Package 'hpgltools'

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Type Package

Title A pile of (hopefully) useful R functions

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Description This is a set of functions I have been using in my various analyses
in the El-Sayed laboratory. The set of tasks included herein run a
spectrum from preprocessing count-tables from RNAseq-like data,
through differential expression analyses, to post-processing tasks
like gene ontology enrichment. Along the way, these function seek
to make plotting analyses consistent, provide multiple entry-points
to the various tools, and handle corner cases which are not
flexibly handled by the packages this is based upon.

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Suggests affy, AnnotationDbi, AnnotationForge, AnnotationHub,
BiocGenerics, BiocManager, biomaRt, Biostrings, BRAIN, BSgenome,
caret, Category, cleaver, clusterProfiler, corpcor, corrplot, curl,
DBI, desc, DESeq2, devEMF, devtools, directlabels, doParallel,
DOSE, doSNOW, DSS,
EBSeq, EDASeq, edgeR, EuPathDB,
fastcluster, fastICA, ffpe, fission,
genbankr, genefilter, GenomicRanges, GenomeInfoDb, genoPlotR, ggdendro,
ggrepel, ggstatsplot, ggthemes, goseq, GO.db, GOstats,
graph, GSVA, GSVAdata, gtools, gplots, gProfileR, gprofiler2, GSEABase,
Heatplus, Hmisc, Homo.sapiens, htmlwidgets, httr,
IHW, inflection, IRanges, isva, iterators,
jsonlite,
KEGGREST, KEGGgraph,
lattice, limma, locfit,
matrixStats, miscTools, MLSeq, motifRG, MSnbase, mygene, mzR,
openxlsx, OrganismDbi,
pander, parallel, pasilla, pathview, pcaMethods, plotly, plyr, preprocessCore, PROPER,
qvalue,

R.utils, RColorBrewer, RCurl, readr, reactome.db, readODS, readxl, reshape2, rGADEM, Rgraphviz,
rhdf5, rjson, rmarkdown, robust, robustbase, Rsamtools, RSQLite, Rtsne,
rtracklayer, ruv, RUVSeq, rvest,
S4Vectors, scales, SeqTools, seqLogo, SmartSVA, statmod, stringi, stringr, survJamda, SWATH2stats,
taxize, testthat, tidyr, topGO, tximport,
UniProt.ws, uwot,
xCell, xml2,
Vennerable, venneuler

Imports data.table, dplyr,
foreach,
ggplot2, GenomicFeatures, glue,
knitr,
magrittr, methods,
rlang,
sva,
variancePartition

Depends Biobase, SummarizedExperiment

VignetteBuilder knitr

ByteCompile true

biocViews DifferentialExpression

Encoding UTF-8

RoxygenNote 7.1.1

Collate '01_hpgltools.r'
'annotation_biomart.r'
'annotation_genbank.r'
'annotation_gff.r'
'annotation_kegg.r'
'annotation_microbesonline.r'
'annotation_orgdb.r'
'annotation_txt.r'
'annotation_uniprot.r'
'annotation_shared.r'
'expt.r'
'de_shared.r'
'de_basic.r'
'de_edger.r'
'de_deseq.r'
'de_ebseq.r'
'de_limma.r'
'de_plots.r'
'de_xlsx.r'
'normalize_shared.r'
'normalize_filter.r'
'normalize_convert.r'

'normalize_transform.r'
'normalize_norm.r'
'normalize_batch.r'
'plot_shared.r'
'plot_bar.r'
'plot_distribution.r'
'plot_dotplot.r'
'plot_heatmap.r'
'plot_hist.r'
'plot_point.r'
'plot_venn.r'
'gsva.r'
'ontology_shared.r'
'ontology_goseq.r'
'ontology_gprofiler.r'
'ontology_gostats.r'
'helpers_misc.r'
'ontology_topgo.r'
'ontology_clusterprofiler.r'
'ontology_plots.r'
'ontology_xlsx.r'
'ontology_kegg.r'
'dimension_reduction.r'
'plot_circos.r'
'plot_genplot.r'
'plot_misc.r'
'model_testing.r'
'alt_splicing.r'
'model_varpartition.r'
'tnseq.r'
'proteomics.r'
'plot_proteomics.r'
'variants.r'
'se.r'
'sequence.r'
'power_estimation.r'
'xlsx.r'
'motif.r'

R topics documented:

%:::% *R CMD check is super annoying about :::.*

Description

In a fit of pique, I did a google search to see if anyone else has been annoyed in the same way as was I. Yihui Xie was, and in his email to r-devel in 2013 he proposed a game of hide-and-seek; which I am repeating here.

Usage

```
pkg %:::% fun
```

Arguments

pkg	on the left hand side
fun	on the right hand side

Details

This just implements ::: as an infix operator that will not trip check.

add_conditional_nas *Replace 0 with NA if not all entries for a given condition are 0.*

Description

This will hopefully handle a troubling corner case in Volker's data: He primarily wants to find proteins which are found in one condition, but _not_ in another. However, due to the unknown unknown problem in DIA acquisition, answering this question is difficult. If one uses a normal expressionset or msnset or whatever, one of two things will happen: either the 0/NA proteins will be entirely removed/ignored, or they will lead to spurious 'significant' calls. MSstats, to its credit, does a lot to try to handle these cases; but in the case Volker is most interested, it will exclude the interesting proteins entirely.

Usage

```
add_conditional_nas(expt, fact = "condition", method = "NA")
```

Arguments

expt	Expressionset to examine.
fact	Experimental design factor to use.
method	Specify whether to leave the NAs as NA, or replace them with the mean of all non-NA values.

Details

So, here is what I am going to do: Iterate through each element of the chosen experimental design factor, check if all samples for that condition are 0, if so; leave them. If not all the samples have 0 for the given condition, then replace the zero entries with NA. This should allow for stuff like rowMeans(na.rm = TRUE) to provide useful information.

Finally, this will add columns to the annotations which tell the number of observations for each protein after doing this.

Value

New expressionset with some, but not all, 0s replaced with NA.

`all_adjusters` *Combine all surrogate estimators and batch correctors into one function.*

Description

For a long time, I have mostly kept my surrogate estimators and batch correctors separate. However, that separation was not complete, and it really did not make sense. This function brings them together. This now contains all the logic from the freshly deprecated get_model_adjust().

Usage

```
all_adjusters(
  input,
  design = NULL,
  estimate_type = "sva",
  batch1 = "batch",
  batch2 = NULL,
  surrogates = "be",
  low_to_zero = FALSE,
  cpus = 4,
  na_to_zero = TRUE,
  expt_state = NULL,
  confounders = NULL,
  chosen_surrogates = NULL,
  adjust_method = "ruv",
  filter = "raw",
  thresh = 1,
  noscale = FALSE,
  prior_plots = FALSE
)
```

Arguments

input	Dataframe or expt or whatever as the data to analyze/modify.
design	If the data is not an expt, then put the design here.
estimate_type	Name of the estimator.
batch1	Column in the experimental design for the first known batch.
batch2	Only used by the limma method, a second batch column.
surrogates	Either a number of surrogates or a method to search for them.
expt_state	If this is not an expt, provide the state of the data here.
confounders	List of confounded factors for smartSVA/iSVA.
...	Extra arguments passed along to other methods.

Details

This applies the methodologies very nicely explained by Jeff Leek at https://github.com/jtleek/svaseq/blob/master/recount.Rm and attempts to use them to acquire estimates which may be applied to an experimental model by either EdgeR, DESeq2, or limma. In addition, it modifies the count tables using these estimates so that one may play with the modified counts and view the changes (with PCA or heatmaps or whatever). Finally, it prints a couple of the plots shown by Leek in his document. In other words, this is entirely derivative of someone much smarter than me.

Value

List containing surrogate estimates, new counts, the models, and some plots, as available.

See Also

[all_adjuster()] [isva] [sva] [limma::removeBatchEffect()] [corpcor] [edgeR] [RUVSeq] [SmartSVA] [variancePartition] [counts_from_surrogates()]

---

all_ontology_searches *Perform ontology searches given the results of a differential expression analysis.*

Description

This takes a set of differential expression results, extracts a subset of up/down expressed genes; passes them to goseq, clusterProfiler, topGO, GOstats, and gProfiler; collects the outputs; and returns them in a (hopefully) consistent fashion. It attempts to handle the differing required annotation/GOid inputs required for each tool and/or provide supported species in ways which the various tools expect.

Usage

```
all_ontology_searches(
  de_out,
  gene_lengths = NULL,
  goids = NULL,
  n = NULL,
  z = NULL,
  lfc = NULL,
  p = NULL,
  overwrite = FALSE,
  species = "unsupported",
  orgdb = "org.Dm.eg.db",
  goid_map = "reference/go/id2go.map",
  gff_file = NULL,
  gff_type = "gene",
  do_goseq = TRUE,
  do_cluster = TRUE,
  do_topgo = TRUE,
  do_gostats = TRUE,
  do_gprofiler = TRUE,
  do_trees = FALSE,
  ...
)
```

Arguments

de_out	List of topTables comprising limma/deseq/edger outputs.
gene_lengths	Data frame of gene lengths for goseq.
goids	Data frame of goids and genes.
n	Number of genes at the top/bottom of the fold-changes to define 'significant.'
z	Number of standard deviations from the mean fold-change used to define 'significant.'
lfc	Log fold-change used to define 'significant'.
p	Maximum pvalue to define 'significant.'
overwrite	Overwrite existing excel results file?
species	Supported organism used by the tools.
orgdb	Provide an organismDbi/Orgdb to hold the various annotation data, in response to the shift of clusterprofiler and friends towards using them.
goid_map	Mapping file used by topGO, if it does not exist then goids_df creates it.
gff_file	gff file containing the annotations used by gff2genetable from clusterprofiler.
gff_type	Column to use from the gff file for the universe of genes.
do_goseq	Perform simple_goseq()?
do_cluster	Perform simple_clusterprofiler()?
do_topgo	Perform simple_topgo()?

do_gostats	Perform simple_gostats()?
do_gprofiler	Perform simple_gprofiler()?
do_trees	make topGO trees from the data?
...	Arguments to pass through in arglist.

Value

a list of up/down ontology results from goseq/clusterprofiler/topgo/gostats, and associated trees.

See Also

[goseq] [clusterProfiler] [topGO] [goStats] [gProfiler] [GO.db]

Examples

```
## Not run:
 many_comparisons = limma_pairwise(expt = an_expt)
 tables = many_comparisons$limma
 this_takes_forever = limma_ontology(tables, gene_lengths = lengthdb,
                                     goids = goids_df, z = 1.5, gff_file='length_db.gff')

## End(Not run)
```

---

all_pairwise *Perform limma, DESeq2, EdgeR pairwise analyses.*

Description

This takes an expt object, collects the set of all possible pairwise comparisons, sets up experimental models appropriate for the differential expression analyses, and performs them.

Usage

```
all_pairwise(
  input = NULL,
  conditions = NULL,
  batches = NULL,
  model_cond = TRUE,
  modify_p = FALSE,
  model_batch = TRUE,
  filter = NULL,
  model_intercept = FALSE,
  extra_contrasts = NULL,
  alt_model = NULL,
  libsize = NULL,
  test_pca = TRUE,
  annot_df = NULL,
```

```
  parallel = TRUE,
  do_basic = TRUE,
  do_deseq = TRUE,
  do_ebseq = NULL,
  do_edger = TRUE,
  do_limma = TRUE,
  convert = "cpm",
  norm = "quant",
  verbose = TRUE,
  ...
)
```

Arguments

input	Dataframe/vector or expt class containing count tables, normalization state, etc.
conditions	Factor of conditions in the experiment.
batches	Factor of batches in the experiment.
model_cond	Include condition in the model? This is likely always true.
modify_p	Depending on how it is used, sva may require a modification of the p-values.
model_batch	Include batch in the model? This may be true/false/"sva" or other methods supported by all_adjusters().
filter	Added because I am tired of needing to filter the data before invoking all_pairwise().
model_intercept	Use an intercept model instead of cell means?
extra_contrasts	Optional extra contrasts beyone the pairwise comparisons. This can be pretty neat, lets say one has conditions A,B,C,D,E and wants to do (C/B)/A and (E/D)/A or (E/D)/(C/B) then use this with a string like: "c_vs_b_ctrla = (C-B)-A, e_vs_d_ctrla = (E-D)-A, de_vs_cb = (E-D)-(C-B)".
alt_model	Alternate model to use rather than just condition/batch.
libsize	Library size of the original data to help voom().
test_pca	Perform some tests of the data before/after applying a given batch effect.
annot_df	Annotations to add to the result tables.
parallel	Use dopar to run limma, deseq, edger, and basic simultaneously.
do_basic	Perform a basic analysis?
do_deseq	Perform DESeq2 pairwise?
do_ebseq	Perform EBSeq (caveat, this is NULL as opposed to TRUE/FALSE so it can choose).
do_edger	Perform EdgeR?
do_limma	Perform limma?
convert	Modify the data with a 'conversion' method for PCA?
norm	Modify the data with a 'normalization' method for PCA?
...	Picks up extra arguments into arglist, currently only passed to write_limma().

Details

Tested in test_29de_shared.R This runs limma_pairwise(), deseq_pairwise(), edger_pairwise(), basic_pairwise() each in turn. It collects the results and does some simple comparisons among them.

Value

A list of limma, deseq, edger results.

See Also

[limma_pairwise()] [edger_pairwise()] [deseq_pairwise()] [ebseq_pairwise()] [basic_pairwise()]

Examples

```
## Not run:
 lotsodata <- all_pairwise(input = expt, model_batch = "svaseq")
 summary(lotsodata)
 ## limma, edger, deseq, basic results; plots; and summaries.

## End(Not run)
```

---

backup_file *Make a backup of an existing file with n revisions, like VMS!*

Description

Sometimes I just want to kick myself for overwriting important files and then I remember using VMS and wish modern computers were a little more like it.

Usage

```
backup_file(backup_file, backups = 4)
```

Arguments

backup_file	Filename to backup.
backups	How many revisions?

base_size *The following sets the ggplot2 default text size.*

Description

The following sets the ggplot2 default text size.

Usage

```
base_size
```

Format

An object of class `numeric` of length 1.

basic_pairwise *The simplest possible differential expression method.*

Description

Perform a pairwise comparison among conditions which takes nothing into account. It _only_ takes the conditions, a mean value/variance among them, divides by condition, and returns the result. No fancy nomalizations, no statistical models, no nothing. It should be the very worst method possible. But, it should also provide a baseline to compare the other tools against, they should all do better than this, always.

Usage

```
basic_pairwise(
  input = NULL,
  design = NULL,
  conditions = NULL,
  batches = NULL,
  model_cond = TRUE,
  model_intercept = FALSE,
  alt_model = NULL,
  model_batch = FALSE,
  force = FALSE,
  fx = "mean",
  ...
)
```

Arguments

input	Count table by sample.
design	Data frame of samples and conditions.
conditions	Not currently used, but passed from all_pairwise()
batches	Not currently used, but passed from all_pairwise()
model_cond	Not currently used, but passed from all_pairwise()
model_intercept	Not currently used, but passed from all_pairwise()
alt_model	Not currently used, but passed from all_pairwise()
model_batch	Not currently used, but passed from all_pairwise()
force	Force as input non-normalized data?
fx	What function to use for mean/median?
...	Extra options passed to arglist.

Details

Tested in test_27de_basic.R This function was written after the corresponding functions in de_deseq.R, de_edger.R, and de_limma.R. Like those, it performs the full set of pairwise comparisons and returns a list of the results. As mentioned above, unlike those, it is purposefully stupid.

Value

Df of pseudo-logFC, p-values, numerators, and denominators.

See Also

[deseq_pairwise()] [limma_pairwise()] [edger_pairwise()] [ebseq_pairwise()]

Examples

```
## Not run:
 expt <- create_expt(metadata = "sample_sheet.xlsx", gene_info = "annotations")
 basic_de <- basic_pairwise(expt)
 basic_tables <- combine_de_tables(basic_de)

## End(Not run)
```

batch_counts *Perform different batch corrections using limma, sva, ruvg, and cbcb-SEQ.*

Description

I found this note which is the clearest explanation of what happens with batch effect data: https://support.bioconductor.org/p/7
Just to be clear, there's an important difference between removing a batch effect and modelling a batch effect. Including the batch in your design formula will model the batch effect in the regression step, which means that the raw data are not modified (so the batch effect is not removed), but instead the regression will estimate the size of the batch effect and subtract it out when performing all other tests. In addition, the model's residual degrees of freedom will be reduced appropriately to reflect the fact that some degrees of freedom were "spent" modelling the batch effects. This is the preferred approach for any method that is capable of using it (this includes DESeq2). You would only remove the batch effect (e.g. using limma's removeBatchEffect function) if you were going to do some kind of downstream analysis that can't model the batch effects, such as training a classifier. I don't have experience with ComBat, but I would expect that you run it on log-transformed CPM values, while DESeq2 expects raw counts as input. I couldn't tell you how to properly use the two methods together.

Usage

```
batch_counts(
  count_table,
  method = TRUE,
  expt_design = NULL,
  batch1 = "batch",
  current_state = NULL,
  current_design = NULL,
  expt_state = NULL,
  surrogate_method = NULL,
  surrogates = NULL,
  low_to_zero = FALSE,
  cpus = 4,
  batch2 = NULL,
  noscale = TRUE,
  ...
)
```

Arguments

count_table	Matrix of (pseudo)counts.
batch1	Column in the design table describing the presumed covariant to remove.
expt_state	Current state of the expt in an attempt to avoid double-normalization.
batch2	Column in the design table describing the second covariant to remove (only used by limma at the moment).

noscale	Used for combatmod, when true it removes the scaling parameter from the invocation of the modified combat.
...	More options for you!
design	Model matrix defining the experimental conditions/batches/etc.
batch	String describing the method to try to remove the batch effect (or FALSE to leave it alone, TRUE uses limma).

Value

The 'batch corrected' count table and new library size. Please remember that the library size which comes out of this may not be what you want for voom/limma and would therefore lead to spurious differential expression values.

See Also

[limma] [edgeR] [RUVSeq] [sva]

Examples

```
## Not run:
 limma_batch <- batch_counts(table, design, batch1='batch', batch2='strain')
 sva_batch <- batch_counts(table, design, batch='sva')

## End(Not run)
```

---

bioc_all *Grab a copy of all bioconductor packages and install them by type*

Description

This uses jsonlite to get a copy of all bioconductor packages by name and then iterates through them with BiocManager to install all of them. It performs a sleep between each installation in an attempt to avoid being obnoxious. As a result, it will of a necessity take forever.

Usage

```
bioc_all(
  release = NULL,
  mirror = "bioconductor.statistik.tu-dortmund.de",
  base = "packages",
  type = "software",
  suppress_updates = TRUE,
  suppress_auto = TRUE,
  force = FALSE
)
```

Arguments

release	Bioconductor release to use, should probably be adjusted to automatically find it.
mirror	Bioconductor mirror to use.
base	Base directory on the mirror to download from.
type	Type in the tree to use (software or annotation)
suppress_updates	For BiocLite(), don't update?
suppress_auto	For BiocLite(), don't update?
force	Install if already installed?

Value

a number of packages installed

See Also

[BiocManager] [jsonlite]

Examples

```
## Not run:
 go_get_some_coffee_this_will_take_a_while <- bioc_all()

## End(Not run)
```

---

cbcb_batch *A function suggested by Hector Corrada Bravo and Kwame Okrah for batch removal.*

Description

During a lab meeting, the following function was suggested as a quick and dirty batch removal tool. It takes data and a model including a 'batch' factor, invokes limma on them, removes the batch factor, does a cross product of the fitted data and modified model and uses that with residuals to get a new data set.

Usage

```
cbcb_batch(
  normalized_counts,
  model,
  conditional_model = NULL,
  batch_model = NULL,
  batch1 = "batch",
  condition = "condition",
```

```
  matrix_scale = "linear",
  return_scale = "linear",
  method = "subtract"
)
```

Arguments

normalized_counts	Data frame of log2cpm counts.
model	Balanced experimental model containing condition and batch factors.
batch1	Column containing the first batch's metadata in the experimental design.
condition	Column containing the condition information in the metadata.
matrix_scale	Is the data on a linear or log scale?
return_scale	Do you want the data returned on the linear or log scale?
method	I found a couple ways to apply the surrogates to the data. One method subtracts the residuals of a batch model, the other adds the conditional.

Value

Dataframe of residuals after subtracting batch from the model.

See Also

[limma::voom()] [limma::lmFit()]

Examples

```
## Not run:
 newdata <- cbcb_batch_effect(counts, expt_model)

## End(Not run)
```

---

cbcb_combat *A modified version of comBatMod.*

Description

This is a hack of Kwame Okrah's combatMod to make it not fail on corner-cases. This was mostly copy/pasted from https://github.com/kokrah/cbcbSEQ/blob/master/R/transform.R

Usage

```
cbcb_combat(dat, batch, mod, noscale = TRUE, prior.plots = FALSE, ...)
```

Arguments

dat	Df to modify.
batch	Factor of batches.
mod	Factor of conditions.
noscale	The normal 'scale' option squishes the data too much, so this defaults to TRUE.
prior.plots	Print out prior plots?
...	Extra options are passed to arglist

Value

Df of batch corrected data

See Also

[sva] [sva::ComBat()]

Examples

```
## Not run:
 df_new = cbcb_combat(df, batches, model)

## End(Not run)
```

---

cbcb_filter_counts *Filter low-count genes from a data set using cpm data and a threshold.*

Description

This was a function written by Kwame Okrah and perhaps also Laura Dillon to remove low-count genes. It drops genes based on a cpm threshold and number of samples.

Usage

```
cbcb_filter_counts(count_table, threshold = 1, min_samples = 2, libsize = NULL)
```

Arguments

count_table	Data frame of (pseudo)counts by sample.
threshold	Lower threshold of counts for each gene.
min_samples	Minimum number of samples.
libsize	Table of library sizes.

Value

Dataframe of counts without the low-count genes.

See Also

[edgeR]

Examples

```
## Not run:
 filtered_table <- cbcb_filter_counts(count_table)

## End(Not run)
```

`check_plot_scale` *Look at the range of the data for a plot and use it to suggest if a plot should be on log scale.*

Description

There are a bunch of plots which often-but-not-always benefit from being displayed on a log scale rather than base 10. This is a quick and dirty heuristic which suggests the appropriate scale. If the data 'should' be on the log scale and it has 0s, then they are moved to 1 so that when logged they will return to 0. Similarly, if there are negative numbers and the intended scale is log, then this will set values less than 0 to zero to avoid imaginary numbers.

Usage

```
check_plot_scale(data, scale = NULL, max_data = 10000, min_data = 10)
```

Arguments

`data`	Data to plot.
`scale`	If known, this will be used to define what (if any) values to change.
`max_data`	Define the upper limit for the heuristic.
`min_data`	Define the lower limit for the heuristic.

`check_xlsx_worksheet` *Create the named worksheet in a workbook, this function was not well named.*

Description

This tries to make sure that some of the problems of creating new worksheets do not occur. E.g. Names must be less than something and must not exist.

Usage

```
check_xlsx_worksheet(wb, sheet)
```

Arguments

wb	Workbook to modify
sheet	Sheet to check/create.

Value

The workbook object hopefully with a new worksheet.

See Also

[openxlsx::addWorksheet()]

---

choose_basic_dataset *Attempt to ensure that input data to basic_pairwise() is suitable.*

Description

basic_pairwise() assumes log2 data as input, use this to ensure that is true.

Usage

```
choose_basic_dataset(input, force = FALSE, ...)
```

Arguments

input	An expressionset containing expt to test and/or modify.
force	If we want to try out other distributed data sets, force it in using me.
...	future options, I think currently unused.

Value

data ready for basic_pairwise()

See Also

[Biobase] [choose_dataset()] [normalize_expt()]

Examples

```
## Not run:
 ready <- choose_basic_dataset(expt)

## End(Not run)
```

choose_binom_dataset *A sanity check that a given set of data is suitable for methods which assume a negative binomial distribution of input.*

Description

Take an expt and poke at it to ensure that it will not result in troubled results.

Usage

```
choose_binom_dataset(input, verbose = TRUE, force = FALSE, ...)
```

Arguments

input	Expressionset containing expt object.
force	Ignore every warning and just use this data.
...	Extra arguments passed to arglist.

Details

Invoked by deseq_pairwise() and edger_pairwise().

Value

dataset suitable for limma analysis

See Also

[DESeq2] [edgeR] [choose_basic_dataset()] [choose_limma_dataset()]

choose_dataset *Choose a suitable data set for Edger/DESeq*

Description

The _pairwise family of functions all demand data in specific formats. This tries to make that consistent.

Usage

```
choose_dataset(input, choose_for = "limma", force = FALSE, verbose = TRUE, ...)
```

Arguments

input	Expt input.
choose_for	One of limma, deseq, edger, or basic. Defines the requested data state.
force	Force non-standard data?
...	More options for future expansion.

Details

Invoked by _pairwise().

Value

List the data, conditions, and batches in the data.

See Also

[choose_binom_dataset()] [choose_limma_dataset()] [choose_basic_dataset()]

Examples

```
## Not run:
 starting_data <- create_expt(metadata)
 modified_data <- normalize_expt(starting_data, transform = "log2", norm = "quant")
 a_dataset <- choose_dataset(modified_data, choose_for = "deseq")
 ## choose_dataset should see that log2 data is inappropriate for DESeq2 and
 ## return it to a base10 state.

## End(Not run)
```

---

choose_limma_dataset *A sanity check that a given set of data is suitable for analysis by limma.*

Description

Take an expt and poke at it to ensure that it will not result in troubled limma results.

Usage

```
choose_limma_dataset(
  input,
  force = FALSE,
  which_voom = "limma",
  verbose = TRUE,
  ...
)
```

Arguments

input	Expressionset containing expt object.
force	Ingore warnings and use the provided data asis.
which_voom	Choose between limma'svoom, voomWithQualityWeights, or the hpgl equivalents.
...	Extra arguments passed to arglist.

Value

dataset suitable for limma analysis

See Also

[limma] [choose_dataset()]

---

choose_model *Try out a few experimental models and return a likely working option.*

Description

The _pairwise family of functions all demand an experimental model. This tries to choose a consistent and useful model for all for them. This does not try to do multi-factor, interacting, nor dependent variable models, if you want those do them yourself and pass them off as alt_model.

Usage

```
choose_model(
  input,
  conditions = NULL,
  batches = NULL,
  model_batch = TRUE,
  model_cond = TRUE,
  model_intercept = FALSE,
  alt_model = NULL,
  alt_string = NULL,
  intercept = 0,
  reverse = FALSE,
  contr = NULL,
  surrogates = "be",
  verbose = TRUE,
  ...
)
```

Arguments

input	Input data used to make the model.
conditions	Factor of conditions in the putative model.
batches	Factor of batches in the putative model.
model_batch	Try to include batch in the model?
model_cond	Try to include condition in the model? (Yes!)
model_intercept	Use an intercept model instead of cell-means?
alt_model	Use your own model.
alt_string	String describing an alternate model.
intercept	Choose an intercept for the model as opposed to 0.
reverse	Reverse condition/batch in the model? This shouldn't/doesn't matter but I wanted to test.
contr	List of contrasts.arg possibilities.
surrogates	Number of or method used to choose the number of surrogate variables.
...	Further options are passed to arglist.

Details

Invoked by the _pairwise() functions.

Value

List including a model matrix and strings describing cell-means and intercept models.

See Also

[stats::model.matrix()]

Examples

```
## Not run:
 a_model <- choose_model(expt, model_batch = TRUE, model_intercept = FALSE)
 a_model$chosen_model
 ## ~ 0 + condition + batch

## End(Not run)
```

circos_arc *Write arcs between chromosomes in circos.*

Description

Ok, so when I said I only do 1 chromosome images, I lied. This function tries to make writing arcs between chromosomes easier. It too works in 3 stages, It writes out a data file using cfgout as a basename and the data from df in the circos arc format into circos/data/bob_arc.txt It then writes out a configuration plot stanza in circos/conf/bob_arc.conf and finally adds an include to circos/bob.conf

Usage

```
circos_arc(
  cfg,
  df,
  first_col = "seqnames",
  second_col = "seqnames.2",
  color = "blue",
  radius = 0.75,
  thickness = 3,
  ribbon = "yes",
  show = "yes",
  z = "0"
)
```

Arguments

cfg	Result of circos_prefix(), contains a bunch of useful material.
df	Dataframe with starts/ends and the floating point information.
first_col	Name of the first chromosome.
second_col	Name of the second chromosome.
color	Color of the chromosomes.
radius	Outer radius at which to add the arcs.
thickness	Integer thickness of the arcs.
ribbon	Print as a ribbon?
show	Show these arcs?
z	Correction parameter.

Details

In its current implementation, this only understands two chromosomes. A minimal amount of logic and data organization will address this weakness.

Value

The file to which the arc configuration information was written.

`circos_heatmap` *Write tiles of arbitrary heat-mappable data in circos.*

Description

This function tries to make the writing circos heatmaps easier. Like circos_plus_minus() and circos_hist() it works in 3 stages, It writes out a data file using cfgout as a basename and the data from df in the circos histogram format into circos/data/bob_heatmap.txt It then writes out a configuration plot stanza in circos/conf/bob_heatmap.conf and finally adds an include to circos/bob.conf

Usage

```
circos_heatmap(
  cfg,
  df,
  colname = "logFC",
  color_mapping = 0,
  min_value = NULL,
  max_value = NULL,
  basename = "",
  colors = NULL,
  color_choice = "spectral-9-div",
  scale_log_base = 1,
  outer = 0.9,
  rules = NULL,
  width = 0.08,
  spacing = 0.02
)
```

Arguments

`cfg`	Result of circos_prefix(), contains a bunch of useful material.
`df`	Dataframe with starts/ends and the floating point information.
`colname`	Name of the column with the data of interest.
`color_mapping`	0 means no overflows for min/max, 1 means overflows of min get a chosen color, 2 means overflows of both min/max get chosen colors.
`min_value`	Minimum value for the data.
`max_value`	Maximum value for the data.
`basename`	Make sure the written configuration files get different names with this.
`colors`	Colors of the heat map.
`color_choice`	Name of the heatmap to use, I forget how this interacts with color...

scale_log_base	Defines how the range of colors will be ranged with respect to the values in the data.
outer	Floating point radius of the circle into which to place the heatmap.
rules	some extra rules?
width	Width of each tile in the heatmap.
spacing	Radial distance between outer, inner, and inner to whatever follows.

Value

Radius after adding the histogram and the spacing.

---

circos_hist *Write histograms of arbitrary floating point data in circos.*

Description

This function tries to make the writing of histogram data in circos easier. Like circos_plus_minus() it works in 3 stages, It writes out a data file using cfgout as a basename and the data from df in the circos histogram format into circos/data/bob_hist.txt It then writes out a configuration plot stanza in circos/conf/bob_hist.conf and finally adds an include to circos/bob.conf

Usage

```
circos_hist(
  cfg,
  df,
  colname = "logFC",
  basename = "",
  color = "blue",
  fill_color = "blue",
  fill_under = "yes",
  extend_bin = "no",
  thickness = "0",
  orientation = "out",
  outer = 0.9,
  width = 0.08,
  spacing = 0
)
```

Arguments

cfg	Result of circos_prefix(), contains a bunch of useful material.
df	Dataframe with starts/ends and the floating point information.
colname	Name of the column with the data of interest.
basename	Location to write the circos data (usually cwd).

color	Color of the plotted data.
fill_color	Guess
fill_under	The circos histogram fill under parameter
extend_bin	Extend bins?
thickness	histogram thickness.
orientation	facing in or out?
outer	Floating point radius of the circle into which to place the data.
width	Radial width of each tile.
spacing	Distance between outer, inner, and inner to whatever follows.

Value

Radius after adding the histogram and the spacing.

`circos_ideogram` *Create the description of chromosome markings.*

Description

This function writes ideogram files for circos.

Usage

```
circos_ideogram(
  name = "default",
  conf_dir = "circos/conf",
  band_url = NULL,
  fill = "yes",
  stroke_color = "black",
  show_bands = "yes",
  fill_bands = "yes",
  thickness = "20",
  stroke_thickness = "2",
  label_font = "condensedbold",
  spacing_default = "0",
  spacing_break = "0",
  fill_color = "black",
  radius = "0.85",
  radius_padding = "0.05",
  label_size = "36",
  band_stroke_thickness = "2"
)
```

Arguments

name	Name of the configuration file to which to add the ideogram.
conf_dir	Where does the configuration live?
band_url	Provide a url for making these imagemaps?
fill	Fill in the strokes?
stroke_color	What color?
show_bands	Show the bands for the ideogram?
fill_bands	and fill them in?
thickness	How thick to color the lines
stroke_thickness	How much of them to fill in
label_font	What font to use.
spacing_default	How much space between elements.
spacing_break	Space between breaks.
fill_color	What color to fill
radius	Where on the circle to put them
radius_padding	How much to pad between radii.
label_size	How large to make the labels in px.
band_stroke_thickness	How big to make the strokes!

Value

The file to which the ideogram configuration was written.

