

Package ‘annotatr’

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Title Annotation of Genomic Regions to Genomic Annotations

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Description Given a set of genomic sites/regions (e.g. ChIP-seq peaks, CpGs, differentially methylated CpGs or regions, SNPs, etc.) it is often of interest to investigate the intersecting genomic annotations. Such annotations include those relating to gene models (promoters, 5'UTRs, exons, introns, and 3'UTRs), CpGs (CpG islands, CpG shores, CpG shelves), or regulatory sequences such as enhancers. The annotatr package provides an easy way to summarize and visualize the intersection of genomic sites/regions with genomic annotations.

Depends R (>= 3.3.0)

Imports AnnotationDbi, AnnotationHub, dplyr, GenomicFeatures, GenomicRanges, GenomeInfoDb (>= 1.10.3), ggplot2, IRanges, methods, org.Dm.eg.db, org.Hs.eg.db, org.Mm.eg.db, org.Rn.eg.db, readr, regioneR, reshape2, rtracklayer, S4Vectors, stats, TxDb.Dmelanogaster.UCSC.dm3.ensGene, TxDb.Dmelanogaster.UCSC.dm6.ensGene, TxDb.Hsapiens.UCSC.hg19.knownGene, TxDb.Hsapiens.UCSC.hg38.knownGene, TxDb.Mmusculus.UCSC.mm9.knownGene, TxDb.Mmusculus.UCSC.mm10.knownGene, TxDb.Rnorvegicus.UCSC.rn4.ensGene, TxDb.Rnorvegicus.UCSC.rn5.refGene, TxDb.Rnorvegicus.UCSC.rn6.refGene, utils

Suggests BiocStyle, devtools, knitr, rmarkdown, roxygen2, testthat

VignetteBuilder knitr

BugReports <https://www.github.com/rcavalcante/annotatr/issues>

License GPL-3

LazyData true

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NeedsCompilation no

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annotate_regions	<i>A function to intersect user region data with annotation data</i>
------------------	--

Description

Annotate genomic regions to selected genomic annotations while preserving the data associated with the genomic regions.

Usage

```
annotate_regions(regions, annotations, minoverlap = 1L,
  ignore.strand = TRUE, quiet = FALSE)
```

Arguments

regions The GRanges object returned by read_regions().

annotations	A character vector of annotations to build. Valid annotation codes are listed with supported_annotatons(). The "basicgenes" shortcut builds the following regions: 1-5Kb upstream of TSSs, promoters, 5UTRs, exons, introns, and 3UTRs. The "cpgs" shortcut builds the following regions: CpG islands, shores, shelves, and interCGI regions. NOTE: Shortcuts need to be appended by the genome, e.g. hg19_basicgenes. Custom annotations whose names are of the form [genome]_custom_[name] should also be included. Custom annotations should be read in and converted to GRanges with read_annotatons(). They can be for a supported_genome(), or for an unsupported genome.
minoverlap	A scalar, positive integer, indicating the minimum required overlap of regions with annotations.
ignore.strand	Logical indicating whether strandedness should be respected in findOverlaps(). Default FALSE.
quiet	Print progress messages (FALSE) or not (TRUE).

Value

A GRanges where the granges are from the regions, and the mcols include the mcols from the regions and a column with the annotation GRanges.

Examples

```
### An example using Gm12878 Stat3 ChIP-seq from ENCODE and an annotation shortcut
file = system.file('extdata', 'Gm12878_Stat3_chr2.bed.gz', package = 'annotatr')
r = read_regions(con = file, genome = 'hg19')

# Select and build annotations
annots = 'hg19_cpg_islands'
annotations = build_annotatons(genome = 'hg19', annotations = annots)

a = annotate_regions(
  regions = r,
  annotations = annotations,
  ignore.strand = TRUE)

### An example with built-in and custom annotations
a = system.file('extdata', 'test_annotatons_3.bed', package='annotatr')
read_annotatons(con = a, name = 'TFBS', genome = 'hg19')

r_file = system.file('extdata', 'test_read_multiple_data_nohead.bed', package='annotatr')
extraCols = c(pval = 'numeric', mu1 = 'integer', mu0 = 'integer', diff_exp = 'character')
r = read_regions(con = r_file, genome = 'hg19', extraCols = extraCols, rename_score = 'coverage')

# Select and build annotations
annots = c('hg19_cpg_islands','hg19_custom_TFBS')
annotations = build_annotatons(genome = 'hg19', annotations = annots)

a = annotate_regions(
  regions = r,
  annotations = annotations,
  ignore.strand = TRUE)
```

annotatr

annotatr: Annotation of Genomic Regions to Functional Annotations

Description

Given a set of genomic sites/regions (e.g. ChIP-seq peaks, CpGs, differentially methylated CpGs or regions, SNPs, etc.) it is often of interest to investigate the intersecting functional annotations. Such annotations include those relating to gene models (promoters, 5'UTRs, exons, introns, and 3'UTRs), CpGs (CpG islands, CpG shores, CpG shelves), the non-coding genome, and enhancers. The annotatr package provides an easy way to summarize and visualize the intersection of genomic sites/regions with the above functional annotations.

annotatr_cache

A global-variable to hold custom annotations loaded in an R session

Description

Code thanks to Martin Morgan. This is a global variable that will store custom annotations that a user reads in during a session in which annotatr is loaded.

