Package 'PING'

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Type Package

Title Probabilistic inference for Nucleosome Positioning with MNase-based or Sonicated Short-read Data

Description Probabilistic inference of ChIP-Seq using an empirical Bayes mixture model approach.

Version 2.49.0

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Depends R(>= 3.5.0)

Imports methods, PICS, graphics, grDevices, stats, Gviz, fda, BSgenome, stats4, BiocGenerics, IRanges, GenomicRanges, S4Vectors

Suggests parallel, ShortRead, rtracklayer

Collate setClasses.R setMethods.R PING.R postPING.R segmentPING.R

License Artistic-2.0

biocViews Clustering, StatisticalMethod, Visualization, Sequencing

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postPING   *Post process Estimation of binding site positions obtained from PING*

Description

Post process Estimation of binding site positions obtained from PING. Refit mixture models with stronger prior in candidate regions contain potential problems, and then convert final result into dataframe.

Usage

```
postPING(
  ping,
  seg,
  rho2 = NULL,
  sigmaB2 = NULL,
  alpha2 = NULL,
  beta2 = NULL,
  min.dist = 100,
  paraEM = NULL,
  paraPrior = NULL,
  score = 0.05,
  dataType = "MNase",
  nCores = 1,
  makePlot = FALSE,
  FragmentLength = 100,
  mart = NULL,
  seg.boundary = NULL,
  DupBound = NULL,
  IP = NULL,
  datname = ""
)
```

Arguments

ping	A `pingList` object containing estimation of nucleosome positions as returned by the `PING` function.
seg	An object of class `segmentReadsList` containing the results for all pre-processed regions as returned by `segmentReads`.
rho2, sigmaB2, alpha2, beta2	
	Integer values, the parameters in the prior of mixture models to be re-fitted.
min.dist	The minimum distance of two adjacent nucleosomes predicted from different candidate regions, smaller than that will be treated as duplicated predictions for the same nucleosomes.
paraEM	A `list` of parameters for the EM algorithm. The default parameters should be good enough for most usages.
paraPrior	A `list` of parameters for the prior distribution. The default parameters should be good enough for most usages.
score	A `numeric`. The score threshold used when calling `FilterPING`.

dataType	A `character` that can be set to use selected default parameters for the algorithm.
nCores	An `integer`. The number of cores that should be used in parallel by the function.
makePlot	A `logical`. Plot a summary of the output.
FragmentLength	An `integer`. The length of XSET profile extension
mart, seg.boundary, DupBound, datname	
	Plotting parameters and options.
IP	A `GRanges` object. The reads used in segmentation process.
minK	An `integer`.The minimum number of binding events per region. If the value is 0, the minimum number is automatically calculated.
maxK	An `integer`. The maximum number of binding events per region. If the value is 0, the maximum number is automatically calculated.
tol	A `numeric`. The tolerance for the EM algorithm.
B	An `integer`. The maximum number of iterations to be used.
mSelect	A `character` specifying the information criteria to be used when selecting the number of binding events. Default="AIC3"
mergePeaks	A `logical` stating whether overlapping binding events should be picked.
mapCorrect	A `logical` stating whether mappability profiles should be incorporated in the estimation, i.e: missing reads estimated.
xi	An `integer`. The average DNA fragment size.
rho	An `integer`. A variance parameter for the average DNA fragment size distribution.
alpha	An `integer`. First hyperparameter of the inverse Gamma distribution for sigma^2 in the PICS model
beta	An `integer`. Second hyperparameter of the inverse Gamma distribution for sigma^2 in the PING model
lambda	An `integer`. The lambda control Gaussian Markov Random Field prior on the distance of adjacent nucleosomes, we do not recommend user change the default value.
dMu	An `integer`. Our best guess for the distance between two neighboring nucleosomes.

Value

A `data.frame` containing the estimated binding site positions

Note

Based on our experiemt on a few real data sets, we suggestion to use following values of parameters. For sonication data we use rho1=1.2; sigmaB2=6400; rho=15; alpha1=10; alpha2=98; beta2=200000. For MNase data we use rho1=3; sigmaB2=4900; rho=8; alpha1=20; alpha2=100; beta2=100000. The value of xi depends on specs of sample, since that affect the length of linker-DNA. For example, we use xi=160 for yeast and xi=200 for mouse.

See Also

PING, plotSummary

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