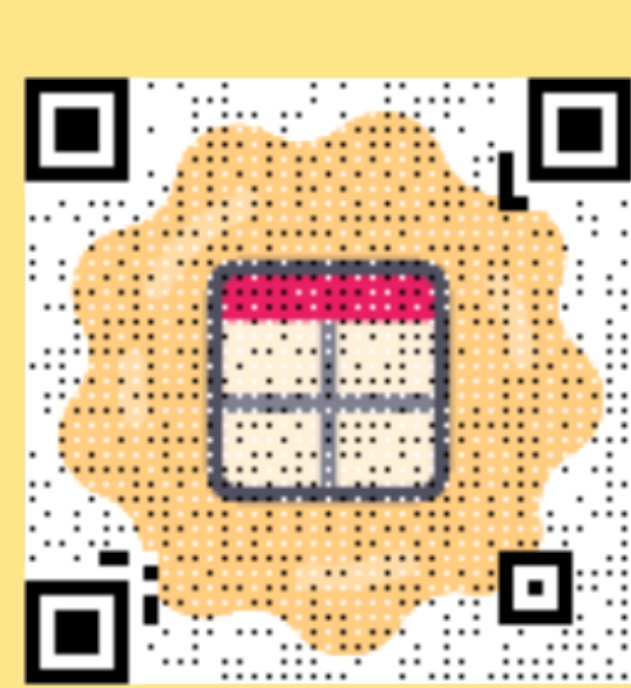


CytoTable: High Performance and Scalable Single-cell Morphology Feature Engineering

