

Description

CAME is a command line tool for identifying chromatin accessibility from nucleosome occupancy and methylome sequencing (NOMe-Seq). The tool is written in Java, therefore no platform-specific compiling of the bytecode is required. A Java Virtual Machine (JVM) with level 1.8 or higher has to be installed on the system; however, it is recommended to update to the newest Java binaries provided by Oracle for the corresponding platform (i.e., Linux, Mac, or Windows).

Usage:

```
java -jar came.jar <input_filepath> <output_filepath> [optional arguments]
```

Input file format

CAME takes tab-eliminated files from commonly used bisulfite alignment programs and methylation calling softwares, such as BSMAP, AMP pipeline.

1. Default format:

- chromosome
- start
- end
- coverage
- methylation score

i.e., example.txt

chr1	24709432	24709435	10	0.74
chr1	24709433	24709436	6	0.96
chr1	24709447	24709450	20	0.99
chr1	24709448	24709451	27	0.99

2. BSMAP format

- chromorome
- coordinate (1-based)
- strand
- sequence context
- methylation ratio
- number of reads covering this locus
- number of unconverted Cs in the reads at this locus

Please reference [BSMAP](#) for details.

3. AMP

- chrBase
- chr
- base
- strand

- coverage
- freqC
- freqT

Please reference [AMP](#) for details.

Output file

CAME will generate a tab-eliminated .bed file that includes:

- chr chromosome name
- start the start position of a closed (open) chromatin region
- end the end position of a closed (open) chromatin region
- #gchs the number of gchs within the closed (open) chromatin region
- score the average methylation score of gchs within the closed (open) chromatin region
- length the length of detected region

Parameters

optional arguments

- -t [0 or 1 or 2] type of input file format. 0: default 1: BSMAP 2: AMP (see Input file format section)
- -s [0-1] methylation score cutoff for seed. GCHs with smaller (larger) methylation score than this cutoff will be selected as seed points for detection of closed (open) chromatin region. (default: 0.2)
- -e [0-1] average methylation score cutoff for extended region. If the average methylation score of the extended region is larger (smaller) than cutoff, extension will be stopped. (default: 0.4)
- -a [0-1] average methylation score cutoff for seed+extended region. If the average methylation score of the (seed+extended) region is larger (smaller) than cutoff, extension will be stopped. (default: 0.4)
- -j [0-1] jump cutoff. If the methylation score of a peak is larger (smaller) than cutoff, extension will be stopped. (default: 0.7)
- -m [0-1] final end points decision parameter. By default, the final values will automatically estimated from non-parametric mixture model. Or defined by users.
- -d [positive integer] distance cutoff for GCHs. (default: 500)
- -i [chrName, start end] interval. Process only for provided region, instead of all chromosomes.
- -o [0 or 1] export open chromatin region. If -o is 1, the open chromatin region will be printed out, instead of closed chromatin region. (default: 0)