Package 'EpiCompare'

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Type Package

Title Comparison, Benchmarking & QC of Epigenomic Datasets

Version 1.11.3

Description EpiCompare is used to compare and analyse epigenetic datasets for quality control and benchmarking purposes.
The package outputs an HTML report consisting of three sections:
(1. General metrics) Metrics on peaks (percentage of blacklisted and non-standard peaks, and peak widths) and fragments (duplication rate) of samples,
(2. Peak overlap) Percentage and statistical significance of overlapping and non-overlapping peaks. Also includes upset plot and
(3. Functional annotation) functional annotation (ChromHMM, ChIPseeker and enrichment analysis) of peaks.
Also includes peak enrichment around TSS.

License GPL-3

URL https://github.com/neurogenomics/EpiCompare

BugReports https://github.com/neurogenomics/EpiCompare/issues

Depends R (>= 4.2.0)

Imports AnnotationHub, ChIPseeker, data.table, genomation, GenomicRanges, IRanges (>= 2.41.3), GenomeInfoDb, ggplot2 (>= 3.5.0), htmltools, methods, plotly, reshape2, rmarkdown, rtracklayer, stats, stringr, utils, BiocGenerics, downloadthis, parallel

Suggests rworkflows, BiocFileCache, BiocParallel, BiocStyle, clusterProfiler, GenomicAlignments, grDevices, knitr, org.Hs.eg.db, testthat (>= 3.0.0), tidyr, TxDb.Hsapiens.UCSC.hg19.knownGene, TxDb.Hsapiens.UCSC.hg38.knownGene, TxDb.Mmusculus.UCSC.mm9.knownGene, TxDb.Mmusculus.UCSC.mm10.knownGene, BSgenome.Hsapiens.UCSC.hg19, BSgenome.Hsapiens.UCSC.hg38, BSgenome.Mmusculus.UCSC.mm9, BSgenome.Mmusculus.UCSC.mm10, ComplexUpset, plyranges, scales, Matrix, consensusSeekeR, heatmaply, viridis

VignetteBuilder knitr

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Contents

as_interactive *As interactive*

Description

Convert a ggplot object to plotly, and enable it to be plotted within an Rmarkdown HTML file.

Usage

```
as_interactive(
  plt,
  to_widget = isTRUE(getOption("knitr.in.progress")),
  add_boxmode = FALSE
)
```

Arguments

plt	ggplot object.
to_widget	Convert to a widget so it works within Rmarkdown HTML files. By default, this will be only be set to TRUE when being run within the context of **knitr** rendering.
add_boxmode	Add extra layout to enable dodged boxplots.

Value

A plotly object or a tagList wrapping the plotly object.

Source

GitHub Issue to check whether knitting

bpplapply *Wrapper for bplapply*

Description

Wrapper function for bplapply that automatically handles issues with **BiocParallel** related to different OS platforms.

Usage

```
bpplapply(
  X,
  FUN,
  apply_fun = parallel::mclapply,
  workers = check_workers(),
  progressbar = workers > 1,
  verbose = workers == 1,
  use_snowparam = TRUE,
  register_now = FALSE,
  ...
)
```

Arguments

X	Any object for which methods length, [, and [[are implemented.
FUN	The function to be applied to each element of X.
apply_fun	Iterator function to use.
workers	Number of threads to parallelize across.
progressbar	logical(1) Enable progress bar (based on plyr:::progress_text).
verbose	Print messages.
use_snowparam	Whether to use SnowParam (default: TRUE) or MulticoreParam (FALSE) when parallelising across multiple workers.
register_now	Register the cores now with register (TRUE), or simply return the BPPARAM object (default: FALSE).
...	Arguments passed on to BiocParallel::bplapply
	BPPARAM An optional BiocParallelParam instance determining the parallel back-end to be used during evaluation, or a list of BiocParallelParam instances, to be applied in sequence for nested calls to **BiocParallel** functions.
	BPREDO A list of output from bplapply with one or more failed elements. When a list is given in BPREDO, bpok is used to identify errors, tasks are rerun and inserted into the original results.
	BPOPTIONS Additional options to control the behavior of the parallel evaluation, see bpoptions.

Value

(Named) list.

Examples

```
X <- stats::setNames(seq_len(length(letters)), letters)
out <- bpplapply(X, print)
```

checkCache *Check cache*

Description

Quick function to check if object is already saved.

Usage

```
checkCache(cache = BiocFileCache::BiocFileCache(ask = FALSE), url)
```

Arguments

cache	BiocFileCache.
url	Path to cached file.

Value

path

check_cell_lines *Check cell lines*

Description

Check whether a list of cell lines matches any of those that are made available through EpiCompare.

Usage

```
check_cell_lines(cell_lines = NULL, verbose = TRUE)
```

Arguments

cell_lines	A character vector of cell line names. If NULL (default), will return names of all cell lines.
verbose	Print messages.

Value

Character vector, or NULL.

check_genome_build *Check genome build*

Description

Check that the genome build is valid and require specific reference datasets to be installed.

Usage

```
check_genome_build(genome_build, type = "txdb")
```

Arguments

genome_build	Genome build name.
type	whether to fetch the txdb or bsgen reference data

Value

txdb or bsgen

check_grlist_cols *Check GRanges list columns*

Description

Check that at least one of the required columns is in a list of GRanges objects. Elements that do not meet this criterion will be dropped from the list.

Usage

```
check_grlist_cols(grlist, target_cols)
```

Arguments

grlist	Named list of GRanges objects.
target_cols	A character vector of column names to search for.

Value

Named list of GRanges objects.

check_list_names *Check peaklist is named*

Description

This function checks whether the peaklist is named. If not, default file names are assigned.

Usage

```
check_list_names(peaklist, default_prefix = "sample")
```

Arguments

peaklist	A list of peak files as GRanges object.
default_prefix	Default prefix to use when creating names for peaklist.

Value

named peaklist

check_workers *Check workers*

Description

Assign parallel worker cores.

Usage

```
check_workers(workers = NULL)
```

Arguments

workers	Number of cores to parallelise across (in applicable functions). If NULL, will set to the total number of available cores minus 1.

Value

Integer

Examples

```
workers <- check_workers()
```

clean_granges *Clean GRanges*

Description

Remove columns from the metadata (`GenomicRanges::mcols`) that conflicts with GRanges conventions.

Usage

```
clean_granges(
  gr,
 nono_cols = c("seqnames", "ranges", "strand", "seqlevels", "seqlengths", "isCircular",
    "start", "end", "width", "element")
)
```

Arguments

`gr`	A GRanges object.
`nono_cols`	Problematic columns to search for and remove (if present).

Value

Cleaned GRanges object.

CnR_H3K27ac *Example CUT&Run peak file*

Description

Human H3K27ac peak file generated with CUT&Run using K562 cell-line from Meers et al., (2019). Human genome build hg19 was used. Raw peak file (.BED) was obtained from GEO (https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR8581604). Peak calling was performed by Leyla Abbasova using MACS2. The peak file was then processed into GRanges object. Peaks located on chromosome 1 were subsetted to reduce the dataset size.

Usage

```
data("CnR_H3K27ac")
```

Format

An object of class `GRanges` of length 2707.

Source

The code to prepare the .Rda file from the raw peak file is:

```
# sequences were directly downloaded from https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR8581604
# and peaks (BED file) were generated by Leyla Abbasova (Neurogenomics Lab, Imperial College
London)
CnR_H3K27ac <- ChIPseeker::readPeakFile("path", as = "GRanges")
CnR_H3K27ac <- CnR_H3K27ac[seqnames(CnR_H3K27ac)== "chr1"]
my_label <-c("name","score","strand","signalValue","pValue","qValue","peak")
colnames(GenomicRanges::mcols(CnR_H3K27ac)) <- my_label
usethis::use_data(CnR_H3K27ac, overwrite = TRUE)
```

CnR_H3K27ac_picard *Example Picard duplication metrics file 2*

Description

Duplication metrics output on CUT&Run H3K27ac file (sample accession: SRR8581604). Raw sequences were aligned to hg19 genome and after, Picard was performed by Leyla Abbasova. The duplication summary output generated by Picard was processed to reduce the size of data.

Usage

```
data("CnR_H3K27ac_picard")
```

Format

An object of class `data.frame` with 1 rows and 10 columns.

Source

The code to prepare the .Rda file is:

```
picard <- read.table("path/to/picard/duplication/output",header = TRUE, fill = TRUE)
CnR_H3K27ac_picard <- picard[1,]
usethis::use_data(CnR_H3K27ac_picard, overwrite = TRUE)
```

CnT_H3K27ac *Example CUT&Tag peak file*

Description

Human H3K27ac peak file generated with CUT&Tag using K562 cell-line from Kaya-Okur et al., (2019). Human genome build hg19 was used. Raw peak file (.BED) was obtained from GEO (https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR8383507). Peak calling was performed by Leyla Abbasova using MACS2. The peak file was then imported as an GRanges object. Peaks located on chromosome 1 were subsetted to reduce the dataset size.

Usage

```
data("CnT_H3K27ac")
```

Format

An object of class GRanges of length 1670.

Source

The code to prepare the .Rda file from the raw peak file is:

```
# sequences were directly downloaded from https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR8383507
# and peaks (BED file) were generated by Leyla Abbasova (Neurogenomics Lab, Imperial College
London)
CnT_H3K27ac <- ChIPseeker::readPeakFile("path", as = "GRanges")
CnT_H3K27ac <- CnT_H3K27ac[seqnames(CnT_H3K27ac)== "chr1"]
my_label <-c("name","score","strand","signalValue","pValue","qValue","peak")
colnames(GenomicRanges::mcols(CnT_H3K27ac)) <- my_label
usethis::use_data(CnT_H3K27ac)
```

CnT_H3K27ac_picard *Example Picard duplication metrics file 1*

Description

Duplication metrics output of CUT&Tag H3K27ac file (sample accession: SRR8581604). Raw sequences were aligned to hg19 genome and Picard was performed by Leyla Abbasova. The duplication summary output generated by Picard was processed to reduce the size of data.

