

# Package ‘HiContacts’

January 20, 2026

**Title** Analysing cool files in R with HiContacts

**Version** 1.12.0

**Date** 2022-08-16

**Description** HiContacts provides a collection of tools to  
analyse and visualize Hi-C datasets imported in R by HiCExperiment.

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**URL** <https://github.com/js2264/HiContacts>

**BugReports** <https://github.com/js2264/HiContacts/issues>

**Depends** R (>= 4.2), HiCExperiment

**Imports** InteractionSet, SummarizedExperiment, GenomicRanges, IRanges,  
GenomeInfoDb, S4Vectors, methods, BiocGenerics, BiocIO,  
BiocParallel, RSpectra, Matrix, tibble, tidyr, dplyr, readr,  
stringr, ggplot2, ggrastr, scales, stats, utils

**Suggests** HiContactsData, rtracklayer, GenomicFeatures, Biostrings,  
BSgenome.Scerevisiae.UCSC.sacCer3, WGCNA, Rfast, terra,  
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arithmetics

*HiContacts arithmetics functionalities*

---

## Description

Different arithmetic operations can be performed on Hi-C contact matrices:

- normalize a contact matrix using iterative correction;
- detrend a contact matrix, i.e. remove the distance-dependent contact trend;
- autocorrelate a contact matrix: this is typically done to highlight large-scale compartments;
- divide one contact matrix by another;
- merge multiple contact matrices;
- despeckle (i.e. smooth out) a contact matrix out;
- aggregate (average) a contact matrices over a set of genomic loci of interest;
- boost Hi-C signal by enhancing long-range interactions while preserving short-range interactions (this is adapted from Boost-HiC);
- subsample interactions using a proportion or a fixed number of final interactions.
- coarsen a contact matrix to a larger (coarser) resolution

**Usage**

```
## S4 method for signature 'HiCExperiment'
aggregate(
  x,
  targets,
  flankingBins = 51,
  maxDistance = NULL,
  BPPARAM = BiocParallel::bpparam()
)

detrend(x, use.scores = "balanced")

autocorrelate(x, use.scores = "balanced", detrend = TRUE, ignore_ndiags = 3)

divide(x, by, use.scores = "balanced", pseudocount = 0)

## S4 method for signature 'HiCExperiment,HiCExperiment'
merge(x, y, ..., use.scores = "balanced", FUN = mean)

despeckle(x, use.scores = "balanced", focal.size = 1)

boost(x, use.scores = "balanced", alpha = 1, full.replace = FALSE)

coarsen(x, bin.size)

## S4 method for signature 'HiCExperiment'
normalize(
  object,
  use.scores = "count",
  niters = 200,
  min.nnz = 10,
  mad.max = 3
)

subsample(x, prop)
```

**Arguments**

|                            |                                                                                                                                                                                                                                                       |
|----------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>x, y, object</code>  | a <code>HiCExperiment</code> object                                                                                                                                                                                                                   |
| <code>targets</code>       | Set of chromosome coordinates for which interaction counts are extracted from the Hi-C contact file, provided as a <code>GRanges</code> object (for diagonal-centered loci) or as a <code>GInteractions</code> object (for off-diagonal coordinates). |
| <code>flankingBins</code>  | Number of bins on each flank of the bins containing input targets.                                                                                                                                                                                    |
| <code>maxDistance</code>   | Maximum distance to use when compiling distance decay                                                                                                                                                                                                 |
| <code>BPPARAM</code>       | <code>BiocParallel</code> parameters                                                                                                                                                                                                                  |
| <code>use.scores</code>    | Which scores to use to perform operations                                                                                                                                                                                                             |
| <code>detrend</code>       | Detrend matrix before performing autocorrelation                                                                                                                                                                                                      |
| <code>ignore_ndiags</code> | ignore N diagonals when calculating correlations                                                                                                                                                                                                      |
| <code>by</code>            | a <code>HiCExperiment</code> object                                                                                                                                                                                                                   |
| <code>pseudocount</code>   | Add a pseudocount when dividing matrices (Default: 0)                                                                                                                                                                                                 |

