

Package ‘FitHiC’

April 2, 2025

Type Package

Title Confidence estimation for intra-chromosomal contact maps

Version 1.33.0

Date 2017-04-12

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

git_url <https://git.bioconductor.org/packages/FitHiC>

git_branch devel

git_last_commit 75885eb

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2025-04-02

Author Ferhat Ay [aut] (Python original,
<https://noble.gs.washington.edu/proj/fit-hi-c/>),
Timothy L. Bailey [aut],
William S. Noble [aut],
Ruyu Tan [aut, cre, trl] (R port)

Maintainer Ruyu Tan <rut003@ucsd.edu>

Contents

| | |
|------------------|---|
| FitHiC | 2 |
|------------------|---|

| | |
|--------|-----------------|
| FitHiC | <i>Fit-Hi-C</i> |
|--------|-----------------|

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)

Ruyu Tan, <rut003@ucsd.edu>

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_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(fragsfile, intersfile, outdir,
  libname="Dixon_hESC_HindIII_hg18_combineFrag10_chr1", noOfBins=200,
  distUpThres=5000000, 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(fragsfile, intersfile, outdir,
  libname="Dixon_mESC_HindIII_mm9_combineFrag10_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)

```

Index

FitHiC, 2