Usage

```
annotatr_cache
```

Format

An object of class list of length 2.

Value

An environment to contain custom annotations from read_annotatations.

Examples

```
# Example usage
annotatr_cache$set("foo", 1:10)
annotatr_cache$get("foo")

# Read in a BED3 file as a custom annotation
file = system.file('extdata', 'test_annotatations_3.bed', package='annotatr')
# The custom annotation is added to the annotatr_cache environment in this function
read_annotatations(con = file, name = 'test', genome = 'hg19')
# The result of read_annotatations() is not visible in .GlobalEnv, instead
# need to use the get method
print(annotatr_cache$get('hg19_custom_test'))
```

build_annotations	<i>A function to build annotations from TxDb.* and AnnotationHub resources</i>
-------------------	--

Description

Create a GRanges object consisting of all the desired annotations. Supported annotation codes are listed by supported_annotations(). The basis for enhancer annotations are FANTOM5 data, the basis for CpG related annotations are CpG island tracks from AnnotationHub, and the basis for genic annotations are from the TxDb.* and org.db group of packages.

Usage

```
build_annotations(genome, annotations)
```

Arguments

genome	The genome assembly.
annotations	A character vector of annotations to build. Valid annotation codes are listed with supported_annotations(). The "basicgenes" shortcut builds the following regions: 1-5Kb upstream of TSSs, promoters, 5UTRs, exons, introns, and 3UTRs. The "cpgs" shortcut builds the following regions: CpG islands, shores, shelves, and interCGI regions. NOTE: Shortcuts need to be appended by the genome, e.g. hg19_basicgenes. Custom annotations whose names are of the form [genome]_custom_[name] should also be included. Custom annotations should be read in and converted to GRanges with read_annotations(). They can be for a supported_genome(), or for an unsupported genome.

Value

A GRanges object of all the annotations combined. The mcols are id, tx_id, gene_id, symbol, type. The id column is a unique name, the tx_id column is either a UCSC knownGene transcript ID (genic annotations) or a Ensembl transcript ID (lncRNA annotations), the gene_id is the Entrez ID, the symbol is the gene symbol from the org.*.eg.db mapping from the Entrez ID, and the type is of the form [genome]_[type]_[name].

Examples

```
# Example with hg19
annots = c('hg19_cpg_islands', 'hg19_cpg_shores', 'hg19_genes_promoters')
annots_gr = build_annotations(genome = 'hg19', annotations = annots)

# Example with a custom annotation
file = system.file('extdata', 'test_annotations_3.bed', package='annotatr')
read_annotations(con = file, name = 'test', genome = 'hg19')
annots = c('hg19_genes_promoters', 'hg19_custom_test')
annots_gr = build_annotations(genome = 'hg19', annotations = annots)
```

build_cpg_annots *A helper function to build CpG related annotations.*

Description

Using the AnnotationHub package, extract CpG island track for the appropriate genome and construct the shores, shelves, and interCGI annotations as desired.

Usage

```
build_cpg_annots(genome = supported_genomes(),
                 annotations = supported_annotations())
```

Arguments

genome The genome assembly.
annotations A character vector with entries of the form [genome]_cpg_{islands, shores, shelves, inter}.

Value

A list of GRanges objects.

build_enhancer_annots *A helper function to build enhancer annotations for hg19 and mm10 from FANTOM5.*

Description

A helper function to build enhancer annotations for hg19 and mm10 from FANTOM5.

Usage

```
build_enhancer_annots(genome = c("hg19", "mm9"))
```

Arguments

genome The genome assembly.

Value

A GRanges object.

build_gene_annots *A helper function to build genic annotations.*

Description

Using the TxDb.* group of packages, construct genic annotations consisting of any combination of 1-5kb upstream of a TSS, promoters (< 1kb from TSS), 5UTRs, CDS, exons, first exons, introns, intron/exon and exon/intron boundaries, 3UTRs, and intergenic.

Usage

```
build_gene_annots(genome = supported_genomes(),
  annotations = supported_annotations())
```

Arguments

genome The genome assembly.
 annotations A character vector with entries of the form [genome]_genes_{1to5kb,promoters,5UTRs,cds,exon}

Value

A list of GRanges objects with unique id of the form [type]:i, tx_id being the UCSC knownGene transcript name, gene_id being the Entrez Gene ID, symbol being the gene symbol from the Entrez ID to symbol mapping in org.db for that species, and type being the annotation type.

build_lncrna_annots *A helper function to build lncRNA annotations.*

Description

Using the AnnotationHub package, retrieve transcript level lncRNA annotations for either human (GRCh38) or mouse (GRCm38). If the genome is 'hg19', use the permalink from GENCODE and rtracklayer::import() to download and process.

Usage

```
build_lncrna_annots(genome = c("hg19", "hg38", "mm10"))
```

Arguments

genome The genome assembly.