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Introduction

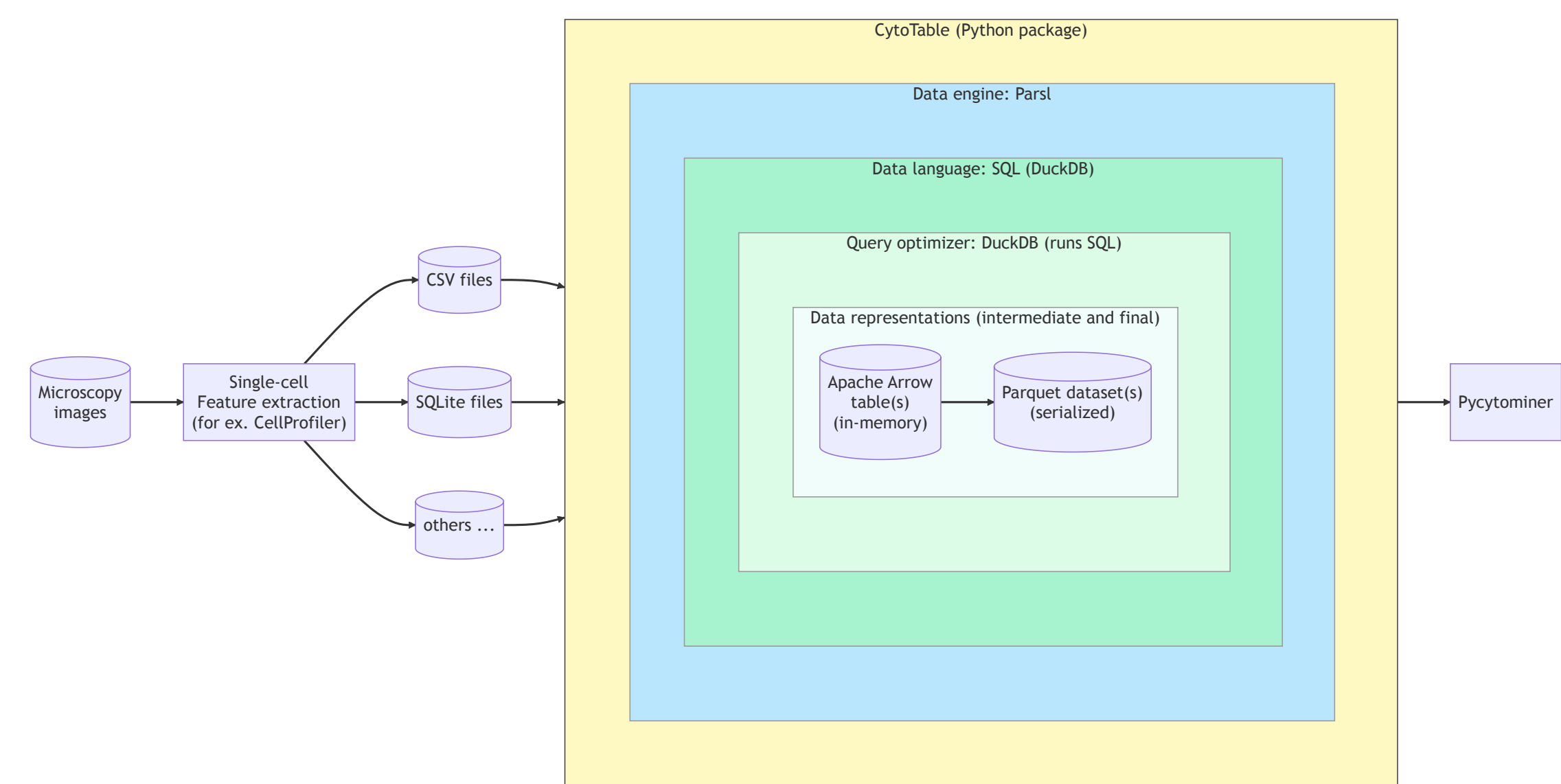


Figure 1. Diagram showing high-dimensional single-cell morphology data flow with relationship to CytoTable modular data stack components.

We are solving significant scalability and replicability challenges with high-dimensional single-cell morphology data (such as those extracted from CellProfiler[1]) by implementing novel and effective capabilities as a modular, portable, and cross-language single-cell data stack[2]: (a) language frontend: SQL (DuckDB[3]), (b) intermediate representation: Apache Arrow[4] and Apache Parquet[5], (c) query optimizer: DuckDB[3], (d) execution engine: Parsl[6] with Pythonic MapReduce design patterns[7], (e) execution runtime, Python package (PyPI, source)(Figure 1).

