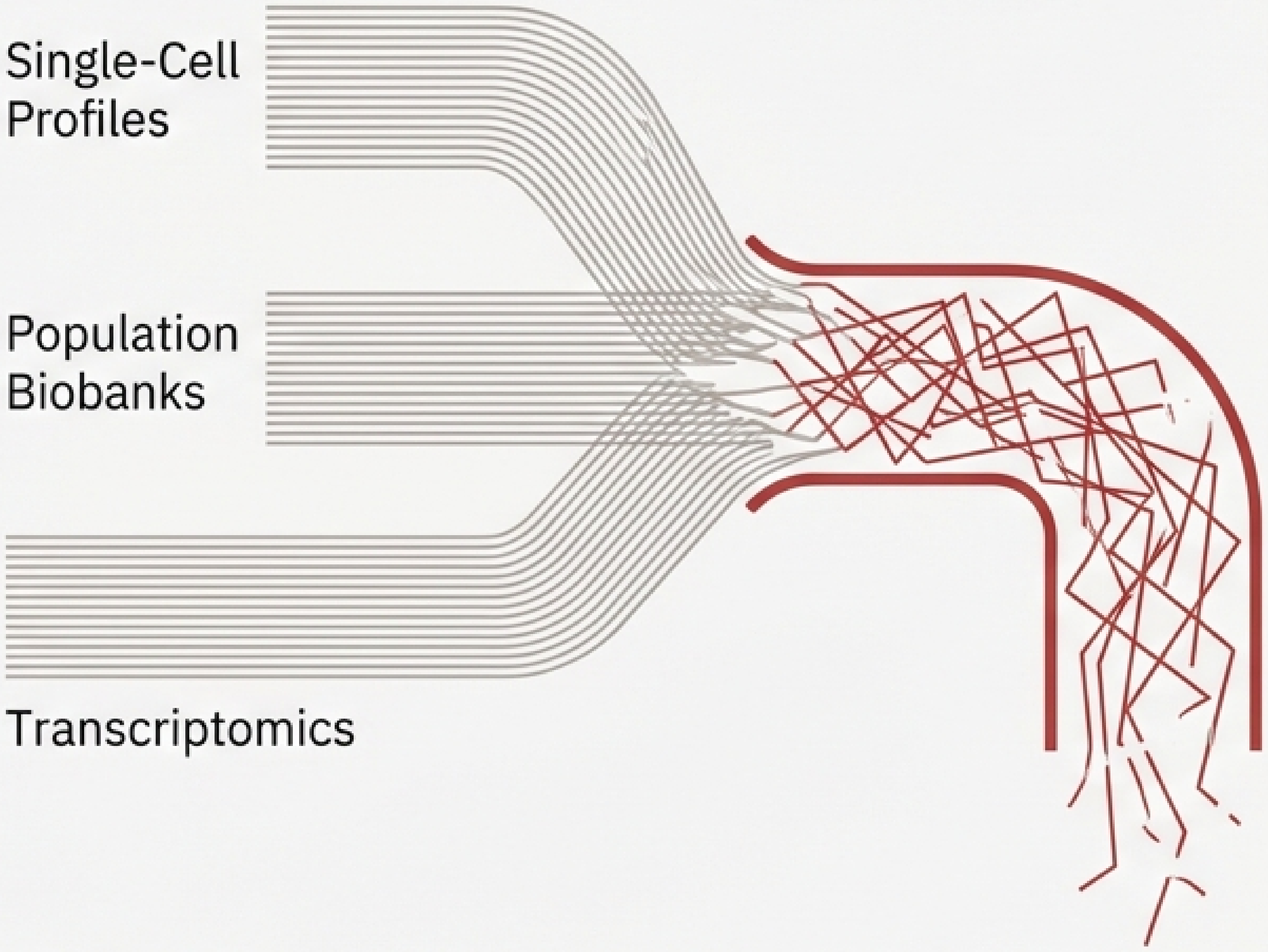
PLAID: Single-Sample Gene Set Enrichment at Ludicrous Speed

