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. FRAGS-FILE 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. INTERS-FILE 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 mid-Points 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. DE-FAULT 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). DE-FAULT is no limit.

distLowThres
: Lower bound on the intra-chromosomal distance range (unit: base pairs). DE-FAULT 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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