Usage

```
data("CnT_H3K27ac_picard")
```

Format

An object of class `data.frame` with 1 rows and 10 columns.

Source

The code to prepare the .Rda file is:

```
picard <- read.table("path/to/picard/duplication/output",header = TRUE, fill = TRUE)]
CnT_H3K27ac_picard <- picard[1,]
usethis::use_data(CnT_H3K27ac_picard, overwrite = TRUE)
```

`compute_consensus_peaks` *Compute consensus peaks*

Description

Compute consensus peaks from a list of GRanges.

Usage

```
compute_consensus_peaks(
  grlist,
  groups = NULL,
  genome_build,
  lower = 2,
  upper = Inf,
  min.gapwidth = 1L,
  method = c("granges", "consensusseeker"),
  ...
)
```

Arguments

`grlist`	Named list of GRanges objects.
`groups`	A character vector of the same length as `grlist` defining how to group GRanges objects when computing consensus peaks.
`genome_build`	Genome build name.
`lower, upper`	The lower and upper bounds for the slice.
`min.gapwidth`	Ranges separated by a gap of at least `min.gapwidth` positions are not merged.
`method`	Method to call peaks with: • "granges" : Simple overlap procedure using GRanges functions. Faster but less accurate. • "consensusseeker" : Uses findConsensusPeakRegions to compute consensus peaks. Slower but more accurate.

... Arguments passed on to consensusSeekeR::findConsensusPeakRegions

narrowPeaks a GRanges containing called peak regions of signal enrichment based on pooled, normalized data for all analyzed experiments. All GRanges entries must have a metadata field called "name" which identifies the region to the called peak. All GRanges entries must also have a row name which identifies the experiment of origin. Each peaks entry must have an associated narrowPeaks entry. A GRanges entry is associated to a narrowPeaks entry by having a identical metadata "name" field and a identical row name.

peaks a GRanges containing called peaks of signal enrichment based on pooled, normalized data for all analyzed experiments. All GRanges entries must have a metadata field called "name" which identifies the called peak. All GRanges entries must have a row name which identifies the experiment of origin. Each peaks entry must have an associated narrowPeaks entry. A GRanges entry is associated to a narrowPeaks entry by having a identical metadata "name" field and a identical row name.

chrInfo a Seqinfo containing the name and the length of the chromosomes to analyze. Only the chomosomes contained in this Seqinfo will be analyzed.

extendingSize a numeric value indicating the size of padding on both sides of the position of the peaks median to create the consensus region. The minimum size of the consensus region is equal to twice the value of the extendingSize parameter. The size of the extendingSize must be a positive integer. Default = 250.

expandToFitPeakRegion a logical indicating if the region size, which is set by the extendingSize parameter is extended to include the entire narrow peak regions of all peaks included in the unextended consensus region. The narrow peak regions of the peaks added because of the extension are not considered for the extension. Default: FALSE.

shrinkToFitPeakRegion a logical indicating if the region size, which is set by the extendingSize parameter is shrinked to fit the narrow peak regions of the peaks when all those regions are smaller than the consensus region. Default: FALSE.

minNbrExp a positive numeric or a positive integer indicating the minimum number of experiments in which at least one peak must be present for a potential consensus region. The numeric must be a positive integer inferior or equal to the number of experiments present in the narrowPeaks and peaks parameters. Default = 1.

nbrThreads a numeric or a integer indicating the number of threads to use in parallel. The nbrThreads must be a positive integer. Default = 1.

Details

NOTE: If you get the error "Error in serialize(data, node$con) : error writing to connection", try running closeAllConnections and rerun compute_consensus_peaks. This error can sometimes occur when compute_consensus_peaks has been disrupted partway through.

Value

Named list of consensus peak GRanges.

Source

GenomicRanges tutorial

consensusSeekeR

Examples

```
data("encode_H3K27ac") # example dataset as GRanges object
data("CnT_H3K27ac") # example dataset as GRanges object
data("CnR_H3K27ac") # example dataset as GRanges object
grlist <- list(CnR=CnR_H3K27ac, CnT=CnT_H3K27ac, ENCODE=encode_H3K27ac)

consensus_peaks <- compute_consensus_peaks(grlist = grlist,
                                           groups = c("Imperial",
                                                      "Imperial",
                                                      "ENCODE"))
```

`compute_corr` *Compute correlation matrix*

Description

Compute correlation matrix on all peak files.

Usage

```
compute_corr(
  peakfiles,
  reference = NULL,
  genome_build,
  keep_chr = NULL,
  drop_empty_chr = FALSE,
  bin_size = 5000,
  method = "spearman",
  intensity_cols = c("total_signal", "qValue", "Peak Score", "score"),
  return_bins = FALSE,
  fill_diag = NA,
  workers = check_workers(),
  save_path = tempfile(fileext = ".corr.csv.gz")
)
```

Arguments

`peakfiles`	A list of peak files as GRanges object and/or as paths to BED files. If paths are provided, EpiCompare imports the file as GRanges object. EpiCompare also accepts a list containing a mix of GRanges objects and paths.Files must be listed and named using `list()`. E.g. `list("name1"=file1, "name2"=file2)`. If no names are specified, default file names will be assigned.

`reference` A named list containing reference peak file(s) as GRanges object. Please ensure that the reference file is listed and named i.e. `list("reference_name" = reference_peak)`. If more than one reference is specified, individual reports for each reference will be generated. However, please note that specifying more than one reference can take awhile. If a reference is specified, it enables two analyses: (1) plot showing statistical significance of overlapping/non-overlapping peaks; and (2) ChromHMM of overlapping/non-overlapping peaks.

`genome_build` The build of **all** peak and reference files to calculate the correlation matrix on. If all peak and reference files are not of the same build use liftover_grlist to convert them all before running. Genome build should be one of hg19, hg38, mm9, mm10.

`keep_chr` Which chromosomes to keep.

`drop_empty_chr` Drop chromosomes that are not present in any of the `peakfiles` (default: `FALSE`).

`bin_size` Default of 100. Base-pair size of the bins created to measure correlation. Use smaller value for higher resolution but longer run time and larger memory usage.

`method` Default spearman (i.e. non-parametric). A character string indicating which correlation coefficient (or covariance) is to be computed. One of "pearson", "kendall", or "spearman": can be abbreviated.

`intensity_cols` Depending on which columns are present, this value will be used to get quantiles and ultimately calculate the correlations:

- "total_signal" : Used by the peak calling software SEACR. *NOTE*: Another SEACR column (e.g. "max_signal") can be used together or instead of "total_signal".
- "qValue"Used by the peak calling software MACS2/3. Should contain the negative log of the p-values after multiple testing correction.
- "Peak Score" : Used by the peak calling software HOMER.

`return_bins` If `TRUE`, returns a named list with both the rebinned (standardised) peaks ("bin") and the correlation matrix ("cor"). If `FALSE` (default), returns only the correlation matrix (unlisted).

`fill_diag` Fill the diagonal of the overlap matrix.

`workers` Number of threads to parallelize across.

`save_path` Path to save a table of correlation results to.

Value

correlation matrix

Examples

```
data("CnR_H3K27ac")
data("CnT_H3K27ac")
data("encode_H3K27ac")
peakfiles <- list(CnR_H3K27ac=CnR_H3K27ac, CnT_H3K27ac=CnT_H3K27ac)
reference <- list("encode_H3K27ac"=encode_H3K27ac)

#increasing bin_size for speed but lower values will give more granular corr
```

```
corr_mat <- compute_corr(peakfiles = peakfiles,
                         reference = reference,
                         genome_build = "hg19",
                         bin_size = 200000,
                         workers = 1)
```

`download_button` *Download local file*

Description

Save an object as RDS and create a download button that can be rendered to Rmarkdown HTML pages. Uses the package **downloadthis**.

Usage

```
download_button(
  object,
  save_output = FALSE,
  outfile_dir = NULL,
  filename = NULL,
  button_label = paste0("Download: ", "<code>", filename, "</code>"),
  output_extension = ".rds",
  icon = "fa fa-save",
  button_type = "success",
  self_contained = TRUE,
  add_download_button = TRUE,
  verbose = TRUE
)
```

Arguments

`object`	R object to serialize.
`save_output`	Default FALSE. If TRUE, all outputs (tables and plots) of the analysis will be saved in a folder (EpiCompare_file).
`outfile_dir`	Directory to save the file to.
`filename`	Name of the file to save.
`button_label`	Character (HTML), button label
`output_extension`	Extension of the output file. Currently, `.csv`, `.xlsx`, and `.rds` are supported. If a (named) list is passed to the function, only `.xlsx` and `.rds` are supported.
`icon`	Fontawesome tag e.g.: "fa fa-save"
`button_type`	Character, one of the standard Bootstrap types
`self_contained`	A boolean to specify whether your HTML output is self-contained. Default to `FALSE`.
`add_download_button`	Add download buttons for each plot or dataset.
`verbose`	Print messages.

Value

Download button as HTML text.

Source

csv2 Issue.

Plotly Issue

Examples

```
button <- download_button(object=mtcars)
```

---

encode_H3K27ac *Example ChIP-seq peak file*

Description

Human H3K27ac peak file generated with ChIP-seq using K562 cell-line. Human genome build hg19 was used. The peak file (.BED) was obtained from ENCODE project (https://www.encodeproject.org/files/ENCFF044JNJ/). The BED file was then imported as an GRanges object. Peaks located on chromosome 1 were subsetted to reduce the dataset size.

Usage

```
data("encode_H3K27ac")
```

Format

An object of class GRanges of length 5142.

