

# Package ‘HiCExperiment’

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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)

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

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'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'  
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## Contents

|                               |           |
|-------------------------------|-----------|
| .pairs2gi . . . . .           | 2         |
| AggrHiCExperiment . . . . .   | 3         |
| AllGenerics . . . . .         | 5         |
| as . . . . .                  | 5         |
| bin-methods . . . . .         | 6         |
| checks . . . . .              | 7         |
| ContactsFile-class . . . . .  | 8         |
| CoolFile-class . . . . .      | 9         |
| data . . . . .                | 10        |
| export-methods . . . . .      | 10        |
| HiCExperiment . . . . .       | 11        |
| HiCExperiment utils . . . . . | 16        |
| HicFile-class . . . . .       | 17        |
| HicproFile-class . . . . .    | 18        |
| import-methods . . . . .      | 19        |
| multi2Query . . . . .         | 21        |
| PairsFile-class . . . . .     | 22        |
| parse-cool . . . . .          | 22        |
| parse-hic . . . . .           | 23        |
| parse-hicpro . . . . .        | 24        |
| reexports . . . . .           | 24        |
| <b>Index</b>                  | <b>25</b> |

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.pairs2gi

*Pairs parsing functions*

---

## Description

Pairs parsing functions

**Usage**

```
.pairs2gi(
  file,
  chr1.field = NULL,
  start1.field = NULL,
  chr2.field = NULL,
  start2.field = NULL,
  strand1.field = NULL,
  strand2.field = NULL,
  frag1.field = NULL,
  frag2.field = NULL,
  nThread = 1,
  nrows = Inf
)
```

**Arguments**

`file` pairs file. Default formatting is `<readname>\t<chr1>\t<start1>\t<chr2>\t<start2>`.  
`chr1.field`, `start1.field`, `chr2.field`, `start2.field`, `strand1.field`,  
`strand2.field`, `frag1.field`, `frag2.field`  
 Index of the column in which each field is contained in the pairs file.

`nThread` Number of CPUs to use to import the pairs file in R

`nrows` Number of pairs to import

**Value**

a GInteractions object

---

|                   |                                   |
|-------------------|-----------------------------------|
| AggrHiCExperiment | AggrHiCExperiment <i>S4 class</i> |
|-------------------|-----------------------------------|

---

**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 diagonal-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 ( <code>\&lt;Pairs\&gt;</code> ), borders ( <code>\&lt;GRanges\&gt;</code> ), viewpoints ( <code>\&lt;GRanges\&gt;</code> ), 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]
```

---

**AllGenerics***Generic functions*

---

**Description**

Generics functions created in HiCExperiment package.

**Arguments**

|       |                                |
|-------|--------------------------------|
| x     | Passed to corresponding method |
| name  | Passed to corresponding method |
| value | Passed to corresponding method |
| ...   | Passed to corresponding method |

---

**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)
```

---

checks

*Checks functions*

---

**Description**

Internal functions to validate the nature/structure of (m)cool files or HiCExperiment objects. All these check functions should return a logical.

**Usage**

```
.check_cool_file(path)
.check_cool_format(path, resolution, ...)
.is_mcool(path)
.is_cool(path)
.check_hic_file(path)
.check_hic_format(path, resolution, ...)
.is_hic(path)
.check_hicpro_files(path, bed)
.is_hicpro_matrix(path)
.is_hicpro_regions(bed)
.check_resolution(contacts, resolution)
.check_scores(contacts, use.scores)
.is_square(pair)
```

**Arguments**

|            |  |
|------------|--|
| path       | Path of a (m)cool file                                       |
| resolution | Resolution   |
| ...        | HiCExperiment object, arguments passed on by other functions |
| bed        | Path to regions file generated by HiC-Pro                    |
| contacts   | A HiCExperiment object                                       |
| use.scores | Name of scores to check                                      |
| pair       | Pairs object with length of 1                                |

**Value**

Logical

---

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 <i>S4 class</i> |
|----------------|--------------------------|

---

## 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 | <i>Example datasets provided in HiCExperiment &amp; HiContactsData</i> |
|------|--|

---

**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 | <i>HiCExperiment export methods</i> |
|----------------|-------------------------------------|