Pathway Level Average Intensity Detection

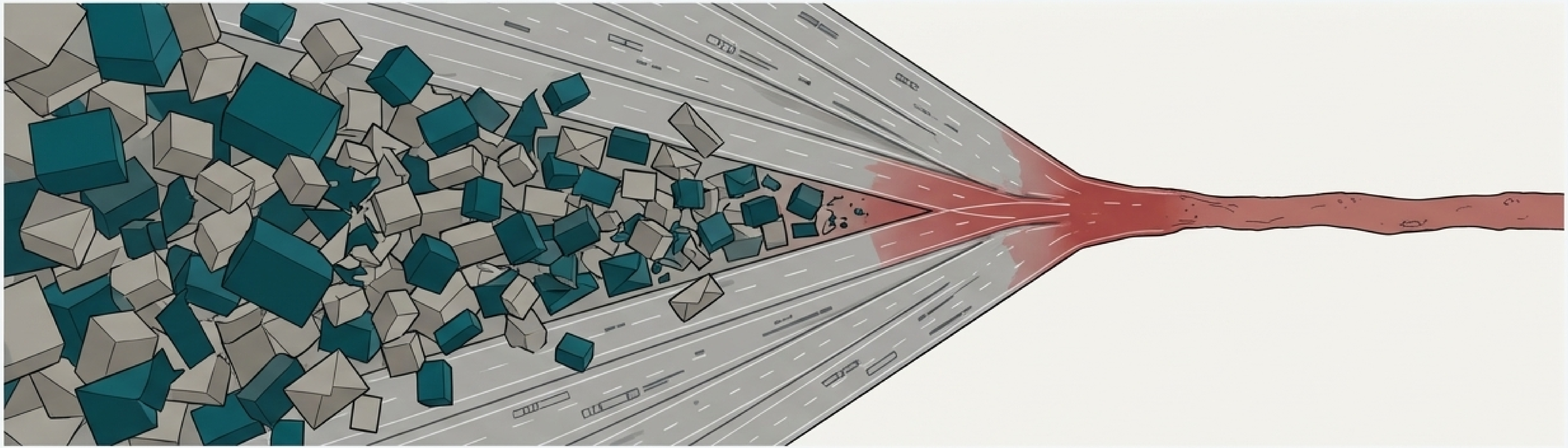
An ultrafast and memory-optimised method to compute single-sample enrichment scores for gene expression and proteomics data

The promise of large-scale biology is hitting a computational wall.

- The rise of single-cell profiles and population biobanks has created an explosion of data.
- These datasets are pivotal for patient stratification and advancing personalised medicine.
- However, existing single-sample enrichment methods were not designed for this scale.



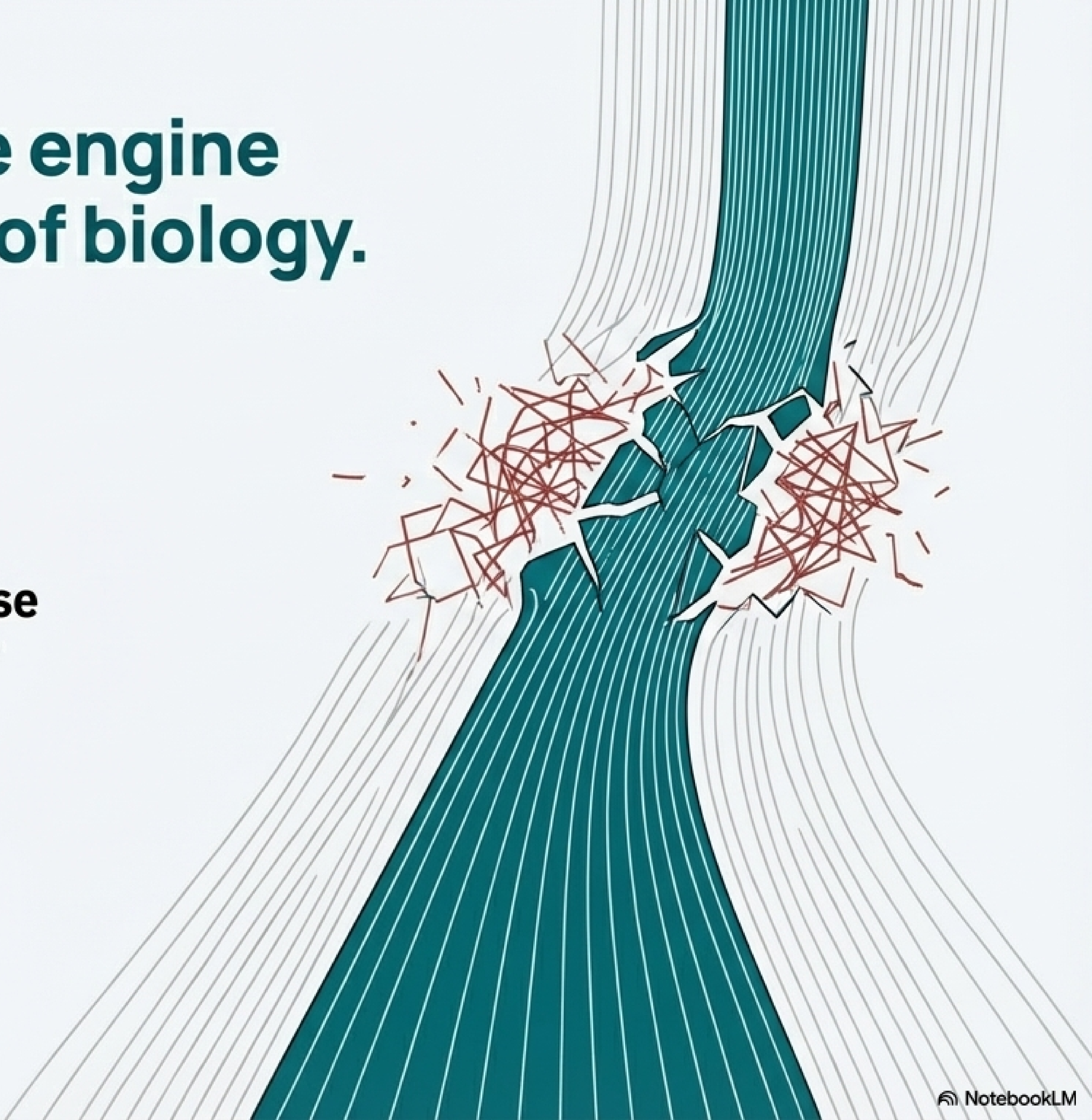
This isn't just slow. It's a bottleneck for discovery.



