
MuG - MACS2 Pipelines Documentation

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Requirements and Installation

1.1 Requirements

1.1.1 Software

- Python 2.7.10+
- Cython 0.25+
- HTSLib
- SAMtools

```
1 sudo apt-get install make build-essential zlib1g-dev libbz2-dev liblzma-dev curl pigz ↵  
↵ libncurses5-dev  
2  
3 pip install Cython  
4  
5 cd ${HOME}/lib  
6 git clone https://github.com/samtools/htslib.git  
7 cd htslib  
8 autoheader  
9 autoconf  
10 ./configure --prefix=${HOME}/lib/htslib  
11 make  
12 make install  
13  
14 cd ${HOME}/lib  
15 git clone https://github.com/samtools/samtools.git  
16 cd samtools  
17 autoheader  
18 autoconf -Wno-syntax  
19 ./configure --prefix=${HOME}/lib/samtools  
20 make  
21 make install
```

The following will then need to be on your \$PATH:

```
1 cd ${HOME}/bin
2
3 ln -s ${HOME}/lib/htslib/bin/bgzip bgzip
4 ln -s ${HOME}/lib/htslib/bin/htsfile htsfile
5 ln -s ${HOME}/lib/htslib/bin/tabix tabix
6
7 ln -s ${HOME}/lib/samtools/bin/ace2sam ace2sam
8 ln -s ${HOME}/lib/samtools/bin/blast2sam.pl blast2sam.pl
9 ln -s ${HOME}/lib/samtools/bin/bowtie2sam.pl bowtie2sam.pl
10 ln -s ${HOME}/lib/samtools/bin/export2sam.pl export2sam.pl
11 ln -s ${HOME}/lib/samtools/bin/interpolate_sam.pl interpolate_sam.pl
12 ln -s ${HOME}/lib/samtools/bin/maq2sam-long maq2sam-long
13 ln -s ${HOME}/lib/samtools/bin/maq2sam-short maq2sam-short
14 ln -s ${HOME}/lib/samtools/bin/md5fa md5fa
15 ln -s ${HOME}/lib/samtools/bin/md5sum-lite md5sum-lite
16 ln -s ${HOME}/lib/samtools/bin/novo2sam.pl novo2sam.pl
17 ln -s ${HOME}/lib/samtools/bin/plot-bamstats plot-bamstats
18 ln -s ${HOME}/lib/samtools/bin/psl2sam.pl psl2sam.pl
19 ln -s ${HOME}/lib/samtools/bin/sam2vcf.pl sam2vcf.pl
20 ln -s ${HOME}/lib/samtools/bin/samtools samtools
21 ln -s ${HOME}/lib/samtools/bin/samtools.pl samtools.pl
22 ln -s ${HOME}/lib/samtools/bin/seq_cache_populate.pl seq_cache_populate.pl
23 ln -s ${HOME}/lib/samtools/bin/soap2sam.pl soap2sam.pl
24 ln -s ${HOME}/lib/samtools/bin/varfilter.py varfilter.py
25 ln -s ${HOME}/lib/samtools/bin/wgsim wgsim
26 ln -s ${HOME}/lib/samtools/bin/wgsim_eval.pl wgsim_eval.pl
27 ln -s ${HOME}/lib/samtools/bin/zoom2sam.pl zoom2sam.pl
```

1.1.2 Python Modules

- mg-tool-api
- mg-common
- pylint
- pytest
- macs2

1.2 Installation

Directly from GitHub:

```
1 git clone https://github.com/Multiscale-Genomics/mg-process-macs2.git
```

Using pip:

```
1 pip install git+https://github.com/Multiscale-Genomics/mg-process-macs2.git
```

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 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] Text file with a single entry

Example

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

```
1 cd /home/compss/code/mg-process-macs2
2 runcompss --lang=python process_masc2.py --config /home/compss/code/mg-process-macs2/
  ↪ tool_config/process_test.json --in_metadata /home/compss/code/mg-process-macs2/
  ↪ tests/json/input_test.json --out_metadata /home/compss/code/mg-process-macs2/tests/
  ↪ results.json
```

2.1.2 Methods

class process_mac_s2.**process_mac_s2** (*configuration=None*)

Functions for demonstrating the pipeline set up.