Morphology Feature Data Scalability

CytoTable and Pycytominer SQLite Processing Time Comparison

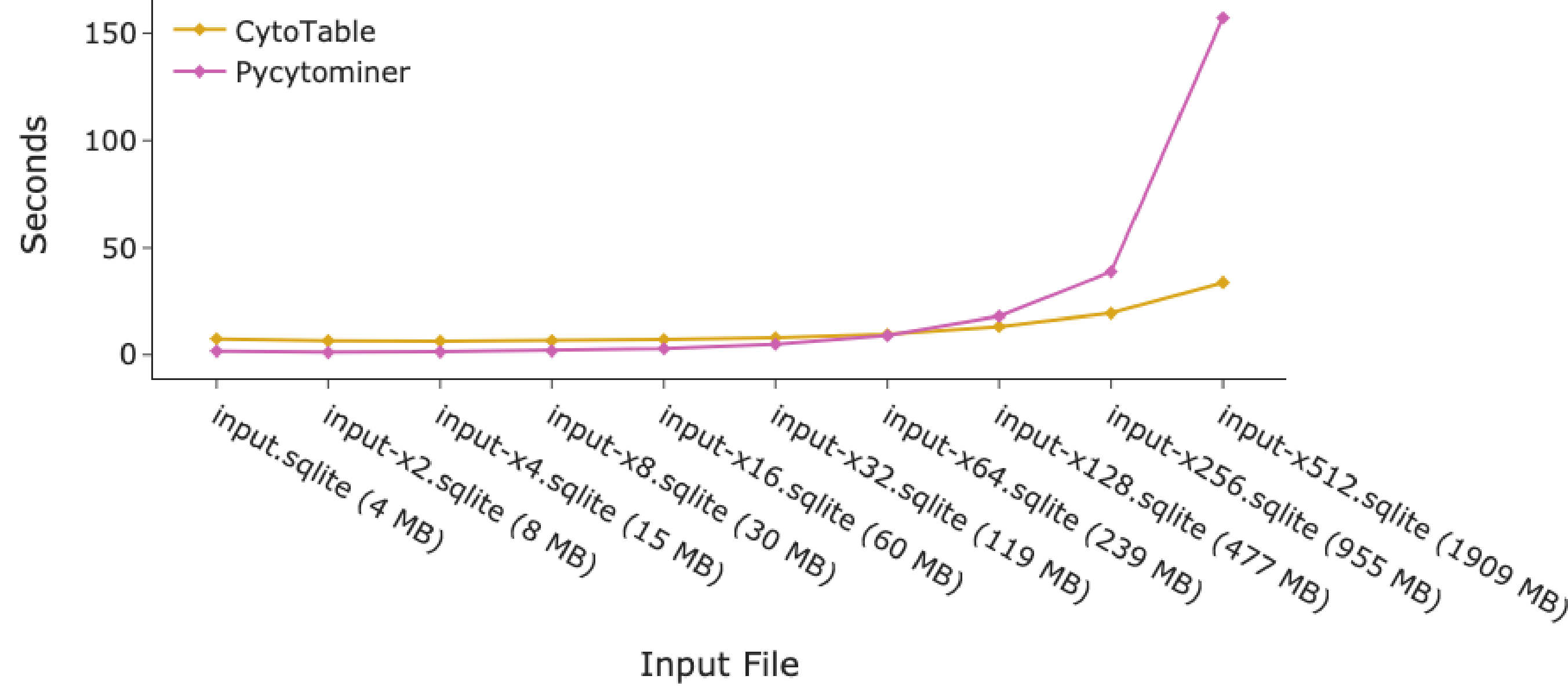


Figure 2. Plot showing processing time duration for CytoTable and Pycytominer for various datasets.