|              |                                                                                                                                                                                                                                                                                       |
|--------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ...          | HiCExperiment objects. For aggregate, targets (a set of GRanges or GInteractions).                                                                                                                                                                                                    |
| FUN          | merging function                                                                                                                                                                                                                                                                      |
| focal.size   | Size of the smoothing rectangle                                                                                                                                                                                                                                                       |
| alpha        | Power law scaling factor. As indicated in Boost-HiC documentation, the alpha parameter influences the weighting of contacts: if $\alpha < 1$ long-range interactions are prioritized; if $\alpha \gg 1$ short-range interactions have more weight when computing the distance matrix. |
| full.replace | Whether to replace the entire set of contacts, rather than only filling the missing interactions (count=0) (Default: FALSE)                                                                                                                                                           |
| bin.size     | Bin size to coarsen a HiCExperiment at                                                                                                                                                                                                                                                |
| niters       | Number of iterations for ICE matrix balancing                                                                                                                                                                                                                                         |
| min.nnz      | Filter bins with less than min.nnz non-zero elements when performing ICE matrix balancing                                                                                                                                                                                             |
| mad.max      | Filter out bins whose log coverage is less than mad.max median absolute deviations below the median bin log coverage.                                                                                                                                                                 |
| prop         | Float between 0 and 1, or integer corresponding to the # of                                                                                                                                                                                                                           |

### Value

a HiCExperiment object with extra scores

### Examples

```
#### -----
#### Normalize a contact matrix
#### -----

library(HiContacts)
contacts_yeast <- contacts_yeast()
normalize(contacts_yeast)

#### -----
#### Detrending a contact matrix
#### -----

detrend(contacts_yeast)

#### -----
#### Auto-correlate a contact matrix
#### -----

autocorrelate(contacts_yeast)

#### -----
#### Divide 2 contact matrices
#### -----

contacts_yeast <- refocus(contacts_yeast, 'II')
contacts_yeast_eco1 <- contacts_yeast_eco1() |> refocus('II')
divide(contacts_yeast_eco1, by = contacts_yeast)

#### -----
```

```

#### Merge 2 contact matrices
#### -----

merge(contacts_yeast_eco1, contacts_yeast)

#### -----
#### Despeckle (smoothen) a contact map
#### -----

despeckle(contacts_yeast)

#### -----
#### Aggregate a contact matrix over centromeres, at different scales
#### -----

contacts <- contacts_yeast() |> zoom(resolution = 1000)
centros <- topologicalFeatures(contacts, 'centromeres')
aggregate(contacts, targets = centros, flankingBins = 51)

#### -----
#### Enhance long-range interaction signal
#### -----

contacts <- contacts_yeast() |> zoom(resolution = 1000) |> refocus('II')
boost(contacts, alpha = 1)

#### -----
#### Subsample & "coarsen" contact matrix
#### -----

subcontacts <- subsample(contacts, prop = 100000)
coarsened_subcontacts <- coarsen(subcontacts, bin.size = 4000)

```

---

checks

*Checks functions*


---

## Description

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

## Usage

```

.is_symmetrical(x)

.is_comparable(...)

.are_HiCExperiment(...)

.is_same_seqinfo(...)

.is_same_resolution(...)

.is_same_bins(...)

```

```
.is_same_regions(...)
```

### Arguments

`x`                      A HiCExperiment object  
`...`                    HiCExperiment objects

### Value

Logical

---

|                            |                      |
|----------------------------|----------------------|
| <code>cisTransRatio</code> | <i>cisTransRatio</i> |
|----------------------------|----------------------|

---

### Description

Quickly computes a cis-trans ratio of interactions.

### Usage

```
cisTransRatio(x)
```

### Arguments

`x`                      A HiCExperiment object over the full genome

### Value

a tibble, listing for each chr. the % of cis/trans interactions

### Examples

```
library(HiContacts)
full_contacts_yeast <- contacts_yeast(full = TRUE)
cisTransRatio(full_contacts_yeast)
```

---

|          |                 |
|----------|-----------------|
| Contacts | <i>Contacts</i> |
|----------|-----------------|

---

### Description

This function has been deprecated in favor of the generic `HiCExperiment()` constructor (from `HiCExperiment` package).