- Current methods demand excessive runtime and memory resources.
- This computational inefficiency makes analysing large datasets **impractical**.
- This limitation is a focus for bioinformatics teams in academia and the pharmaceutical industry, as it directly impacts basic and clinical biomedical research.

Introducing PLAID: The engine built for the new scale of biology.

- To address this critical need, we developed PLAID, an ultrafast and memory-optimised algorithm.
- The core innovation is its use of **sparse matrix computation** to deliver highly accurate gene set scoring.
- It is designed to surpass the performance of current methods in single-cell, bulk transcriptomics, and proteomics data.

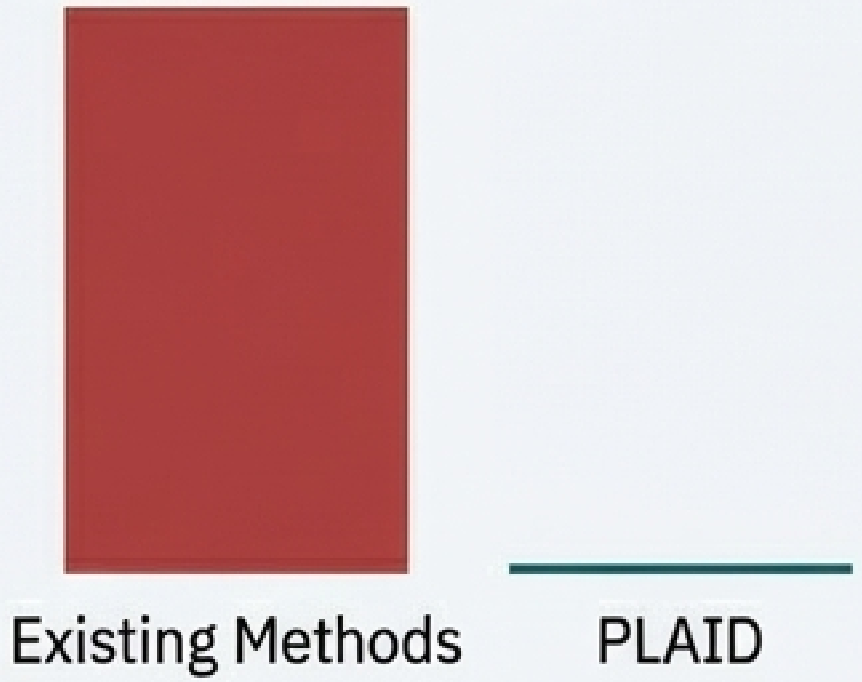


The PLAID performance leap is not incremental. It's a paradigm shift.

