

Package ‘FitHiC’

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Type Package

Title Confidence estimation for intra-chromosomal contact maps

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Description Fit-Hi-C is a tool for assigning statistical confidence estimates to intra-chromosomal contact maps produced by genome-wide genome architecture assays such as Hi-C.

License GPL (>= 2)

biocViews DNA3DStructure, Software

Imports data.table, fdrtool, grDevices, graphics, Rcpp, stats, utils

LinkingTo Rcpp

RoxygenNote 5.0.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

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FitHiC

*Fit-Hi-C***Description**

Fit-Hi-C is a tool for assigning statistical confidence estimates to intra-chromosomal contact maps produced by genome-wide genome architecture assays such as Hi-C.

Usage

```
FitHiC( fragsfile, intersfile, outdir, biasfile = "none", noOfPasses = 1,
        noOfBins = 100, mappabilityThreshold = 1, libname = "",
        distUpThres = -1, distLowThres = -1, visual = FALSE,
        useHiCPro = FALSE)
```

Arguments

| | |
|----------------------|--|
| fragsfile | The path specifies where FRAGSFILE is located in the file system. FRAGSFILE stores the information about midpoints (or start indices) of the fragments. It should consist of 5 columns: first column stands for chromosome name; third column stands for the midPoint; fourth column stands for the hitCount; second column and fifth column can be arbitrary. |
| intersfile | The path specifies where INTERSFILE is located in the file system. INTERSFILE stores the information about interactions between fragment pairs. It should consist of 5 columns: first column and third column stand for the chromosome names of the fragment pair; second column and fourth column stand for midPoints of the fragment pair; fifth column stands for hitCount. |
| outdir | The path specifies where the output files will be stored in the file system. If the path does not exist, it will be automatically created. |
| biasfile | The path specifies where BIASFILE is located in the file system. BIASFILE stores the information about biases calculated by ICE for each locus. It should consist of 3 columns: first column stands for chromosome name; second column stands for the midPoint; third column stands for the bias. This argument is OPTIONAL. |
| noOfPasses | Number of passes after the initial (before) fit. DEFAULT is 1 (after). |
| noOfBins | Number of equal-occupancy (count) bins. Default is 100. |
| mappabilityThreshold | Minimum number of hits per locus that has to exist to call it mappable. DEFAULT is 1. |
| libname | Name of the library that is analyzed to be used for plots. DEFAULT is empty. |
| distUpThres | Upper bound on the intra-chromosomal distance range (unit: base pairs). DEFAULT is no limit. |
| distLowThres | Lower bound on the intra-chromosomal distance range (unit: base pairs). DEFAULT is no limit. |
| visual | Use this flag for generating plots. DEFAULT is False. |
| useHiCPro | Whether to use HiC-Pro preprocessed data. DEFAULT is False. |

Value

None

Author(s)

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Examples

```

fragsfile <- system.file("extdata", "fragmentLists/Duan_yeast_EcoRI.gz",
  package = "FitHiC")
intersfile <- system.file("extdata", "contactCounts/Duan_yeast_EcoRI.gz",
  package = "FitHiC")
outdir <- file.path(getwd(), "Duan_yeast_EcoRI")
FitHiC(fragfile, intersfile, outdir, libname="Duan_yeast_EcoRI",
  distUpThres=250000, distLowThres=10000)

fragsfile <- system.file("extdata", "fragmentLists/Duan_yeast_HindIII.gz",
  package = "FitHiC")
intersfile <- system.file("extdata", "contactCounts/Duan_yeast_HindIII.gz",
  package = "FitHiC")
outdir <- file.path(getwd(), "Duan_yeast_HindIII")
FitHiC(fragfile, intersfile, outdir, libname="Duan_yeast_HindIII",
  distUpThres=250000, distLowThres=10000)

fragsfile <- system.file("extdata",
  "fragmentLists/Dixon_hESC_HindIII_hg18_combineFrag10_chr1.gz",
  package = "FitHiC")
intersfile <- system.file("extdata",
  "contactCounts/Dixon_hESC_HindIII_hg18_combineFrag10_chr1.gz",
  package = "FitHiC")
outdir <- file.path(getwd(), "Dixon_hESC_HindIII_hg18_combineFrag10_chr1")
FitHiC(fragfile, intersfile, outdir,
  libname="Dixon_hESC_HindIII_hg18_combineFrag10_chr1", noOfBins=200,
  distUpThres=500000, distLowThres=50000)

fragsfile <- system.file("extdata",
  "fragmentLists/Dixon_mESC_HindIII_mm9_combineFrag10_chr1.gz",
  package = "FitHiC")
intersfile <- system.file("extdata",
  "contactCounts/Dixon_mESC_HindIII_mm9_combineFrag10_chr1.gz",
  package = "FitHiC")
outdir <- file.path(getwd(), "Dixon_mESC_HindIII_mm9_combineFrag10_chr1")
FitHiC(fragfile, intersfile, outdir,
  libname="Dixon_mESC_HindIII_mm9_combineFrag10_chr1", noOfBins=200,
  distUpThres=500000, distLowThres=50000)

fragsfile <- system.file("extdata",
  "fragmentLists/Dixon_hESC_HindIII_hg18_w40000_chr1.gz",
  package = "FitHiC")
intersfile <- system.file("extdata",
  "contactCounts/Dixon_hESC_HindIII_hg18_w40000_chr1.gz",
  package = "FitHiC")
outdir <- file.path(getwd(), "Dixon_hESC_HindIII_hg18_w40000_chr1")
FitHiC(fragfile, intersfile, outdir,
  libname="Dixon_hESC_HindIII_hg18_w40000_chr1", noOfBins=50,

```

```
distUpThres=5000000, distLowThres=50000)

fragsfile <- system.file("extdata",
  "fragmentLists/Dixon_hESC_HindIII_hg18_w40000_chr1.gz",
  package = "FitHiC")
intersfile <- system.file("extdata",
  "contactCounts/Dixon_hESC_HindIII_hg18_w40000_chr1.gz",
  package = "FitHiC")
outdir <- file.path(getwd(), "Dixon_hESC_HindIII_hg18_w40000_chr1.afterICE")
biasfile <- system.file("extdata",
  "biasPerLocus/Dixon_hESC_HindIII_hg18_w40000_chr1.gz",
  package = "FitHiC")
FitHiC(fragfile, intersfile, outdir, biasfile,
  libname="Dixon_hESC_HindIII_hg18_w40000_chr1", noOfBins=50,
  distUpThres=5000000, distLowThres=50000)

fragsfile <- system.file("extdata", "fragmentLists/data_5000000_abs.bed.gz",
  package = "FitHiC")
intersfile <- system.file("extdata", "contactCounts/data_5000000.matrix.gz",
  package = "FitHiC")
biasfile <- system.file("extdata",
  "biasPerLocus/data_5000000_iced.matrix.biases.gz", package = "FitHiC")
outdir <- file.path(getwd(), "data_5000000")
FitHiC(fragfile, intersfile, outdir, biasfile, libname="data_5000000",
  distUpThres=500000000, distLowThres=5000000, useHiCPro=TRUE)
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