Package 'GRaNIE'

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Title GRaNIE: Reconstruction cell type specific gene regulatory networks including enhancers using single-cell or bulk chromatin accessibility and RNA-seq data

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Description Genetic variants associated with diseases often affect non-coding regions, thus likely having a regulatory role. To understand the effects of genetic variants in these regulatory regions, identifying genes that are modulated by specific regulatory elements (REs) is crucial. The effect of gene regulatory elements, such as enhancers, is often cell-type specific, likely because the combinations of transcription factors (TFs) that are regulating a given enhancer have cell-type specific activity. This TF activity can be quantified with existing tools such as diffTF and captures differences in binding of a TF in open chromatin regions. Collectively, this forms a gene regulatory network (GRN) with cell-type and data-specific TF-RE and RE-gene links. Here, we reconstruct such a GRN using single-cell or bulk RNAseq and open chromatin (e.g., using ATACseq or ChIPseq for open chromatin marks) and optionally (Capture) Hi-C data. Our network contains different types of links, connecting TFs to regulatory elements, the latter of which is connected to genes in the vicinity or within the same chromatin domain (TAD). We use a statistical framework to assign empirical FDRs and weights to all links using a permutation-based approach.

Imports futile.logger, checkmate, patchwork (>= 1.2.0), reshape2, data.table, matrixStats, Matrix, GenomicRanges, RColorBrewer, ComplexHeatmap, DESeq2, circlize, progress, utils, methods, stringr, tools, scales, igraph, S4Vectors, ggplot2, rlang, Biostrings, GenomeInfoDb (>= 1.34.8), SummarizedExperiment, forcats, gridExtra, limma, tidyselect, readr, grid, tidyr (>= 1.3.0), dplyr, stats, grDevices, graphics, magrittr, tibble, viridis, colorspace, biomaRt, topGO, AnnotationHub, ensembldb

Depends R (>= 4.2.0)

Suggests knitr, BSgenome.Hsapiens.UCSC.hg19, BSgenome.Hsapiens.UCSC.hg38, BSgenome.Mmusculus.UCSC.mm39, BSgenome.Mmusculus.UCSC.mm10, BSgenome.Mmusculus.UCSC.mm9, BSgenome.Rnorvegicus.UCSC.rn6, BSgenome.Rnorvegicus.UCSC.rn7, BSgenome.Dmelanogaster.UCSC.dm6,

BSgenome.Mmulatta.UCSC.rheMac10,
TxDb.Hsapiens.UCSC.hg19.knownGene,
TxDb.Hsapiens.UCSC.hg38.knownGene,
TxDb.Mmusculus.UCSC.mm39.knownGene,
TxDb.Mmusculus.UCSC.mm10.knownGene,
TxDb.Mmusculus.UCSC.mm9.knownGene,
TxDb.Rnorvegicus.UCSC.rn6.refGene,
TxDb.Rnorvegicus.UCSC.rn7.refGene,
TxDb.Dmelanogaster.UCSC.dm6.ensGene,
TxDb.Mmulatta.UCSC.rheMac10.refGene, org.Hs.eg.db,
org.Mm.eg.db, org.Rn.eg.db, org.Dm.eg.db, org.Mmu.eg.db, IHW,
clusterProfiler, ReactomePA, DOSE, BiocFileCache, ChIPseeker,
testthat (>= 3.0.0), BiocStyle, csaw, BiocParallel, WGCNA,
variancePartition, purrr, EDASeq, JASPAR2022, JASPAR2024,
RSQLite, TFBSTools, motifmatchr, rbioapi, LDlinkR

VignetteBuilder knitr

biocViews Software, GeneExpression, GeneRegulation, NetworkInference,
GeneSetEnrichment, BiomedicalInformatics, Genetics,
Transcriptomics, ATACSeq, RNASeq, GraphAndNetwork, Regression,
Transcription, ChIPSeq

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Author Christian Arnold [cre, aut],
Judith Zaugg [aut],
Rim Moussa [aut],
Armando Reyes-Palomares [ctb],
Giovanni Palla [ctb],
Maksim Kholmatov [ctb]

Maintainer Christian Arnold <chrarnold@web.de>

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addConnections_peak_gene *Add peak-gene connections to a GRN object*

Description

After the execution of this function, QC plots can be plotted with the function plotDiagnosticPlots_peakGene unless this has already been done by default due to plotDiagnosticPlots = TRUE

Usage

```
addConnections_peak_gene(
  GRN,
  overlapTypeGene = "TSS",
  corMethod = "pearson",
  promoterRange = 250000,
  TADs = NULL,
  TADs_mergeOverlapping = FALSE,
  knownLinks = NULL,
  knownLinks_separator = c(":", "-"),
  knownLinks_useExclusively = FALSE,
  shuffleRNACounts = TRUE,
  nCores = 4,
  plotDiagnosticPlots = TRUE,
  plotGeneTypes = list(c("all"), c("protein_coding")),
  outputFolder = NULL,
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
overlapTypeGene	Character. "TSS" or "full". Default "TSS". If set to "TSS", only the TSS of the gene is used as reference for finding genes in the neighborhood of a peak. If set to "full", the whole annotated gene (including all exons and introns) is used instead.
corMethod	Character. One of pearson, spearman or bicor. Default pearson. Method for calculating the correlation coefficient. For pearson and spearman , see cor for details. bicor denotes the *biweight midcorrelation*, a correlation measure based on medians as calculated by WGCNA::bicorAndPvalue. Both spearman and bicor are considered more robust measures that are less prone to be affected by outliers.

promoterRange
: Integer >=0. Default 250000. The size of the neighborhood in bp to correlate peaks and genes in vicinity. Only peak-gene pairs will be correlated if they are within the specified range. Increasing this value leads to higher running times and more peak-gene pairs to be associated, while decreasing results in the opposite.

TADs
: Data frame with TAD domains. Default NULL. If provided, the neighborhood of a peak is defined by the TAD domain the peak is in rather than a fixed-sized neighborhood. The expected format is a BED-like data frame with at least 3 columns in this particular order: chromosome, start, end, the 4th column is optional and will be taken as ID column. All additional columns as well as column names are ignored. For the first 3 columns, the type is checked as part of a data integrity check.

TADs_mergeOverlapping
: TRUE or FALSE. Default FALSE. Should overlapping TADs be merged? Only relevant if TADs are provided.

knownLinks
: NULL or a data frame with exactly two columns. Both columns must be of type character and they must both contain genomic coordinates in the usual format: chr:start-end, while the 2 separators between the three elements can be chosen by the user. The first column denotes the **bait**, the promoter coordinates that are overlapped with the genes (usually their TSS, unless specified otherwise via the parameter overlapTypeGene, while the second column denotes the **other end (OE)** coordinates, which is overlapped with the peaks/enhancers from the GRN object. **NOTE: The provided column names are ignored and column 1 is interpreted as bait column and column 2 as OE column unless column names are exactly 'bait' and 'OE'.**. For more details, see the Workflow vignette.)

knownLinks_separator
: Character vector of length 1 or 2. Default c(":", "-"). Separator(s) for the character columns that specify the genomic locations. The first entry splits the chromosome from the position, while the second entry splits the start and end coordinates. If only one separator is given, the same will be used for both.

knownLinks_useExclusively
: TRUE or FALSE. Default FALSE. If kept at FALSE (the default), specified knownLinks will be used in addition to the regular peak-gene links that are identified via the default method. If set to TRUE, only the knownLinks will be used.

shuffleRNACounts
: TRUE or FALSE. Default TRUE. Should the RNA sample labels be shuffled in addition to testing random peak-gene pairs for the background? When set to FALSE, only peak-gene pairs are shuffled, but for each pair, the counts from peak and RNA that are correlated are matched (i.e., sample 1 counts from peak data are compared to sample 1 counts from RNA). If set to TRUE, however, the RNA sample labels are in addition shuffled so that sample 1 counts from peak data are compared to sample 4 data from RNA, for example. Shuffling truly randomizes the resulting background eGRN. Note that this parameter and its influence is still being investigated. Until version 1.0.7, this parameter (although not existent explicitly) was implicitly set to TRUE.

nCores — Integer >0. Default 1. Number of cores to use. A value >1 requires the BiocParallel package (as it is listed under Suggests, it may not be installed yet).

plotDiagnosticPlots — TRUE or FALSE. Default TRUE. Run and plot various diagnostic plots? If set to TRUE, PDF files will be produced and saved in the output directory (in a subfolder called plots).

plotGeneTypes — List of character vectors. Default list(c("all"), c("protein_coding")). Each list element may consist of one or multiple gene types that are plotted collectively in one PDF. The special keyword "all" denotes all gene types that are found (be aware: this typically contains 20+ gene types, see https://www.gencodegenes.org/pages/biotypes.html for details).

outputFolder — Character or NULL. Default NULL. If set to NULL, the default output folder as specified when initiating the object in initializeGRN will be used. Otherwise, all output from this function will be put into the specified folder. If a folder is provided, while we recommend specifying an absolute path, a relative one also works.

forceRerun — TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

An updated GRN object, with additional information added from this function.

See Also

plotDiagnosticPlots_peakGene

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = addConnections_peak_gene(GRN, promoterRange=10000, plotDiagnosticPlots = FALSE)
```

---

addConnections_TF_peak

Add TF-peak connections to a GRN object

Description

After the execution of this function, QC plots can be plotted with the function plotDiagnosticPlots_TFPeaks unless this has already been done by default due to plotDiagnosticPlots = TRUE

Usage

```
addConnections_TF_peak(
  GRN,
  plotDiagnosticPlots = TRUE,
  plotDetails = FALSE,
  outputFolder = NULL,
  corMethod = "pearson",
  connectionTypes = c("expression"),
  removeNegativeCorrelation = c(FALSE),
  maxFDRToStore = 0.3,
  addForBackground = TRUE,
  useGCCorrection = FALSE,
  percBackground_size = 75,
  percBackground_resample = TRUE,
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
plotDiagnosticPlots	TRUE or FALSE. Default TRUE. Run and plot various diagnostic plots? If set to TRUE, PDF files will be produced and saved in the output directory (in a subfolder called plots).
plotDetails	TRUE or FALSE. Default FALSE. Print additional plots that may help for debugging and QC purposes? Note that these plots are currently less documented or not at all.
outputFolder	Character or NULL. Default NULL. If set to NULL, the default output folder as specified when initiating the object in initializeGRN will be used. Otherwise, all output from this function will be put into the specified folder. If a folder is provided, while we recommend specifying an absolute path, a relative one also works.
corMethod	Character. One of pearson, spearman or bicor. Default pearson. Method for calculating the correlation coefficient. For pearson and spearman , see cor for details. bicor denotes the *biweight midcorrelation*, a correlation measure based on medians as calculated by WGCNA::bicorAndPvalue. Both spearman and bicor are considered more robust measures that are less prone to be affected by outliers.
connectionTypes	Character vector. Default expression. Vector of connection types to include for the TF-peak connections. If an additional connection type is specified here, it has to be available already within the object (EXPERIMENTAL). See the function addData_TFActivity for details.
removeNegativeCorrelation	Vector of TRUE or FALSE. Default FALSE. EXPERIMENTAL. Must be a logical vector of the same length as the parameter connectionType. Should negatively correlated TF-peak connections be removed for the specific connection type?

For connection type expression, the default is FALSE, while for any TF Activity related connection type, we recommend setting this to TRUE.

maxFDRToStore Numeric[0,1]. Default 0.3. Maximum TF-peak FDR value to permanently store a particular TF-peak connection in the object? This parameter has a large influence on the overall memory size of the object, and we recommend not storing connections with a high FDR due to their sheer number.

addForBackground
TRUE or FALSE. Default TRUE. Add connections also for background data. Leave at TRUE unless you know what you are doing.

useGCCorrection
TRUE or FALSE. Default FALSE. EXPERIMENTAL. Should a GC-matched background be used when calculating FDRs? For more details, see the Package Details vignette.

percBackground_size
Numeric[0,100]. Default 75. EXPERIMENTAL. Percentage of the background to use as basis for sampling. If set to 0, an automatic iterative procedure will identify the maximum percentage so that all relevant GC bins with a rel. frequency above 5% from the foreground can be matched. For more details, see the Package Details vignette. Only relevant if useGCCorrection is set to TRUE, ignored otherwise.

percBackground_resample
TRUE or FALSE. Default TRUE. EXPERIMENTAL. Should resampling be enabled for those GC bins for which not enough background peaks are available?. For more details, see the Package Details vignette. Only relevant if useGCCorrection is set to TRUE, ignored otherwise.

forceRerun TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

An updated GRN object, with additional information added from this function.

See Also

plotDiagnosticPlots_TFPeaks

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = addConnections_TF_peak(GRN, plotDiagnosticPlots = FALSE, forceRerun = FALSE)
```

addData *Add data to a GRN object.*

Description

This function adds both RNA and peak data to a GRN object, along with data normalization. In addition, and highly recommended, sample metadata can be optionally provided.

Usage

```
addData(
  GRN,
  counts_peaks,
  normalization_peaks = "DESeq2_sizeFactors",
  idColumn_peaks = "peakID",
  counts_rna,
  normalization_rna = "limma_quantile",
  idColumn_RNA = "ENSEMBL",
  sampleMetadata = NULL,
  additionalParams.l = list(),
  allowOverlappingPeaks = FALSE,
  keepOriginalReadCounts = FALSE,
  EnsemblVersion = NULL,
  genomeAnnotationSource = "AnnotationHub",
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
counts_peaks	Data frame. No default. Counts for the peaks, with raw or normalized counts for each peak (rows) across all samples (columns). In addition to the count data, it must also contain one ID column with a particular format, see the argument idColumn_peaks below. Row names are ignored, column names must be set to the sample names and must match those from the RNA counts and the sample metadata table.
normalization_peaks	Character. Default DESeq2_sizeFactors. Normalization procedure for peak data. Must be one of limma_cyclicloess, limma_quantile, limma_scale, csaw_cyclicLoess_orig, csaw_TMM, EDASeq_GC_peaks, gcqn_peaks, DESeq2_sizeFactors, none.
idColumn_peaks	Character. Default peakID. Name of the column in the counts_peaks data frame that contains peak IDs. The required format must be chr:start-end, with chr denoting the abbreviated chromosome name, and start and end the begin and end of the peak coordinates, respectively. End must be bigger than start. Examples for valid peak IDs are chr1:400-800 or chrX:20-25.

counts_rna
: Data frame. No default. Counts for the RNA-seq data, with raw or normalized counts for each gene (rows) across all samples (columns). In addition to the count data, it must also contain one ID column with a particular format, see the argument idColumn_rna below. Row names are ignored, column names must be set to the sample names and must match those from the RNA counts and the sample metadata table.

normalization_rna
: Character. Default limma_quantile. Normalization procedure for peak data. Must be one of limma_cyclicloess, limma_quantile, limma_scale, csaw_cyclicLoess_orig, csaw_TMM, DESeq2_sizeFactors, none.

idColumn_RNA
: Character. Default ENSEMBL. Name of the column in the counts_rna data frame that contains Ensembl IDs.

sampleMetadata
: Data frame. Default NULL. Optional, additional metadata for the samples, such as age, sex, gender etc. If provided, the @seealso [plotPCA_all()] function can then incorporate and plot it. Sample names must match with those from both peak and RNA-Seq data. The first column is expected to contain the sample IDs, the actual column name is irrelevant.

additionalParams.l
: Named list. Default list(). Additional parameters for the chosen normalization method. Currently, only the GC-aware normalization methods EDASeq_GC_peaks and gcqn_peaks are supported here. Both support the parameters roundResults (logical flag, TRUE or FALSE) and nBins (Integer > 0), and EDASeq_GC_peaks supports three additional parameters: withinLane_method (one of: "loess","median","upper","full") and betweenLane_method (one of: "median","upper","full"). For more information, see the EDASeq vignette.

allowOverlappingPeaks
: TRUE or FALSE. Default FALSE. Should overlapping peaks be allowed (then only a warning is issued when overlapping peaks are found) or (the default) should an error be raised?

keepOriginalReadCounts
: TRUE or FALSE. Default FALSE. Should the original read counts as provided to the function be kept in addition to storing the rad counts after a (if any) normalization? This increases the memory footprint of the object because 2 additional count matrices have to be stored.

EnsemblVersion
: NULL or Character(1). Default NULL. The Ensembl version to use for genome annotation retrieval via biomaRt, which is only used to populate the gene annotation metadata that is stored in GRN@annotation$genes. By default (NULL), the newest version is selected for the most recent genome assembly versions is used (see biomaRt::listEnsemblArchives() for supported versions). This parameter can override this to use a custom (older) version instead.

genomeAnnotationSource
: AnnotationHub or biomaRt. Default AnnotationHub. Annotation source to retrieve genome annotation data from.

forceRerun
: TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Details

If the ChIPseeker package is installed, additional peak annotation is provided in the annotation slot and a peak annotation QC plot is produced as part of peak-gene QC. This is fully optional, however, and has no consequences for downstream functions. Normalizing the data sensibly is very important. When quantileis chose, limma::normalizeQuantiles is used, which in essence does the following: Each quantile of each column is set to the mean of that quantile across arrays. The intention is to make all the normalized columns have the same empirical distribution. This will be exactly true if there are no missing values and no ties within the columns: the normalized columns are then simply permutations of one another.

Value

An updated GRN object, with added data from this function(e.g., slots GRN@data$peaks and GRN@data$RNA)

See Also

plotPCA_all

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
# library(readr)
# rna.df   = read_tsv("https://www.embl.de/download/zaugg/GRaNIE/rna.tsv.gz")
# peaks.df = read_tsv("https://www.embl.de/download/zaugg/GRaNIE/peaks.tsv.gz")
# meta.df  = read_tsv("https://www.embl.de/download/zaugg/GRaNIE/sampleMetadata.tsv.gz")
# GRN = loadExampleObject()
# We omit sampleMetadata = meta.df in the following line, becomes too long otherwise
# GRN = addData(GRN, counts_peaks = peaks.df, counts_rna = rna.df, forceRerun = FALSE)
```