---

**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     | Whether 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 ( $\langle$ GInteractions $\rangle$ ), borders ( $\langle$ GRanges $\rangle$ ), viewpoints ( $\langle$ GRanges $\rangle$ ), 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)]

```

---

HiCExperiment utils    *Utils functions*

---

### Description

Utilities to facilitate parsing/handling of coordinates, GInteractions, Pairs, ... These functions are not exported.

### Usage

```

splitCoords(coords)

coords2char(coords, big.mark = ",")

char2coords(char)

sortPairs(pairs)

```



```

asGInteractions(df)

sdiag(A, k = 0)

.df2symmmat(diag, score)

distanceDecay(dump, threshold = NULL)

detrendingModel(file, resolution)

.fixRegions(gis, bins, coords)

```

### Arguments

|            |  |
|------------|--|
| coords     | A set of genomic coordinates (either as a GRanges object or as a character string) |
| big.mark   | Separator for thousands when printing out genomic coordinates as character         |
| char       | char (e.g. "II:30001-50000" or "II:30001-50000II:60001-80000")                     |
| pairs      | Pairs object   |
| df         | a data.frame to turn into a GInteraction object.                                   |
| A          | Numerical matrix   |
| k          | secondary diagonal k   |
| diag       | vector of distances to diagonal  |
| score      | scores to parse into symmetrical matrix  |
| dump       | dumped contacts as GInteractions, e.g. from .dumpCool                              |
| threshold  | maximum distance to compute distance decay for                                     |
| file       | path to a HiC contact matrix file  |
| resolution | Resolution to use with the HiC contact matrix file                                 |
| gis        | GInteractions object   |
| bins       | Larger set of regions (usually bins from HiCExperiment)                            |

### Value

Reformatted coordinates or GInteractions.

---

|               |                         |
|---------------|-------------------------|
| HicFile-class | HicFile <i>S4 class</i> |
|---------------|-------------------------|

---

### 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(f).
- 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')
```

multi2Query

*Querying multiple slices of a contact matrix***Description**

These functions are the workhorse internal functions used to extract counts from multiple genomic coordinates in a Hi-C contact matrix.

**Usage**

```
.multi2DQuery(
  file,
  resolution,
  pairs,
  maxDistance = NULL,
  bed = NULL,
  BPPARAM = BiocParallel::bpparam()
)
```

**Arguments**

|             |  |
|-------------|--|
| file        | path to a Hi-C contact file (can be any format, (m)cool, .hic, or HiC-Pro-derived) |
| resolution  | resolution to use to import matrix over specified targets                          |
| pairs       | slices to read, provided as a Pairs object   |
| maxDistance | Maximum distance to use when compiling distance decay                              |
| bed         | associated bed file for HiC-Pro derived contact matrix.                            |
| BPPARAM     | BiocParallel parameters  |

**Value**

a GInteractions object with count, balanced, detrended and expected scores

---

|                 |                           |
|-----------------|---------------------------|
| PairsFile-class | PairsFile <i>S4</i> 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)
```

---

|            |                              |
|------------|------------------------------|
| parse-cool | <i>Parsing (m)cool files</i> |
|------------|------------------------------|

---

### Description

These functions are the workhorse internal functions used to import a `.(m)cool` file as `GInteractions` (wrapped into a `HiCExperiment` object by `HiCExperiment()` function).

### Usage

```
.getCoolAnchors(file, resolution = NULL, balanced = "cooler")
.getCountsFromPair(file, pair, anchors, resolution = NULL)
.getCounts(file, coords, anchors, resolution = NULL)
.fetchCool(file, path, resolution = NULL, idx = NULL, ...)
.dumpCool(file, resolution = NULL)
.lsCoolFiles(file, verbose = FALSE)
.lsCoolResolutions(file, verbose = FALSE)
.cool2seqinfo(file, resolution = NULL)
.cool2gi(file, coords = NULL, resolution = NULL)
```

**Arguments**

|            |   |
|------------|---|
| file       | path to a Hi-C contact file (in (m)cool format)   |
| resolution | resolution of the contact matrix  |
| balanced   | import balancing scores   |
| pair       | Genomic coordinates to extract contacts for, stored as a Pairs of GRanges (e.g. S4Vectors::Pairs(GRanges("II:200000-300000"), GRanges("II:70000-100000"))). |
| anchors    | anchors from .getCoolAnchors()  |
| coords     | Genomic coordinates to extract contacts for, stored as a GRanges object   |
| path       | Internal path of the cool file to check   |
| idx        | Index to extract from the cool (HDF5) file  |
| ...        | Other arguments passed to .fetchCool  |
| verbose    | Print resolutions in the console  |

**Value**

Silently, a numerical vector of resolutions stored in the cool file

---

parse-hic

*Parsing hic files*

---

**Description**

These functions are the workhorse internal functions used to import a .hic file as GInteractions (wrapped into a HiCExperiment object by HiCExperiment() function).

**Usage**

