Package: HiCExperiment (via r-universe)

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Title Bioconductor class for interacting with Hi-C files in R

Version 1.5.0

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Description R generic interface to Hi-C contact matrices in
`.(m)cool`, `.hic` or HiC-Pro derived formats, as well as other
Hi-C processed file formats. Contact matrices can be partially
parsed using a random access method, allowing a
memory-efficient representation of Hi-C data in R. The
`HiCExperiment` class stores the Hi-C contacts parsed from
local contact matrix files. `HiCExperiment` instances can be
further investigated in R using the `HiContacts` analysis
package.

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URL https://github.com/js2264/HiCExperiment

BugReports https://github.com/js2264/HiCExperiment/issues

Depends R (>= 4.2)

Imports InteractionSet, strawr, GenomeInfoDb, GenomicRanges, IRanges,
S4Vectors, BiocGenerics, BiocIO, BiocParallel, methods, rhdf5,
Matrix, vroom, dplyr, stats

Suggests HiContacts, HiContactsData, BiocFileCache, rtracklayer,
testthat (>= 3.0.0), BiocStyle, knitr, rmarkdown

biocViews HiC, DNA3DStructure, DataImport

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Collate 'HiCExperiment-class.R' 'AggrHiCExperiment-class.R'
'AllGenerics.R' 'HiCExperiment-methods.R'
'AggrHiCExperiment-methods.R' 'PairsFile-class.R'
'ContactsFile-class.R' 'ContactsFile-methods.R'
'CoolFile-class.R' 'CoolFile-methods.R' 'HicFile-class.R'
'HicFile-methods.R' 'HicproFile-class.R' 'HicproFile-methods.R'
'PairsFile-methods.R' 'import-methods.R' 'available.R' 'bin.R'
'checks.R' 'coerce.R' 'data.R' 'export-methods.R' 'globals.R'
'parse-cool.R' 'parse-hic.R' 'parse-hicpro.R' 'parse-pairs.R'
'parse-slices.R' 'reexports.R' 'utils.R' 'zzz.R'

Repository https://bioc.r-universe.dev

RemoteUrl https://github.com/bioc/HiCExperiment

RemoteRef HEAD

RemoteSha 6d012594e08a7283a0707db668d755441b01e93f

Contents

AggrHiCExperiment   AggrHiCExperiment *S4 class*

Description

The `AggrHiCExperiment` extends `HiCExperiment` class.

Usage

```
AggrHiCExperiment(
  file,
  resolution = NULL,
  targets,
  flankingBins = 50,
```

```
  metadata = list(),
  topologicalFeatures = S4Vectors::SimpleList(),
  pairsFile = NULL,
  bed = NULL,
  maxDistance = NULL,
  BPPARAM = BiocParallel::bpparam()
)

## S4 method for signature 'AggrHiCExperiment,missing'
slices(x)

## S4 method for signature 'AggrHiCExperiment,character'
slices(x, name)

## S4 method for signature 'AggrHiCExperiment,numeric'
slices(x, name)

## S4 method for signature 'AggrHiCExperiment'
show(object)
```

Arguments

`file`	CoolFile or plain path to a Hi-C contact file
`resolution`	Resolution to use with the Hi-C contact file
`targets`	Set of chromosome coordinates for which interaction counts are extracted from the Hi-C contact file, provided as a GRanges object (for diagnoal-centered loci) or as a GInteractions object (for off-diagonal coordinates).
`flankingBins`	Number of bins on each flank of the bins containing input targets.
`metadata`	list of metadata
`topologicalFeatures`	
	topologicalFeatures provided as a named SimpleList
`pairsFile`	Path to an associated .pairs file
`bed`	Path to regions file generated by HiC-Pro
`maxDistance`	Maximum distance to use when compiling distance decay
`BPPARAM`	BiocParallel parameters
`x`, `object`	A `AggrHiCExperiment` object.
`name`	The name/index of slices to extract.

Value

An `AggrHiCExperiment` object.

Slots

`fileName` Path of Hi-C contact file

`resolutions` Resolutions available in the Hi-C contact file.

resolution Current resolution

interactions Genomic Interactions extracted from the Hi-C contact file

scores Available interaction scores.

slices Available interaction slices.

topologicalFeatures Topological features associated with the dataset (e.g. loops (\<Pairs\>), borders (\<GRanges\>), viewpoints (\<GRanges\>), etc...)

pairsFile Path to the .pairs file associated with the Hi-C contact file

metadata metadata associated with the Hi-C contact file.

