

Package ‘HiContacts’

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Title Analysing cool files in R with HiContacts

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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	<i>HiContacts arithmetics functionalities</i>
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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)
<code>...</code>	<code>HiCExperiment</code> objects. For aggregate, targets (a set of <code>GRanges</code> or <code>GInteractions</code>).
<code>FUN</code>	merging function
<code>focal.size</code>	Size of the smoothing rectangle
<code>alpha</code>	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.
<code>full.replace</code>	Whether to replace the entire set of contacts, rather than only filling the missing interactions (<code>count=0</code>) (Default: <code>FALSE</code>)
<code>bin.size</code>	Bin size to coarsen a <code>HiCExperiment</code> at
<code>niters</code>	Number of iterations for ICE matrix balancing
<code>min.nnz</code>	Filter bins with less than <code>min.nnz</code> non-zero elements when performing ICE matrix balancing
<code>mad.max</code>	Filter out bins whose log coverage is less than <code>mad.max</code> median absolute deviations below the median bin log coverage.
<code>prop</code>	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
```

cisTransRatio	<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	<i>Compute the law of distance-dependent contact frequency, a.k.a. $P(s)$</i>
-------------	--

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 or DNASTringSet object associated with the Hi-C contact matrix.
chromosomes	character or integer vector indicating which
neigens	Number 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 *Contact map insulation*

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	<i>HiContacts plotting functionalities</i>
------------------	--

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	<i>Matrix palettes</i>
----------	------------------------

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

Plotting virtual 4C profiles

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*Plotting a $P(s)$ distance law*

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'
)
scalo <- scalogram(contacts_yeast['II'])
plotScalogram(scalo)
```

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

Description

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

HiCExperiment [contacts_yeast](#), [contacts_yeast_eco1](#)

scalogram	<i>Compute a scalogram of contacts</i>
-----------	--

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

```

tracks

*Aligning tracks with HiCExperiment objects***Description**

Aligning tracks with HiCExperiment objects

Usage

```

## S4 method for signature 'HiExperiment'
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

Computing virtual 4C profiles

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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