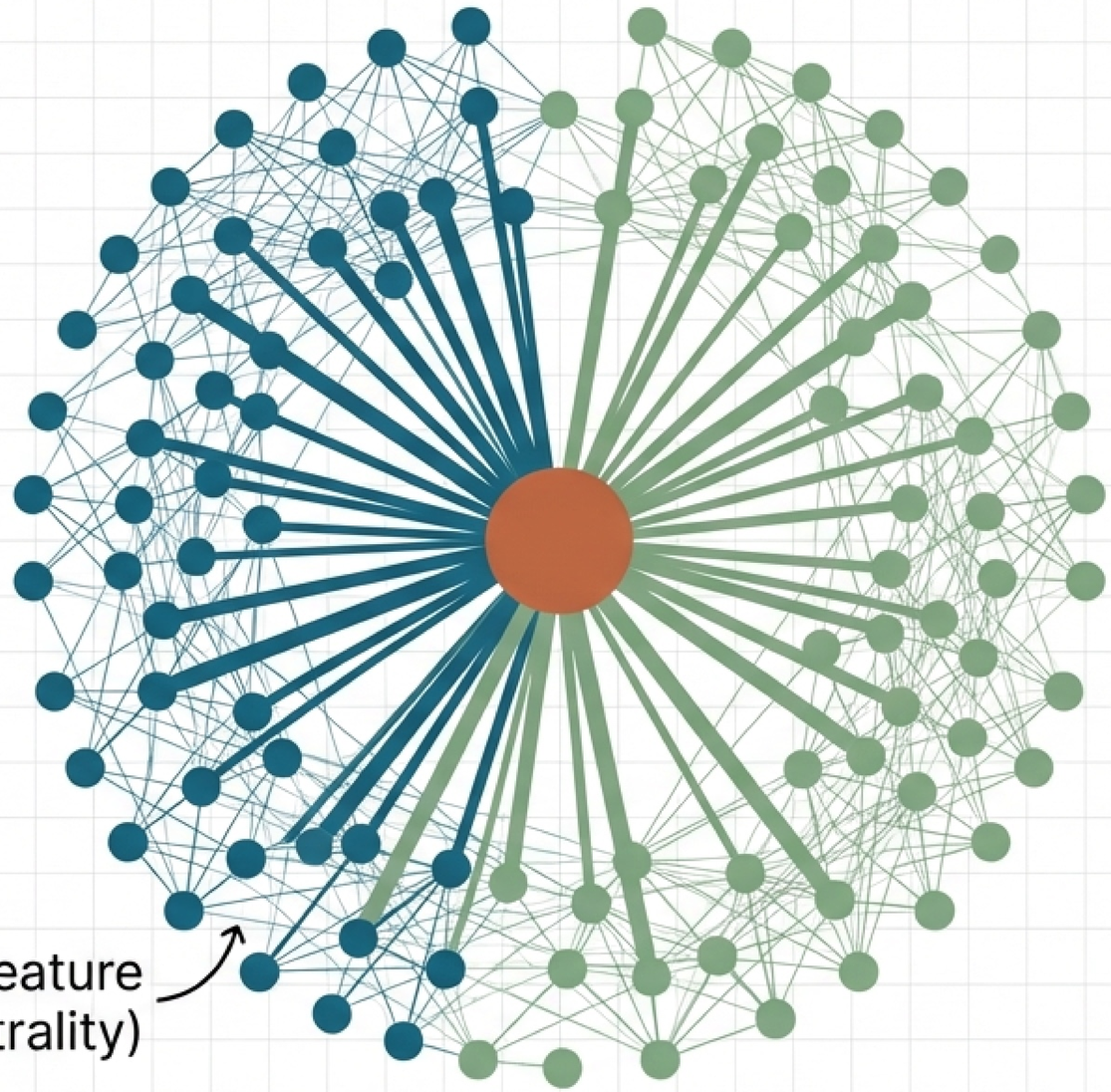
Identifies topological hubs (Degree, Betweenness, PageRank).

Combined Scoring

Recommended: Weighted approach integrating association, variance, and centrality.

Identifying Biological Hubs

Hubs act as bridges between molecular layers, revealing potential biomarkers.