Source

The code to prepare the .Rda file from the raw peak file is:

```
# dataset was directly downloaded from
# https://www.encodeproject.org/files/ENCFF044JNJ/ encode_H3K27ac <- ChIPseeker::readPeakFile("path",
as = "GRanges")
encode_H3K27ac <-encode_H3K27ac[seqnames(encode_H3K27ac) == "chr1"]
my_label <- c("name","score","strand","signalValue","pValue","qValue","peak")
colnames(GenomicRanges::mcols(encode_H3K27ac)) <- my_label
usethis::use_data(encode_H3K27ac, overwrite = TRUE)
```

EpiCompare *Compare epigenomic datasets*

Description

This function compares and analyses multiple epigenomic datasets and outputs an HTML report containing all results of the analysis. The report is mainly divided into three sections: (1) General Metrics on Peakfiles, (2) Peak Overlaps and (3) Functional Annotation of Peaks.

Usage

```
EpiCompare(
  peakfiles,
  genome_build,
  genome_build_output = "hg19",
  blacklist = NULL,
  picard_files = NULL,
  reference = NULL,
  upset_plot = FALSE,
  stat_plot = FALSE,
  chromHMM_plot = FALSE,
  chromHMM_annotation = "K562",
  chipseeker_plot = FALSE,
  enrichment_plot = FALSE,
  tss_plot = FALSE,
  tss_distance = c(-3000, 3000),
  precision_recall_plot = FALSE,
  n_threshold = 20,
  corr_plot = FALSE,
  bin_size = 5000,
  interact = TRUE,
  add_download_button = FALSE,
  save_output = FALSE,
  output_filename = "EpiCompare",
  output_timestamp = FALSE,
  output_dir,
  display = NULL,
  run_all = FALSE,
  workers = 1,
  quiet = FALSE,
  error = FALSE,
  debug = FALSE
)
```

Arguments

peakfiles	A list of peak files as GRanges object and/or as paths to BED files. If paths are provided, EpiCompare imports the file as GRanges object. EpiCompare also

accepts a list containing a mix of GRanges objects and paths.Files must be listed and named using `list()`. E.g. `list("name1"=file1, "name2"=file2)`. If no names are specified, default file names will be assigned.

`genome_build` A named list indicating the genome build used to generate each of the following inputs:

- "peakfiles" : Genome build for the `peakfiles` input. Assumes genome build is the same for each element in the `peakfiles` list.
- "reference" : Genome build for the `reference` input.
- "blacklist" : Genome build for the `blacklist` input.

Example input list:
`genome_build = list(peakfiles="hg38", reference="hg19", blacklist="hg19")`

Alternatively, you can supply a single character string instead of a list. This should *only* be done in situations where all three inputs (`peakfiles`, `reference`, `blacklist`) are of the same genome build. For example:
`genome_build = "hg19"`

Supported genome builds are: "hg19", "hg38", "mm9" and "mm10".

`genome_build_output`
Genome build to standardise all inputs to. Liftovers will be performed automatically as needed. Default: "hg19".

Note: Cross-species liftovers are supported.

`blacklist` A GRanges object containing blacklisted genomic regions. Blacklists included in **EpiCompare** are:

- `NULL` (default): Automatically selects the appropriate blacklist based on the `genome_build_output` argument.
- "hg19_blacklist": Regions of hg19 genome that have anomalous and/or unstructured signals. hg19_blacklist
- "hg38_blacklist": Regions of hg38 genome that have anomalous and/or unstructured signals. hg38_blacklist
- "mm10_blacklist": Regions of mm10 genome that have anomalous and/or unstructured signals. mm10_blacklist
- "mm9_blacklist": Blacklisted regions of mm10 genome that have been lifted over from mm10_blacklist. mm9_blacklist
- `<user_input>`: A custom user-provided blacklist in GRanges format.

`picard_files` A list of summary metrics output from Picard. Files must be in data.frame format and listed using `list()` and named using `names()`. To import Picard duplication metrics (.txt file) into R as data frame, use:
`picard <- read.table("/path/to/picard/output", header = TRUE, fill = TRUE)`.

`reference` A named list containing reference peak file(s) as GRanges object. Please ensure that the reference file is listed and named i.e. `list("reference_name" = reference_peak)`. If more than one reference is specified, individual reports for each reference will be generated. However, please note that speci-

fying more than one reference can take awhile. If a reference is specified, it enables two analyses: (1) plot showing statistical significance of overlapping/non-overlapping peaks; and (2) ChromHMM of overlapping/non-overlapping peaks.

`upset_plot` Default FALSE. If TRUE, the report includes upset plot of overlapping peaks.

`stat_plot` Default FALSE. If TRUE, the function creates a plot showing the statistical significance of overlapping/non-overlapping peaks. Reference peak file must be provided.

`chromHMM_plot` Default FALSE. If TRUE, the function outputs ChromHMM heatmap of individual peak files. If a reference peak file is provided, ChromHMM annotation of overlapping and non-overlapping peaks is also provided.

`chromHMM_annotation`
ChromHMM annotation for ChromHMM plots. Default K562 cell-line. Cell-line options are:

- "K562" = K-562 cells
- "Gm12878" = Cellosaurus cell-line GM12878
- "H1hesc" = H1 Human Embryonic Stem Cell
- "Hepg2" = Hep G2 cell
- "Hmec" = Human Mammary Epithelial Cell
- "Hsmm" = Human Skeletal Muscle Myoblasts
- "Huvec" = Human Umbilical Vein Endothelial Cells
- "Nhek" = Normal Human Epidermal Keratinocytes
- "Nhlf" = Normal Human Lung Fibroblasts

`chipseeker_plot`
Default FALSE. If TRUE, the report includes a barplot of ChIPseeker annotation of peak files.

`enrichment_plot`
Default FALSE. If TRUE, the report includes dotplots of KEGG and GO enrichment analysis of peak files.

`tss_plot` Default FALSE. If TRUE, the report includes peak count frequency around transcriptional start site. Note that this can take awhile.

`tss_distance` A vector specifying the distance upstream and downstream around transcription start sites (TSS). The default value is `c(-3000,3000)`; meaning peak frequency 3000bp upstream and downstream of TSS will be displayed.

`precision_recall_plot`
Default is FALSE. If TRUE, creates a precision-recall curve plot and an F1 plot using plot_precision_recall.

`n_threshold` Number of thresholds to test.

`corr_plot` Default is FALSE. If TRUE, creates a correlation plot across all peak files using plot_corr.

`bin_size` Default of 100. Base-pair size of the bins created to measure correlation. Use smaller value for higher resolution but longer run time and larger memory usage.

`interact` Default TRUE. By default, plots are interactive. If set FALSE, all plots in the report will be static.

add_download_button
: Add download buttons for each plot or dataset.

save_output
: Default FALSE. If TRUE, all outputs (tables and plots) of the analysis will be saved in a folder (EpiCompare_file).

output_filename
: Default EpiCompare.html. If otherwise, the html report will be saved in the specified name.

output_timestamp
: Default FALSE. If TRUE, date will be included in the file name.

output_dir
: Path to where output HTML file should be saved.

display
: After completion, automatically display the HTML report file in one of the following ways:

  - "browser" : Display the report in your default web browser.
  - "rsstudio" : Display the report in Rstudio.
  - NULL (default) : Do not display the report.

run_all
: Convenience argument that enables all plots/features (without specifying each argument manually) by overriding the default values. Default: `FALSE`.

workers
: Number of threads to parallelize across.

quiet
: An option to suppress printing during rendering from knitr, pandoc command line and others. To only suppress printing of the last "Output created: " message, you can set `rmarkdown.render.message` to `FALSE`

error
: If `TRUE`, the Rmarkdown report will continue to render even when some chunks encounter errors (default: `FALSE`). Passed to opts_chunk.

debug
: Run in debug mode, where are messages and warnings are printed within the HTML report (default: `FALSE`).

Value

Path to one or more HTML report files.

Examples

```
### Load Data ###
data("encode_H3K27ac") # example dataset as GRanges object
data("CnT_H3K27ac") # example dataset as GRanges object
data("CnR_H3K27ac") # example dataset as GRanges object
data("CnT_H3K27ac_picard") # example Picard summary output
data("CnR_H3K27ac_picard") # example Picard summary output

#### Prepare Input ####
# create named list of peakfiles
peakfiles <- list(CnR=CnR_H3K27ac, CnT=CnT_H3K27ac)
# create named list of picard outputs
picard_files <- list(CnR=CnR_H3K27ac_picard, CnT=CnT_H3K27ac_picard)
# reference peak file
reference <- list("ENCODE" = encode_H3K27ac)
```

```
### Run EpiCompare ###
output_html <- EpiCompare(peakfiles = peakfiles,
           genome_build = list(peakfiles="hg19",
                               reference="hg19"),
           picard_files = picard_files,
           reference = reference,
           output_filename = "EpiCompare_test",
           output_dir = tempdir())
# utils::browseURL(output_html)
```

`fig_length` *Dynamic Figure Length Generator*

Description

This function calculates the appropriate figure height depending on the number of items.

Usage

```
fig_length(default_size, number_of_items, max_items)
```

Arguments

`default_size`	The default figure length. Must be numeric.
`number_of_items`	Number of peak files, or terms.
`max_items`	Maximum number of peak files, or terms.

Value

Figure height/width. A number.

`fragment_info` *Summary on fragments*

Description

This function outputs a summary on fragments using metrics generated by Picard. Provides the number of mapped fragments, duplication rate and number of unique fragments.

Usage

```
fragment_info(picard_list)
```

Arguments

picard_list	Named list of duplication metrics generated by Picard as data frame. Data frames must be named and listed using `list()`. e.g. `list("name1"=file1, "name2"=file2)`. To import Picard duplication metrics (.txt file) into R as data frame, use `picard <- read.table("/path/to/picard/output", header = TRUE,fill = TRUE)`.

Value

A table summarizing metrics on fragments.

Examples

```
### Load Data ###
data(CnT_H3K27ac_picard) # example picard output
data(CnR_H3K27ac_picard) # example picard output
### Import Picard Metrics ###
# To import Picard duplication metrics (.txt file) into R as data frame
# CnT_H3K27ac_picard <- read.table("/path/to/picard/output.txt",
#  header = TRUE,fill = TRUE)
### Create Named List ###
picard_list <- list("CnT_H3K27ac"=CnT_H3K27ac_picard,
                "CnR_H3K27ac"=CnR_H3K27ac_picard)
df <- fragment_info(picard_list = picard_list)
```

---

gather_files *Gather files*

Description

Recursively find peak/picard files stored within subdirectories and import them as a list of GRanges objects.