See Also

HiCExperiment()

Examples

```
fpath <- HiContactsData::HiContactsData('yeast_wt', 'mcool')
data(centros_yeast)
x <- AggrHiCExperiment(
  file = fpath,
  resolution = 8000,
  targets = centros_yeast[c(4, 7)]
)
x
slices(x, 'count')[1:10, 1:10, 1]
```

---

as   *Coercing functions*

Description

Coercing functions available for HiCExperiment objects.

Usage

```
## S4 method for signature 'HiCExperiment'
as.matrix(x, use.scores = "balanced", sparse = FALSE)

## S4 method for signature 'HiCExperiment'
as.data.frame(x)

gi2cm(gi, use.scores = "score")

cm2matrix(cm, replace_NA = NA, sparse = FALSE)

df2gi(
  df,
```

```
    seqnames1 = "seqnames1",
    start1 = "start1",
    end1 = "end1",
    seqnames2 = "seqnames2",
    start2 = "start2",
    end2 = "end2"
)
```

Arguments

x	HiCExperiment object
use.scores	Which scores to use to inflate GInteractions
sparse	Whether to return the contact matrix as a sparse matrix
gi	GInteractions object
cm	A `ContactMatrix` object
replace_NA	Replace NA values
df	A `data.frame` object
seqnames1, start1, end1, seqnames2, start2, end2	
	Names (as strings) of columns containing corresponding information in a data.frame parsed into GInteractions (default: FALSE)

Examples

```
mcoolPath <- HiContactsData::HiContactsData('yeast_wt', 'mcool')
contacts <- import(mcoolPath, focus = 'XVI', resolution = 16000, format = 'cool')
gis <- interactions(contacts)
cm <- gi2cm(gis, 'balanced')
cm
cm2matrix(cm)[1:10, 1:10]
df2gi(data.frame(
    chr1 = 'I', start1 = 10, end1 = 100,
    chr2 = 'I', start2 = 40, end2 = 1000,
    score = 12,
    weight = 0.234,
    filtered = TRUE
), seqnames1 = 'chr1', seqnames2 = 'chr2')
```

---

bin-methods   *HiCExperiment binning methods*

Description

HiCExperiment binning methods

Usage

```
## S4 method for signature 'GInteractions,numeric'
bin(x, resolution, seqinfo = NULL)

## S4 method for signature 'PairsFile,numeric'
bin(x, resolution, seqinfo = NULL)
```

Arguments

x	A PairsFile or GInteractions object
resolution	Which resolution to use to bin the interactions
seqinfo	Seqinfo object

Examples

```
pairsf <- HiContactsData::HiContactsData('yeast_wt', 'pairs.gz')
pf <- PairsFile(pairsf)
```

ContactsFile-class   ContactsFile *S4 class*

Description

The `ContactsFile` class describes a `BiocFile` object, pointing to the location of an Hi-C matrix file (cool, mcool, hic, hicpro, ...) and containing additional slots:

1. resolution: at which resolution the associated mcool file should be parsed

2. pairsFile: the path (in plain character) to an optional pairs file (stored as a `PairsFile` object);

3. metadata: a list. If the CoolFile is created by `HiCool`, it will contain two elements: `log` (path to `HiCool` processing log file) and `stats` (aggregating some stats from `HiCool` mapping).

ContactsFile methods.

Arguments

path	String; path to an Hi-C matrix file (cool, mcool, hic, hicpro)
resolution	numeric; resolution to use with Hi-C matrix file
pairsFile	String; path to a pairs file
metadata	list.
object	A `ContactsFile` object.
x	A `ContactsFile` object.

Slots

resolution numeric value or NULL

pairsFile PairsFile object

metadata list

See Also

[CoolFile()](), [HicFile()](), [HicproFile()]()

CoolFile-class   CoolFile *S4 class*

Description

The `CoolFile` class describes a `BiocFile` object, pointing to the location of an Hi-C matrix file (cool, mcool, hic, hicpro, ...) and containing additional slots:

1. resolution: at which resolution the associated mcool file should be parsed

2. pairsFile: the path (in plain character) to an optional pairs file (stored as a `PairsFile` object);

3. metadata: a list. If the CoolFile is created by `HiCool`, it will contain two elements: `log` (path to `HiCool` processing log file) and `stats` (aggregating some stats from `HiCool` mapping).