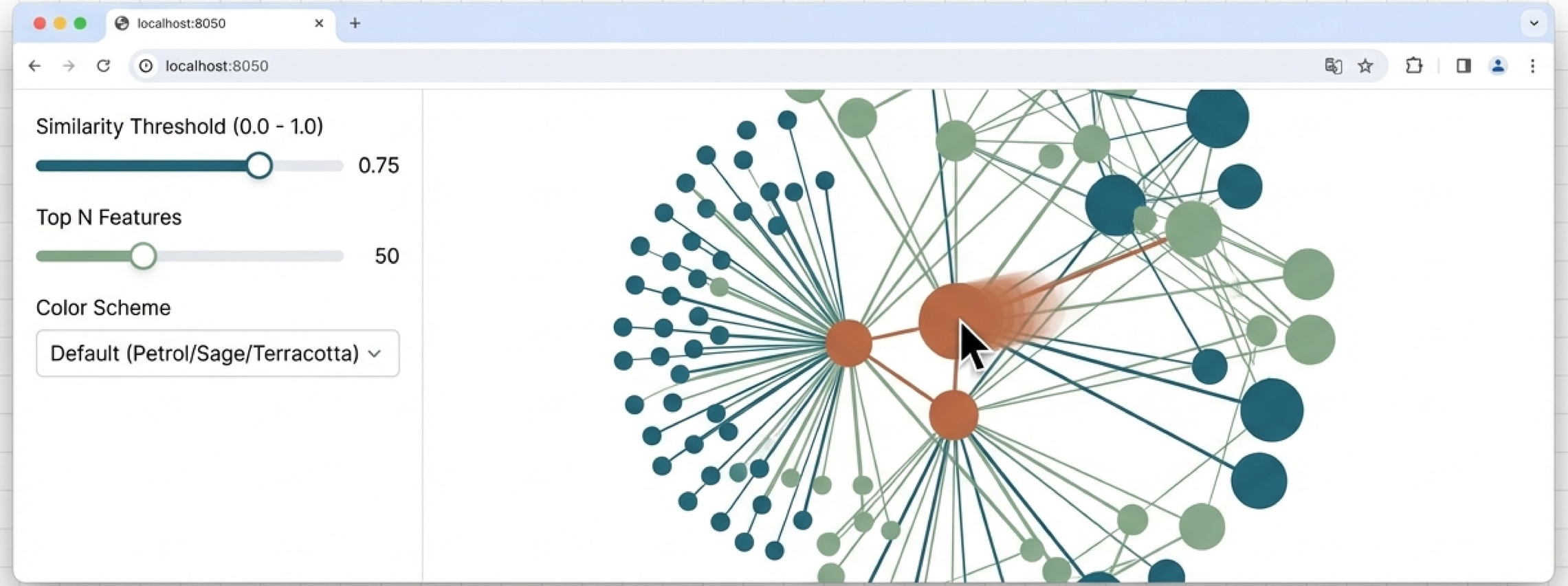


- Gene Expression
- Metabolites

```
hubs = get_hub_features(method='degree')
```

Interactive Dashboard

Real-time exploration and hypothesis generation.



Adjust parameters on the fly. Auto-launches in your local browser.

Implementation: From Data to Integration

Simple, readable syntax to load disparate datasets.

```python
from omicsnet import OmicsIntegrator

# Initialize
integrator = OmicsIntegrator()

# Add Transcriptomics (Binary Outcome)
integrator.add_modality(
    name='transcriptomics',
    data=tx_data,
    outcome=binary_outcome,
    modality_type='gene',
    outcome_type='binary'
)

# Add Proteomics (Continuous Outcome)
integrator.add_modality(
    name='proteomics',
    data=px_data,
    outcome=age_outcome,
    outcome_type='continuous',
    correlation_method='pearson'
)
```