---

circos_karyotype *Create the description of (a)chromosome(s) for circos.*

Description

This function tries to save me from having to get the lengths of arcs for bacterial chromosomes manually correct, and writes them as a circos compatible karyotype file. The outfile parameter was chosen to match the configuration directive outlined in circos_prefix(), however that will need to be changed in order for this to work in variable conditions. Next time I make one of these graphs I will do that I suspect. In addition, this currently only understands how to write bacterial chromosomes, that will likely be fixed when I am asked to write out a L.major karyotype. These defaults were chosen because I have a chromosome of this length that is correct.

Usage

```
circos_karyotype(
  cfg,
  segments = 6,
  color = "white",
  fasta = NULL,
  lengths = NULL
)
```

Arguments

cfg	Result from circos_prefix(), contains a bunch of useful things.
segments	How many segments to cut the chromosome into?
color	Color segments of the chromosomal arc?
fasta	Fasta file to use to create the karyotype.
lengths	If no sequence file is provided, use a named numeric vector to provide them.

Value

The output filename.

---

circos_make *Write a simple makefile for circos.*

Description

I regenerate all my circos pictures with make(1). This is my makefile.

Usage

```
circos_make(cfg, target = "", circos = "circos", verbose = FALSE)
```

Arguments

cfg	Configuration from circos_prefix().
target	Default make target.
circos	Location of circos. I have a copy in home/bin/circos and use that sometimes.

Value

a kitten

`circos_plus_minus` *Write tiles of bacterial ontology groups using the categories from microbesonline.org.*

Description

This function tries to save me from writing out ontology definitions and likely making mistakes. It uses the start/ends from the gff annotation along with the 1 letter GO-like categories from microbesonline.org. It then writes two data files circos/data/bob_plus_go.txt, circos/data/bob_minus_go.txt along with two configuration files circos/conf/bob_minus_go.conf and circos/conf/bob_plus_go.conf and finally adds an include to circos/bob.conf

Usage

```
circos_plus_minus(
  cfg,
  outer = 1,
  width = 0.08,
  thickness = 95,
  spacing = 0,
  padding = 1,
  margin = 0,
  plus_orientation = "out",
  minus_orientation = "in",
  layers = 1,
  layers_overflow = "hide",
  acol = "orange",
  bcol = "reds-9-seq",
  ccol = "yellow",
  dcol = "vlpurple",
  ecol = "vlgreen",
  fcol = "dpblue",
  gcol = "vlgreen",
  hcol = "vlpblue",
  icol = "vvdpgreen",
  jcol = "dpred",
  kcol = "orange",
  lcol = "vvlorange",
  mcol = "dpgreen",
  ncol = "vvlpblue",
  ocol = "vvlgreen",
  pcol = "vvdpred",
  qcol = "ylgn-3-seq",
  rcol = "vlgrey",
  scol = "grey",
  tcol = "vlpurple",
  ucol = "greens-3-seq",
```

```
  vcol = "vlred",
  wcol = "vvdppurple",
  xcol = "black",
  ycol = "lred",
  zcol = "vlpblue"
)
```

Arguments

cfg	Result from circos_prefix().
outer	Floating point radius of the circle into which to place the plus-strand data.
width	Radial width of each tile.
thickness	How wide to make the bars.
spacing	Radial distance between outer, inner, and inner to whatever follows.
padding	How much space between them.
margin	Margin between elements.
plus_orientation	Orientation of the plus pieces.
minus_orientation	Orientation of the minus pieces.
layers	How many layers to use
layers_overflow	How to handle too many layers.
acol	A color: RNA processing and modification.
bcol	B color: Chromatin structure and dynamics.
ccol	C color: Energy production conversion.
dcol	D color: Cell cycle control, mitosis and meiosis.
ecol	E color: Amino acid transport metabolism.
fcol	F color: Nucleotide transport and metabolism.
gcol	G color: Carbohydrate transport and metabolism.
hcol	H color: Coenzyme transport and metabolism.
icol	I color: Lipid transport and metabolism.
jcol	J color: Translation, ribosome structure and biogenesis.
kcol	K color: Transcription.
lcol	L color: Replication, recombination, and repair.
mcol	M color: Cell wall/membrane biogenesis.
ncol	N color: Cell motility
ocol	O color: Posttranslational modification, protein turnover, chaperones.
pcol	P color: Inorganic ion transport and metabolism.
qcol	Q color: Secondary metabolite biosynthesis, transport, and catabolism.

rcol	R color: General function prediction only.
scol	S color: Function unknown.
tcol	T color: Signal transduction mechanisms.
ucol	U color: Intracellular trafficking(sp?) and secretion.
vcol	V color: Defense mechanisms.
wcol	W color: Extracellular structures.
xcol	X color: Not in COG.
ycol	Y color: Nuclear structure.
zcol	Z color: Cytoskeleton.

Value

Radius after adding the plus/minus information and the spacing between them.

`circos_prefix` *Write the beginning of a circos configuration file.*

Description

A few parameters need to be set when starting circos. This sets some of them and gets ready for plot stanzas.

Usage

```
circos_prefix(
  annotation,
  name = "mgas",
  basedir = "circos",
  chr_column = "seqnames",
  cog_column = "COGFun",
  start_column = "start",
  stop_column = "end",
  strand_column = "strand",
  id_column = NULL,
  cog_map = NULL,
  radius = 1800,
  chr_units = 1000,
  band_url = NULL,
  ...
)
```

Arguments

annotation	Annotation data frame.
name	Name of the map, called with 'make name'.
basedir	Base directory for writing the data.
chr_column	Name of the column containing the chromosome names in the annotations.
cog_column	Name of the column containing the COG groups in the annotations.
start_column	Name of the column containing the starts in the annotations.
stop_column	Name of the column containing the stops in the annotations.
strand_column	Name of the column containing the strand information.
id_column	Where do the gene IDs live? NULL means rownames.
cog_map	Not yet used, but used to provide an alternate map of groups/colors.
radius	Size of the image.
chr_units	How often to print chromosome in 'prefix' units.
band_url	Place to imagemap link.
...	Extra arguments passed to the tick/karyotype makers.

Details

In its current implementation, this really assumes that there will be no highlight stanzas and at most 1 link stanza. chromosomes. A minimal amount of logic and data organization will address these weaknesses.

Value

The master configuration file name.

---

circos_suffix *Write the end of a circos master configuration.*

Description

circos configuration files need an ending. This writes it.

Usage

```
circos_suffix(cfg)
```

Arguments

cfg	Result from circos_prefix()

Value

Filename of the configuration.

`circos_ticks` *Create the ticks for a circos plot.*

Description

This function writes ticks for circos. This has lots of options, the defaults are all taken from the circos example documentation for a bacterial genome.

Usage

```
circos_ticks(
  name = "default",
  conf_dir = "circos/conf",
  show_ticks = "yes",
  show_tick_labels = "yes",
  show_grid = "no",
  skip_first_label = "yes",
  skip_last_label = "no",
  tick_separation = 2,
  min_label_distance = 0,
  label_separation = 5,
  label_offset = 5,
  label_size = 8,
  multiplier = 0.001,
  main_color = "black",
  main_thickness = 3,
  main_size = 20,
  first_size = 10,
  first_spacing = 1,
  first_color = "black",
  first_show_label = "no",
  first_label_size = 12,
  second_size = 15,
  second_spacing = 5,
  second_color = "black",
  second_show_label = "yes",
  second_label_size = 16,
  third_size = 18,
  third_spacing = 10,
  third_color = "black",
  third_show_label = "yes",
  third_label_size = 16,
  fourth_spacing = 100,
  fourth_color = "black",
  fourth_show_label = "yes",
  suffix = " kb",
  fourth_label_size = 36,
```

```
  include_first_label = TRUE,
  include_second_label = TRUE,
  include_third_label = TRUE,
  include_fourth_label = TRUE,
  ...
)
```

Arguments

name	Name of the configuration file to which to add the ideogram.
conf_dir	Where does the configuration live.
show_ticks	Show them or not.
show_tick_labels	Show the tick labels, or do not.
show_grid	Print a grid behind.
skip_first_label	Like a clock.
skip_last_label	Ditto.
tick_separation	Top-level separation between tick marks.
min_label_distance	distance to the edge of the plot for labels.
label_separation	radial distance between labels.
label_offset	The offset for the labels.
label_size	Top-level label size.
multiplier	When writing the position, by what factor to lower the numbers?
main_color	Color for top-level labels?
main_thickness	Top-level thickness of lines etc.
main_size	Top-level size of text.
first_size	Second level size of text.
first_spacing	Second level spacing of ticks.
first_color	Second-level text color.
first_show_label	Show a label for the second level ticks?
first_label_size	Text size for second level labels?
second_size	Size of ticks for the third level.
second_spacing	third-level spacing
second_color	Text color for the third level.
second_show_label	Give them a label?

second_label_size
: And a size.

third_size
: Now for the size of the almost-largest ticks

third_spacing
: How far apart?

third_color
: and their color

third_show_label
: give a label?

third_label_size
: and a size.

fourth_spacing
: The largest ticks!

fourth_color
: The largest color.

fourth_show_label
: Provide a label?

suffix
: String for printing chromosome distances.

fourth_label_size
: They are big!

include_first_label
: Provide the smallest labels?

include_second_label
: Second smallest labels?

include_third_label
: Second biggest labels?

include_fourth_label
: Largest labels?

...
: Extra arguments from circos_prefix().

Value

The file to which the ideogram configuration was written.

`circos_tile` *Write tiles of arbitrary categorical point data in circos.*

Description

This function tries to make the writing circos tiles easier. Like circos_plus_minus() and circos_hist() it works in 3 stages, It writes out a data file using cfgout as a basename and the data from df in the circos histogram format into circos/data/bob_tile.txt It then writes out a configuration plot stanza in circos/conf/bob_tile.conf and finally adds an include to circos/bob.conf

Usage

```
circos_tile(
  cfg,
  df,
  colname = "logFC",
  basename = "",
  colors = NULL,
  thickness = 80,
  padding = 1,
  margin = 0,
  stroke_thickness = 0,
  orientation = "out",
  outer = 0.9,
  width = 0.08,
  spacing = 0
)
```

Arguments

cfg	Result from circos_prefix().
df	Dataframe with starts/ends and the floating point information.
colname	Name of the column with the data of interest. chromosome)
basename	Used to make unique filenames for the data/conf files.
colors	Colors of the data.
thickness	How thick to make the tiles in radial units.
padding	Space between tiles.
margin	How much space between other rings and the tiles?
stroke_thickness	Size of the tile outlines.
orientation	Facing in or out.
outer	Floating point radius of the circle into which to place the categorical data.
width	Width of each tile.
spacing	Radial distance between outer, inner, and inner to whatever follows.

Value

Radius after adding the histogram and the spacing.

`clear_session` *Clear an R session, this is probably unwise given what I have read about R.*

Description

Clear an R session, this is probably unwise given what I have read about R.

Usage

```
clear_session(keepers = NULL, depth = 10)
```

Arguments

`keepers`	List of namespaces to leave alone (unimplemented).
`depth`	Cheesy forloop of attempts to remove packages stops after this many tries.

Value

A spring-fresh R session, hopefully.

See Also

[R.utils]

`cleavage_histogram` *Make a histogram of how many peptides are expected at every integer dalton from a given start to end size for a given enzyme digestion.*

Description

This is very similar to plot_cleaved() above, but tries to be a little bit smarter.

Usage

```
cleavage_histogram(
  pep_sequences,
  enzyme = "trypsin",
  start = 600,
  end = 1500,
  color = "black"
)
```

Arguments

pep_sequences	Protein sequences as per plot_cleaved().
enzyme	Compatible enzyme name from cleaver.
start	Print histogram from here
end	to here.
color	Make the bars this color.

Value

List containing the plot and size distribution.

---

cluster_trees *Take clusterprofile group data and print it on a tree as per topGO.*

Description

TopGO's ontology trees can be very illustrative. This function shoe-horns clusterProfiler data into the format expected by topGO and uses it to make those trees.

Usage

```
cluster_trees(
  de_genes,
  cpdata,
  goid_map = "id2go.map",
  go_db = NULL,
  score_limit = 0.2,
  overwrite = FALSE,
  selector = "topDiffGenes",
  pval_column = "adj.P.Val"
)
```

Arguments

de_genes	List of genes deemed 'interesting'.
cpdata	Data from simple_clusterprofiler().
goid_map	Mapping file of IDs to GO ontologies.
go_db	Dataframe of mappings used to build goid_map.
score_limit	Scoring limit above which to ignore genes.
overwrite	Overwrite an existing goid mapping file?
selector	Name of a function for applying scores to the trees.
pval_column	Name of the column in the GO table from which to extract scores.

Value

plots! Trees! oh my!

See Also

[Ramigo] [topGO::showSigOfNotes()]

Examples

```
## Not run:
 cluster_data <- simple_clusterprofiler(genes, stuff)
 ctrees <- cluster_trees(genes, cluster_data)

## End(Not run)
```

---

combine_de_tables *Combine portions of deseq/limma/edger table output.*

Description

This hopefully makes it easy to compare the outputs from limma/DESeq2/EdgeR on a table-by-table basis.

Usage

```
combine_de_tables(
  apr,
  extra_annot = NULL,
  excel = NULL,
  sig_excel = NULL,
  abundant_excel = NULL,
  excel_title = "Table SXXX: Combined Differential Expression of YYY",
  keepers = "all",
  excludes = NULL,
  adjp = TRUE,
  include_limma = TRUE,
  include_deseq = TRUE,
  include_edger = TRUE,
  include_ebseq = TRUE,
  include_basic = TRUE,
  rownames = TRUE,
  add_plots = TRUE,
  loess = FALSE,
  plot_dim = 6,
  compare_plots = TRUE,
  padj_type = "ihw",
  lfc_cutoff = 1,
```

```
  p_cutoff = 0.05,
  de_types = c("limma", "deseq", "edger"),
  ...
)
```

Arguments

apr	Output from all_pairwise().
extra_annot	Add some annotation information?
excel	Filename for the excel workbook, or null if not printed.
sig_excel	Filename for writing significant tables.
abundant_excel	Filename for writing abundance tables.
excel_title	Title for the excel sheet(s). If it has the string 'YYY', that will be replaced by the contrast name.
keepers	List of reformatted table names to explicitly keep certain contrasts in specific orders and orientations.
excludes	List of columns and patterns to use for excluding genes.
adjp	Perhaps you do not want the adjusted p-values for plotting?
include_limma	Include limma analyses in the table?
include_deseq	Include deseq analyses in the table?
include_edger	Include edger analyses in the table?
include_ebseq	Include ebseq analyses in the table?
include_basic	Include my stupid basic logFC tables?
rownames	Add rownames to the xlsx printed table?
add_plots	Add plots to the end of the sheets with expression values?
loess	Add time intensive loess estimation to plots?
plot_dim	Number of inches squared for the plot if added.
compare_plots	Add some plots comparing the results.
padj_type	Add a consistent p adjustment of this type.
...	Arguments passed to significance and abundance tables.

Value

Table combining limma/edger/deseq outputs.

See Also

[all_pairwise()] [extract_significant_genes()]

Examples

```
## Not run:
 expt <- create_expt(metadata = "some_metadata.xlsx", gene_info = funkytown)
 big_result <- all_pairwise(expt, model_batch = FALSE)
 pretty <- combine_de_tables(big_result, table='t12_vs_t0')
 pretty <- combine_de_tables(big_result, table='t12_vs_t0',
                             keepers = list("avsb" = c("a","b")))
 pretty <- combine_de_tables(big_result, table='t12_vs_t0',
                             keepers = list("avsb" = c("a","b")),
                             excludes = list("description" = c("sno","rRNA")))

## End(Not run)
```

---

combine_expts *Take two expressionsets and smoosh them together.*

Description

Because of the extra sugar I added to expressionSets, the combine() function needs a little help when combining expts. Notably, the information from tximport needs some help.

Usage

```
combine_expts(
  expt1,
  expt2,
  condition = "condition",
  batch = "batch",
  merge_meta = TRUE
)
```

Arguments

expt1	First expt object.
expt2	Second expt object.
condition	Column with which to reset the conditions.
batch	Column with which to reset the batches.
merge_meta	Merge the metadata when they mismatch? This should perhaps default to TRUE.

Value

Larger expt.

See Also

[set_expt_batches()] [set_expt_conditions()] [set_expt_colors()] [set_expt_genenames()] [set_expt_samplenames()] [subset_expt()] [create_expt()]

Examples

```
 ## Not run:
  ## I am trying to get rid of all my dontrun sections, but I don't have two
  ## expressionsets to combine.
  expt1 <- create_expt(first_meta)
  expt2 <- create_expt(second_meta)
  combined <- combine_expts(expt1, expt2, merge_meta = TRUE)

## End(Not run)
```

`combine_extracted_plots` *Gather data required to make MA/Volcano plots for pairwise comparisons.*

Description

It should be possible to significantly simplify the arguments passed to this function, but I have thus far focused only on getting it to work with the newly split-apart combine_de_tables() functions.

Usage

```
combine_extracted_plots(
  name,
  combined,
  denominator,
  numerator,
  plot_inputs,
  include_basic = TRUE,
  include_deseq = TRUE,
  include_edger = TRUE,
  include_limma = TRUE,
  include_ebseq = FALSE,
  loess = FALSE,
  logfc = 1,
  p = 0.05,
  do_inverse = FALSE,
  found_table = NULL
)
```

Arguments

`name`	Name of the table to plot.
`combined`	Modified pairwise result, containing the various DE methods.
`denominator`	Name of the denominator coefficient.
`numerator`	Name of the numerator coefficient.

plot_inputs	The individual outputs from limma etc.
include_basic	Add basic data?
include_deseq	Add deseq data?
include_edger	Add edger data?
include_limma	Add limma data?
include_ebseq	Add ebseq data?
loess	Add a loess estimation?
do_inverse	Flip the numerator/denominator?
found_table	The table name actually used.

`combine_single_de_table` *Given a limma, edger, and deseq table, combine them into one.*

Description

This combines the outputs from the various differential expression tools and formalizes some column names to make them a little more consistent.

Usage

```
combine_single_de_table(
  li = NULL,
  ed = NULL,
  eb = NULL,
  de = NULL,
  ba = NULL,
  table_name = "",
  final_table_names = c(),
  annot_df = NULL,
  do_inverse = FALSE,
  adjp = TRUE,
  padj_type = "fdr",
  include_deseq = TRUE,
  include_edger = TRUE,
  include_ebseq = TRUE,
  include_limma = TRUE,
  include_basic = TRUE,
  lfc_cutoff = 1,
  p_cutoff = 0.05,
  excludes = NULL,
  sheet_count = 0
)
```

Arguments

li	Limma output table.
ed	Edger output table.
eb	EBSeq output table
de	DESeq2 output table.
ba	Basic output table.
table_name	Name of the table to merge.
final_table_names	Vector of the final table names.
annot_df	Add some annotation information?
do_inverse	Invert the fold changes?
adjp	Use adjusted p-values?
padj_type	Add this consistent p-adjustment.
include_deseq	Include tables from deseq?
include_edger	Include tables from edger?
include_ebseq	Include tables from ebseq?
include_limma	Include tables from limma?
include_basic	Include the basic table?
lfc_cutoff	Preferred logfoldchange cutoff.
p_cutoff	Preferred pvalue cutoff.
excludes	Set of genes to exclude from the output.
sheet_count	What sheet is being written?

Value

List containing a) Dataframe containing the merged limma/edger/deseq/basic tables, and b) A summary of how many genes were observed as up/down by output table.

See Also

[data.table] [hpgl_padjust()] [extract_keepers_all()] [extract_keepers_lst()] [extract_keepers_single()]

compare_de_results *Compare the results of separate all_pairwise() invocations.*

Description

Where compare_led_tables looks for changes between limma and friends, this function looks for differences/similarities across the models/surrogates/etc across invocations of limma/deseq/edger.

Usage

```
compare_de_results(
  first,
  second,
  cor_method = "pearson",
  try_methods = c("limma", "deseq", "edger")
)
```

Arguments

first	One invocation of combine_de_tables to examine.
second	A second invocation of combine_de_tables to examine.
cor_method	Method to use for cor.test().
try_methods	List of methods to attempt comparing.

Details

Tested in 29de_shared.R

Value

A list of compared columns, tables, and methods.

See Also

[all_pairwise()]

Examples

```
## Not run:
 first <- all_pairwise(expt, model_batch = FALSE, excel = "first.xlsx")
 second <- all_pairwise(expt, model_batch = "svaseq", excel = "second.xlsx")
 comparison <- compare_de_results(first$combined, second$combined)

## End(Not run)
```

compare_go_searches *Compare the results from different ontology tools*

Description

Combine the results from goseq, cluster profiler, topgo, and gostats; poke at them with a stick and see what happens. The general idea is to pull the p-value data from each tool and contrast that to the set of all possibile ontologies. This allows one to do a correlation coefficient between them. In addition, take the 1-pvalue for each ontology for each tool. Thus for strong p-values the score will be near 1 and so we can sum the scores for all the tools. Since topgo has 4 tools, the total possible is 7 if everything has a p-value equal to 0.

Usage

```
compare_go_searches(goseq = NULL, cluster = NULL, topgo = NULL, gostats = NULL)
```

Arguments

goseq	Result from simple_goseq()
cluster	Result from simple_clusterprofiler()
topgo	Result from topGO
gostats	Result from GOstats

Value

Summary of the similarities of ontology searches

See Also

[goseq] [clusterProfiler] [topGO] [goStats]

compare_logfc_plots *Compare logFC values from limma and friends*

Description

There are some peculiar discrepencies among these tools, what is up with that?

Usage

```
compare_logfc_plots(combined_tables)
```

Arguments

combined_tables	The combined tables from limma et al.

Details

Invoked by combine_de_tables() in order to compare the results.

Value

Some plots

See Also

[plot_linear_scatter()]

Examples

```
## Not run:
 limma_vs_deseq_vs_edger <- compare_logfc_plots(combined)
 ## Get a list of plots of logFC by contrast of LvD, LvE, DvE
 ## It provides comparisons against the basic analysis, but who cares about that.

## End(Not run)
```

---

compare_significant_contrasts

Implement a cleaner version of 'subset_significants' from analyses with Maria Adelaida.

Description

This should provide nice venn diagrams and some statistics to compare 2 or 3 contrasts in a differential expression analysis.

Usage

```
compare_significant_contrasts(
  sig_tables,
  compare_by = "deseq",
  weights = FALSE,
  contrasts = c(1, 2, 3)
)
```

Arguments

sig_tables	Set of significance tables to poke at.
compare_by	Use which program for the comparisons?
weights	When printing venn diagrams, weight them?
contrasts	List of contrasts to compare.

Value

List containing the intersections of the contrasts and plots describing them.

See Also

[Vennerable]

`compare_surrogate_estimates` *Perform a comparison of the surrogate estimators demonstrated by Jeff Leek.*

Description

This is entirely derivative, but seeks to provide similar estimates for one's own actual data and catch corner cases not taken into account in that document (for example if the estimators don't converge on a surrogate variable). This will attempt each of the surrogate estimators described by Leek: pca, sva supervised, sva unsupervised, ruv supervised, ruv residuals, ruv empirical. Upon completion it will perform the same limma expression analysis and plot the ranked t statistics as well as a correlation plot making use of the extracted estimators against condition/batch/whatever else. Finally, it does the same ranking plot against a linear fitting Leek performed and returns the whole pile of information as a list.

Usage

```
compare_surrogate_estimates(
  expt,
  extra_factors = NULL,
  filter_it = TRUE,
  filter_type = TRUE,
  do_catplots = FALSE,
  surrogates = "be",
  ...
)
```

Arguments

`expt`	Experiment containing a design and other information.
`extra_factors`	Character list of extra factors which may be included in the final plot of the data.
`filter_it`	Most of the time these surrogate methods get mad if there are 0s in the data. Filter it?
`filter_type`	Type of filter to use when filtering the input data.
`do_catplots`	Include the catplots? They don't make a lot of sense yet, so probably no.
`surrogates`	Use 'be' or 'leek' surrogate estimates, or choose a number.
`...`	Extra arguments when filtering.

Value

List of the results.

See Also

[normalize_expt()] [plot_pca()] [all_adjuster()] [corrplot] [ffpe]

`concatenate_runs` *Sum the reads/gene for multiple sequencing runs of a single condition/batch.*

Description

On occasion we have multiple technical replicates of a sequencing run. This can use a column in the experimental design to identify those replicates and sum the counts into a single column in the count tables.

Usage

```
concatenate_runs(expt, column = "replicate")
```

Arguments

`expt`	Experiment class containing the requisite metadata and count tables.
`column`	Column of the design matrix used to specify which samples are replicates.

Details

Untested as of 2016-12-01, but used in a couple of projects where sequencing runs got repeated.

Value

Expt with the concatenated counts, new design matrix, batches, conditions, etc.

See Also

[Biobase] [exprs()] [fData()] [pData()] [create_expt()]

Examples

```
## Not run:
 compressed <- concatenate_runs(expt)

## End(Not run)
```

convert_counts *Perform a cpm/rpkm/whatever transformation of a count table.*

Description

I should probably tell it to also handle a simple df/vector/list of gene lengths, but I haven't. cp_seq_m is a cpm conversion of the data followed by a rp-ish conversion which normalizes by the number of the given oligo. By default this oligo is 'TA' because it was used for tnseq which should be normalized by the number of possible transposition sites by mariner. It could, however, be used to normalize by the number of methionines, for example – if one wanted to do such a thing.

Usage

```
convert_counts(count_table, method = "raw", ...)
```

Arguments

method	Type of conversion to perform: edgecpm/cpm/rpkm/cp_seq_m.
...	Options I might pass from other functions are dropped into arglist, used by rpkm (gene lengths) and divide_seq (genome, pattern to match, and annotation type).
data	Matrix of count data.

Value

Dataframe of cpm/rpkm/whatever(counts)

See Also

[edgeR] [Biobase]

Examples

```
## Not run:
 converted_table = convert_counts(count_table, method='cbcbcpm')

## End(Not run)
```

`convert_gsc_ids` *Use AnnotationDbi to translate geneIDs from type x to type y.*

Description

This is intended to convert all the IDs in a geneSet from one ID type to another and giving back the geneSet with the new IDs. FIXME: This should use convert_ids() to simplify itself

Usage

```
convert_gsc_ids(
  gsc,
  orgdb = "org.Hs.eg.db",
  from_type = NULL,
  to_type = "ENTREZID"
)
```

Arguments

`gsc`	geneSetCollection with IDs of a type one wishes to change.
`orgdb`	Annotation object containing the various IDs.
`from_type`	Name of the ID which your gsc is using. This can probably be automagically detected...
`to_type`	Name of the ID you wish to use.

Details

One caveat: this will collapse redundant IDs via unique().

Value

Fresh gene set collection replete with new names.

See Also

[AnnotationDbi] [guess_orgdb_keytypes()] [convert_ids()] [GSEABase]

convert_ids *Change gene IDs to the format expected by gsva using an orgdb.*

Description

Though it is possible to use gsva without ENTREZ IDs, it is not trivial. This function attempts to ensure that the IDs in one's expressionset are therefore entrez IDs. It is possible that this function is at least partially redundant with other functions in this package and should be replaced.

Usage

```
convert_ids(ids, from = "ENSEMBL", to = "ENTREZID", orgdb = "org.Hs.eg.db")
```

Arguments

ids	Vector of IDS to modify.
from	Change from this format.
to	Change to this format.
orgdb	Using this orgdb instance.

Value

New vector of ENTREZ IDs.

See Also

[AnnotationDbi]

cordist *Similarity measure which combines elements from Pearson correlation and Euclidean distance.*

Description

Here is Keith's summary: Where the cor returns the Pearson correlation matrix for the input matrix, and the dist function returns the Euclidean distance matrix for the input matrix. The LHS of the equation is simply the sign of the correlation function, which serves to preserve the sign of the interaction. The RHS combines the Pearson correlation and the log inverse Euclidean distance with equal weights. The result is a number in the range from -1 to 1 where values close to -1 indicate a strong negative correlation and values close to 1 indicate a strong positive corelation. While the Pearson correlation and Euclidean distance each contribute equally in the above equation, one could also assign tuning parameters to each of the metrics to allow for unequal contributions.

Usage

```
cordist(
  data,
  cor_method = "pearson",
  dist_method = "euclidean",
  cor_weight = 0.5,
  ...
)
```

Arguments

data	Matrix of data
cor_method	Which correlation method to use?
dist_method	Which distance method to use?
cor_weight	0-1 weight of the correlation, the distance weight will be 1-cor_weight.
...	extra arguments for cor/dist

Value

Matrix of the correlation-modified distances of the original matrix.

Author(s)

Keigth Hughitt

---

correlate_de_tables *See how similar are results from limma/deseq/edger/ebseq.*

Description

limma, DEseq2, and EdgeR all make somewhat different assumptions. and choices about what makes a meaningful set of differentially. expressed genes. This seeks to provide a quick and dirty metric describing the degree to which they (dis)agree.

Usage

```
correlate_de_tables(results, annot_df = NULL, extra_contrasts = NULL)
```

Arguments

results	Data from do_pairwise()
annot_df	Include annotation data?

Details

Invoked by all_pairwise().

Value

Heatmap showing how similar they are along with some correlations betwee the three players.

See Also

[limma_pairwise()] [edger_pairwise()] [deseq_pairwise()]

Examples

```
## Not run:
 l = limma_pairwise(expt)
 d = deseq_pairwise(expt)
 e = edger_pairwise(expt)
 fun = compare_led_tables(limma = l, deseq = d, edger = e)

## End(Not run)
```

---

count_expt_snps *Gather snp information for an expt*

Description

This function attempts to gather a set of variant positions using an extant expressionset. This therefore seeks to keep the sample metadata consistent with the original data. In its current iteration, it therefore makes some potentially bad assumptions about the naming conventions for its input files. It furthermore assumes inputs from the variant calling methods in cyoa.

Usage

```
count_expt_snps(
  expt,
  type = "counts",
  annot_column = "bcftable",
  tolower = TRUE,
  snp_column = "diff_count"
)
```

Arguments

expt	an expressionset from which to extract information.
type	Use counts / samples or ratios?
annot_column	Column in the metadata for getting the table of bcftools calls.
tolower	Lowercase stuff like 'HPGL'?
snp_column	Which column of the parsed bcf table contains our interesting material?

Value

A new expt object

See Also

[Biobase]

Examples

```
 ## Not run:
expt <- create_expt(metadata, gene_information)
snp_expt <- count_expt_snps(expt)
## This assumes that the metadata has a column named 'bcftable' with one file per
## cell.  These files in turn should have a column named 'diff_count' which will
## be the source of the numbers found when doing exprs(snp_expt).

## End(Not run)
```

---

count_nmer *Count n-mers in a given data set using Biostrings*

Description

This just calls PDict() and vcountPDict() on a sequence database given a pattern and number of mismatches. This may be used by divide_seq() normalization.

Usage

```
count_nmer(genome, pattern = "ATG", mismatch = 0)
```

Arguments

genome	Sequence database, genome in this case.
pattern	Count off this string.
mismatch	How many mismatches are acceptable?

Value

Set of counts by sequence.

`counts_from_surrogates` *A single place to extract count tables from a set of surrogate variables.*

Description

Given an initial set of counts and a series of surrogates, what would the resulting count table look like? Hopefully this function answers that question.

Usage

```
counts_from_surrogates(
  data,
  adjust = NULL,
  design = NULL,
  method = "ruv",
  cond_column = "condition",
  batch_column = "batch",
  matrix_scale = "linear",
  return_scale = "linear",
  ...
)
```

Arguments

`data`	Original count table, may be an expt/expressionset or df/matrix.
`adjust`	Surrogates with which to adjust the data.
`design`	Experimental design if it is not included in the expressionset.
`method`	Which methodology to follow, ideally these agree but that seems untrue.
`cond_column`	design column containing the condition data.
`matrix_scale`	Was the input for the surrogate estimator on a log or linear scale?
`return_scale`	Does one want the output linear or log?
`...`	Arguments passed to downstream functions.

Value

A data frame of adjusted counts.

See Also

[sva] [RUVSeq] [crossprod()] [tcrossprod()] [solve()]

cp_options *Set up appropriate option sets for clusterProfiler*

Description

This hard-sets some defaults for orgdb/kegg databases when using clusterProfiler.

Usage

```
cp_options(species)
```

Arguments

species	Currently it only works for humans and fruit flies.

create_expt *Wrap bioconductor's expressionset to include some extra information.*

Description

The primary innovation of this function is that it will check the metadata for columns containing filenames for the count tables, thus hopefully making the collation and care of metadata/counts easier. For example, I have some data which has been mapped against multiple species. I can use this function and just change the file_column argument to pick up each species' tables.

