Package: HiCExperiment (via r-universe)

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

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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)

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'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'
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Contents

AggrHiCExperiment 2
as 4
bin-methods 6
ContactsFile-class 6
CoolFile-class 7
data 8
export-methods 9
HiCExperiment 9
HicFile-class 15
HicproFile-class 16
import-methods 17
PairsFile-class 19

Index **20**

`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)
```

Index

[,HiCExperiment,GInteractions,ANY,ANY-method (HiCExperiment), 9
[,HiCExperiment,GRanges,ANY,ANY-method (HiCExperiment), 9
[,HiCExperiment,Pairs,ANY,ANY-method (HiCExperiment), 9
[,HiCExperiment,character,ANY,ANY-method (HiCExperiment), 9
[,HiCExperiment,logical,ANY,ANY-method (HiCExperiment), 9
[,HiCExperiment,numeric,ANY,ANY-method (HiCExperiment), 9
[,HiCExperiment-method (HiCExperiment), 9
$,HiCExperiment-method (HiCExperiment), 9
$<-,HiCExperiment-method (HiCExperiment), 9

AggrHiCExperiment, 2
AggrHiCExperiment(), *13*
AggrHiCExperiment-class (AggrHiCExperiment), 2
anchors,HiCExperiment-method (HiCExperiment), 9
as, 4
availableChromosomes,ANY-method (import-methods), 17
availableChromosomes,CoolFile-method (import-methods), 17
availableChromosomes,HicFile-method (import-methods), 17
availableChromosomes,HicproFile-method (import-methods), 17
availableResolutions,ANY-method (import-methods), 17
availableResolutions,CoolFile-method (import-methods), 17
availableResolutions,HicFile-method (import-methods), 17
availableResolutions,HicproFile-method (import-methods), 17

bin,GInteractions,character-method (bin-methods), 6
bin,GInteractions,numeric-method (bin-methods), 6
bin,PairsFile,numeric-method (bin-methods), 6
bin-methods, 6
bins,HiCExperiment-method (HiCExperiment), 9

centros_yeast (data), 8
cis,HiCExperiment-method (HiCExperiment), 9
cm2matrix (as), 4
coerce,HiCExperiment,ContactMatrix-method (as), 4
coerce,HiCExperiment,data.frame-method (as), 4
coerce,HiCExperiment,GInteractions-method (as), 4
coerce,HiCExperiment,InteractionSet-method (as), 4
coerce,HiCExperiment,matrix-method (as), 4
contacts_yeast (data), 8
contacts_yeast_eco1 (data), 8
ContactsFile (ContactsFile-class), 6
ContactsFile-class, 6
ContactsFile-methods (ContactsFile-class), 6
CoolFile (CoolFile-class), 7
CoolFile(), *7*, *13*, *15*, *16*, *19*
CoolFile-class, 7
CoolFile-methods (CoolFile-class), 7

data, 8
df2gi (as), 4

export (export-methods), 9
export,HiCExperiment,missing,character-method (export-methods), 9
export-methods, 9

fileName,HiCExperiment-method (HiCExperiment), 9
focus,HiCExperiment-method (HiCExperiment), 9
focus<-,HiCExperiment,character-method (HiCExperiment), 9
focus<-,HiCExperiment-method (HiCExperiment), 9

gi2cm (as), 4

HiCExperiment, 9
HiCExperiment(), *4*
HiCExperiment-class (HiCExperiment), 9
HicFile (HicFile-class), 15
HicFile(), *7, 8*, *13*, *16*, *19*
HicFile-class, 15
HicFile-methods (HicFile-class), 15
HicproFile (HicproFile-class), 16
HicproFile(), *7, 8*, *13*, *15*, *19*
HicproFile-class, 16
HicproFile-methods (HicproFile-class), 16