Implementation: Computation & Visualization

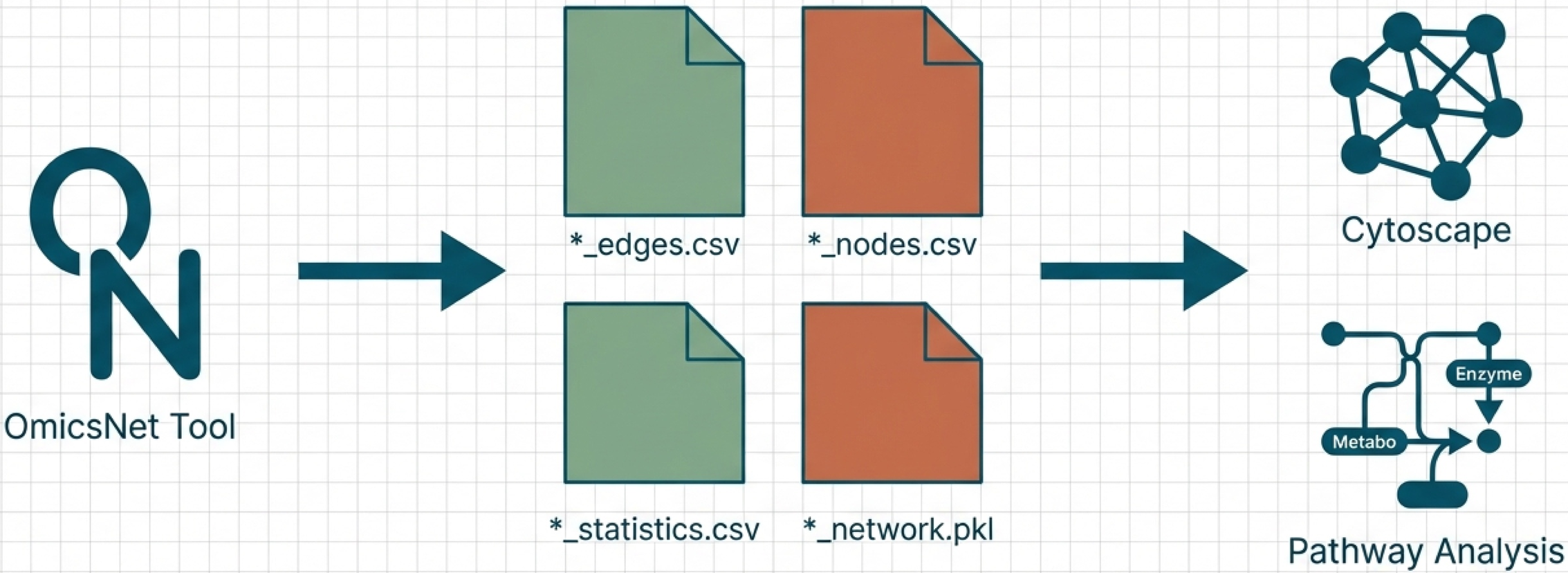
Generate publication figures or launch the web app in three lines.

omicsnet_viz.py

```python
from omicsnet import NetworkVisualizer, launch_dashboard

# Compute & Build
integrator.compute_similarity_matrices()
network = integrator.build_network(similarity_threshold=0.85)

# Static Plot (for publication)
visualizer = NetworkVisualizer(network)
visualizer.plot_static(save_path='network.png')

# Interactive Dashboard (for discovery)
launch_dashboard(network=network, port=8050)
```

Outputs Designed for Downstream Analysis

OmicsNet integrates seamlessly into existing bioinformatics pipelines.

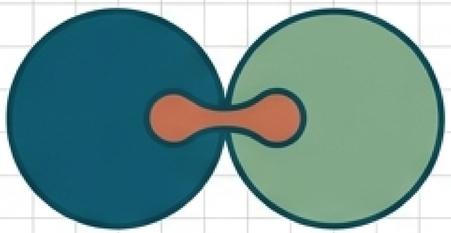


Is OmicsNet Right for You?

- You have multiple omics datasets (e.g., Genes, Proteins, Metabolites).
- These datasets come from different patient cohorts (Zero Sample Overlap).
- You possess a shared outcome variable (Clinical, Phenotypic, or Imaging).
- You need to identify functional relationships across molecular layers.

Summary of Capabilities

Zero Sample Overlap



Integrates disparate cohorts using association-based similarity.

Multi-Modal Support

Transcriptomics, Proteomics, Metabolomics, Cell Painting.

Interactive Discovery

Drag-and-drop dashboard for real-time hypothesis generation.

Publication Ready

High-quality static plots and standard statistical exports.

Get Started with OmicsNet

```
> pip install .
> git clone https://github.com/shivaprasad-patil/OmicsNet
```

License: Apache 2.0 (Open Source)

Citation: OmicsNet: Multi-Omics Network Integration, Shivaprasad Patil (2025)