In typical use cases, PLAID is:

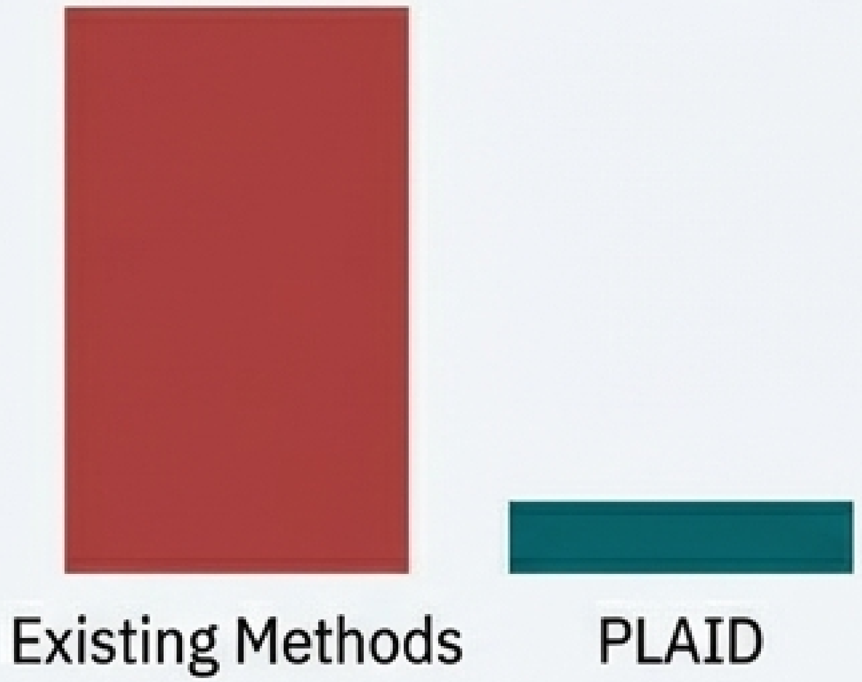
>100x

Faster



10x

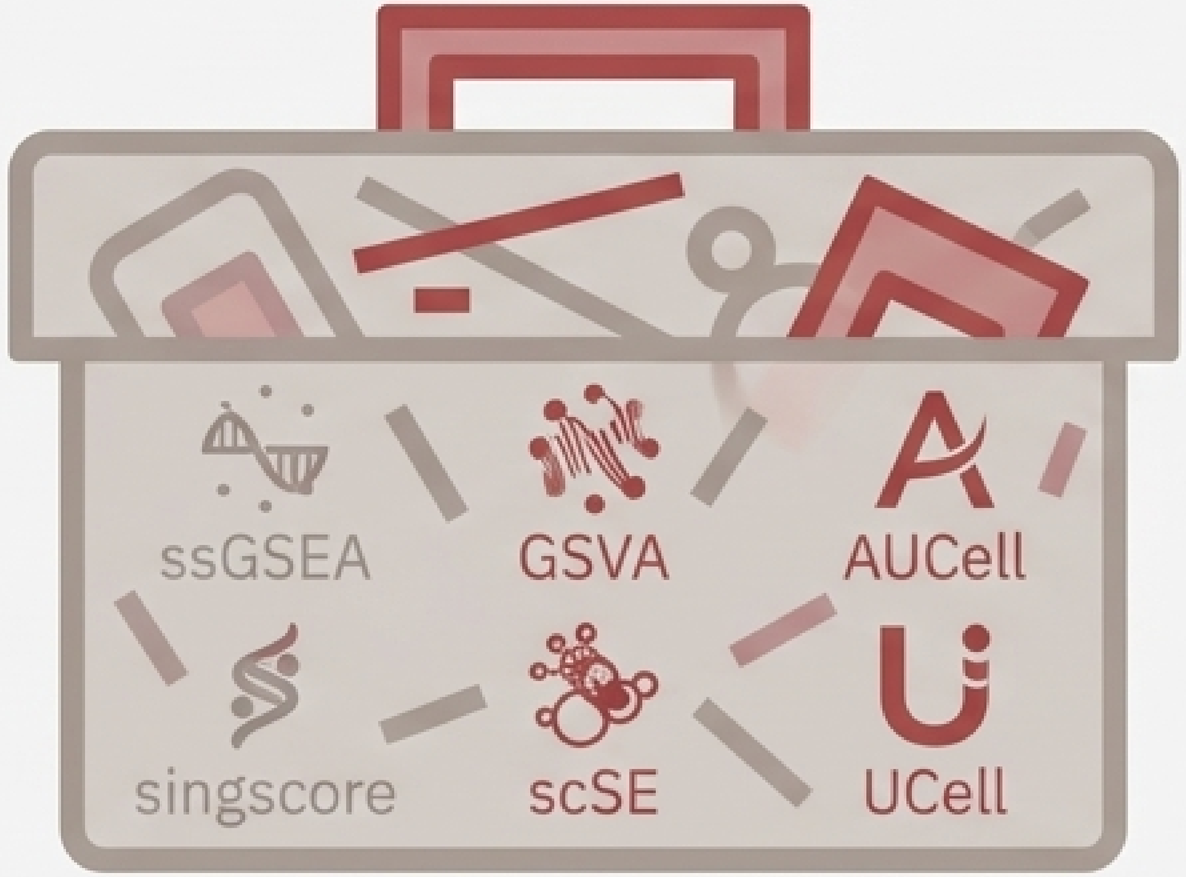
Less Memory