Value

A GRanges object with id giving the transcript_type from the GENCODE file, tx_id being the Ensembl transcript ID, gene_id being the Entrez ID coming from a mapping of gene symbol to Entrez ID, symbol being the gene_name from the GENCODE file, and the type being [genome]_lncrna_gencode.

check_annotations *Function to check for valid annotations*

Description

Gives errors if any annotations are not in supported_annotations() (and they are not in the required custom format), basicgenes are used, or the genome prefixes are not the same for all annotations.

Usage

```
check_annotations(annotations)
```

Arguments

annotations A character vector of annotations possibly using the shortcuts

Value

If all the checks on the annotations pass, returns NULL to allow code to move forward.

expand_annotations *Function to expand annotation shortcuts*

Description

Function to expand annotation shortcuts

Usage

```
expand_annotations(annotations)
```

Arguments

annotations A character vector of annotations, possibly using the shortcut accessors

Value

A vector of data accession-ized names that are ordered from upstream to downstream in the case of knownGenes and islands to interCGI in the case of cpgs.

get_orgdb_name	<i>Function to get correct org.* package name based on genome</i>
----------------	---

Description

Function to get correct org.* package name based on genome

Usage

```
get_orgdb_name(genome = supported_genomes())
```

Arguments

genome A string giving the genome assembly.

Value

A string giving the correct org for org.db packages. e.g. hg19 -> Hs.

get_txdb_name	<i>Function to get correct TxDb.* package name based on genome</i>
---------------	--

Description

Function to get correct TxDb.* package name based on genome

Usage

```
get_txdb_name(genome = supported_genomes())
```

Arguments

genome A string giving the genome assembly.

Value

A string giving the name of the correct TxDb.* package name based on genome.

plot_annotation	<i>Plot the number of regions per annotation</i>
-----------------	--

Description

Given a GRanges of annotated regions, plot the number of regions with the corresponding genomic annotations used in `annotation_order`. If a region is annotated to multiple annotations of the same `annot.type`, the region will only be counted once in the corresponding bar plot. For example, if a region were annotated to multiple exons, it would only count once toward the exon bar in the plot, but if it were annotated to an exon and an intron, it would count towards both.

Usage

```
plot_annotation(annotated_regions, annotated_random, annotation_order = NULL,
               plot_title, x_label, y_label, quiet = FALSE)
```

Arguments

<code>annotated_regions</code>	The GRanges result of <code>annotate_regions()</code> .
<code>annotated_random</code>	The GRanges result of <code>annotate_regions()</code> on the randomized regions created from <code>randomize_regions()</code> .
<code>annotation_order</code>	A character vector which doubles as the subset of annotations desired for the plot as well as the ordering. If <code>NULL</code> , all annotations are displayed.
<code>plot_title</code>	A string used for the title of the plot. If missing, no title is displayed.
<code>x_label</code>	A string used for the x-axis label. If missing, no x-axis label is displayed.
<code>y_label</code>	A string used for the y-axis label. If missing, no y-axis label is displayed.
<code>quiet</code>	Print progress messages (<code>FALSE</code>) or not (<code>TRUE</code>).

Value

A ggplot object which can be viewed by calling it, saved with `ggplot2::ggsave`, or edited.

Examples

```
#####
# An example of ChIP-seq peaks with signalValue used for score

# Select and build annotations
annots = c('hg19_cpg_islands', 'hg19_cpg_shores')
annotations = build_annotations(genome = 'hg19', annotations = annots)

chip_bed = system.file('extdata', 'Gm12878_Stat3_chr2.bed.gz', package = 'annotatr')
chip_regions = read_regions(con = chip_bed, genome = 'hg19')

chip_rnd = randomize_regions(regions = chip_regions)

chip_annots = annotate_regions(
  regions = chip_regions,
```

```

        annotations = annotations,
        ignore.strand = TRUE)

chip_rnd_annots = annotate_regions(
  regions = chip_rnd,
  annotations = annotations,
  ignore.strand = TRUE)

annots_order = c(
  'hg19_cpg_islands',
  'hg19_cpg_shores')

p_annots = plot_annotation(annotated_regions = chip_annots,
  annotation_order = annots_order)
p_annots_rnd = plot_annotation(annotated_regions = chip_annots,
  annotated_random = chip_rnd_annots, annotation_order = annots_order)

```

plot_categorical	<i>Plot a categorical data variable over another</i>
------------------	--

Description

Given a GRanges of annotated regions from `annotate_regions()`, visualize the the distribution of categorical data fill in categorical data x. A bar representing the distribution of all fill in x will be added according to the contents of fill. This is the distribution over all values of x. Additionally, when `annotated_random` is not missing, a "Random Regions" bar shows the distribution of random regions over fill.

Usage

```

plot_categorical(annotated_regions, annotated_random, x, fill = NULL,
  x_order = NULL, fill_order = NULL, position = "stack", plot_title,
  legend_title, x_label, y_label, quiet = FALSE)

```

Arguments

<code>annotated_regions</code>	The GRanges result of <code>annotate_regions()</code> .
<code>annotated_random</code>	The GRanges result of <code>annotate_regions()</code> on the randomized regions created from <code>randomize_regions()</code> . Random regions can only be used with <code>fill == 'annot.type'</code> .
<code>x</code>	One of <code>'annot.type'</code> or a categorical data column, indicating whether annotation classes or data classes will appear on the x-axis.
<code>fill</code>	One of <code>'annot.type'</code> , a categorical data column, or <code>NULL</code> , indicating whether annotation classes or data classes will fill the bars. If <code>NULL</code> then the bars will be the total counts of the x classes.
<code>x_order</code>	A character vector that subsets and orders the x classes. Default <code>NULL</code> , uses existing values.
<code>fill_order</code>	A character vector that subsets and orders the fill classes. Default <code>NULL</code> , uses existing values.

