# Package: PING (via r-universe)

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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

**RoxygenNote** 7.0.1

**Repository** https://bioc.r-universe.dev

**RemoteUrl** https://github.com/bioc/PING

**RemoteRef** HEAD

**RemoteSha** 4eff825a5cc1a7ae3dd8d56023a23b7c57d906dc

## Contents

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

# Index