```
.hic2gi(file, coords = NULL, resolution = NULL)
.lsHicResolutions(file, verbose = FALSE)
.getHicAnchors(file, resolution = NULL)
.hic2seqinfo(file)
.dumpHic(file, resolution = NULL)
```

**Arguments**

|            |  |
|------------|--|
| file       | path to a Hi-C contact file in .hic format   |
| coords     | NULL, character, or GRanges. Can also be a Pairs object of paired GRanges (length of 1). |
| resolution | resolution of the contact matrix to use  |
| verbose    | Print resolutions in the console   |

**Value**

a GInteractions object  
vector

---

|              |  |
|--------------|--|
| parse-hicpro | <i>Parsing hicpro files (matrix &amp; bed)</i> |
|--------------|--|

---

**Description**

These functions are the workhorse internal functions used to import HiC-Pro .matrix and .bed files as GInteractions (wrapped into a HiCExperiment object by HiCExperiment() function).

**Usage**

```
.hicpro2gi(file, bed)
.getHicproAnchors(bed)
.hicpro2seqinfo(bed)
.dumpHicpro(file, bed)
```

**Arguments**

|      |   |
|------|---|
| file | path to a matrix file from HiC-Pro            |
| bed  | path to the regions file generated by HiC-Pro |

**Value**

a GInteractions object

---

|           |   |
|-----------|---|
| reexports | <i>Objects exported from other packages</i> |
|-----------|---|

---

**Description**

These objects are imported from other packages. Follow the links below to see their documentation.

**S4Vectors** [metadata](#)



# Index

## \* internal

- .pairs2gi, 2
- AllGenerics, 5
- checks, 7
- HiCExperiment utils, 16
- multi2Query, 21
- parse-cool, 22
- parse-hic, 23
- parse-hicpro, 24
- reexports, 24
- .check\_cool\_file (checks), 7
- .check\_cool\_format (checks), 7
- .check\_hic\_file (checks), 7
- .check\_hic\_format (checks), 7
- .check\_hicpro\_files (checks), 7
- .check\_resolution (checks), 7
- .check\_scores (checks), 7
- .cool2gi (parse-cool), 22
- .cool2seqinfo (parse-cool), 22
- .df2symmmat (HiCExperiment utils), 16
- .dumpCool (parse-cool), 22
- .dumpHic (parse-hic), 23
- .dumpHicpro (parse-hicpro), 24
- .fetchCool (parse-cool), 22
- .fixRegions (HiCExperiment utils), 16
- .getCoolAnchors (parse-cool), 22
- .getCounts (parse-cool), 22
- .getCountsFromPair (parse-cool), 22
- .getHicAnchors (parse-hic), 23
- .getHicproAnchors (parse-hicpro), 24
- .hic2gi (parse-hic), 23
- .hic2seqinfo (parse-hic), 23
- .hicpro2gi (parse-hicpro), 24
- .hicpro2seqinfo (parse-hicpro), 24
- .is\_cool (checks), 7
- .is\_hic (checks), 7
- .is\_hicpro\_matrix (checks), 7
- .is\_hicpro\_regions (checks), 7
- .is\_mcool (checks), 7
- .is\_square (checks), 7
- .lsCoolFiles (parse-cool), 22
- .lsCoolResolutions (parse-cool), 22
- .lsHicResolutions (parse-hic), 23
- .multi2DQuery (multi2Query), 21
- .pairs2gi, 2
- [,HiCExperiment,GInteractions,ANY,ANY-method (HiCExperiment), 11
- [,HiCExperiment,GRanges,ANY,ANY-method (HiCExperiment), 11
- [,HiCExperiment,Pairs,ANY,ANY-method (HiCExperiment), 11
- [,HiCExperiment,character,ANY,ANY-method (HiCExperiment), 11
- [,HiCExperiment,logical,ANY,ANY-method (HiCExperiment), 11
- [,HiCExperiment,numeric,ANY,ANY-method (HiCExperiment), 11
- [,HiCExperiment-method (HiCExperiment), 11
- \$,HiCExperiment-method (HiCExperiment), 11
- \$<-,HiCExperiment-method (HiCExperiment), 11
- AggrHiCExperiment, 3
- AggrHiCExperiment(), 15
- AggrHiCExperiment-class (AggrHiCExperiment), 3