<code>position</code>	A string which has the same possible values as in <code>ggplot2::geom_bar(..., position)</code> , i.e., 'stack', 'fill', 'dodge', etc.
<code>plot_title</code>	A string used for the title of the plot. If missing, no title is displayed.
<code>legend_title</code>	A string used for the legend title to describe fills (if fill is not NULL). Default displays corresponding variable name.
<code>x_label</code>	A string used for the x-axis label. If missing, corresponding variable name used.
<code>y_label</code>	A string used for the y-axis label. If missing, corresponding variable name used.
<code>quiet</code>	Print progress messages (FALSE) or not (TRUE).

Details

For example, if a differentially methylated region has the categorical label `hyper`, and is annotated to a promoter, a 5UTR, two exons, and an intron. Each annotation will appear in the All bar once. Likewise for the hyper bar if the differential methylation status is chosen as `x` with `annot.type` chosen as `fill`.

Value

A ggplot object which can be viewed by calling it, or saved with `ggplot2::ggsave`.

Examples

```
# Select and build annotations
annots = c('hg19_cpgs')
annotations = build_annotations(genome = 'hg19', annotations = annots)

dm_file = system.file('extdata', 'IDH2mut_v_NBM_multi_data_chr9.txt.gz', package = 'annotatr')
extraCols = c(diff_meth = 'numeric', mu1 = 'numeric', mu0 = 'numeric')
dm_regions = read_regions(con = dm_file, extraCols = extraCols, genome = 'hg19',
  rename_score = 'pval', rename_name = 'DM_status', format = 'bed')

dm_annots = annotate_regions(
  regions = dm_regions,
  annotations = annotations,
  ignore.strand = TRUE)

dm_order = c(
  'hyper',
  'hypo')
cpg_order = c(
  'hg19_cpg_islands',
  'hg19_cpg_shores',
  'hg19_cpg_shelves',
  'hg19_cpg_inter')

dm_vn = plot_categorical(
  annotated_regions = dm_annots,
  x = 'DM_status',
  fill = 'annot.type',
  x_order = dm_order,
  fill_order = cpg_order,
  position = 'fill',
  legend_title = 'knownGene Annotations',
  x_label = 'DM status',
```

```

    y_label = 'Proportion')

# Create randomized regions
dm_rnd_regions = randomize_regions(regions = dm_regions)
dm_rnd_annots = annotate_regions(
    regions = dm_rnd_regions,
    annotations = annotations,
    ignore.strand = TRUE)

dm_vn_rnd = plot_categorical(
    annotated_regions = dm_annots,
    annotated_random = dm_rnd_annots,
    x = 'DM_status',
    fill = 'annot.type',
    x_order = dm_order,
    fill_order = cpg_order,
    position = 'fill',
    legend_title = 'knownGene Annotations',
    x_label = 'DM status',
    y_label = 'Proportion')

```

plot_coannotations *Plot pair-wise annotations across regions*

Description

All co-occurring annotations associated with a region are computed and displayed as a heatmap.

Usage

```
plot_coannotations(annotated_regions, annotation_order = NULL, plot_title,
  axes_label, quiet = FALSE)
```

Arguments

annotated_regions	The GRanges result of <code>annotate_regions()</code> .
annotation_order	A character vector which doubles as the subset of annotations desired for plot as well as the ordering. If NULL, all annotations are displayed.
plot_title	A string used for the title of the plot. If missing, no plot title label is displayed.
axes_label	A string used for the axis labels. If missing, corresponding variable name used.
quiet	Print progress messages (FALSE) or not (TRUE).

Details

As with `plot_annotation()`, the number in each cell is the number of unique regions annotated to the pair of annotations.

For example, if a region is annotated to both a CpG shore and to two different exons simultaneously, the region will only be counted once in the CpG shore / exon cell. NOTE, this same region will count once in both the CpG shore and exon cells on the diagonal.

Value

A ggplot object which can be viewed by calling it, saved with `ggplot2::ggsave`, or edited.

Examples

```
# Select and build annotations
annots = c('hg19_cpgs')
annotations = build_annotations(genome = 'hg19', annotations = annots)

dm_file = system.file('extdata', 'IDH2mut_v_NBM_multi_data_chr9.txt.gz', package = 'annotatr')
extraCols = c(diff_meth = 'numeric', mu1 = 'numeric', mu0 = 'numeric')
dm_regions = read_regions(con = dm_file, extraCols = extraCols, genome = 'hg19',
  rename_score = 'pval', rename_name = 'DM_status', format = 'bed')

dm_annots = annotate_regions(
  regions = dm_regions,
  annotations = annotations,
  ignore.strand = TRUE)

all_order = c(
  'hg19_cpg_islands',
  'hg19_cpg_shores',
  'hg19_cpg_shelves',
  'hg19_cpg_inter')

dm_vs_ca = plot_coannotations(
  annotated_regions = dm_annots,
  annotation_order = all_order,
  axes_label = 'Annotations',
  plot_title = 'Co-occurrence of Annotations')
```

plot_numerical

Plot numerical data over regions or regions summarized over annotations

Description

This function produces either histograms over facet, or x-y scatterplots over facet. In the case of histograms over facets, the All distribution (hollow histogram with red outline) is the distribution of x over all the regions in the data. The facet specific distributions (solid gray) are the distribution of x over the regions in each facet. For example, a CpG with associated percent methylation annotated to a CpG island and a promoter will count once in the All distribution, but will count once each in the CpG island and promoter facet distributions.

