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Overview

BCTool is a free, open-source application developed in Python to find biclusters using biclustering algorithms.

This application presents a **Python-based implementation for biclustering algorithms**, motivated by the need for broader accessibility, enhanced usability, and easier integration with modern bioinformatics workflows. BCTool is tested with the *Saccharomyces cerevisiae* dataset.

Functionality

BCTool takes in the datasets, selected algorithms of the five, and the selected arguments. It outputs the biclusters found. We provide the users with the ability to see every single bicluster.

Implemented Methods and Features

BCTool incorporates several established biclustering methods, offering researchers a suite of tools to use. These algorithms are the following:

- **LAS (Large Average Submatrix)**: Detects large submatrices with significantly high average values using statistical testing.
- **Chen and Church Algorithm**: Being the simplest method among all, it works by minimizing the mean squared residue to find coherent submatrices in gene expression data.
- **ISA (Iterative Signature Algorithm)**: Uses an iterative approach to discover co-expressed gene modules and condition-specific patterns.
- **OPSM (Order-Preserving Submatrix)**: Identifies submatrices in which genes follow a consistent linear ordering across conditions.
- **BiVisu**: Combines biclustering with built-in visualization to aid in understanding structure and expression profiles.

Conclusion

BCTool presents a modern, Python-based implementation with advanced functionalities. Our version offers great flexibility, extensibility, and accessibility to the broad scientific community.