Usage

```
create_expt(
  metadata = NULL,
  gene_info = NULL,
  count_dataframe = NULL,
  sanitize_rownames = FALSE,
  sample_colors = NULL,
  title = NULL,
  notes = NULL,
  countdir = NULL,
  include_type = "all",
  include_gff = NULL,
  file_column = "file",
  id_column = NULL,
  savefile = NULL,
  low_files = FALSE,
  ...
)
```

Arguments

metadata	Comma separated file (or excel) describing the samples with information like condition, batch, count_filename, etc.
gene_info	Annotation information describing the rows of the data set, this often comes from a call to import.gff() or biomart or organismdbi.
count_dataframe	If one does not wish to read the count tables from the filesystem, they may instead be fed as a data frame here.
sanitize_rownames	Clean up weirdly written gene IDs?
sample_colors	List of colors by condition, if not provided it will generate its own colors using colorBrewer.
title	Provide a title for the expt?
notes	Additional notes?
countdir	Directory containing count tables.
include_type	I have usually assumed that all gff annotations should be used, but that is not always true, this allows one to limit to a specific annotation type.
include_gff	Gff file to help in sorting which features to keep.
file_column	Column to use in a gene information dataframe for
id_column	Column which contains the sample IDs.
savefile	Rdata filename prefix for saving the data of the resulting expt.
low_files	Explicitly lowercase the filenames when searching the filesystem?
...	More parameters are fun!

Value

experiment an expressionset

See Also

[Biobase] [cdm_expt_rda] [example_gff] [sb_annot] [sb_data] [extract_metadata()] [set_expt_conditions()] [set_expt_batches()] [set_expt_samplenames()] [subset_expt()] [set_expt_colors()] [set_expt_genenames()] [tximport] [load_annotations()]

Examples

```
cdm_expt_rda <- system.file("share", "cdm_expt.rda", package = "hpgltools")
load(file = cdm_expt_rda)
head(cdm_counts)
head(cdm_metadata)
## The gff file has differently labeled locus tags than the count tables, also
## the naming standard changed since this experiment was performed, therefore I
## downloaded a new gff file.
example_gff <- system.file("share", "gas.gff", package = "hpgltools")
gas_gff_annot <- load_gff_annotations(example_gff)
```

```
rownames(gas_gff_annot) <- make.names(gsub(pattern = "(Spy)_", replacement = "\\1",
                                           x = gas_gff_annot[["locus_tag"]]), unique = TRUE)
mgas_expt <- create_expt(metadata = cdm_metadata, gene_info = gas_gff_annot,
                         count_dataframe = cdm_counts)
head(pData(mgas_expt))
## An example using count tables referenced in the metadata.
sb_annot <- system.file("share", "sb", "trinotate_head.csv.xz", package = "hpgltools")
sb_annot <- load_trinotate_annotations(trinotate = sb_annot)
sb_annot <- as.data.frame(sb_annot)
rownames(sb_annot) <- make.names(sb_annot[["transcript_id"]], unique = TRUE)
sb_annot[["rownames"]] <- NULL
sb_data <- system.file("share", "sb", "preprocessing.tar.xz", package = "hpgltools")
untarred <- utils::untar(tarfile = sb_data)
sb_expt <- create_expt(metadata = "preprocessing/kept_samples.xlsx",
                       gene_info = sb_annot)
dim(exprs(sb_expt))
dim(fData(sb_expt))
pData(sb_expt)
## There are lots of other ways to use this, for example:
## Not run:
 new_experiment <- create_expt(metadata = "some_csv_file.csv", gene_info = gene_df)
 ## Remember that this depends on an existing data structure of gene annotations.
 meta <- extract_metadata("some_supplementary_materials_xls_file_I_downloaded.xls")
 another_expt <- create_expt(metadata = meta, gene_info = annotations, count_dataframe = df_I_downloaded)

## End(Not run)
```

---

de_venn *Create venn diagrams describing how well deseq/limma/edger agree.*

Description

The sets of genes provided by limma and friends would ideally always agree, but they do not. Use this to see out how much the (dis)agree.

Usage

```
de_venn(table, adjp = FALSE, p = 0.05, lfc = 0, ...)
```

Arguments

table	Which table to query?
adjp	Use adjusted p-values
p	p-value cutoff, I forget what for right now.
lfc	What fold-change cutoff to include?
...	More arguments are passed to arglist.

Value

A list of venn plots

See Also

[Vennerable] [get_sig_genes()]

Examples

```
## Not run:
 bunchovenns <- de_venn(pairwise_result)

## End(Not run)
```

`default_norm` *Perform a default normalization of some data*

Description

This just calls normalize expt with the most common arguments except log2 transformation, but that may be appended with 'transform = log2', so I don't feel bad. Indeed, it will allow you to overwrite any arguments if you wish. In our work, the most common normalization is: quantile(cpm(low-filter(data))).

Usage

```
default_norm(expt, ...)
```

Arguments

`expt`	An expressionset containing expt object
`...`	More options to pass to normalize_expt()

Value

The normalized expt

See Also

[normalize_expt()]

`default_proper` *Invoke PROPER and replace its default data set with data of interest.*

Description

Recent reviewers of Najib's grants have taken an increased interest in knowing the statistical power of the various experiments. He queried Dr. Corrada-Bravo who suggested PROPER. I spent some time looking through it and, with some revervations, modified its workflow to (at least in theory) be able to examine any dataset. The workflow in question is particularly odd and warrants further discussion/analysis. This function invokes PROPER exactly as it was performed in their paper.

Usage

```
default_proper(
  de_tables,
  p = 0.05,
  experiment = "cheung",
  nsims = 20,
  reps = c(3, 5, 7, 10),
  de_method = "edger",
  alpha_type = "fdr",
  alpha = 0.1,
  stratify = "expr",
  target = "lfc",
  filter = "none",
  delta = 0.5
)
```

Arguments

`de_tables`	A set of differential expression results, presumably from EdgeR or DESeq2.
`p`	Cutoff
`experiment`	The default data set in PROPER is entitled 'cheung'.
`nsims`	Number of simulations to perform.
`reps`	Simulate these number of experimental replicates.
`de_method`	There are a couple choices here for tools which are pretty old, my version of this only accepts deseq or edger.
`alpha_type`	I assume p-adjust type.
`alpha`	Accepted fdr rate.
`stratify`	There are a few options here, I don't fully understand them.
`target`	Cutoff.
`filter`	Apply a filter?
`delta`	Not epsilon! (E.g. I forget what this does).

Value

List containing the various results and plots from proper.

See Also

[PROPER]

`deparse_go_value` *Extract more easily readable information from a GOTERM datum.*

Description

The output from the GOTERM/GO.db functions is inconsistent, to put it nicely. This attempts to extract from that heterogeneous datatype something easily readable. Example: Synonym() might return any of the following: NA, NULL, "NA", "NULL", c("NA",NA,"GO:00001"), "GO:00002", c("Some text",NA, NULL, "GO:00003") This function will boil that down to 'not found', '', 'GO:00004', or "GO:0001, some text, GO:00004"

Usage

```
deparse_go_value(value)
```

Arguments

`value`	Result of try(as.character(somefunction(GOTERM[id])), silent = TRUE). somefunction would be 'Synonym' 'Secondary' 'Ontology', etc...

Value

something more sane (hopefully).

See Also

[GO.db]

Examples

```
## Not run:
 ## goterms = GOTERM[ids]
 ## sane_goterms = deparse_go_value(goterms)

## End(Not run)
```

`deseq_pairwise` *deseq_pairwise() Because I can't be trusted to remember '2'.*

Description

This calls deseq2_pairwise(...) because I am determined to forget typing deseq2.

Usage

```
deseq_pairwise(...)
```

Arguments

...	I like cats.

Value

stuff deseq2_pairwise results.

See Also

[deseq2_pairwise()]

`deseq_try_sv` *Given a set of surrogate variables from sva and friends, try adding them to a DESeqDataSet.*

Description

Sometimes sva returns a set of surrogate variable estimates which lead to models which are invalid according to DESeq2. This function will try before buying and tell the user if the sva model additions are valid according to DESeq.

Usage

```
deseq_try_sv(data, summarized, svs, num_sv = NULL)
```

Arguments

`data`	DESeqDataSet to test out.
`summarized`	Existing DESeq metadata to append svs.
`svs`	Surrogates from sva and friends to test out.
`num_sv`	Optionally, provide the number of SVs, primarily used if recursing in the hunt for a valid number of surrogates.

Value

DESeqDataSet with at least some of the SVs appended to the model.

See Also

[sva] [RUVSeq] [all_adjusters()] [normalize_batch()]

`deseq2_pairwise` *Set up model matrices contrasts and do pairwise comparisons of all conditions using DESeq2.*

Description

Invoking DESeq2 is confusing, this should help.

Usage

```
deseq2_pairwise(
  input = NULL,
  conditions = NULL,
  batches = NULL,
  model_cond = TRUE,
  model_batch = TRUE,
  model_intercept = FALSE,
  alt_model = NULL,
  extra_contrasts = NULL,
  annot_df = NULL,
  force = FALSE,
  deseq_method = "long",
  ...
)
```

Arguments

`input`	Dataframe/vector or expt class containing data, normalization state, etc.
`conditions`	Factor of conditions in the experiment.
`batches`	Factor of batches in the experiment.
`model_cond`	Is condition in the experimental model?
`model_batch`	Is batch in the experimental model?
`model_intercept`	Use an intercept model?
`alt_model`	Provide an arbitrary model here.
`extra_contrasts`	Provide extra contrasts here.
`annot_df`	Include some annotation information in the results?

force	Force deseq to accept data which likely violates its assumptions.
deseq_method	The DESeq2 manual shows a few ways to invoke it, I make 2 of them available here.
...	Triple dots! Options are passed to arglist.

Details

Like the other _pairwise() functions, this attempts to perform all pairwise contrasts in the provided data set. The details are of course slightly different when using DESeq2. Thus, this uses the function choose_binom_dataset() to try to ensure that the incoming data is appropriate for DESeq2 (if one normalized the data, it will attempt to revert to raw counts, for example). It continues on to extract the conditions and batches in the data, choose an appropriate experimental model, and run the DESeq analyses as described in the manual. It defaults to using an experimental batch factor, but will accept a string like 'sva' instead, in which case it will use sva to estimate the surrogates, and append them to the experimental design. The deseq_method parameter may be used to apply different DESeq2 code paths as outlined in the manual. If you want to play with non-standard data, the force argument will round the data and shoe-horn it into DESeq2.

Value

List including the following information: run = the return from calling DESeq() denominators = list of denominators in the contrasts numerators = list of the numerators in the contrasts conditions = the list of conditions in the experiment coefficients = list of coefficients making the contrasts all_tables = list of DE tables

See Also

[DESeq2] [basic_pairwise()] [limma_pairwise()] [edger_pairwise()] [ebseq_pairwise()]

Examples

```
## Not run:
 pretend = deseq2_pairwise(data, conditions, batches)

## End(Not run)
```

---

disjunct_pvalues *Test for infected/control/beads – a placebo effect?*

Description

This was a function I copied out of Keith/Hector/Laura/Cecilia's paper in which they sought to discriminate the effect of inert beads on macrophages vs. the effect of parasites. The simpler way of expressing it is: take the worst p-value observed for the pair of contrasts, infected/uninfected and beads/uninfected.

Usage

```
disjunct_pvalues(contrast_fit, cellmeans_fit, conj_contrasts, disj_contrast)
```

Arguments

contrast_fit	Result of lmFit.
cellmeans_fit	Result of a cellmeans fit.
conj_contrasts	Result from the makeContrasts of the first set.
disj_contrast	Result of the makeContrasts of the second set.

Details

The goal is therefore to find responses different than beads The null hypothesis is (H0): (infected == uninfected) | (infected == beads) The alt hypothesis is (HA): (infected != uninfected) & (infected != beads)

---

divide_seq *Express a data frame of counts as reads per pattern per million.*

Description

This uses a sequence pattern rather than length to normalize sequence. It is essentially fancy pants rpkm.

Usage

```
divide_seq(counts, ...)
```

Arguments

counts	Read count matrix.
...	Options I might pass from other functions are dropped into arglist.

Value

The RPseqM counts

See Also

[edgeR] [Rsamtools::FaFile()] [Biostrings::PDict()] [Biostrings::vcountPDict()] [GenomeInfoDb] [GenomicRanges]

Examples

```
## Not run:
 cptam <- divide_seq(cont_table, fasta = "mgas_5005.fasta.xz", gff = "mgas_5005.gff.xz")

## End(Not run)
```

do_pairwise *Generalize pairwise comparisons*

Description

I want to multithread my pairwise comparisons, this is the first step in doing so.

Usage

```
do_pairwise(type, ...)
```

Arguments

type	Which type of pairwise comparison to perform
...	Set of arguments intended for limma_pairwise(), edger_pairwise(), and friends.

Details

Used to make parallel operations easier.

Value

Result from limma/deseq/edger/basic

See Also

[all_pairwise()]

do_topgo *An attempt to make topgo invocations a bit more standard.*

Description

My function 'simple_topgo()' was excessively long and a morass of copy/pasted fragments. This attempts to simplify that and converge on a single piece of code for all the methodologies provided by topgo.

Usage

```
do_topgo(
  type,
  go_map = NULL,
  fisher_genes = NULL,
  ks_genes = NULL,
  selector = "topDiffGenes",
  sigforall = TRUE,
  numchar = 300,
  pval_column = "adj.P.Val",
  overwrite = FALSE,
  cutoff = 0.05,
  densities = FALSE,
  pval_plots = TRUE
)
```

Arguments

type	Type of topgo search to perform: fisher, KS, EL, or weight.
go_map	Mappings of gene and GO IDs.
fisher_genes	List of genes used for fisher analyses.
ks_genes	List of genes used for KS analyses.
selector	Function to use when selecting genes.
sigforall	Provide significance metrics for all ontologies observed, not only the ones deemed statistically significant.
numchar	A limit on characters printed when printing topgo tables (used?)
pval_column	Column from which to extract DE p-values.
overwrite	Overwrite an existing gene ID/GO mapping?
cutoff	Define 'significant'?
densities	Perform gene density plots by ontology?
pval_plots	Print p-values plots as per clusterProfiler?

Value

List of results from the various tests in topGO.

See Also

[topGO]

download_gbk *A genbank accession downloader scurrilously stolen from ape.*

Description

This takes and downloads genbank accessions.

Usage

```
download_gbk(accessions = "AE009949", write = TRUE)
```

Arguments

accessions	An accession – actually a set of them.
write	Write the files? Otherwise return a list of the strings

Details

Tested in test_40ann_biomartgenbank.R In this function I stole the same functionality from the ape package and set a few defaults so that it hopefully fails less often.

Value

A list containing the number of files downloaded and the character strings acquired.

Author(s)

The ape authors with some modifications by atb.

See Also

[ape]

Examples

```
written <- download_gbk(accessions = "AE009949")
written$written_file
```

download_microbesonline_files

Download the various file formats from microbesoline.

Description

Microbesonline provides an interesting set of file formats to download. Each format proves useful under one condition or another, ergo this defaults to iterating through them all and getting every file.

Usage

```
download_microbesonline_files(id = "160490", type = NULL)
```

Arguments

id	Species ID to query.
type	File type(s) to download, if left null it will grab the genbank, tab, protein fasta, transcript fasta, and genome.

Value

List describing the files downloaded and their locations.

download_uniprot_proteome

Download the txt uniprot data for a given accession/species.

Description

Uniprot is an astonishing resource, but man is it a pain to use. Hopefully this function will help. It takes either a uniprot accession, taxonomy ID, or species name and does its best to find the appropriate uniprot data. This is therefore primarily used by load_uniprot_annotations().

Usage

```
download_uniprot_proteome(
  accession = NULL,
  species = NULL,
  taxonomy = NULL,
  all = FALSE,
  first = FALSE
)
```

Arguments

accession	Which accession to grab?
species	Or perhaps species?
taxonomy	Query for a specific taxonomy ID rather than species/accession?
all	If there are more than 1 hit, grab them all?
first	Or perhaps just grab the first hit?

Value

A filename/accession tuple.

See Also

[xml2] [rvest]

Examples

```
uniprot_sc_downloaded <- download_uniprot_proteome(species = "Saccharomyces cerevisiae S288c")
uniprot_sc_downloaded$filename
uniprot_sc_downloaded$species
```

---

ebseq_few *Invoke EBMultiTest() when we do not have too many conditions to deal with.*

Description

Starting at approximately 5 conditions, ebseq becomes too unwieldy to use effectively. But, its results until then are pretty neat.

Usage

```
ebseq_few(
  data,
  conditions,
  patterns = NULL,
  ng_vector = NULL,
  rounds = 10,
  target_fdr = 0.05,
  norm = "median"
)
```

Arguments

data	Expressionset/matrix
conditions	Factor of conditions in the data to compare.
patterns	Set of patterns as described in the ebseq documentation to query.
ng_vector	Passed along to ebmultitest().
rounds	Passed to ebseq.
target_fdr	Passed to ebseq.
norm	Normalization method to apply to the data.

See Also

[ebseq_pairwise()]

---

ebseq_pairwise *Set up model matrices contrasts and do pairwise comparisons of all conditions using EBSeq.*

Description

Invoking EBSeq is confusing, this should help.

Usage

```
ebseq_pairwise(
  input = NULL,
  patterns = NULL,
  conditions = NULL,
  batches = NULL,
  model_cond = NULL,
  model_intercept = NULL,
  alt_model = NULL,
  model_batch = NULL,
  ng_vector = NULL,
  rounds = 10,
  target_fdr = 0.05,
  method = "pairwise_subset",
  norm = "median",
  force = FALSE,
  ...
)
```

Arguments

input	Dataframe/vector or expt class containing data, normalization state, etc.
patterns	Set of expression patterns to query.
conditions	Not currently used, but passed from all_pairwise()
batches	Not currently used, but passed from all_pairwise()
model_cond	Not currently used, but passed from all_pairwise()
model_intercept	Not currently used, but passed from all_pairwise()
alt_model	Not currently used, but passed from all_pairwise()
model_batch	Not currently used, but passed from all_pairwise()
ng_vector	I think this is for isoform quantification, but am not yet certain.
rounds	Number of iterations for doing the multi-test
target_fdr	Definition of 'significant'
method	The default ebseq methodology is to create the set of all possible 'patterns' in the data; for data sets which are more than trivially complex, this is not tenable, so this defaults to subsetting the data into pairs of conditions.
norm	Normalization method to use.
force	Force ebseq to accept bad data (notably NA containing stuff from proteomics.
...	Extra arguments currently unused.

Value

List containing tables from ebseq, the conditions tested, and the ebseq table of conditions.

See Also

[limma_pairwise()] [deseq_pairwise()] [edger_pairwise()] [basic_pairwise()]

Examples

```
 ## Not run:
  expt <- create_expt(metadata = "sample_sheet.xlsx", gene_info = annotations)
  ebseq_de <- ebseq_pairwise(input = expt)

## End(Not run)
```

`ebseq_pairwise_subset` *Perform pairwise comparisons with ebseq, one at a time.*

Description

This uses the same logic as in the various *_pairwise functions to invoke the 'normal' ebseq pairwise comparison for each pair of conditions in an expressionset. It therefore avoids the strange logic inherent in the ebseq multitest function.

Usage

```
ebseq_pairwise_subset(
  input,
  ng_vector = NULL,
  rounds = 10,
  target_fdr = 0.05,
  model_batch = FALSE,
  model_cond = TRUE,
  model_intercept = FALSE,
  alt_model = NULL,
  conditions = NULL,
  norm = "median",
  force = FALSE,
  ...
)
```

Arguments

`input`	Expressionset/expt to perform de upon.
`ng_vector`	Passed on to ebseq, I forget what this does.
`rounds`	Passed on to ebseq, I think it defines how many iterations to perform before return the de estimates
`target_fdr`	If we reach this fdr before iterating rounds times, return.
`model_batch`	Provided by all_pairwise() I do not think a Bayesian analysis really cares about models, but if one wished to try to add a batch factor, this would be the place to do it. It is currently ignored.
`model_cond`	Provided by all_pairwise(), ibid.
`model_intercept`	Ibid.
`alt_model`	Ibid.
`conditions`	Factor of conditions in the data, used to define the contrasts.
`norm`	EBseq normalization method to apply to the data.
`force`	Flag used to force inappropriate data into the various methods.
`...`	Extra arguments passed downstream, noably to choose_model()

Value

A pairwise comparison of the various conditions in the data.

See Also

[ebseq_pairwise()]

`ebseq_size_factors` *Choose the ebseq normalization method to apply to the data.*

Description

EBSeq provides three normaliation methods. Median, Quantile, and Rank. Choose among them here.

Usage

```
ebseq_size_factors(data_mtrx, norm = NULL)
```

Arguments

`data_mtrx`	This is exprs(expressionset)
`norm`	The method to pass along.

Value

a new matrix using the ebseq specific method of choice.

See Also

[EBSeq]

`ebseq_two` *The primary function used in my EBSeq implementation.*

Description

Most of the time, my invocation of ebseq will fall into this function.

Usage

```
ebseq_two(
  pair_data,
  conditions,
  numerator = 2,
  denominator = 1,
  ng_vector = NULL,
  rounds = 10,
  target_fdr = 0.05,
  norm = "median",
  force = FALSE
)
```

Arguments

pair_data	Matrix containing the samples comprising two experimental factors of interest.
conditions	Factor of conditions in the data.
numerator	Which factor has the numerator in the data.
denominator	Which factor has the denominator in the data.
ng_vector	Passed to ebseq.
rounds	Passed to ebseq.
target_fdr	Passed to ebseq.
norm	Normalization method of ebseq to apply.
force	Force inappropriate data into ebseq?

Value

EBSeq result table with some extra formatting.

See Also

[ebseq_pairwise()]

---

edger_pairwise *Set up a model matrix and set of contrasts to do pairwise comparisons using EdgeR.*

Description

This function performs the set of possible pairwise comparisons using EdgeR.

Usage

```
edger_pairwise(
  input = NULL,
  conditions = NULL,
  batches = NULL,
  model_cond = TRUE,
  model_batch = TRUE,
  model_intercept = FALSE,
  alt_model = NULL,
  extra_contrasts = NULL,
  annot_df = NULL,
  force = FALSE,
  edger_method = "long",
  ...
)
```

Arguments

input	Dataframe/vector or expt class containing data, normalization state, etc.
conditions	Factor of conditions in the experiment.
batches	Factor of batches in the experiment.
model_cond	Include condition in the experimental model?
model_batch	Include batch in the model? In most cases this is a good thing(tm).
model_intercept	Use an intercept containing model?
alt_model	Alternate experimental model to use?
extra_contrasts	Add some extra contrasts to add to the list of pairwise contrasts. This can be pretty neat, lets say one has conditions A,B,C,D,E and wants to do (C/B)/A and (E/D)/A or (E/D)/(C/B) then use this with a string like: "c_vs_b_ctrla = (C-B)-A, e_vs_d_ctrla = (E-D)-A, de_vs_cb = (E-D)-(C-B),"
annot_df	Annotation information to the data tables?
force	Force edgeR to accept inputs which it should not have to deal with.
edger_method	I found a couple/few ways of doing edger in the manual, choose with this.
...	The elipsis parameter is fed to write_edger() at the end.

Details

Like the other _pairwise() functions, this attempts to perform all pairwise contrasts in the provided data set. The details are of course slightly different when using EdgeR. Thus, this uses the function choose_binom_dataset() to try to ensure that the incoming data is appropriate for EdgeR (if one normalized the data, it will attempt to revert to raw counts, for example). It continues on to extract the conditions and batches in the data, choose an appropriate experimental model, and run the EdgeR analyses as described in the manual. It defaults to using an experimental batch factor, but will accept a string like 'sva' instead, in which case it will use sva to estimate the surrogates,

and append them to the experimental design. The edger_method parameter may be used to apply different EdgeR code paths as outlined in the manual. If you want to play with non-standard data, the force argument will round the data and shoe-horn it into EdgeR.

Value

List including the following information: contrasts = The string representation of the contrasts performed. lrt = A list of the results from calling glmLRT(), one for each contrast. contrast_list = The list of each call to makeContrasts() I do this to avoid running into the limit on # of contrasts addressable by topTags() all_tables = a list of tables for the contrasts performed.

See Also

[edgeR] [deseq_pairwise()] [ebseq_pairwise()] [limma_pairwise()] [basic_pairwise()]

Examples

```
## Not run:
 expt <- create_expt(metadata = "metadata.xlsx", gene_info = annotations)
 pretend <- edger_pairwise(expt, model_batch = "sva")

## End(Not run)
```

---

exclude_genes_expt *Exclude some genes given a pattern match*

Description

Because I am too lazy to remember that expressionsets use matrix subsets for gene and sample. Also those methods lead to shenanigans when I want to know what happened to the data over the course of the subset.

Usage

```
exclude_genes_expt(
  expt,
  column = "txtype",
  method = "remove",
  ids = NULL,
  warning_cutoff = 90,
  patterns = c("snRNA", "tRNA", "rRNA"),
  ...
)
```

Arguments

expt	Expressionset containing expt object.
column	fData column to use for subsetting.
method	Either remove explicit rows, or keep them.
ids	Specific IDs to exclude.
patterns	Character list of patterns to remove/keep
...	Extra arguments are passed to arglist, currently unused.

Value

A smaller expt

See Also

[create_expt()] [Biobase]

Examples

```
 ## Not run:
  all_expt <- create_expt(metadata)
  ## This assumes a column in the metadata named 'txtype' containing the
  ## information telling us what type of transcript each gene is.
  no_ribosomes <- exclude_genes_expt(all_expt, column = "txtype",
                                     patterns = c("snRNA", "tRNA", "rRNA"))
  i_hate_these_genes <- exclude_genes_expt(all_expt, ids = c("gene1", "gene2"))
  only_ribosomes <- exclude_genes_expt(all_expt, method = "keep")

## End(Not run)
```

---

expt *An expt is an ExpressionSet superclass with a shorter name.*

Description

It is also a simple list so that one may summarize it more simply, provides colors and some slots to make one's life easier. It is created via the function create_expt() which perhaps should be changed.

Usage

```
expt(...)
```

Arguments

...	Parameters for create_expt()

Details

Another important caveat: expressionSets and their methods are all S4; but I did not want to write S4 methods, so I made my expt a S3 class. As a result, in order to make use of exprs, notes, pData, fData, and friends, I made use of setMethod() to set up calls for the expressionSet portion of the expt objects.

Slots

`title` Title for the expressionSet.

`notes` Notes for the expressionSet (redundant with S4 notes()).

`design` Copy of the experimental metadata (redundant with pData()).

`annotation` Gene annotations (redundant with fData()).

`gff_file` filename of a gff file which feeds this data.

`state` What is the state of the data vis a vis normalization, conversion, etc.

`conditions` Usually the condition column from pData.

`batches` Usually the batch column from pData.

`libsize` Library sizes of the data in its current state.

`colors` Chosen colors for plotting the data.

`tximport` Data provided by tximport() to create the exprs() data.

`extract_abundant_genes` *Extract the sets of genes which are significantly more abundant than the rest.*

Description

Given the output of something_pairwise(), pull out the genes for each contrast which are the most/least abundant. This is in contrast to extract_significant_genes(). That function seeks out the most changed, statistically significant genes.

Usage

```
extract_abundant_genes(
  pairwise,
  according_to = "all",
  n = 200,
  z = NULL,
  unique = FALSE,
  excel = "excel/abundant_genes.xlsx",
  ...
)
```

Arguments

pairwise	Output from _pairwise()().
according_to	What tool(s) define 'most?' One may use deseq, edger, limma, basic, all.
n	How many genes to pull?
z	Instead take the distribution of abundances and pull those past the given z score.
unique	One might want the subset of unique genes in the top-n which are unique in the set of available conditions. This will attempt to provide that.
excel	Excel file to write.
...	Arguments passed into arglist.

Value

The set of most/least abundant genes by contrast/tool.

See Also

openxlsx

---

extract_coefficient_scatter

Perform a coefficient scatter plot of a limma/deseq/edger/basic table.

Description

Plot the gene abundances for two coefficients in a differential expression comparison. By default, genes past 1.5 z scores from the mean are colored red/green.

Usage

```
extract_coefficient_scatter(
  output,
  toptable = NULL,
  type = "limma",
  x = 1,
  y = 2,
  z = 1.5,
  p = NULL,
  lfc = NULL,
  n = NULL,
  loess = FALSE,
  alpha = 0.4,
  color_low = "#DD0000",
  z_lines = FALSE,
  color_high = "#7B9F35",
  ...
)
```

Arguments

output	Result from the de_ family of functions, all_pairwise, or combine_de_tables().
toptable	Chosen table to query for abundances.
type	Query limma, deseq, edger, or basic outputs.
x	The x-axis column to use, either a number of name.
y	The y-axis column to use.
z	Define the range of genes to color (FIXME: extend this to p-value and fold-change).
p	Set a p-value cutoff for coloring the scatter plot (currently not supported).
lfc	Set a fold-change cutoff for coloring points in the scatter plot (currently not supported.)
n	Set a top-n fold-change for coloring the points in the scatter plot (this should work, actually).
loess	Add a loess estimation (This is slow.)
alpha	How see-through to make the dots.
color_low	Color for the genes less than the mean.
z_lines	Add lines to show the z-score demarcations.
color_high	Color for the genes greater than the mean.
...	More arguments are passed to arglist.

See Also

[plot_linear_scatter()]

Examples

```
## Not run:
 expt <- create_expt(metadata = "some_metadata.xlsx", gene_info = annotations)
 pairwise_output <- all_pairwise(expt)
 scatter_plot <- extract_coefficient_scatter(pairwise_output,
                                             type = "deseq", x = "uninfected", y = "infected")

## End(Not run)
```

---

extract_de_plots *Make a MA plot of some limma output with pretty colors and shapes.*

Description

Yay pretty colors and shapes! This function should be reworked following my rewrite of combine_de_tables(). It is certainly possible to make the logic here much simpler now.

Usage

```
extract_de_plots(
  pairwise,
  type = "edger",
  table = NULL,
  logfc = 1,
  p_type = "adj",
  p = 0.05,
  invert = FALSE,
  ...
)
```

Arguments

pairwise	The result from all_pairwise(), which should be changed to handle other invocations too.
type	Type of table to use: deseq, edger, limma, basic.
table	Result from edger to use, left alone it chooses the first.
logfc	What logFC to use for the MA plot horizontal lines.
p_type	Adjusted or raw pvalues?
p	Cutoff to define 'significant' by p-value.
invert	Invert the plot?
...	Extra arguments are passed to arglist.

Value

a plot!

See Also

[plot_ma_de()] [plot_volcano_de()]

Examples

```
## Not run:
 prettyplot <- edger_ma(all_aprwise) ## [sic, I'm witty! and can speel]

## End(Not run)
```

extract_go *Extract a set of geneID to GOID mappings from a suitable data source.*

Description

Like extract_lengths above, this is primarily intended to read gene ID and GO ID mappings from a OrgDb/OrganismDbi object.

Usage

```
extract_go(db, metadf = NULL, keytype = "ENTREZID")
```

Arguments

db	Data source containing mapping information.
metadf	Data frame containing extant information.
keytype	Keytype used for querying

Value

Dataframe of 2 columns: geneID and goID.

See Also

[AnnotationDbi]

extract_keepers_all *When no set of 'keeper' contrasts is specified, grab them all.*

Description

This has a couple of cousin functions, extract_keepers_list and _single. These handle extracting one or more contrasts out of the various tables produced by all_pairwise().

Usage

```
extract_keepers_all(
  apr,
  extracted,
  keepers,
  table_names,
  all_coefficients,
  limma,
  edger,
  ebseq,
```

```
  deseq,
  basic,
  adjp,
  annot_df,
  include_deseq,
  include_edger,
  include_ebseq,
  include_limma,
  include_basic,
  excludes,
  padj_type,
  loess = FALSE,
  lfc_cutoff = 1,
  p_cutoff = 0.05
)
```

Arguments

apr	Result from all_pairwise().
extracted	Table of extracted data.
keepers	In this case, one may assume either NULL or 'all'.
table_names	The set of tables produced by all_pairwise().
all_coefficients	The set of all experimental conditions in the experimental metadata.
limma	The limma data from all_pairwise().
edger	The edger data from all_pairwise().
ebseq	The ebseq data from all_pairwise().
deseq	The deseq data from all_pairwise().
basic	The basic data from all_pairwise().
adjp	Pull out the adjusted p-values from the data?
annot_df	What annotations should be added to the table?
include_deseq	Whether or not to include the deseq data.
include_edger	Whether or not to include the edger data.
include_ebseq	Whether or not to include the ebseq data.
include_limma	Whether or not to include the limma data.
include_basic	Whether or not to include the basic data.
excludes	Set of genes to exclude.
padj_type	Choose a specific p adjustment.
loess	Include a loess estimator in the plots?

`extract_keepers_lst` *When a list of 'keeper' contrasts is specified, extract it from the data.*

Description

This is the most interesting of the extract_keeper functions. It must check that the numerators and denominators match the desired contrast and flip the signs in the logFCs when appropriate.

