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 sytem. 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(fragsfile, 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(fragsfile, intersfile, outdir, libname="Duan_yeast_HindIII",
    distUpThres=250000, distLowThres=10000)

fragsfile <- system.file("extdata",
    "fragmentLists/Dixon_hESC_HindIII_hg18_combineFrags10_chr1.gz",
    package = "FitHiC")
intersfile <- system.file("extdata",
    "contactCounts/Dixon_hESC_HindIII_hg18_combineFrags10_chr1.gz",
    package = "FitHiC")
outdir <- file.path(getwd(), "Dixon_hESC_HindIII_hg18_combineFrags10_chr1")
FitHiC(fragsfile, intersfile, outdir,
    libname="Dixon_hESC_HindIII_hg18_combineFrags10_chr1", noOfBins=200,
    distUpThres=5000000, distLowThres=50000)

fragsfile <- system.file("extdata",
    "fragmentLists/Dixon_mESC_HindIII_mm9_combineFrags10_chr1.gz",
    package = "FitHiC")
intersfile <- system.file("extdata",
    "contactCounts/Dixon_mESC_HindIII_mm9_combineFrags10_chr1.gz",
    package = "FitHiC")
outdir <- file.path(getwd(), "Dixon_mESC_HindIII_mm9_combineFrags10_chr1")
FitHiC(fragsfile, intersfile, outdir,
    libname="Dixon_mESC_HindIII_mm9_combineFrags10_chr1", noOfBins=200,
    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")
FitHiC(fragsfile, 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(fragsfile, 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(fragsfile, intersfile, outdir, biasfile, libname="data_5000000",
    distUpThres=500000000, distLowThres=5000000, useHiCPro=TRUE)
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