

# Package ‘FitHiC’

November 19, 2025

**Type** Package

**Title** Confidence estimation for intra-chromosomal contact maps

**Version** 1.37.0

**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** 4a22ef6

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.23

**Date/Publication** 2025-11-19

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## Contents

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

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=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(fragfile, 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(fragfile, intersfile, outdir,
    libname="Dixon_hESC_HindIII_hg18_w40000_chr1", noOfBins=50,
    distUpThres=5000000, distLowThres=50000)

fragfile <- 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)

fragfile <- 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)

```

# Index

FitHiC, [2](#)