---

addData_TFActivity *Add TF activity data to GRN object using a simplified procedure for estimating it. EXPERIMENTAL.*

Description

We do not yet provide full support for this function. It is currently being tested. Use at our own risk.

Usage

```
addData_TFActivity(
  GRN,
  normalization = "cyclicLoess",
  name = "TF_activity",
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
normalization	Character. Default cyclicLoess. One of cyclicLoess, sizeFactors, quantile, or none. Normalization procedure. When set to cyclicLoess, the csaw package is required (as it is listed under Suggests, it may not be installed).
name	Name in object under which it should be stored. This corresponds to the connectionType afterwards that some functions iterate over.
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

An updated GRN object, with added data from this function (GRN@data$TFs[[name]] in particular, with name referring to the value of tje name parameter)

---

addSNPData *Add SNP data to a GRN object and associate SNPs to peaks.*

Description

This function accepts a vector of SNP IDs (rsID), retrieves their genomic positions and overlaps them with the peaks to extend the peak metadata ('GRN@data$peaks$counts_metadata') by storing the number, positions and rsids of all overlapping SNPs per peak (new columns starting with 'SNP_'). Optionally, SNPs in LD with the user-provided SNPs can be identified using the LDlinkR package. Note that only SNPs in LD are associated with a peak for those SNPs directly overlapping a peak. That is, if a user-provided SNP does not overlap with any peak, neither the SNP itself nor any of the SNPs in LD will be associated with any peak, even if an LD SNP overlaps another peak. The results of are stored in GRN@annotation$SNPs (full, unfiltered table) and GRN@annotation$SNPs_filtered (filtered table), and rapid re-filtering is possible without re-querying the database (time-consuming)

Usage

```
addSNPData(
  GRN,
  SNP_IDs,
  EnsemblVersion = NULL,
  add_SNPs_LD = FALSE,
  requeryLD = FALSE,
  population = "CEU",
  r2d = "r2",
  token = NULL,
  filter = "R2 > 0.8",
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
SNP_IDs	Character vector. No default. Vector of SNP IDs (rsID) that should be integrated and overlapped with the peaks.
EnsemblVersion	NULL or Character(1). Default NULL. Only relevant if source is not set to custom, ignored otherwise. The Ensembl version to use for the retrieval of gene IDs from their provided database names (e.g., JASPAR) via biomaRt. By default (NULL), the newest version is selected for the most recent genome assembly versions is used (see biomaRt::listEnsemblArchives() for supported versions). This parameter can override this to use a custom (older) version instead.
add_SNPs_LD	TRUE or FALSE. Default FALSE. Should SNPs in LD with any of the user-provided SNPs that overlap a peak be identified and added to the peak? If set to TRUE, LDlinkR::LDproxy_batch will be used to identify SNPs in LD based on the user-provided SNP_IDs argument, a specific (set of) populations (argument population) and a value for r2d. The full table (stored in GRN@annotation$SNPs) is then subsequently filtered, see also the filter argument.
requeryLD	TRUE or FALSE. Default FALSE. Only applicable if add_SNPs_LD = TRUE and ignored otherwise. Should LDlinkR::LDproxy_batch be re-executed if already present? As this is very time-consuming, querying the database is only performed if this parameter is set to TRUE or if GRN@annotation$SNPs is missing.
population	Character vector. Default CEU. Only applicable if add_SNPs_LD = TRUE and ignored otherwise. Population code(s) from the 1000 Genomes project to be used for LDlinkR::LDproxy_batch. Multiple codes are allowed. For all valid codes, see https://ftp.1000genomes.ebi.ac.uk/vol1/ftp/README_populations.md
r2d	r2 or d. Default r2. Only applicable if add_SNPs_LD = TRUE and ignored otherwise. See the help of the function LDlinkR::LDproxy_batch for more details.
token	Character or NULL. Default NULL. Only applicable if add_SNPs_LD = TRUE and ignored otherwise. LDlink provided user token. Register for token at https://ldlink.nih.gov/?tab=apiaccess Has to be done only once and is very simple and straight forward but unfortunately necessary. An example, non-functional token is 2c49a3b54g04.
filter	Character. Default R2 > 0.8. Only applicable if add_SNPs_LD = TRUE and ignored otherwise. Filter criteria for the output table as generated by LDlinkR::LDproxy_batch. dplyr::filter style is used to specify filters, and multiple filtering criteria can be used (e.g., R2 > 0.8 & MAF > 0.01). The filtered table is stored in GRN@annotation$SNPs_filtered. Note that re-filtering is quick without the need to re-query the database unless requeryLD = TRUE.
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Details

'biomaRt' is used to retrieve genomic positions for the user-defined SNPs, which can take a long time depending on the number of SNPs provided. Similarly, querying the LDlink servers may take a long time.

Value

An updated GRN object, with additional information added from this function.

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = addSNPData(GRN, SNP_IDs = c("rs7570219", "rs6445264", "rs12067275"), forceRerun = FALSE)
```

---

addTFBS *Add TFBS to a GRN object.*

Description

For this, a folder that contains one TFBS file per TF in bed or bed.gz format must be given (see details). The folder must also contain a so-called translation table, see the argument `translationTable` for details. We provide example files for selected supported genome assemblies (hg19, hg38 and mm10, mm39) that are fully compatible with GRaNIE as separate downloads. For more information, check https://difftf.readthedocs.io/en/latest/chapter2.html#dir-tfbs.

Usage

```
addTFBS(
  GRN,
  source = "custom",
  motifFolder = NULL,
  TFs = "all",
  translationTable = "translationTable.csv",
  translationTable_sep = " ",
  filesTFBSPattern = "_TFBS",
  fileEnding = ".bed",
  nTFMax = NULL,
  EnsemblVersion = NULL,
  JASPAR_useSpecificTaxGroup = NULL,
  JASPAR_removeAmbiguousTFs = TRUE,
  forceRerun = FALSE,
  ...
)
```

Arguments

GRN	Object of class GRN
source	Character. One of `custom`, `JASPAR2022` or `JASPAR2024`. Default `custom`. If a custom source is being used, further details about the motif folder and files will be provided (see the other function arguments). If set to `JASPAR2022`, the JASPAR2022 database is used. If set to `JASPAR2024`, the JASPAR2024 database is used.

motifFolder Character. No default. Only relevant if source = "custom". Path to the folder that contains the TFBS predictions. The files must be in BED format, 6 columns, one file per TF. See the other parameters for more details. The folder must also contain a so-called translation table, see the argument translationTable for details.

TFs Character vector. Default all. Only relevant if source = "custom". Vector of TF names to include. The special keyword all can be used to include all TF found in the folder as specified by motifFolder. If all is specified anywhere, all TFs will be included. TF names must otherwise match the file names that are found in the folder, without the file suffix.

translationTable
Character. Default translationTable.csv. Only relevant if source = "custom". Name of the translation table file that is also located in the folder along with the TFBS files. This file must have the following structure: at least 2 columns, called ENSEMBL and ID. ID denotes the ID for the TF that is used throughout the pipeline (e.g., AHR) and the prefix of how the corresponding file is called (e.g., AHR.0.B if the file for AHR is called AHR.0.B_TFBS.bed.gz), while ENSEMBL denotes the ENSEMBL ID (dot suffix; e.g., ENSG00000106546, are removed automatically if present).

translationTable_sep
Character. Default " " (white space character). Only relevant if source = "custom". The column separator for the translationTable file.

filesTFBSPattern
Character. Default "_TFBS". Only relevant if source = "custom". Suffix for the file names in the TFBS folder that is not part of the TF name. Can be empty. For example, for the TF CTCF, if the file is called CTCF.all.TFBS.bed, set this parameter to ".all.TFBS".

fileEnding Character. Default ".bed". Only relevant if source = "custom". File ending for the files from the motif folder.

nTFMax NULL or Integer[1,]. Default NULL. Maximal number of TFs to import. Can be used for testing purposes, e.g., setting to 5 only imports 5 TFs even though the whole motifFolder has many more TFs defined.

EnsemblVersion NULL or Character(1). Default NULL. Only relevant if source is not set to custom, ignored otherwise. The Ensembl version to use for the retrieval of gene IDs from their provided database names (e.g., JASPAR) via biomaRt. By default (NULL), the newest version is selected for the most recent genome assembly versions is used (see biomaRt::listEnsemblArchives() for supported versions). This parameter can override this to use a custom (older) version instead.

JASPAR_useSpecificTaxGroup
NULL or Character(1). Default NULL. Should a tax group instead of th specific genome assembly be used for retrieving the TF list? This is useful for genomes that are not human or mouse for which JASPAR otherwise returns too few TFs otherwise. If set to NULL, the specific genome version as provided in the object is used within TFBSTools::getMatrixSet in the opts list for species, while tax_group will be used instead if this argument is not set to NULL. For example, it can be set to vertebrates to use the vertebrates TF collection. For more details, see ?TFBSTools::getMatrixSet.

JASPAR_removeAmbiguousTFs
: TRUE or FALSE. Default TRUE. Remove TFs for which the name as provided b JASPAR cannot be mapped uniquely to one and only Ensembl ID? By default (NULL), the newest version is selected (see biomaRt::listEnsemblArchives() for supported versions). This parameter can override this to use a custom (older) version instead.

forceRerun
: TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

...
: Additional named elements for the opts function argument from ?TFBSTools::getMatrixSet that is used to query the JASPAR database.

Value

An updated GRN object, with additional information added from this function(GRN@annotation$TFs in particular)

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
```

---

add_featureVariation *Quantify and interpret multiple sources of biological and technical variation for features (TFs, peaks, and genes) in a GRN object*

Description

Runs the main function fitExtractVarPartModel of the package variancePartition: Fits a linear (mixed) model to estimate contribution of multiple sources of variation while simultaneously correcting for all other variables for the features in a GRN object (TFs, peaks, and genes) given particular metadata. The function reports the fraction of variance attributable to each metadata variable. **Note: The results are not added to** GRN@connections$all.filtered**, rerun the function** getGRNConnections **and set** include_variancePartitionResults **to** TRUE **to do so**. The results object is stored in GRN@stats$variancePartition and can be used for the various diagnostic and plotting functions from variancePartition.

Usage

```
add_featureVariation(
  GRN,
  formula = "auto",
  metadata = c("all"),
  features = "all_filtered",
  nCores = 1,
  forceRerun = FALSE,
  ...
)
```

Arguments

GRN	Object of class GRN
formula	Character(1). Either auto or a manually defined formula to be used for the model fitting. Default auto. Must include only terms that are part of the metadata as specified with the metadata parameter. If set to auto, the formula will be build automatically based on all metadata variables as specified with the metadata parameter. By default, numerical variables will be modeled as fixed effects, while variables that are defined as factors or can be converted to factors (characters and logical variables) are modeled as random effects as recommended by the variancePartition package.
metadata	Character vector. Default all. Vector of column names from the metadata data frame that was provided when using the function addData. Must either contain the special keyword all to denote that all (!) metadata columns from GRN@data$metadata are taken or if not, a subset of the column names from GRN@data$metadatato include in the model fitting for fitExtractVarPartModel..
features	Character(1). Either all_filtered or all. Default all_filtered. Should variancePartition only be run for the features (TFs, peaks and genes) from the filtered set of connections (the result of filterGRNAndConnectGenes) or for all genes that are defined in the object? If set to all, the running time is greatly increased.
nCores	Integer >0. Default 1. Number of cores to use. A value >1 requires the BiocParallel package (as it is listed under Suggests, it may not be installed yet).
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.
...	Additional parameters passed on to variancePartition::fitExtractVarPartModel beyond exprObj, formula and data. See the function help for more information

Details

The normalized count matrices are used as input for fitExtractVarPartModel.

Value

An updated GRN object, with additional information added from this function to GRN@stats$variancePartition as well as the elements genes, consensusPeaks and TFs within GRN@annotation. As noted above, the results are not added to GRN@connections$all.filtered; rerun the function getGRNConnections and set include_variancePartitionResults to TRUE to include the results in the eGRN output table.

See Also

addData

getGRNConnections

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
# GRN = loadExampleObject()
# GRN = add_featureVariation(GRN, metadata = c("mt_frac"), forceRerun = TRUE)
```

---

add_TF_gene_correlation

Add TF-gene correlations to a GRN object.

Description

The information is currently stored in GRN@connections$TF_genes.filtered. Note that raw p-values are not adjusted.

Usage

```
add_TF_gene_correlation(
  GRN,
  corMethod = "pearson",
  nCores = 1,
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
corMethod	Character. One of pearson, spearman or bicor. Default pearson. Method for calculating the correlation coefficient. For pearson and spearman , see cor for details. bicor denotes the *biweight midcorrelation*, a correlation measure based on medians as calculated by WGCNA::bicorAndPvalue. Both spearman and bicor are considered more robust measures that are less prone to be affected by outliers.
nCores	Integer >0. Default 1. Number of cores to use. A value >1 requires the BiocParallel package (as it is listed under Suggests, it may not be installed yet).
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

An updated GRN object, with additional information added from this function.

