

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

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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()
)

detrond(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

| | |
|----------------------------|----------------------|
| <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

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

| | |
|----------------------------------|---|
| <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 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

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 R1e |
| 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 symmetrical 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

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

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

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

| | |
|-------------------------|---------------------------------|
| <code>x</code> | a HiCExperiment object |
| <code>viewpoint</code> | viewpoint, defined as a GRanges |
| <code>use.scores</code> | 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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