**Usage**

```

Contacts(
  file,
  resolution = NULL,
  focus = NULL,
  metadata = list(),
  topologicalFeatures = S4Vectors::SimpleList(loops =
    S4Vectors::Pairs(GenomicRanges::GRanges(), GenomicRanges::GRanges()), borders =
    GenomicRanges::GRanges(), compartments = GenomicRanges::GRanges(), viewpoints =
    GenomicRanges::GRanges()),
  pairsFile = NULL
)

```

**Arguments**

|                                  |                                                                                                                                                                                                            |
|----------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>file</code>                | Path to a (m)cool file                                                                                                                                                                                     |
| <code>resolution</code>          | Resolution to use with mcool file                                                                                                                                                                          |
| <code>focus</code>               | focus Chr. coordinates for which interaction counts are extracted from the .(m)cool file, provided as a character string (e.g. "II:4001-5000"). If not provided, the entire (m)cool file will be imported. |
| <code>metadata</code>            | list of metadata                                                                                                                                                                                           |
| <code>topologicalFeatures</code> | topologicalFeatures provided as a named SimpleList                                                                                                                                                         |
| <code>pairsFile</code>           | Path to an associated .pairs file                                                                                                                                                                          |

**Value**

a new HiCExperiment object.

**Examples**

```

library(HiContacts)
library(HiContactsData)
mcool_path <- HiContactsData::HiContactsData('yeast_wt', 'mcool')
Contacts(mcool_path, resolution = 1000)

```

---

distanceLaw

---

*Compute the law of distance-dependent contact frequency, a.k.a.  $P(s)$* 


---

**Description**

$P(s)$  will be approximated if no pairs are provided, or the exact  $P(s)$  will be computed if a .pairs file is added to the HiCExperiment object using `pairsFile(x) <- "..."`.

**Usage**

```

distanceLaw(x, coords, ...)

## S4 method for signature 'GInteractions,missing'
distanceLaw(x, by_chr = FALSE)

## S4 method for signature 'HiCExperiment,missing'
distanceLaw(
  x,
  by_chr = FALSE,
  filtered_chr = c("XII", "chrXII", "chr12", "12", "Mito", "MT", "chrM")
)

## S4 method for signature 'PairsFile,missing'
distanceLaw(
  x,
  by_chr = FALSE,
  filtered_chr = c("XII", "chrXII", "chr12", "12", "Mito", "MT", "chrM"),
  chunk_size = 1e+05
)

## S4 method for signature 'HiCExperiment,GRanges'
distanceLaw(x, coords, chunk_size = 1e+05)

## S4 method for signature 'PairsFile,GRanges'
distanceLaw(x, coords, chunk_size = 1e+05)

localDistanceLaw(x, coords = coords)

```

**Arguments**

|              |                                                                                                                         |
|--------------|-------------------------------------------------------------------------------------------------------------------------|
| x            | A HiCExperiment object                                                                                                  |
| coords       | GRanges to specify which genomic loci to use when computing P(s)                                                        |
| ...          | Arguments passed to corresponding method                                                                                |
| by_chr       | by_chr                                                                                                                  |
| filtered_chr | filtered_chr                                                                                                            |
| chunk_size   | For pairs files which do not fit in memory, pick a number of pairs to parse by chunks (1e7 should be a good compromise) |

**Value**

a tibble

**Examples**

```

contacts_yeast <- contacts_yeast()
ps <- distanceLaw(contacts_yeast)
ps
local_ps <- localDistanceLaw(
  contacts_yeast,
  GenomicRanges::GRanges(
    c("telomere" = "II:1-20000", "arm" = "II:300001-700000")
  )
)

```



```

    )
  )
  local_ps

```

---

|                 |                                 |
|-----------------|---------------------------------|
| getCompartments | <i>Contact map compartments</i> |
|-----------------|---------------------------------|

---

## Description

Computes eigen vectors for each chromosome using cis contacts and extract chromosome compartments.

## Usage

```

getCompartments(
  x,
  resolution = NULL,
  genome = NULL,
  chromosomes = NULL,
  neigens = 3,
  sort_eigens = FALSE,
  BPPARAM = BiocParallel::bpparam()
)

```

## Arguments

|             |                                                                            |
|-------------|----------------------------------------------------------------------------|
| x           | A HiCExperiment object over a full genome                                  |
| resolution  | Which resolution to use to compute eigen vectors                           |
| genome      | a BSgenome of DNASTringSet object associated with the Hi-C contact matrix. |
| chromosomes | character or integer vector indicating which                               |
| neigens     | Numver of eigen vectors to extract                                         |
| sort_eigens | Can be FALSE or one of c('Spearman', 'Pearson')                            |
| BPPARAM     | BiocParallel parallelization settings                                      |

## Value

A HiCExperiment object with additional eigens metadata containing the normalized eigenvectors and a new "compartments" topologicalFeatures storing A and B compartments as a GRanges object.

