

# Package ‘PING’

January 4, 2025

**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** 2.51.0

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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

**git\_url** <https://git.bioconductor.org/packages/PING>

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 postPING
 

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


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### 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 experient on a few real data sets, we suggestion to use following values of parameters. For sonication data we use  $\rho_1=1.2$ ;  $\sigma_B=6400$ ;  $\rho=15$ ;  $\alpha_1=10$ ;  $\alpha_2=98$ ;  $\beta_2=200000$ . For MNase data we use  $\rho_1=3$ ;  $\sigma_B=4900$ ;  $\rho=8$ ;  $\alpha_1=20$ ;  $\alpha_2=100$ ;  $\beta_2=100000$ . 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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