BSpipe.Visualization Documentation

Description: Creates files for visualization on UCSC genome browser
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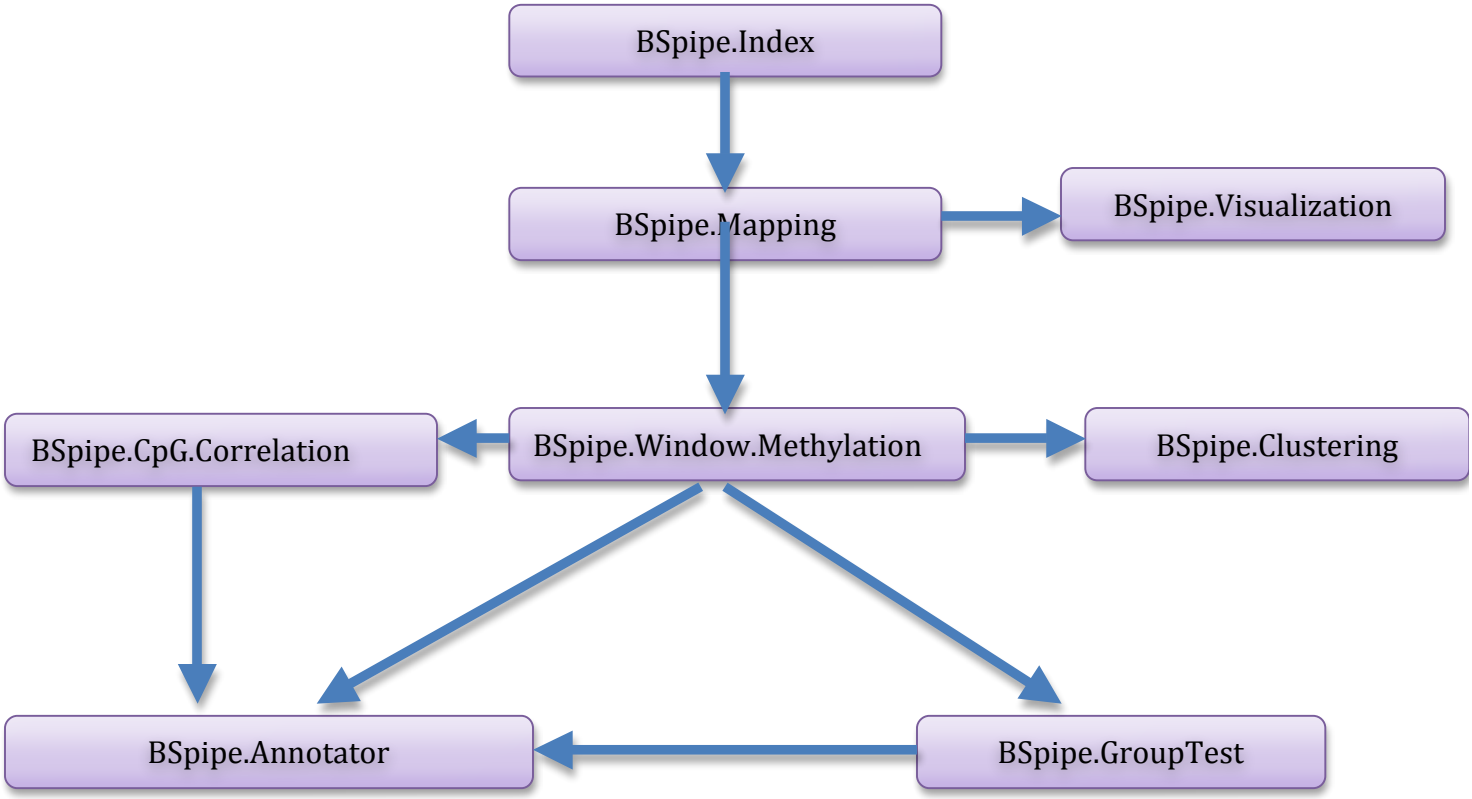
BSpipe Version: 1.0

Bisulfite sequencing is a powerful technique to study DNA cytosine methylation. Bisulfite treatment followed by PCR amplification specifically converts unmethylated cytosines to thymine. Coupled with next generation sequencing technology, it is able to detect the methylation status of every cytosine in the genome. BSpipe is an efficient bisulfite mapping software. It comes with a couple of utilities for annotation, calculation of CpG correlation etc.

The following is the flowchart of use of utilities in BSpipe package.



BSpipe.Visualization is a specific utility under BSpipe package that creates necessary files that can be used for visualization on UCSC genome browser

Parameters:

Name	Type	Description
Input.file*	bam	Include any bam from the mapping results directory
Reference.configuration.file*	tab delimited txt (.conf)	Refer next section
Reference.base	directory	Base directory containing reference file (optional)
URL*	text	Base URL for all UCSC track files
Bam	Yes/No	Create track file for the BAM file [default – Yes]
Bigwig	Yes/No	Create track file for the bigwig file [default –Yes]
CpG bed	Yes/No	Create track file for

		bed files representing CpG methylation [default – Yes]
CpH bed	Yes/No	Create track file for bed files representing CpH methylation [default – Yes]

Configuration files:

- **Reference Configuration file**

  This file saves information of the reference file. For convenience, BSpipe.Index can be run with the reference fasta file, which creates all necessary files and a reference configuration file.

  The file is organized as below:
  ref *reference name*
  seq *reference fasta (full path)*
  length *reference fasta.length (full path)*
  tc *reference c.fasta (full path)*
  ag *reference g.fasta (full path)*
  index_tc *program name* *bsbowtie reference.c prefix*
  index_ag *program name* *bsbowtie reference.g prefix*
  mspi *path to mspi.bed file.*

A sample reference configuration file for hg19 is shown below.

```
  GNU nano 1.3.12

ref      chr19
seq      chr19.fa
length   chr19.fa.length
tc       chr19.c.fa
ag       chr19.g.fa
index_tc         bowtie   chr19.c
index_ag         bowtie   chr19.g
mspi     chr19.mspi.bed
```

- **Running jobs on SGE**

  Users can submit mapping jobs to the Sun Grid Engine (SGE), by including the SGE configuration file (optional). This option is not set by default. Administrators can edit the wrapper shell script to include the sge.conf file using the prefix '-c' in the command line.

  N.B: For convenience, sge.conf file is available with the uploaded scripts in genepattern, which can be edited by the administrators.

Output files:

The program creates UCSC track files based on the user input.