Usage

```
plot_numerical(annotated_regions, x, y, facet = "annot.type",
  facet_order = NULL, bin_width = 10, plot_title, x_label, y_label,
  quiet = FALSE)
```

Arguments

annotated_regions	A GRanges returned from <code>annotate_regions()</code> . If the data is not summarized, the data is at the region level. If it is summarized, it represents the average or standard deviation of the regions by the character vector used for by in <code>summarize_numerical()</code> .
x	A string indicating the column of the GRanges to use for the x-axis.
y	A string indicating the column of the GRanges to use for the y-axis. If missing, a histogram over x will be plotted. If not missing, a scatterplot is plotted.
facet	A string indicating which categorical variable in the GRanges to make <code>ggplot2</code> facets over. Default is <code>annot.type</code> .
facet_order	A character vector which give the order of the facets, and can be used to subset the column in the GRanges used for the facet. For example, if <code>facet = 'annot.type'</code> , then the annotations maybe subsetted to just CpG annotations. Default is <code>NULL</code> , meaning all annotations in their default order are used.
bin_width	An integer indicating the bin width of the histogram used for score. Default 10. Select something appropriate for the data. NOTE: This is only used if y is <code>NULL</code> .
plot_title	A string used for the title of the plot. If missing, no title is displayed.
x_label	A string used for the x-axis label. If missing, no x-axis label is displayed.
y_label	A string used for the y-axis label. If missing, no y-axis label is displayed.
quiet	Print progress messages (<code>FALSE</code>) or not (<code>TRUE</code>).

Value

A `ggplot` object which can be viewed by calling it, or saved with `ggplot2::ggsave`.

Examples

```
# An example with multi-columned data

# Select and build annotations
annots = c('hg19_cpgs')
annotations = build_annotations(genome = 'hg19', annotations = annots)

dm_file = system.file('extdata', 'IDH2mut_v_NBM_multi_data_chr9.txt.gz', package = 'annotatr')
extraCols = c(diff_meth = 'numeric', mu1 = 'numeric', mu0 = 'numeric')
dm_regions = read_regions(con = dm_file, extraCols = extraCols, genome = 'hg19',
  rename_score = 'pval', rename_name = 'DM_status', format = 'bed')

# Annotate the regions
dm_annots = annotate_regions(
  regions = dm_regions,
  annotations = annotations,
  ignore.strand = TRUE)

# Plot histogram of group 1 methylation rates across the CpG annotations.
# NOTE: Overall distribution (everything in \code{facet_order})
# is plotted in each facet for comparison.
dm_vs_regions_mu1 = plot_numerical(
  annotated_regions = dm_annots,
  x = 'mu1',
  facet = 'annot.type',
```

```

facet_order = c('hg19_cpg_islands','hg19_cpg_shores',
                'hg19_cpg_shelves','hg19_cpg_inter'),
bin_width = 5,
plot_title = 'Group 1 Methylation over CpG Annotations',
x_label = 'Group 1 Methylation')

# Can also use the result of annotate_regions() to plot two numerical
# data columns against each other for each region, and facet by annotations.
dm_vs_regions_annot = plot_numerical(
  annotated_regions = dm_annots,
  x = 'mu0',
  y = 'mu1',
  facet = 'annot.type',
  facet_order = c('hg19_cpg_islands','hg19_cpg_shores',
                  'hg19_cpg_shelves','hg19_cpg_inter'),
  plot_title = 'Region Methylation: Group 0 vs Group 1',
  x_label = 'Group 0',
  y_label = 'Group 1')

# Another example, but using differential methylation status as the facets.
dm_vs_regions_name = plot_numerical(
  annotated_regions = dm_annots,
  x = 'mu0',
  y = 'mu1',
  facet = 'DM_status',
  facet_order = c('hyper','hypo','none'),
  plot_title = 'Region Methylation: Group 0 vs Group 1',
  x_label = 'Group 0',
  y_label = 'Group 1')

```

plot_numerical_coannotations

Plot numerical data occurring in pairs of annotations

Description

Plot numerical data associated with regions occurring in annot1, annot2 and in both. As with `plot_numerical()`, the result is a plot of histograms or x-y scatterplots.

