
MuG - Process BamQC Pipelines Documentation

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1.1 Requirements

1.1.1 Software

- Python 2.7.10+
- Java 8+
- Ant
- BamQC

1.1.2 Python Modules

- mg-tool-api
- pylint
- pytest

1.2 Installation

Directly from GitHub:

```
git clone https://github.com/Multiscale-Genomics/Bam_QC.git
```

Using pip:

```
pip install git+https://github.com/Multiscale-Genomics/Bam_QC.git
```


2.1 Bam QC Tool

This is a pipeline using BamQC for bam file stats.

2.1.1 Running from the command line

Parameters

config [file] Location of the config file for the workflow

in_metadata [file] Location of the input list of files required by the process

out_metadata [file] Location of the output results.json file for returned files

Returns

output [file] Html file with all the statistics

Example

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

```
1 cd /home/compss/code/Bam_QC
2 runcompss --lang=python Bam_QC/process_bamqc.py --config /home/compss/code/Bam_QC/
  ↪ tool_config/process_bamqc.json --in_metadata /home/compss/code/Bam_QC/tests/json/
  ↪ input_bamqc.json --out_metadata /home/compss/code/Bam_QC/tests/results.json
```

2.1.2 Methods

class `process_bamqc.process_bamqc` (*configuration=None*)

Functions for demonstrating the pipeline set up.

run (*input_files, metadata, output_files*)

This pipeline analyses a given bam file and produces html file as the reporting output file.

Parameters

- **input_files** (*dict*) – Dictionary of file locations. These should include:
 - **bam** [str] Location for the bam file
- **metadata** (*list*) – Required meta data
- **output_files** (*dict*) – Locations of the output html files returned by the pipeline

Returns

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

3.1 Test Tool

class Bam_QC.tool.bamqc.bamQC (*configuration=None*)

Tool for statistical and qualitative analysis of a Bam file

bamqc (***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

static **get_bamqc_params** (*params*)

Function to handle for extraction of commandline parameters :param params: :type params: dict

Returns

Return type list

run (*input_files, input_metadata, output_files*)

The main function to run the bamqc tool

Parameters

- **input_files** (*dict*) – Input bam file
- **input_metadata** (*dict*) – Matching metadata for the file, plus any additional data
- **output_files** (*dict*) – html file containing reports.

Returns

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

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CHAPTER 5

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