CytoTable and Pycytominer SQLite Total Memory Consumption

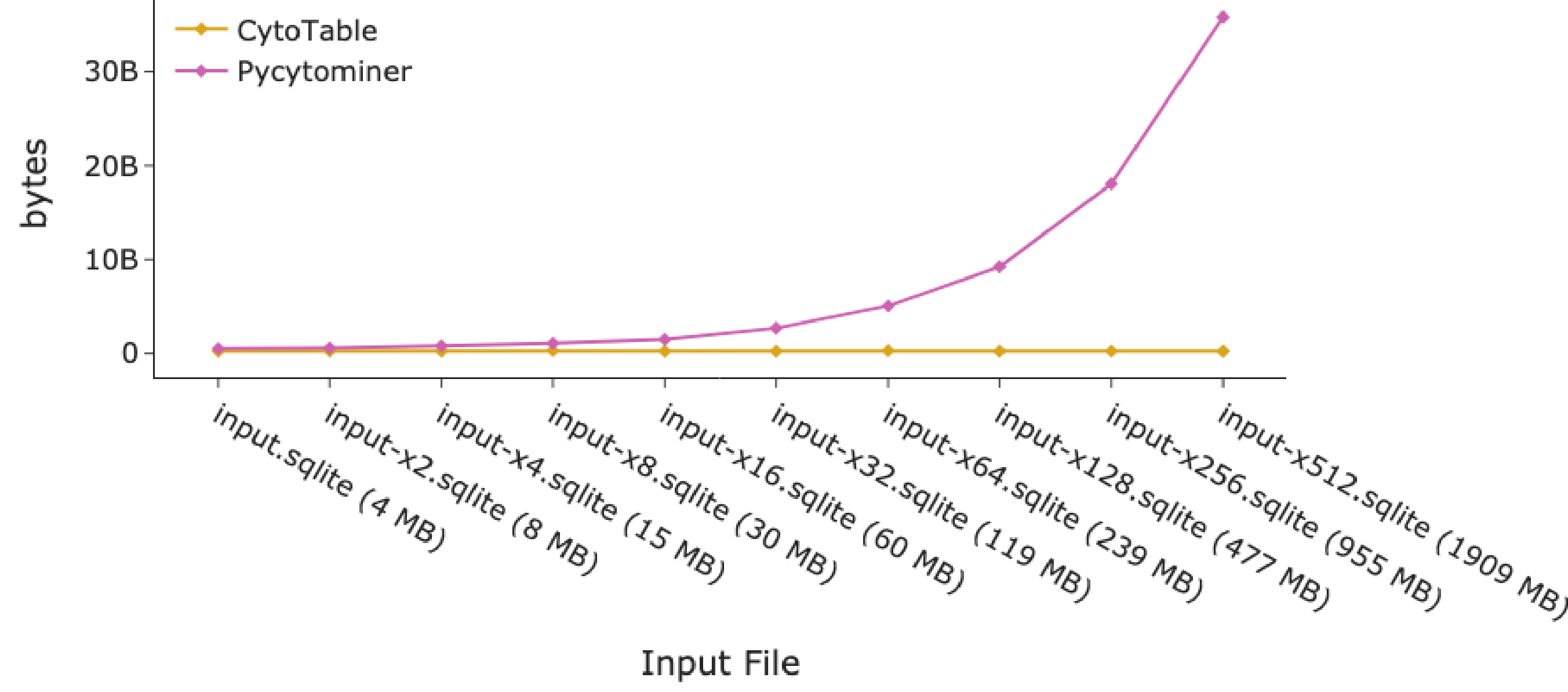


Figure 3. Plot showing total memory consumption for CytoTable and Pycytominer for various datasets.

CytoTable builds upon the shoulders of Pycytominer, helping to streamline the SingleCells.merge_single_cells(...) method. We decrease overall processing completion time (Figure 2) and memory consumption (Figure 3) for large amounts of data by leveraging composable data stack elements.

Empowering the Cytomining Ecosystem

Orchestration: CytoSnake

Authors: Erik Serrano, Jenna Tomkinson, Roshan Kern, Vince Rubinetti, Dave Bunten, Gregory P. Way