...than the original algorithms it simulates.

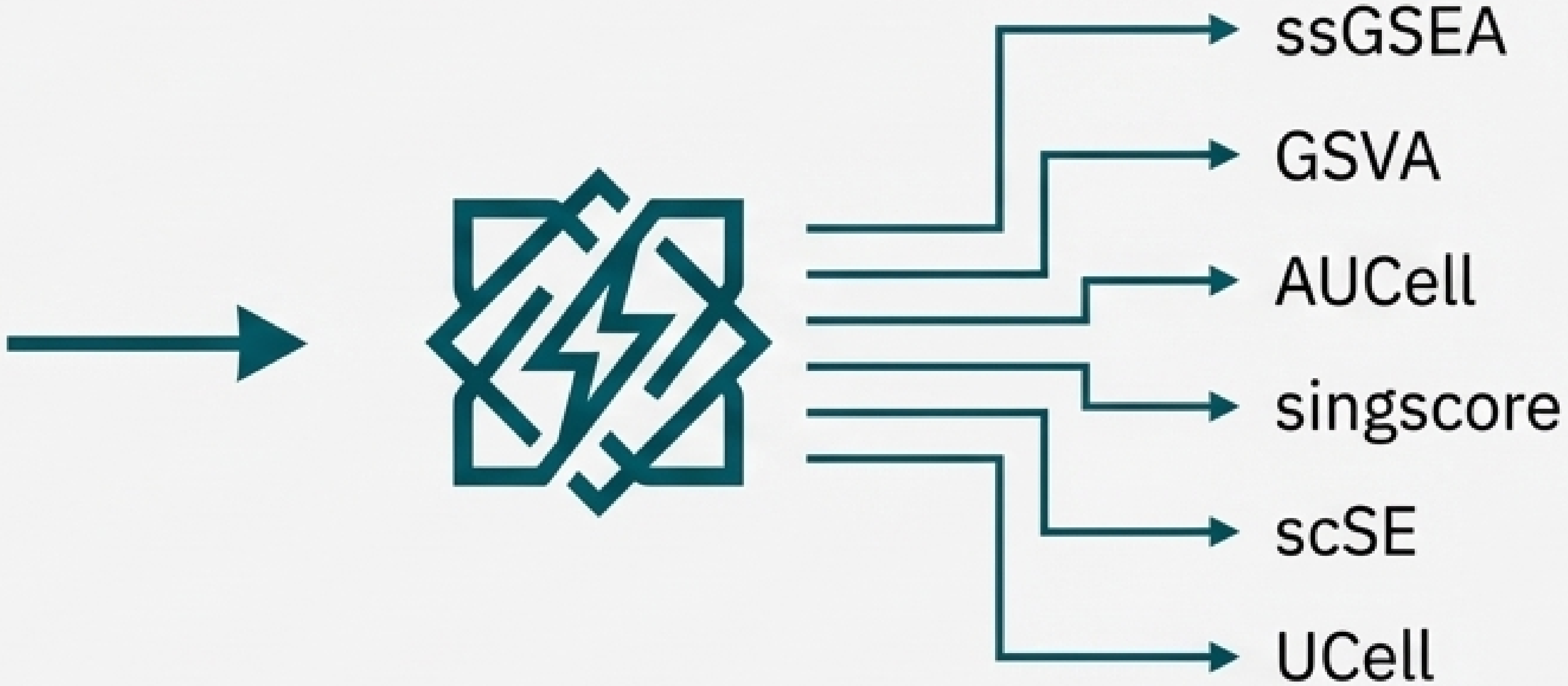
One unified engine. Multiple industry-standard methods.