Usage

```
extract_keepers_lst(
  extracted,
  keepers,
  table_names,
  all_coefficients,
  limma,
  edger,
  ebseq,
  deseq,
  basic,
  adjp,
  annot_df,
  include_deseq,
  include_edger,
  include_ebseq,
  include_limma,
  include_basic,
  excludes,
  padj_type,
  loess = FALSE,
  lfc_cutoff = 1,
  p_cutoff = 0.05
)
```

Arguments

`extracted`	Tables extracted from the all_pairwise data.
`keepers`	In this case, one may assume either NULL or 'all'.
`table_names`	The set of tables produced by all_pairwise().
`all_coefficients`	The set of all experimental conditions in the experimental metadata.
`limma`	The limma data from all_pairwise().
`edger`	The edger data from all_pairwise().
`ebseq`	The ebseq data from all_pairwise().
`deseq`	The deseq data from all_pairwise().

basic	The basic data from all_pairwise().
adjp	Pull out the adjusted p-values from the data?
annot_df	What annotations should be added to the table?
include_deseq	Whether or not to include the deseq data.
include_edger	Whether or not to include the edger data.
include_ebseq	Whether or not to include the ebseq data.
include_limma	Whether or not to include the limma data.
include_basic	Whether or not to include the basic data.
excludes	Set of genes to exclude.
padj_type	Choose a specific p adjustment.
loess	Add a loess to plots?
apr	Result from all_pairwise()

`extract_keepers_single` *When a single 'keeper' contrast is specified, find and extract it.*

Description

When a single 'keeper' contrast is specified, find and extract it.

Usage

```
extract_keepers_single(
  apr,
  extracted,
  keepers,
  table_names,
  all_coefficients,
  limma,
  edger,
  ebseq,
  deseq,
  basic,
  adjp,
  annot_df,
  include_deseq,
  include_edger,
  include_ebseq,
  include_limma,
  include_basic,
  excludes,
  padj_type,
```

```
  loess = FALSE,
  lfc_cutoff = 1,
  p_cutoff = 0.05
)
```

Arguments

apr	Data from all_pairwise().
extracted	Tables extracted in combine_de_tables().
keepers	In this case, one may assume either NULL or 'all'.
table_names	The set of tables produced by all_pairwise().
all_coefficients	The set of all experimental conditions in the experimental metadata.
limma	The limma data from all_pairwise().
edger	The edger data from all_pairwise().
ebseq	The ebseq data from all_pairwise().
deseq	The deseq data from all_pairwise().
basic	The basic data from all_pairwise().
adjp	Pull out the adjusted p-values from the data?
annot_df	What annotations should be added to the table?
include_deseq	Whether or not to include the deseq data.
include_edger	Whether or not to include the edger data.
include_ebseq	Whether or not to include the ebseq data.
include_limma	Whether or not to include the limma data.
include_basic	Whether or not to include the basic data.
excludes	Set of genes to exclude.
padj_type	Choose a specific p adjustment.
loess	Add a loess to plots?

---

extract_lengths *Take gene/exon lengths from a suitable data source (gff/TxDb/OrganismDbi)*

Description

Primarily goseq, but also other tools on occasion require a set of gene IDs and lengths. This function is resposible for pulling that data from either a gff, or TxDb/OrganismDbi.

Usage

```
extract_lengths(
  db = NULL,
  gene_list = NULL,
  type = "GenomicFeatures::transcripts",
  id = "TXID",
  possible_types = c("GenomicFeatures::genes", "GenomicFeatures::cds",
    "GenomicFeatures::transcripts"),
  ...
)
```

Arguments

db	Object containing data, if it is a string then a filename is assumed to a gff file.
gene_list	Set of genes to query.
type	Function name used for extracting data from TxDb objects.
id	Column from the resulting data structure to extract gene IDs.
possible_types	Character list of types I have previously used.
...	More arguments are passed to arglist.

Value

Dataframe containing 2 columns: ID, length

See Also

[GenomicFeatures]

---

extract_mayu_pps_fdr *Read output from mayu to get the IP/PP number corresponding to a given FDR value.*

Description

Read output from mayu to get the IP/PP number corresponding to a given FDR value.

Usage

```
extract_mayu_pps_fdr(file, fdr = 0.01)
```

Arguments

file	Mayu output file.
fdr	Chosen fdr value to acquire.

Value

List of two elements: the full mayu table sorted by fdr and the number corresponding to the chosen fdr value.

`extract_metadata` *Pull metadata from a table (xlsx/xls/csv/whatever)*

Description

I find that when I acquire metadata from a paper or collaborator, annoyingly often there are many special characters or other shenanigans in the column names. This function performs some simple sanitizations. In addition, if I give it a filename it calls my generic 'read_metadata()' function before sanitizing.

Usage

```
extract_metadata(metadata, id_column = "sampleid", ...)
```

Arguments

`metadata`	file or df of metadata
`id_column`	Column in the metadat containing the sample names.
`...`	Arguments to pass to the child functions (read_csv etc).

Value

Metadata dataframe hopefully cleaned up to not be obnoxious.

Examples

```
 ## Not run:
  sanitized <- extract_metadata("some_random_supplemental.xls")
  saniclean <- extract_metadata(some_goofy_df)

## End(Not run)
```

`extract_msraw_data` *Read a bunch of mzXML files to acquire their metadata.*

Description

I have had difficulties getting the full set of correct parameters for a DDA/DIA experiment. After some poking, I eventually found most of these required prameters in the mzXML raw files. Ergo, this function uses them. 20190310: I had forgotten about the mzR library. I think much (all?) of this is redundant with respect to it and perhaps should be removed in deference to the more complete and fast implementation included in mzR.

Usage

```
extract_msraw_data(
  metadata,
  write_windows = TRUE,
  id_column = "sampleid",
  file_column = "raw_file",
  allow_window_overlap = FALSE,
  start_add = 0,
  format = "mzXML",
  parallel = TRUE,
  savefile = NULL,
  ...
)
```

Arguments

`metadata`	Data frame describing the samples, including the mzXML filenames.
`write_windows`	Write out SWATH window frames.
`id_column`	What column in the sample sheet provides the ID for the samples?
`file_column`	Which column in the sample sheet provides the filenames?
`allow_window_overlap`	What it says on the tin, some tools do not like DIA windows to overlap, if TRUE, this will make sure each annotated window starts at the end of the previous window if they overlap.
`start_add`	Another strategy is to just add a static amount to each window.
`format`	Currently this handles mzXML or mzML files.
`parallel`	Perform operations using an R foreach cluster?
`savefile`	If not null, save the resulting data structure to an rda file.
`...`	Extra arguments, presumably color palettes and column names and stuff like that.

Value

List of data extracted from every sample in the MS run (DIA or DDA).

extract_mzML_scans *Parse a mzML file and return the relevant data.*

Description

This does the actual work for extract_scan_data(). This levers mzR to provide the data and goes a step further to pull out the windows acquired in the MS/MS scan and print them in formats acceptable to TPP/OpenMS (eg. with and without headers).

Usage

```
extract_mzML_scans(
  file,
  id = NULL,
  write_acquisitions = TRUE,
  allow_window_overlap = FALSE,
  start_add = 0
)
```

Arguments

file	Input mzML file to parse.
id	Chosen ID for the given file.
write_acquisitions	Write acquisition windows.
allow_window_overlap	Some downstream tools cannot deal with overlapping windows. Toggle that here.
start_add	Other downstream tools appear to expect some padding at the beginning of each window. Add that here.

Value

The list of metadata, scan data, etc from the mzXML file.

extract_mzXML_scans *Parse a mzXML file and return the relevant data.*

Description

This does the actual work for extract_scan_data(). When I wrote this function, I had forgotten about the mzR library; with that in mind, this seems to give a bit more information and be a bit faster than my short tests with mzR (note however that my tests were to compare mzR parsing mzML files vs. this function with mzXML, which is a classic apples to oranges).

Usage

```
extract_mzXML_scans(
  file,
  id = NULL,
  write_acquisitions = TRUE,
  allow_window_overlap = FALSE,
  start_add = 0
)
```

Arguments

file	Input mzXML file to parse.
id	Chosen ID for the given file.
write_acquisitions	Write acquisition windows.
allow_window_overlap	Some downstream tools cannot deal with overlapping windows. Toggle that here.
start_add	Other downstream tools appear to expect some padding at the beginning of each window. Add that here.

Details

This goes a step further to pull out the windows acquired in the MS/MS scan and print them in formats acceptable to TPP/OpenMS (eg. with and without headers).

Value

The list of metadata, scan data, etc from the mzXML file.

---

extract_peprophet_data

Get some data from a peptideprophet run.

Description

I am not sure what if any parameters this should have, but it seeks to extract the useful data from a peptide prophet run. In the situation in which I wish to use it, the input command was: > xinteract -dDECOY_ -OARPpd -Nfdr_library.xml comet_result.pep.xml Eg. It is a peptideprophet result provided by TPP. I want to read the resulting xml table and turn it into a data.table so that I can plot some metrics from it.

Usage

```
extract_peprophet_data(pepxml, decoy_string = "DECOY_", ...)
```

Arguments

pepxml	The file resulting from the xinteract invocation.
decoy_string	What prefix do decoys have in the data.
...	Catch extra arguments passed here, currently unused.

Value

data table of all the information I saw fit to extract The columns are: * protein: The name of the matching sequence (DECOYs allowed here) * decoy: TRUE/FALSE, is this one of our decoys? * peptide: The sequence of the matching spectrum. * start_scan: The scan in which this peptide was observed * end scan: Ibid * index This seems to just increment * precursor_neutral_mass: Calculated mass of this fragment assuming no isotope shenanigans (yeah, looking at you C13). * assumed_charge: The expected charge state of this peptide. * retention_time_sec: The time at which this peptide eluted during the run. * peptide_prev_aa: The amino acid before the match. * peptide_next_aa: and the following amino acid. * num_tot_proteins: The number of matches not counting decoys. * num_matched_ions: How many ions for this peptide matched? * tot_num_ions: How many theoretical ions are in this fragment? * matched_ion_ratio: num_matched_ions / tot_num_ions, bigger is better! * cal_neutral_pep_mass: This is redundant with precursor_neutral_mass, but recalculated by peptideProphet, so if there is a discrepency we should yell at someone! * massdiff How far off is the observed mass vs. the calculated? (also redundant with massd later) * num_tol_term: The number of peptide termini which are consistent with the cleavage (hopefully 2), but potentially 1 or even 0 if digestion was bad. (redundant with ntt later) * num_missed_cleavages: How many cleavages must have failed in order for this to be a good match? * num_matched_peptides: Number of alternate possible peptide matches. * xcorr: cross correlation of the experimental and theoretical spectra (this is supposedly only used by sequest, but I seem to have it here...) * deltacn: The normalized difference between the xcorr values for the best hit and next best hit. Thus higher numbers suggest better matches. * deltacnstar: Apparently 'important for things like phospho-searches containing homologous top-scoring peptides when analyzed by peptideprophet...' – the comet release notes. * spscore: The raw value of preliminary score from the sequest algorithm. * sprank: The rank of the match in a preliminary score. 1 is good. * expect: E-value of the given peptide hit. Thus how many identifications one expect to observe by chance, lower is therefore better * prophet_probability: The peptide prophet probability score, higher is better. * fval: 0.6(the dot function + 0.4(the delta dot function) - (the dot bias penalty function) – which is to say... well I dunno, but it is supposed to provide information about how similar this match is to other potential matches, so I presume higher means the match is more ambiguous. * ntt: Redundant with num_tol_term above, but this time from peptide prophet. * nmc: Redundant with num_missed_cleavages, except it coalesces them. * massd: Redundant with massdiff * isomassd: The mass difference, but taking into account stupid C13. * RT: Retention time * RT_score: The score of the retention time! * modified_peptides: A string describing modifications in the found peptide * variable_mods: A comma separated list of the variable modifications observed. * static_mods: A comma separated list of the static modifications observed.

---

extract_pyprophet_data

Read a bunch of scored swath outputs from pyprophet to acquire their metrics.

Description

This function is mostly cribbed from the other extract_ functions in this file. With it, I hope to be able to provide some metrics of a set of openswath runs, thus potentially opening the door to being able to objectively compare the same run with different options and/or different runs.

Usage

```
extract_pyprophet_data(
  metadata,
  pyprophet_column = "diascored",
  savefile = NULL,
  ...
)
```

Arguments

metadata	Data frame describing the samples, including the mzXML filenames.
pyprophet_column	Which column from the metadata provides the requisite filenames?
savefile	If not null, save the data from this to the given filename.
...	Extra arguments, presumably color palettes and column names and stuff like that.

Details

Likely columns generated by exporting OpenMS data via pyprophet include: transition_group_id: Incrementing ID of the transition in the MS(.pqp) library used for matching (I am pretty sure). decoy: Is this match of a decoy peptide? run_id: This is a bizarre encoding of the run, OpenMS/pyprophet re-encodes the run ID from the filename to a large signed integer. filename: Which raw mzXML file provides this particular intensity value? rt: Retention time in seconds for the matching peak group. assay_rt: The expected retention time after normalization with the iRT. (how does the iRT change this value?) delta_rt: The difference between rt and assay_rt irt: (As described in the abstract of Claudia Escher's 2012 paper: "Here we present iRT, an empirically derived dimensionless peptide-specific value that allows for highly accurate RT prediction. The iRT of a peptide is a fixed number relative to a standard set of reference iRT-peptides that can be transferred across laboratories and chromatographic systems.") assay_irt: The iRT observed in the actual chromatographic run. delta_irt: The difference. I am seeing that all the delta iRTs are in the -4000 range for our actual experiment; since this is in seconds, does that mean that it is ok as long as they stay in a similar range? id: unique long signed integer for the peak group. sequence: The sequence of the matched peptide fullunimodpeptidename: The sequence, but with unimod formatted modifications included. charge: The assumed charge of the observed peptide. mz: The m/z value of the precursor ion. intensity: The sum of all transition intensities in the peak group. aggr_prec_peak_area: Semi-colon separated list of intensities (peak areas) of the MS traces for this match. aggr_prec_peak_apex: Intensity peak apexes of the MS1 traces. leftwidth: The start of the peak group in seconds. rightwidth: The end of the peak group in seconds. peak_group_rank: When multiple peak groups match, which one is this? d_score: I think this is the score as retured by openMS (higher is better). m_score: I am pretty sure this is the result of a SELECT QVALUE operation in pyprophet. aggr_peak_area: The intensities of this fragment ion separated by semicolons. aggr_peak_apex: The intensities of this

fragment ion separated by semicolons. aggr_fragment_annotation: Annotations of the fragment ion traces by semicolon. proteinname: Name of the matching protein. m_score_protein_run_specific: I am guessing the fdr for the pvalue for this run. mass: Mass of the observed fragment.

Value

List of data from each sample in the pyprophet scored DIA run.

`extract_scan_data` *Read a mzML/mzXML file and extract from it some important metadata.*

Description

When working with swath data, it is fundamentally important to know the correct values for a bunch of the input variables. These are not trivial to acquire. This function attempts to make this easier (but slow) by reading the mzXML file and parsing out helpful data.

Usage

```
extract_scan_data(
  file,
  id = NULL,
  write_acquisitions = TRUE,
  format = "mzXML",
  allow_window_overlap = FALSE,
  start_add = 0
)
```

Arguments

`file`	Filename to read.
`id`	An id to give the result.
`write_acquisitions`	If a filename is provided, write a tab separated table of windows.
`format`	Either mzXML or mzML.
`allow_window_overlap`	One may choose to foce windows to not overlap.
`start_add`	Add a minute to the start of the windows to avoid overlaps?

Value

List containing a table of scan and precursor data.

extract_siggenes *Alias for extract_significant_genes because I am dumb.*

Description

Alias for extract_significant_genes because I am dumb.

Usage

```
extract_siggenes(...)
```

Arguments

...	The parameters for extract_significant_genes()

Value

It should return a reminder for me to remember my function names or change them to something not stupid.

extract_significant_genes *Extract the sets of genes which are significantly up/down regulated from the combined tables.*

Description

Given the output from combine_de_tables(), extract the genes in which we have the greatest likely interest, either because they have the largest fold changes, lowest p-values, fall outside a z-score, or are at the top/bottom of the ranked list.

Usage

```
extract_significant_genes(
  combined,
  according_to = "all",
  lfc = 1,
  p = 0.05,
  sig_bar = TRUE,
  z = NULL,
  n = NULL,
  top_percent = NULL,
  ma = TRUE,
  p_type = "adj",
  invert_barplots = FALSE,
```

```
  excel = NULL,
  siglfc_cutoffs = c(0, 1, 2),
  ...
)
```

Arguments

combined	Output from combine_de_tables().
according_to	What tool(s) decide 'significant?' One may use the deseq, edger, limma, basic, meta, or all.
lfc	Log fold change to define 'significant'.
p	(Adjusted)p-value to define 'significant'.
sig_bar	Add bar plots describing various cutoffs of 'significant'?
z	Z-score to define 'significant'.
n	Take the top/bottom-n genes.
top_percent	Use a percentage to get the top-n genes.
ma	Add ma plots to the sheets of 'up' genes?
p_type	use an adjusted p-value?
invert_barplots	Invert the significance barplots as per Najib's request?
excel	Write the results to this excel file, or NULL.
siglfc_cutoffs	Set of cutoffs used to define levels of 'significant.'
...	Arguments passed into arglist.

Value

The set of up-genes, down-genes, and numbers therein.

See Also

combine_de_tables

---

factor_rsquared *Collect the r^2 values from a linear model fitting between a singular value decomposition and factor.*

Description

Collect the r^2 values from a linear model fitting between a singular value decomposition and factor.

Usage

```
factor_rsquared(datum, fact, type = "factor")
```

Arguments

datum	Result from corpcor::fast.svd.
fact	Experimental factor from the original data.
type	Make this categorical or continuous with factor/continuous.

Value

The r^2 values of the linear model as a percentage.

See Also

[corpcor] [stats::lm()]

---

features_greater_than *Count the number of features(genes) greater than x in a data set.*

Description

Sometimes I am asked how many genes have >= x counts. Well, here you go.

Usage

```
features_greater_than(data, cutoff = 1, hard = TRUE, inverse = FALSE)
```

Arguments

data	Dataframe/exprs/matrix/whatever of counts.
cutoff	Minimum number of counts.
hard	Greater-than is hard, greater-than-equals is not.
inverse	when inverted, this provides features less than the cutoff.

Details

Untested as of 2016-12-01 but used with Lucia. I think it would be interesting to iterate this function from small to large cutoffs and plot how the number of kept genes decreases.

Value

A list of two elements, the first comprised of the number of genes greater than the cutoff, the second with the identities of said genes.

See Also

[Biobase]

Examples

```
## Not run:
 features <- features_greater_than(expt)
 fewer <- features_greater_than(expt, cutoff = 100)

## End(Not run)
```

`features_in_single_condition` *I want an easy way to answer the question: what features are in only condition x?*

Description

The answer to this lies in a combination of subset_expt() and features_greater_than().

Usage

```
features_in_single_condition(
  expt,
  cutoff = 2,
  factor = "condition",
  chosen = NULL
)
```

Arguments

`expt`	An experiment to query.
`cutoff`	What is the minimum number of counts required to define 'included.'
`factor`	What metadata factor to query?
`chosen`	Either choose a subset or all conditions to query.

Value

A set of features.

See Also

[subset_expt()]

Examples

```
## Not run:
 unique_genes

## End(Not run)
```

features_less_than *Do features_greater_than() inverted!*

Description

Do features_greater_than() inverted!

Usage

```
features_less_than(...)
```

Arguments

...	Arguments passed to features_greather_than()

Value

The set of features less than whatever you would have done with features_greater_than().

See Also

[features_greater_than()]

filter_counts *Call various count filters.*

Description

This calls the various filtering functions in genefilter along with suggestions made in our lab meetings; defaulting to the threshold based filter suggested by Hector.

Usage

```
filter_counts(
  count_table,
  method = "cbcb",
  p = 0.01,
  A = 1,
  k = 1,
  cv_min = 0.01,
  cv_max = 1000,
  thresh = 2,
  min_samples = 2,
  ...
)
```

Arguments

count_table	Some counts to filter.
method	Filtering method to apply (cbcb, pofa, kofa, cv right now).
p	Used by genefilter's pofa().
A	Also for pofa().
k	Used by genefilter's kofa().
cv_min	Used by genefilter's cv().
cv_max	Also used by cv().
thresh	Minimum threshold across samples for cbcb.
min_samples	Minimum number of samples for cbcb.
...	More options might be needed, especially if I fold cv/p/etc into ...

Value

Data frame of filtered counts.

See Also

[genefilter]

Examples

```
## Not run:
 new <- filter_counts(old)

## End(Not run)
```

---

find_working_mart *Find a functional biomart instance.*

Description

In my experience, the various biomart mirrors are not varyingly likely to be functional at any given time. In addition, I often find it useful to use an archive instance rather than the most recent ensembl instance. This function therefore iterates over the various mirrors; or if archive = TRUE it will try a series of archive servers from 1, 2, and 3 years ago.

Usage

```
find_working_mart(
 default_hosts = c("useast.ensembl.org", "uswest.ensembl.org", "www.ensembl.org",
    "asia.ensembl.org"),
 trymart = "ENSEMBL_MART_ENSEMBL",
 archive = FALSE,
 year = NULL,
 month = NULL
)
```

Arguments

default_hosts	List of biomart mirrors to try.
trymart	Specific mart to query.
archive	Try an archive server instead of a mirror? If this is a character, it will assume it is a specific archive hostname.
year	Choose specific year(s) for the archive servers?
month	Choose specific month(s) for the archive servers?

Value

Either a mart instance or NULL if no love was forthcoming.

See Also

[biomaRt::useMart()] [biomaRt::listMarts()]

---

flanking_sequence *Extract sequence flanking a set of annotations (generally coding sequences)*

Description

Given a set of annotations and genome, one might want to get the set of adjacent sequences.

Usage

```
flanking_sequence(
  bsgenome,
  annotation,
  distance = 200,
  type = "gene",
  prefix = ""
)
```

Arguments

bsgenome	Genome sequence
annotation	Set of annotations
distance	How far from each annotation is desired?
type	What type of annotation is desired?
prefix	Provide a prefix to the names to distinguish them from the existing annotations.

Value

List of sequences before and after each sequence.

See Also

[load_gff_annotations()] [GenomicRanges] [IRanges]

`gather_eupath_utrs_padding` *Given an eupathdb species lacking UTR boundaries, extract an arbitrary region before/after each gene.*

Description

This is a very domain-specific function.

Usage

```
gather_eupath_utrs_padding(
  species_name = "Leishmania major",
  entry = NULL,
  webservice = "tritrypdb",
  padding = 200,
  ...
)
```

Arguments

`species_name`	Species name for which to query the eupathdb.
`entry`	EuPathDB metadatum entry.
`webservice`	If specified, makes the query faster, I always used tritrypdb.org.
`padding`	Number of nucleotides to gather.
`...`	Extra arguments for the various EuPathDB functions.

Value

Set of padding UTR sequences/coordinates.

`gather_genes_orgdb` *Use the orgdb instances from clusterProfiler to gather annotation data for GO.*

Description

Since clusterprofiler no longer builds gomaps, I need to start understanding how to properly get information from orgDBs.

Usage

```
gather_genes_orgdb(goseq_data, orgdb_go, orgdb_ensembl)
```

Arguments

`goseq_data`	Some data from goseq and friends.
`orgdb_go`	The orgDb instance with GO data.
`orgdb_ensembl`	The orgDb instance with ensembl data.

Value

GO mapping

See Also

[goseq]

`gather_masses` *Use BRAIN to find the peptide mass from a sequence.*

Description

This rounds the avgMass from BRAIN to deal with isotopes, maybe this should be changed.

Usage

```
gather_masses(sequence)
```

Arguments

`sequence`	Sequence to count.

Value

Rounded average mass.

`gather_ontology_genes` *Given a set of goseq data from simple_goseq(), make a list of genes represented in each ontology.*

Description

This function uses the GO2ALLEG data structure to reverse map ontology categories to a list of genes represented. It therefore assumes that the GO2ALLEG.rda data structure has been deposited in pwd(). This in turn may be generated by clusterProfilers buildGOmap() function if it doesn't exist. For some species it may also be auto-generated. With little work this can be made much more generic, and it probably should.

Usage

```
gather_ontology_genes(
  result,
  ontology = NULL,
  column = "over_represented_pvalue",
  pval = 0.1,
  include_all = FALSE,
  ...
)
```

Arguments

`result`	List of results as generated by simple_*().
`ontology`	Ontology to search (MF/BP/CC).
`column`	Which column to use for extracting ontologies?
`pval`	Maximum accepted pvalue to include in the list of categories to cross reference.
`include_all`	Include all genes in the ontology search?
`...`	Extra options without a purpose just yet.

Value

Data frame of categories/genes.

See Also

[simple_goseq()]

Examples

```
 ## Not run:
 data <- simple_goseq(sig_genes = limma_output, lengths = annotation_df, goids = goids_df)
  genes_in_cats <- gather_genes(data, ont='BP')

## End(Not run)
```

gather_utrs_padding *Take a BSgenome and data frame of chr/start/end/strand, provide 5' and 3' padded sequence.*

Description

For some species, we do not have a fully realized set of UTR boundaries, so it can be useful to query some arbitrary and consistent amount of sequence before/after every CDS sequence. This function can provide that information. Note, I decided to use tibble for this so that if one accidently prints too much it will not freak out.

Usage

```
gather_utrs_padding(
  bsgenome,
  annot_df,
  gid = NULL,
  name_column = "gid",
  chr_column = "chromosome",
  start_column = "start",
  end_column = "end",
  strand_column = "strand",
  type_column = "annot_gene_type",
  gene_type = "protein coding",
  padding = 120,
  ...
)
```

Arguments

bsgenome	BSgenome object containing the genome of interest.
annot_df	Annotation data frame containing all the entries of interest, this is generally extracted using a function in the load_something_annotations() family (load_orgdb_annotations() being the most likely).
gid	Specific GID(s) to query.
name_column	Give each gene a name using this column.
chr_column	Column name of the chromosome names.
start_column	Column name of the start information.
end_column	Ibid, end column.
strand_column	Ibid, strand.
type_column	Subset the annotation data using this column, if not null.
gene_type	Subset the annotation data using the type_column with this type.
padding	Return this number of nucleotides for each gene.
...	Arguments passed to child functions (I think none currently).

Value

Dataframe of UTR, CDS, and UTR+CDS sequences.

`gather_utrs_txdb` *Get UTR sequences using information provided by TxDb and fiveUTRsByTranscript*

Description

For species like Mus musculus, load_orgdb_annotations(Mus.musculus) should return a list including the requisite GRanges for the 5'/3' UTRs.

Usage

```
gather_utrs_txdb(
  bsgenome,
  fivep_utr = NULL,
  threep_utr = NULL,
  start_column = "start",
  end_column = "end",
  strand_column = "strand",
  chr_column = "seqnames",
  name_column = "group_name",
  ...
)
```

Arguments

`bsgenome`	A BSGenome instance containing the encoded genome.
`fivep_utr`	Locations of the 5' UTRs.
`threep_utr`	Locations of the 3' UTRs.
`start_column`	What column in the annotation data contains the starts?
`end_column`	Column in the data with the end locations.
`strand_column`	What column in the annotation data contains the sequence strands?
`chr_column`	Column in the df with the chromosome names.
`name_column`	Finally, where are the gene names?
`...`	Parameters passed to child functions.

Value

UTRs!

`genefilter_cv_counts` *Filter genes from a dataset outside a range of variance.*

Description

This function from genefilter removes genes surpassing a variance cutoff. It is not therefore a low-count filter per se.

Usage

```
genefilter_cv_counts(count_table, cv_min = 0.01, cv_max = 1000)
```

Arguments

`count_table`	Input data frame of counts by sample.
`cv_min`	Minimum coefficient of variance.
`cv_max`	Maximum coefficient of variance.

Value

Dataframe of counts without the high/low variance genes.

See Also

[genefilter::kOverA()]

Examples

```
## Not run:
 filtered_table = genefilter_kofa_counts(count_table)

## End(Not run)
```

`genefilter_kofa_counts`
Filter low-count genes from a data set using genefilter's kOverA().

Description

This is the most similar to the function suggested by Hector I think.

Usage

```
genefilter_kofa_counts(count_table, k = 1, A = 1)
```

Arguments

count_table	Input data frame of counts by sample.
k	Minimum number of samples to have >A counts.
A	Minimum number of counts for each gene's sample in kOverA().

Value

Dataframe of counts without the low-count genes.

See Also

[genefilter::kOverA()]

Examples

```
## Not run:
 filtered_table = genefilter_kofa_counts(count_table)

## End(Not run)
```

---

genefilter_pofa_counts

Filter low-count genes from a data set using genefilter's pOverA().

Description

I keep thinking this function is pofa... oh well. Of the various tools in genefilter, this one to me is the most intuitive. Take the ratio of counts/samples and make sure it is >= a score.

Usage

```
genefilter_pofa_counts(count_table, p = 0.01, A = 100)
```

Arguments

count_table	Input data frame of counts by sample.
p	Minimum proportion of each gene's counts/sample to be greater than a minimum(A).
A	Minimum number of counts in the above proportion.

Value

Dataframe of counts without the low-count genes.

See Also

[genefilter::pOverA()]

Examples

```
## Not run:
 filtered_table = genefilter_pofa_counts(count_table)

## End(Not run)
```

`generate_expt_colors` *Set up default colors for a data structure containing usable metadata*

Description

In theory this function should be useful in any context when one has a blob of metadata and wants to have a set of colors. Since my taste is utterly terrible, I rely entirely upon RColorBrewer, but also allow one to choose his/her own colors.

Usage

```
generate_expt_colors(
  sample_definitions,
  cond_column = "condition",
  by = "sampleid",
  ...
)
```

Arguments

`sample_definitions`	Metadata, presumably containing a 'condition' column.
`cond_column`	Which column in the sample data provides the set of 'conditions' used to define the colors?
`by`	Name the factor of colors according to this column.
`...`	Other arguments like a color palette, etc.

Value

Colors!

See Also

[create_expt()]

`genoplot_chromosome` *Try plotting a chromosome (region)*

Description

genoplotr is cool, I don't yet understand it though

Usage

```
genoplot_chromosome(
  accession = "AE009949",
  start = NULL,
  end = NULL,
  title = "Genome plot"
)
```

Arguments

`accession`	An accession to plot, this will download it.
`start`	First segment to plot (doesn't quite work yet).
`end`	Final segment to plot (doesn't quite work yet).
`title`	Put a title on the resulting plot.

Value

Hopefully a pretty plot of a genome

See Also

[genoPlotR]

`get_abundant_genes` *Find the set of most/least abundant genes according to limma and friends following a differential expression analysis.*

Description

Given a data set provided by limma, deseq, edger, etc; one might want to know what are the most and least abundant genes, much like get_sig_genes() does to find the most significantly different genes for each contrast.

Usage

```
get_abundant_genes(datum, type = "limma", n = NULL, z = NULL, unique = FALSE)
```

Arguments

datum	Output from the _pairwise() functions.
type	Extract abundant genes according to what?
n	Perhaps take just the top/bottom n genes.
z	Or take genes past a given z-score.
unique	Unimplemented: take only the genes unique among the conditions surveyed.

Value

List of data frames containing the genes of interest.

See Also

[get_sig_genes()]

Examples

```
## Not run:
 abundant <- get_abundant_genes(all_pairwise_output, type = "deseq", n = 100)
 ## Top 100 most abundant genes from deseq
 least <- get_abundant_genes(all_pairwise_output, type = "deseq", n = 100, least = TRUE)
 ## Top 100 least abundant genes from deseq
 abundant <- get_abundant_genes(all_pairwise_output, type = "edger", z = 1.5)
 ## Get the genes more than 1.5 standard deviations from the mean.

## End(Not run)
```

---

get_circos_data *Extra fonts and useful bits and bobs for working with circos.*

Description

This is a tarball of the circos etc/ directory from my Debian linux installation. I discovered to my annoyance that other systems were missing the fonts required to make circos plots work properly along with something else. In a fit of pique I tarred them up and left them here.

Usage

```
get_circos_data()
```

get_genesizes *Grab gene length/width/size from an annotation database.*

Description

This function tries to gather an appropriate gene length column from whatever annotation data source is provided.

Usage

```
get_genesizes(
  annotation = NULL,
  type = "gff",
  gene_type = "gene",
  type_column = "type",
  key = NULL,
  length_names = NULL,
  ...
)
```

Arguments

annotation	There are a few likely data sources when getting gene sizes, choose one with this.
type	What type of annotation data are we using?
gene_type	Annotation type to use (3rd column of a gff file).
type_column	Type identifier (10th column of a gff file).
key	What column has ID information?
length_names	Provide some column names which give gene length information?
...	Extra arguments likely for load_annotations()

Value

Data frame of gene IDs and widths.

See Also

[rtracklayer] [load_gff_annotations()]

Examples

```
pa_gff <- system.file("share", "paeruginosa_pa14.gff", package = "hpgltools")
pa_genesizes <- get_genesizes(gff = pa_gff)
head(pa_genesizes)
```

get_git_commit *Get the current git commit for hpgltools*

Description

One might reasonably ask about this function: "Why?" I invoke this function at the end of my various knitr documents so that if necessary I can do a > git reset <commit id> and get back to the exact state of my code.

Usage

```
get_git_commit(gitdir = "~/hpgltools")
```

Arguments

gitdir	Directory containing the git repository.

get_group_gsva_means *Create dataframe which gets the maximum within group mean gsva score for each gene set*

Description

Create dataframe which gets the maximum within group mean gsva score for each gene set

Usage

```
get_group_gsva_means(gsva_scores, groups, keep_single = TRUE, method = "mean")
```

Arguments

groups	list of groups for which to calculate the means
keep_single	Keep categories with only 1 element.
method	mean or median?
gsva_result	Result from simple_gsva()

Value

dataframe containing max_gsva_score, and within group means for gsva scores

See Also

[simple_gsva()]

get_gsvadb_names *Extract the GeneSets corresponding to the provided name(s).*

Description

Many of the likely GSCs contain far more gene sets than one actually wants to deal with. This will subset them according to a the desired 'requests'.