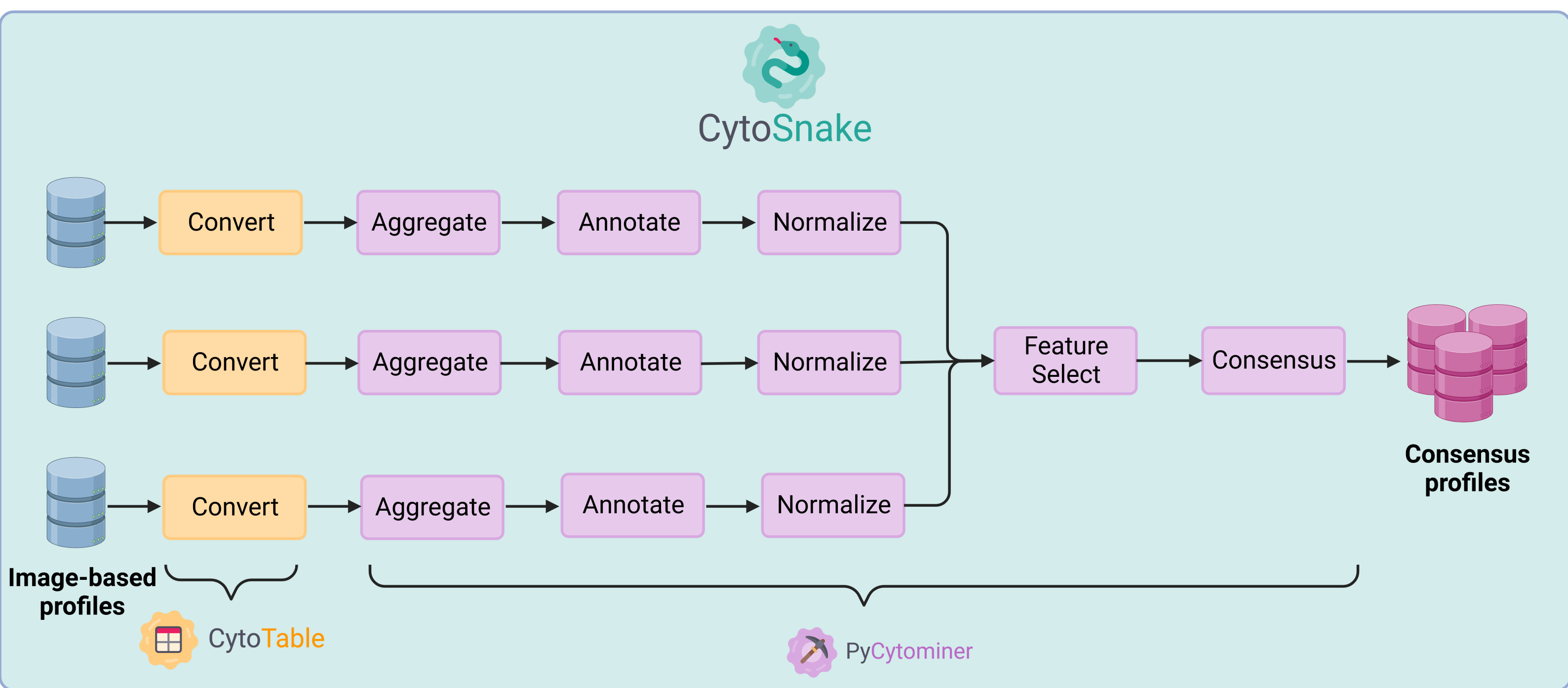


Figure 4. Diagram showing how CytoSnake orchestration applied in multiple pipelines.

CytoSnake is an innovative tool for orchestrating high-dimensional cell morphology data processing pipelines, including those which leverage CytoTable and other applied usecases.