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = add_TF_gene_correlation(GRN, forceRerun = FALSE)
```

AR_classification_wrapper *Run the activator-repressor classification for the TFs for a GRN object*

Description

Run the activator-repressor classification for the TFs for a GRN object

Usage

```
AR_classification_wrapper(
  GRN,
  significanceThreshold_Wilcoxon = 0.05,
  plot_minNoTFBS_heatmap = 100,
  deleteIntermediateData = TRUE,
  plotDiagnosticPlots = TRUE,
  outputFolder = NULL,
  corMethod = "pearson",
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
significanceThreshold_Wilcoxon	Numeric[0,1]. Default 0.05. Significance threshold for Wilcoxon test that is run in the end for the final classification. See the Vignette and *diffTF* paper for details.
plot_minNoTFBS_heatmap	Integer[1,]. Default 100. Minimum number of TFBS for a TF to be included in the heatmap that is part of the output of this function.
deleteIntermediateData	TRUE or FALSE. Default TRUE. Should intermediate data be deleted before returning the object after a successful run? Due to the size of the produced intermediate data, we recommend setting this to TRUE, but if memory or object size are not an issue, the information can also be kept.
plotDiagnosticPlots	TRUE or FALSE. Default TRUE. Run and plot various diagnostic plots? If set to TRUE, PDF files will be produced and saved in the output directory (in a subfolder called plots).
outputFolder	Character or NULL. Default NULL. If set to NULL, the default output folder as specified when initiating the object in initializeGRN will be used. Otherwise, all output from this function will be put into the specified folder. If a folder is provided, while we recommend specifying an absolute path, a relative one also works.

corMethod — Character. One of pearson, spearman or bicor. Default pearson. Method for calculating the correlation coefficient. For pearson and spearman , see cor for details. bicor denotes the *biweight midcorrelation*, a correlation measure based on medians as calculated by WGCNA::bicorAndPvalue. Both spearman and bicor are considered more robust measures that are less prone to be affected by outliers.

forceRerun — TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

An updated GRN object, with additional information added from this function.

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
# GRN = loadExampleObject()
# GRN = AR_classification_wrapper(GRN, outputFolder = ".", forceRerun = FALSE)
```

---

build_eGRN_graph *Builds a graph out of a set of connections*

Description

This function requires a filtered set of connections in the GRN object as generated by filterGRNAndConnectGenes

Usage

```
build_eGRN_graph(
  GRN,
  model_TF_gene_nodes_separately = FALSE,
  allowLoops = FALSE,
  removeMultiple = FALSE,
  directed = FALSE,
  forceRerun = FALSE
)
```

Arguments

GRN — Object of class GRN

model_TF_gene_nodes_separately — TRUE or FALSE. Default FALSE. Should TF and gene nodes be modeled separately? If set to TRUE,this may lead to unwanted effects in case of TF-TF connections (i.e., a TF regulating another TF)

allowLoops — TRUE or FALSE. Default FALSE. Allow loops in the network (i.e., a TF that regulates itself)

removeMultiple	TRUE or FALSE. Default FALSE. Remove loops with the same start and end point? This can happen if multiple TF originate from the same gene, for example.
directed	TRUE or FALSE. Default FALSE. Should the network be directed?
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

An updated GRN object, with the graph(s) being stored in the slot 'graph' (i.e., 'GRN@graph' for both TF-gene and TF-peak-gene graphs)

See Also

filterGRNAndConnectGenes

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = build_eGRN_graph(GRN, forceRerun = FALSE)
```

---

calculateCommunitiesEnrichment

Run an enrichment analysis for the genes in each community in the filtered GRN object

---

Description

The enrichment analysis is based on the subset of the network connected to a particular community as identified by calculateCommunitiesStats , see calculateTFEnrichment and calculateGeneralEnrichment for TF-specific and general enrichment, respectively. This function requires the existence of the eGRN graph in the GRN object as produced by build_eGRN_graph as well as community information as calculated by calculateCommunitiesStats. Results can subsequently be visualized with the function plotCommunitiesEnrichment.

Usage

```
calculateCommunitiesEnrichment(
  GRN,
  ontology = c("GO_BP", "GO_MF"),
  algorithm = "weight01",
  statistic = "fisher",
  background = "neighborhood",
  background_geneTypes = "all",
  selection = "byRank",
  communities = NULL,
  pAdjustMethod = "BH",
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
ontology	Character vector of ontologies. Default c("GO_BP", "GO_MF"). Valid values are "GO_BP", "GO_MF", "GO_CC", "KEGG", "DO", and "Reactome", referring to *GO Biological Process*, *GO Molecular Function*, *GO Cellular Component*, *KEGG*, *Disease Ontology*, and *Reactome Pathways*, respectively. GO ontologies require the topGO, "KEGG" the clusterProfiler, "DO" the DOSE, and "Reactome" the ReactomePA packages, respectively. As they are listed under Suggests, they may not yet be installed, and the function will throw an error if they are missing.
algorithm	Character. Default "weight01". One of: "classic", "elim", "weight", "weight01", "lea", "parentchild". Only relevant if ontology is GO related (GO_BP, GO_MF, GO_CC), ignored otherwise. Name of the algorithm that handles the GO graph structures. Valid inputs are those supported by the topGO library. For general information about the algorithms, see https://academic.oup.com/bioinformatics/article/22/13/1600/193669. weight01 is a mixture between the elim and the weight algorithms.
statistic	Character. Default "fisher". One of: "fisher", "ks", "t". Statistical test to be used. Only relevant if ontology is GO related (GO_BP, GO_MF, GO_CC), and valid inputs are a subset of those supported by the topGO library (we had to remove some as they do not seem to work properly in topGO either), ignored otherwise. For the other ontologies the test statistic is always Fisher.
background	Character. Default "neighborhood". One of: "all_annotated", "all_RNA", "all_RNA_filtered", "neighborhood". Set of genes to be used to construct the background for the enrichment analysis. This can either be all annotated genes in the reference genome (all_annotated), all genes from the provided RNA data (all_RNA), all genes from the provided RNA data excluding those marked as filtered after executing filterData (all_RNA_filtered), or all the genes that are within the neighborhood of any peak (before applying any filters except for the user-defined promoterRange value in addConnections_peak_gene) (neighborhood).
background_geneTypes	Character vector of gene types that should be considered for the background. Default "all". Only gene types as defined in the GRN object, slot GRN@annotation$genes$gene.type are allowed. The special keyword "all" means no filter on gene type.
selection	Character. Default "byRank". One of: "byRank", "byLabel". Specify whether the communities enrichment will by calculated based on their rank, where the largest community (with most vertices) would have a rank of 1, or by their label. Note that the label is independent of the rank.
communities	NULL or numeric vector or character vector. Default NULL. If set to NULL, all community enrichments that have been calculated before are plotted. If a numeric vector is specified (when selection = "byRank"), the rank of the communities is specified. For example, communities = c(1,4) then denotes the first and fourth largest community. If a character vector is specified (when selection = "byLabel"), the name of the communities is specified instead. For example, communities = c("1","4") then denotes the communities with the names "1" and "4", which may or may not be the largest and fourth largest communities among all.

pAdjustMethod	Character. Default "BH". One of: "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr". This parameter is only relevant for the following ontologies: KEGG, DO, Reactome. For the other ontologies, the algorithm serves as an adjustment.
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Details

All enrichment functions use the TF-gene graph as defined in the 'GRN' object. See the 'ontology' argument for currently supported ontologies. Also note that some parameter combinations for 'algorithm' and 'statistic' are incompatible, an error message will be thrown in such a case.

Value

An updated GRN object, with the enrichment results stored in the stats$Enrichment$byCommunity slot.

See Also

plotCommunitiesEnrichment

plotGeneralEnrichment

calculateGeneralEnrichment

calculateCommunitiesStats

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = calculateCommunitiesEnrichment(GRN, ontology = c("GO_BP"), forceRerun = FALSE)
```

---

calculateCommunitiesStats

Generate graph communities and their summarizing statistics

Description

The results can subsequently be visualized with the function plotCommunitiesStats This function requires a filtered set of connections in the GRN object as generated by filterGRNAndConnectGenes. It then generates the TF-gene graph from the filtered connections, and clusters its vertices into communities using established community detection algorithms.

Usage

```
calculateCommunitiesStats(GRN, clustering = "louvain", forceRerun = FALSE, ...)
```

Arguments

GRN	Object of class GRN
clustering	Character. Default louvain. One of: louvain, leiden, leading_eigen, fast_greedy, optimal, walktrap. The community detection algorithm to be used. Please bear in mind the robustness and time consumption of the algorithms when opting for an alternative to the default.
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.
...	Additional parameters for the used clustering method, see the igraph::cluster_* methods for details on the specific parameters and what they do. For leiden clustering, for example, you may add a resolution_parameter to control the granularity of the community detection or n_iterations to modify the number of iterations.

Value

An updated GRN object, with a table that consists of the connections clustered into communities stored in the GRN@graphTF_geneclusterGraph slot as well as within the igraph object in GRN@graphTF_genegraph (retrievable via igraph using igraph::vertex.attributes(GRN@graphTF_genegraph)$c
for example.)

See Also

plotCommunitiesStats

calculateCommunitiesEnrichment

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = calculateCommunitiesStats(GRN, forceRerun = FALSE)
```

---

calculateGeneralEnrichment

Run an enrichment analysis for the genes in the whole network in the filtered GRN object

---

Description

The enrichment analysis is based on the whole network, see calculateCommunitiesEnrichment and calculateTFEnrichment for community- and TF-specific enrichment, respectively. This function requires the existence of the eGRN graph in the GRN object as produced by build_eGRN_graph. Results can subsequently be visualized with the function plotGeneralEnrichment.

Usage

```
calculateGeneralEnrichment(
  GRN,
  ontology = c("GO_BP", "GO_MF"),
  algorithm = "weight01",
  statistic = "fisher",
  background = "neighborhood",
  background_geneTypes = "all",
  pAdjustMethod = "BH",
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
ontology	Character vector of ontologies. Default c("GO_BP", "GO_MF"). Valid values are "GO_BP", "GO_MF", "GO_CC", "KEGG", "DO", and "Reactome", referring to *GO Biological Process*, *GO Molecular Function*, *GO Cellular Component*, *KEGG*, *Disease Ontology*, and *Reactome Pathways*, respectively. GO ontologies require the topGO, "KEGG" the clusterProfiler, "DO" the DOSE, and "Reactome" the ReactomePA packages, respectively. As they are listed under Suggests, they may not yet be installed, and the function will throw an error if they are missing.
algorithm	Character. Default "weight01". One of: "classic", "elim", "weight", "weight01", "lea", "parentchild". Only relevant if ontology is GO related (GO_BP, GO_MF, GO_CC), ignored otherwise. Name of the algorithm that handles the GO graph structures. Valid inputs are those supported by the topGO library. For general information about the algorithms, see https://academic.oup.com/bioinformatics/article/22/13/1600/193669. weight01 is a mixture between the elim and the weight algorithms.
statistic	Character. Default "fisher". One of: "fisher", "ks", "t". Statistical test to be used. Only relevant if ontology is GO related (GO_BP, GO_MF, GO_CC), and valid inputs are a subset of those supported by the topGO library (we had to remove some as they do not seem to work properly in topGO either), ignored otherwise. For the other ontologies the test statistic is always Fisher.
background	Character. Default "neighborhood". One of: "all_annotated", "all_RNA", "all_RNA_filtered", "neighborhood". Set of genes to be used to construct the background for the enrichment analysis. This can either be all annotated genes in the reference genome (all_annotated), all genes from the provided RNA data (all_RNA), all genes from the provided RNA data excluding those marked as filtered after executing filterData (all_RNA_filtered), or all the genes that are within the neighborhood of any peak (before applying any filters except for the user-defined promoterRange value in addConnections_peak_gene) (neighborhood).
background_geneTypes	Character vector of gene types that should be considered for the background. Default "all". Only gene types as defined in the GRN object, slot GRN@annotation$genes$gene.type are allowed. The special keyword "all" means no filter on gene type.

pAdjustMethod	Character. Default "BH". One of: "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr". This parameter is only relevant for the following ontologies: KEGG, DO, Reactome. For the other ontologies, the algorithm serves as an adjustment.
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Details

All enrichment functions use the TF-gene graph as defined in the 'GRN' object. See the 'ontology' argument for currently supported ontologies. Also note that some parameter combinations for 'algorithm' and 'statistic' are incompatible, an error message will be thrown in such a case.

Value

An updated GRN object, with the enrichment results stored in the stats$Enrichment$general slot.

See Also

plotGeneralEnrichment

calculateCommunitiesEnrichment

calculateTFEnrichment

plotCommunitiesEnrichment

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN =  loadExampleObject()
GRN =  calculateGeneralEnrichment(GRN, ontology = "GO_BP", forceRerun = FALSE)
```

---

calculateTFEnrichment *Run an enrichment analysis for the set of genes connected to a particular TF or sets of TFs in the filtered GRN object*

Description

The enrichment analysis is based on the subset of the network connected to particular TFs (TF regulons), see calculateCommunitiesEnrichment and calculateGeneralEnrichment for community- and general enrichment, respectively. This function requires the existence of the eGRN graph in the GRN object as produced by build_eGRN_graph. Results can subsequently be visualized with the function plotTFEnrichment.

Usage

```
calculateTFEnrichment(
  GRN,
  rankType = "degree",
  n = 3,
  TF.IDs = NULL,
  ontology = c("GO_BP", "GO_MF"),
  algorithm = "weight01",
  statistic = "fisher",
  background = "neighborhood",
  background_geneTypes = "all",
  pAdjustMethod = "BH",
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
rankType	Character. Default "degree". One of: "degree", "EV", "custom". This parameter will determine the criterion to be used to identify the "top" TFs. If set to "degree", the function will select top TFs based on the number of connections to genes they have, i.e. based on their degree-centrality. If set to "EV" it will select the top TFs based on their eigenvector-centrality score in the network. If set to custom, a set of TF IDs will have to be passed to the "TF.IDs" parameter.
n	Numeric. Default 3. If this parameter is passed as a value between 0 and 1, it is treated as a percentage of top nodes. If the value is passed as an integer it will be treated as the number of top nodes. This parameter is not relevant if rankType = "custom".
TF.IDs	Character vector. Default NULL. If the rank type is set to "custom", a vector of TF IDs for which the GO enrichment should be calculated should be passed to this parameter.
ontology	Character vector of ontologies. Default c("GO_BP", "GO_MF"). Valid values are "GO_BP", "GO_MF", "GO_CC", "KEGG", "DO", and "Reactome", referring to *GO Biological Process*, *GO Molecular Function*, *GO Cellular Component*, *KEGG*, *Disease Ontology*, and *Reactome Pathways*, respectively. GO ontologies require the topGO, "KEGG" the clusterProfiler, "DO" the DOSE, and "Reactome" the ReactomePA packages, respectively. As they are listed under Suggests, they may not yet be installed, and the function will throw an error if they are missing.
algorithm	Character. Default "weight01". One of: "classic", "elim", "weight", "weight01", "lea", "parentchild". Only relevant if ontology is GO related (GO_BP, GO_MF, GO_CC), ignored otherwise. Name of the algorithm that handles the GO graph structures. Valid inputs are those supported by the topGO library. For general information about the algorithms, see https://academic.oup.com/bioinformatics/article/22/13/1600/193669. weight01 is a mixture between the elim and the weight algorithms.
statistic	Character. Default "fisher". One of: "fisher", "ks", "t". Statistical test to be used. Only relevant if ontology is GO related (GO_BP, GO_MF, GO_CC), and

valid inputs are a subset of those supported by the topGO library (we had to remove some as they do not seem to work properly in topGO either), ignored otherwise. For the other ontologies the test statistic is always Fisher.

background Character. Default "neighborhood". One of: "all_annotated", "all_RNA", "all_RNA_filtered", "neighborhood". Set of genes to be used to construct the background for the enrichment analysis. This can either be all annotated genes in the reference genome (all_annotated), all genes from the provided RNA data (all_RNA), all genes from the provided RNA data excluding those marked as filtered after executing filterData (all_RNA_filtered), or all the genes that are within the neighborhood of any peak (before applying any filters except for the user-defined promoterRange value in addConnections_peak_gene) (neighborhood).

background_geneTypes
Character vector of gene types that should be considered for the background. Default "all". Only gene types as defined in the GRN object, slot GRN@annotation$genes$gene.type are allowed. The special keyword "all" means no filter on gene type.

pAdjustMethod Character. Default "BH". One of: "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr". This parameter is only relevant for the following ontologies: KEGG, DO, Reactome. For the other ontologies, the algorithm serves as an adjustment.

forceRerun TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Details

All enrichment functions use the TF-gene graph as defined in the 'GRN' object. See the 'ontology' argument for currently supported ontologies. Also note that some parameter combinations for 'algorithm' and 'statistic' are incompatible, an error message will be thrown in such a case.