Usage

```
gather_files(
  dir,
  type = "peaks.stringent",
  nfcore_cutandrun = FALSE,
  return_paths = FALSE,
  rbind_list = FALSE,
  workers = check_workers(),
  verbose = TRUE
)
```

Arguments

dir	Directory to search within.
type	File type to search for. Options include: • "<pattern>"Finds files matching an arbitrary regex pattern specified by user. • "peaks.stringent"Finds files ending in "*.stringent.bed$" • "peaks.consensus"Finds files ending in "*.consensus.peaks.bed$" • "peaks.consensus.filtered" Finds files ending in"*.consensus.peaks.filtered.awk.bed$" • "picard"Finds files ending in "*.target.markdup.MarkDuplicates.metrics.txt$"
nfcore_cutandrun	Whether the files were generated by the nf-core/cutandrun Nextflow pipeline. If TRUE, can use the standardised folder structure to automatically generate more descriptive file names with sample IDs.
return_paths	Return only the file paths without actually reading them in as GRanges.
rbind_list	Bind all objects into one.
workers	Number of cores to parallelise across (in applicable functions). If NULL, will set to the total number of available cores minus 1.
verbose	Print messages.

Details

For "peaks.stringent" files called with SEACR, column names will be automatically added:

- total_signal : Total signal contained within denoted coordinates.
- max_signalMaximum bedgraph signal attained at any base pair within denoted coordinates.
- max_signal_region Region representing the farthest upstream and farthest downstream bases within the denoted coordinates that are represented by the maximum bedgraph signal.

Value

A named list of GRanges objects.

Examples

```
#### Make example files ####
save_paths <- EpiCompare::write_example_peaks()
dir <- unique(dirname(save_paths))
#### Gather/import files ####
peaks <- EpiCompare::gather_files(dir=dir,
                                  type="peaks.narrow",
                                  workers = 1)
```

gather_files_names *Make file names*

Description

Support function for gather_files.

Usage

```
gather_files_names(paths, type, nfcore_cutandrun, verbose = TRUE)
```

Arguments

paths	Character vector of file paths.
type	File type to search for. Options include: • "<pattern>"Finds files matching an arbitrary regex pattern specified by user. • "peaks.stringent"Finds files ending in "*.stringent.bed$" • "peaks.consensus"Finds files ending in "*.consensus.peaks.bed$" • "peaks.consensus.filtered" Finds files ending in"*.consensus.peaks.filtered.awk.bed$" • "picard"Finds files ending in "*.target.markdup.MarkDuplicates.metrics.txt$"
nfcore_cutandrun	Whether the files were generated by the nf-core/cutandrun Nextflow pipeline. If TRUE, can use the standardised folder structure to automatically generate more descriptive file names with sample IDs.
verbose	Print messages.

Value

Named character vector.

get_bpparam *Get BiocParallel parameters*

Description

Get (and optionally register) BiocParallel parameter (BPPARAM). SnowParam is the default function as it tends to be more robust. However, because it doesn't work on Windows, this function automatically detected the Operating System and switches to SerialParam as needed.

Usage

```
get_bpparam(
  workers,
  progressbar = workers > 1,
  use_snowparam = TRUE,
  register_now = FALSE
)
```

Arguments

workers	Number of threads to parallelize across.
progressbar	logical(1) Enable progress bar (based on plyr:::progress_text).
use_snowparam	Whether to use SnowParam (default: TRUE) or MulticoreParam (FALSE) when parallelising across multiple workers.
register_now	Register the cores now with register (TRUE), or simply return the BPPARAM object (default: FALSE).

Value

BPPARAM

---

get_chromHMM_annotation

Download ChromHMM annotation file(s)

Description

Download ChromHMM annotation file(s) for a given cell-line (returned as a GRanges object) or a list of cell-lines (returned as a named list of GRanges objects). All annotations are aligned to the hg19 genome build. All data can be found on the UCSC Genome Browser here.

Usage

```
get_chromHMM_annotation(
  cell_line,
  cache = BiocFileCache::BiocFileCache(ask = FALSE)
)
```

Arguments

cell_line	ChromHMM annotation for user-specified cell-line. Cell-line options are: • "K562" = K-562 cells • "Gm12878" = Cellosaurus cell-line GM12878 • "H1hesc" = H1 Human Embryonic Stem Cell • "Hepg2" = Hep G2 cell

- "Hmec" = Human Mammary Epithelial Cell
- "Hsmm" = Human Skeletal Muscle Myoblasts
- "Huvec" = Human Umbilical Vein Endothelial Cells
- "Nhek" = Normal Human Epidermal Keratinocytes
- "Nhlf" = Normal Human Lung Fibroblasts

Value

Cell-line specific ChromHMM annotation file. Default K562 cell-line.

`group_files` *Group files*

Description

Assign group names to each file in a named list based on a series of string searches based on combinations of relevant metadata factors.

Usage

```
group_files(peakfiles, searches)
```

Arguments

`peakfiles`	A list of peak files as GRanges object and/or as paths to BED files. If paths are provided, EpiCompare imports the file as GRanges object. EpiCompare also accepts a list containing a mix of GRanges objects and paths.Files must be listed and named using `list()`. E.g. `list("name1"=file1, "name2"=file2)`. If no names are specified, default file names will be assigned.
`searches`	A named list of substrings to group `peakfiles` by.

Value

Named peak files

Examples

```
data("encode_H3K27ac") # example dataset as GRanges object
data("CnT_H3K27ac") # example dataset as GRanges object
data("CnR_H3K27ac") # example dataset as GRanges object
peakfiles <- list(CnR_H3K27ac=CnR_H3K27ac,
                  CnT_H3K27ac=CnT_H3K27ac,
                  encode_H3K27ac=encode_H3K27ac)

peaks_grouped <- group_files(peakfiles = peakfiles,
                             searches=list(assay=c("H3K27ac"),
                                           source=c("Cn","ENCODE")))
```

hg19_blacklist *Human genome hg19 blacklisted regions*

Description

Obtained from https://www.encodeproject.org/files/ENCFF001TDO/. The ENCODE blacklist includes regions of the hg19 genome that have anomalous and/or unstructured signals independent of the cell-line or experiment. Removal of ENCODE blacklist is recommended for quality measure.

Usage

```
data("hg19_blacklist")
```

Format

An object of class GRanges of length 411.

Source

The code to prepare the .Rda file is:

```
# blacklisted regions were directly downloaded
# from https://www.encodeproject.org/files/ENCFF001TDO/
hg19_blacklist <-ChIPseeker::readPeakFile(file.path(path), as = "GRanges")
usethis::use_data(hg19_blacklist, overwrite = TRUE)
```

hg38_blacklist *Human genome hg38 blacklisted regions*

Description

Obtained from https://www.encodeproject.org/files/ENCFF356LFX/. The ENCODE blacklist includes regions of the hg38 genome that have anomalous and/or unstructured signals independent of the cell-line or experiment. Removal of ENCODE blacklist is recommended for quality measure.

Usage

```
data("hg38_blacklist")
```

Format

An object of class GRanges of length 910.

Source

The code to prepare the .Rda file is:

```
## blacklisted regions were directly downloaded
## from https://www.encodeproject.org/files/ENCFF356LFX/
hg38_blacklist <-ChIPseeker::readPeakFile(file.path(path), as = "GRanges")
usethis::use_data(hg38_blacklist, overwrite = TRUE)
```

---

is_granges *Is an object of class GRanges*

Description

Check whether an object is of the class GRanges.

Usage

```
is_granges(obj)
```

Arguments

obj	Any R object.

Value

Boolean.

---

liftover_grlist *Liftover peak list*

Description

Perform genome build liftover to one or more GRanges objects at once.

Usage

```
liftover_grlist(
  grlist,
  input_build,
  output_build = "hg19",
  style = "UCSC",
  keep_chr = paste0("chr", c(seq_len(22), "X", "Y")),
  as_grangeslist = FALSE,
  merge_all = FALSE,
  verbose = TRUE
)
```

Arguments

grlist	A named list of GRanges objects, or simply a single unlisted GRanges object. Can perform liftover within species or across species.
input_build	The genome build of grlist.
output_build	Desired genome build for grlist to be lifted over to.
style	Chromosome style, set by seqlevelsStyle. • "UCSC" : Uses the chromosome style "chr1". • "NCBI" : Uses the chromosome style "1"
keep_chr	Which chromosomes to keep.
as_grangeslist	Return as a GRangesList.
merge_all	Merge all GRanges into a single GRanges object.
verbose	Print messages.

Value

Named list of lifted GRanges objects.

Examples

```
grlist <- list("gr1"=GenomicRanges::GRanges("4:1-100000"),
               "gr2"=GenomicRanges::GRanges("6:1-100000"),
               "gr3"=GenomicRanges::GRanges("8:1-100000"))

grlist_lifted <- liftover_grlist(grlist = grlist,
                                 input_build = "hg19",
                                 output_build="hg38")
```

---

messager *Print messages*

Description

Conditionally print messages. Allows developers to easily control verbosity of functions, and meet Bioconductor requirements that dictate the message must first be stored to a variable before passing to message.

Usage

```
messager(..., v = TRUE, parallel = FALSE)
```

Arguments

v	Whether to print messages or not.
parallel	Whether to enable message print when wrapped in parallelised functions.

Value

Null

`message_parallel` *Message parallel*

Description

Send messages to console even from within parallel processes

Usage

```
message_parallel(...)
```

Value

A message

`mm10_blacklist` *Mouse genome mm10 blacklisted regions*

Description

Obtained from https://www.encodeproject.org/files/ENCFF547MET/. The ENCODE blacklist includes regions of the mm10 genome that have anomalous and/or unstructured signals independent of the cell-line or experiment. Removal of ENCODE blacklist is recommended for quality measure.