## Examples

```

library(HiContacts)
full_contacts_yeast <- contacts_yeast(full = TRUE)
comps <- getCompartments(full_contacts_yeast)
metadata(comps)$eigens

```

---

|                      |                               |
|----------------------|-------------------------------|
| getDiamondInsulation | <i>Contact map insulation</i> |
|----------------------|-------------------------------|

---

### Description

Computes diamond insulation score along the entire genome

### Usage

```
getDiamondInsulation(x, window_size = NULL, BPPARAM = BiocParallel::bpparam())

getBorders(x, weak_threshold = 0.2, strong_threshold = 0.5)
```

### Arguments

|                  |                                                                                         |
|------------------|-----------------------------------------------------------------------------------------|
| x                | A HiCExperiment object over a full genome                                               |
| window_size      | Which window size to use to compute diamond insulation score (default: 10 * resolution) |
| BPPARAM          | BiocParallel parallelization settings                                                   |
| weak_threshold   | Less stringent cutoff to call borders in the diamond insulation score                   |
| strong_threshold | More stringent cutoff to call borders in the diamond insulation score                   |

### Value

a HiCExperiment object with additional insulation metadata, containing the diamond insulation score computed

### Examples

```
library(HiContacts)
hic <- contacts_yeast() |>
  refocus('II:1-300000') |>
  zoom(1000)
diams <- getDiamondInsulation(hic)
getDiamondInsulation(diams)
```

---

|          |                                     |
|----------|-------------------------------------|
| getLoops | <i>Finding loops in contact map</i> |
|----------|-------------------------------------|

---

### Description

Find loops using chromosight.

This function is actually provided by the HiCool package rather than the HiContacts package. HiCool provides a self-managed conda environment, and this limits

### Usage

```
getLoops(...)
```

**Arguments**

... Parameters passed to `HiCool::getLoops()`.

---

HiContacts-plots

*HiContacts plotting functionalities*


---

**Description**

Several plots can be generated in HiContacts:

- Hi-C contact matrices
- Distance-dependant interaction frequency decay (a.k.a. "Distance law" or "P(s)")
- Virtual 4C profiles
- Scalograms
- Saddle plots

---

palettes

*Matrix palettes*


---

**Description**

Matrix palettes

**Usage**

```
bwrColors()
```

```
bbrColors()
```

```
bgrColors()
```

```
afmhotrColors()
```

```
coolerColors()
```

```
rainbowColors()
```

**Value**

A vector of colours carefully picked for Hi-C contact heatmaps

**Examples**

```
bwrColors()
```

```
bbrColors()
```

```
bgrColors()
```

```
afmhotrColors()
```

```
coolerColors()
```

```
rainbowColors()
```

---

|        |                                     |
|--------|-------------------------------------|
| plot4C | <i>Plotting virtual 4C profiles</i> |
|--------|-------------------------------------|

---

**Description**

Plotting virtual 4C profiles

**Usage**

```
plot4C(x, mapping = ggplot2::aes(x = center, y = score, col = seqnames))
```

**Arguments**

|         |                                                                                          |
|---------|------------------------------------------------------------------------------------------|
| x       | GRanges, generally the output of virtual4C()                                             |
| mapping | aes to pass on to ggplot2 (default: ggplot2::aes(x = center, y = score, col = seqnames)) |

**Value**

ggplot

**Examples**

```
contacts_yeast <- contacts_yeast()
v4C <- virtual4C(contacts_yeast, GenomicRanges::GRanges('II:490001-510000'))
plot4C(v4C)
```

---

|            |                                  |
|------------|----------------------------------|
| plotMatrix | <i>Plotting a contact matrix</i> |
|------------|----------------------------------|