import (import-methods), 17
import,CoolFile,ANY,ANY-method (import-methods), 17
import,CoolFile-method (import-methods), 17
import,HicFile,ANY,ANY-method (import-methods), 17
import,HicFile-method (import-methods), 17
import,HicproFile,ANY,ANY-method (import-methods), 17
import,HicproFile-method (import-methods), 17
import,PairsFile,ANY,ANY-method (import-methods), 17
import,PairsFile-method (import-methods), 17
import-methods, 17
interactions,HiCExperiment-method (HiCExperiment), 9
interactions<-,HiCExperiment,GInteractions-method (HiCExperiment), 9
interactions<-,HiCExperiment-method (HiCExperiment), 9

length,HiCExperiment-method (HiCExperiment), 9

makeHiCExperimentFromGInteractions (HiCExperiment), 9
McoolFile-class (CoolFile-class), 7
metadata<-,ContactsFile,list-method (ContactsFile-class), 6
metadata<-,ContactsFile-method (ContactsFile-class), 6
metadata<-,HiCExperiment,list-method (HiCExperiment), 9
metadata<-,HiCExperiment-method (HiCExperiment), 9

PairsFile (PairsFile-class), 19
PairsFile(), *13*
pairsFile,ContactsFile-method (ContactsFile-class), 6
pairsFile,HiCExperiment-method (HiCExperiment), 9
pairsFile,PairsFile-method (PairsFile-class), 19
PairsFile-class, 19
pairsFile<-,HiCExperiment,character-method (HiCExperiment), 9
pairsFile<-,HiCExperiment-method (HiCExperiment), 9

refocus,HiCExperiment,character-method (HiCExperiment), 9
regions,HiCExperiment-method (HiCExperiment), 9
resolution,ContactsFile-method (ContactsFile-class), 6
resolution,HiCExperiment-method (HiCExperiment), 9
resolutions,HiCExperiment-method (HiCExperiment), 9

scores,HiCExperiment,character-method (HiCExperiment), 9
scores,HiCExperiment,missing-method (HiCExperiment), 9

scores,HiCExperiment,numeric-method
(HiCExperiment), 9
scores,HiCExperiment-method
(HiCExperiment), 9
scores<-,HiCExperiment,character,numeric-method
(HiCExperiment), 9
scores<-,HiCExperiment-method
(HiCExperiment), 9
seqinfo,HiCExperiment-method
(HiCExperiment), 9
show,AggrHiCExperiment-method
(AggrHiCExperiment), 2
show,CoolFile-method (CoolFile-class), 7
show,HiCExperiment-method
(HiCExperiment), 9
show,HicFile-method (HicFile-class), 15
show,HicproFile-method
(HicproFile-class), 16
slices,AggrHiCExperiment,character-method
(AggrHiCExperiment), 2
slices,AggrHiCExperiment,missing-method
(AggrHiCExperiment), 2
slices,AggrHiCExperiment,numeric-method
(AggrHiCExperiment), 2
subsetByOverlaps,HiCExperiment,GInteractions-method
(HiCExperiment), 9
subsetByOverlaps,HiCExperiment,GRanges-method
(HiCExperiment), 9
subsetByOverlaps,HiCExperiment,logical-method
(HiCExperiment), 9
subsetByOverlaps,HiCExperiment,numeric-method
(HiCExperiment), 9
subsetByOverlaps,HiCExperiment,Pairs-method
(HiCExperiment), 9

topologicalFeatures,HiCExperiment,character-method
(HiCExperiment), 9
topologicalFeatures,HiCExperiment,missing-method
(HiCExperiment), 9
topologicalFeatures,HiCExperiment,numeric-method
(HiCExperiment), 9
topologicalFeatures,HiCExperiment-method
(HiCExperiment), 9
topologicalFeatures<-,HiCExperiment,character,GRangesOrGInteractions-method
(HiCExperiment), 9
topologicalFeatures<-,HiCExperiment-method
(HiCExperiment), 9
trans,HiCExperiment-method
(HiCExperiment), 9
zoom,HiCExperiment,numeric-method
(HiCExperiment), 9