

BSpice.Annotator Documentation

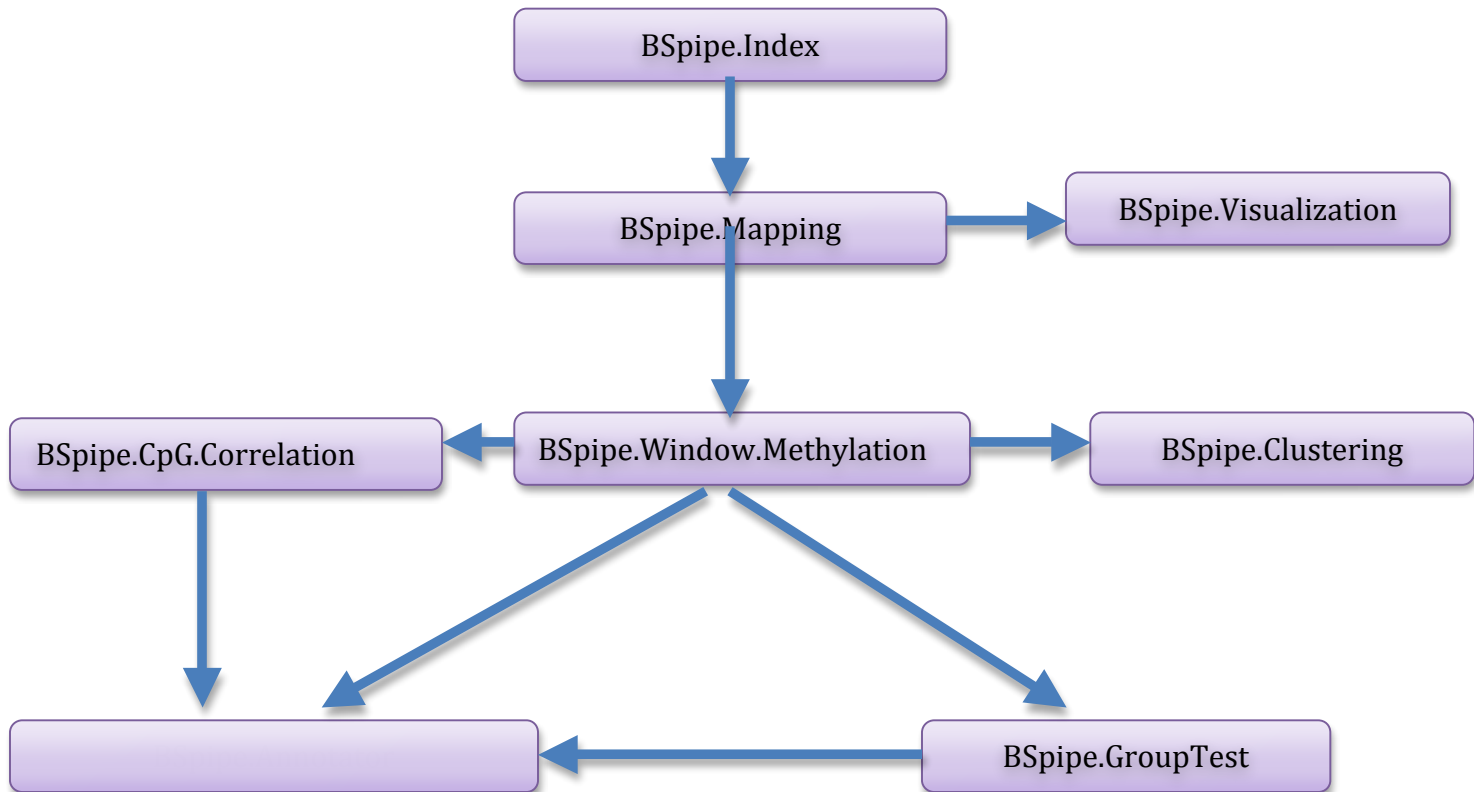
Description: Annotates windows or CpG regions.

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BSpice 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. BSpice is an efficient bisulfite mapping software. It comes with a couple of utilities that includes mapping, annotation, calculation of CpG correlation etc.

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



BSpice.Annotator is a specific utility under BSpice package that annotates CpGs or windows.

Parameters:

Name	Type	Description
Input.file	*.xls or *.bed.gz	Input file that needs to be annotated. This can be *.xls file created by either BSpice.Window.Methylation or BSpice.GroupTest or BSpice.CpG.Correlation.
Annotation directory	directory	Include a directory containing ucsc annotation files. The directory should contain cpgIslandExt.*, kgXref.*, knownGene.*, refGene.*, rnsk.* and rnaGene.* files
Size	int	Upstream and downstream size in bp [default - 1000]

Configuration files:

- **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 output files include summary files (*.summary), annotation files (*.ann), summary statistics files (*.stat).