Usage

```
data("mm10_blacklist")
```

Format

An object of class GRanges of length 164.

Source

The code to prepare the .Rda file is:

```
## blacklisted regions were directly downloaded
## from https://www.encodeproject.org/files/ENCFF547MET/
mm10_blacklist <-ChIPseeker::readPeakFile(file.path(path), as = "GRanges")
usethis::use_data(mm10_blacklist, overwrite = TRUE)
```

mm9_blacklist *Mouse genome mm9 blacklisted regions*

Description

Blaklisted regions of the mm9 genome build btained by lifting over the `mm10_blacklist`.

Usage

```
data("mm9_blacklist")
```

Format

An object of class `GRanges` of length 292.

Source

```
tmp <- base::get("mm10_blacklist", asNamespace("EpiCompare")) mm9_blacklist <- liftover_grlist(grlist
= tmp, input_build = "mm10", output_build = "mm9", keep_chr = NULL) usethis::use_data(mm9_blacklist,
overwrite = TRUE)
```

overlap_heatmap *Generate heatmap of percentage overlap*

Description

This function generates a heatmap showing percentage of overlapping peaks between peak files.

Usage

```
overlap_heatmap(
  peaklist,
  interact = TRUE,
  draw_cellnote = TRUE,
  fill_diag = NA,
  verbose = TRUE
)
```

Arguments

`peaklist`	A list of peak files as GRanges object. Files must be listed and named using `list()`. e.g. `list("name1"=file1, "name2"=file2)`. If not named, default file names will be assigned.
`interact`	Default TRUE. By default heatmap is interactive. If FALSE, heatmap is static.
`draw_cellnote`	Draw the numeric values within each heatmap cell.
`fill_diag`	Fill the diagonal of the overlap matrix.
`verbose`	Print messages.

Value

An interactive heatmap

Examples

```
### Load Data ###
data("encode_H3K27ac") # example peakfile GRanges object
data("CnT_H3K27ac") # example peakfile GRanges object
### Create Named List ###
peaklist <- list("encode"=encode_H3K27ac, "CnT"=CnT_H3K27ac)
### Run ###
my_heatmap <- overlap_heatmap(peaklist = peaklist)
```

`overlap_percent` *Calculate percentage of overlapping peaks*

Description

This function calculates the percentage of overlapping peaks and outputs a table or matrix of results.

Usage

```
overlap_percent(
  peaklist1,
  peaklist2,
  invert = FALSE,
  precision_recall = TRUE,
  suppress_messages = TRUE
)
```

Arguments

`peaklist1`	A list of peak files as GRanges object. Files must be listed and named using `list()`. e.g. `list("name1"=file1, "name2"=file2)`. If not named, default file names will be assigned.
`peaklist2`	peaklist1 A list of peak files as GRanges object. Files must be listed and named using `list()`. e.g. `list("name1"=file1, "name2"=file2)`.
`invert`	If `TRUE`, keep only the ranges in `x` that do *not* overlap `ranges`.
`precision_recall`	Return percision-recall results for all combinations of `peaklist1` (the "query") and `peaklist2` (the "subject"). See subsetByOverlaps for more details on this terminology.
`suppress_messages`	Suppress messages.

Value

data frame

Examples

```
### Load Data ###
data("encode_H3K27ac") # example peakfile GRanges object
data("CnT_H3K27ac") # example peakfile GRanges object
data("CnR_H3K27ac") # example peakfile GRanges object

### Create Named Peaklist ###
peaks <- list("CnT"=CnT_H3K27ac, "CnR"=CnR_H3K27ac)
reference_peak <- list("ENCODE"=encode_H3K27ac)

### Run ###
overlap <- overlap_percent(peaklist1=peaks,
                           peaklist2=reference_peak)
```

---

overlap_stat_plot *Statistical significance of overlapping peaks*

Description

This function calculates the statistical significance of overlapping/ non-overlapping peaks against a reference peak file. If the reference peak file has the BED6+4 format (peak called by MACS2), the function generates a series of box plots showing the distribution of q-values for sample peaks that are overlapping and non-overlapping with the reference. If the reference peak file does not have the BED6+4 format, the function uses enrichPeakOverlap from **ChIPseeker** package to calculate the statistical significance of overlapping peaks only. In this case, please provide an annotation file as a TxDb object.

Usage

```
overlap_stat_plot(
  reference,
  peaklist,
  txdb = NULL,
  interact = FALSE,
  nShuffle = 50,
  digits = 4,
  workers = check_workers()
)
```

Arguments

reference	A reference peak file as GRanges object.
peaklist	A list of peak files as GRanges object. Files must be listed and named using `list()`. E.g. `list("name1"=file1, "name2"=file2)`. If not named, default file names will be assigned.
txdb	A TxDb annotation object from Bioconductor. This is required only if the reference file does not have BED6+4 format.

interact	Default TRUE. By default, plots are interactive. If set FALSE, all plots in the report will be static.
nShuffle	shuffle numbers
digits	integer indicating the number of decimal places (round) or significant digits (signif) to be used. For round, negative values are allowed (see 'Details').
workers	Number of threads to parallelize across.

Value

A named list.

- "plot"boxplot/barplot showing the statistical significance of overlapping/non-overlapping peaks.
- "data"Plot data.

Examples

```
### Load Data ###
data("encode_H3K27ac") # example peakfile GRanges object
data("CnT_H3K27ac") # example peakfile GRanges object
data("CnR_H3K27ac") # example peakfile GRanges object
### Create Named Peaklist & Reference ###
peaklist <- list('CnT'=CnT_H3K27ac, "CnR"=CnR_H3K27ac)
reference <- list("ENCODE"=encode_H3K27ac)
out <- overlap_stat_plot(reference = reference,
                         peaklist = peaklist,
                         workers = 1)
```

---

overlap_upset_plot *Generate Upset plot for overlapping peaks*

Description

This function generates upset plot of overlapping peaks files using the **ComplexUpset** package.

Usage

```
overlap_upset_plot(peaklist, verbose = TRUE)
```

Arguments

peaklist	A named list of peak files as GRanges object. Objects must be listed and named using list(). e.g. list("name1"=file1, "name2"=file2). If not named, default file names are assigned.
verbose	Print messages

Value

Upset plot of overlapping peaks.

Examples

```
### Load Data ###
data("encode_H3K27ac") # load example data
data("CnT_H3K27ac") # load example data
peaklist <- list("encode"=encode_H3K27ac, "CnT"=CnT_H3K27ac)
my_plot <- overlap_upset_plot(peaklist = peaklist)
```

---

peak_info *Summary of Peak Information*

Description

This function outputs a table summarizing information on the peak files. Provides the total number of peaks and the percentage of peaks in blacklisted regions.

Usage

```
peak_info(peaklist, blacklist)
```

Arguments

peaklist	A named list of peak files as GRanges object. Objects listed using `list("name1" = peak, "name2" = peak2)`.
blacklist	A GRanges object containing blacklisted regions.

Value

A summary table of peak information

Examples

```
### Load Data ###
data("encode_H3K27ac") # example peakfile GRanges object
data("CnT_H3K27ac") # example peakfile GRanges object
data("hg19_blacklist") # example blacklist GRanges object

### Named Peaklist ###
peaklist <- list("encode"=encode_H3K27ac, "CnT"=CnT_H3K27ac)

### Run ###
df <- peak_info(peaklist = peaklist,
                blacklist = hg19_blacklist)
```

plot_ChIPseeker_annotation
Create ChIPseeker annotation plot

Description

This function annotates peaks using `ChIPseeker::annotatePeak`. It outputs functional annotation of each peak file in a barplot.

Usage

```
plot_ChIPseeker_annotation(
  peaklist,
  txdb = NULL,
  tss_distance = c(-3000, 3000),
  interact = FALSE
)
```

Arguments

`peaklist`	A list of peak files as GRanges object. Files must be listed and named using `list()`. e.g. `list("name1"=file1, "name2"=file2)`. If not named, default file names will be assigned.
`txdb`	A TxDb annotation object from Bioconductor.
`tss_distance`	A vector specifying the distance upstream and downstream around transcription start sites (TSS). The default value is `c(-3000,3000)`; meaning peak frequency 3000bp upstream and downstream of TSS will be displayed.
`interact`	Default TRUE. By default, plots are interactive. If set FALSE, all plots in the report will be static.

Value

ggplot barplot

Examples

```
### Load Data ###
data("CnT_H3K27ac") # example peakfile GRanges object
data("CnR_H3K27ac") # example peakfile GRanges object
peaklist <- list("CnT"=CnT_H3K27ac, "CnR"=CnR_H3K27ac)
my_plot <- plot_ChIPseeker_annotation(peaklist = peaklist,
                                      tss_distance = c(-50,50))
```

plot_chromHMM *Plot ChromHMM heatmap*

Description

Creates a heatmap using outputs from ChromHMM using ggplot2.The function takes a list of peakfiles, performs ChromHMM and outputs a heatmap. ChromHMM annotation file must be loaded prior to using this function. ChromHMM annotations are aligned to hg19, and will be automatically lifted over to the genome_build to match the build of the peaklist.

Usage

```
plot_chromHMM(
  peaklist,
  chromHMM_annotation,
  genome_build,
  cell_line = NULL,
  interact = FALSE,
  return_data = FALSE
)
```

Arguments

peaklist	A named list of peak files as GRanges object. If list is not named, default names will be assigned.
chromHMM_annotation	ChromHMM annotation list.
genome_build	The human genome reference build used to generate peakfiles. "hg19" or "hg38".
cell_line	If not cell_line, will replace chromHMM_annotation by importing chromHMM data for a given cell line using get_chromHMM_annotation.
interact	Default TRUE. By default, the heatmaps are interactive. IfFALSE, the function generates a static ChromHMM heatmap.
return_data	Return the plot data as in addition to the plot itself.

Value

ChromHMM heatmap, or a named list.

