Package: EpiCompare (via r-universe)

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Type Package

Title Comparison, Benchmarking & QC of Epigenomic Datasets

Version 1.16.0

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.

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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), Seqinfo (>= 0.99.2), GenomeInfoDb (>= 1.45.7), 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

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Contents

`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)
```

---

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()
```

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,
  peak_score_plot = FALSE,
  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 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.

`peak_score_plot`
Default FALSE. If TRUE, the report includes boxplots showing the distribution of peak scores in each peak file.

`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)
```

---

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)
```

---

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)
```

---

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")
```

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_peak_scores *Plot Peak Scores boxplot*

Description

This function creates a boxplot showing the distribution of peak scores in each peak file.

Usage

```
plot_peak_scores(
  peaklist,
  score_cols = c("score", "signal.value"),
  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)
score_cols	Depending on which columns are present, this value will be used to get peak scores to plot from the metadata columns.
interact	Default TRUE. By default, plots are interactive. If set FALSE, all plots in the report will be static.

Value

A boxplot of peak scores.

Examples

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

---

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,
  rows = "peaklist2",
```

```
  cols = NULL,
  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.
rows, cols	A set of variables or expressions quoted by `vars()` and defining faceting groups on the rows or columns dimension. The variables can be named (the names are passed to `labeller`). For compatibility with the classic interface, `rows` can also be a formula with the rows (of the tabular display) on the LHS and the columns (of the tabular display)

	on the RHS; the dot in the formula is used to indicate there should be no faceting on this dimension (either row or column).
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)
```

`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)
```

`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)
```

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()
```

`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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