- AllGenerics, 5
- anchors,HiCExperiment-method (HiCExperiment), 11
- as, 5
- asGInteractions (HiCExperiment utils), 16
- availableChromosomes (AllGenerics), 5
- availableChromosomes,ANY-method (import-methods), 19
- availableChromosomes,CoolFile-method (import-methods), 19
- availableChromosomes,HicFile-method (import-methods), 19
- availableChromosomes,HicproFile-method (import-methods), 19
- availableResolutions (AllGenerics), 5
- availableResolutions,ANY-method (import-methods), 19

- availableResolutions, CoolFile-method (import-methods), 19
- availableResolutions, HicFile-method (import-methods), 19
- availableResolutions, HicproFile-method (import-methods), 19
- bin (AllGenerics), 5
- 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 (AllGenerics), 5
- bins, HiCExperiment-method (HiCExperiment), 11
- centros\_yeast (data), 10
- char2coords (HiCExperiment utils), 16
- checks, 7
- cis (AllGenerics), 5
- cis, HiCExperiment-method (HiCExperiment), 11
- cm2matrix (as), 5
- coerce, HiCExperiment, ContactMatrix-method (as), 5
- coerce, HiCExperiment, data.frame-method (as), 5
- coerce, HiCExperiment, GInteractions-method (as), 5
- coerce, HiCExperiment, InteractionSet-method (as), 5
- coerce, HiCExperiment, matrix-method (as), 5
- contacts\_yeast (data), 10
- contacts\_yeast\_eco1 (data), 10
- ContactsFile (ContactsFile-class), 8
- ContactsFile-class, 8
- ContactsFile-methods (ContactsFile-class), 8
- CoolFile (CoolFile-class), 9
- CoolFile(), 8, 15, 18, 19, 22
- CoolFile-class, 9
- CoolFile-methods (CoolFile-class), 9
- coords2char (HiCExperiment utils), 16
- data, 10
- detrendingModel (HiCExperiment utils), 16
- df2gi (as), 5
- distanceDecay (HiCExperiment utils), 16
- export (export-methods), 10
- export, HiCExperiment, missing, character-method (export-methods), 10
- export-methods, 10
- fileName, HiCExperiment-method (HiCExperiment), 11
- focus (AllGenerics), 5
- focus, HiCExperiment-method (HiCExperiment), 11
- focus<- (AllGenerics), 5
- focus<-, HiCExperiment, character-method (HiCExperiment), 11
- focus<-, HiCExperiment-method (HiCExperiment), 11
- gi2cm (as), 5
- HiCExperiment, 11
- HiCExperiment utils, 16
- HiCExperiment(), 5
- HiCExperiment-class (HiCExperiment), 11
- HicFile (HicFile-class), 17
- HicFile(), 8, 9, 15, 19, 22
- HicFile-class, 17
- HicFile-methods (HicFile-class), 17
- HicproFile (HicproFile-class), 18
- HicproFile(), 8, 9, 15, 18, 22
- HicproFile-class, 18
- HicproFile-methods (HicproFile-class), 18
- import (import-methods), 19
- import, CoolFile, ANY, ANY-method (import-methods), 19
- import, CoolFile-method (import-methods), 19
- import, HicFile, ANY, ANY-method (import-methods), 19
- import, HicFile-method (import-methods), 19
- import, HicproFile, ANY, ANY-method (import-methods), 19
- import, HicproFile-method (import-methods), 19
- import, PairsFile, ANY, ANY-method (import-methods), 19
- import, PairsFile-method (import-methods), 19
- import-methods, 19
- interactions, HiCExperiment-method (HiCExperiment), 11
- interactions<-, HiCExperiment, GInteractions-method (HiCExperiment), 11

- interactions<- ,HiCExperiment-method  
(HiCExperiment), 11
- length,HiCExperiment-method  
(HiCExperiment), 11
- makeHiCExperimentFromGInteractions  
(HiCExperiment), 11
- McoolFile-class (CoolFile-class), 9
- metadata, 24
- metadata (reexports), 24