---

**Description**

Plotting a contact matrix

**Usage**

```
plotMatrix(x, ...)

montage(x, ...)

## S4 method for signature 'HiCExperiment'
plotMatrix(
  x,
  compare.to = NULL,
  use.scores = "balanced",
  scale = "log10",
  maxDistance = NULL,
  loops = NULL,
  borders = NULL,
  tracks = NULL,
```

```
limits = NULL,
dpi = 500,
rasterize = TRUE,
symmetrical = TRUE,
chrom_lines = TRUE,
show_grid = FALSE,
cmap = NULL,
caption = TRUE
)

## S4 method for signature 'GInteractions'
plotMatrix(
  x,
  use.scores = NULL,
  scale = "log10",
  maxDistance = NULL,
  loops = NULL,
  borders = NULL,
  tracks = NULL,
  limits = NULL,
  dpi = 500,
  rasterize = TRUE,
  symmetrical = TRUE,
  chrom_lines = TRUE,
  show_grid = FALSE,
  cmap = NULL
)

## S4 method for signature 'matrix'
plotMatrix(
  x,
  scale = "log10",
  limits = NULL,
  dpi = 500,
  rasterize = TRUE,
  cmap = NULL
)

## S4 method for signature 'AggrHiCExperiment'
plotMatrix(
  x,
  use.scores = "balanced",
  scale = "log10",
  maxDistance = NULL,
  loops = NULL,
  borders = NULL,
  limits = NULL,
  dpi = 500,
  rasterize = TRUE,
  chrom_lines = TRUE,
  show_grid = FALSE,
  cmap = NULL,
```

```

    caption = TRUE
  )

## S4 method for signature 'AggrHiCExperiment'
montage(
  x,
  use.scores = "balanced",
  scale = "log10",
  limits = NULL,
  dpi = 500,
  rasterize = TRUE,
  cmap = NULL
)

```

### Arguments

|                          |                                                                                                  |
|--------------------------|--------------------------------------------------------------------------------------------------|
| <code>x</code>           | A HiCExperiment object                                                                           |
| <code>...</code>         | Extra arguments passed to the corresponding method.                                              |
| <code>compare.to</code>  | Compare to a second HiC matrix in the lower left corner                                          |
| <code>use.scores</code>  | Which scores to use in the heatmap                                                               |
| <code>scale</code>       | Any of 'log10', 'log2', 'linear', 'exp0.2' (Default: 'log10')                                    |
| <code>maxDistance</code> | maximum distance. If provided, the heatmap is plotted horizontally                               |
| <code>loops</code>       | Loops to plot on top of the heatmap, provided as GInteractions                                   |
| <code>borders</code>     | Borders to plot on top of the heatmap, provided as GRanges                                       |
| <code>tracks</code>      | Named list of bigwig tracks imported as Rle                                                      |
| <code>limits</code>      | color map limits                                                                                 |
| <code>dpi</code>         | DPI to create the plot (Default: 500)                                                            |
| <code>rasterize</code>   | Whether the generated heatmap is rasterized or vectorized (Default: TRUE)                        |
| <code>symmetrical</code> | Whether to enforce a symmetrical heatmap (Default: TRUE)                                         |
| <code>chrom_lines</code> | Whether to display separating lines between chromosomes, should any be necessary (Default: TRUE) |
| <code>show_grid</code>   | Whether to display an underlying grid (Default: FALSE)                                           |
| <code>cmap</code>        | Color scale to use. (Default: bgrColors() if limits are c(-1, 1) and coolerColors() otherwise)   |
| <code>caption</code>     | Whether to display a caption (Default: TRUE)                                                     |

### Value

ggplot object

### Examples

```

contacts_yeast <- contacts_yeast()
plotMatrix(
  contacts_yeast,
  use.scores = 'balanced',
  scale = 'log10',
  limits = c(-4, -1)
)

```

---

|        |                                     |
|--------|-------------------------------------|
| plotPs | <i>Plotting a P(s) distance law</i> |
|--------|-------------------------------------|

---

## Description

Plotting a P(s) distance law

## Usage

```
plotPs(x, mapping, xlim = c(5000, 499000), ylim = c(1e-08, 1e-04))
```

```
plotPsSlope(x, mapping, xlim = c(5000, 499000), ylim = c(-3, 0))
```

## Arguments

|         |                                               |
|---------|-----------------------------------------------|
| x       | the output data.frame of distanceLaw function |
| mapping | aes to pass on to ggplot2                     |
| xlim    | xlim                                          |
| ylim    | ylim                                          |

## Value

ggplot

## Examples

```
## Single P(s)

contacts_yeast <- contacts_yeast()
ps <- distanceLaw(contacts_yeast)
plotPs(ps, ggplot2::aes(x = binned_distance, y = norm_p))

## Comparing several P(s)

contacts_yeast <- contacts_yeast()
contacts_yeast_eco1 <- contacts_yeast_eco1()
ps_wt <- distanceLaw(contacts_yeast)
ps_wt$sample <- 'WT'
ps_eco1 <- distanceLaw(contacts_yeast_eco1)
ps_eco1$sample <- 'eco1'
ps <- rbind(ps_wt, ps_eco1)
plotPs(ps, ggplot2::aes(x = binned_distance, y = norm_p, group = sample, color = sample))
plotPsSlope(ps, ggplot2::aes(x = binned_distance, y = slope, group = sample))
```