Value

An updated GRN object, with the enrichment results stored in the stats$Enrichment$byTF slot.

See Also

plotTFEnrichment

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN =  loadExampleObject()
GRN =  calculateTFEnrichment(GRN, n = 5, ontology = "GO_BP", forceRerun = FALSE)
```

`changeOutputDirectory` *Change the output directory of a GRN object*

Description

Change the output directory of a GRN object

Usage

```
changeOutputDirectory(GRN, outputDirectory = ".")
```

Arguments

`GRN`	Object of class `GRN`
`outputDirectory`	Character. Default `.` . New output directory for all output files unless overwritten via the parameter `outputFolder`.

Value

An updated `GRN` object, with the output directory being adjusted accordingly

Examples

```
GRN = loadExampleObject()
GRN = changeOutputDirectory(GRN, outputDirectory = ".")
```

`deleteIntermediateData` *Optional convenience function to delete intermediate data from the function `AR_classification_wrapper` and summary statistics that may occupy a lot of space*

Description

Optional convenience function to delete intermediate data from the function `AR_classification_wrapper` and summary statistics that may occupy a lot of space

Usage

```
deleteIntermediateData(GRN)
```

Arguments

`GRN`	Object of class `GRN`

Value

An updated GRN object, with some slots being deleted (GRN@dataTFsclassification as well as GRN@stats$connectionDetails.l)

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = deleteIntermediateData(GRN)
```

---

filterConnectionsForPlotting

Filter connections for subsequent visualization with 'visualizeGRN()' from the filtered eGRN

Description

This helper function provides an easy and flexible way to retain particular connections for plotting and discard all others. Note that this filtering is only relevant and applicable for the function 'visualizeGRN()' and ignored anywhere else. This makes it possible to visualize only specific TF regulons or to plot only connections that fulfill particular filter criteria. Due to the flexibility of the implementation by allowing arbitrary filters that are passed directly to dplyr::filter, users can visually investigate the eGRN, which is particularly useful when the eGRNs is large and has many connections.

Usage

```
filterConnectionsForPlotting(GRN, plotAll = TRUE, ..., forceRerun = FALSE)
```

Arguments

GRN	Object of class GRN
plotAll	TRUE or FALSE. Default TRUE. Should all connections be included for plotting? If set to TRUE, all connections are marked for plotting and everything else is ignored. This resets any previous setting. If set FALSE, the filter expressions (if any) are used to determine which connection to plot
...	An arbitrary set of arguments that is used directly, without modification, as input for dplyr::filter and therefore has to be valid expression that dplyr::filter understands. The filtering is based on the all.filtered table as stored in GRN@connections$all.filtered$`0`. Thus, the specific filters can be completely arbitrary for ultimate flexibility and must only adhere to the column names and types as defined in GRN@connections$all.filtered$`0`. See the examples also for what you can do.
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

An updated GRN object, with added data from this function.

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = filterConnectionsForPlotting (GRN, plotAll = FALSE, TF.ID == "E2F6.0.A")
GRN = filterConnectionsForPlotting (GRN, plotAll = FALSE, TF_peak.r > 0.7 | TF_peak.fdr < 0.2)
GRN = filterConnectionsForPlotting (GRN, plotAll = FALSE, TF_peak.r > 0.7, TF_peak.fdr < 0.2)
```

---

filterData *Filter RNA-seq and/or peak data from a GRN object*

Description

This function marks genes and/or peaks as `filtered` depending on the chosen filtering criteria and is based on the count data AFTER potential normalization as chosen when using the addData function. Most of the filters may not be meaningful and useful anymore to apply after using particular normalization schemes that can give rise to, for example, negative values such as cyclic loess normalization. If normalized counts do not represents counts anymore but rather a deviation from a mean or something a like, the filtering critieria usually do not make sense anymore. Filtered genes / peaks will then be disregarded when adding connections in subsequent steps via addConnections_TF_peak and addConnections_peak_gene. **This function does NOT (re)filter existing connections when the GRN object already contains connections. Thus, upon re-execution of this function with different filtering criteria, all downstream steps have to be re-run.**

Usage

```
filterData(
  GRN,
  minNormalizedMean_peaks = NULL,
  maxNormalizedMean_peaks = NULL,
  minNormalizedMeanRNA = NULL,
  maxNormalizedMeanRNA = NULL,
  chrToKeep_peaks = NULL,
  minSize_peaks = 20,
  maxSize_peaks = 10000,
  minCV_peaks = NULL,
  maxCV_peaks = NULL,
  minCV_genes = NULL,
  maxCV_genes = NULL,
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
minNormalizedMean_peaks	Numeric[0,] or NULL. Default 5. Minimum mean across all samples for a peak to be retained for the normalized counts table. Set to NULL for not applying the filter. Be aware that depending on the chosen normalization, this filter may not make sense and should NOT be applied. See the notes for this function.
maxNormalizedMean_peaks	Numeric[0,] or NULL. Default NULL. Maximum mean across all samples for a peak to be retained for the normalized counts table. Set to NULL for not applying the filter. Be aware that depending on the chosen normalization, this filter may not make sense and should NOT be applied. See the notes for this function.
minNormalizedMeanRNA	Numeric[0,] or NULL. Default 5. Minimum mean across all samples for a gene to be retained for the normalized counts table. Set to NULL for not applying the filter. Be aware that depending on the chosen normalization, this filter may not make sense and should NOT be applied. See the notes for this function.
maxNormalizedMeanRNA	Numeric[0,] or NULL. Default NULL. Maximum mean across all samples for a gene to be retained for the normalized counts table. Set to NULL for not applying the filter. Be aware that depending on the chosen normalization, this filter may not make sense and should NOT be applied. See the notes for this function.
chrToKeep_peaks	Character vector or NULL. Default NULL. Vector of chromosomes that peaks are allowed to come from. This filter can be used to filter sex chromosomes from the peaks, for example (e.g, `c(paste0("chr", 1:22), "chrX", "chrY")`)
minSize_peaks	Integer[1,] or NULL. Default 20. Minimum peak size (width, end - start) for a peak to be retained. Set to NULL for not applying the filter.
maxSize_peaks	Integer[1,] or NULL. Default 10000. Maximum peak size (width, end - start) for a peak to be retained. Set to NULL for not applying the filter.
minCV_peaks	Numeric[0,] or NULL. Default NULL. Minimum CV (coefficient of variation, a unitless measure of variation) for a peak to be retained. Set to NULL for not applying the filter. Be aware that depending on the chosen normalization, this filter may not make sense and should NOT be applied. See the notes for this function.
maxCV_peaks	Numeric[0,] or NULL. Default NULL. Maximum CV (coefficient of variation, a unitless measure of variation) for a peak to be retained. Set to NULL for not applying the filter. Be aware that depending on the chosen normalization, this filter may not make sense and should NOT be applied. See the notes for this function.
minCV_genes	Numeric[0,] or NULL. Default NULL. Minimum CV (coefficient of variation, a unitless measure of variation) for a gene to be retained. Set to NULL for not applying the filter. Be aware that depending on the chosen normalization, this filter may not make sense and should NOT be applied. See the notes for this function.

maxCV_genes	Numeric[0,] or NULL. Default NULL. Maximum CV (coefficient of variation, a unitless measure of variation) for a gene to be retained. Set to NULL for not applying the filter. Be aware that depending on the chosen normalization, this filter may not make sense and should NOT be applied. See the notes for this function.
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Details

All this function does is setting (or modifying) the filtering flag in GRN@data$peaks$counts_metadata and GRN@dataRNAcounts_metadata, respectively.

Value

An updated GRN object, with added data from this function.

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = filterData(GRN, forceRerun = FALSE)
```

---

filterGRNAndConnectGenes

Filter TF-peaks and peak-gene connections and combine them to TF-peak-gene connections to construct an eGRN.

Description

This is one of the main integrative functions of the GRaNIE package. It has two main functions: First, filtering both TF-peak and peak-gene connections according to different criteria such as FDR and other properties Second, joining the three major elements that an eGRN consist of (TFs, peaks, genes) into one data frame, with one row per unique TF-peak-gene connection. **After successful execution, the connections (along with additional feature metadata) can be retrieved with the function getGRNConnections. Note that a previously stored eGRN graph is reset upon successful execution of this function along with printing a descriptive warning, and re-running the function build_eGRN_graph is necessary when any of the network functions of the package shall be executed. If the filtered connections changed, all network related enrichment functions also have to be rerun.** Internally, before joining them, both TF-peak links and peak-gene connections are filtered separately for reasons of memory and computational efficacy: First filtering out unwanted links dramatically reduces the memory needed for the full eGRN. Peak-gene p-value adjustment is only done after all filtering steps on the remaining set of connections to lower the statistical burden of multiple-testing adjustment; therefore, this may lead to initially counter-intuitive effects such as a particular connections not being included anymore as compared to a filtering based on different thresholds, or the FDR being different for the same reason.

Usage

```
filterGRNAndConnectGenes(
  GRN,
  TF_peak.fdr.threshold = 0.2,
  TF_peak.connectionTypes = "all",
  peak.SNP_filter = list(min_nSNPs = 0, filterType = "orthogonal"),
  peak_gene.p_raw.threshold = NULL,
  peak_gene.fdr.threshold = 0.2,
  peak_gene.fdr.method = "BH",
  peak_gene.IHW.covariate = NULL,
  peak_gene.IHW.nbins = "auto",
  outputFolder = NULL,
  gene.types = c("all"),
  allowMissingTFs = FALSE,
  allowMissingGenes = TRUE,
  peak_gene.r_range = c(0, 1),
  peak_gene.selection = "all",
  peak_gene.maxDistance = NULL,
  filterTFs = NULL,
  filterGenes = NULL,
  filterPeaks = NULL,
  TF_peak_FDR_selectViaCorBins = FALSE,
  filterLoops = TRUE,
  resetGraphAndStoreInternally = TRUE,
  silent = FALSE,
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
TF_peak.fdr.threshold	Numeric[0,1]. Default 0.2. Maximum FDR for the TF-peak links. Set to 1 or NULL to disable this filter.
TF_peak.connectionTypes	Character vector. Default all. TF-peak connection types to consider. The special keyword all denotes all connection types (e.g., expression and TFActivity) that are found in the GRN object. By default, only expression is present in the object, so all and expression are usually equivalent unless calculation of TF-peak links based on TF activity has also been enabled.
peak.SNP_filter	Named list. Default list(min_nSNPs = 0, filterType = "orthogonal"). Filters related to SNP data if they have been added with the function addSNPData, ignored otherwise. The named list must contain at least two elements: First, min_nSNPs, an integer >= 0 that denotes how many SNPs a peak has to overlap with at least to pass the filter or be considered for inclusion. Second, filterType, a character that must either be orthogonal or extra and denotes whether the SNP filter is orthogonal to the other filters (i.e, an alternative way of when a

peak is considered for being kept) or whether the SNP filter is in addition to all other filters. For more help, see the Vignettes.

`peak_gene.p_raw.threshold`
: Numeric[0,1]. Default NULL. Threshold for the peak-gene connections, based on the raw p-value. All peak-gene connections with a larger raw p-value will be filtered out.

`peak_gene.fdr.threshold`
: Numeric[0,1]. Default 0.2. Threshold for the peak-gene connections, based on the FDR. All peak-gene connections with a larger FDR will be filtered out.

`peak_gene.fdr.method`
: Character. Default "BH". One of: "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none", "IHW". Method for adjusting p-values for multiple testing. If set to "IHW", the package `IHW` is required (as it is listed under `Suggests`, it may not be installed), and independent hypothesis weighting will be performed, and a suitable covariate has to be specified for the parameter `peak_gene.IHW.covariate`.

`peak_gene.IHW.covariate`
: Character. Default `NULL`. Name of the covariate to use for IHW (column name from the table that is returned with the function `getGRNConnections`. Only relevant if `peak_gene.fdr.method` is set to "IHW". You have to make sure the specified covariate is suitable for IHW, see the diagnostic plots that are generated in this function for this. For many datasets, the peak-gene distance (called `peak_gene.distance` in the object) seems suitable.

`peak_gene.IHW.nbins`
: Integer or "auto". Default "auto". Number of bins for IHW. Only relevant if `peak_gene.fdr.method` is set to "IHW".

`outputFolder`
: Character or `NULL`. Default `NULL`. If set to `NULL`, the default output folder as specified when initiating the object in `initializeGRN` will be used. Otherwise, all output from this function will be put into the specified folder. If a folder is provided, while we recommend specifying an absolute path, a relative one also works.

`gene.types`
: Character vector of supported gene types. Default `"all"`. Filter for gene types to retain, genes with gene types not listed here are filtered. The special keyword "all" indicates no filter and retains all gene types. To filter for only protein-coding genes, use `"protein_coding"`. The specified names must match the names as stored in the `GRN` object (see `GRN@annotation$genes$gene.type`) and correspond 1:1 to the gene type names as provided by `biomaRt`, with the exception of `lncRNAs`, which is internally renamed to `lincRNAs` when first fetching all gene types. This is done due to a recent change in `biomaRt` and aims at keeping backwards compatibility with `GRN` objects.

`allowMissingTFs`
: `TRUE` or `FALSE`. Default `FALSE`. Should connections be returned for which the TF is NA (i.e., connections consisting only of peak-gene links?). If set to `TRUE`, this generally greatly increases the number of connections but it may not be what you aim for.

`allowMissingGenes`
: `TRUE` or `FALSE`. Default `TRUE`. Should connections be returned for which the gene

is NA (i.e., connections consisting only of TF-peak links?). If set to TRUE, this generally increases the number of connections.

peak_gene.r_range
: Numeric(2). Default c(0,1). Filter for lower and upper limit for the peak-gene links. Only links will be retained if the correlation coefficient is within the specified interval. This filter is usually used to filter out negatively correlated peak-gene links.

peak_gene.selection
: "all" or "closest". Default "all". Filter for the selection of genes for each peak. If set to "all", all previously identified peak-gene are used, while "closest" only retains the closest gene for each peak that is retained until the point the filter is applied.

peak_gene.maxDistance
: Integer >0. Default NULL. Maximum peak-gene distance to retain a peak-gene connection.

filterTFs
: Character vector. Default NULL. Vector of TFs (as named in the GRN object) to retain. All TFs not listed will be filtered out.

filterGenes
: Character vector. Default NULL. Vector of gene IDs (as named in the GRN object) to retain. All genes not listed will be filtered out.

filterPeaks
: Character vector. Default NULL. Vector of peak IDs (as named in the GRN object) to retain. All peaks not listed will be filtered out.

TF_peak_FDR_selectViaCorBins
: TRUE or FALSE. Default FALSE. Use a modified procedure for selecting TF-peak links. Instead of selecting solely based on the user-specified FDR, this procedure first identifies the correlation bin closest to 0 that contains at least one significant TF-peak link according to the chosen TF_peak.fdr.threshold. This is done spearately for both FDR directions. It then retains all TF-peak links that have a correlation bin at least as extreme as the identified pair. For example, if the correlation bin [0.35,0.40] contains a significant TF-peak link while [0,0.05], [0.05,0.10], ..., [0.30,0.35] do not, all TF-peak links with a correlation of at least 0.35 or above are selected (i.e, bins [0.35,0.40], [0.40,0.45], ..., [0.95,1.00]). Thus, for the final selection, also links with a higher FDR but a more extreme correlation may be selected.

filterLoops
: TRUE or FALSE. Default TRUE. If a TF regulates itself (i.e., the TF and the gene are the same entity), should such loops be filtered from the GRN?

resetGraphAndStoreInternally
: TRUE or FALSE. Default TRUE. If set to TRUE, the stored eGRN graph (slot graph) is reset due to the potentially changed connections that would otherwise cause conflicts in the information stored in the object. Also, a GRN object is returned. If set to FALSE, only the new filtered connections are returned and the object is not altered.

silent
: TRUE or FALSE. Default FALSE. Print progress messages and filter statistics.

forceRerun
: TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

An updated GRN object, with additional information added from this function. The filtered and merged TF-peak and peak-gene connections in the slot GRN@connections$all.filtered and can be retrieved (along with other feature metadata) using the function getGRNConnections.