Usage

```
get_gsvadb_names(sig_data, requests = NULL)
```

Arguments

sig_data	The pile of GeneSets, probably from GSVAdata.
requests	Character list of sources to keep.

Value

Whatever GeneSets remain.

get_hsapiens_data *Subset of a human RNASeq expressionset.*

Description

This is a portion of an expressionset used to examine changes caused by infection with Leishmania panamensis.

Usage

```
get_hsapiens_data()
```

get_individual_snps *Extract the observed snps unique to individual categories in a snp set.*

Description

The result of get_snp_sets provides sets of snps for all possible categories. This is cool and all, but most of the time we just want the results of a single group in that rather large set (2^number of categories)

Usage

```
get_individual_snps(retlist)
```

Arguments

retlist	The result from get_snp_sets().

get_kegg_genes *Extract the set of geneIDs matching pathways for a given species.*

Description

This uses KEGGREST to extract the mappings for all genes for a species and pathway or 'all'. Because downloading them takes a while, it will save the results to kegg_species.rda. When run interactively, it will give some information regarding the number of genes observed in each pathway.

Usage

```
get_kegg_genes(
  pathway = "all",
  abbreviation = NULL,
  species = "leishmania major",
  savefile = NULL
)
```

Arguments

pathway	Either a single pathway kegg id or 'all'.
abbreviation	Optional 3 letter species kegg id.
species	Stringified species name used to extract the 3 letter abbreviation.
savefile	Filename to which to save the relevant data.

Value

Dataframe of the various kegg data for each pathway, 1 row/gene.

See Also

[KEGGREST]

Examples

```
## Not run:
 kegg_info <- get_kegg_genes(species = "Canis familiaris")

## End(Not run)
```

`get_kegg_orgn` *Search KEGG identifiers for a given species name.*

Description

KEGG identifiers do not always make sense. For example, how am I supposed to remember that Leishmania major is lmj? This takes in a human readable string and finds the KEGG identifiers that match it.

Usage

```
get_kegg_orgn(species = "Leishmania", short = TRUE)
```

Arguments

`species`	Search string (Something like 'Homo sapiens').
`short`	Only pull the orgid?

Value

Data frame of possible KEGG identifier codes, genome ID numbers, species, and phylogenetic classifications.

See Also

[RCurl]

Examples

```
## Not run:
 fun = get_kegg_orgn('Canis')
 ## >     Tid     orgid      species                    phylogeny
 ## >  17 T01007   cfa Canis familiaris (dog) Eukaryotes;Animals;Vertebrates;Mammals

## End(Not run)
```

get_kegg_sub *Provide a set of simple substitutions to convert geneIDs from KEGG->TriTryDB*

Description

This function should provide 2 character lists which, when applied sequentially, will result in a hopefully coherent set of mapped gene IDs matching the TriTypDB/KEGG specifications.

Usage

```
get_kegg_sub(species = "lma")
```

Arguments

species	3 letter abbreviation for a given kegg type

Value

2 character lists containing the patterns and replace arguments for gsub(), order matters!

See Also

[KEGGREST]

get_lmajor_data *The UTR regions of every highly translated L.major gene.*

Description

Once upon a time I performed a ribosome profiling experiment in Leishmania major. Sadly, we still have not published it. This file contains the UTRs of every highly translated gene in procyclic promastigotes. I used it in some motif analyses for fun.

Usage

```
get_lmajor_data()
```

get_microbesonline_taxid

Extract microbesonline taxon IDs without having to click on the weird boxes at the top of the website.

Description

This should simplify getting material from microbesonline.

Usage

```
get_microbesonline_taxid(species = "Acyrthosiphon pisum virus")
```

Arguments

species	String to search the set of microbesonline taxa.

Value

NULL or 1 or more taxon ids.

See Also

[xml2]

Examples

```
coli_taxids <- get_microbesonline_taxid(species = "coli S88")
head(coli_taxids)
```

get_msigdb_metadata

Create a metadata dataframe of msigdb data, this hopefully will be usable to fill the fData slot of a gsva returned expressionset.

Description

Create a metadata dataframe of msigdb data, this hopefully will be usable to fill the fData slot of a gsva returned expressionset.

Usage

```
get_msigdb_metadata(
  gsva_result = NULL,
  msig_xml = "msigdb_v6.2.xml",
  wanted_meta = c("ORGANISM", "DESCRIPTION_BRIEF", "AUTHORS", "PMID")
)
```

Arguments

gsva_result	Some data from GSVA to modify.
msig_xml	msig XML file downloaded from broad.

Value

list containing 2 data frames: all metadata from broad, and the set matching the sig_data GeneSets.

See Also

[xml2] [rvest]

---

get_mtuberculosis_data

Portion of a sample sheet used in a DIA-SWATH proteomics experiment.

Description

In this experiment, Dr. Briken sought to learn about proteins which are exported by Mycobacterium tuberculosis. He therefore performed a DIA SWATH experiment using two strains and collected the supernatant fraction (to get the exported proteins) and the intracellular fraction. This file contains the metadata for a portion of that experiment. I used a fairly exhaustive set of open source tools to interpret Dr. Briken's data. These files comprise the endpoint of the preprocessing and the inputs for the R package 'SWATH2stats'. This file is excessively large, but the smallest by far of the various inputs I wanted to include to test my various proteomics functions. In a separate series of experiments, we sought to look at the effect of infection on splicing in the host. Thus I performed rmats and suppa and attempted to compare the results to see how reliable they are. (spoiler: not very).

Usage

```
get_mtuberculosis_data()
```

---

get_paeruginosa_data *Pseudomonas areuginosa strain PA14 data files.*

Description

The sample sheet from an experiment with another ESKAPE pathogen, Pesudomonas! This is emblematic of how I like to organize samples. The most relevant columns for creating an expressionset with create_expt() include: 'Sample ID', 'Condition', 'Batch', and 'file'. This actually provides a subset of an experiment in which we were looking simultaneously at the 'large' and 'small' RNA populations in two PA strains, one of which is deficient in an oligonucleotide degradation enzyme 'orn'. We were also seeking to find changes from exponential growth to stationary. The portions of the experiment included in this sample sheet are only 3 replicates of the large RNA samples. The gff and fasta correspond to the genome and annotations used when mapping and may be recreated with the accompanying genbank flat file. Finally, 'counts' contains the count directory from the Pseudomonas experiment subset, which is an archive file containing the raw tables created via bowtie2 -> samtools -> htseq-count.

Usage

```
get_paeruginosa_data()
```

---

get_pairwise_gene_abundances

A companion function for get_abundant_genes()

Description

Instead of pulling to top/bottom abundant genes, get all abundances and variances or stderr.

Usage

```
get_pairwise_gene_abundances(datum, type = "limma", excel = NULL)
```

Arguments

datum	Output from _pairwise() functions.
type	According to deseq/limma/ed ger/basic?
excel	Print this to an excel file?

Value

List containing the expression values and some metrics of variance/error.

See Also

[get_abundant_genes()]

Examples

```
## Not run:
 abundance_excel <- get_pairwise_gene_abundances(combined, excel = "abundances.xlsx")
 ## This should provide a set of abundances after voom by condition.

## End(Not run)
```

`get_res` *Attempt to get residuals from tsne data*

Description

I strongly suspect that this is not correct, but it is a start.

Usage

```
get_res(
  svd_result,
  design,
  factors = c("condition", "batch"),
  res_slot = "v",
  var_slot = "d"
)
```

Arguments

`svd_result`	The set of results from one of the many potential svd-ish methods.
`design`	Experimental design from which to get experimental factors.
`factors`	Set of experimental factors for which to calculate rsquared values.
`res_slot`	Where is the res data in the svd result?
`var_slot`	Where is the var data in the svd result?

Value

Data frame of rsquared values and cumulative sums.

get_sagalactiae_data *Sample sheet used for a portion of a Group B Streptococcal TNSeq experiment.*

Description

TNSeq is sort of the inverse of RNASeq, one is instead looking for the genes _not_ represented in the dataset. This sample sheet lays out the experimental design for an in vitro TNSeq experiment from Streptococcus agalactiae strain CJB111. At the time of the experiment, there was not a very good genome for this strain. We therefore chose to use strain A909 as the reference. Since then, Lindsey's lab made a complete genome, though the annotations remain a bit sparse. One thing I like to do with TNSeq data is to treat it similarly to RNASeq data in order to get a sense of the changing 'fitness' of each gene. The data has all the same distribution attributes of a RNASeq dataset, after all; so why not use the same plots and tests to see if it is valid? The Essentiality package from the DeJesus lab uses a Bayesian framework to look for genes which are essential in a TNSeq experiment. In my pipeline, I invoke this tool with multiple parameters in an attempt to find the parameters which provide the most likely 'true' result. This archive contains those results for our GBS TNSeq experiment. My preprocessing pipeline uses the bam alignments from bowtie to extract all reads which start/end on a mariner insertion site (TA) and count how many occured at every position of the genome. These files are the result of that process, thus each line is the position of a 'T' in the 'TA' followed by the number of reads which start/end with it.

Usage

```
get_sagalactiae_data()
```

get_sbetaceum_data *Portion of the RNASeq results from Solanum betaceum.*

Description

I had the opportunity to work the Sandra Correia, she was awesome. She was seeking to learn about differences among embryogenic cells in the Tree tomato. I therefore got to learn first-hand a tiny portion of what is meant when one says 'plant genetics are hard.' I had it far easier than Sandra. I just used Trinity to make some de-novo transcriptomes and attempt to provide some metrics about which ones are real and really different across conditions in her experiment. Her work was many thousands of times more difficult. The full S.betaceum trinotate annotation is quite large, so I just pulled a portion as an example for this package.

Usage

```
get_sbetaceum_data()
```

`get_sig_genes` *Get a set of up/down differentially expressed genes.*

Description

Take one or more criteria (fold change, rank order, (adj)p-value, z-score from median FC) and use them to extract the set of genes which are defined as 'differentially expressed.' If no criteria are provided, it arbitrarily chooses all genes outside of 1-z.

Usage

```
get_sig_genes(
  table,
  n = NULL,
  z = NULL,
  lfc = NULL,
  p = NULL,
  column = "logFC",
  fold = "plusminus",
  p_column = "adj.P.Val"
)
```

Arguments

`table`	Table from limma/edger/deseq.
`n`	Rank-order top/bottom number of genes to take.
`z`	Number of z-scores >/< the median to take.
`lfc`	Fold-change cutoff.
`p`	P-value cutoff.
`column`	Table's column used to distinguish top vs. bottom.
`fold`	Identifier reminding how to get the bottom portion of a fold-change (plusminus says to get the negative of the positive, otherwise 1/positive is taken). This effectively tells me if this is a log fold change or not.
`p_column`	Table's column containing (adjusted or not)p-values.

Details

Tested in test_29de_shared.R

Value

Subset of the up/down genes given the provided criteria.

See Also

[extract_significant_genes()] [get_abundant_genes()]

Examples

```
## Not run:
 sig_table <- get_sig_genes(table, lfc = 1)

## End(Not run)
```

`get_sig_gsva_categories` *Attempt to score the results from simple_gsva()*

Description

This function uses a couple of methods to try to get an idea of whether the results from gsva are actually interesting. It does so via the following methods: 1. Use limma on the expressionset returned by simple_gsva(), this might provide an idea of if there are changing signatures among the sample types. 2. Perform a simplified likelihood estimate to get a sense of the significant categories.

Usage

```
get_sig_gsva_categories(
  gsva_result,
  cutoff = 0.95,
  excel = "excel/gsva_subset.xlsx",
  model_batch = FALSE,
  factor_column = "condition",
  factor = NULL,
  label_size = NULL,
  col_margin = 6,
  row_margin = 12,
  type = "mean"
)
```

Arguments

`gsva_result`	Result from simple_gsva()
`cutoff`	Significance cutoff
`excel`	Excel file to write the results.
`model_batch`	Add batch to limma's model.
`factor_column`	When extracting significance information, use this metadata factor.
`factor`	Use this metadata factor as the reference.
`label_size`	Used to make the category names easier to read at the expense of dropping some.
`col_margin`	Attempt to make heatmaps fit better on the screen with this and...
`row_margin`	this parameter

Value

List containing the gsva results, limma results, scores, some plots, etc.

See Also

[score_gsva_likelihoods()] [get_group_gsva_means()] [limma_pairwise()] [simple_gsva()]

`get_snp_sets` *Create all possible sets of variants by sample (types).*

Description

I like this function. It generates an exhaustive catalog of the snps by chromosome for all the various categories as defined by factor.

Usage

```
get_snp_sets(
  snp_expt,
  factor = "pathogenstrain",
  limit = 1,
  do_save = FALSE,
  savefile = "variants.rda"
)
```

Arguments

`snp_expt`	The result of count_expt_snps()
`factor`	Experimental factor to use for cutting and splicing the data.
`limit`	Minimum median number of hits / factor to define a position as a hit.
`do_save`	Save the result?
`savefile`	Prefix for a savefile if one chooses to save the result.

Value

A funky list by chromosome containing: 'medians', the median number of hits / position by sample type; 'possibilities', the; 'intersections', the groupings as detected by Vennerable; 'chr_data', the raw data; 'set_names', a character list of the actual names of the groupings; 'invert_names', the opposite of set_names which is to say the names of groups which do _not_ include samples x,y,z; 'density', a list of snp densities with respect to chromosomes. Note that this last one is approximate as I just calculate with the largest chromosome position number, not the explicit number of nucleotides in the chromosome.

See Also

[medians_by_factor()]

Examples

```
 ## Not run:
expt <- create_expt(metadata, gene_information)
snp_expt <- count_expt_snps(expt)
snp_sets <- get_snp_sets(snp_expt, factor = "condition")
## This assumes a column in the metadata for the expt named 'condition'.

## End(Not run)
```

`get_spyogenes_data` *Get the filenames of the Streptococcus pyogenes strain 5005 data.*

Description

This should return the Group A Streptococcus pyogenes strain 5005 GFF file, fasta genome, and some count tables. The gff contains the annotations which correspond to NC_007297. The rda file contains an expt which comprises a subset of a RNASeq experiment performed with the McIver lab. The goal was to examine changes in transcription across two media types (the very permissive THY and restrictive CDM). In addition, this used two strains, one which is more and less pathogenic.

Usage

```
get_spyogenes_data()
```

`get_tcruzi_data` *Sample sheet from a portion of an RNASeq experiment of Trypanosoma cruzi CL-Brener.*

Description

This contains a portion of an experiment performed with Santuza in which we were comparing two closely related T.cruzi strains: CL-14 and CL-Brener, which are super-similar but vastly different in terms of their pathogenicity. (I would much rather be infected with CL-14!). The count tables were created via TopHat2 mapping of the CL-Br and CL-14 samples using the CL-Brener genome. One of the interesting and bizarre things about CL-Brener: it is a multi-haplotype strain, containing bits and pieces from two lineages, named 'Esmeraldo' and 'Non-Esmeraldo'. In addition, there is a large portion which has not been characterized and is therefore called 'Unassigned'. Thus, when mapping the data, we create a concatenated genome with all three haplotypes. One thing we did not include in the paper (because I didn't think of it until later), was an analysis of the single nucleotide variants between the two strains. RNASeq data is of course not an ideal format for performing these analyses, but I think I figured out a reasonable method to extract mostly robust differences (in snp.r).

Usage

```
get_tcruzi_data()
```

getEdgeWeights *Plot the ontology DAG.*

Description

This function was stolen from topgo in order to figure out where it was failing.

Usage

```
getEdgeWeights(graph)
```

Arguments

graph	Graph from topGO

Value

Weights!

gff2irange *Extract annotation information from a gff file into an irange object.*

Description

Try to make import.gff a little more robust; I acquire (hopefully) valid gff files from various sources: yeastgenome.org, microbesonline, tritrypdb, ucsc, ncbi. To my eyes, they all look like reasonably good gff3 files, but some of them must be loaded with import.gff2, import.gff3, etc. That is super annoying. Also, I pretty much always just do as.data.frame() when I get something valid from rtracklayer, so this does that for me, I have another function which returns the iranges etc. This function wraps import.gff/import.gff3/import.gff2 calls in try() because sometimes those functions fail in unpredictable ways.

Usage

```
gff2irange(gff, type = NULL)
```

Arguments

gff	Gff filename.
type	Subset to extract.

Details

This is essentially load_gff_annotations(), but returns data suitable for getSet() This is another place which should be revisited for improvements via mcols(). Check snp.r. for ideas.

Value

Iranges! (useful for getSeq().)

See Also

[rtracklayer] [load_gff_annotations()] import.gff

Examples

```
example_gff <- system.file("share", "gas.gff", package = "hpgltools")
gas_iranges <- gff2irange(example_gff)
colnames(as.data.frame(gas_iranges))
```

---

ggplotly_url *Add a little logic to ggplotly to simplify adding clicky link.*

Description

There are some other ease of life improvements I have in a few of my plotly invocations which I should add here.

Usage

```
ggplotly_url(
  plot,
  filename,
  id_column = "id",
  title = NULL,
  url_data = NULL,
  url_column = "url",
  tooltip = "all"
)
```

Arguments

plot	Plot generated via ggplot2.
filename	filename to save the output html plot.
id_column	Column containing the gene IDs.
title	Provide a title for the generated html file.
url_data	Either a glue() string or column of urls.
url_column	Name of the column in the ggplot data containing the URLs.
tooltip	Passed to ggplotly().

Value

plotly with clicky links.

`ggplt` *Simplify plotly ggplot conversion so that there are no shenanigans.*

Description

I am a fan of ggplotly, but its conversion to an html file is not perfect. This hopefully will get around the most likely/worst problems.

Usage

```
ggplt(
  gg,
  filename = "ggplot.html",
  selfcontained = TRUE,
  libdir = NULL,
  background = "white",
  title = class(gg)[[1]],
  knitrOptions = list(),
  ...
)
```

Arguments

`gg`	Plot from ggplot2.
`filename`	Output filename.
`selfcontained`	htmlwidgets: Return the plot as a self-contained file with images re-encoded base64.
`libdir`	htmlwidgets: Directory into which to put dependencies.
`background`	htmlwidgets: String for the background of the image.
`title`	htmlwidgets: Title of the page!
`knitrOptions`	htmlwidgets: I am not a fan of camelCase, but nonetheless, options from knitr for htmlwidgets.
`...`	Any remaining elipsis options are passed to ggplotly.

Value

The final output filename

See Also

[htmlwidgets] [plotly] [ggplot2]

godef *Get a go long-form definition from an id.*

Description

Sometimes it is nice to be able to read the full definition of some GO terms.

Usage

```
godef(go = "GO:0032432")
```

Arguments

go	GO ID, this may be a character or list (assuming the elements are goids).

Value

Some text providing the long definition of each provided GO id.

See Also

[AnnotationDbi] [GO.db]

Examples

```
## Not run:
 godef("GO:0032432")
 ## > GO:0032432
 ## > "An assembly of actin filaments that are on the same axis but may be
 ## > same or opposite polarities and may be packed with different levels of tightness."

## End(Not run)
```

golev *Get a go level approximation from an ID.*

Description

Sometimes it is useful to know how far up/down the ontology tree a given id resides. This attmepts to answer that question.

Usage

```
golev(go)
```

Arguments

go	GO id, this may be a character or list (assuming the elements are goids).

Value

Set of numbers corresponding to approximate tree positions of the GO ids.

See Also

[AnnotationDbi] [GO.db]

Examples

```
## Not run:
 golev("GO:0032559")
 ## > 3

## End(Not run)
```

---

golevel *Get a go level approximation from a set of IDs.*

Description

This just wraps golev() in mapply.

Usage

```
golevel(go = c("GO:0032559", "GO:0000001"))
```

Arguments

go	Character list of IDs.

Value

Set pf approximate levels within the onlogy.

See Also

[golev()]

Examples

```
## Not run:
 golevel(c("GO:0032559", "GO:0000001")
 ## > 3 4

## End(Not run)
```

golevel_df *Extract a dataframe of golevels using getGOLevel() from clusterProfiler.*

Description

This function is way faster than my previous iterative golevel function. That is not to say it is very fast, so it saves the result to ontlevel.rda for future lookups.

Usage

```
golevel_df(ont = "MF", savefile = "ontlevel.rda")
```

Arguments

ont	Ontology to recurse.
savefile	File to save the results for future lookups.

Value

Dataframe of goids<->highest level

See Also

[clusterProfiler]

goont *Get a go ontology name from an ID.*

Description

Get a go ontology name from an ID.

Usage

```
goont(go = c("GO:0032432", "GO:0032433"))
```

Arguments

go	GO id, this may be a character or list (assuming the elements are goids).

Value

The set of ontology IDs associated with the GO ids, thus 'MF' or 'BP' or 'CC'.

See Also

[AnnotationDbi] [GO.db]

Examples

```
## Not run:
 goont(c("GO:0032432", "GO:0032433"))
 ## > GO:0032432 GO:0032433
 ## > "CC" "CC"

## End(Not run)
```

---

gosec *Get a GO secondary ID from an id.*

Description

Unfortunately, GOTERM's returns for secondary IDs are not consistent, so this function has to have a whole bunch of logic to handle the various outputs.

Usage

```
gosec(go = "GO:0032432")
```

Arguments

go	GO ID, this may be a character or list(assuming the elements, not names, are goids).

Value

Some text comprising the secondary GO id(s).

See Also

[AnnotationDbi] [GO.db]

Examples

```
## Not run:
 gosec("GO:0032432")
 ## > GO:0032432
 ## > "GO:0000141" "GO:0030482"

## End(Not run)
```

goseq_msigdb *Pass MSigDB categorical data to goseq and run it.*

Description

goseq is probably the easiest method to push varying data types into. Thus it was the first thing I thought of when looking to push MSigDB data into a GSEA method.

Usage

```
goseq_msigdb(
  sig_genes,
  signatures = "c2BroadSets",
  data_pkg = "GSVAdata",
  signature_category = "c2",
  current_id = "ENSEMBL",
  required_id = "ENTREZID",
  length_db = NULL,
  doplot = TRUE,
  adjust = 0.1,
  pvalue = 0.1,
  length_keytype = "transcripts",
  go_keytype = "entrezid",
  goseq_method = "Wallenius",
  padjust_method = "BH",
  bioc_length_db = "ensGene",
  excel = NULL,
  orgdb = "org.Hs.eg.db"
)
```

Arguments

sig_genes	Character list of genes deemed significant. I think in the current implementation this must be just a list of IDs as opposed to the full dataframe of interesting genes because we likely need to convert IDs.
signatures	Used by load_gmt_signatures(), the signature file or set.
data_pkg	Used by load_gmt_signatures().
signature_category	Ibid, but the name of the signatures group.
current_id	Used by convert_msig_ids(), when converting IDs, the name of the existing type.
required_id	What type to convert to in convert_msig_ids().
length_db	Dataframe of lengths. It is worth noting that goseq explicitly states that one might wish to use other potentially confounding factors here, but they only examine lenghts in their paper. Starting with this parameter, everything is just passed directly to simple_goseq()

doplot	Print the prior plot?
adjust	passed to simple_goseq()
pvalue	passed to simple_goseq()
length_keytype	passed to simple_goseq()
go_keytype	passed to simple_goseq()
goseq_method	passed to simple_goseq()
padjust_method	passed to simple_goseq()
bioc_length_db	passed to simple_goseq()
excel	passed to simple_goseq()

Value

Some goseq data!

See Also

[gsva] [goseq]

---

goseq_table *Enhance the goseq table of gene ontology information.*

Description

While goseq has some nice functionality, the table of outputs it provides is somewhat lacking. This attempts to increase that with some extra helpful data like ontology categories, definitions, etc.

Usage

```
goseq_table(df, file = NULL)
```

Arguments

df	Dataframe of ontology information. This is intended to be the output from goseq including information like numbers/category, GOids, etc. It requires a column 'category' which contains: GO:000001 and such.
file	Csv file to which to write the table.

Value

Ontology table with annotation information included.

See Also

[goseq] [GO.db]

Examples

```
## Not run:
 annotated_go = goseq_table(go_ids)
 head(annotated_go, n = 1)
 ## >        category numDEInCat numInCat over_represented_pvalue
 ## > 571  GO:0006364          9       26            4.655108e-08
 ## >      under_represented_pvalue       qvalue ontology
 ## > 571                 1.0000000 6.731286e-05       BP
 ## >                                    term
 ## > 571                 rRNA processing
 ## >                                  synonym
 ## > 571        "35S primary transcript processing, GO:0006365"
 ## >        secondary    definition
 ## > 571    GO:0006365   Any process involved in the conversion of a primary ribosomal
 ##          RNA (rRNA) transcript into one or more mature rRNA molecules.

## End(Not run)
```

`goseq_trees` *Make fun trees a la topgo from goseq data.*

Description

This seeks to force goseq data into a format suitable for topGO and then use its tree plotting function to make it possible to see significantly increased ontology trees.

Usage

```
goseq_trees(
  goseq,
  goid_map = "id2go.map",
  score_limit = 0.01,
  overwrite = FALSE,
  selector = "topDiffGenes",
  pval_column = "adj.P.Val"
)
```

Arguments

`goseq`	Data from goseq.
`goid_map`	File to save go id mapping.
`score_limit`	Score limit for the coloring.
`overwrite`	Overwrite the trees?
`selector`	Function for choosing genes.
`pval_column`	Column to acquire pvalues.

Value

A plot!

See Also

[Ramigo]

`gostats_kegg` *Use gostats() against kegg pathways.*

Description

This sets up a GSEABase analysis using KEGG pathways rather than gene ontologies. Does this even work? I don't think I have ever tested it yet. oh, it sort of does, maybe if I export it I will rembmer it.

Usage

```
gostats_kegg(
  organism = "Homo sapiens",
  pathdb = "org.Hs.egPATH",
  godb = "org.Hs.egGO"
)
```

Arguments

`organism`	The organism used to make the KEGG frame, human readable no taxonomic.
`pathdb`	Name of the pathway database for this organism.
`godb`	Name of the ontology database for this organism.

Value

Results from hyperGTest using the KEGG pathways.

See Also

[AnnotationDbi] [GSEABase] [Category]

gostats_trees *Take gostats data and print it on a tree as topGO does.*

Description

This shoehorns gostats data into a format acceptable by topgo and uses it to print pretty ontology trees showing the over represented ontologies.

Usage

```
gostats_trees(
  gostats_result,
  goid_map = "id2go.map",
  score_limit = 0.01,
  overwrite = FALSE,
  selector = "topDiffGenes",
  pval_column = "adj.P.Val"
)
```

Arguments

gostats_result	Return from simple_gostats().
goid_map	Mapping of IDs to GO in the Ramigo expected format.
score_limit	Maximum score to include as 'significant'.
overwrite	Overwrite the goid_map?
selector	Function to choose differentially expressed genes in the data.
pval_column	Column in the data to be used to extract pvalue scores.

Value

plots! Trees! oh my!

See Also

topGO gostats

gosyn *Get a go synonym from an ID.*

Description

I think I will need to do similar parsing of the output for this function as per gosec() In some cases this also returns stuff like c("some text", "GO:someID") versus "some other text" versus NULL versus NA. This function just goes a mapply(gosn, go).

Usage

```
gosyn(go = "GO:0000001")
```

Arguments

go	GO id, this may be a character or list(assuming the elements are goids).

Value

Some text providing the synonyms for the given id(s).

See Also

[AnnotationDbi] [GO.db]

Examples

```
## Not run:
 text =  gosyn("GO:0000001")
 text
 ## > GO:000001
 ## > "mitochondrial inheritance"

## End(Not run)
```

goterm *Get a go term from ID.*

Description

Get a go term from ID.

Usage

```
goterm(go = "GO:0032559")
```

Arguments

go	GO id or a list thereof, this may be a character or list(assuming the elements, not names, are goids).

Value

Some text containing the terms associated with GO id(s).

See Also

[AnnotationDbi] [GO.db]

Examples

```
## Not run:
 goterm("GO:0032559")
 ## > GO:0032559
 ## > "adenyl ribonucleotide binding"

## End(Not run)
```

---

gotest *Test GO ids to see if they are useful.*

Description

This just wraps gotst in mapply.

Usage

```
gotest(go)
```

Arguments

go	go IDs as characters.

Value

Some text

See Also

[GO.db]

Examples

```
## Not run:
 gotest("GO:0032559")
 ## > 1
 gotest("GO:0923429034823904")
 ## > 0

## End(Not run)
```

---

graph_metrics *Make lots of graphs!*

Description

Plot out a set of metrics describing the state of an experiment including library sizes, # non-zero genes, heatmaps, boxplots, density plots, pca plots, standard median distance/correlation, and qq plots.

Usage

```
graph_metrics(
  expt,
  cormethod = "pearson",
  distmethod = "euclidean",
  title_suffix = NULL,
  qq = FALSE,
  ma = FALSE,
  gene_heat = FALSE,
  ...
)
```

Arguments

expt	an expt to process
cormethod	The correlation test for heatmaps.
distmethod	define the distance metric for heatmaps.
title_suffix	Text to add to the titles of the plots.
qq	Include qq plots?
ma	Include pairwise ma plots?
gene_heat	Include a heatmap of the gene expression data?
...	Extra parameters optionally fed to the various plots

Value

a loooong list of plots including the following:

1. nonzero = a ggplot2 plot of the non-zero genes vs library size
2. libsize = a ggplot2 bar plot of the library sizes
3. boxplot = a ggplot2 boxplot of the raw data
4. corheat = a recordPlot()ed pairwise correlation heatmap of the raw data
5. smc = a recordPlot()ed view of the standard median pairwise correlation of the raw data
6. disheat = a recordPlot()ed pairwise euclidean distance heatmap of the raw data
7. smd = a recordPlot()ed view of the standard median pairwise distance of the raw data
8. pcaplot = a recordPlot()ed PCA plot of the raw samples
9. pcatable = a table describing the relative contribution of condition/batch of the raw data
10. pcares = a table describing the relative contribution of condition/batch of the raw data
11. pcavar = a table describing the variance of the raw data
12. qq = a recordPlotted() view comparing the quantile/quantiles between the mean of all data and every raw sample
13. density = a ggplot2 view of the density of each raw sample (this is complementary but more fun than a boxplot)

See Also

[plot_nonzero()] [plot_legend()] [plot_libsize()] [plot_disheat()] [plot_corheat()] [plot_topn()] [plot_pca()] [plot_sm()] [plot_boxplot()]

Examples

```
## Not run:
 toomany_plots <- graph_metrics(expt)
 toomany_plots$pcaplot
 norm <- normalize_expt(expt, convert = "cpm", batch = TRUE, filter_low = TRUE,
                        transform = "log2", norm = "rle")
 holy_asscrackers <- graph_metrics(norm, qq = TRUE, ma = TRUE)

## End(Not run)
```

---

guess_orgdb_keytype *Iterate over keytypes looking for matches against a set of IDs.*

Description

Sometimes, one does not know what the correct keytype is for a given set of IDs. This will hopefully find them.

Usage

```
guess_orgdb_keytype(ids, orgdb = NULL, verbose = FALSE)
```

Arguments

ids	Set of gene IDs to seek.
orgdb	Orgdb instance to iterate through.
verbose	talky talk

Value

Likely keytype which provides the desired IDs.

See Also

[org.Dm.eg.db]

Examples

```
ids <- c("Dm.9", "Dm.2294", "Dm.4971")
dm_orgdb <- "org.Dm.eg.db"
keytype_guess <- guess_orgdb_keytype(ids, dm_orgdb)
keytype_guess
```

---

heatmap.3 *a minor change to heatmap.2 makes heatmap.3*

Description

heatmap.2 is the devil.

