

GenePattern Flow Cytometry Suite

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1 Module StageFiles

Summary: A utility for users to stage and share a common input file for use by modules within a pipeline.

Version: 2

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1.1 Description

In some GenePattern¹ pipelines, the input files for processing are the same. When executing these pipelines, users will have to specify and upload the input file several times. This module allows users to stage and share a common input file for use by modules within a pipeline.

1.2 Requirements:

- GenePattern \geq 3.2.0
- Java \geq 1.5

1.3 Installation instructions:

1. Install the *StageFiles* module in GenePattern from the StageFiles.zip file or from an appropriate GenePattern module repository.

1.4 Memory, CPU and Time considerations:

Maximum memory and processing time was estimated based on processing an FCS file with 1,000,000 events and 24 parameters stored as FCS 3.0 in floating point data type.

- Maximum RAM: 50 MB
- Maximum run time: 10 seconds

1.5 Parameters

- * **Input file** – The input file that will be uploaded and staged on the GenePattern server.
- * **Output file name** – If required, specify the desired filename of the staged file.

1.6 Results

- **Staged file** – The output file is a duplicate of the submitted file and is now accessible by other modules within the same pipeline. The final output filename is dependent on the GenePattern server settings “input.file.mode” used. If “move” mode is used and the input and output filenames are the same, the module will prefix the final output filename with “staged_”. The filename will not change if “path” mode was used instead.

1.7 Related Modules

None

References

- [1] Michael Reich, Ted Liefeld, Joshua Gould, Jim Lerner, Pablo Tamayo, and Jill P. Mesirov. Genepattern 2.0. *Nature Genetics*, 38(5):500–501, May 2006.

*Required