See Also

visualizeGRN

addConnections_TF_peak

addConnections_peak_gene

build_eGRN_graph

getGRNConnections

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = filterGRNAndConnectGenes(GRN)
```

---

generateStatsSummary *Generate a summary for the number of connections for different filtering criteria for a GRN object.*

Description

This functions calls filterGRNAndConnectGenes repeatedly and stores the total number of connections and other statistics each time to summarize them afterwards. All arguments are identical to the ones in filterGRNAndConnectGenes, see the help for this function for details. The function plot_stats_connectionSummary can be used afterwards for plotting.

Usage

```
generateStatsSummary(
  GRN,
  TF_peak.fdr = c(0.001, 0.01, 0.05, 0.1, 0.2),
  TF_peak.connectionTypes = "all",
  peak_gene.fdr = c(0.001, 0.01, 0.05, 0.1, 0.2),
  peak_gene.r_range = c(0, 1),
  gene.types = c("all"),
  allowMissingGenes = c(FALSE, TRUE),
  allowMissingTFs = c(FALSE),
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
TF_peak.fdr	Numeric vector[0,1]. Default c(0.001, 0.01, 0.05, 0.1, 0.2). TF-peak FDR values to iterate over.
TF_peak.connectionTypes	Character vector. Default all. TF-peak connection types to consider. The special keyword all denotes all connection types (e.g., expression and TFActivity) that are found in the GRN object. By default, only expression is present in the object, so all and expression are usually equivalent unless calculation of TF-peak links based on TF activity has also been enabled.
peak_gene.fdr	Numeric vector[0,1]. Default c(0.001, 0.01, 0.05, 0.1, 0.2). Peak-gene FDR values to iterate over.
peak_gene.r_range	Numeric vector of length 2[-1,1]. Default c(0,1). The correlation range of peak-gene connections to keep.
gene.types	Character vector of supported gene types. Default "all". Filter for gene types to retain, genes with gene types not listed here are filtered. The special keyword "all" indicates no filter and retains all gene types. To filter for only protein-coding genes, use "protein_coding". The specified names must match the names as stored in the GRN object (see GRN@annotation$genes$gene.type) and correspond 1:1 to the gene type names as provided by biomaRt, with the exception of lncRNAs, which is internally renamed to lincRNAs when first fetching all gene types. This is done due to a recent change in biomaRt and aims at keeping backwards compatibility with GRN objects.
allowMissingGenes	Logical vector of length 1 or 2. Default c(FALSE, TRUE). Allow genes to be missing for peak-gene connections? If both FALSE and TRUE are given, the code loops over both
allowMissingTFs	Logical vector of length 1 or 2. Default c(FALSE). Allow TFs to be missing for TF-peak connections? If both FALSE and TRUE are given, the code loops over both
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

An updated GRN object, with additional information added from this function.

See Also

plot_stats_connectionSummary

filterGRNAndConnectGenes

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = generateStatsSummary(GRN, TF_peak.fdr = c(0.01, 0.1), peak_gene.fdr = c(0.01, 0.1))
```

`getCounts` *Get counts for the various data defined in a* `GRN` *object*

Description

Get counts for the various data defined in a `GRN` object. **Note: This function, as all** `get` **functions from this package, does NOT return a** `GRN` **object.**

Usage

```
getCounts(
  GRN,
  type,
  permuted = FALSE,
  asMatrix = FALSE,
  includeIDColumn = TRUE,
  includeFiltered = FALSE
)
```

Arguments

`GRN`	Object of class `GRN`
`type`	Character. Either `peaks` or `rna`. `peaks` corresponds to the counts for the open chromatin data, while `rna` refers to th RNA-seq counts. If set to `rna`, both real (foreground) and background data can be retrieved, while for `peaks`, only the real (i.e., the one with index `0`) can be retrieved.
`permuted`	`TRUE` or `FALSE`. Default `FALSE`. Should the permuted data be taken (`TRUE`) or the non-permuted, original one (`FALSE`)?
`asMatrix`	Logical. `TRUE` or `FALSE`. Default `FALSE`. If set to `FALSE`, counts are returned as a data frame with or without an ID column (see `includeIDColumn`). If set to `TRUE`, counts are returned as a matrix with the ID column as row names.
`includeIDColumn`	Logical. `TRUE` or `FALSE`. Default `TRUE`. Only relevant if `asMatrix = FALSE`. If set to `TRUE`, an explicit ID column is returned (no row names). If set to `FALSE`, the IDs are in the row names instead.
`includeFiltered`	Logical. `TRUE` or `FALSE`. Default `FALSE`. If set to `FALSE`, genes or peaks marked as filtered (after running the function `filterData`) will not be returned. If set to `TRUE`, all elements are returned regardless of the currently active filter status.

Value

Data frame of counts, with the type as indicated by the function parameters. This function does **NOT** return a GRN object.

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
counts.df = getCounts(GRN, type = "peaks", permuted = FALSE)
```

`getGRNConnections` *Extract connections or links from a GRN object as a data frame.*

Description

Returns stored connections/links (either TF-peak, peak-genes, TF-genes or the filtered set of connections as produced by `filterGRNAndConnectGenes`). Additional meta columns (TF, peak and gene metadata) can be added optionally. **Note: This function, as all `get` functions from this package, does NOT return a GRN object.**

Usage

```
getGRNConnections(
  GRN,
  type = "all.filtered",
  background = FALSE,
  include_TF_gene_correlations = FALSE,
  include_TFMetadata = FALSE,
  include_peakMetadata = FALSE,
  include_geneMetadata = FALSE,
  include_variancePartitionResults = FALSE
)
```

Arguments

GRN	Object of class GRN
type	Character. One of `TF_peaks`, `peak_genes`, `TF_genes` or `all.filtered`. Default `all.filtered`. The type of connections to retrieve.
background	Integer (0 or 1). Default `0`. Either `0` or `1`). Here, `0` refers to the real (foreground) while `1` to the background.
include_TF_gene_correlations	Logical. `TRUE` or `FALSE`. Default `FALSE`. Should TFs and gene correlations be returned as well? If set to `TRUE`, they must have been computed beforehand with `add_TF_gene_correlation`.
include_TFMetadata	Logical. `TRUE` or `FALSE`. Default `FALSE`. Should TF metadata be returned as well?

include_peakMetadata
: Logical. TRUE or FALSE. Default FALSE. Should peak metadata be returned as well?

include_geneMetadata
: Logical. TRUE or FALSE. Default FALSE. Should gene metadata be returned as well?

include_variancePartitionResults
: Logical. TRUE or FALSE. Default FALSE. Should the results from the function add_featureVariation be included? If set to TRUE, they must have been computed beforehand with add_featureVariation; otherwise, an error is thrown.

Value

A data frame with the requested connections. This function does **NOT** return a GRN object. Depending on the arguments, the data frame that is returned has different columns, which however can be divided into the following classes according to their name:

- TF-related: Starting with TF.:
  - TF.name and TF.ID: Name / ID of the TF
  - TF.ENSEMBL: Ensembl ID (unique)
- peak-related: Starting with peak.:
  - peak.ID: ID (coordinates)
  - peak.mean, peak.median, peak.CV: peak mean, median and its coefficient of variation (CV) across all samples
  - peak.annotation: Peak annotation as determined by ChIPseeker such as Promoter, 5' UTR, 3' UTR, Exon, Intron, Downstream, Intergenic
  - peak.nearestGene*: Additional metadata for the nearest gene such as position (chr, start, end, strand), name (name, symbol and ENSEMBL), and distance to the TSS (distanceToTSS)
  - peak.GC.perc: GC percentage
- gene-related: Starting with gene.:
  - gene.name and gene.ENSEMBL: gene name and Ensembl ID
  - gene.type: gene type (such as protein_coding, lincRNA) as retrieved by biomaRt
  - gene.mean, gene.median, gene.CV: gene mean, median and its coefficient of variation (CV) across all samples
- TF-peak-related: Starting with TF_peak.:
  - TF_peak.r and TF_peak.r_bin: Correlation coefficient of the TF-peak pair and its correlation bin (in bins of width 0.05, such as (-0.55,-0.5] for r = -0.53)
  - TF_peak.fdr and TF_peak.fdr_direction: TF-peak FDR and the directionality from which it was derived (see Methods in the paper, pos or neg)
  - TF_peak.connectionType: TF-peak connection type. This is by default expression, meaning that expression was used to construct the TF and peak
- peak-gene-related: Starting with peak_gene.:
  - peak_gene.source: Source/Origin of the identified connection. Either neighborhood, TADs or knownLinks, depending on the parameters used when running the function addConnections_peak_gene

  - peak_gene.bait_OE_ID: Only present when known links have been provided (see addConnections_peak_gene). This column denotes the original IDs of the bait and OE coordinates that identified this link.
  - peak_gene.tad_ID: Only present when TADs have been provided (see addConnections_peak_gene). This column denotes the original ID of the TAD ID that identified this link.
  - peak_gene.distance: Peak-gene distance (usually taken the TSS of the gene as reference unless specified otherwise, see the parameter overlapTypeGene for more information from addConnections_peak_gene). If the peak-gene connection is across chromosomes (as defined by the known links, see addConnections_peak_gene), the distance is set to NA.
  - peak_gene.r: Correlation coefficient of the peak-gene pair
  - peak_gene.p_raw and peak_gene.p_adj: Raw and adjusted p-value of the peak-gene pair
- TF-gene-related: Starting with TF_gene.:
  - TF_gene.r: Correlation coefficient of the TF-gene pair
  - TF_gene.p_raw: Raw p-value of the TF-gene pair

See Also

filterGRNAndConnectGenes

add_featureVariation

add_TF_gene_correlation

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN_con.all.df = getGRNConnections(GRN)
```

---

getGRNSummary — *Summarize a GRN object to a named list for comparison with other GRN objects.*

Description

Note: This function, as all get functions from this package, does NOT return a GRN object.

Usage

```
getGRNSummary(GRN, silent = FALSE)
```

Arguments

GRN	Object of class GRN
silent	TRUE or FALSE. Default FALSE. Should the function be silent and print nothing?

Value

A named list summarizing the GRN object. This function does **NOT** return a GRN object, but instead a named lsit with the following elements:

- data:
  - peaks, genes and TFs:
  - sharedSamples:
  - metadata:
- parameters and config: GRN parameters and config information
- connections: Connection summary for different connection types
  - TF_peak: TF-peak (number of connections for different FDR thresholds)
  - peak_genes: Peak-gene
  - TF_peak_gene: TF-peak-gene
- network: Network-related summary, including the number of nodes, edges, communities and enrichment for both the TF-peak-gene and TF-gene network
  - TF_gene
  - TF_peak_gene

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
summary.l = getGRNSummary(GRN)
```

---

getParameters — *Retrieve parameters for previously used function calls and general parameters for a GRN object.*

Description

Note: This function, as all get functions from this package, does NOT return a GRN object.

Usage

```
getParameters(GRN, type = "parameter", name = "all")
```

Arguments

GRN	Object of class GRN
type	Character. Either function or parameter. Default parameter. When set to function, a valid GRaNIE function name must be given that has been run before. When set to parameter, in combination with name, returns a specific parameter (as specified in GRN@config)).
name	Character. Default all. Name of parameter or function name to retrieve. Set to the special keyword all to retrieve all parameters.

Value

The requested parameters. This function does **NOT** return a GRN object.

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
params.l = getParameters(GRN, type = "parameter", name = "all")
```

`getTopNodes` *Retrieve the top nodes (TFs or genes) with respect to either degree or Eigenvector centrality in the filtered GRN object.*

Description

This function requires a filtered set of connections in the GRN object as generated by `filterGRNAndConnectGenes`. **Note: This function, as all `get` functions from this package, does NOT return a GRN object.**

Usage

```
getTopNodes(GRN, nodeType, rankType, n = 0.1, use_TF_gene_network = TRUE)
```

Arguments

GRN	Object of class GRN
nodeType	Character. One of: "gene" or "TF". Node type.
rankType	Character. One of: "degree", "EV". This parameter will determine the criterion to be used to identify the "top" nodes. If set to "degree", the function will select top nodes based on the number of connections they have, i.e. based on their degree-centrality. If set to "EV" it will select the top nodes based on their eigenvector-centrality score in the network.
n	Numeric. Default 0.1. If this parameter is passed as a value between [0,1], it is treated as a percentage of top nodes. If the value is passed as an integer >=1 it will be treated as the number of top nodes.
use_TF_gene_network	TRUE or FALSE. Default TRUE. Should the TF-gene network be used (TRUE) or the TF-peak-gene network (FALSE)?

Value

A data frame with the node names and the corresponding scores used to rank them

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
topGenes = getTopNodes(GRN, nodeType = "gene", rankType = "degree", n = 3)
topTFs = getTopNodes(GRN, nodeType = "TF", rankType = "EV", n = 5)
```

GRaNIE **GRaNIE** *(**G**ene **R**egul**a**tory **N**etwork **I**nference including **E**nhancers): Reconstruction and evaluation of data-driven, cell type specific gene regulatory networks including enhancers using chromatin accessibility and RNAseq data (general package information)*

Description

Genetic variants associated with diseases often affect non-coding regions, thus likely having a regulatory role. To understand the effects of genetic variants in these regulatory regions, identifying genes that are modulated by specific regulatory elements (REs) is crucial. The effect of gene regulatory elements, such as enhancers, is often cell-type specific, likely because the combinations of transcription factors (TFs) that are regulating a given enhancer have celltype specific activity. This TF activity can be quantified with existing tools such as `diffTF` and captures differences in binding of a TF in open chromatin regions. Collectively, this forms a gene regulatory network (`eGRN`) with cell-type and data-specific TF-RE and RE-gene links. Here, we reconstruct such a `eGRN` using bulk RNAseq and open chromatin (e.g., using ATACseq or ChIPseq for open chromatin marks) and optionally TF activity data. Our network contains different types of links, connecting TFs to regulatory elements, the latter of which is connected to genes in the vicinity or within the same chromatin domain (TAD). We use a statistical framework to assign empirical FDRs and weights to all links using a permutation-based approach.

Package functions

See the Vignettes for a workflow example and more generally https://grp-zaugg.embl-community.io/GRaNIE for all project-related information.

GRN object

The `GRaNIE` package works with `GRN` objects. See `GRN` for details.

Contact Information

Please check out https://grp-zaugg.embl-community.io/GRaNIE for how to get in contact with us.

Author(s)

Maintainer: Christian Arnold <chrarnold@web.de>

Authors:

- Judith Zaugg <judith.zaugg@embl.de>
- Rim Moussa <rim.moussa01@gmail.com>

Other contributors:

- Armando Reyes-Palomares <armandorp@gmail.com> [contributor]

- Giovanni Palla <giov.pll@gmail.com> [contributor]
- Maksim Kholmatov <maksim.kholmatov@embl.de> [contributor]

See Also

Useful links:

- https://grp-zaugg.embl-community.io/GRaNIE
- Report bugs at https://git.embl.de/grp-zaugg/GRaNIE/issues

`GRN-class` *Create, represent, investigate, quantify and visualize enhancer-mediated gene regulatory networks (***eGRNs***)*

Description

The class `GRN` stores data and information related to our `eGRN` approach to construct enhancer-mediated gene regulatory networks out of open chromatin and RNA-Seq data. See the description below for more details, and **visit our project website at https://grp-zaugg.embl-community.io/GRaNIE and have a look at the various Vignettes**.