Usage

```
heatmap.3(
  x,
  Rowv = TRUE,
  Colv = if (symm) "Rowv" else TRUE,
  distfun = dist,
  hclustfun = fastcluster::hclust,
  dendrogram = c("both", "row", "column", "none"),
  reorderfun = function(d, w) reorder(d, w),
  symm = FALSE,
  scale = c("none", "row", "column"),
  na.rm = TRUE,
  revC = identical(Colv, "Rowv"),
  add.expr,
  breaks,
```

```
symbreaks = min(x < 0, na.rm = TRUE) || scale != "none",
col = "heat.colors",
colsep,
rowsep,
sepcolor = "white",
sepwidth = c(0.05, 0.05),
cellnote,
notecex = 1,
notecol = "cyan",
na.color = par("bg"),
trace = c("column", "row", "both", "none"),
tracecol = "cyan",
hline = median(breaks),
vline = median(breaks),
linecol = tracecol,
margins = c(5, 5),
ColSideColors,
RowSideColors,
cexRow = 0.2 + 1/log10(nr),
cexCol = 0.2 + 1/log10(nc),
labRow = NULL,
labCol = NULL,
srtRow = NULL,
srtCol = NULL,
adjRow = c(0, NA),
adjCol = c(NA, 0),
offsetRow = 0.5,
offsetCol = 0.5,
key = TRUE,
keysize = 1.5,
density.info = c("histogram", "density", "none"),
denscol = tracecol,
symkey = min(x < 0, na.rm = TRUE) || symbreaks,
densadj = 0.25,
key.title = NULL,
key.xlab = NULL,
key.ylab = NULL,
key.xtickfun = NULL,
key.ytickfun = NULL,
key.par = list(),
main = NULL,
xlab = NULL,
ylab = NULL,
lmat = NULL,
lhei = NULL,
lwid = NULL,
extrafun = NULL,
linewidth = 1,
```

```
  ...
)
```

Arguments

x	data
Rowv	add rows?
Colv	add columns?
distfun	distance function to use
hclustfun	clustering function to use
dendrogram	which axes to put trees on
reorderfun	reorder the rows/columns?
symm	symmetrical?
scale	add the scale?
na.rm	remove nas from the data?
revC	reverse the columns?
add.expr	no clue
breaks	also no clue
symbreaks	still no clue
col	colors!
colsep	column separator
rowsep	row separator
sepcolor	color to put between columns/rows
sepwidth	how much to separate
cellnote	mur?
notecex	size of the notes
notecol	color of the notes
na.color	a parameter call to bg
trace	do a trace for rows/columns?
tracecol	color of the trace
hline	the hline
vline	the vline
linecol	the line color
margins	margins are good
ColSideColors	colors for the columns as annotation
RowSideColors	colors for the rows as annotation
cexRow	row size
cexCol	column size
labRow	hmmmm

labCol	still dont know
srtRow	srt the row?
srtCol	srt the column?
adjRow	adj the row?
adjCol	adj the column?
offsetRow	how far to place the text from the row
offsetCol	how far to place the text from the column
key	add a key?
keysize	if so, how big?
density.info	for the key, what information to add
denscol	tracecol hmm ok
symkey	I like keys
densadj	adj the dens?
key.title	title for the key
key.xlab	text for the x axis of the key
key.ylab	text for the y axis of the key
key.xtickfun	add text to the ticks of the key x axis
key.ytickfun	add text to the ticks of the key y axis
key.par	parameters for the key
main	the main title of the plot
xlab	main x label
ylab	main y label
lmat	the lmat
lhei	the lhei
lwid	the lwid
extrafun	I do enjoy me some extra fun
linewidth	the width of lines
...	because this function did not already have enough options

Value

a heatmap!

See Also

heatmap.2

`hpgl_arescore` *Implement the arescan function in R*

Description

This function was taken almost verbatim from AREScore() in SeqTools Available at: https://github.com/lianos/seqtools.git At least on my computer I could not make that implementation work So I rewrapped its apply() calls and am now hoping to extend its logic a little to make it more sensitive and get rid of some of the spurious parameters or at least make them more transparent.

Usage

```
hpgl_arescore(
  x,
  basal = 1,
  overlapping = 1.5,
  d1.3 = 0.75,
  d4.6 = 0.4,
  d7.9 = 0.2,
  within.AU = 0.3,
  aub.min.length = 10,
  aub.p.to.start = 0.8,
  aub.p.to.end = 0.55
)
```

Arguments

`x`	DNA/RNA StringSet containing the UTR sequences of interest
`basal`	I dunno.
`overlapping`	default = 1.5
`d1.3`	default = 0.75 These parameter names are so stupid, lets be realistic
`d4.6`	default = 0.4
`d7.9`	default = 0.2
`within.AU`	default = 0.3
`aub.min.length`	default = 10
`aub.p.to.start`	default = 0.8
`aub.p.to.end`	default = 0.55

Value

a DataFrame of scores

See Also

[IRanges] [Biostrings] [GenomicRanges]

Examples

```
## Not run:
 ## Extract all the genes from my genome, pull a static region 120nt following the stop
 ## and test them for potential ARE sequences.
 ## FIXME: There may be an error in this example, another version I have
 ## handles the +/- strand genes separately, I need to return to this and check
 ## if it is providing the 5' UTR for 1/2 the genome, which would be
 ## unfortunate -- but the logic for testing remains the same.
 are_candidates <- hpgl_arescore(genome)
 utr_genes <- subset(lmajor_annotations, type == 'gene')
 threep <- GenomicRanges::GRanges(seqnames = Rle(utr_genes[,1]),
                              ranges = IRanges(utr_genes[,3], end=(utr_genes[,3] + 120)),
                                   strand = Rle(utr_genes[,5]),
                                   name = Rle(utr_genes[,10]))
 threep_seqstrings <- Biostrings::getSeq(lm, threep)
 are_test <- hpgltools::hpgl_arescore(x = threep_seqstrings)
 are_genes <- rownames(are_test[ which(are_test$score > 0), ])

## End(Not run)
```

---

hpgl_cor *Wrap cor() to include robust correlations.*

Description

Take covRob's robust correlation coefficient and add it to the set of correlations available when one calls cor(). I should reimplement this using S4.

Usage

```
hpgl_cor(df, method = "pearson", ...)
```

Arguments

df	Data frame to test.
method	Correlation method to use. Includes pearson, spearman, kendal, robust.
...	Other options to pass to stats::cor().

Value

Some fun correlation statistics.

See Also

[robust]

Examples

```
## Not run:
 hpgl_cor(df = df)
 hpgl_cor(df = df, method = "robust")

## End(Not run)
```

`hpgl_dist` *Because I am not smart enough to remember t()*

Description

It seems to me there should be a function as easy for distances are there is for correlations.

Usage

```
hpgl_dist(df, method = "euclidean", ...)
```

Arguments

`df`	data frame from which to calculate distances.
`method`	Which distance calculation to use?
`...`	Extra arguments for dist.

`hpgl_filter_counts` *Filter low-count genes from a data set using cpm data and a threshold.*

Description

This is identical to cbcb_filter_counts except it does not do the somewhat tortured log2CPM() but instead just uses a 4 cpm non-log threshold. It should therefore give basically the same result, but without the shenanigans.

Usage

```
hpgl_filter_counts(
  count_table,
  threshold = 2,
  min_samples = 2,
  libsize = NULL,
  ...
)
```

Arguments

count_table	Data frame of (pseudo)counts by sample.
threshold	Lower threshold of counts for each gene.
min_samples	Minimum number of samples.
libsize	Table of library sizes.
...	Arguments passed to cpm and friends.

Value

Dataframe of counts without the low-count genes.

See Also

[edgeR]

Examples

```
## Not run:
 filtered_table <- cbcb_filter_counts(count_table)

## End(Not run)
```

---

hpgl_GOplot *A minor hack of the topGO GOplot function.*

Description

This allows me to change the line widths from the default.

Usage

```
hpgl_GOplot(
  dag,
  sigNodes,
  dag.name = "GO terms",
  edgeTypes = TRUE,
  nodeShape.type = c("box", "circle", "ellipse", "plaintext")[3],
  genNodes = NULL,
  wantedNodes = NULL,
  showEdges = TRUE,
  useFullNames = TRUE,
  oldSigNodes = NULL,
  nodeInfo = NULL,
  maxchars = 30
)
```

Arguments

dag	DAG tree of ontologies.
sigNodes	Set of significant ontologies (with p-values).
dag.name	Name for the graph.
edgeTypes	Types of the edges for graphviz.
nodeShape.type	Shapes on the tree.
genNodes	Generate the nodes?
wantedNodes	Subset of the ontologies to plot.
showEdges	Show the arrows?
useFullNames	Full names of the ontologies (they can get long).
oldSigNodes	I dunno.
nodeInfo	Hmm.
maxchars	Maximum characters per line inside the shapes.

Value

Topgo plot!

See Also

[topGO]

---

hpgl_GroupDensity *A hack of topGO's groupDensity()*

Description

This just adds a couple wrappers to avoid errors in groupDensity.

Usage

```
hpgl_GroupDensity(object, whichGO, ranks = TRUE, rm.one = FALSE)
```

Arguments

object	TopGO enrichment object.
whichGO	Individual ontology group to compare against.
ranks	Rank order the set of ontologies?
rm.one	Remove pvalue = 1 groups?

Value

plot of group densities.

hpgl_log2cpm *Converts count matrix to log2 counts-per-million reads.*

Description

Based on the method used by limma as described in the Law et al. (2014) voom paper.

Usage

```
hpgl_log2cpm(counts, lib.size = NULL)
```

Arguments

counts	Read count matrix.
lib.size	Library size.

Value

log2-CPM read count matrix.

See Also

[edgeR]

Examples

```
## Not run:
 l2cpm <- hpgl_log2cpm(counts)

## End(Not run)
```

hpgl_norm *Normalize a dataframe/expt, express it, and/or transform it*

Description

There are many possible options to this function. Refer to normalize_expt() for a more complete list.

Usage

```
hpgl_norm(data, ...)
```

Arguments

data	Some data as a df/expt/whatever.
...	I should put all those other options here

Value

edgeR's DGEList expression of a count table. This seems to me to be the easiest to deal with.

See Also

[edgeR] [DESeq2] [edgeR::cpm()] [filter_counts()] [batch_counts()] [convert_counts()] [transform_counts()]

Examples

```
## Not run:
 df_raw = hpgl_norm(expt = expt)  ## Only performs low-count filtering
 df_raw = hpgl_norm(df = a_df, design = a_design) ## Same, but using a df
 df_ql2rpkm = hpgl_norm(expt = expt, norm='quant', transform='log2',
                        convert='rpkm')  ## Quantile, log2, rpkm
 count_table = df_ql2rpkm$counts

## End(Not run)
```

---

hpgl_padjust *Wrap p.adjust to add IHW adjustments as an option.*

Description

IHW and apeglm are the two new toys I found, this adds the former as a way to adjust p-values.

Usage

```
hpgl_padjust(
  data,
  pvalue_column = "pvalue",
  mean_column = "base_mean",
  method = "fdr",
  significance = 0.05,
  type = NULL
)
```

Arguments

data	Column or table containing values to adjust.
pvalue_column	Name of the column in a table containing the p-values.
mean_column	Name of the column in a table containing the mean count values to weight.
method	p adjustment method to apply.
significance	Passed to IHW
type	Assuming a DE table, what type of DE is this?

Value

Newly adjusted p-values using either p.adjust() or IHW.

See Also

[IHW]

`hpgl_qshrink` *A hacked copy of Kwame's qsmooth/qstats code.*

Description

I made a couple small changes to Kwame's qstats() function to make it not fail when on corner-cases. I sent him a diff, but haven't checked to see if it was useful yet.

Usage

```
hpgl_qshrink(
  data = NULL,
  groups = NULL,
  refType = "mean",
  groupLoc = "mean",
  window = 99,
  groupCol = NULL,
  plot = TRUE,
  ...
)
```

Arguments

`data`	Count table to modify
`groups`	Factor of the experimental conditions
`refType`	Method for grouping conditions
`groupLoc`	Method for grouping groups
`window`	Window, for looking!
`groupCol`	Column to define conditions
`plot`	Plot the quantiles?
`...`	More options

Value

New data frame of normalized counts

See Also

[qsmooth]

Examples

```
## Not run:
 df <- hpgl_qshrink(data)

## End(Not run)
```

`hpgl_qstats` *A hacked copy of Kwame's qsmooth/qstats code.*

Description

I made a couple small changes to Kwame's qstats() function to make it not fail when on corner-cases. I sent him a diff, but haven't checked to see if it was useful yet.

Usage

```
hpgl_qstats(data, groups, refType = "mean", groupLoc = "mean", window = 99)
```

Arguments

`data`	Initial count data
`groups`	Experimental conditions as a factor.
`refType`	Method to separate groups, mean or median.
`groupLoc`	I don't remember what this is for.
`window`	Window for basking!

Value

Some new data.

See Also

[matrixStats]

Examples

```
## Not run:
 qstatted <- hpgl_qstats(data, conditions)

## End(Not run)
```

hpgl_rpkm *Reads/(kilobase(gene) * million reads)*

Description

Express a data frame of counts as reads per kilobase(gene) per million(library). This function wraps EdgeR's rpkm in an attempt to make sure that the required gene lengths get sent along.

Usage

```
hpgl_rpkm(count_table, ...)
```

Arguments

count_table	Data frame of counts, alternately an edgeR DGEList.
...	extra options including annotations for defining gene lengths.

Value

Data frame of counts expressed as rpkm.

See Also

[edgeR::rpkm()]

Examples

```
## Not run:
 rpkm_df = hpgl_rpkm(df, annotations = gene_annotations)

## End(Not run)
```

hpgl_voom *A slight modification of limma's voom().*

Description

Estimate mean-variance relationship between samples and generate 'observational-level weights' in preparation for linear modeling RNAseq data. This particular implementation was primarily scabbed from cbcbSEQ, but changes the mean-variance plot slightly and attempts to handle corner cases where the sample design is confounded by setting the coefficient to 1 for those samples rather than throwing an unhelpful error. Also, the Elist output gets a 'plot' slot which contains the plot rather than just printing it.

Usage

```
hpgl_voom(
  dataframe,
  model = NULL,
  libsize = NULL,
  normalize.method = "none",
  span = 0.5,
  stupid = FALSE,
  logged = FALSE,
  converted = FALSE,
  ...
)
```

Arguments

dataframe	Dataframe of sample counts which have been normalized and log transformed.
model	Experimental model defining batches/conditions/etc.
libsize	Size of the libraries (usually provided by edgeR).
normalize.method	Normalization method used in voom().
span	The span used in voom().
stupid	Cheat when the resulting matrix is not solvable?
logged	Is the input data is known to be logged?
converted	Is the input data is known to be cpm converted?
...	Extra arguments are passed to arglist.

Value

EList containing the following information: E = The normalized data weights = The weights of said data design = The resulting design lib.size = The size in pseudocounts of the library plot = A ggplot of the mean/variance trend with a blue loess fit and red trend fit

See Also

[limma::voom()]

Examples

```
## Not run:
 funkytown = hpgl_voom(samples, model)

## End(Not run)
```

`hpgl_voomweighted` *A minor change to limma's voom with quality weights to attempt to address some corner cases.*

Description

This copies the logic employed in hpgl_voom(). I suspect one should not use it.

Usage

```
hpgl_voomweighted(
  data,
  fun_model,
  libsize = NULL,
  normalize.method = "none",
  plot = TRUE,
  span = 0.5,
  var.design = NULL,
  method = "genebygene",
  maxiter = 50,
  tol = 1e-10,
  trace = FALSE,
  replace.weights = TRUE,
  col = NULL,
  ...
)
```

Arguments

`data`	Some data!
`fun_model`	A model for voom() and arrayWeights()
`libsize`	Library sizes passed to voom().
`normalize.method`	Passed to voom()
`plot`	Do the plot of mean variance?
`span`	yes
`var.design`	maybe
`method`	kitty!
`maxiter`	50 is good
`tol`	I have no tolerance.
`trace`	no trace for you.
`replace.weights`	Replace the weights?
`col`	yay columns!
`...`	more arguments!

Value

a voom return

See Also

[limma::voom()]

Examples

```
## Not run:
## No seriously, dont run this, I think it is wiser to use the functions
## provided by limma. But this provides a place to test stuff out.
 voom_result <- hpgl_voomweighted(dataset, model)

## End(Not run)
```

---

hpgltools *hpgltools: a suite of tools to make our analyses easier*

Description

This provides a series of helpers for working with sequencing data

Details

It falls under a few main topics

- Data exploration, look for trends in sequencing data and identify batch effects or skewed distributions.
- Differential expression analyses, use DESeq2/limma/EdgeR in a hopefully robust and flexible fashion.
- Ontology analyses, use goseq/clusterProfiler/topGO/GOStats/gProfiler in hopefully robust ways.
- Perform some simple TnSeq analyses.

To see examples of this in action, check out the vignettes: `browseVignettes(package = 'hpgltools')`

`ihw_adjust` *Make sure the outputs from limma and friends are in a format suitable for IHW.*

Description

IHW seems like an excellent way to improve the confidence in the p-values provided by the various DE methods. It expects inputs fairly specific to DESeq2, however, it is trivial to convert other methods to this, ergo this function.

Usage

```
ihw_adjust(
  de_result,
  pvalue_column = "pvalue",
  type = NULL,
  mean_column = "baseMean",
  significance = 0.05
)
```

Arguments

`de_result`	Table which should have the 2 types of requisite columns: mean value of counts and p-value.
`pvalue_column`	Name of the column of p-values.
`type`	If specified, this will explicitly perform the calculation for the given type of differential expression analysis: limma, edger, deseq, etc.
`mean_column`	Name of the column of mean values.
`significance`	IHW uses this parameter, I don't know why.

Details

https://bioconductor.org/packages/release/bioc/vignettes/IHW/inst/doc/introduction_to_ihw.html

Value

weight adjusted p-values.

See Also

[IHW]

`import_deseq` *Try to add data to DESeq in a flexible fashion. This currently only handles matrices, htseq data, and tximport data.*

Description

This will hopefully make adding counts to a DESeq data set easier, as it tries to handle the various arguments with minimal fuss.

Usage

```
import_deseq(data, column_data, model_string, tximport = NULL)
```

Arguments

`data`	Counts from htseq/mtrx/tximport/etc
`column_data`	I think this is the sample names, I forget.
`model_string`	Model describing the data by sample names.
`tximport`	Where is this data coming from?

See Also

[DESeq2::DESeqDataSetFromMatrix]

`import_edger` *Import tximport information into edgeR.*

Description

This was taken from the tximport manual with minor modifications.

Usage

```
import_edger(data, conditions, tximport = NULL)
```

Arguments

`data`	data to be coerced into edgeR.
`conditions`	Set of conditions used to make the DGEList.
`tximport`	Tell this if the data is actually coming from tximport.

Value

Hopefully valid DGEList for edgeR.

See Also

[import_deseq()]

`impute_expt` *Impute missing values using code from DEP reworked for expressionsets.*

Description

[impute_expt()] imputes missing values in a proteomics dataset.

Usage

```
impute_expt(
  expt,
  filter = TRUE,
  p = 0.5,
 fun = c("bpca", "knn", "QRILC", "MLE", "MinDet", "MinProb", "min", "zero", "mixed",
    "nbavg"),
  ...
)
```

Arguments

`expt`	An ExpressionSet (well, expt), I think it is assumed that this should have been normalized and filtered for features which have no values across 'most' samples.
`filter`	Use normalize_expt() to filter the data?
`p`	When filtering with pofa, use this p parameter.
`fun`	"bpca", "knn", "QRILC", "MLE", "MinDet", "MinProb", "man", "min", "zero", "mixed" or "nbavg", Function used for data imputation based on [MSnbase::imputemethods()]
`...`	Additional arguments for imputation functions.

Value

An imputed expressionset.

See Also

[MSnbase]

`init_xlsx` *Initialize an xlsx file with a little bit of logic to make sure there are no annoying downstream errors.*

Description

Initialize an xlsx file with a little bit of logic to make sure there are no annoying downstream errors.

Usage

```
init_xlsx(excel = "excel/something.xlsx")
```

Arguments

`excel`	Excel file to create.

Value

List containing the basename of the excel file along with the openxlsx workbook data structure.

See Also

[openxlsx::createWorkbook()]

`intersect_signatures` *Take a result from simple_gsva(), a list of gene IDs, and intersect them.*

Description

Najib is curious about the relationship of genes in sets, the sets, and the genes that comprise those sets. This is pushing gsva towards a oroborous-ish state.

Usage

```
intersect_signatures(
  gsva_result,
  lst,
  freq_cutoff = 2,
  sig_weights = TRUE,
  gene_weights = TRUE
)
```

Arguments

gsva_result	Result from simple_gsva().
lst	List of genes of interest.
freq_cutoff	Minimum number of observations to be counted.
sig_weights	When making venn diagrams, weight them?
gene_weights	When venning genes, weight them?

Value

List containing some venns, lists, and such.

See Also

[Vennerable] [simple_gsva()]

---

intersect_significant *Find the sets of intersecting significant genes*

Description

Use extract_significant_genes() to find the points of agreement between limma/deseq/edger.

Usage

```
intersect_significant(
  combined,
  lfc = 1,
  p = 0.05,
  padding_rows = 2,
  z = NULL,
  p_type = "adj",
  selectors = c("limma", "deseq", "edger"),
  order = "inverse",
  excel = "excel/intersect_significant.xlsx",
  ...
)
```

Arguments

combined	Result from combine_de_tables().
lfc	Define significant via fold-change.
p	Or p-value.
padding_rows	How much space to put between groups of data?
z	Use a z-score filter?

p_type	Use normal or adjusted p-values.
selectors	List of methods to intersect.
order	When set to the default 'inverse', go from the set with the most least intersection to the most. E.g. Start with abc,bc,ac,c,ab,b,a as opposed to a,b,ab,c,ac,bc,abc.
excel	An optional excel workbook to which to write.
...	Extra arguments for extract_significant_genes() and friends.

Value

List containing the intersections between the various DE methods for both the up and down sets of genes. It should also provide some venn diagrams showing the degree of similarity between the methods.

Examples

```
 ## Not run:
  expt <- create_expt(metadata = "some_metadata.xlsx", gene_info = funkytown)
  big_result <- all_pairwise(expt, model_batch = FALSE)
  pretty <- combine_de_tables(big_result, excel = "excel/combined_expt.xlsx")
  intersect <- intersect_significant(pretty, excel = "excel/intersecting_genes.xlsx")

## End(Not run)
```

---

kegg_vector_to_df *Convert a potentially non-unique vector from kegg into a normalized data frame.*

Description

This function seeks to reformat data from KEGGREST into something which is rather easier to use.

Usage

```
kegg_vector_to_df(vector, final_colname = "first", flatten = TRUE)
```

Arguments

vector	Information from KEGGREST
final_colname	Column name for the new information
flatten	Flatten nested data?

Details

This could probably benefit from a tidyr-ish revisitation.

Value

A normalized data frame of gene IDs to whatever.

See Also

[KEGGREST] [load_kegg_annotations()]

`limma_pairwise` *Set up a model matrix and set of contrasts for pairwise comparisons using voom/limma.*

Description

Creates the set of all possible contrasts and performs them using voom/limma.

Usage

```
limma_pairwise(
  input = NULL,
  conditions = NULL,
  batches = NULL,
  model_cond = TRUE,
  model_batch = TRUE,
  model_intercept = FALSE,
  alt_model = NULL,
  extra_contrasts = NULL,
  annot_df = NULL,
  libsize = NULL,
  force = FALSE,
  ...
)
```

Arguments

`input`	Dataframe/vector or expt class containing count tables, normalization state, etc.
`conditions`	Factor of conditions in the experiment.
`batches`	Factor of batches in the experiment.
`model_cond`	Include condition in the model?
`model_batch`	Include batch in the model? If this is a character instead of a logical, then it is passed to all_adjusers() to attempt to find model parameters which describe surrogate variables in the data.
`model_intercept`	Perform a cell-means or intercept model? A little more difficult for me to understand. I have tested and get the same answer either way.
`alt_model`	Separate model matrix instead of the normal condition/batch.

extra_contrasts
: Some extra contrasts to add to the list. This can be pretty neat, lets say one has conditions A,B,C,D,E and wants to do (C/B)/A and (E/D)/A or (E/D)/(C/B) then use this with a string like: "c_vs_b_ctrla = (C-B)-A, e_vs_d_ctrla = (E-D)-A, de_vs_cb = (E-D)-(C-B),"

annot_df
: Data frame for annotations.

libsize
: I've recently figured out that libsize is far more important than I previously realized. Play with it here.

force
: Force data which may not be appropriate for limma into it?

...
: Use the elipsis parameter to feed options to write_limma().

Value

List including the following information: macb = the mashing together of condition/batch so you can look at it macb_model = The result of calling model.matrix(~0 + macb) macb_fit = The result of calling lmFit(data, macb_model) voom_result = The result from voom() voom_design = The design from voom (redundant from voom_result, but convenient) macb_table = A table of the number of times each condition/batch pairing happens cond_table = A table of the number of times each condition appears (the denominator for the identities) batch_table = How many times each batch appears identities = The list of strings defining each condition by itself all_pairwise = The list of strings defining all the pairwise contrasts contrast_string = The string making up the makeContrasts() call pairwise_fits = The result from calling contrasts.fit() pairwise_comparisons = The result from eBayes() limma_result = The result from calling write_limma()

See Also

[limma] [Biobase] [deseq_pairwise()] [edger_pairwise()] [basic_pairwise()]

Examples

```
## Not run:
 pretend <- limma_pairwise(expt)

## End(Not run)
```

---

load_annotations *Use one of the load_*_annotations() functions to gather annotation data.*

Description

We should be able to have an agnostic annotation loader which can take some standard arguments and figure out where to gather data on its own.

Usage

```
load_annotations(type = NULL, ...)
```

Arguments

type	Explicitly state the type of annotation data to load. If not provided, try to figure it out automagically.
...	Arguments passed to the other load_*_annotations().

Value

Some annotations, hopefully.

See Also

[load_biomart_annotations()] [load_gff_annotations()] [load_genbank_annotations()] [load_kegg_annotations()] [load_trinotate_annotations()] [load_microbesonline_annotations()] [load_uniprot_annotations()]

Examples

```
example_gff <- get_paeruginosa_data()[["gff"]]
gff_annotations <- load_annotations(type = "gff", gff = example_gff)
dim(gff_annotations)
```

---

load_biomart_annotations

Extract annotation information from biomart.

Description

Biomart is an amazing resource of information, but using it is a bit annoying. This function hopes to alleviate some common headaches.

Usage

```
load_biomart_annotations(
  species = "hsapiens",
  overwrite = FALSE,
  do_save = TRUE,
  host = NULL,
  trymart = "ENSEMBL_MART_ENSEMBL",
  archive = TRUE,
 default_hosts = c("useast.ensembl.org", "uswest.ensembl.org", "www.ensembl.org",
    "asia.ensembl.org"),
  year = NULL,
  month = NULL,
  drop_haplotypes = TRUE,
  trydataset = NULL,
  gene_requests = c("ensembl_gene_id", "version", "ensembl_transcript_id",
    "transcript_version", "hgnc_symbol", "description", "gene_biotype"),
  length_requests = c("ensembl_transcript_id", "cds_length", "chromosome_name",
```

```
    "strand", "start_position", "end_position"),
  include_lengths = TRUE
)
```

Arguments

species	Choose a species.
overwrite	Overwite an existing save file?
do_save	Create a savefile of annotations for future runs?
host	Ensembl hostname to use.
trymart	Biomart has become a circular dependency, this makes me sad, now to list the marts, you need to have a mart loaded.
archive	Try an archive server instead of a mirror? If this is a character, it will assume it is a specific archive hostname.
default_hosts	List of biomart mirrors to try.
year	Choose specific year(s) for the archive servers?
month	Choose specific month(s) for the archive server?
drop_haplotypes	Some chromosomes have stupid names because they are from non-standard haplotypes and they should go away. Setting this to false stops that.
trydataset	Choose the biomart dataset from which to query.
gene_requests	Set of columns to query for description-ish annotations.
length_requests	Set of columns to query for location-ish annotations.
include_lengths	Also perform a search on structural elements in the genome?

Details

Tested in test_40ann_biomart.R This goes to some lengths to find the relevant tables in biomart. But biomart is incredibly complex and one should carefully inspect the output if it fails to see if there are more appropriate marts, datasets, and columns to download.

Value

List containing: a data frame of the found annotations, a copy of The mart instance to help with finding problems, the hostname queried, the name of the mart queried, a vector of rows queried, vector of the available attributes, and the ensembl dataset queried.

See Also

[biomaRt::listDatasets()] [biomaRt::getBM()] [find_working_mart()]

Examples

```
## This downloads the hsapiens annotations by default.
hs_biomart_annot <- load_biomart_annotations()
summary(hs_biomart_annot)
dim(hs_biomart_annot$annotation)
```

---

load_biomart_go *Extract gene ontology information from biomart.*

Description

I perceive that every time I go to acquire annotation data from biomart, they have changed something important and made it more difficult for me to find what I want. I recently found the *.archive.ensembl.org, and so this function uses that to try to keep things predictable, if not consistent.

Usage

```
load_biomart_go(
  species = "hsapiens",
  overwrite = FALSE,
  do_save = TRUE,
  host = NULL,
  trymart = "ENSEMBL_MART_ENSEMBL",
  archive = TRUE,
 default_hosts = c("useast.ensembl.org", "uswest.ensembl.org", "www.ensembl.org",
    "asia.ensembl.org"),
  year = NULL,
  month = NULL,
  drop_haplotypes = TRUE,
  secondtry = "_gene",
  dl_rows = c("ensembl_gene_id", "go_accession"),
  dl_rowsv2 = c("ensembl_gene_id", "go_id")
)
```

Arguments

species	Species to query.
overwrite	Overwrite existing savefile?
do_save	Create a savefile of the annotations? (if not false, then a filename.)
host	Ensembl hostname to use.
trymart	Biomart has become a circular dependency, this makes me sad, now to list the marts, you need to have a mart loaded.
archive	Try an archive server instead of a mirror? If this is a character, it will assume it is a specific archive hostname.
default_hosts	List of biomart mirrors to try.

year	Choose specific year(s) for the archive servers?
month	Choose specific month(s) for the archive servers?
drop_haplotypes	Some chromosomes have stupid names because they are from non-standard haplotypes and they should go away. Setting this to false stops that.
secondtry	The newer mart name.
dl_rows	List of rows from the final biomart object to download.
dl_rowsv2	A second list of potential rows.

Details

Tested in test_40ann_biomart.R This function makes a couple of attempts to pick up the correct tables from biomart. It is worth noting that it uses the archive.ensembl host(s) because of changes in table organization after December 2015 as well as an attempt to keep the annotation sets relatively consistent.

Value

List containing the following: data frame of ontology data, a copy of the biomart instance for further querying, the host queried, the biomart queried, a vector providing the attributes queried, and the ensembl dataset queried.

See Also

[biomaRt::listMarts()] [biomaRt::useDatasets()] [biomaRt::getBM()]

Examples

```
hs_biomart_ontology <-load_biomart_go()
summary(hs_biomart_ontology)
dim(hs_biomart_ontology$go)
```

---

load_biomart_orthologs

Use biomart to get orthologs between supported species.

Description

Biomart's function getLDS is incredibly powerful, but it makes me think very polite people are going to start knocking on my door, and it fails weirdly pretty much always. This function attempts to alleviate some of that frustration.

Usage

```
load_biomart_orthologs(
  gene_ids = NULL,
  first_species = "hsapiens",
  second_species = "mmusculus",
  host = "dec2016.archive.ensembl.org",
  trymart = "ENSEMBL_MART_ENSEMBL",
  attributes = "ensembl_gene_id"
)
```

Arguments

gene_ids	List of gene IDs to translate.
first_species	Linnean species name for one species.
second_species	Linnean species name for the second species.
host	Ensembl server to query.
trymart	Assumed mart name to use.
attributes	Key to query

Details

Tested in test_40ann_biomart.R As with my other biomart functions, this one grew out of frustrations when attempting to work with the incredibly unforgiving biomart service. It does not attempt to guarantee a useful biomart connection, but will hopefully point out potentially correct marts and attributes to use for a successful query. I can say with confidence that it works well between mice and humans.

Value

list of 4 elements: The first is the set of all ids, as getLDS seems to always send them all; the second is the subset corresponding to the actual ids of interest, and the 3rd/4th are other, optional ids from other datasets.

See Also

[biomaRt::getLDS()]

Examples

```
mouse_yeast_orthologs <- load_biomart_orthologs(gene_ids = NULL, first_species = "mmusculus",
                                                second_species = "scerevisiae")
head(mouse_yeast_orthologs$all_linked_genes)
```

load_genbank_annotations *Given a genbank accession, make a txDb object along with sequences, etc.*

Description

Let us admit it, sometimes biomart is a pain. It also does not have easily accessible data for microbes. Genbank does!

Usage

```
load_genbank_annotations(
  accession = "AE009949",
  reread = TRUE,
  savetxdb = FALSE
)
```

Arguments

accession	Accession to download and import
reread	Re-read (download) the file from genbank
savetxdb	Attempt saving a txdb object?

Details

Tested in test_40ann_biomartgenbank.R and test_70expt_spyogenes.R This primarily sets some defaults for the genbankr service in order to facilitate downloading genomes from genbank and dumping them into a local txdb instance.

Value

List containing a txDb, sequences, and some other stuff which I haven't yet finalized.

See Also

[Biostrings] [GenomicFeatures] [genbankr::import()] [genbankr::readGenBank()]

Examples

```
sagalacticae_genbank_annot <- load_genbank_annotations(accession = "AE009948")
dim(as.data.frame(sagalacticae_genbank_annot$cds))
```

load_gff_annotations *Extract annotation information from a gff file into a df*

Description

Try to make import.gff a little more robust; I acquire (hopefully) valid gff files from various sources: yeastgenome.org, microbesonline, tritrypdb, ucsc, ncbi. To my eyes, they all look like reasonably good gff3 files, but some of them must be loaded with import.gff2, import.gff3, etc. That is super annoying. Also, I pretty much always just do as.data.frame() when I get something valid from rtracklayer, so this does that for me, I have another function which returns the iranges etc. This function wraps import.gff/import.gff3/import.gff2 calls in try() because sometimes those functions fail in unpredictable ways.