Examples

```
### Load Data ###
data("CnT_H3K27ac") # example dataset as GRanges object
data("CnR_H3K27ac") # example dataset as GRanges object
### Create Named Peaklist ###
peaklist <- list(CnT=CnT_H3K27ac, CnR=CnR_H3K27ac)
### Run ###
```

```
my_plot <- plot_chromHMM(peaklist = peaklist,
                         cell_line = "K562",
                         genome_build = "hg19")
```

---

plot_corr *Plot correlation of peak files*

Description

Plot correlation by binning genome and measuring correlation of peak quantile ranking. This ranking is based on p-value or other peak intensity measure dependent on the peak calling approach.

Usage

```
plot_corr(
  peakfiles,
  reference = NULL,
  genome_build,
  bin_size = 5000,
  keep_chr = NULL,
  drop_empty_chr = FALSE,
  method = "spearman",
  intensity_cols = c("total_signal", "qValue", "Peak Score", "score"),
  interact = FALSE,
  draw_cellnote = TRUE,
  fill_diag = NA,
  workers = check_workers(),
  show_plot = TRUE,
  save_path = tempfile(fileext = ".corr.csv.gz")
)
```

Arguments

peakfiles	A list of peak files as GRanges object and/or as paths to BED files. If paths are provided, EpiCompare imports the file as GRanges object. EpiCompare also accepts a list containing a mix of GRanges objects and paths.Files must be listed and named using `list()`. E.g. `list("name1"=file1, "name2"=file2)`. If no names are specified, default file names will be assigned.
reference	A named list containing reference peak file(s) as GRanges object. Please ensure that the reference file is listed and named i.e. `list("reference_name" = reference_peak)`. If more than one reference is specified, individual reports for each reference will be generated. However, please note that specifying more than one reference can take awhile. If a reference is specified, it enables two analyses: (1) plot showing statistical significance of overlapping/non-overlapping peaks; and (2) ChromHMM of overlapping/non-overlapping peaks.

genome_build	The build of **all** peak and reference files to calculate the correlation matrix on. If all peak and reference files are not of the same build use liftover_grlist to convert them all before running. Genome build should be one of hg19, hg38, mm9, mm10.
bin_size	Default of 100. Base-pair size of the bins created to measure correlation. Use smaller value for higher resolution but longer run time and larger memory usage.
keep_chr	Which chromosomes to keep.
drop_empty_chr	Drop chromosomes that are not present in any of the peakfiles (default: FALSE).
method	Default spearman (i.e. non-parametric). A character string indicating which correlation coefficient (or covariance) is to be computed. One of "pearson", "kendall", or "spearman": can be abbreviated.
intensity_cols	Depending on which columns are present, this value will be used to get quantiles and ultimately calculate the correlations: • "total_signal" : Used by the peak calling software SEACR. *NOTE*: Another SEACR column (e.g. "max_signal") can be used together or instead of "total_signal". • "qValue"Used by the peak calling software MACS2/3. Should contain the negative log of the p-values after multiple testing correction. • "Peak Score" : Used by the peak calling software HOMER.
interact	Default TRUE. By default heatmap is interactive. If FALSE, heatmap is static.
draw_cellnote	Draw the numeric values within each heatmap cell.
fill_diag	Fill the diagonal of the overlap matrix.
workers	Number of threads to parallelize across.
show_plot	Show the plot.
save_path	Path to save a table of correlation results to.

Value

list with correlation plot (corr_plot) and correlation matrix (data)

Examples

```
data("CnR_H3K27ac")
data("CnT_H3K27ac")
data("encode_H3K27ac")
peakfiles <- list(CnR_H3K27ac=CnR_H3K27ac, CnT_H3K27ac=CnT_H3K27ac)
reference <- list("encode_H3K27ac"=encode_H3K27ac)
## Increasing bin_size for speed here,
## but lower values will give more precise results (and lower correlations)
cp <- plot_corr(peakfiles = peakfiles,
                reference = reference,
                genome_build = "hg19",
                bin_size = 5000,
                workers = 1)
```

plot_enrichment *Generate enrichment analysis plots*

Description

This function runs KEGG and GO enrichment analysis of peak files and generates dot plots.

Usage

```
plot_enrichment(
  peaklist,
  txdb = NULL,
  tss_distance = c(-3000, 3000),
  pvalueCutoff = 0.05,
  interact = FALSE,
  verbose = TRUE
)
```

Arguments

peaklist	A list of peak files as GRanges object. Files must be listed and named using `list()`. e.g. `list("name1"=file1, "name2"=file2)`. If not named, default file names will be assigned.
txdb	A TxDb annotation object from Bioconductor.
tss_distance	A vector specifying the distance upstream and downstream around transcription start sites (TSS). The default value is `c(-3000,3000)`; meaning peak frequency 3000bp upstream and downstream of TSS will be displayed.
pvalueCutoff	P-value cutoff, passed to compareCluster.
interact	Default TRUE. By default, plots are interactive. If set FALSE, all plots in the report will be static.
verbose	Print messages.

Value

KEGG and GO dot plots

Examples

```
### Load Data ###
data("CnT_H3K27ac") # example peakfile GRanges object
data("CnR_H3K27ac") # example peakfile GRanges object
### Create Named Peaklist ###
peaklist <- list("CnT"=CnT_H3K27ac, "CnR"=CnR_H3K27ac)
enrich_res <- plot_enrichment(peaklist = peaklist, pvalueCutoff=1,
                              tss_distance = c(-50,50))
```

`plot_precision_recall` *Plot precision-recall curves*

Description

Plot precision-recall curves (and optionally F1 plots) by iteratively testing for peak overlap across a series of thresholds used to filter `peakfiles`. Each GRanges object in `peakfiles` will be used as the "query" against each GRanges object in `reference` as the subject. Will automatically use any columns that are specified with `thresholding_cols` and present within each GRanges object to create percentiles for thresholding. *NOTE* : Assumes that all GRanges in `peakfiles` and `reference` are already aligned to the same genome build.

Usage

```
plot_precision_recall(
  peakfiles,
  reference,
  thresholding_cols = c("total_signal", "qValue", "Peak Score"),
  initial_threshold = 0,
  n_threshold = 20,
  max_threshold = 1,
  workers = check_workers(),
  plot_f1 = TRUE,
  subtitle = NULL,
  color = "peaklist1",
  shape = color,
  facets = "peaklist2 ~ .",
  interact = FALSE,
  show_plot = TRUE,
  save_path = tempfile(fileext = "precision_recall.csv"),
  verbose = TRUE
)
```

Arguments

`peakfiles`	A list of peak files as GRanges object and/or as paths to BED files. If paths are provided, EpiCompare imports the file as GRanges object. EpiCompare also accepts a list containing a mix of GRanges objects and paths.Files must be listed and named using `list()`. E.g. `list("name1"=file1, "name2"=file2)`. If no names are specified, default file names will be assigned.
`reference`	A named list containing reference peak file(s) as GRanges object. Please ensure that the reference file is listed and named i.e. `list("reference_name" = reference_peak)`. If more than one reference is specified, individual reports for each reference will be generated. However, please note that specifying more than one reference can take awhile. If a reference is specified, it enables two analyses: (1) plot showing statistical significance of overlapping/non-overlapping peaks; and (2) ChromHMM of overlapping/non-overlapping peaks.

`thresholding_cols`
: Depending on which columns are present, GRanges will be filtered at each threshold according to one or more of the following:
  - "total_signal" : Used by the peak calling software SEACR. *NOTE*: Another SEACR column (e.g. "max_signal") can be used together or instead of "total_signal".
  - "qValue"Used by the peak calling software MACS2/3. Should contain the negative log of the p-values after multiple testing correction.
  - "Peak Score" : Used by the peak calling software HOMER.

`initial_threshold`
: Numeric threshold that was provided to SEACR (via the parameter `--ctrl`) when calling peaks without an IgG control.

`n_threshold` Number of thresholds to test.

`max_threshold` Maximum threshold to test.

`workers` Number of threads to parallelize across.

`plot_f1` Generate a plot with the F1 score vs. threshold as well.

`subtitle` Plot subtitle.

`color` Variable to color data points by.

`shape` Variable to set data point shapes by.

`facets` **[Deprecated]** Please use `rows` and `cols` instead.

`interact` Default TRUE. By default, plots are interactive. If set FALSE, all plots in the report will be static.

`show_plot` Show the plot.

`save_path` File path to save precision-recall results to.

`verbose` Print messages.

Value

list with data and precision recall and F1 plots

Examples

```
data("CnR_H3K27ac")
data("CnT_H3K27ac")
data("encode_H3K27ac")
peakfiles <- list(CnR_H3K27ac=CnR_H3K27ac, CnT_H3K27ac=CnT_H3K27ac)
reference <- list("encode_H3K27ac" = encode_H3K27ac)

pr_out <- plot_precision_recall(peakfiles = peakfiles,
                                reference = reference,
                                workers = 1)
```

`precision_recall` *Compute precision-recall*

Description

Compute precision and recall using each GRanges object in `peakfiles` as the "query" against each GRanges object in `reference` as the subject.

Usage

```
precision_recall(
  peakfiles,
  reference,
  thresholding_cols = c("total_signal", "qValue", "Peak Score"),
  initial_threshold = 0,
  n_threshold = 20,
  max_threshold = 1,
  cast = TRUE,
  workers = 1,
  verbose = TRUE,
  save_path = tempfile(fileext = "precision_recall.csv"),
  ...
)
```

Arguments

`peakfiles` A list of peak files as GRanges object and/or as paths to BED files. If paths are provided, EpiCompare imports the file as GRanges object. EpiCompare also accepts a list containing a mix of GRanges objects and paths.Files must be listed and named using `list()`. E.g. `list("name1"=file1, "name2"=file2)`. If no names are specified, default file names will be assigned.

`reference` A named list containing reference peak file(s) as GRanges object. Please ensure that the reference file is listed and named i.e. `list("reference_name" = reference_peak)`. If more than one reference is specified, individual reports for each reference will be generated. However, please note that specifying more than one reference can take awhile. If a reference is specified, it enables two analyses: (1) plot showing statistical significance of overlapping/non-overlapping peaks; and (2) ChromHMM of overlapping/non-overlapping peaks.

