Package 'HiContacts'

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Title Analysing cool files in R with HiContacts

Version 1.6.0

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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,
patchwork, testthat (>= 3.0.0), BiocStyle, knitr, rmarkdown

biocViews HiC, DNA3DStructure

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VignetteBuilder knitr

LazyData false

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Contents

`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 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

x, y, object	a HiCExperiment object
targets	Set of chromosome coordinates for which interaction counts are extracted from the Hi-C contact file, provided as a GRanges object (for diagnoal-centered loci) or as a GInteractions object (for off-diagonal coordinates).
flankingBins	Number of bins on each flank of the bins containing input targets.
maxDistance	Maximum distance to use when compiling distance decay
BPPARAM	BiocParallel parameters
use.scores	Which scores to use to perform operations
detrend	Detrend matrix before performing autocorrelation

ignore_ndiags	ignore N diagonals when calculating correlations
by	a HiCExperiment object
pseudocount	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 » 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

`cisTransRatio` *cisTransRatio*

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 *Contacts*

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

`file`	Path to a (m)cool file
`resolution`	Resolution to use with mcool file
`focus`	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.
`metadata`	list of metadata
`topologicalFeatures`	topologicalFeatures provided as a named SimpleList
`pairsFile`	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 *Contact map compartments*

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 *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 *Finding loops in contact map*

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 *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 *Plotting a contact matrix*

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

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

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 *Plotting scalograms*

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

---

tracks *Aligning tracks with HiCExperiment objects*

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` *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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