- PLAID uniquely integrates and can simulate the most widely used single-sample gene set scoring algorithms.
- Apply multiple methods for cross-validation with outstanding runtime efficiency and minimal memory.



Before

Supported Methods



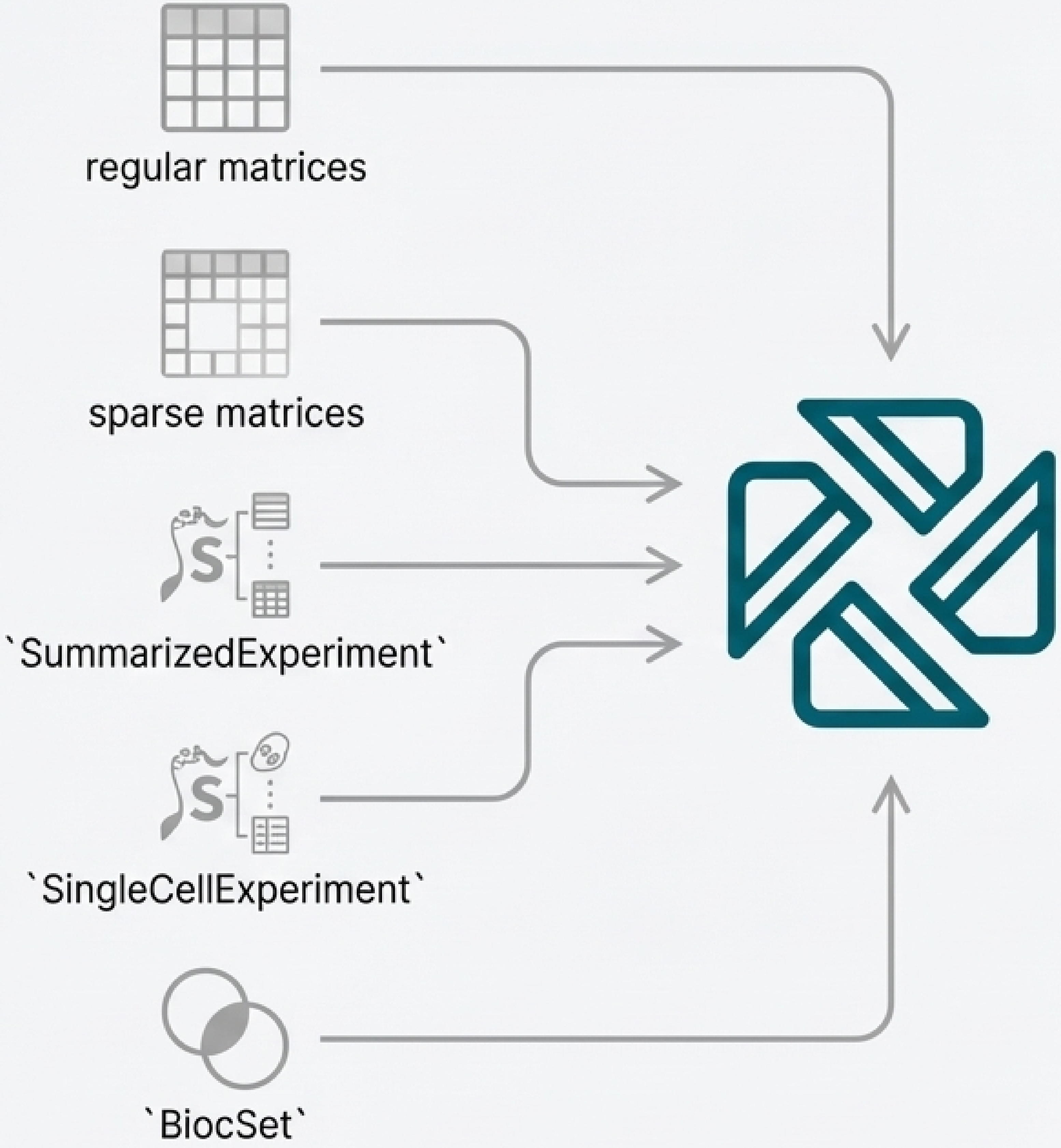
- ssGSEA
- GSVA
- AUCell
- singscore
- scSE
- UCell

After

Built to work with the tools you already use.

PLAID is designed for maximum compatibility and ease of use.