CoolFile methods.

Arguments

path	String; path to a (m)cool file
resolution	numeric; resolution to use with mcool file
pairsFile	String; path to a pairs file
metadata	list; if the CoolFile object was generated by HiCool::HiCool, this list contains the path to log file, some statistics regarding the number of pairs obtained by hicstuff as well as the arguments and the hash ID used by HiCool.
object	A `CoolFile` object.

See Also

[HicFile()](), [HicproFile()]()

Examples

```
mcoolPath <- HiContactsData::HiContactsData('yeast_wt', 'mcool')
pairsPath <- HiContactsData::HiContactsData('yeast_wt', 'pairs.gz')
cf <- CoolFile(
  mcoolPath,
  resolution = 2000,
  pairsFile = pairsPath,
  metadata = list(info = 'Yeast WT Hi-C exp.')
)
cf
resolution(cf)
pairsFile(cf)
metadata(cf)
```

---

data   *Example datasets provided in* HiCExperiment *&* HiContactsData

---

Description

Example datasets provided in HiCExperiment & HiContactsData

Usage

```
data(centros_yeast)

contacts_yeast(full = FALSE)

contacts_yeast_eco1(full = FALSE)
```

Arguments

full   Whether to import all interactions

Format

An object of class ″GRanges″.

Source

HiContacts

Examples

```
data(centros_yeast)
centros_yeast
contacts_yeast()
```

---

export-methods   *HiCExperiment export methods*

Description

Export methods to save a HiCExperiment object into a set of HiC-Pro-style files (matrix & regions files)

Usage

```
## S4 method for signature 'HiCExperiment,missing,character'
export(object, prefix, format, ...)
```

Arguments

object	A HiCExperiment object
prefix	Prefix used when generating output file(s).
format	File format. Available: cool and HiC-Pro.
...	Extra arguments to use when exporting to cool. Can be metadata <string> or chunksize <integer>.

Value

Path to saved files

Examples

```
###################################################################
## ----------- Importing .(m)cool contact matrices ---------- ##
###################################################################

mcoolPath <- HiContactsData::HiContactsData('yeast_wt', 'mcool')
hic <- import(mcoolPath, format = 'mcool', resolution = 16000)
export(hic["II"], prefix = 'subset_chrII', format = 'cool')
export(hic["II"], prefix = 'subset_chrII', format = 'HiC-Pro')
```

HiCExperiment   HiCExperiment *S4 class*

Description

The HiCExperiment class describes Hi-C contact files imported in R, either through the HiCExperiment constructor function or using the import method implemented by HiCExperiment package.