Slots

`data` Currently stores 4 different types of data:

- `peaks`:
  - `counts`:
  - `counts_metadata`:
- `RNA`:
  - `counts`:
  - `counts_metadata`:
  - `counts_permuted_index`:
- `TFs`:
  - `TF_activity`:
  - `TF_peak_overlap`:
  - `classification`:

`config` Contains general configuration data and parameters such as parameters, files, directories, flags, and recorded function parameters.

`connections` Stores various types of connections

`annotation` Stores annotation data for peaks and genes

`stats` Stores statistical and summary information for a `GRN` network. Currently, connection details are stored here.

`graph` Stores the eGRN graph related information and data structures

Constructors

Currently, a GRN object is created by executing the function initializeGRN.

Accessors

In the following code snippets, GRN is a GRN object.

Get general annotation of a GRN object from the GRaNIE package

nPeaks(GRN)), nTFs(GRN)) and nGenes(GRN)): Retrieve the number of peaks, TFs and genes, respectively, that have been added to the object (both before and after filtering)

---

importTFData *Import externally derived TF Activity data. EXPERIMENTAL.*

Description

We do not yet provide full support for this function. It is currently being tested. Use at our own risk.

Usage

```
importTFData(
  GRN,
  data,
  name,
  idColumn = "ENSEMBL",
  nameColumn = "TF.name",
  normalization = "none",
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
data	Data frame. No default. Data with TF data.
name	Name in object under which it should be stored. This corresponds to the connectionType afterwards that some functions iterate over.
idColumn	Character. Default ENSEMBL. Name of the ID column. Must not be unique as some TFs may correspond to the same ID.
nameColumn	Character. Default TF.name. Must be unique for each TF / row.
normalization	Character. Default cyclicLoess. One of cyclicLoess, sizeFactors, quantile, or none. Normalization procedure. When set to cyclicLoess, the csaw package is required (as it is listed under Suggests, it may not be installed).
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

An updated GRN object, with added data from this function.

`initializeGRN` *Create and initialize an empty GRN object.*

Description

Executing this function is the very first step in the *GRaNIE* workflow. After its execution, data can be added to the object.

Usage

```
initializeGRN(objectMetadata = list(), outputFolder = ".", genomeAssembly)
```

Arguments

`objectMetadata`	List. Default `list()`. Optional (named) list with an arbitrary number of elements, all of which capture metadata for the object. **Only atomic data types are allowed for each list element (see ?is.atomic for more help: logical, integer, numeric, complex, character, raw, and NULL), and this slot is not supposed to store real data**. This is mainly used to distinguish GRN objects from one another by storing object-specific metadata along with the data.
`outputFolder`	Output folder, either absolute or relative to the current working directory. Default `"."`. Default output folder where all pipeline output will be put unless specified otherwise. We recommend specifying an absolute path. Note that for Windows-based systems, the path must be correctly specified with "/" as path separator.
`genomeAssembly`	Character. No default. The genome assembly of all data that to be used within this object. Currently, supported genomes are: `hg19`, `hg38`, `mm9`, `mm10`, `mm39`, `rn6`, `rn7`, `dm6`. If you need additional genomes, let us know. See function description for further information and notes.

Value

Empty GRN object

Examples

```
meta.l = list(name = "exampleName", date = "01.03.22")
GRN = initializeGRN(objectMetadata = meta.l, outputFolder = "output", genomeAssembly = "hg38")
```

loadExampleObject *Load example GRN dataset*

Description

Loads an example GRN object with 6 TFs, ~61.000 peaks, ~19.000 genes, 259 filtered connections and pre-calculated enrichments. This function uses `BiocFileCache` if installed to cache the example object, which is considerably faster than re-downloading the file anew every time the function is executed. If not, the file is re-downloaded every time anew. Thus, to enable caching, you may install the package `BiocFileCache`.

Usage

```
loadExampleObject(
  forceDownload = FALSE,
  fileURL = "https://git.embl.de/grp-zaugg/GRaNIE/-/raw/master/data/GRN.rds"
)
```

Arguments

`forceDownload`	`TRUE` or `FALSE`. Default `FALSE`. Should the download be enforced even if the local cached file is already present?
`fileURL`	Character. Default `https://git.embl.de/grp-zaugg/GRaNIE/-/raw/master/data/GRN.rds`. URL to the GRN example object in rds format.

Value

An small example `GRN` object

Examples

```
GRN = loadExampleObject()
```

nGenes *Get the number of genes for a `GRN` object.*

Description

Returns the number of genes (all or only non-filtered ones) from the provided RNA-seq data in the `GRN` object.

Usage

```
nGenes(GRN, filter = TRUE)
```

Arguments

GRN	Object of class GRN
filter	TRUE or FALSE. Default TRUE. Should genes marked as filtered be included in the count?

Value

Integer. Number of genes that are defined in the GRN object, either by excluding (filter = TRUE) or including (filter = FALSE) genes that are currently marked as *filtered*.

See Also

nTFs

nPeaks

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
nGenes(GRN, filter = TRUE)
nGenes(GRN, filter = FALSE)
```

---

nPeaks *Get the number of peaks for a GRN object.*

Description

Returns the number of peaks (all or only non-filtered ones) from the provided peak datain the GRN object.

Usage

```
nPeaks(GRN, filter = TRUE)
```

Arguments

GRN	Object of class GRN
filter	TRUE or FALSE. Default TRUE. Should peaks marked as filtered be included in the count?

Value

Integer. Number of peaks that are defined in the GRN object, either by excluding (filter = TRUE) or including (filter = FALSE) peaks that are currently marked as *filtered*.

See Also

nTFs

nGenes

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
nPeaks(GRN, filter = TRUE)
nPeaks(GRN, filter = FALSE)
```

---

nTFs *Get the number of TFs for a GRN object.*

Description

Returns the number of TFs from the provided TFBS data in the GRN object.

Usage

```
nTFs(GRN)
```

Arguments

GRN	Object of class GRN

Value

Integer. Number of TFs that are defined in the GRN object.

See Also

nGenes

nPeaks

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
nTFs(GRN)
```

overlapPeaksAndTFBS *Overlap peaks and TFBS for a GRN object*

Description

If the source was set to JASPAR in addTFBS, the argument nCores is ignored.

Usage

```
overlapPeaksAndTFBS(GRN, nCores = 2, forceRerun = FALSE, ...)
```

Arguments

GRN	Object of class GRN
nCores	Integer >0. Default 1. Number of cores to use. A value >1 requires the BiocParallel package (as it is listed under Suggests, it may not be installed yet).
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.
...	No default. Only relevant if source = "JASPAR" has been selected in addTFBS, ignored otherwise. Additional arguments for motifmatchr::matchMotifs such as custom background nucleotide frequencies or p-value cutoffs. For more information, type ?motifmatchr::matchMotifs

Value

An updated GRN object, with added data from this function (GRN@dataTFsTF_peak_overlap in particular)

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = overlapPeaksAndTFBS(GRN, nCores = 2, forceRerun = FALSE)
```

performAllNetworkAnalyses

Perform all network-related statistical and descriptive analyses, including community and enrichment analyses. See the functions it executes in the @seealso section below.

Description

A convenience function that calls all network-related functions in one-go, using selected default parameters and a set of adjustable ones also. For full adjustment, run the individual functions separately. This function requires a filtered set of connections in the GRN object as generated by filterGRNAndConnectGenes

Usage

```
performAllNetworkAnalyses(
  GRN,
  ontology = c("GO_BP", "GO_MF"),
  algorithm = "weight01",
  statistic = "fisher",
  background = "neighborhood",
  clustering = "louvain",
  communities = NULL,
  selection = "byRank",
  topnGenes = 20,
  topnTFs = 20,
  maxWidth_nchar_plot = 50,
  display_pAdj = FALSE,
  outputFolder = NULL,
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
ontology	Character vector of ontologies. Default c("GO_BP", "GO_MF"). Valid values are "GO_BP", "GO_MF", "GO_CC", "KEGG", "DO", and "Reactome", referring to *GO Biological Process*, *GO Molecular Function*, *GO Cellular Component*, *KEGG*, *Disease Ontology*, and *Reactome Pathways*, respectively. GO ontologies require the topGO, "KEGG" the clusterProfiler, "DO" the DOSE, and "Reactome" the ReactomePA packages, respectively. As they are listed under Suggests, they may not yet be installed, and the function will throw an error if they are missing.
algorithm	Character. Default "weight01". One of: "classic", "elim", "weight", "weight01", "lea", "parentchild". Only relevant if ontology is GO related (GO_BP, GO_MF, GO_CC), ignored otherwise. Name of the algorithm that handles the GO graph structures. Valid inputs are those supported by the topGO library. For general information about the algorithms, see https://academic.oup.com/bioinformatics/article/22/13/1600/193669. weight01 is a mixture between the elim and the weight algorithms.
statistic	Character. Default "fisher". One of: "fisher", "ks", "t". Statistical test to be used. Only relevant if ontology is GO related (GO_BP, GO_MF, GO_CC), and valid inputs are a subset of those supported by the topGO library (we had to remove some as they do not seem to work properly in topGO either), ignored otherwise. For the other ontologies the test statistic is always Fisher.
background	Character. Default "neighborhood". One of: "all_annotated", "all_RNA", "all_RNA_filtered", "neighborhood". Set of genes to be used to construct the background for the enrichment analysis. This can either be all annotated genes in the reference genome (all_annotated), all genes from the provided RNA data (all_RNA), all genes from the provided RNA data excluding those marked as filtered after executing filterData (all_RNA_filtered), or all the genes that are within the neighborhood of any peak (before applying any filters

except for the user-defined promoterRange value in addConnections_peak_gene) (neighborhood).

clustering — Character. Default louvain. One of: louvain, leiden, leading_eigen, fast_greedy, optimal, walktrap. The community detection algorithm to be used. Please bear in mind the robustness and time consumption of the algorithms when opting for an alternative to the default.

communities — NULL or numeric vector or character vector. Default NULL. If set to NULL, all community enrichments that have been calculated before are plotted. If a numeric vector is specified (when selection = "byRank"), the rank of the communities is specified. For example, communities = c(1,4) then denotes the first and fourth largest community. If a character vector is specified (when selection = "byLabel"), the name of the communities is specified instead. For example, communities = c("1","4") then denotes the communities with the names "1" and "4", which may or may not be the largest and fourth largest communities among all.

selection — Character. Default "byRank". One of: "byRank", "byLabel". Specify whether the communities will be selected based on their rank or explicitly by their label. Note that the label is independent of the rank. When set to "byRank", the largest community (with most vertices) always has a rank of 1.

topnGenes — Integer > 0. Default 20. Number of genes to plot, sorted by their rank or label.

topnTFs — Integer > 0. Default 20. Number of TFs to plot, sorted by their rank or label.

maxWidth_nchar_plot — Integer (>=10). Default 50. Maximum number of characters for a term before it is truncated.

display_pAdj — TRUE or FALSE. Default FALSE. Is the p-value being displayed in the plots the adjusted p-value? This parameter is relevant for KEGG, Disease Ontology, and Reactome enrichments, and does not affect GO enrichments.

outputFolder — Character or NULL. Default NULL. If set to NULL, the default output folder as specified when initiating the object in initializeGRN will be used. Otherwise, all output from this function will be put into the specified folder. If a folder is provided, while we recommend specifying an absolute path, a relative one also works.

forceRerun — TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

An updated GRN object, with added data from this function.

See Also

build_eGRN_graph

plotGeneralGraphStats

calculateGeneralEnrichment

plotGeneralEnrichment

calculateCommunitiesStats

plotCommunitiesStats

calculateCommunitiesEnrichment

plotCommunitiesEnrichment

calculateTFEnrichment

plotTFEnrichment

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
# GRN = loadExampleObject()
# GRN = performAllNetworkAnalyses(GRN, outputFolder = ".", forceRerun = FALSE)
```

---

plotCommunitiesEnrichment

Plot community-based enrichment results for a filtered GRN object

---

Description

Similarly to plotGeneralEnrichment and plotTFEnrichment, the results of the community-based enrichment analysis are plotted. This function produces multiple plots. First, one plot per community to summarize the community-specific enrichment. Second, a summary heatmap of all significantly enriched terms across all communities and for the whole eGRN. The latter allows to compare the results with the general network enrichment. Third, a subset of the aforementioned heatmap, showing only the top most significantly enriched terms per community and for the whole eGRN (as specified by nID) for improved visibility

Usage

```
plotCommunitiesEnrichment(
  GRN,
  outputFolder = NULL,
  basenameOutput = NULL,
  selection = "byRank",
  communities = NULL,
  topn_pvalue = 30,
  p = 0.05,
  nSignificant = 2,
  nID = 10,
  maxWidth_nchar_plot = 50,
  display_pAdj = FALSE,
  plotAsPDF = TRUE,
  pdf_width = 12,
  pdf_height = 12,
  pages = NULL,
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
outputFolder	Character or NULL. Default NULL. If set to NULL, the default output folder as specified when initiating the object in initializeGRN will be used. Otherwise, all output from this function will be put into the specified folder. If a folder is provided, while we recommend specifying an absolute path, a relative one also works.
basenameOutput	NULL or character. Default NULL. Basename of the output files that are produced. If set to NULL, a default basename is chosen. If a custom basename is specified, all output files will have the chosen basename as file prefix, be careful with not overwriting already existing files (if forceRerun is set to TRUE)
selection	Character. Default "byRank". One of: "byRank", "byLabel". Specify whether the communities will be selected based on their rank or explicitly by their label. Note that the label is independent of the rank. When set to "byRank", the largest community (with most vertices) always has a rank of 1.
communities	NULL or numeric vector or character vector. Default NULL. If set to NULL, all community enrichments that have been calculated before are plotted. If a numeric vector is specified (when selection = "byRank"), the rank of the communities is specified. For example, communities = c(1,4) then denotes the first and fourth largest community. If a character vector is specified (when selection = "byLabel"), the name of the communities is specified instead. For example, communities = c("1","4") then denotes the communities with the names "1" and "4", which may or may not be the largest and fourth largest communities among all.
topn_pvalue	Numeric. Default 30. Maximum number of ontology terms that meet the p-value significance threshold to display in the enrichment dot plot
p	Numeric. Default 0.05. p-value threshold to determine significance.
nSignificant	Numeric > 0. Default 3. Threshold to filter out an ontology term with less than nSignificant overlapping genes.
nID	Numeric > 0. Default 10. For the reduced summary heatmap, number of top terms to select per community / for the general enrichment.
maxWidth_nchar_plot	Integer (>=10). Default 50. Maximum number of characters for a term before it is truncated.
display_pAdj	TRUE or FALSE. Default FALSE. Is the p-value being displayed in the plots the adjusted p-value? This parameter is relevant for KEGG, Disease Ontology, and Reactome enrichments, and does not affect GO enrichments.
plotAsPDF	TRUE or FALSE. Default TRUE.Should the plots be printed to a PDF file? If set to TRUE, a PDF file is generated, the name of which depends on the value of basenameOutput. If set to FALSE, all plots are printed to the currently active device. Note that most functions print more than one plot, which means you may only see the last plot depending on your active graphics device.
pdf_width	Number>0. Default 12. Width of the PDF, in cm.
pdf_height	Number >0. Default 12. Height of the PDF, in cm.

pages	Integer vector or NULL. Default NULL. Page number(s) to plot. Can be used to plot only specific pages to a PDF or the currently active graphics device.
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

The same GRN object, without modifications.