`thresholding_cols`
Depending on which columns are present, GRanges will be filtered at each threshold according to one or more of the following:

- "total_signal" : Used by the peak calling software SEACR. *NOTE*: Another SEACR column (e.g. "max_signal") can be used together or instead of "total_signal".
- "qValue"Used by the peak calling software MACS2/3. Should contain the negative log of the p-values after multiple testing correction.

- "Peak Score" : Used by the peak calling software HOMER.

`initial_threshold`
: Numeric threshold that was provided to SEACR (via the parameter `--ctrl`) when calling peaks without an IgG control.

`n_threshold`
: Number of thresholds to test.

`max_threshold`
: Maximum threshold to test.

`cast`
: Cast the data into a format that's more compatible with **ggplot2**.

`workers`
: Number of threads to parallelize across.

`verbose`
: Print messages.

`save_path`
: File path to save precision-recall results to.

`...`
: Arguments passed on to `bpplapply`

`apply_fun` Iterator function to use.

`register_now` Register the cores now with register (`TRUE`), or simply return the `BPPARAM object` (default: `FALSE`).

`use_snowparam` Whether to use SnowParam (default: `TRUE`) or MulticoreParam (`FALSE`) when parallelising across multiple `workers`.

`progressbar logical(1)` Enable progress bar (based on plyr:::progress_text).

`X` Any object for which methods `length`, `[`, and `[[` are implemented.

`FUN` The `function` to be applied to each element of `X`.

Value

Overlap

Examples

```
data("CnR_H3K27ac")
data("CnT_H3K27ac")
data("encode_H3K27ac")
peakfiles <- list(CnR_H3K27ac=CnR_H3K27ac, CnT_H3K27ac=CnT_H3K27ac)
reference <- list("encode_H3K27ac" = encode_H3K27ac)

pr_df <- precision_recall(peakfiles = peakfiles,
                          reference = reference,
                          workers = 1)
```

`precision_recall_matrix`

Create a precision-recall matrix

Description

Converts a list of peak files to a symmetric matrix where the y-axis indicates precision and the x-axis indicates recall.

Usage

```
precision_recall_matrix(peaklist, fill_diag = NA, verbose = TRUE)
```

Arguments

fill_diag	Fill the diagonal of the overlap matrix.
verbose	Print messages.

Value

matrix

---

predict_precision_recall

Predict precision-recall

Description

Predict specific values of precision or recall by fitting a model to a precision-recall curve. Predictions that are <0 will automatically be set to 0. Predictions that are >100 will automatically be set to 100.

Usage

```
predict_precision_recall(
  pr_df,
  fun = stats::loess,
  precision = seq(10, 100, 10),
  recall = seq(10, 100, 10)
)
```

Arguments

pr_df	Precision-recall data.frame generated by precision_recall.
fun	Function to fit the data with.
precision	Precision values to predict recall from.
recall	Recall values to predict precision from.

Value

A named list of fitted models and predictions.

Source

Fix for producing NAs from loess fun.

Examples

```
data("CnR_H3K27ac")
data("CnT_H3K27ac")
data("encode_H3K27ac")
peakfiles <- list(CnR_H3K27ac=CnR_H3K27ac, CnT_H3K27ac=CnT_H3K27ac)
reference <- list("encode_H3K27ac" = encode_H3K27ac)
pr_df <- precision_recall(peakfiles = peakfiles,
                          reference = reference)
predictions <- predict_precision_recall(pr_df = pr_df)
```

---

predict_values *Predict values*

Description

Fit a model and make predictions from it.

Usage

```
predict_values(df, fun, values, input_var, predicted_var)
```

Arguments

df	data.frame
fun	Function to fit the data with.
values	Values to make predictions from.
input_var	Input variable column name.
predicted_var	Predicted variable name.

Value

data.frame

---

prepare_blacklist *Prepare blacklist as GRanges*

Description

Selects the appropriate blacklist in a variety of conditions.

Usage

```
prepare_blacklist(
  blacklist,
  output_build,
  blacklist_build = NULL,
  verbose = TRUE
)
```

Arguments

output_build	Desired genome build for grlist to be lifted over to.
blacklist_build	Genome build of the blacklist. Only used when blacklist is a user-supplied GRanges object.
verbose	Print messages.

Value

A GRanges objects of blacklisted genomic regions from the relevant genome build.

---

prepare_genome_builds *Prepare genome builds*

Description

Parse the genome_build argument into peaklist_build and reference_build.

Usage

```
prepare_genome_builds(genome_build, blacklist = NULL)
```

Arguments

genome_build	A named list indicating the genome build used to generate each of the following inputs: • "peakfiles" : Genome build for the peakfiles input. Assumes genome build is the same for each element in the peakfiles list. • "reference" : Genome build for the reference input. • "blacklist" : Genome build for the blacklist input. Example input list: genome_build = list(peakfiles="hg38", reference="hg19", blacklist="hg19") Alternatively, you can supply a single character string instead of a list. This should *only* be done in situations where all three inputs (peakfiles, reference, blacklist) are of the same genome build. For example: genome_build = "hg19"

Supported genome builds are: "hg19", "hg38", "mm9" and "mm10".

`blacklist` A GRanges object containing blacklisted genomic regions. Blacklists included in **EpiCompare** are:

- `NULL` (default): Automatically selects the appropriate blacklist based on the `genome_build_output` argument.
- "hg19_blacklist": Regions of hg19 genome that have anomalous and/or unstructured signals. hg19_blacklist
- "hg38_blacklist": Regions of hg38 genome that have anomalous and/or unstructured signals. hg38_blacklist
- "mm10_blacklist": Regions of mm10 genome that have anomalous and/or unstructured signals. mm10_blacklist
- "mm9_blacklist": Blacklisted regions of mm10 genome that have been lifted over from mm10_blacklist. mm9_blacklist
- `<user_input>`: A custom user-provided blacklist in GRanges format.

Value

Named list.

`prepare_peaklist` *Prepare peaklist as GRanges*

Description

Prepare peaklist as GRanges

Usage

```
prepare_peaklist(peaklist, remove_empty = TRUE, as_grangeslist = FALSE)
```

Arguments

`peaklist`	A named list of peaks as GRanges or paths to BED files.
`remove_empty`	Remove any empty elements in the list.
`as_grangeslist`	Convert output to class GRangesList before returning.

Value

A list of GRanges objects

prepare_reference *Prepare referemce as GRanges*

Description

Prepare referemce as GRanges

Usage

```
prepare_reference(
  reference,
  max_elements = NULL,
  remove_empty = TRUE,
  as_list = TRUE,
  as_grangeslist = FALSE
)
```

Arguments

reference	A named list of GRanges objects, or a single GRanges object to be converted into a named list.
max_elements	Max number of elements to use within the list. Set to NULL (default) to use all elements.
remove_empty	Remove any empty elements in the list.
as_list	Return as a list.
as_grangeslist	Return as a GRangesList (overrides as_list).

Value

A list of GRanges objects

read_bowtie *Read bowtie*

Description

Read a bowtie file.

Usage

```
read_bowtie(path, verbose = TRUE)
```

Arguments

path	Path to bowtie file.
verbose	Print messages.

Value

data.table

`read_peaks` *Read peaks*

Description

Read peak files.

Usage

```
read_peaks(path, type, verbose = TRUE)
```

Arguments

`path`	Path to peak file.
`type`	File type to search for. Options include: • "<pattern>"Finds files matching an arbitrary regex pattern specified by user. • "peaks.stringent"Finds files ending in "*.stringent.bed$" • "peaks.consensus"Finds files ending in "*.consensus.peaks.bed$" • "peaks.consensus.filtered" Finds files ending in"*.consensus.peaks.filtered.awk.bed$" • "picard"Finds files ending in "*.target.markdup.MarkDuplicates.metrics.txt$"
`verbose`	Print messages.

Value

GRanges

`rebin_peaks` *Rebin peaks*

Description

Standardise a list of peak files by rebinning them into fixd-width tiles across the genome.

Usage

```
rebin_peaks(
  peakfiles,
  genome_build,
  intensity_cols = c("total_signal", "qValue", "Peak Score", "score"),
  bin_size = 5000,
  keep_chr = NULL,
  sep = c(":", "-"),
  drop_empty_chr = FALSE,
  as_sparse = TRUE,
  workers = check_workers(),
  verbose = TRUE,
  ...
)
```

Arguments

peakfiles	A list of peak files as GRanges object and/or as paths to BED files. If paths are provided, EpiCompare imports the file as GRanges object. EpiCompare also accepts a list containing a mix of GRanges objects and paths.Files must be listed and named using `list()`. E.g. `list("name1"=file1, "name2"=file2)`. If no names are specified, default file names will be assigned.
genome_build	The build of **all** peak and reference files to calculate the correlation matrix on. If all peak and reference files are not of the same build use liftover_grlist to convert them all before running. Genome build should be one of hg19, hg38, mm9, mm10.
intensity_cols	Depending on which columns are present, this value will be used to get quantiles and ultimately calculate the correlations: • "total_signal" : Used by the peak calling software SEACR. *NOTE*: Another SEACR column (e.g. "max_signal") can be used together or instead of "total_signal". • "qValue"Used by the peak calling software MACS2/3. Should contain the negative log of the p-values after multiple testing correction. • "Peak Score" : Used by the peak calling software HOMER.
bin_size	Default of 100. Base-pair size of the bins created to measure correlation. Use smaller value for higher resolution but longer run time and larger memory usage.
keep_chr	Which chromosomes to keep.
sep	Separator to be used after chromosome name (first item) and between start/end genomic coordinates (second item).
drop_empty_chr	Drop chromosomes that are not present in any of the `peakfiles` (default: `FALSE`).
as_sparse	Return the rebinned peaks as a sparse matrix (default: `TRUE`), which is more efficiently stored than a dense matrix (`FALSE`).
workers	Number of threads to parallelize across.
verbose	Print messages.
...	Arguments passed on to `bpplapply`

apply_fun Iterator function to use.

register_now Register the cores now with register (TRUE), or simply return the BPPARAM object (default: FALSE).

use_snowparam Whether to use SnowParam (default: TRUE) or MulticoreParam (FALSE) when parallelising across multiple workers.

progressbar logical(1) Enable progress bar (based on plyr:::progress_text).