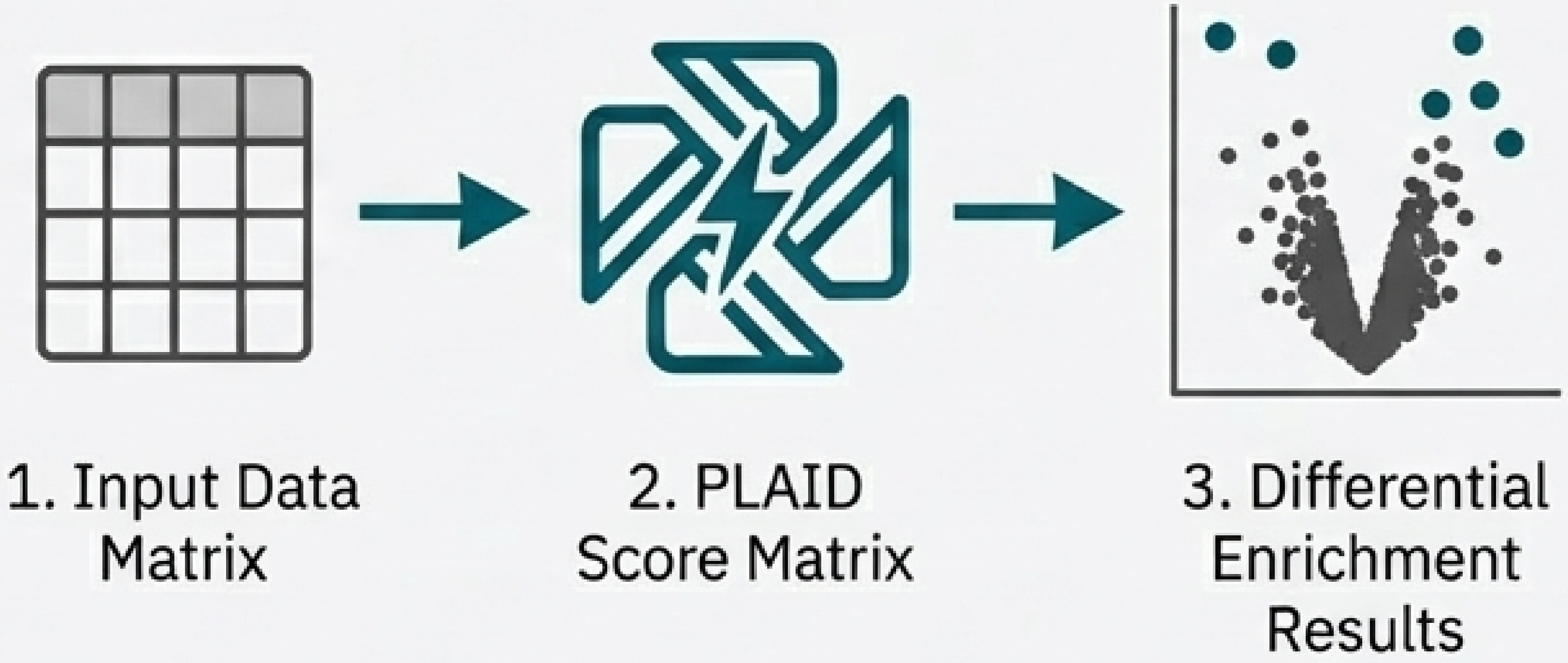
- **Data Types:** Works directly with regular and sparse matrices.
- **Bioconductor Native:** Automatically detects and handles key Bioconductor objects, including:
    - `SummarizedExperiment`
    - `SingleCellExperiment`
    - `BiocSet`



Go from scoring to discovery with built-in differential testing.

PLAID is more than just a scoring algorithm.

- The package includes **built-in differential enrichment testing**.
- This enables you to move directly from calculating sample-level scores to identifying statistically significant differences between experimental groups, all within a single, efficient workflow.