See Also

plotGeneralEnrichment

plotTFEnrichment

calculateCommunitiesEnrichment

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = plotCommunitiesEnrichment(GRN, plotAsPDF = FALSE, pages = 1)
```

---

plotCommunitiesStats *Plot general structure & connectivity statistics for each community in a filtered GRN*

Description

Similarly to the statistics produced by plotGeneralGraphStats, summaries regarding the vertex degrees and the most important vertices per community are generated. Note that the communities need to first be calculated using the calculateCommunitiesStats function

Usage

```
plotCommunitiesStats(
  GRN,
  outputFolder = NULL,
  basenameOutput = NULL,
  selection = "byRank",
  communities = seq_len(5),
  topnGenes = 20,
  topnTFs = 20,
  plotAsPDF = TRUE,
  pdf_width = 12,
  pdf_height = 12,
  pages = NULL,
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
outputFolder	Character or NULL. Default NULL. If set to NULL, the default output folder as specified when initiating the object in initializeGRN will be used. Otherwise, all output from this function will be put into the specified folder. If a folder is provided, while we recommend specifying an absolute path, a relative one also works.
basenameOutput	NULL or character. Default NULL. Basename of the output files that are produced. If set to NULL, a default basename is chosen. If a custom basename is specified, all output files will have the chosen basename as file prefix, be careful with not overwriting already existing files (if forceRerun is set to TRUE)
selection	Character. Default "byRank". One of: "byRank", "byLabel". Specify whether the communities will be selected based on their rank or explicitly by their label. Note that the label is independent of the rank. When set to "byRank", the largest community (with most vertices) always has a rank of 1.
communities	NULL or numeric vector or character vector. Default NULL. If set to NULL, all community enrichments that have been calculated before are plotted. If a numeric vector is specified (when selection = "byRank"), the rank of the communities is specified. For example, communities = c(1,4) then denotes the first and fourth largest community. If a character vector is specified (when selection = "byLabel"), the name of the communities is specified instead. For example, communities = c("1","4") then denotes the communities with the names "1" and "4", which may or may not be the largest and fourth largest communities among all.
topnGenes	Integer > 0. Default 20. Number of genes to plot, sorted by their rank or label.
topnTFs	Integer > 0. Default 20. Number of TFs to plot, sorted by their rank or label.
plotAsPDF	TRUE or FALSE. Default TRUE.Should the plots be printed to a PDF file? If set to TRUE, a PDF file is generated, the name of which depends on the value of basenameOutput. If set to FALSE, all plots are printed to the currently active device. Note that most functions print more than one plot, which means you may only see the last plot depending on your active graphics device.
pdf_width	Number>0. Default 12. Width of the PDF, in cm.
pdf_height	Number >0. Default 12. Height of the PDF, in cm.
pages	Integer vector or NULL. Default NULL. Page number(s) to plot. Can be used to plot only specific pages to a PDF or the currently active graphics device.
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

The same GRN object, without modifications.

See Also

plotGeneralGraphStats

calculateCommunitiesStats

calculateCommunitiesEnrichment

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = plotCommunitiesStats(GRN, plotAsPDF = FALSE, pages = 1)
```

---

plotCorrelations *Plot scatter plots of the underlying count data for either TF-peak, peak-gene or TF-gene pairs for a GRN object*

Description

The user can select multiple filters to plot only pairs of interest. The data that is shown is the same that has been used to construct the eGRN.

Usage

```
plotCorrelations(
  GRN,
  type = "all.filtered",
  TF.IDs = NULL,
  peak.IDs = NULL,
  gene.IDs = NULL,
  min_abs_r = 0,
  TF_peak_maxFDR = 0.2,
  peak_gene_max_rawP = 0.2,
  TF_gene_max_rawP = 0.2,
  nMax = 10,
  nSelectionType = "random",
  dataType = c("real"),
  corMethod = NULL,
  outputFolder = NULL,
  basenameOutput = NULL,
  plotAsPDF = TRUE,
  plotsPerPage = c(2, 2),
  pdf_width = 10,
  pdf_height = 8,
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN

type — Character(1). Default "all.filtered". Either "TF-peak", "peak-gene", "TF-gene", or "all.filtered". Default "all.filtered". Which connections to plot? "all.filtered" plots all TF-peak and peak-gene pairs from the filtered eGRN as stored in the object.

TF.IDs — Character(). Default NULL. Character vector of TF IDs to include. If set to NULL, this filter will be ignored. Only applicable when type = "TF-peak" or type = "TF-gene".

peak.IDs — Character(). Default NULL. Character vector of peak IDs to include. If set to NULL, this filter will be ignored. Only applicable when type = "TF-peak" or type = "peak-gene".

gene.IDs — Character(). Default NULL. Character vector of gene IDs (Ensembl) to include. If set to NULL, this filter will be ignored. Only applicable when type = "TF-gene" or type = "peak-gene".

min_abs_r — Numeric[0,1]. Default 0. Filter for all types of pairs: Minimum correlation coefficient (absolute value) required to include a particular pair.

TF_peak_maxFDR — Numeric[0,1]. Default 0.2. Filter for TF-peak pairs: Which maximum FDR should a pair to plot have? Only applicable when type = "TF-peak".

peak_gene_max_rawP — Numeric[0,1]. Default 0.2. Filter for peak-gene pairs: Which maximum FDR should a pair to plot have? Only applicable when type = "peak-gene".

TF_gene_max_rawP — Numeric[0,1]. Default 0.2. Filter for TF-gene pairs: Which maximum FDR should a pair to plot have? Only applicable when type = "TF-gene".

nMax — Numeric(1). Default 10. Filter for all types of pairs: maximum number of selected pairs that fulfill all other filters that should be plotted. If set to 0, this filter will be disabled and all pairs that fulfill the user-defined criteria will be plotted. If set to a value > 0, different pairs may be selected each time the function is run (if the total number of remaining pairs is large enough)

nSelectionType — random or top. Default top. Only applicable if nMax is set to a value > 0. If set to top, only the top features will be plotted while random plots randomly selected features.

dataType — Character vector. One of, or both of, real or background. Default real. For which type, real or background data, to produce the diagnostic plots?

corMethod — Character. Either NULL (the default) or one of pearson, spearman or bicor. Method for calculating the correlation coefficient. If set to NULL, the correlation method that has been used in the GraNIE object is used. For testing nd visualizing data, this can be changed, though. For pearson and spearman , see cor for details. bicor denotes the *biweight midcorrelation*, a correlation measure based on medians as calculated by WGCNA::bicorAndPvalue. Both spearman and bicor are considered more robust measures that are less prone to be affected by outliers.

outputFolder — Character or NULL. Default NULL. If set to NULL, the default output folder as specified when initiating the object in initializeGRN will be used. Otherwise, all output from this function will be put into the specified folder. If a folder is provided, while we recommend specifying an absolute path, a relative one also works.

basenameOutput	NULL or character. Default NULL. Basename of the output files that are produced. If set to NULL, a default basename is chosen. If a custom basename is specified, all output files will have the chosen basename as file prefix, be careful with not overwriting already existing files (if forceRerun is set to TRUE)
plotAsPDF	TRUE or FALSE. Default TRUE.Should the plots be printed to a PDF file? If set to TRUE, a PDF file is generated, the name of which depends on the value of basenameOutput. If set to FALSE, all plots are printed to the currently active device. Note that most functions print more than one plot, which means you may only see the last plot depending on your active graphics device.
plotsPerPage	Integer vector of length 2. Default c(2,2). How man plots should be put on one page? The first number denotes the number of rows, the second one the number of columns.
pdf_width	Number>0. Default 12. Width of the PDF, in cm.
pdf_height	Number >0. Default 12. Height of the PDF, in cm.
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

An updated GRN object.

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = plotCorrelations(GRN, nMax = 1, min_abs_r = 0.8, plotsPerPage = c(1,1), plotAsPDF = FALSE)
```

---

plotDiagnosticPlots_peakGene

Plot diagnostic plots for peak-gene connections for a GRN object

---

Description

Plot diagnostic plots for peak-gene connections for a GRN object

Usage

```
plotDiagnosticPlots_peakGene(
  GRN,
  outputFolder = NULL,
  basenameOutput = NULL,
  gene.types = list(c("all"), c("protein_coding")),
  useFiltered = FALSE,
  plotDetails = FALSE,
  plotPerTF = FALSE,
  plotAsPDF = TRUE,
```

```
  pdf_width = 12,
  pdf_height = 12,
  pages = NULL,
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
outputFolder	Character or NULL. Default NULL. If set to NULL, the default output folder as specified when initiating the object in initializeGRN will be used. Otherwise, all output from this function will be put into the specified folder. If a folder is provided, while we recommend specifying an absolute path, a relative one also works.
basenameOutput	NULL or character. Default NULL. Basename of the output files that are produced. If set to NULL, a default basename is chosen. If a custom basename is specified, all output files will have the chosen basename as file prefix, be careful with not overwriting already existing files (if forceRerun is set to TRUE)
gene.types	List of character vectors. Default list(c("all"), c("protein_coding")). Vectors of gene types to consider for the diagnostic plots. Multiple distinct combinations of gene types can be specified. For example, if set to list(c("protein_coding", "lincRNA"), c("protein_coding"), c("all")), 3 distinct PDFs will be produced, one for each element of the list. The first file would only consider protein-coding and lincRNA genes, while the second plot only considers protein-coding ones. The special keyword "all" denotes all gene types found (usually, there are many gene types present, also more exotic and rare ones).
useFiltered	Logical. TRUE or FALSE. Default FALSE. If set to FALSE, the diagnostic plots will be produced based on all peak-gene connections. This is the default and will usually be best to judge whether the background behaves as expected. If set to TRUE, the diagnostic plots will be produced based on the filtered set of connections. For this, the function filterGRNAndConnectGenes must have been run before.
plotDetails	TRUE or FALSE. Default FALSE. Print additional plots that may help for debugging and QC purposes? Note that these plots are currently less documented or not at all.
plotPerTF	Logical. TRUE or FALSE. Default FALSE. If set to FALSE, the diagnostic plots will be done across all TF (the default), while setting it to TRUE will generate the QC plots TF-specifically, including "all" TF, sorted by the number of connections.
plotAsPDF	TRUE or FALSE. Default TRUE.Should the plots be printed to a PDF file? If set to TRUE, a PDF file is generated, the name of which depends on the value of basenameOutput. If set to FALSE, all plots are printed to the currently active device. Note that most functions print more than one plot, which means you may only see the last plot depending on your active graphics device.
pdf_width	Number>0. Default 12. Width of the PDF, in cm.
pdf_height	Number >0. Default 12. Height of the PDF, in cm.

pages	Integer vector or NULL. Default NULL. Page number(s) to plot. Can be used to plot only specific pages to a PDF or the currently active graphics device.
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

An updated GRN object.

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
types = list(c("protein_coding"))
GRN = plotDiagnosticPlots_peakGene(GRN, gene.types=types, plotAsPDF = FALSE, pages = 1)
```

---

plotDiagnosticPlots_TFPeaks

Plot diagnostic plots for TF-peak connections for a GRN object

---

Description

Plot diagnostic plots for TF-peak connections for a GRN object

Usage

```
plotDiagnosticPlots_TFPeaks(
  GRN,
  outputFolder = NULL,
  basenameOutput = NULL,
  plotDetails = FALSE,
  dataType = c("real", "background"),
  nTFMax = NULL,
  plotAsPDF = TRUE,
  pdf_width = 12,
  pdf_height_base = 8,
  pages = NULL,
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
outputFolder	Character or NULL. Default NULL. If set to NULL, the default output folder as specified when initiating the object in initializeGRN will be used. Otherwise, all output from this function will be put into the specified folder. If a folder is provided, while we recommend specifying an absolute path, a relative one also works.

basenameOutput	NULL or character. Default NULL. Basename of the output files that are produced. If set to NULL, a default basename is chosen. If a custom basename is specified, all output files will have the chosen basename as file prefix, be careful with not overwriting already existing files (if forceRerun is set to TRUE)
plotDetails	TRUE or FALSE. Default FALSE. Print additional plots that may help for debugging and QC purposes? Note that these plots are currently less documented or not at all.
dataType	Character vector. One of, or both of, "real" or "background". For which type, real or background data, to produce the diagnostic plots?
nTFMax	NULL or Integer > 0. Default NULL. Maximum number of TFs to process. Can be used for testing purposes by setting this to a small number i(.e., 10)
plotAsPDF	TRUE or FALSE. Default TRUE.Should the plots be printed to a PDF file? If set to TRUE, a PDF file is generated, the name of which depends on the value of basenameOutput. If set to FALSE, all plots are printed to the currently active device. Note that most functions print more than one plot, which means you may only see the last plot depending on your active graphics device.
pdf_width	Number>0. Default 12. Width of the PDF, in cm.
pdf_height_base	Number. Default 8. Base height of the PDF, in cm, per connection type. The total height is automatically determined based on the number of connection types that are found in the object (e.g., expression or TF activity). For example, when two connection types are found, the base height is multiplied by 2.
pages	Integer vector or NULL. Default NULL. Page number(s) to plot. Can be used to plot only specific pages to a PDF or the currently active graphics device.
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

An updated GRN object.

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = plotDiagnosticPlots_TFPeaks(GRN, outputFolder = ".", dataType = "real", nTFMax = 2, pages = 1)
```

---

plotDiagnosticPlots_TFPeaks_GC

Plot GC-specific diagnostic plots for TF-peak connections for a GRN object

---

Description

Note: The arguments nTFMax and pages are not implemented yet

Usage

```
plotDiagnosticPlots_TFPeaks_GC(
  GRN,
  outputFolder = NULL,
  basenameOutput = NULL,
  dataType = c("real", "background"),
  nTFMax = NULL,
  plotAsPDF = TRUE,
  pdf_width = 12,
  pdf_height_base = 15,
  pages = NULL,
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
outputFolder	Character or NULL. Default NULL. If set to NULL, the default output folder as specified when initiating the object in initializeGRN will be used. Otherwise, all output from this function will be put into the specified folder. If a folder is provided, while we recommend specifying an absolute path, a relative one also works.
basenameOutput	NULL or character. Default NULL. Basename of the output files that are produced. If set to NULL, a default basename is chosen. If a custom basename is specified, all output files will have the chosen basename as file prefix, be careful with not overwriting already existing files (if forceRerun is set to TRUE)
dataType	Character vector. One of, or both of, "real" or "background". For which type, real or background data, to produce the diagnostic plots?
nTFMax	NULL or Integer > 0. Default NULL. Maximum number of TFs to process. Can be used for testing purposes by setting this to a small number i(.e., 10)
plotAsPDF	TRUE or FALSE. Default TRUE.Should the plots be printed to a PDF file? If set to TRUE, a PDF file is generated, the name of which depends on the value of basenameOutput. If set to FALSE, all plots are printed to the currently active device. Note that most functions print more than one plot, which means you may only see the last plot depending on your active graphics device.
pdf_width	Number>0. Default 12. Width of the PDF, in cm.
pdf_height_base	Number. Default 8. Base height of the PDF, in cm, per connection type. The total height is automatically determined based on the number of connection types that are found in the object (e.g., expression or TF activity). For example, when two connection types are found, the base height is multiplied by 2.
pages	Integer vector or NULL. Default NULL. Page number(s) to plot. Can be used to plot only specific pages to a PDF or the currently active graphics device.
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

`plotGeneralEnrichment` *Plot the general enrichement results*

Description

This function plots the results of the general enrichment analysis for every specified ontology.