Usage

```
plot_numerical_coannotations(annotated_regions, x, y, annot1, annot2,
  bin_width = 10, plot_title, x_label, y_label, quiet = FALSE)
```

Arguments

annotated_regions	A GRanges returned from <code>annotate_regions()</code> .
x	A string indicating the column of the GRanges to use for the x-axis.
y	A string indicating the column of the GRanges to use for the y-axis. If missing, a histogram over x will be plotted. If not missing, a scatterplot is plotted.
annot1	A string indicating the first annotation type.

annot2	A string indicating the second annotation type.
bin_width	An integer indicating the bin width of the histogram used for score. Default 10. Select something appropriate for the data. NOTE: This is only used if y is NULL.
plot_title	A string used for the title of the plot. If missing, no title is displayed.
x_label	A string used for the x-axis label. If missing, no x-axis label is displayed.
y_label	A string used for the y-axis label. If missing, no y-axis label is displayed.
quiet	Print progress messages (FALSE) or not (TRUE).

Details

For example, a CpG with associated percent methylation annotated to a CpG island and a promoter will count once in the All distribution and once in the CpG island / promoter facet distribution. However, a CpG associated only with a promoter will count once in the All distribution and once in the promoter / promoter distribution.

Value

A ggplot object which can be viewed by calling it, or saved with `ggplot2::ggsave`.

Examples

```
# Select and build annotations
annots = c('hg19_cpg_islands', 'hg19_genes_promoters')
annotations = build_annotations(genome = 'hg19', annotations = annots)

dm_file = system.file('extdata', 'IDH2mut_v_NBM_multi_data_chr9.txt.gz', package = 'annotatr')
extraCols = c(diff_meth = 'numeric', mu1 = 'numeric', mu0 = 'numeric')
dm_regions = read_regions(con = dm_file, extraCols = extraCols, genome = 'hg19',
  rename_score = 'pval', rename_name = 'DM_status', format = 'bed')

dm_annots = annotate_regions(
  regions = dm_regions,
  annotations = annotations,
  ignore.strand = TRUE)

dm_vs_num_co = plot_numerical_coannotations(
  annotated_regions = dm_annots,
  x = 'mu0',
  annot1 = 'hg19_cpg_islands',
  annot2 = 'hg19_genes_promoters',
  bin_width = 5,
  plot_title = 'Group 0 Perc. Meth. in CpG Islands and Promoters',
  x_label = 'Percent Methylation')
```

Description

randomize_regions is a wrapper function for `regioneR::randomizeRegions()` that simplifies the creation of randomized regions for an input set of regions read with `read_regions()`. It relies on the `seqlengths` of regions in order to build the appropriate genome object for `regioneR::randomizeRegions()`.

Usage

```
randomize_regions(regions, allow.overlaps = TRUE, per.chromosome = TRUE,
  quiet = FALSE)
```

Arguments

`regions` A GRanges object from `read_regions`.

`allow.overlaps` A logical stating whether random regions can overlap input regions (TRUE) or not (FALSE). Default TRUE.

`per.chromosome` A logical stating whether the random regions should remain on the same chromosome (TRUE) or not (FALSE). Default TRUE.

`quiet` Print progress messages (FALSE) or not (TRUE).

Details

NOTE: The data associated with the input regions are not passed on to the random regions.

Value

A GRanges object of randomized regions based on regions from `read_regions()`. NOTE: Data associated with the original regions is not attached to the randomized regions.

Examples

```
# Create random region set based on ENCODE ChIP-seq data
file = system.file('extdata', 'Gm12878_Stat3_chr2.bed.gz', package = 'annotatr')
r = read_regions(con = file, genome = 'hg19')

random_r = randomize_regions(regions = r)
```

read_annotations *Read custom annotations*

Description

`read_annotations()` is a wrapper for the `rtracklayer::import()` function that creates a GRanges object matching the structure of annotations built with `build_annotations()`. The structure is defined by GRanges, with the `mcols()` with names `c('id', 'gene_id', 'symbol', 'type')`.

Usage

```
read_annotations(con, name, genome = NA, format, extraCols = character(),
  ...)
```

Arguments

con	A path, URL, connection or BEDFile object. See <code>rtracklayer::import.bed()</code> documentation.
name	A string for the name of the annotations to be used in the name of the object, <code>[genome]_custom_[name]</code>
genome	From <code>rtracklayer::import()</code> : The identifier of a genome, or NA if unknown. Typically, this is a UCSC identifier like 'hg19'. An attempt will be made to derive the <code>seqinfo</code> on the return value using either an installed <code>BSgenome</code> package or UCSC, if network access is available.
format	From <code>rtracklayer::import()</code> : The format of the output. If not missing, should be one of 'bed', 'bed15', 'bedGraph' or 'bedpe'. If missing and 'con' is a filename, the format is derived from the file extension. This argument is unnecessary when 'con' is a derivative of 'RTLFile'.
extraCols	From <code>rtracklayer::import.bed()</code> : A character vector in the same form as 'colClasses' from 'read.table'. It should indicate the name and class of each extra/special column to read from the BED file. As BED does not encode column names, these are assumed to be the last columns in the file. This enables parsing of the various BEDX+Y formats.
...	Parameters to pass onto the format-specific method of <code>rtracklayer::import()</code> .

Value

A GRanges object stored in `annotatr_cache`. To view a custom annotation, do `annotatr_cache$get(name)`. To add a custom annotation to the set of annotations, include '`[name]_custom_[genome]`' in the call to `build_annotations()`. See example below.