Usage

```
load_gff_annotations(
  gff,
  type = NULL,
  id_col = "ID",
  ret_type = "data.frame",
  second_id_col = "locus_tag",
  try = NULL,
  row.names = NULL
)
```

Arguments

gff	Gff filename.
type	Subset the gff file for entries of a specific type.
id_col	Column in a successful import containing the IDs of interest.
ret_type	Return a data.frame or something else?
second_id_col	Second column to check.
try	Give your own function call to use for importing.
row.names	Choose another column for setting the rownames of the data frame.

Value

Dataframe of the annotation information found in the gff file.

See Also

[rtracklayer] [GenomicRanges]

Examples

```
example_gff <- system.file("share", "gas.gff", package = "hpgltools")
gas_gff_annot <- load_gff_annotations(example_gff)
dim(gas_gff_annot)
```

`load_gmt_signatures` *Load signatures from either a gmt file, xml file, or directly from the GSVAdata data set in R.*

Description

There are a bunch of places from which to acquire signature data. This function attempts to provide a single place to load them. The easiest way to get up to date signatures is to download them from msigdb and set the signatures parameter to the downloaded filename.

Usage

```
load_gmt_signatures(
  signatures = "c2BroadSets",
  data_pkg = "GSVAdata",
  signature_category = "c2"
)
```

Arguments

`signatures`	Either the filename downloaded or the variable's name as found in the environment created by data_pkg.
`data_pkg`	Used when signatures is not a filename to load a data package, presumably GSVAdata.
`signature_category`	Probably not needed unless you download a signature file containing lots of different categories.

Value

signature dataset which may be used by gsva()

See Also

[GSEABase]

load_kegg_annotations *Create a data frame of pathways to gene IDs from KEGGREST*

Description

This seeks to take the peculiar format from KEGGREST for pathway<->genes and make it easier to deal with. Sadly, this only works for a subset of species now.

Usage

```
load_kegg_annotations(species = "coli", abbreviation = NULL, flatten = TRUE)
```

Arguments

species	String to use to query KEGG abbreviation.
abbreviation	If you already know the abbreviation, use it.
flatten	Flatten nested tables?

Value

dataframe with rows of KEGG gene IDs and columns of NCBI gene IDs and KEGG paths.

See Also

[KEGGREST]

Examples

```
sc_kegg_annot <- load_kegg_annotations(species = "cerevisiae")
head(sc_kegg_annot)
```

load_microbesonline_annotations
Skip the db and download all the text annotations for a given species.

Description

The microbesonline publicly available mysqldb is rather more complex than I prefer. This skips that process and just grabs a tsv copy of everything and loads it into a dataframe. I have not yet figured out how to so-easily query microbesonline for species IDs, thus one will have to manually query the database to find species of interest.

Usage

```
load_microbesonline_annotations(species = NULL, id = NULL)
```

Arguments

species	Microbesonline species.
id	Microbesonline ID to query.

Details

Tested in test_70expt_spyogenes.R There is so much awesome information in microbesonline, but damn is it annoying to download. This function makes that rather easier, or so I hope at least.

Value

Dataframe containing the annotation information.

See Also

[rvest] [xml2] [readr]

Examples

```
pa14_microbesonline_annot <- load_microbesonline_annotations(species = "PA14")
colnames(pa14_microbesonline_annot)
```

---

load_microbesonline_go

Extract the set of GO categories by microbesonline locus

Description

The microbesonline is such a fantastic resource, it is a bit of a shame that it is such a pain to query.

Usage

```
load_microbesonline_go(
  id = NULL,
  species = NULL,
  table_df = NULL,
  id_column = "name",
  data_column = "GO",
  name = NULL
)
```

Arguments

id	Which species to query.
species	Microbesonline species.
table_df	Pre-existing data frame of annotations containing GO stuff.
id_column	This no longer uses MySQL, so which column from the html table to pull?
data_column	Similar to above, there are lots of places from which one might extract the data.
name	Allowing for non-specific searches by species name.

Details

Tested in test_42ann_microbes.R I am not 100 ontology accessions. At the very least, it does return a large number of them, which is a start.

Value

data frame of GO terms from www.microbesonline.org

See Also

[tidyr]

Examples

```
pa14_microbesonline_go <- load_microbesonline_go(species = "PA14")
head(pa14_microbesonline_go)
```

---

load_orgdb_annotations

Load organism annotation data from an orgdb sqlite package.

Description

Creates a dataframe gene and transcript information for a given set of gene ids using the AnnotationDbi interface.

Usage

```
load_orgdb_annotations(
  orgdb = NULL,
  gene_ids = NULL,
  include_go = FALSE,
  keytype = "ensembl",
  strand_column = "cdsstrand",
  start_column = "cdsstart",
  end_column = "cdsend",
  chromosome_column = "cdschrom",
```

```
  type_column = "gene_type",
  name_column = "cdsname",
  fields = NULL,
  sum_exon_widths = FALSE
)
```

Arguments

orgdb	OrganismDb instance.
gene_ids	Search for a specific set of genes?
include_go	Ask the Dbi for gene ontology information?
keytype	mmm the key type used?
strand_column	There are a few fields I want to gather by default: start, end, strand, chromosome, type, and name; but these do not necessarily have consistent names, use this column for the chromosome strand.
start_column	Use this column for the gene start.
end_column	Use this column for the gene end.
chromosome_column	Use this column to identify the chromosome.
type_column	Use this column to identify the gene type.
name_column	Use this column to identify the gene name.
fields	Columns included in the output.
sum_exon_widths	Perform a sum of the exons in the data set?

Details

Tested in test_45ann_organdb.R This defaults to a few fields which I have found most useful, but the brave or pathological can pass it 'all'.

Value

Table of geneids, chromosomes, descriptions, strands, types, and lengths.

See Also

[AnnotationDbi] [AnnotationDbi::select()] [GenomicFeatures]

Examples

```
hs_orgdb_annot <- load_orgdb_annotations()
summary(hs_orgdb_annot$genes)
```

load_orgdb_go *Retrieve GO terms associated with a set of genes.*

Description

AnnotationDbi provides a reasonably complete set of GO mappings between gene ID and ontologies. This will extract that table for a given set of gene IDs.

Usage

```
load_orgdb_go(
  orgdb = NULL,
  gene_ids = NULL,
  keytype = "ensembl",
  columns = c("go", "goall", "goid")
)
```

Arguments

orgdb	OrganismDb instance.
gene_ids	Identifiers of the genes to retrieve annotations.
keytype	The mysterious keytype returns yet again to haunt my dreams.
columns	The set of columns to request.

Details

Tested in test_45ann_organdb.R This is a nice way to extract GO data primarily because the Orgdb data sets are extremely fast and flexible, thus by changing the keytype argument, one may use a lot of different ID types and still score some useful ontology data.

Value

Data frame of gene IDs, go terms, and names.

Author(s)

I think Keith provided the initial implementation of this, but atb messed with it pretty extensively.

See Also

[AnnotationDbi] [GO.db]

Examples

```
drosophila_orgdb_go <- load_orgdb_go(orgdb = "org.Dm.eg.db")
head(drosophila_orgdb_go)
```

load_trinotate_annotations

Read a csv file from trinotate and make an annotation data frame.

Description

Trinotate performs some neat sequence searches in order to seek out likely annotations for the trinity contigs. The resulting csv file is encoded in a peculiar fashion, so this function attempts to make it easier to read and put them into a format usable in an expressionset.

Usage

```
load_trinotate_annotations(trinotate = "reference/trinotate.csv")
```

Arguments

trinotate	CSV of trinotate annotation data.

Value

Dataframe of fun data.

See Also

[tidyr] [readr]

Examples

```
sb_annot <- get_sbetaceum_data()[["annot"]]
a_few_trinotate <- load_trinotate_annotations(trinotate = sb_annot)
dim(a_few_trinotate)
```

load_trinotate_go

Read a csv file from trinotate and extract ontology data from it.

Description

Trinotate performs some neat sequence searches in order to seek out likely annotations for the trinity contigs. This function extracts ontology data from it. Keep in mind that this data is primarily from Blast2GO.

Usage

```
load_trinotate_go(trinotate = "reference/trinotate.csv")
```

Arguments

trinotate	CSV of trinotate annotation data.

Value

List of the extracted GO data, a table of it, length data, and the resulting length table.

See Also

[load_trinotate_annotations()]

Examples

```
sb_annot <- get_sbetaceum_data()[["annot"]]
trinotate_go <- load_trinotate_go(trinotate = sb_annot)
dim(trinotate_go$go_data)
dim(trinotate_go$go_table)
```

---

load_uniprot_annotations

Read a uniprot text file and extract as much information from it as possible.

Description

I spent entirely too long fighting with Uniprot.ws, finally got mad and wrote this.

Usage

```
load_uniprot_annotations(file = NULL, species = NULL, savefile = TRUE)
```

Arguments

file	Uniprot file to read and parse
species	Species name to download/load.
savefile	Do a save?

Value

Big dataframe of annotation data.

See Also

[download_uniprot_proteome()]

Examples

```
uniprot_sc_downloaded <- download_uniprot_proteome(species = "Saccharomyces cerevisiae S288c")
sc_uniprot_annot <- load_uniprot_annotations(file = uniprot_sc_downloaded$filename)
dim(sc_uniprot_annot)
```

`load_uniprot_go` *Extract ontology information from a uniprot dataframe.*

Description

Extract ontology information from a uniprot dataframe.

Usage

```
load_uniprot_go(input)
```

Arguments

`input`	uniprot filename or dataframe.

Value

Ontology dataframe

See Also

[load_uniprot_annotations()] [stringr] [tidyr]

Examples

```
## Not run:
uniprot_sc_downloaded <- download_uniprot_proteome(species = "Saccharomyces cerevisiae S288c")
sc_uniprot_annot <- load_uniprot_annotations(file = uniprot_sc_downloaded$filename)
sc_uniprot_go <- load_uniprot_go(sc_uniprot_annot)
head(sc_uniprot_go)

## End(Not run)
```

loadme *Load a backup rdata file*

Description

I often use R over a sshfs connection, sometimes with significant latency, and I want to be able to save/load my R sessions relatively quickly. Thus this function uses my backup directory to load its R environment.

Usage

```
loadme(directory = "savefiles", filename = "Rdata.rda.xz")
```

Arguments

directory	Directory containing the RData.rda.xz file.
filename	Filename to which to save.

Value

a bigger global environment

See Also

[saveme()]

Examples

```
## Not run:
 loadme()

## End(Not run)
```

local_get_value *Perform a get_value for delimited files*

Description

Keith wrote this as .get_value() but functions which start with . trouble me.

Usage

```
local_get_value(x, delimiter = ": ")
```

Arguments

x	Some stuff to split
delimiter	The tritrypdb uses ': ' ergo the default.

Value

A value!

`make_exampledata` *Small hack of limma's exampleData() to allow for arbitrary data set sizes.*

Description

exampleData has a set number of genes/samples it creates. This relaxes that restriction.

Usage

```
make_exampledata(ngenes = 1000, columns = 5)
```

Arguments

ngenes	How many genes in the fictional data set?
columns	How many samples in this data set?

Value

Matrix of pretend counts.

See Also

[limma] [DESeq2] [stats]

Examples

```
## Not run:
 pretend = make_exampledata()

## End(Not run)
```

make_gsc_from_abundant *Given a pairwise result, make a gene set collection.*

Description

If I want to play with gsva and friends, then I need GeneSetCollections! Much like make_gsc_from_significant(), this function extract the genes deemed 'abundant' and generates gene sets accordingly.

Usage

```
make_gsc_from_abundant(
  pairwise,
  according_to = "deseq",
  orgdb = "org.Hs.eg.db",
  researcher_name = "elsayed",
  study_name = "macrophage",
  category_name = "infection",
  phenotype_name = NULL,
  pair_names = "high",
  current_id = "ENSEMBL",
  required_id = "ENTREZID",
  ...
)
```

Arguments

pairwise	A pairwise result, or combined de result, or extracted genes.
according_to	When getting significant genes, use this method.
orgdb	Annotation dataset.
researcher_name	Prefix of the name for the generated set(s).
study_name	Second element in the name of the generated set(s).
category_name	Third element in the name of the generated set(s).
phenotype_name	Optional phenotype data for the generated set(s).
pair_names	The suffix of the generated set(s).
current_id	What type of ID is the data currently using?
required_id	What type of ID should the use?
...	Extra arguments for extract_abundant_genes().

Value

List containing 3 GSCs, one containing both the highs/lows called 'colored', one of the highs, and one of the lows.

See Also

[extract_abundant_genes()] [make_gsc_from_ids()] [GSEABase]

`make_gsc_from_ids` *Create a gene set collection from a set of arbitrary IDs.*

Description

This function attempts to simplify the creation of a gsva compatible GeneSet. Some important caveats when working with gsva, notably the gene IDs we use are not usually compatible with the gene IDs used by gsva, thus the primary logic in this function is intended to bridge these IDs.

Usage

```
make_gsc_from_ids(
  first_ids,
  second_ids = NULL,
  orgdb = "org.Hs.eg.db",
  researcher_name = "elsayed",
  study_name = "macrophage",
  category_name = "infection",
  phenotype_name = NULL,
  pair_names = "up",
  current_id = "ENSEMBL",
  required_id = "ENTREZID"
)
```

Arguments

`first_ids`	The required IDs for a single set.
`second_ids`	Potentially null optionally used for a second, presumably contrasting set.
`orgdb`	Orgdb annotation, used to translate IDs to the required type.
`researcher_name`	Prefix of the name for the generated set(s).
`study_name`	Second element in the name of the generated set(s).
`category_name`	Third element in the name of the generated set(s).
`phenotype_name`	Optional phenotype data for the generated set(s).
`pair_names`	The suffix of the generated set(s).
`current_id`	What type of ID is the data currently using?
`required_id`	What type of ID should the use?

Value

Small list comprised of the created gene set collection(s).

See Also

[GSEABase]

`make_gsc_from_pairwise` *Given a pairwise result, make a gene set collection.*

Description

If I want to play with gsva and friends, then I need GeneSetCollections! To that end, this function uses extract_significant_genes() in order to gather sets of genes deemed 'significant'. It then passes these sets to make_gsc_from_ids().

Usage

```
make_gsc_from_pairwise(
  pairwise,
  according_to = "deseq",
  orgdb = "org.Hs.eg.db",
  pair_names = c("ups", "downs"),
  category_name = "infection",
  phenotype_name = "parasite",
  set_name = "elsayed_macrophage",
  color = TRUE,
  current_id = "ENSEMBL",
  required_id = "ENTREZID",
  ...
)
```

Arguments

`pairwise`	A pairwise result, or combined de result, or extracted genes.
`according_to`	When getting significant genes, use this method.
`orgdb`	Annotation dataset.
`pair_names`	Describe the contrasts of the GSC: up vs. down, high vs. low, etc.
`category_name`	What category does the GSC describe?
`phenotype_name`	When making color sets, use this phenotype name.
`set_name`	A name for the created gene set.
`color`	Make a colorSet?
`current_id`	Usually we use ensembl IDs, but that does not _need_ to be the case.
`required_id`	gsva uses entrezids by default.
`...`	Extra arguments for extract_significant_genes().

Value

List containing 3 GSCs, one containing both the ups/downs called 'colored', one of the ups, and one of the downs.

See Also

[combine_de_tables()] [extract_significant_genes()] [make_gsc_from_ids()] [GSEABase]

`make_id2gomap` *Make a go mapping from IDs in a format suitable for topGO.*

Description

When using a non-supported organism, one must write out mappings in the format expected by topgo. This handles that process and gives a summary of the new table.

Usage

```
make_id2gomap(
  goid_map = "reference/go/id2go.map",
  go_db = NULL,
  overwrite = FALSE
)
```

Arguments

`goid_map`	TopGO mapping file.
`go_db`	If there is no goid_map, create it with this data frame.
`overwrite`	Rewrite the mapping file?

Value

Summary of the new goid table.

See Also

[topGO]

make_kegg_df *Use pathfindR to get a dataframe of KEGG IDs.*

Description

The various KEGG conversion methods from KEGGREST appear to only work for a small subset of species now. This uses a differnt query format to get a less flexible version of the same information. But at least it works.

Usage

```
make_kegg_df(org_code)
```

Arguments

org_code	Organism code from KEGG.

Value

Dataframe of gene IDs to KEGG IDs.

make_limma_tables *Writes out the results of a limma search using toptable().*

Description

However, this will do a couple of things to make one's life easier: 1. Make a list of the output, one element for each comparison of the contrast matrix 2. Write out the toptable() output in separate .csv files and/or sheets in excel 3. Since I have been using qvalues a lot for other stuff, add a column for them.

Usage

```
make_limma_tables(
  fit = NULL,
  adjust = "BH",
  n = 0,
  coef = NULL,
  annot_df = NULL,
  intercept = FALSE
)
```

Arguments

fit	Result from lmFit()/eBayes()
adjust	Pvalue adjustment chosen.
n	Number of entries to report, 0 says do them all.
coef	Which coefficients/contrasts to report, NULL says do them all.
annot_df	Optional data frame including annotation information to include with the tables.
intercept	Intercept model?

Value

List of data frames comprising the toptable output for each coefficient, I also added a qvalue entry to these toptable() outputs.

See Also

[limma] [write_xlsx()]

Examples

```
## Not run:
 finished_comparison = eBayes(limma_output)
 table = make_limma_tables(finished_comparison, adjust = "fdr")

## End(Not run)
```

---

make_pairwise_contrasts

Run makeContrasts() with all pairwise comparisons.

Description

In order to have uniformly consistent pairwise contrasts, I decided to avoid potential human erors(sic) by having a function generate all contrasts.

Usage

```
make_pairwise_contrasts(
  model,
  conditions,
  do_identities = FALSE,
  do_extras = TRUE,
  do_pairwise = TRUE,
  extra_contrasts = NULL,
  ...
)
```

Arguments

model	Describe the conditions/batches/etc in the experiment.
conditions	Factor of conditions in the experiment.
do_identities	Include all the identity strings? Limma can use this information while edgeR can not.
do_pairwise	Include all pairwise strings? This shouldn't need to be set to FALSE, but just in case.
extra_contrasts	Optional string of extra contrasts to include.
...	Extra arguments passed here are caught by arglist.

Details

Invoked by the _pairwise() functions.

Value

List including the following information:

1. all_pairwise_contrasts = the result from makeContrasts(...)
2. identities = the string identifying each condition alone
3. all_pairwise = the string identifying each pairwise comparison alone
4. contrast_string = the string passed to R to call makeContrasts(...)
5. names = the names given to the identities/contrasts

See Also

[limma::makeContrasts()]

Examples

```
## Not run:
 pretend <- make_pairwise_contrasts(model, conditions)

## End(Not run)
```

---

make_pombe_expt *Create a Schizosaccharomyces cerevisiae expt.*

Description

This just saves some annoying typing if one wishes to make a standard expressionset superclass out of the publicly available fission data set.

Usage

```
make_pombe_expt(annotation = TRUE)
```

Arguments

annotation	Add annotation data?

Value

Expressionset/expt of fission.

See Also

[fission] [create_expt()]

---

make_simplified_contrast_matrix

Create a contrast matrix suitable for MSstats and similar tools.

Description

I rather like makeContrasts() from limma. I troubled me to have to manually create a contrast matrix when using MSstats. It turns out it troubled me for good reason because I managed to reverse the terms and end up with the opposite contrasts of what I intended. Ergo this function.

Usage

```
make_simplified_contrast_matrix(numerators, denominators)
```

Arguments

numerators	Character list of conditions which are the numerators of a series of a/b comparisons.
denominators	Character list of conditions which are the denominators of a series of a/b comparisons.

Details

Feed make_simplified_contrast_matrix() a series of numerators and denominators names after the conditions of interest in an experiment and it returns a contrast matrix in a format acceptable to MSstats.

Value

Contrast matrix suitable for use in tools like MSstats.

See Also

[MSstats]

map_kegg_dbs *Maps KEGG identifiers to ENSEMBL gene ids.*

Description

Takes a list of KEGG gene identifiers and returns a list of ENSEMBL ids corresponding to those genes.

Usage

```
map_kegg_dbs(kegg_ids)
```

Arguments

kegg_ids	List of KEGG identifiers to be mapped.

Value

Ensembl IDs as a character list.

See Also

[KEGGREST::keggGet()]

Examples

```
kegg_df <- load_kegg_annotations(species = "coli")
kegg_ids <- head(kegg_df[["kegg_geneid"]])
mapped <- map_kegg_dbs(kegg_ids)
mapped
```

map_orgdb_ids *Map AnnotationDbi keys from one column to another.*

Description

Given a couple of keytypes, this provides a quick mapping across them. I might have an alternate version of this hiding in the gsva code, which requires ENTREZIDs. In the mean time, this creates a dataframe of the mapped columns for a given set of gene ids using the in a sqlite instance.

Usage

```
map_orgdb_ids(orgdb, gene_ids = NULL, mapto = "ensembl", keytype = "geneid")
```

Arguments

orgdb	OrganismDb instance.
gene_ids	Gene identifiers for retrieving annotations.
mapto	Key to map the IDs against.
keytype	Choose a keytype, this will yell if it doesn't like your choice.

Value

a table of gene information

Author(s)

Keith Hughitt with changes by atb.

See Also

[AnnotationDbi]

Examples

```
dm_unigene_to_ensembl <- map_orgdb_ids("org.Dm.eg.db", mapto = "ensembl", keytype = "unigene")
head(dm_unigene_to_ensembl)
```

---

mean_by_bioreplicate *An attempt to address a troubling question when working with DIA data.*

Description

My biggest concern when treating DIA data in a RNASeqish manner is the fact that if a given peptide is not identified, that is not the same thing as stating that it was not translated. It is somewhat reminiscent of the often mocked and repeated Donald Rumsfeld statement regarding known unknowns vs. unknown unknowns. Thus, in an RNASeq experiment, if one sees a zero, one may assume that transcript was not transcribed, it may be assumed to be a known zero(unknown). In contrast, if the same thing happens in a DIA data set, that represents an unknown unknown. Perhaps it was not translated, and perhaps it was not identified.

Usage

```
mean_by_bioreplicate(expt, fact = "bioreplicate", fun = "mean")
```

Arguments

expt	Starting expressionset to mangle.
fact	Metadata factor to use when taking the mean of biological replicates.
fun	Assumed to be mean, but one might want median.

Details

This function therefore does the following: 1. Backfill all 0s in the matrix to NA. 2. Performs a mean across all samples which are known technical replicates of the same biological replicate. This mean is performed using na.rm = TRUE. Thus the entries which used to be 0 should no longer affect the result. 3. Recreate the expressionset with the modified set of samples.

Value

new expressionset

`median_by_factor` *Create a data frame of the medians of rows by a given factor in the data.*

Description

This assumes of course that (like expressionsets) there are separate columns for each replicate of the conditions. This will just iterate through the levels of a factor describing the columns, extract them, calculate the median, and add that as a new column in a separate data frame.

Usage

```
median_by_factor(data, fact = "condition", fun = "median")
```

Arguments

`data`	Data frame, presumably of counts.
`fact`	Factor describing the columns in the data.
`fun`	Optionally choose mean or another function.

Details

Used in write_expt() as well as a few random collaborations.

Value

Data frame of the medians.

See Also

[Biobase] [matrixStats]

Examples

```
## Not run:
 compressed = median_by_factor(data, experiment$condition)

## End(Not run)
```

mesg *message() but with a verbose flag.*

Description

message() but with a verbose flag.

Usage

```
mesg(..., verbosity = NULL)
```

Arguments

...	parameters for message()
verbose	actually print the message?

model_test *Make sure a given experimental factor and design will play together.*

Description

Have you ever wanted to set up a differential expression analysis and after minutes of the computer churning away it errors out with some weird error about rank? Then this is the function for you!

Usage

```
model_test(design, goal = "condition", factors = NULL, ...)
```

Arguments

design	Dataframe describing the design of the experiment.
goal	Experimental factor you actually want to learn about.
factors	Experimental factors you rather wish would just go away.
...	I might decide to add more options from other functions.

Value

List of booleans telling if the factors + goal will work.

See Also

[model.matrix()] [qr()]

`my_identifyAUBlocks` *copy/paste the function from SeqTools and figure out where it falls on its ass.*

Description

Yeah, I do not remember what I changed in this function.

Usage

```
my_identifyAUBlocks(x, min.length = 20, p.to.start = 0.8, p.to.end = 0.55)
```

Arguments

`x`	Sequence object
`min.length`	I dunno.
`p.to.start`	P to start of course
`p.to.end`	The p to end – wtf who makes names like this?

Value

a list of IRanges which contain a bunch of As and Us.

`my_isva` *There are some funky scoping problems in isva::DoISVA().*

Description

Thus I copy/pasted the function and attempted to address them here.

Usage

```
my_isva(
  data.m,
  pheno.v,
  cf.m = NULL,
  factor.log = FALSE,
  pvthCF = 0.01,
  th = 0.05,
  ncomp = NULL,
  icamethod = "fastICA"
)
```

Arguments

data.m	Input matrix.
pheno.v	Vector of conditions of interest in the data.
cf.m	Matrix of confounded conditions in the data.
factor.log	I forget.
pvthCF	Minimal p-value for considering.
th	threshold for inclusion.
ncomp	Number of SVA components to estimate.
icamethod	Which ICA implementation to use?

See Also

[isva]

---

my_runsims *A version of PROPER:::runsims which is (hopefully) a little more robust.*

Description

When I was testing PROPER, it fell down mysteriously on a few occasions. The source ended up being in runsims(), ergo this function.

Usage

```
my_runsims(
  Nreps = c(3, 5, 7, 10),
  Nreps2,
  nsims = 100,
  sim.opts,
  DEmethod = c("edgeR", "DSS", "DESeq", "DESeq2"),
  verbose = TRUE
)
```

Arguments

Nreps	Vector of numbers of replicates to simulate.
Nreps2	Second vector of replicates.
nsims	How many simulations to perform?
sim.opts	Options provided in a list which include information about the expression, numbers of genes, logFC values, etc.
DEmethod	I suggest using only either edgeR or DESeq2.
verbose	Print some information along the way?

See Also

[PROPER]

`mymakeContrasts` *A copy of limma::makeContrasts() with special sauce.*

Description

This is a copy of limma::makeContrasts without the test of make.names() Because I want to be able to use it with interaction models potentially and if a model has first:second, make.names() turns the ':' to a '.' and then the equivalence test fails, causing makeContrasts() to error spuriously (I think).

Usage

```
mymakeContrasts(..., contrasts = NULL, levels)
```

Arguments

`...`	Conditions used to make the contrasts.
`contrasts`	Actual contrast names.
`levels`	contrast levels used.

Value

Same contrasts as used in makeContrasts, but with unique names.

See Also

[limma::makeContrasts()]

`myretrieveKGML` *A couple functions from KEGGgraph that have broken*

Description

Some material in KEGGREST is borken.

Usage

```
myretrieveKGML(
  pathway,
  organism,
  destfile,
  silent = TRUE,
  hostname = "http://www.kegg.jp",
  ...
)
```

Arguments

pathway	The path to query.
organism	Which organism to query?
destfile	File to which to download.
silent	Send stdout and stderr to dev null?
hostname	Host to download from (this is what is broken.)
...	Arglist!

---

normalize_counts *Perform a simple normalization of a count table.*

Description

This provides shortcut interfaces for normalization functions from deseq2/edger and friends.

Usage

```
normalize_counts(data, design = NULL, method = "raw", ...)
```

Arguments

data	Matrix of count data.
design	Dataframe describing the experimental design. (conditions/batches/etc)
...	More arguments might be necessary.
norm	Normalization to perform: 'sf|quant|qsmooth|tmm|upperquartile|tmm|rle' I keep wishy-washing on whether design is a required argument.

Value

Dataframe of normalized(counts)

See Also

[edgeR] [limma] [DESeq2] [preprocessCore] [BiocGenerics]

Examples

```
## Not run:
 norm_table = normalize_counts(count_table, design = design, norm='qsmooth')

## End(Not run)
```

`normalize_expt` *Normalize the data of an expt object. Save the original data, and note what was done.*

Description

It is the responsibility of normalize_expt() to perform any arbitrary normalizations desired as well as to ensure that the data integrity is maintained. In order to do this, it writes the actions performed in expt$state and saves the intermediate steps of the normalization in expt$intermediate_counts. Furthermore, it should tell you every step of the normalization process, from count filtering, to normalization, conversion, transformation, and batch correction.

Usage

```
normalize_expt(
  expt,
  transform = "raw",
  norm = "raw",
  convert = "raw",
  batch = "raw",
  filter = FALSE,
  annotations = NULL,
  fasta = NULL,
  entry_type = "gene",
  use_original = FALSE,
  batch1 = "batch",
  batch2 = NULL,
  batch_step = 4,
  low_to_zero = TRUE,
  thresh = 2,
  min_samples = 2,
  p = 0.01,
  A = 1,
  k = 1,
  cv_min = 0.01,
  cv_max = 1000,
  na_to_zero = FALSE,
  adjust_method = "ruv",
  verbose = TRUE,
  ...
)
```

Arguments

`expt`	Original expt.
`transform`	Transformation desired, usually log2.
`norm`	How to normalize the data? (raw, quant, sf, upperquartile, tmm, rle)

convert	Conversion to perform? (raw, cpm, rpkm, cp_seq_m)
batch	Batch effect removal tool to use? (limma sva fsva ruv etc)
filter	Filter out low/undesired features? (cbcb, pofa, kofa, others?)
annotations	Used for rpkm – probably not needed as this is in fData now.
fasta	Fasta file for cp_seq_m counting of oligos.
entry_type	For getting genelengths by feature type (rpkm or cp_seq_m).
use_original	Use the backup data in the expt class?
batch1	Experimental factor to extract first.
batch2	Second factor to remove (only with limma's removebatcheffect()).
batch_step	From step 1-5, when should batch correction be applied?
low_to_zero	When log transforming, change low numbers (< 0) to 0 to avoid NaN?
thresh	Used by cbcb_lowfilter().
min_samples	Also used by cbcb_lowfilter().
p	Used by genefilter's pofa().
A	Also used by genefilter's pofa().
k	Used by genefilter's kofa().
cv_min	Used by genefilter's cv().
cv_max	Also used by genefilter's cv().
na_to_zero	Sometimes rpkm gives some NA values for very low numbers.
verbose	Print what is happening while the normalization is performed? I am not sure why, but I think they should be 0.
...	more options

Value

Expt object with normalized data and the original data saved as 'original_expressionset'

See Also

[convert_counts()] [normalize_counts()] [batch_counts()] [filter_counts()] [transform_counts()]

Examples

```
## Not run:
 normed <- normalize_expt(exp, transform='log2', norm='rle', convert='cpm',
                          batch='raw', filter='pofa')
 normed_batch <- normalize_expt(exp, transform='log2', norm='rle', convert='cpm',
                                batch='sva', filter='pofa')

## End(Not run)
```

orgdb_from_ah *Get an orgdb from an AnnotationHub taxonID.*

Description

Ideally, annotationhub will one day provide a one-stop shopping source for a tremendous wealth of curated annotation databases, sort of like a non-obnoxious biomart. But for the moment, this function is more fragile than I would like.

Usage

```
orgdb_from_ah(ahid = NULL, title = NULL, species = NULL, type = "OrgDb")
```

Arguments

ahid	TaxonID from AnnotationHub
title	Title for the annotation hub instance
species	Species to download
type	Datatype to download

Value

An Orgdb instance

See Also

[AnnotationHub] [S4Vectors]

Examples

```
## Not run:
 org <- mytaxIdToOrgDb(species = "Leishmania", type = "TxDb")

## End(Not run)
```

pattern_count_genome *Find how many times a given pattern occurs in every gene of a genome.*

Description

There are times when knowing how many times a given string appears in a genome/CDS is helpful. This function provides that information and is primarily used by cp_seq_m().

Usage

```
pattern_count_genome(
  fasta,
  gff = NULL,
  pattern = "TA",
  type = "gene",
  key = NULL
)
```

Arguments

fasta	Genome sequence.
gff	Gff of annotation information from which to acquire CDS (if not provided it will just query the entire genome).
pattern	What to search for? This was used for tnseq and TA is the mariner insertion point.
type	Column to use in the gff file.
key	What type of entry of the gff file to key from?

Details

This is once again a place where mcols() usage might improve the overall quality of life.

Value

Data frame of gene names and number of times the pattern appears/gene.

See Also

[Biostrings] [Rsamtools::FaFile()] [Biostrings::PDict()]

Examples

```
pa_data <- get_paeruginosa_data()
pa_fasta <- pa_data[["fasta"]]
pa_gff <- pa_data[["gff"]]
ta_count <- pattern_count_genome(pa_fasta, pa_gff)
head(ta_count)
```

pca_highscores *Get the highest/lowest scoring genes for every principle component.*

Description

This function uses princomp to acquire a principle component biplot for some data and extracts a dataframe of the top n genes for each component by score.

Usage

```
pca_highscores(expt, n = 20, cor = TRUE, vs = "means", logged = TRUE)
```

Arguments

expt	Experiment to poke.
n	Number of genes to extract.
cor	Perform correlations?
vs	Do a mean or median when getting ready to perform the pca?
logged	Check for the log state of the data and adjust as deemed necessary?

Value

a list including the princomp biplot, histogram, and tables of top/bottom n scored genes with their scores by component.