Applied research: NF1 Schwann cell project

Authors: Jenna Tomkinson, Cameron Mattson, Erik Serrano, Gregory P. Way

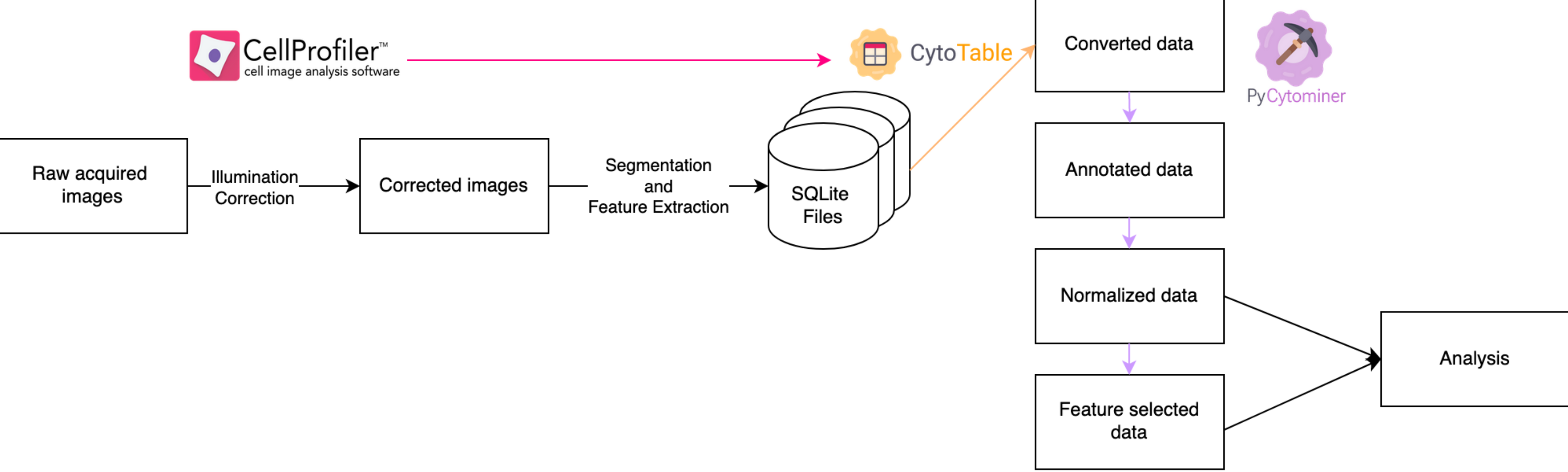


Figure 5. Diagram showing NF1 pipeline implementation details including CytoTable and Pycytominer.

Comprehensive dataset analyses for cell painting assays, enabling the further understanding of cellular morphology NF1 Schwann cells and rare disease treatment.

Applied research: Pyroptosis signature project

Authors: Michael J. Lippincott, Jenna Tomkinson, Gregory P. Way

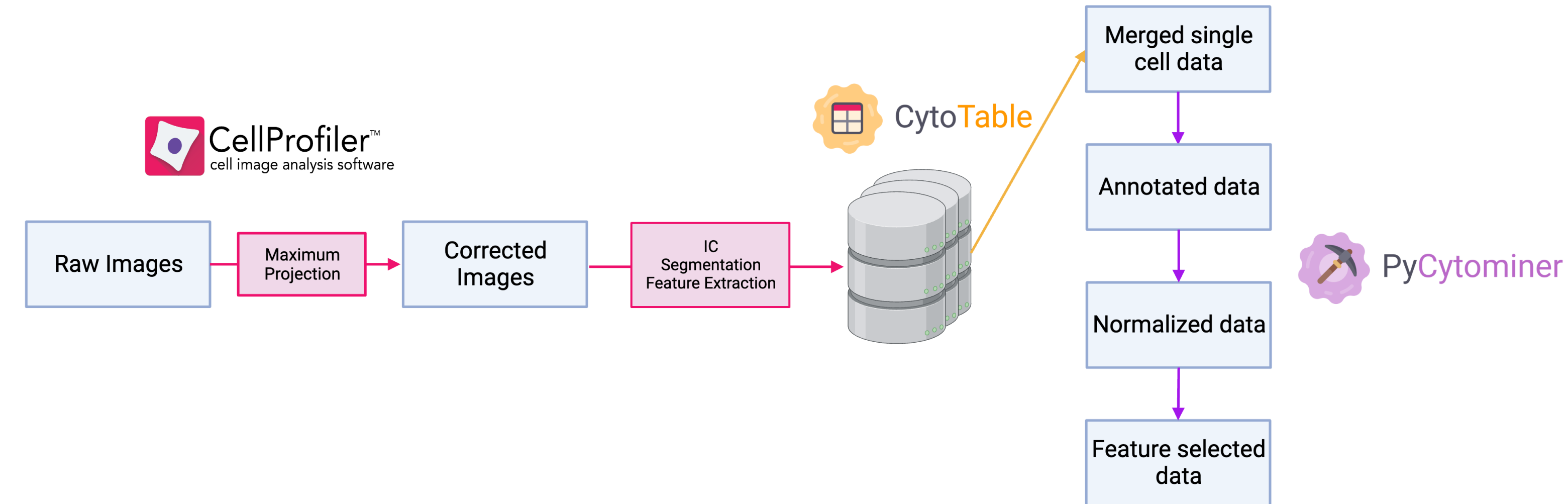


Figure 6. Diagram showing pyroptotic cell changes which are studied as part of the Pyroptosis signature project.