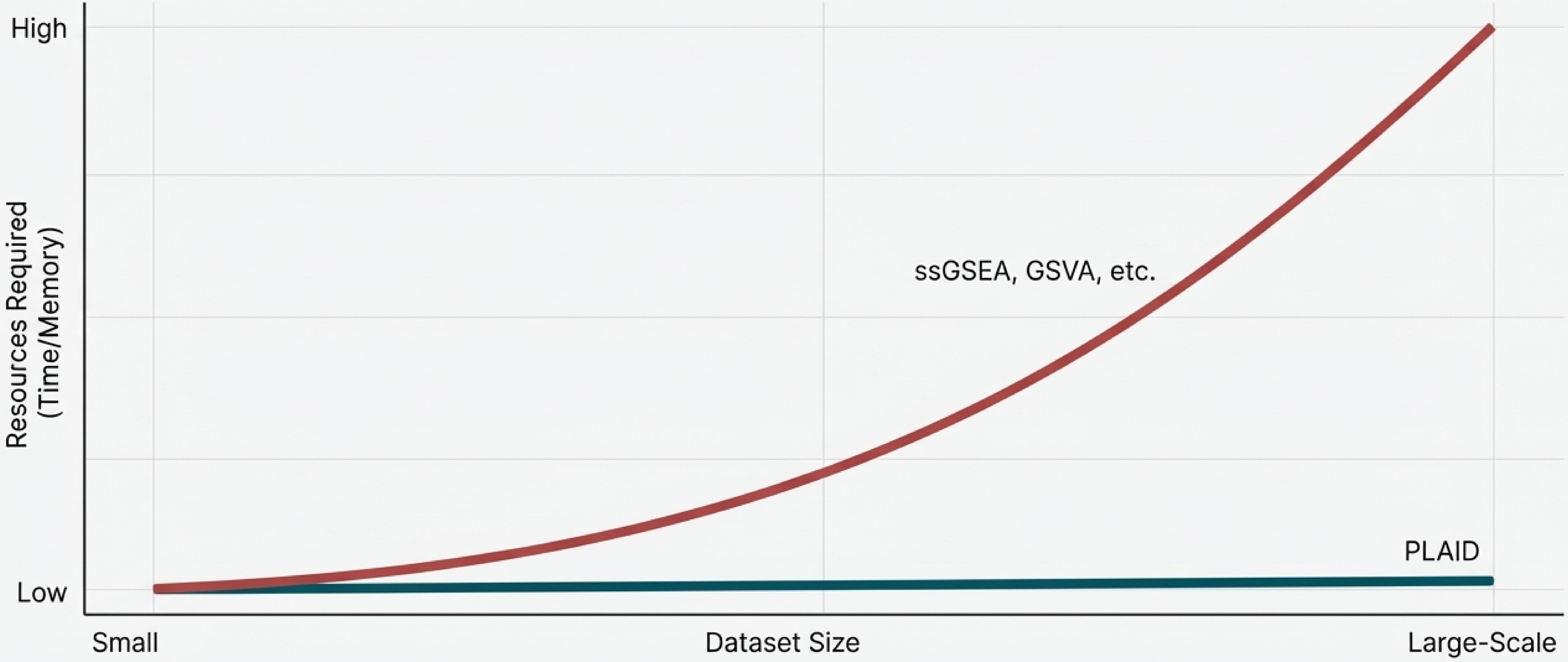

1. Input Data Matrix

2. PLAID Score Matrix

3. Differential Enrichment Results

Performance remains stable as your datasets grow.

This chart illustrates the conceptual relationship between dataset size (e.g., number of cells/samples) and computational resources required. While existing methods show exponential increases in runtime and memory, PLAID maintains efficiency at scale.



Professionally developed, peer-reviewed, and community trusted.

Published Research

Zito A., et al. PLAID: ultrafast single-sample gene set enrichment scoring. *Bioinformatics*, 2025, btaf621.

Community Standard

Available through **Bioconductor**, the standard repository for R-based bioinformatics software.

Developed By

The Bioinformatics Data Science Team at **BigOmics Analytics**.

Platform Integration

PLAID is the main single-sample gene set scoring algorithm in **OmicsPlayground**, a comprehensive self-service bioinformatics platform.

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BigOmics Analytics

Bioconductor

Install PLAID from Bioconductor in a single line of code.

Open your R console and run the following command:

```r
BiocManager::install("plaid")
```

For the latest development version, you can also install directly from GitHub:

```r
remotes::install_github("bigomics/plaid")
```

Explore the documentation and get support.

Source Code & Issues

`github.com/bigomics/plaid`

Detailed Tutorials & Examples

Vignette: *Getting Started with PLAID*

Vignette: *Comparing PLAID with other methods*

Professional Support

For questions, reach out to the BigOmics Analytics team at `help@bigomics.ch`

A final warning.

“PLAID is fast. Ludicrously fast. Please fasten your seatbelts before usage.”

Stop waiting for your analysis. Start unlocking the insights in your data.