- metadata<- (AllGenerics), 5
- metadata<- ,ContactsFile, list-method  
(ContactsFile-class), 8
- metadata<- ,ContactsFile-method  
(ContactsFile-class), 8
- metadata<- ,HiCExperiment, list-method  
(HiCExperiment), 11
- metadata<- ,HiCExperiment-method  
(HiCExperiment), 11
- multi2Query, 21
- PairsFile (PairsFile-class), 22
- pairsFile (AllGenerics), 5
- PairsFile(), 15
- pairsFile, ContactsFile-method  
(ContactsFile-class), 8
- pairsFile, HiCExperiment-method  
(HiCExperiment), 11
- pairsFile, PairsFile-method  
(PairsFile-class), 22
- PairsFile-class, 22
- pairsFile<- (AllGenerics), 5
- pairsFile<- ,HiCExperiment, character-method  
(HiCExperiment), 11
- pairsFile<- ,HiCExperiment-method  
(HiCExperiment), 11
- parse-cool, 22
- parse-hic, 23
- parse-hicpro, 24
- reexports, 24
- refocus (AllGenerics), 5
- refocus, HiCExperiment, character-method  
(HiCExperiment), 11
- regions, HiCExperiment-method  
(HiCExperiment), 11
- resolution (AllGenerics), 5
- resolution, ContactsFile-method  
(ContactsFile-class), 8
- resolution, HiCExperiment-method  
(HiCExperiment), 11
- resolutions (AllGenerics), 5
- resolutions, HiCExperiment-method  
(HiCExperiment), 11
- scores (AllGenerics), 5
- scores, HiCExperiment, character-method  
(HiCExperiment), 11
- scores, HiCExperiment, missing-method  
(HiCExperiment), 11
- scores, HiCExperiment, numeric-method  
(HiCExperiment), 11
- scores, HiCExperiment-method  
(HiCExperiment), 11
- scores<- (AllGenerics), 5
- scores<- ,HiCExperiment, character, numeric-method  
(HiCExperiment), 11
- scores<- ,HiCExperiment-method  
(HiCExperiment), 11
- sdiag (HiCExperiment utils), 16
- seqinfo, HiCExperiment-method  
(HiCExperiment), 11
- show, AggrHiCExperiment-method  
(AggrHiCExperiment), 3
- show, CoolFile-method (CoolFile-class), 9
- show, HiCExperiment-method  
(HiCExperiment), 11
- show, HicFile-method (HicFile-class), 17
- show, HicproFile-method  
(HicproFile-class), 18
- slices (AllGenerics), 5
- slices, AggrHiCExperiment, character-method  
(AggrHiCExperiment), 3
- slices, AggrHiCExperiment, missing-method  
(AggrHiCExperiment), 3
- slices, AggrHiCExperiment, numeric-method  
(AggrHiCExperiment), 3
- sortPairs (HiCExperiment utils), 16
- splitCoords (HiCExperiment utils), 16
- subsetByOverlaps, HiCExperiment, GInteractions-method  
(HiCExperiment), 11
- subsetByOverlaps, HiCExperiment, GRanges-method  
(HiCExperiment), 11
- subsetByOverlaps, HiCExperiment, logical-method  
(HiCExperiment), 11
- subsetByOverlaps, HiCExperiment, numeric-method  
(HiCExperiment), 11
- subsetByOverlaps, HiCExperiment, Pairs-method  
(HiCExperiment), 11
- topologicalFeatures (AllGenerics), 5
- topologicalFeatures, HiCExperiment, character-method  
(HiCExperiment), 11
- topologicalFeatures, HiCExperiment, missing-method  
(HiCExperiment), 11

topologicalFeatures,HiCExperiment,numeric-method  
    (HiCExperiment), [11](#)

topologicalFeatures,HiCExperiment-method  
    (HiCExperiment), [11](#)

topologicalFeatures<- (AllGenerics), [5](#)

topologicalFeatures<- ,HiCExperiment,character,GRangesOrGInteractions-method  
    (HiCExperiment), [11](#)

topologicalFeatures<- ,HiCExperiment-method  
    (HiCExperiment), [11](#)

trans (AllGenerics), [5](#)

trans,HiCExperiment-method  
    (HiCExperiment), [11](#)

zoom (AllGenerics), [5](#)

zoom,HiCExperiment,numeric-method  
    (HiCExperiment), [11](#)