Usage

```
HiCExperiment(
  file,
  resolution = NULL,
  focus = NULL,
  metadata = list(),
  topologicalFeatures = S4Vectors::SimpleList(compartments = GenomicRanges::GRanges(),
    borders = GenomicRanges::GRanges(), loops =
   InteractionSet::GInteractions(GenomicRanges::GRanges(), GenomicRanges::GRanges()),
    viewpoints = GenomicRanges::GRanges()),
  pairsFile = NULL,
  bed = NULL
)

makeHiCExperimentFromGInteractions(gi)

## S4 method for signature 'HiCExperiment'
resolutions(x)

## S4 method for signature 'HiCExperiment'
resolution(x)

## S4 method for signature 'HiCExperiment'
focus(x)

## S4 replacement method for signature 'HiCExperiment,character'
focus(x) <- value

## S4 method for signature 'HiCExperiment,numeric'
zoom(x, resolution)

## S4 method for signature 'HiCExperiment,character'
refocus(x, focus)

## S4 method for signature 'HiCExperiment,missing'
scores(x)

## S4 method for signature 'HiCExperiment,character'
scores(x, name)

## S4 method for signature 'HiCExperiment,numeric'
scores(x, name)

## S4 replacement method for signature 'HiCExperiment,character,numeric'
scores(x, name) <- value

## S4 method for signature 'HiCExperiment,missing'
topologicalFeatures(x)
```

```
## S4 method for signature 'HiCExperiment,character'
topologicalFeatures(x, name)

## S4 method for signature 'HiCExperiment,numeric'
topologicalFeatures(x, name)

## S4 replacement method for signature 'HiCExperiment,character,GRangesOrGInteractions'
topologicalFeatures(x, name) <- value

## S4 method for signature 'HiCExperiment'
pairsFile(x)

## S4 replacement method for signature 'HiCExperiment,character'
pairsFile(x) <- value

## S4 replacement method for signature 'HiCExperiment,list'
metadata(x) <- value

## S4 method for signature 'HiCExperiment,numeric'
subsetByOverlaps(x, ranges)

## S4 method for signature 'HiCExperiment,logical'
subsetByOverlaps(x, ranges)

## S4 method for signature 'HiCExperiment,GRanges'
subsetByOverlaps(x, ranges, type = c("within", "any"))

## S4 method for signature 'HiCExperiment,GInteractions'
subsetByOverlaps(x, ranges)

## S4 method for signature 'HiCExperiment,Pairs'
subsetByOverlaps(x, ranges)

## S4 method for signature 'HiCExperiment,numeric,ANY,ANY'
x[i]

## S4 method for signature 'HiCExperiment,GRanges,ANY,ANY'
x[i]

## S4 method for signature 'HiCExperiment,logical,ANY,ANY'
x[i]

## S4 method for signature 'HiCExperiment,GInteractions,ANY,ANY'
x[i]

## S4 method for signature 'HiCExperiment,Pairs,ANY,ANY'
x[i]
```

```
## S4 method for signature 'HiCExperiment,character,ANY,ANY'
x[i]

## S4 method for signature 'HiCExperiment'
fileName(object)

## S4 method for signature 'HiCExperiment'
interactions(x, fillout.regions = FALSE)

## S4 replacement method for signature 'HiCExperiment,GInteractions'
interactions(x) <- value

## S4 method for signature 'HiCExperiment'
length(x)

## S4 replacement method for signature 'HiCExperiment'
x$name <- value

## S4 method for signature 'HiCExperiment'
x$name

## S4 method for signature 'HiCExperiment'
seqinfo(x)

## S4 method for signature 'HiCExperiment'
bins(x)

## S4 method for signature 'HiCExperiment'
anchors(x)

## S4 method for signature 'HiCExperiment'
regions(x)

## S4 method for signature 'HiCExperiment'
cis(x)

## S4 method for signature 'HiCExperiment'
trans(x)
```

Arguments

`file`	CoolFile or plain path to a Hi-C contact file
`resolution`	Resolution to use with the Hi-C contact file
`focus`	Chromosome coordinates for which interaction counts are extracted from the Hi-C contact file, provided as a character string (e.g. "II:4001-5000"). If not provided, the entire Hi-C contact file will be imported.
`metadata`	list of metadata

topologicalFeatures

> topologicalFeatures provided as a named SimpleList

pairsFile   Path to an associated .pairs file (optional)

bed   Path to regions file generated by HiC-Pro (optional)

gi   GInteractions object

x   A `HiCExperiment` object.

value   Value to add to topologicalFeatures, scores, pairsFile or metadata slots.

name   Name of the element to access in topologicalFeatures or scores SimpleLists.

type   any of `within` or any, to subset interactions by overlap with a provided GRanges.

i, ranges   a GRanges, coordinates in character, or boolean vector to subset a HiCExperiment

object   A `HiCExperiment` object.

fillout.regions

> Whehter to add missing regions to GInteractions' regions?

Value

An `HiCExperiment` object.

Slots

fileName Path of Hi-C contact file

focus Chr. coordinates for which interaction counts are extracted from the Hi-C contact file.

resolutions Resolutions available in the Hi-C contact file.

resolution Current resolution

interactions Genomic Interactions extracted from the Hi-C contact file

scores Available interaction scores.

topologicalFeatures Topological features associated with the dataset (e.g. loops (\<GInteractions\>), borders (\<GRanges\>), viewpoints (\<GRanges\>), etc...)

pairsFile Path to the .pairs file associated with the Hi-C contact file

metadata metadata associated with the Hi-C contact file.