Examples

```
# Read in a BED3 file as a custom annotation
file = system.file('extdata', 'test_annotations_3.bed', package='annotatr')
read_annotations(con = file, name = 'test', genome = 'hg19')
annotations = build_annotations(genome = 'hg19', annotations = 'hg19_custom_test')
```

read_regions

Read genomic regions in BEDX+Y format

Description

`read_regions()` reads genomic regions by calling the `rtracklayer::import()` function. This function can automatically deal with BEDX files from BED3 to BED6. For BED6+Y, the `extraCols` argument should be used to correctly interpret the extra columns.

Usage

```
read_regions(con, genome = NA, format, extraCols = character(), rename_name,
  rename_score, ...)
```

Arguments

con	A path, URL, connection or BEDFile object. See <code>rtracklayer::import()</code> documentation.
genome	From <code>rtracklayer::import()</code> : The identifier of a genome, or NA if unknown. Typically, this is a UCSC identifier like 'hg19'. An attempt will be made to derive the <code>seqinfo</code> on the return value using either an installed <code>BSgenome</code> package or UCSC, if network access is available.
format	From <code>rtracklayer::import()</code> : The format of the output. If not missing, should be one of 'bed', 'bed15', 'bedGraph' or 'bedpe'. If missing and 'con' is a filename, the format is derived from the file extension. This argument is unnecessary when 'con' is a derivative of 'RTLFile'.
extraCols	From <code>rtracklayer::import()</code> : A character vector in the same form as 'colClasses' from 'read.table'. It should indicate the name and class of each extra/special column to read from the BED file. As BED does not encode column names, these are assumed to be the last columns in the file. This enables parsing of the various BEDX+Y formats.
rename_name	A string to rename the name column of the BED file. For example, if the name column actually contains a categorical variable.
rename_score	A string to rename the score column of the BED file. For example, if the score column represents a quantity about the data besides the score in the BED specification.
...	Parameters to pass onto the format-specific method of <code>rtracklayer::import()</code> .

Details

NOTE: The name (4th) and score (5th) columns are so named. If these columns have a particular meaning for your data, they should be renamed with the `rename_name` and/or `rename_score` parameters.

Value

A `GRanges` object.

Examples

```
# Example of reading a BED3 file
file = system.file('extdata', 'Gm12878_Stat3_chr2.bed.gz', package = 'annotatr')
gr = read_regions(con = file, genome = 'hg19')

# Example of reading a BED6+3 file where the last 3 columns are non-standard
file = system.file('extdata', 'IDH2mut_v-NBM_multi_data_chr9.txt.gz', package = 'annotatr')
extraCols = c(diff_meth = 'numeric', mu0 = 'numeric', mu1 = 'numeric')
gr = read_regions(con = file, genome = 'hg19', extraCols = extraCols, format = 'bed',
  rename_name = 'DM_status', rename_score = 'pval')
```

subset_order_tbl	<i>Function to subset a tbl_df or grouped_df by a column</i>
------------------	--

Description

Function to subset a `tbl_df` or `grouped_df` by a column

Usage

```
subset_order_tbl(tbl, col, col_order)
```

Arguments

<code>tbl</code>	A <code>tbl_df</code> or <code>grouped_df</code> .
<code>col</code>	A string indicating which column of <code>tbl</code> to subset and order
<code>col_order</code>	A character vector indicating the order of <code>col</code> .

Value

A modified version of `summary` with `col` subsetted by `col_order`.

summarize_annotations	<i>Summarize annotation counts</i>
-----------------------	------------------------------------

Description

Given a `GRanges` of annotated regions, count the number of regions in each annotation type. If `annotated_random` is not `NULL`, then the same is computed for the random regions.

Usage

```
summarize_annotations(annotated_regions, annotated_random, quiet = FALSE)
```

Arguments

<code>annotated_regions</code>	The <code>GRanges</code> result of <code>annotate_regions()</code> .
<code>annotated_random</code>	The <code>GRanges</code> result of <code>annotate_regions()</code> on the randomized regions created from <code>randomize_regions()</code> .
<code>quiet</code>	Print progress messages (<code>FALSE</code>) or not (<code>TRUE</code>).

Details

If a region is annotated to multiple annotations of the same `annot.type`, the region will only be counted once. For example, if a region were annotated to multiple exons, it would only count once toward the exons, but if it were annotated to an exon and an intron, it would count towards both.

Value

A `tbl_df` of the number of regions per annotation type.

Examples

```
### An example of ChIP-seq peaks with signalValue

# Select and build annotations
annots = c('hg19_cpg_islands', 'hg19_cpg_shores')
annotations = build_annotations(genome = 'hg19', annotations = annots)

file = system.file('extdata', 'Gm12878_Stat3_chr2.bed.gz', package = 'annotatr')
r = read_regions(con = file, genome = 'hg19')

a = annotate_regions(
  regions = r,
  annotations = annotations,
  ignore.strand = TRUE,
  quiet = FALSE)

rnd = randomize_regions(regions = r)

rnd_annots = annotate_regions(
  regions = rnd,
  annotations = annotations,
  ignore.strand = TRUE,
  quiet = FALSE)

# Summarize the annotated regions without randomized regions
s = summarize_annotations(annotated_regions = a)

# Summarize the annotated regions with randomized regions
s_rnd = summarize_annotations(
  annotated_regions = a,
  annotated_random = rnd_annots)
```

`summarize_categorical` *Summarize categorical data over groupings of annotated regions*

Description

Given a `GRanges` of annotated regions, count the number of regions when the annotations are grouped by categorical columns.