Usage

```
plotGeneralEnrichment(
  GRN,
  outputFolder = NULL,
  basenameOutput = NULL,
  ontology = NULL,
  topn_pvalue = 30,
  p = 0.05,
  display_pAdj = FALSE,
  maxWidth_nchar_plot = 50,
  plotAsPDF = TRUE,
  pdf_width = 12,
  pdf_height = 12,
  pages = NULL,
  forceRerun = FALSE
)
```

Arguments

`GRN`	Object of class `GRN`
`outputFolder`	Character or `NULL`. Default `NULL`. If set to `NULL`, the default output folder as specified when initiating the object in `initializeGRN` will be used. Otherwise, all output from this function will be put into the specified folder. If a folder is provided, while we recommend specifying an absolute path, a relative one also works.
`basenameOutput`	`NULL` or character. Default `NULL`. Basename of the output files that are produced. If set to `NULL`, a default basename is chosen. If a custom basename is specified, all output files will have the chosen basename as file prefix, be careful with not overwriting already existing files (if `forceRerun` is set to `TRUE`)
`ontology`	Character. `NULL` or vector of ontology names. Default `NULL`. Vector of ontologies to plot. The results must have been previously calculated otherwise an error is thrown.
`topn_pvalue`	Numeric. Default 30. Maximum number of ontology terms that meet the p-value significance threshold to display in the enrichment dot plot
`p`	Numeric. Default 0.05. p-value threshold to determine significance.
`display_pAdj`	`TRUE` or `FALSE`. Default `FALSE`. Is the p-value being displayed in the plots the adjusted p-value? This parameter is relevant for KEGG, Disease Ontology, and Reactome enrichments, and does not affect GO enrichments.

maxWidth_nchar_plot
: Integer (>=10). Default 50. Maximum number of characters for a term before it is truncated.

plotAsPDF
: TRUE or FALSE. Default TRUE.Should the plots be printed to a PDF file? If set to TRUE, a PDF file is generated, the name of which depends on the value of basenameOutput. If set to FALSE, all plots are printed to the currently active device. Note that most functions print more than one plot, which means you may only see the last plot depending on your active graphics device.

pdf_width
: Number>0. Default 12. Width of the PDF, in cm.

pdf_height
: Number >0. Default 12. Height of the PDF, in cm.

pages
: Integer vector or NULL. Default NULL. Page number(s) to plot. Can be used to plot only specific pages to a PDF or the currently active graphics device.

forceRerun
: TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

The same GRN object, without modifications.

See Also

plotCommunitiesEnrichment

plotTFEnrichment

calculateGeneralEnrichment

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = plotGeneralEnrichment(GRN, plotAsPDF = FALSE, pages = 1)
```

---

plotGeneralGraphStats *Plot general structure and connectivity statistics for a filtered GRN object*

Description

This function generates graphical summaries about the structure and connectivity of the TF-peak-gene and TF-gene graphs. These include, distribution of vertex types (TF, peak, gene) and edge types (tf-peak, peak-gene), the distribution of vertex degrees, and the most "important" vertices according to degree centrality and eigenvector centrality scores.

Usage

```
plotGeneralGraphStats(
  GRN,
  outputFolder = NULL,
  basenameOutput = NULL,
  plotAsPDF = TRUE,
  pdf_width = 12,
  pdf_height = 12,
  pages = NULL,
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
outputFolder	Character or NULL. Default NULL. If set to NULL, the default output folder as specified when initiating the object in initializeGRN will be used. Otherwise, all output from this function will be put into the specified folder. If a folder is provided, while we recommend specifying an absolute path, a relative one also works.
basenameOutput	NULL or character. Default NULL. Basename of the output files that are produced. If set to NULL, a default basename is chosen. If a custom basename is specified, all output files will have the chosen basename as file prefix, be careful with not overwriting already existing files (if forceRerun is set to TRUE)
plotAsPDF	TRUE or FALSE. Default TRUE.Should the plots be printed to a PDF file? If set to TRUE, a PDF file is generated, the name of which depends on the value of basenameOutput. If set to FALSE, all plots are printed to the currently active device. Note that most functions print more than one plot, which means you may only see the last plot depending on your active graphics device.
pdf_width	Number>0. Default 12. Width of the PDF, in cm.
pdf_height	Number >0. Default 12. Height of the PDF, in cm.
pages	Integer vector or NULL. Default NULL. Page number(s) to plot. Can be used to plot only specific pages to a PDF or the currently active graphics device.
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

The same GRN object, without modifications.

See Also

plotGeneralEnrichment

plotCommunitiesStats

plotCommunitiesEnrichment

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = plotGeneralGraphStats(GRN, plotAsPDF = FALSE, pages = 1)
```

---

plotPCA_all *Produce a PCA plot of the data from a GRN object*

Description

Produce a PCA plot of the data from a GRN object

Usage

```
plotPCA_all(
  GRN,
  outputFolder = NULL,
  basenameOutput = NULL,
  data = c("rna", "peaks"),
  topn = c(500, 1000, 5000),
  type = "normalized",
  removeFiltered = TRUE,
  plotAsPDF = TRUE,
  pdf_width = 12,
  pdf_height = 12,
  pages = NULL,
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
outputFolder	Character or NULL. Default NULL. If set to NULL, the default output folder as specified when initiating the object in initializeGRN will be used. Otherwise, all output from this function will be put into the specified folder. If a folder is provided, while we recommend specifying an absolute path, a relative one also works.
basenameOutput	NULL or character. Default NULL. Basename of the output files that are produced. If set to NULL, a default basename is chosen. If a custom basename is specified, all output files will have the chosen basename as file prefix, be careful with not overwriting already existing files (if forceRerun is set to TRUE)
data	Character. Either "peaks" or "rna" or "all". Default c("rna", "peaks"). Type of data to plot a PCA for. "peaks" corresponds to the the open chromatin data, while "rna" refers to the RNA-seq counts. If set to "all", PCA will be done for both data modalities. In any case, PCA will be based on the original provided data before any additional normalization has been run (i.e., usually the raw data).

topn	Integer vector. Default c(500,1000,5000). Number of top variable features to do PCA for. Can be a vector of different numbers (see default).
type	Character. Must be "normalized". On which data type (raw or normalized) should the PCA plots be done? We removed support for raw and currently only support normalized.
removeFiltered	Logical. TRUE or FALSE. Default TRUE. Should features marked as filtered as determined by filterData be removed?
plotAsPDF	TRUE or FALSE. Default TRUE.Should the plots be printed to a PDF file? If set to TRUE, a PDF file is generated, the name of which depends on the value of basenameOutput. If set to FALSE, all plots are printed to the currently active device. Note that most functions print more than one plot, which means you may only see the last plot depending on your active graphics device.
pdf_width	Number>0. Default 12. Width of the PDF, in cm.
pdf_height	Number >0. Default 12. Height of the PDF, in cm.
pages	Integer vector or NULL. Default NULL. Page number(s) to plot. Can be used to plot only specific pages to a PDF or the currently active graphics device.
forceRerun	TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

An updated GRN object with the data of the screeplot and PCA stored in GRN@stats$PCA. Already existing slots are overwritten.

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = plotPCA_all(GRN, topn = 500, data = "rna", type = "normalized", plotAsPDF = FALSE, pages = 1)
```

---

plotTFEnrichment *Plot TF-based GO enrichment results*

Description

Similarly to plotGeneralEnrichment and plotCommunitiesEnrichment, the results of the TF-based enrichment analysis are plotted. This function produces multiple plots. First, one plot per community to summarize the TF-specific enrichment. Second, a summary heatmap of all significantly enriched terms across all TFs and for the whole eGRN. The latter allows to compare the results with the general network enrichment. Third, a subset of the aforementioned heatmap, showing only the top most significantly enriched terms per TF and for the whole eGRN (as specified by nID) for improved visibility .

Usage

```
plotTFEnrichment(
  GRN,
  rankType = "degree",
  n = NULL,
  TF.IDs = NULL,
  topn_pvalue = 30,
  p = 0.05,
  nSignificant = 2,
  nID = 10,
  display_pAdj = FALSE,
  maxWidth_nchar_plot = 50,
  outputFolder = NULL,
  basenameOutput = NULL,
  plotAsPDF = TRUE,
  pdf_width = 12,
  pdf_height = 12,
  pages = NULL,
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
rankType	Character. One of: "degree", "EV", "custom". This parameter will determine the criterion to be used to identify the "top" nodes. If set to "degree", the function will select top nodes based on the number of connections they have, i.e. based on their degree-centrality. If set to "EV" it will select the top nodes based on their eigenvector-centrality score in the network.
n	NULL or numeric. Default NULL. If set to NULL, all previously calculated TF enrichments will be plotted. If set to a value between (0,1), it is treated as a percentage of top nodes. If the value is passed as an integer it will be treated as the number of top nodes. This parameter is not relevant if rankType = "custom".
TF.IDs	NULL or character vector. Default NULL. For rankType="custom" the IDs of the TFs to plot. Ignored otherwise.
topn_pvalue	Numeric. Default 30. Maximum number of ontology terms that meet the p-value significance threshold to display in the enrichment dot plot
p	Numeric. Default 0.05. p-value threshold to determine significance.
nSignificant	Numeric > 0. Default 3. Threshold to filter out an ontology term with less than nSignificant overlapping genes.
nID	Numeric > 0. Default 10. For the reduced summary heatmap, number of top terms to select per community / for the general enrichment.
display_pAdj	TRUE or FALSE. Default FALSE. Is the p-value being displayed in the plots the adjusted p-value? This parameter is relevant for KEGG, Disease Ontology, and Reactome enrichments, and does not affect GO enrichments.

maxWidth_nchar_plot
: Integer (>=10). Default 50. Maximum number of characters for a term before it is truncated.

outputFolder
: Character or NULL. Default NULL. If set to NULL, the default output folder as specified when initiating the object in initializeGRN will be used. Otherwise, all output from this function will be put into the specified folder. If a folder is provided, while we recommend specifying an absolute path, a relative one also works.

basenameOutput
: NULL or character. Default NULL. Basename of the output files that are produced. If set to NULL, a default basename is chosen. If a custom basename is specified, all output files will have the chosen basename as file prefix, be careful with not overwriting already existing files (if forceRerun is set to TRUE)

plotAsPDF
: TRUE or FALSE. Default TRUE.Should the plots be printed to a PDF file? If set to TRUE, a PDF file is generated, the name of which depends on the value of basenameOutput. If set to FALSE, all plots are printed to the currently active device. Note that most functions print more than one plot, which means you may only see the last plot depending on your active graphics device.

pdf_width
: Number>0. Default 12. Width of the PDF, in cm.

pdf_height
: Number >0. Default 12. Height of the PDF, in cm.

pages
: Integer vector or NULL. Default NULL. Page number(s) to plot. Can be used to plot only specific pages to a PDF or the currently active graphics device.

forceRerun
: TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

The same GRN object, without modifications.

See Also

plotGeneralEnrichment

plotCommunitiesEnrichment

calculateTFEnrichment

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = plotTFEnrichment(GRN, n = 5, plotAsPDF = FALSE, pages = 1)
```

plot_stats_connectionSummary *Plot various network connectivity summaries for a GRN object*

Description

Plot various network connectivity summaries for a GRN object

Usage

```
plot_stats_connectionSummary(
  GRN,
  type = "heatmap",
  outputFolder = NULL,
  basenameOutput = NULL,
  plotAsPDF = TRUE,
  pdf_width = 12,
  pdf_height = 12,
  pages = NULL,
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
type	Character. Either "heatmap" or "boxplot". Default "heatmap". Which plot type to produce?
outputFolder	Character or NULL. Default NULL. If set to NULL, the default output folder as specified when initiating the object in initializeGRN will be used. Otherwise, all output from this function will be put into the specified folder. If a folder is provided, while we recommend specifying an absolute path, a relative one also works.
basenameOutput	NULL or character. Default NULL. Basename of the output files that are produced. If set to NULL, a default basename is chosen. If a custom basename is specified, all output files will have the chosen basename as file prefix, be careful with not overwriting already existing files (if forceRerun is set to TRUE)
plotAsPDF	TRUE or FALSE. Default TRUE.Should the plots be printed to a PDF file? If set to TRUE, a PDF file is generated, the name of which depends on the value of basenameOutput. If set to FALSE, all plots are printed to the currently active device. Note that most functions print more than one plot, which means you may only see the last plot depending on your active graphics device.
pdf_width	Number>0. Default 12. Width of the PDF, in cm.
pdf_height	Number >0. Default 12. Height of the PDF, in cm.
pages	Integer vector or NULL. Default NULL. Page number(s) to plot. Can be used to plot only specific pages to a PDF or the currently active graphics device.

forceRerun TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

The same GRN object, without modifications.

Examples

```
# See the Workflow vignette on the GRaNIE website for examples
GRN = loadExampleObject()
GRN = plot_stats_connectionSummary(GRN, forceRerun = FALSE, plotAsPDF = FALSE, pages = 1)
```

---

visualizeGRN *Visualize a filtered eGRN in a flexible manner.*

Description

This function can visualize a filtered eGRN in a very flexible manner and requires a GRN object as generated by build_eGRN_graph.

Usage

```
visualizeGRN(
  GRN,
  outputFolder = NULL,
  basenameOutput = NULL,
  plotAsPDF = TRUE,
  pdf_width = 12,
  pdf_height = 12,
  title = NULL,
  maxEdgesToPlot = 500,
  nCommunitiesMax = 8,
  graph = "TF-gene",
  colorby = "type",
  layout = "fr",
  vertice_color_TFs = list(h = 10, c = 85, l = c(25, 95)),
  vertice_color_peaks = list(h = 135, c = 45, l = c(35, 95)),
  vertice_color_genes = list(h = 260, c = 80, l = c(30, 90)),
  vertexLabel_cex = 0.4,
  vertexLabel_dist = 0,
  forceRerun = FALSE
)
```

Arguments

GRN	Object of class GRN
outputFolder	Character or NULL. Default NULL. If set to NULL, the default output folder as specified when initiating the object in initializeGRN will be used. Otherwise, all output from this function will be put into the specified folder. If a folder is provided, while we recommend specifying an absolute path, a relative one also works.
basenameOutput	NULL or character. Default NULL. Basename of the output files that are produced. If set to NULL, a default basename is chosen. If a custom basename is specified, all output files will have the chosen basename as file prefix, be careful with not overwriting already existing files (if forceRerun is set to TRUE)
plotAsPDF	TRUE or FALSE. Default TRUE.Should the plots be printed to a PDF file? If set to TRUE, a PDF file is generated, the name of which depends on the value of basenameOutput. If set to FALSE, all plots are printed to the currently active device. Note that most functions print more than one plot, which means you may only see the last plot depending on your active graphics device.
pdf_width	Number>0. Default 12. Width of the PDF, in cm.
pdf_height	Number >0. Default 12. Height of the PDF, in cm.
title	NULL or Character. Default NULL. Title to be assigned to the plot.
maxEdgesToPlot	Integer > 0. Default 500. Refers to the maximum number of connections to be plotted. If the network size is above this limit, nothing will be drawn. In such a case, it may help to either increase the value of this parameter or set the filtering criteria for the network to be more stringent, so that the network becomes smaller.
nCommunitiesMax	Integer > 0. Default 8. Maximum number of communities that get a distinct coloring. All additional communities will be colored with the same (gray) color.
graph	Character. Default TF-gene. One of: TF-gene, TF-peak-gene. Whether to plot a graph with links from TFs to peaks to gene, or the graph with the inferred TF to gene connections.
colorby	Character. Default type. Either type or community. Color the vertices by either type (TF/peak/gene) or community. See calculateCommunitiesStats
layout	Character. Default fr. One of star, fr, sugiyama, kk, lgl, graphopt, mds, sphere
vertice_color_TFs	Named list. Default list(h = 10, c = 85, l = c(25, 95)). The list must specify the color in hcl format (hue, chroma, luminence). See the colorspace package for more details and examples
vertice_color_peaks	Named list. Default list(h = 135, c = 45, l = c(35, 95)).
vertice_color_genes	Named list. Default list(h = 260, c = 80, l = c(30, 90)).
vertexLabel_cex	Numeric. Default 0.4. Font size (multiplication factor, device-dependent)

vertexLabel_dist
: Numeric. Default 0 vertex. Distance between the label and the vertex.

forceRerun
: TRUE or FALSE. Default FALSE. Force execution, even if the GRN object already contains the result. Overwrites the old results.

Value

The same GRN object, without modifications.

See Also

build_eGRN_graph

Examples

```
GRN = loadExampleObject()
GRN = visualizeGRN(GRN, maxEdgesToPlot = 700, graph = "TF-gene", colorby = "type")
```

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