See Also

[AggrHiCExperiment()](#), [CoolFile()](#), [HicFile()](#), [HicproFile()](#), [PairsFile()](#)

Examples

```
#####################################################################
## Create a HiCExperiment object from a disk-stored contact matrix ##
#####################################################################

mcool_file <- HiContactsData::HiContactsData("yeast_wt", "mcool")
pairs_file <- HiContactsData::HiContactsData("yeast_wt", "pairs.gz")
contacts <- HiCExperiment(
```

```
    file = mcool_file,
    resolution = 8000L,
    pairsFile = pairs_file
)
contacts


#######################################################################
## ----- Manually create a HiCExperiment from GInteractions ------ ##
#######################################################################

gis <- interactions(contacts)[1:1000]
contacts2 <- makeHiCExperimentFromGInteractions(gis)
contacts2


#######################################################################
## -------- Slots present in an HiCExperiment object ------------ ##
#######################################################################

fileName(contacts)
focus(contacts)
resolutions(contacts)
resolution(contacts)
interactions(contacts)
scores(contacts)
topologicalFeatures(contacts)
pairsFile(contacts)


#######################################################################
## --------------------- Slot getters ------------------------- ##
#######################################################################

scores(contacts, 1) |> head()
scores(contacts, 'balanced') |> head()
topologicalFeatures(contacts, 1)


#######################################################################
## --------------------- Slot setters ------------------------- ##
#######################################################################

scores(contacts, 'random') <- runif(length(contacts))
topologicalFeatures(contacts, 'loops') <- InteractionSet::GInteractions(
  GenomicRanges::GRanges('II:15324'),
  GenomicRanges::GRanges('II:24310')
)
pairsFile(contacts) <- HiContactsData('yeast_wt', 'pairs.gz')


#######################################################################
## ----------------- Subsetting functions --------------------- ##
#######################################################################

contacts[1:100]
contacts['II']
contacts[c('II', 'III')]
```

```
contacts['II|III']
contacts['II:10001-30000|III:50001-90000']

#####################################################################
## -------------------- Utils functions ---------------------- ##
#####################################################################
## Adapted from other packages

seqinfo(contacts)
bins(contacts)
anchors(contacts)
regions(contacts)

#####################################################################
## ------------- Coercing HiCExperiment objects ----------------- ##
#####################################################################

as(contacts, 'GInteractions')
as(contacts, 'ContactMatrix')
as(contacts, 'matrix')[seq_len(10), seq_len(10)]
as(contacts, 'data.frame')[seq_len(10), seq_len(10)]
```

HicFile-class   HicFile *S4 class*

Description

The HicFile class describes a BiocFile object, pointing to the location of a .hic file (usually created with juicer) and containing 3 additional slots:

1. resolution: at which resolution the associated .hic file should be parsed;

2. pairsFile: the path (in plain character) to an optional pairs file (stored as a PairsFile object);

3. metadata: a list metadata

HicFile methods.

Arguments

path	String; path to a .hic file
resolution	numeric; resolution to use with mcool file
pairsFile	String; path to a pairs file
metadata	list.
object	A HicFile object.

See Also

[CoolFile()](), [HicproFile()]()

Examples

```
hicPath <- HiContactsData::HiContactsData('yeast_wt', 'hic')
pairsPath <- HiContactsData::HiContactsData('yeast_wt', 'pairs.gz')
hic <- HicFile(
  hicPath,
  resolution = 16000,
  pairsFile = pairsPath,
  metadata = list(type = 'example')
)
hic
resolution(hic)
pairsFile(hic)
metadata(hic)
```

HicproFile-class   HicproFile *S4 class*

Description

The `HicproFile` class describes a `BiocFile` object, pointing to the location of a HiC-Pro-generated
matrix file and containing 4 additional slots:

1. bed: path to the matching `.bed` file generated by HiC-Pro;

2. resolution: at which resolution the associated mcool file should be parsed ;

3. pairsFile: the path (in plain character) to an optional pairs file (stored as a `PairsFile` object);

4. metadata: a list metadata

HicproFile methods.

Arguments

path	String; path to the HiC-Pro output .matrix file (matrix file)
bed	String; path to the HiC-Pro output .bed file (regions file)
pairsFile	String; path to a pairs file
metadata	list.
object	A `HicproFile` object.