Usage

```
summarize_categorical(annotated_regions, by = c("annot.type", "annot.id"),
  quiet = FALSE)
```

Arguments

- `annotated_regions` The GRanges result of `annotate_regions()`.
- `by` A character vector to group the data in `as.data.frame(annotated_regions)` by and tally over. Default is `c('annot.type', 'annot.id')`.
- `quiet` Print progress messages (FALSE) or not (TRUE).

Details

If a region is annotated to multiple annotations of the same `annot.type`, the region will only be counted once. For example, if a region were annotated to multiple exons, it would only count once toward the exons, but if it were annotated to an exon and an intron, it would count towards both.

Value

A grouped `dplyr::tbl_df` of the counts of groupings according to the `by` vector.

Examples

```
# Select and build annotations
annots = c('hg19_cpg_islands', 'hg19_genes_promoters')
annotations = build_annotations(genome = 'hg19', annotations = annots)

r_file = system.file('extdata', 'test_read_multiple_data_nohead.bed', package='annotatr')
extraCols = c(pval = 'numeric', mu1 = 'integer', mu0 = 'integer', diff_exp = 'character')
r = read_regions(con = r_file, genome = 'hg19', extraCols = extraCols, rename_score = 'coverage')

a = annotate_regions(
  regions = r,
  annotations = annotations,
  ignore.strand = TRUE)

sc = summarize_categorical(
  annotated_regions = a,
  by = c('annot.type', 'name'),
  quiet = FALSE)
```

`summarize_numerical` *Summarize numerical data over groupings of annotated regions*

Description

Given a GRanges of annotated regions, summarize numerical data columns based on a grouping.

Usage

```
summarize_numerical(annotated_regions, by = c("annot.type", "annot.id"), over,
  quiet = FALSE)
```

Arguments

annotated_regions	The GRanges result of <code>annotate_regions()</code> .
by	A character vector of the columns of <code>as.data.frame(annotated_regions)</code> to group over. Default is <code>c(annot.type, annot.id)</code> .
over	A character vector of the numerical columns in <code>as.data.frame(annotated_regions)</code> to count, take the mean, and take the sd over after grouping according to the by column. NOTE: If more than one value is used, the naming scheme for the resulting <code>dplyr::tbl</code> summary columns are <code>COLNAME_n</code> , <code>COLNAME_mean</code> , <code>COLNAME_sd</code> . If over has length one, then the column names are <code>n</code> , <code>mean</code> , <code>sd</code> .
quiet	Print progress messages (FALSE) or not (TRUE).

Details

NOTE: We do not take the distinct values of `seqnames`, `start`, `end`, `annot.type` as in the other `summarize_*`() functions because in the case of a region that intersected two distinct exons, using `distinct_()` would destroy the information of the mean of the numerical column over one of the exons, which is not desirable.

Value

A grouped `dplyr::tbl_df`, and the count, mean, and sd of the cols by the groupings.

Examples

```
### Test on a very simple bed file to demonstrate different options

# Select and build annotations
annots = c('hg19_cpg_islands', 'hg19_genes_promoters')
annotations = build_annotations(genome = 'hg19', annotations = annots)

r_file = system.file('extdata', 'test_read_multiple_data_nohead.bed', package='annotatr')
extraCols = c(pval = 'numeric', mu1 = 'integer', mu0 = 'integer', diff_exp = 'character')
r = read_regions(con = r_file, genome = 'hg19', extraCols = extraCols, rename_score = 'coverage')

a = annotate_regions(
  regions = r,
  annotations = annotations,
  ignore.strand = TRUE)

# Testing over normal by
sn1 = summarize_numerical(
  annotated_regions = a,
  by = c('annot.type', 'annot.id'),
  over = c('coverage', 'mu1', 'mu0'),
  quiet = FALSE)

# Testing over a different by
sn2 = summarize_numerical(
  annotated_regions = a,
  by = c('diff_exp'),
  over = c('coverage', 'mu1', 'mu0'))
```

supported_annotatations *Function listing which annotations are available.*

Description

This includes the shortcuts. The `expand_annotatations()` function helps handle the shortcuts.

Usage

```
supported_annotatations()
```

Value

A character vector of available annotations.

Examples

```
supported_annotatations()
```

supported_genomes *Function returning supported TxDb.* genomes*

Description

Function returning supported TxDb.* genomes

Usage

```
supported_genomes()
```

Value

A character vector of genomes for supported TxDb.* packages

Examples

```
supported_genomes()
```

tidy_annotations	<i>Function to tidy up annotation accessors for visualization</i>
------------------	---

Description

Function to tidy up annotation accessors for visualization

Usage

```
tidy_annotations(annotations)
```

Arguments

annotations	A character vector of annotations, in the order they are to appear in the visualization.
-------------	--

Value

A list of mappings from original annotation names to names ready for visualization.

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