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

3.1 MACS2

class `mg_process_macsf2.tool.macsf2.Macsf2` (*configuration=None*)

Tool for peak calling for ChIP-seq data

static `get_macsf2_params` (*params*)

Function to handle to extraction of commandline parameters and formatting them for use in the aligner for BWA ALN

Parameters *params* (*dict*) –

Returns *list* – List of lists with each list is the parameter and the matching value

Return type *list*

macsf2_peak_calling (***kwargs*)

Function to run MACS2 for peak calling on aligned sequence files and normalised against a provided background set of alignments.

Parameters

- **name** (*str*) – Name to be used to identify the files
- **bam_file** (*str*) – Location of the aligned FASTQ files as a bam file
- **bai_file** (*str*) – Location of the bam index file
- **bam_file_bgd** (*str*) – Location of the aligned FASTQ files as a bam file representing background values for the cell
- **bai_file_bgd** (*str*) – Location of the background bam index file
- **narrowpeak** (*str*) – Location of the output narrowpeak file
- **summits_bed** (*str*) – Location of the output summits bed file
- **broadpeak** (*str*) – Location of the output broadpeak file
- **gappedpeak** (*str*) – Location of the output gappedpeak file

- **chromosome** (*str*) – If the tool is to be run over a single chromosome the matching chromosome name should be specified. If None then the whole bam file is analysed

Returns

- **narrowPeak** (*file*) – BED6+4 file - ideal for transcription factor binding site identification
- **summitPeak** (*file*) – BED4+1 file - Contains the peak summit locations for every peak
- **broadPeak** (*file*) – BED6+3 file - ideal for histone binding site identification
- **gappedPeak** (*file*) – BED12+3 file - Contains a merged set of the broad and narrow peak files
- *Definitions defined for each of these files have come from the MACS2*
- **documentation described in the docs at [https \(//github.com/taoliu/MACS\)](https://github.com/taoliu/MACS)**

macs2_peak_calling_nobgd (***kwargs*)

Function to run MACS2 for peak calling on aligned sequence files without a background dataset for normalisation.

Parameters

- **name** (*str*) – Name to be used to identify the files
- **bam_file** (*str*) – Location of the aligned FASTQ files as a bam file
- **bai_file** (*str*) – Location of the bam index file
- **narrowpeak** (*str*) – Location of the output narrowpeak file
- **summits_bed** (*str*) – Location of the output summits bed file
- **broadpeak** (*str*) – Location of the output broadpeak file
- **gappedpeak** (*str*) – Location of the output gappedpeak file
- **chromosome** (*str*) – If the tool is to be run over a single chromosome the matching chromosome name should be specified. If None then the whole bam file is analysed

Returns

- **narrowPeak** (*file*) – BED6+4 file - ideal for transcription factor binding site identification
- **summitPeak** (*file*) – BED4+1 file - Contains the peak summit locations for every peak
- **broadPeak** (*file*) – BED6+3 file - ideal for histone binding site identification
- **gappedPeak** (*file*) – BED12+3 file - Contains a merged set of the broad and narrow peak files
- *Definitions defined for each of these files have come from the MACS2*
- **documentation described in the docs at [https \(//github.com/taoliu/MACS\)](https://github.com/taoliu/MACS)**

run (*input_files, input_metadata, output_files*)

The main function to run MACS 2 for peak calling over a given BAM file and matching background BAM file.

Parameters

- **input_files** (*list*) – List of input bam file locations where 0 is the bam data file and 1 is the matching background bam file
- **metadata** (*dict*) –

Returns

- **output_files** (*list*) – List of locations for the output files.
- **output_metadata** (*list*) – List of matching metadata dict objects

CHAPTER 4

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