---

|            |                              |
|------------|------------------------------|
| plotSaddle | <i>Plotting saddle plots</i> |
|------------|------------------------------|

---

**Description**

Plotting saddle plots

**Usage**

```
plotSaddle(  
  x,  
  nbins = 50,  
  limits = c(-1, 1),  
  plotBins = FALSE,  
  BPPARAM = BiocParallel::bpparam()  
)
```

**Arguments**

|          |                                                             |
|----------|-------------------------------------------------------------|
| x        | a HiCExperiment object with a stored eigens metadata        |
| nbins    | Number of bins to use to discretize the eigenvectors        |
| limits   | limits for color map being used                             |
| plotBins | Whether to plot the distribution of bins on top of the plot |
| BPPARAM  | a BiocParallel registered method                            |

**Value**

ggplot

---

|               |                            |
|---------------|----------------------------|
| plotScalogram | <i>Plotting scalograms</i> |
|---------------|----------------------------|

---

**Description**

Plotting scalograms

**Usage**

```
plotScalogram(x, ylim = c(500, 1e+05))
```

**Arguments**

|      |                                                    |
|------|----------------------------------------------------|
| x    | GRanges, the output of scalogram()                 |
| ylim | Range of distances to use for y-axis in scalograms |

**Value**

ggplot



**Examples**

```

contacts_yeast <- HiCExperiment::contacts_yeast()
pairsFile(contacts_yeast) <- HiContactsData::HiContactsData(
  'yeast_wt', format = 'pairs.gz'
)
scalogram <- scalogram(contacts_yeast['II'])
plotScalogram(scalogram)

```

reexports

*Objects exported from other packages***Description**

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

**HiCExperiment** [contacts\\_yeast](#), [contacts\\_yeast\\_eco1](#)

scalogram

*Compute a scalogram of contacts***Description**

Compute a scalogram of contacts

**Usage**

```
scalogram(x, dist_min = 0, nbins = 250, probs = c(0.25, 0.5, 0.75))
```

**Arguments**

|          |                                                     |
|----------|-----------------------------------------------------|
| x        | A HiCExperiment object                              |
| dist_min | Minimum distance for interactions to be considered. |
| nbins    | Number of bins to divide each chromosome            |
| probs    | Quantiles of interactions                           |

**Value**

a tibble  
a tibble

**Examples**

```

contacts_yeast <- HiCExperiment::contacts_yeast()
pairsFile(contacts_yeast) <- HiContactsData::HiContactsData(
  'yeast_wt', format = 'pairs.gz'
)
scalogram <- scalogram(contacts_yeast['II'])
scalogram

```

---

|        |                                                   |
|--------|---------------------------------------------------|
| tracks | <i>Aligning tracks with HiCExperiment objects</i> |
|--------|---------------------------------------------------|

---

**Description**

Aligning tracks with HiCExperiment objects

**Usage**

```
## S4 method for signature 'HiCExperiment'
coverage(x, use.pairs = FALSE, bin.size = resolution(x))
```

**Arguments**

|           |                                                            |
|-----------|------------------------------------------------------------|
| x         | A HiCExperiment object over a full genome                  |
| use.pairs | logical. Whether to use pairsFile to compute Hi-C coverage |
| bin.size  | if use.pairs == TRUE, to which resolution                  |

**Value**

A HiCExperiment object with 2 added columns in regions(x)

**Examples**

```
mcool_file <- HiContactsData::HiContactsData('yeast_wt', format = 'mcool')
hic <- import(mcool_file, format = 'mcool', resolution = 1000)
coverage(hic)
```

---

|           |                                      |
|-----------|--------------------------------------|
| virtual4C | <i>Computing virtual 4C profiles</i> |
|-----------|--------------------------------------|

---

**Description**

From a (m)cool pre-imported in memory, computes a 4C profile using a user-specified viewpoint.

**Usage**

```
virtual4C(x, viewpoint, use.scores = "balanced")
```

**Arguments**

|            |                                 |
|------------|---------------------------------|
| x          | a HiCExperiment object          |
| viewpoint  | viewpoint, defined as a GRanges |
| use.scores | use.scores                      |

**Value**

A tibble with the contact frequency of the viewpoint, per bin along the imported genomic range.

**Examples**

```
library(HiContacts)
contacts_yeast <- contacts_yeast()
v4C <- virtual4C(contacts_yeast, GenomicRanges::GRanges('II:490001-510000'))
v4C
```

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