X Any object for which methods length, [, and [[are implemented.

FUN The function to be applied to each element of X.

Value

Binned peaks matrix

Examples

```
data("CnR_H3K27ac")
data("CnT_H3K27ac")
peakfiles <- list(CnR_H3K27ac=CnR_H3K27ac, CnT_H3K27ac=CnT_H3K27ac)

#increasing bin_size for speed
peakfiles_rebinned <- rebin_peaks(peakfiles = peakfiles,
                                  genome_build = "hg19",
                                  bin_size = 5000,
                                  workers = 1)
```

---

remove_nonstandard_chrom

Remove non-standard chromosomes

Description

Remove non-standard chromosomes from a list of GRanges objects.

Usage

```
remove_nonstandard_chrom(
  grlist,
  keep_chr = paste0("chr", c(seq_len(22), "X", "Y")),
  verbose = TRUE
)
```

Arguments

grlist	Named list of GRanges objects.
keep_chr	Which chromosomes to keep.
verbose	Print messages.

Value

Named list of GRanges objects.

`report_command` *Report command*

Description

Reconstruct the EpiCompare command used to generate the current Rmarkdown report.

Usage

```
report_command(params, peaklist_tidy, reference_tidy)
```

Arguments

`params`	Parameters supplied to the Rmarkdown template.
`peaklist_tidy`	Post-processed target peaks.
`reference_tidy`	Post-processed reference peaks.

Value

String reconstructing R function call.

Examples

```
# report_command()
```

`report_header` *Report header*

Description

Generate a header for EpiCompare reports generated using the *EpiCompare.Rmd* template.

Usage

```
report_header()
```

Value

Header string to be rendering within Rmarkdown file.

Examples

```
report_header()
```

save_output *Save output*

Description

This function saves data frames and plots generated by EpiCompare.

Usage

```
save_output(
  save_output = FALSE,
  file,
  file_type,
  filename,
  outpath,
  interactive = FALSE,
  verbose = TRUE
)
```

Arguments

save_output	Default FALSE. If TRUE, outputs are saved.
file	Tables and plots to be saved.
file_type	Type of file to be saved. "data.frame", "ggplot", "image"
filename	Name of file.
outpath	Outpath
interactive	Default FALSE. If TRUE, interactive plots are saved as html.
verbose	Print messages.

Value

Saved data frames and plots.

set_min_max *Set min/max*

Description

Set the min/max values in a data.frame.

Usage

```
set_min_max(df, colname, min_val = 0, max_val = 100)
```

Arguments

df	data.frame
colname	Column name to check.
min_val	Minimum value.
max_val	Maximum value.

Value

data.frame

---

stopper *Stop messages*

Description

Conditionally print stop messages. Allows developers to easily control verbosity of functions, and meet Bioconductor requirements that dictate the stop message must first be stored to a variable before passing to stop.

Usage

```
stopper(..., v = TRUE)
```

Arguments

v	Whether to print messages or not.

Value

Null

---

tidy_chromosomes *Remove odd chromosomes from GRanges objects*

Description

This convenience function removes non-standard, mitochondrial, and/or sex chromosomes from any GRanges object.

Usage

```
tidy_chromosomes(
  gr,
  keep.X = TRUE,
  keep.Y = TRUE,
  keep.M = FALSE,
  keep.nonstandard = FALSE,
  genome = NULL
)
```

Arguments

gr	Any GRanges object, or any another object with associated seqinfo (or a Seqinfo object itself). The object should typically have a standard genome associated with it, e.g. genome(gr) <- "hg38". gr can also be a list of such GRanges objects.
keep.X, keep.Y, keep.M, keep.nonstandard	Logicals indicating which non-autosomes should be kept. By default, sex chromosomes are kept, but mitochondrial and non-standard chromosomes are removed.
genome	An optional string that, if supplied, will be used to set the genome of gr.

Details

This function is adapted from tidyChromosomes in the BRGenomics package licensed under the Artistic License 2.0. Original author: Mike DeBerardine <https://github.com/mdeber>

Standard chromosomes are defined using the standardChromosomes function from the GenomeInfoDb package.

Value

A GRanges object in which both ranges and seqinfo associated with trimmed chromosomes have been removed.

Author(s)

Mike DeBerardine

See Also

GenomeInfoDb::standardChromosomes

Examples

```
# make a GRanges
chrom <- c("chr2", "chr3", "chrX", "chrY", "chrM", "junk")
gr <- GenomicRanges::GRanges(seqnames = chrom,
              ranges = IRanges::IRanges(start = 2*(1:6), end = 3*(1:6)),
              strand = "+",
```

```
              seqinfo = GenomeInfoDb::Seqinfo(chrom))
GenomeInfoDb::genome(gr) <- "hg38"

gr

tidy_chromosomes(gr)

tidy_chromosomes(gr, keep.M = TRUE)

tidy_chromosomes(gr, keep.M = TRUE, keep.Y = FALSE)

tidy_chromosomes(gr, keep.nonstandard = TRUE)
```

`tidy_peakfile` *Tidy peakfiles in GRanges*

Description

This function filters peak files by removing peaks in blacklisted regions and in non-standard chromosomes. It also checks that the input list of peakfiles is named. If no names are provided, default file names will be used.

Usage

```
tidy_peakfile(peaklist, blacklist)
```

Arguments

`peaklist`	A named list of peak files as GRanges object. Objects must be named and listed using `list()`. e.g. `list("name1"=file1, "name2"=file2)` If not named, default names are assigned.
`blacklist`	Peakfile specifying blacklisted regions as GRanges object.

Value

list of GRanges object

Examples

```
### Load Data ###
data("encode_H3K27ac") # example peakfile GRanges object
data("CnT_H3K27ac") # example peakfile GRanges object
data("hg19_blacklist") # blacklist region for hg19 genome

### Create Named Peaklist ###
peaklist <- list("encode"=encode_H3K27ac, "CnT"=CnT_H3K27ac)

### Run ###
```

```
peaklist_tidy <- tidy_peakfile(peaklist = peaklist,
                               blacklist = hg19_blacklist)
```

`translate_genome` *Translate genome*

Description

Translate the name of a genome build from one format to another.

Usage

```
translate_genome(
  genome,
  style = c("UCSC", "Ensembl", "NCBI"),
  default_genome = NULL,
  omit_subversion = TRUE
)
```

Arguments

`genome`	A character vector of genomes equivalent to UCSC version or Ensembl Assemblies
`style`	A single value equivalent to "UCSC" or "Ensembl" specifying the output genome
`default_genome`	Default genome build when `genome` is `NULL`.
`omit_subversion`	Omit any subversion suffixes after the ".".

Value

Standardized genome build name as a character string.

Examples

```
genome <- translate_genome(genome="hg38", style="Ensembl")
genome2 <- translate_genome(genome="mm10", style="UCSC")
```

tss_plot *Read count frequency around TSS*

Description

This function generates a plot of read count frequency around TSS.

Usage

```
tss_plot(
  peaklist,
  txdb = NULL,
  tss_distance = c(-3000, 3000),
  conf = 0.95,
  resample = 500,
  interact = FALSE,
  workers = check_workers()
)
```

Arguments

peaklist	A list of peak files as GRanges object. Files must be listed and named using `list()`. e.g. `list("name1"=file1, "name2"=file2)` If not named, default file names will be assigned.
txdb	A TxDb annotation object from Bioconductor.
tss_distance	A vector specifying the distance upstream and downstream around transcription start sites (TSS). The default value is `c(-3000,3000)`; meaning peak frequency 3000bp upstream and downstream of TSS will be displayed.
conf	Confidence interval threshold estimated by bootstrapping (`0.95` means 95 Argument passed to plotAvgProf.
resample	Number of bootstrapped iterations to run. Argument passed to plotAvgProf.
interact	Default TRUE. By default, plots are interactive. If set FALSE, all plots in the report will be static.
workers	Number of cores to parallelise bootstrapping across. Argument passed to plotAvgProf.

Value

A named list of profile plots.

Examples

```
### Load Data ###
data("CnT_H3K27ac") # example peaklist GRanges object
data("CnR_H3K27ac") # example peaklist GRanges object
### Create Named Peaklist ###
```

```
peaklist <- list("CnT"=CnT_H3K27ac, "CnR"=CnR_H3K27ac)
my_plot <- tss_plot(peaklist = peaklist,
                    tss_distance=c(-50,50),
                    workers = 1)
```

`width_boxplot` *Peak width boxplot*

Description

This function creates boxplots showing the distribution of widths in each peak file.

Usage

```
width_boxplot(peaklist, interact = FALSE)
```

Arguments

`peaklist`	A list of peak files as GRanges object. Files must be named and listed using `list()`. e.g. `list("name1"=file1, "name2"=file2)`
`interact`	Default TRUE. By default, plots are interactive. If set FALSE, all plots in the report will be static.

Value

A boxplot of peak widths.

Examples

```
### Load Data ###
data("encode_H3K27ac") # example peaklist GRanges object
data("CnT_H3K27ac") # example peaklist GRanges object
peaklist <- list("encode"=encode_H3K27ac, "CnT"=CnT_H3K27ac)
my_plot <- width_boxplot(peaklist = peaklist)
```

`write_example_peaks` *Write example peaks*

Description

Write example peaks datasets to disk.

Usage

```
write_example_peaks(
  dir = file.path(tempdir(), "processed_results"),
  datasets = c("encode_H3K27ac", "CnT_H3K27ac", "CnR_H3K27ac")
)
```

Arguments

dir	Directory to save peak files to.
datasets	Example datasets from **EpiCompare** to write.

Value

Named vector of paths to saved peak files.

Examples

```
save_paths <- EpiCompare::write_example_peaks()
```

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