Identifying and characterizing pyroptosis signatures in cellular systems, aiding in the study of inflammatory cell death pathways as part of the Interstellar collaboration.

Applied research: CFReT project

Authors: Jenna Tomkinson, Erik Serrano, Gregory P. Way

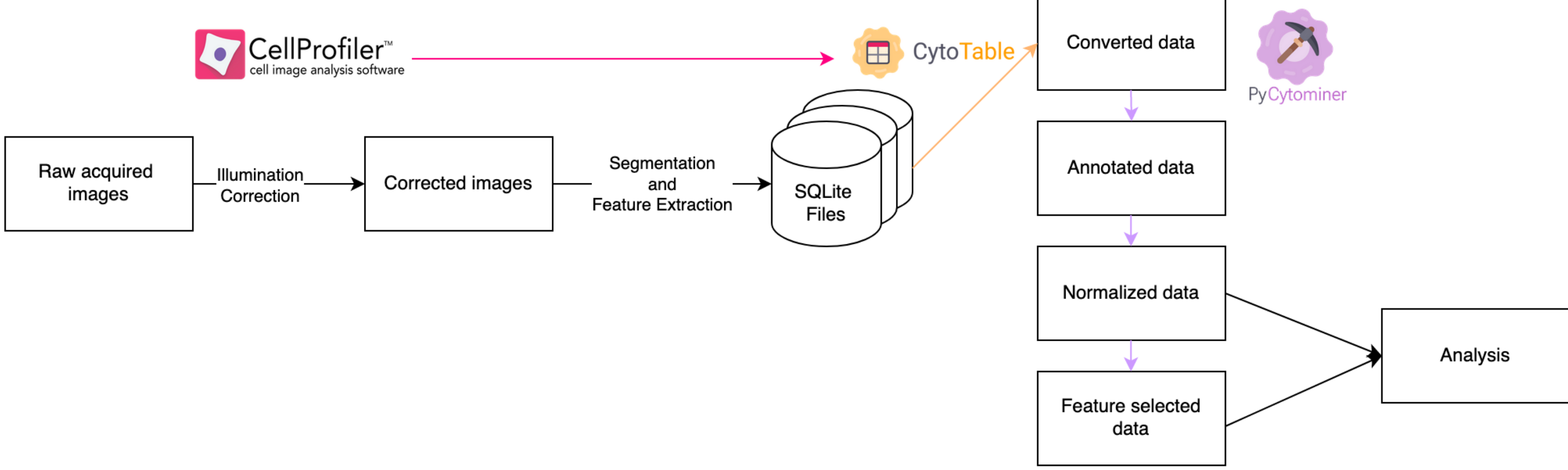


Figure 7. Diagram showing CFReT pipeline implementation details including CytoTable and Pycytominer.

Image-based analysis of cardiac fibroblast datasets to uncover proprietary drug impact on reversing fibrosis.

Using CytoTable

```
import cytotable
result_file = cytotable.convert(
    source_path="path/to/feature-data",
    dest_path="destination/path.parquet",
    dest_datatype="parquet",
    preset="cellprofiler_csv",
)
```

Figure 8. Code block showing Pythonic syntax for using CytoTable.

CytoTable includes a Pythonic API which can be customized as needed or leverage existing presets (Figure 8). See the CytoTable documentation for more detail: <https://cytomining.github.io/CytoTable/>

Shape the future with us!



Figure 9. Cytomining Ecosystem software logos.

The Cytomining Ecosystem cultivates groundbreaking science and research software engineering in the realm of high-dimensional single-cell science, guiding in a new era of bioinformatic innovation.

Interested in collaborating?
We welcome your input, contributions, and guidance!

Find us at <https://github.com/cytomining>.

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