Slots

bed Path to the matching `.bed` file generated by HiC-Pro

See Also

[CoolFile()](), [HicFile()]()

Examples

```
hicproMatrixPath <- HiContactsData::HiContactsData('yeast_wt', 'hicpro_matrix')
hicproBedPath <- HiContactsData::HiContactsData('yeast_wt', 'hicpro_bed')
pairsPath <- HiContactsData::HiContactsData('yeast_wt', 'pairs.gz')
hicpro <- HicproFile(
  hicproMatrixPath, bed = hicproBedPath, pairs = pairsPath ,
  metadata = list(type = 'example')
)
hicpro
resolution(hicpro)
pairsFile(hicpro)
metadata(hicpro)
```

---

import-methods   *HiCExperiment import methods*

Description

Import methods to parse Hi-C files (`.(m)cool`, `.hic`, HiC-Pro derived matrices, pairs files) into data structures implemented in the HiCExperiment package.

Usage

```
import(con, format, text, ...)

## S4 method for signature 'ANY'
availableResolutions(x, ...)

## S4 method for signature 'CoolFile'
availableResolutions(x)

## S4 method for signature 'HicFile'
availableResolutions(x)

## S4 method for signature 'HicproFile'
availableResolutions(x)

## S4 method for signature 'ANY'
availableChromosomes(x, ...)

## S4 method for signature 'CoolFile'
availableChromosomes(x)

## S4 method for signature 'HicFile'
availableChromosomes(x)

## S4 method for signature 'HicproFile'
availableChromosomes(x)
```

Arguments

`...`	Extra parameters to pass to format-specific methods. A list of possible arguments is provided in the next section.
`con, x`	Path or connection to a cool, mcool, .hic or HiC-Pro derived files. Can also be a path to a pairs file.
`format`	The format of the output. If missing and 'con' is a filename, the format is derived from the file extension. This argument is unnecessary when files are directly provided as `CoolFile`, `HicFile`, `HicproFile` or `PairsFile`.
`text`	If 'con' is missing, this can be a character vector directly providing the string data to import.

Value

A `HiCExperiment` or `GInteractions` object

import arguments for ContactFile class

`ContactFile` class gathers `CoolFile`, `HicFile` and `HicproFile` classes. When importing a `ContactFile` object in R, two main arguments can be provided besides the `ContactFile` itself:

- resolution: Resolutions available in the disk-stored contact matrix can be listed using `availableResolutions(file)`
- focus: A genomic locus (or pair of loci) provided as a string. It can be any of the following string structures:
  - `"II"` or `"II:20001-30000"`: this will extract a symmetrical square HiCExperiment object, of an entire chromosome or an portion of it.
  - `"II|III"` or `"II:20001-30000|III:40001-90000"`: this will extract a non-symmetrical HiCExperiment object, with an entire or portion of different chromosomes on each axis.

Examples

```
################################################################
## ----------- Importing .(m)cool contact matrices ---------- ##
################################################################

mcoolPath <- HiContactsData::HiContactsData('yeast_wt', 'mcool')
availableResolutions(mcoolPath)
availableChromosomes(mcoolPath)
import(mcoolPath, resolution = 16000, focus = 'XVI', format = 'cool')

################################################################
## ----------- Importing .hic contact matrices ------------- ##
################################################################

hicPath <- HiContactsData::HiContactsData('yeast_wt', 'hic')
availableResolutions(hicPath)
availableChromosomes(hicPath)
import(hicPath, resolution = 16000, focus = 'XVI', format = 'hic')

################################################################
```

```
## ------- Importing HiC-Pro derived contact matrices ------- ##
################################################################

hicproMatrixPath <- HiContactsData::HiContactsData('yeast_wt', 'hicpro_matrix')
hicproBedPath <- HiContactsData::HiContactsData('yeast_wt', 'hicpro_bed')
availableResolutions(hicproMatrixPath, hicproBedPath)
availableChromosomes(hicproMatrixPath, hicproBedPath)
import(hicproMatrixPath, bed = hicproBedPath, format = 'hicpro')
```

PairsFile-class	PairsFile *S4 class*

Description

The `PairsFile` class describes a `BiocFile` object, pointing to the location of pairs file, typically generated by `HiCool::HiCool()`.

PairsFile methods

Arguments

x   Path to a pairs file

See Also

[CoolFile()](), [HicFile()](), [HicproFile()]()

Examples

```
pairsPath <- HiContactsData::HiContactsData('yeast_wt', 'pairs.gz')
pf <- PairsFile(pairsPath)
pf
pairsFile(pf)
```

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