MuG - Process Test Pipelines Documentation

Release 0.1

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Requirements and Installation

1.1 Requirements

1.1.1 Software

• Python 2.7.10+

1.1.2 Python Modules

- mg-tool-api
- pylint
- pytest

1.2 Installation

Directly from GitHub:

git clone https://github.com/Multiscale-Genomics/mg-process-test.git

Using pip:

pip install git+https://github.com/Multiscale-Genomics/mg-process-test.git

Pipelines

2.1 Test Tool

This is a demonstration pipeline using the testTool.

2.1.1 Running from the command line

Parameters

config [file] Location of the config file for the workflowin_metadata [file] Location of the input list of files required by the processout_metadata [file] Location of the output results.json file for returned files

Returns

output [file] Text file with a single entry

Example

When using a local verion of the [COMPS virtual machine](http://www.bsc.es/computer-sciences/grid-computing/comp-superscalar/downloads-and-documentation):

Tools

3.1 Test Tool

```
\begin{tabular}{ll} \textbf{class} & \verb|mg_process_test.tool.testTool.testTool(configuration=None) \\ & Tool for writing to a file \\ \end{tabular}
```

run (input_files, input_metadata, output_files)

The main function to run the test_writer tool

Parameters

- input_files (dict) List of input files In this case there are no input files required
- input_metadata (dict) Matching metadata for each of the files, plus any additional data
- output_files (dict) List of the output files that are to be generated

Returns

- **output_files** (*dict*) List of files with a single entry.
- output_metadata (dict) List of matching metadata for the returned files

test_writer(**kwargs)

Count the number of characters in a file and return a file with the count

Parameters

- **file_in_loc** (str) Location of the input file
- **file_out_loc** (str) Location of an output file

Returns Writes to the file, which is returned by pyCOMPSs to the defined location

Return type bool

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Workflows

4.1 Test Tool

class mg_process_test.workflow.test_workflow.process_test(configuration=None)
 Functions for demonstrating the pipeline set up.

 ${\tt run}~(input_files, metadata, output_files)$

Main run function for processing a test file.

Parameters

- input_files (dict) Dictionary of file locations
- metadata (list) Required meta data
- output_files (dict) Locations of the output files to be returned by the pipeline

Returns

- **output_files** (*dict*) Locations for the output txt
- output_metadata (dict) Matching metadata for each of the files

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