See Also

[stats] [stats::princomp]

Examples

```
## Not run:
 information <- pca_highscores(df = df, conditions = cond, batches = bat)
 information$pca_bitplot  ## oo pretty

## End(Not run)
```

pca_information *Gather information about principle components.*

Description

Calculate some information useful for generating PCA plots. pca_information seeks to gather together interesting information to make principle component analyses easier, including: the results from (fast.)svd, a table of the r^2 values, a table of the variances in the data, coordinates used to make a pca plot for an arbitrarily large set of PCs, correlations and fstats between experimental factors and the PCs, and heatmaps describing these relationships. Finally, it will provide a plot showing how much of the variance is provided by the top-n genes and (optionally) the set of all PCA plots with respect to one another. (PCx vs. PCy)

Usage

```
pca_information(
  expt,
  expt_design = NULL,
  expt_factors = c("condition", "batch"),
  num_components = NULL,
  plot_pcas = FALSE,
  ...
)
```

Arguments

expt	Data to analyze (usually exprs(somedataset)).
expt_design	Dataframe describing the experimental design, containing columns with useful information like the conditions, batches, number of cells, whatever...
expt_factors	Character list of experimental conditions to query for R^2 against the fast.svd of the data.
num_components	Number of principle components to compare the design factors against. If left null, it will query the same number of components as factors asked for.
plot_pcas	Plot the set of PCA plots for every pair of PCs queried.
...	Extra arguments for the pca plotter

Value

a list of fun pca information: svd_u/d/v: The u/d/v parameters from fast.svd rsquared_table: A table of the rsquared values between each factor and principle component pca_variance: A table of the pca variances pca_data: Coordinates for a pca plot pca_cor: A table of the correlations between the factors and principle components anova_fstats: the sum of the residuals with the factor vs without (manually calculated) anova_f: The result from performing anova(withfactor, withoutfactor), the F slot anova_p: The p-value calculated from the anova() call anova_sums: The RSS value from the above anova() call cor_heatmap: A heatmap from recordPlot() describing pca_cor.

Warning

This function has gotten too damn big and needs to be split up.

See Also

[corpcor] [plot_pca()] [plot_pcs()] [stats::lm()]

Examples

```
## Not run:
 pca_info = pca_information(exprs(some_expt$expressionset), some_design, "all")
 pca_info

## End(Not run)
```

---

pct_all_kegg *Extract the percent differentially expressed genes for all KEGG pathways.*

Description

KEGGgraph provides some interesting functionality for mapping KEGGids and examining the pieces. This attempts to use that in order to evaluate how many 'significant' genes are in a given pathway.

Usage

```
pct_all_kegg(
  all_ids,
  sig_ids,
  organism = "dme",
  pathways = "all",
  pathdir = "kegg_pathways",
  verbose = FALSE,
  ...
)
```

Arguments

all_ids	Set of all gene IDs in a given analysis.
sig_ids	Set of significant gene IDs.
organism	KEGG organism identifier.
pathways	What pathways to look at?
pathdir	Directory into which to copy downloaded pathway files.
verbose	Talky talky?
...	Options I might pass from other functions are dropped into arglist.

Value

Dataframe including the filenames, percentages, nodes included, and differential nodes.

See Also

[KEGGgraph] [KEGGREST]

`pct_kegg_diff` *Extract the percent differentially expressed genes in a given KEGG pathway.*

Description

KEGGgraph provides some interesting functionality for mapping KEGGids and examining the pieces. This attempts to use that in order to evaluate how many 'significant' genes are in a given pathway.

Usage

```
pct_kegg_diff(
  all_ids,
  sig_ids,
  pathway = "00500",
  organism = "dme",
  pathdir = "kegg_pathways",
  ...
)
```

Arguments

`all_ids`	Set of all gene IDs in a given analysis.
`sig_ids`	Set of significant gene IDs.
`pathway`	Numeric pathway identifier.
`organism`	KEGG organism identifier.
`pathdir`	Directory into which to copy downloaded pathway files.
`...`	Options I might pass from other functions are dropped into arglist.

Value

Percent genes/pathway deemed significant.

See Also

[KEGGgraph] [KEGGREST]

please_install *Automatic loading and/or installing of packages.*

Description

Load a library, install it first if necessary.

Usage

```
please_install(lib, update = FALSE)
```

Arguments

lib	String name of a library to check/install.
update	Update packages?

Details

This was taken from: http://sbamin.com/2012/11/05/tips-for-working-in-r-automatically-install-missing-package/ and initially provided by Ramzi Temanni.

Value

0 or 1, whether a package was installed or not.

See Also

[BiocManager] [install.packages()]

Examples

```
## Not run:
 require.auto("ggplot2")

## End(Not run)
```

plot_3d_pca *Something silly for Najib.*

Description

This will make him very happy, but I remain skeptical.

Usage

```
plot_3d_pca(pc_result, components = c(1, 2, 3), file = "3dpca.html")
```

Arguments

pc_result	The result from plot_pca()
components	List of three axes by component.
file	File to write the created plotly object.

Value

List containing the plotly data and filename for the html widget.

See Also

[plotly] [htmlwidgets]

---

plot_batchsv *Make a dotplot of known batches vs. SVs.*

Description

This should make a quick df of the factors and surrogates and plot them. Maybe it should be folded into plot_svfactor? Hmm, I think first I will write this and see if it is better.

Usage

```
plot_batchsv(
  expt,
  svs,
  sv = 1,
  batch_column = "batch",
  factor_type = "factor",
  id_column = "sampleid"
)
```

Arguments

expt	Experiment from which to acquire the design, counts, etc.
svs	Set of surrogate variable estimations from sva/svg or batch estimates.
sv	Which surrogate variable to show?
batch_column	Which experimental design column to use?
factor_type	This may be a factor or range, it is intended to plot a scatterplot if it is a range, a dotplot if a factor.

Value

Plot of batch vs surrogate variables as per Leek's work.

See Also

[sva] [ggplot2]

Examples

```
## Not run:
 estimate_vs_snps <- plot_batchsv(start, surrogate_estimate, "snpcategory")

## End(Not run)
```

---

plot_bcv *Steal edgeR's plotBCV() and make it a ggplot2.*

Description

This was written primarily to understand what that function is doing in edgeR.

Usage

```
plot_bcv(data)
```

Arguments

data	Dataframe/expt/exprs with count data

Value

Plot of the BCV a la ggplot2.

See Also

[edgeR::plotBCV()] [ggplot2]

Examples

```
## Not run:
 bcv <- plot_bcv(expt)
 summary(bcv$data)
 bcv$plot

## End(Not run)
```

plot_boxplot *Make a ggplot boxplot of a set of samples.*

Description

Boxplots and density plots provide complementary views of data distributions. The general idea is that if the box for one sample is significantly shifted from the others, then it is likely an outlier in the same way a density plot shifted is an outlier.

Usage

```
plot_boxplot(
  data,
  colors = NULL,
  title = NULL,
  violin = FALSE,
  scale = NULL,
  expt_names = NULL,
  label_chars = 10,
  ...
)
```

Arguments

data	Expt or data frame set of samples.
colors	Color scheme, if not provided will make its own.
title	A title!
violin	Print this as a violin rather than a just box/whiskers?
scale	Whether to log scale the y-axis.
expt_names	Another version of the sample names for printing.
label_chars	Maximum number of characters for abbreviating sample names.
...	More parameters are more fun!

Value

Ggplot2 boxplot of the samples. Each boxplot contains the following information: a centered line describing the median value of counts of all genes in the sample, a box around the line describing the inner-quartiles around the median (quartiles 2 and 3 for those who are counting), a vertical line above/below the box which shows 1.5x the inner quartile range (a common metric of the non-outliers), and single dots for each gene which is outside that range. A single dot is transparent.

See Also

[ggplot2]

Examples

```
## Not run:
 a_boxplot <- plot_boxplot(expt)
 a_boxplot  ## ooo pretty boxplot look at the lines

## End(Not run)
```

`plot_cleaved` *Plot the average mass and expected intensity of a set of sequences given an enzyme.*

Description

This uses the cleaver package to generate a plot of expected intensities vs. weight for a list of protein sequences.

Usage

```
plot_cleaved(pep_sequences, enzyme = "trypsin", start = 600, end = 1500)
```

Arguments

`pep_sequences`	Set of protein sequences.
`enzyme`	One of the allowed enzymes for cleaver.
`start`	Limit the set of fragments from this point
`end`	to this point.

Value

List containing the distribution of weights and the associated plot.

`plot_corheat` *Make a heatmap.3 description of the correlation between samples.*

Description

Given a set of count tables and design, this will calculate the pairwise correlations and plot them as a heatmap. It attempts to standardize the inputs and eventual output.

Usage

```
plot_corheat(
  expt_data,
  expt_colors = NULL,
  expt_design = NULL,
  method = "pearson",
  expt_names = NULL,
  batch_row = "batch",
  plot_title = NULL,
  label_chars = 10,
  ...
)
```

Arguments

expt_data	Dataframe, expt, or expressionset to work with.
expt_colors	Color scheme for the samples, not needed if this is an expt.
expt_design	Design matrix describing the experiment, not needed if this is an expt.
method	Correlation statistic to use. (pearson, spearman, kendall, robust).
expt_names	Alternate names to use for the samples.
batch_row	Name of the design row used for 'batch' column colors.
label_chars	Limit on the number of label characters.
...	More options are wonderful!
title	Title for the plot.

Value

Gplots heatmap describing describing how the samples are clustering vis a vis pairwise correlation.

See Also

[grDevice] [gplot2::heatmap.2()]

Examples

```
## Not run:
 corheat_plot <- hpgl_corheat(expt = expt, method = "robust")

## End(Not run)
```

`plot_de_pvals` *Given a DE table with p-values, plot them.*

Description

Plot a multi-histogram containing (adjusted)p-values.

Usage

```
plot_de_pvals(
  combined_data,
  type = "limma",
  p_type = "both",
  columns = NULL,
  ...
)
```

Arguments

`combined_data`	Table to extract the values from.
`type`	If provided, extract the type_p and type_adjp columns.
`p_type`	Which type of pvalue to show (adjusted, raw, or all)?
`columns`	Otherwise, extract whatever columns are provided.
`...`	Arguments passed through to the histogram plotter

Details

The assumption of this plot is that the adjustment will significantly decrease the representation of genes in the 'highly significant' range of p-values. However, it is hoped that it will not utterly remove them.

Value

Multihistogram of the result.

See Also

[plot_histogram()]

plot_density *Create a density plot, showing the distribution of each column of data.*

Description

Density plots and boxplots are cousins and provide very similar views of data distributions. Some people like one, some the other. I think they are both colorful and fun!

Usage

```
plot_density(
  data,
  colors = NULL,
  expt_names = NULL,
  position = "identity",
  direct = TRUE,
  fill = NULL,
  title = NULL,
  scale = NULL,
  colors_by = "condition",
  label_chars = 10,
  ...
)
```

Arguments

data	Expt, expressionset, or data frame.
colors	Color scheme to use.
expt_names	Names of the samples.
position	How to place the lines, either let them overlap (identity), or stack them.
direct	Use direct.labels for labeling the plot?
fill	Fill the distributions? This might make the plot unreasonably colorful.
title	Title for the plot.
scale	Plot on the log scale?
colors_by	Factor for coloring the lines
label_chars	Maximum number of characters in sample names before abbreviation.
...	sometimes extra arguments might come from graph_metrics()

Value

ggplot2 density plot!

See Also

[ggplot2]

Examples

```
## Not run:
 funkytown <- plot_density(data)

## End(Not run)
```

`plot_disheat` *Make a heatmap.3 of the distances (euclidean by default) between samples.*

Description

Given a set of count tables and design, this will calculate the pairwise distances and plot them as a heatmap. It attempts to standardize the inputs and eventual output.

Usage

```
plot_disheat(
  expt_data,
  expt_colors = NULL,
  expt_design = NULL,
  method = "euclidean",
  expt_names = NULL,
  batch_row = "batch",
  plot_title = NULL,
  label_chars = 10,
  ...
)
```

Arguments

`expt_data`	Dataframe, expt, or expressionset to work with.
`expt_colors`	Color scheme (not needed if an expt is provided).
`expt_design`	Design matrix (not needed if an expt is provided).
`method`	Distance metric to use.
`expt_names`	Alternate names to use for the samples.
`batch_row`	Name of the design row used for 'batch' column colors.
`label_chars`	Limit on the number of label characters.
`...`	More parameters!
`title`	Title for the plot.

Value

a recordPlot() heatmap describing the distance between samples.

See Also

[gplots::heatmap.2()]

Examples

```
## Not run:
 disheat_plot = plot_disheat(expt = expt, method = "euclidean")

## End(Not run)
```

`plot_dist_scatter` *Make a scatter plot between two sets of numbers with a cheesy distance metric and some statistics of the two sets.*

Description

The distance metric should be codified and made more intelligent. Currently it creates a dataframe of distances which are absolute distances from each axis, multiplied by each other, summed by axis, then normalized against the maximum.

Usage

```
plot_dist_scatter(
  df,
  tooltip_data = NULL,
  gvis_filename = NULL,
  size = 2,
  xlab = NULL,
  ylab = NULL
)
```

Arguments

`df`	Dataframe likely containing two columns.
`tooltip_data`	Df of tooltip information for gvis graphs.
`gvis_filename`	Filename to write a fancy html graph.
`size`	Size of the dots.
`xlab`	x-axis label.
`ylab`	y-axis label.

Value

Ggplot2 scatter plot. This plot provides a "bird's eye" view of two data sets. This plot assumes the two data structures are not correlated, and so it calculates the median/mad of each axis and uses these to calculate a stupid, home-grown distance metric away from both medians. This distance metric is used to color dots which are presumed the therefore be interesting because they are far from 'normal.' This will make a fun clicky googleVis graph if requested.

See Also

[ggplot2::geom_point()] [plot_linear_scatter()]

Examples

```
## Not run:
 dist_scatter(lotsofnumbers_intwo_columns, tooltip_data = tooltip_dataframe,
                   gvis_filename = "html/fun_scatterplot.html")

## End(Not run)
```

---

plot_epitrochoid *Make epitrochoid plots!*

Description

7, 2, 6, 7 should give a pretty result.

Usage

```
plot_epitrochoid(
  radius_a = 7,
  radius_b = 2,
  dist_b = 6,
  revolutions = 7,
  increments = 6480
)
```

Arguments

radius_a	Radius of the major circle
radius_b	And the smaller circle.
dist_b	between b and the drawing point.
revolutions	How many times to revolve through the spirograph.
increments	How many dots to lay down while writing.

`plot_essentiality` *Plot the essentiality of a library as per DeJesus et al.*

Description

This provides a plot of the essentiality metrics 'zbar' with respect to gene. In my pipeline, I use their stand alone mh_ess and tn_hmm packages. The result files produced are named mh_ess-sequence_prefix-mapping_parameters_gene_tas_m_parameter.csv where sequence_prefix is the basename() of the input sequence file, mapping_parameters are a string describing the bowtie mapping used, and m_parameter is usually one of 1,2,4,8,16,32 and defines the lower limit of read depth to be considered useful by the mh_ess package. Thus, before using this, one may want to look at the result from tnseq_saturation() to see if there is a most-appropriate m_parameter. I think I should figure out a heuristic to choose the m, but I am not sure what it would be, perhaps the median of the hits summary?

Usage

```
plot_essentiality(
  file,
  order_by = "posterior_zbar",
  keep_esses = FALSE,
  min_sig = 0.0371,
  max_sig = 0.9902
)
```

Arguments

`file`	Result from the DeJesus essentiality package. I think this has been effectively replaced by their TRANSIT package.
`order_by`	What column to use when ordering the data?
`keep_esses`	Keep entries in the data which are 'S' meaning insufficient evidence.
`min_sig`	Minimal value below which a gene is deemed non-essential and above which it is uncertain.
`max_sig`	Maximum value above which a gene is deemed essential and below which it is uncertain.

Value

A couple of plots

See Also

[ggplot2]

`plot_fun_venn` *A quick wrapper around venneuler to help label stuff*

Description

venneuler makes pretty venn diagrams, but no labels!

Usage

```
plot_fun_venn(
  ones = c(),
  twos = c(),
  threes = c(),
  fours = c(),
  fives = c(),
  factor = 0.9
)
```

Arguments

`ones`	Character list of singletone categories
`twos`	Character list of doubletone categories
`threes`	Character list of tripletone categories
`fours`	Character list of quad categories
`fives`	Character list of quint categories
`factor`	Currently unused, but intended to change the radial distance to the label from the center of each circle.

Value

Two element list containing the venneuler data and the plot.

See Also

[venneuler]

`plot_goseq_pval` *Make a pvalue plot from goseq data.*

Description

With minor changes, it is possible to push the goseq results into a clusterProfiler-ish pvalue plot. This handles those changes and returns the ggplot results.

Usage

```
plot_goseq_pval(
  goterms,
  wrapped_width = 30,
  cutoff = 0.1,
  n = 30,
  mincat = 5,
  level = NULL,
  ...
)
```

Arguments

`goterms`	Some data from goseq!
`wrapped_width`	Number of characters before wrapping to help legibility.
`cutoff`	Pvalue cutoff for the plot.
`n`	How many groups to include?
`mincat`	Minimum size of the category for inclusion.
`level`	Levels of the ontology tree to use.
`...`	Arguments passed from simple_goseq()

Value

Plots!

See Also

[ggplot2]

`plot_gostats_pval` *Make a pvalue plot similar to that from clusterprofiler from gostats data.*

Description

clusterprofiler provides beautiful plots describing significantly overrepresented categories. This function attempts to expand the repetoire of data available to them to include data from gostats. The pval_plot function upon which this is based now has a bunch of new helpers now that I understand how the ontology trees work better, this should take advantage of that, but currently does not.

Usage

```
plot_gostats_pval(
  gs_result,
  wrapped_width = 20,
  cutoff = 0.1,
  n = 30,
  group_minsize = 5
)
```

Arguments

`gs_result`	Ontology search results.
`wrapped_width`	Make the text large enough to read.
`cutoff`	What is the maximum pvalue allowed?
`n`	How many groups to include in the plot?
`group_minsize`	Minimum group size before inclusion.

Value

Plots!

See Also

[ggplot2]

`plot_gprofiler_pval` *Make a pvalue plot from gprofiler data.*

Description

The p-value plots from clusterProfiler are pretty, this sets the gprofiler data into a format suitable for plotting in that fashion and returns the resulting plots of significant ontologies.

Usage

```
plot_gprofiler_pval(
  gp_result,
  wrapped_width = 30,
  cutoff = 0.1,
  n = 30,
  group_minsize = 5,
  scorer = "recall",
  ...
)
```

Arguments

`gp_result`	Some data from gProfiler.
`wrapped_width`	Maximum width of the text names.
`cutoff`	P-value cutoff for the plots.
`n`	Maximum number of ontologies to include.
`group_minsize`	Minimum ontology group size to include.
`scorer`	Which column to use for scoring the data.
`...`	Options I might pass from other functions are dropped into arglist.

Value

List of MF/BP/CC pvalue plots.

See Also

[ggplot2]

`plot_heatmap` *Make a heatmap.3 plot, does the work for plot_disheat and plot_corheat.*

Description

This does what is says on the tin. Sets the colors for correlation or distance heatmaps, handles the calculation of the relevant metrics, and plots the heatmap.

Usage

```
plot_heatmap(
  expt_data,
  expt_colors = NULL,
  expt_design = NULL,
  method = "pearson",
  expt_names = NULL,
  type = "correlation",
  batch_row = "batch",
  plot_title = NULL,
  label_chars = 10,
  ...
)
```

Arguments

`expt_data`	Dataframe, expt, or expressionset to work with.
`expt_colors`	Color scheme for the samples.
`expt_design`	Design matrix describing the experiment vis a vis conditions and batches.
`method`	Distance or correlation metric to use.
`expt_names`	Alternate names to use for the samples.
`type`	Defines the use of correlation, distance, or sample heatmap.
`batch_row`	Name of the design row used for 'batch' column colors.
`label_chars`	Limit on the number of label characters.
`...`	I like elipses!
`title`	Title for the plot.

Value

a recordPlot() heatmap describing the distance between samples.

See Also

[gplots::heatmap.2()]

`plot_heatplus` *Potential replacement for heatmap.2 based plots.*

Description

Heatplus is an interesting tool, I have a few examples of using it and intend to include them here.

Usage

```
plot_heatplus(
  expt,
  type = "correlation",
  method = "pearson",
  annot_columns = "batch",
  annot_rows = "condition",
  cutoff = 1,
  cluster_colors = NULL,
  scale = "none",
  cluster_width = 2,
  cluster_function = NULL,
  heatmap_colors = NULL
)
```

Arguments

`expt`	Experiment to try plotting.
`type`	What comparison method to use on the data (distance or correlation)?
`method`	What distance/correlation method to perform?
`annot_columns`	Set of columns to include as terminal columns next to the heatmap.
`annot_rows`	Set of columns to include as terminal rows below the heatmap.
`cutoff`	Cutoff used to define color changes in the annotated clustering.
`cluster_colors`	Choose colors for the clustering?
`scale`	Scale the heatmap colors?
`cluster_width`	How much space to include between clustering?
`cluster_function`	Choose an alternate clustering function than hclust()?
`heatmap_colors`	Choose your own heatmap cluster palette?

Value

List containing the returned heatmap along with some parameters used to create it.

See Also

[Heatplus] [fastcluster]

plot_histogram *Make a pretty histogram of something.*

Description

A shortcut to make a ggplot2 histogram which makes an attempt to set reasonable bin widths and set the scale to log if that seems a good idea.

Usage

```
plot_histogram(
  df,
  binwidth = NULL,
  log = FALSE,
  bins = 500,
  adjust = 1,
  fillcolor = "darkgrey",
  color = "black"
)
```

Arguments

df	Dataframe of lots of pretty numbers.
binwidth	Width of the bins for the histogram.
log	Replot on the log scale?
bins	Number of bins for the histogram.
adjust	The prettification parameter in the ggplot2 density.
fillcolor	Change the fill colors of the plotted elements?
color	Change the color of the lines of the plotted elements?

Value

Ggplot histogram.

See Also

[ggplot2]

Examples

```
## Not run:
 kittytime = plot_histogram(df)

## End(Not run)
```

plot_hypotrochoid *Make hypotrochoid plots!*

Description

3,7,1 should give the classic 7 leaf clover

Usage

```
plot_hypotrochoid(
  radius_a = 3,
  radius_b = 7,
  dist_b = 1,
  revolutions = 7,
  increments = 6480
)
```

Arguments

radius_a	Radius of the major circle
radius_b	And the smaller circle.
dist_b	between b and the drawing point.
revolutions	How many times to revolve through the spirograph.
increments	How many dots to lay down while writing.

plot_intensity_mz *Plot mzXML peak intensities with respect to m/z.*

Description

I want to have a pretty plot of peak intensities and m/z. The plot provided by this function is interesting, but suffers from some oddities; notably that it does not currently separate the MS1 and MS2 data.

Usage

```
plot_intensity_mz(
  mzxml_data,
  loess = FALSE,
  alpha = 0.5,
  ms1 = TRUE,
  ms2 = TRUE,
  x_scale = NULL,
  y_scale = NULL,
  ...
)
```

Arguments

mzxml_data	The data structure from extract_mzxml or whatever it is.
loess	Do a loess smoothing from which to extract a function describing the data? This is terribly slow, and in the data I have examined so far, not very helpful, so it is FALSE by default.
alpha	Make the plotted dots opaque to this degree.
ms1	Include MS1 data in the plot?
ms2	Include MS2 data in the plot?
x_scale	Plot the x-axis on a non linear scale?
y_scale	Plot the y-axis on a non linear scale?
...	Extra arguments for the downstream functions.

Value

ggplot2 goodness.

---

plot_legend *Scab the legend from a PCA plot and print it alone*

Description

This way I can have a legend object to move about.

Usage

```
plot_legend(stuff)
```

Arguments

stuff	This can take either a ggplot2 pca plot or some data from which to make one.

Value

A legend!

plot_libsize *Make a ggplot graph of library sizes.*

Description

It is often useful to have a quick view of which samples have more/fewer reads. This does that and maintains one's favorite color scheme and tries to make it pretty!

Usage

```
plot_libsize(
  data,
  condition = NULL,
  colors = NULL,
  text = TRUE,
  order = NULL,
  title = NULL,
  yscale = NULL,
  expt_names = NULL,
  label_chars = 10,
  ...
)
```

Arguments

data	Expt, dataframe, or expressionset of samples.
condition	Vector of sample condition names.
colors	Color scheme if the data is not an expt.
text	Add the numeric values inside the top of the bars of the plot?
order	Explicitly set the order of samples in the plot?
title	Title for the plot.
yscale	Whether or not to log10 the y-axis.
expt_names	Design column or manually selected names for printing sample names.
label_chars	Maximum number of characters before abbreviating sample names.
...	More parameters for your good time!

Value

a ggplot2 bar plot of every sample's size

See Also

[ggplot2] [prettyNum] [plot_sample_bars()]

Examples

```
## Not run:
 libsize_plot <- plot_libsize(expt = expt)
 libsize_plot  ## ooo pretty bargraph

## End(Not run)
```

`plot_libsize_prepost` *Visualize genes observed before/after filtering.*

Description

Thanks to Sandra Correia for this! This function attempts to represent the change in the number of genes which are well/poorly represented in the data before and after performing a low-count filter.

Usage

```
plot_libsize_prepost(expt, low_limit = 2, filter = TRUE, ...)
```

Arguments

`expt`	Input expressionset.
`low_limit`	Threshold to define 'low-representation.'
`filter`	Method used to low-count filter the data.
`...`	Extra arbitrary arguments to pass to normalize_expt()

Value

Bar plot showing the number of genes below the low_limit before and after filtering the data.

See Also

[plot_libsize()] [filter_counts()]

plot_linear_scatter *Make a scatter plot between two groups with a linear model superimposed and some supporting statistics.*

Description

Make a scatter plot between two groups with a linear model superimposed and some supporting statistics.

Usage

```
plot_linear_scatter(
  df,
  tooltip_data = NULL,
  gvis_filename = NULL,
  cormethod = "pearson",
  size = 2,
  loess = FALSE,
  identity = FALSE,
  gvis_trendline = NULL,
  z_lines = FALSE,
  first = NULL,
  second = NULL,
  base_url = NULL,
  pretty_colors = TRUE,
  xlab = NULL,
  ylab = NULL,
  color_high = NULL,
  color_low = NULL,
  alpha = 0.4,
  ...
)
```

Arguments

df	Dataframe likely containing two columns.
tooltip_data	Df of tooltip information for gvis graphs.
gvis_filename	Filename to write a fancy html graph.
cormethod	What type of correlation to check?
size	Size of the dots on the plot.
loess	Add a loess estimation?
identity	Add the identity line?
gvis_trendline	Add a trendline to the gvis plot? There are a couple possible types, I think linear is the most common.
z_lines	Include lines defining the z-score boundaries.

first	First column to plot.
second	Second column to plot.
base_url	Base url to add to the plot.
pretty_colors	Colors!
xlab	Alternate x-axis label.
ylab	Alternate x-axis label.
color_high	Chosen color for points significantly above the mean.
color_low	Chosen color for points significantly below the mean.
alpha	Choose an alpha channel to define how see-through the dots are.
...	Extra args likely used for choosing significant genes.

Value

List including a ggplot2 scatter plot and some histograms. This plot provides a "bird's eye" view of two data sets. This plot assumes a (potential) linear correlation between the data, so it calculates the correlation between them. It then calculates and plots a robust linear model of the data using an 'SMDM' estimator (which I don't remember how to describe, just that the document I was reading said it is good). The median/mad of each axis is calculated and plotted as well. The distance from the linear model is finally used to color the dots on the plot. Histograms of each axis are plotted separately and then together under a single cdf to allow tests of distribution similarity. This will make a fun clicky googleVis graph if requested.

See Also

[robust] [stats] [ggplot2] [robust::lmRob] [stats::weights] [plot_histogram()]

Examples

```
## Not run:
 plot_linear_scatter(lotsofnumbers_intwo_columns, tooltip_data = tooltip_dataframe,
                     gvis_filename = "html/fun_scatterplot.html")

## End(Not run)
```

---

plot_ma_de *Make a pretty MA plot from one of limma, deseq, edger, or basic.*

Description

Because I can never remember, the following from wikipedia: "An MA plot is an application of a Bland-Altman plot for visual representation of two channel DNA microarray gene expression data which has been transformed onto the M (log ratios) and A (mean average) scale."

Usage

```
plot_ma_de(
  table,
  expr_col = "logCPM",
  fc_col = "logFC",
  p_col = "qvalue",
  p = 0.05,
  alpha = 0.4,
  logfc = 1,
  label_numbers = TRUE,
  size = 2,
  tooltip_data = NULL,
  gvis_filename = NULL,
  shapes = TRUE,
  invert = FALSE,
  label = NULL,
  ...
)
```

Arguments

table	Df of linear-modelling, normalized counts by sample-type,
expr_col	Column showing the average expression across genes.
fc_col	Column showing the logFC for each gene.
p_col	Column containing the relevant p values.
p	Name of the pvalue column to use for cutoffs.
alpha	How transparent to make the dots.
logfc	Fold change cutoff.
label_numbers	Show how many genes were 'significant', 'up', and 'down'?
size	How big are the dots?
tooltip_data	Df of tooltip information for gvis.
gvis_filename	Filename to write a fancy html graph.
shapes	Provide different shapes for up/down/etc?
invert	Invert the ma plot?
label	Label the top/bottom n logFC values?
...	More options for you

Value

ggplot2 MA scatter plot. This is defined as the rowmeans of the normalized counts by type across all sample types on the x axis, and the log fold change between conditions on the y-axis. Dots are colored depending on if they are 'significant.' This will make a fun clicky googleVis graph if requested.

See Also

[limma_pairwise()] [deseq_pairwise()] [edger_pairwise()] [basic_pairwise()]

Examples

```
 ## Not run:
  plot_ma(voomed_data, table, gvis_filename = "html/fun_ma_plot.html")
  ## Currently this assumes that a variant of toptable was used which
  ## gives adjusted p-values.  This is not always the case and I should
  ## check for that, but I have not yet.

## End(Not run)
```

`plot_multihistogram` *Make a pretty histogram of multiple datasets.*

Description

If there are multiple data sets, it might be useful to plot them on a histogram together and look at the t.test results between distributions.

Usage

```
plot_multihistogram(
  data,
  log = FALSE,
  binwidth = NULL,
  bins = NULL,
  colors = NULL
)
```

Arguments

`data`	Dataframe of lots of pretty numbers, this also accepts lists.
`log`	Plot the data on the log scale?
`binwidth`	Set a static bin width with an unknown # of bins? If neither of these are provided, then bins is set to 500, if both are provided, then bins wins.
`bins`	Set a static # of bins of an unknown width?
`colors`	Change the default colors of the densities?

Value

List of the ggplot histogram and some statistics describing the distributions.

See Also

[stats::pairwise.t.test()] [ggplot2]

Examples

```
## Not run:
 kittytime = plot_multihistogram(df)

## End(Not run)
```

`plot_multiplot` *Make a grid of plots.*

Description

Make a grid of plots.

Usage

```
plot_multiplot(plots, file, cols = NULL, layout = NULL)
```

Arguments

`plots`	List of plots
`file`	File to write to
`cols`	Number of columns in the grid
`layout`	Set the layout specifically

Value

a multiplot!

`plot_mzxml_boxplot` *Make a boxplot out of some of the various data available in the mzxml data.*

Description

There are a few data within the mzXML raw data files which are likely candidates for simple summary via a boxplot/densityplot/whatever. For the moment I am just doing boxplots of a few of them. Since my metadata extractor dumps a couple of tables, one must choose a desired table and column from it to plot.

Usage

```
plot_mzxml_boxplot(
  mzxml_data,
  table = "precursors",
  column = "precursorintensity",
  violin = FALSE,
  names = NULL,
  title = NULL,
  scale = NULL,
  ...
)
```

Arguments

mzxml_data	Provide a list of mzxml data, one element for each sample.
table	One of precursors or scans
column	One of the columns from the table; if 'scans' is chosen, then likely choices include: 'peakscount', 'basepeakmz', 'basepeakintensity'; if 'precursors' is chosen, then the only likely choice for the moment is 'precursorintensity'.
violin	Print the samples as violins rather than only box/whiskers?
names	Names for the x-axis of the plot.
title	Title the plot?
scale	Put the data on a specific scale?
...	Further arguments, presumably for colors or some such.

Value

Boxplot describing the requested column of data in the set of mzXML files.

---

plot_nonzero *Make a ggplot graph of the number of non-zero genes by sample.*

Description

This puts the number of genes with > 0 hits on the y-axis and CPM on the x-axis. Made by Ramzi Temanni <temanni at umd dot edu>.

Usage

```
plot_nonzero(
  data,
  design = NULL,
  colors = NULL,
  plot_labels = NULL,
  expt_names = NULL,
```

```
  label_chars = 10,
  plot_legend = FALSE,
  title = NULL,
  ...
)
```

Arguments

data	Expt, expressionset, or dataframe.
design	Eesign matrix.
colors	Color scheme.
plot_labels	How do you want to label the graph? 'fancy' will use directlabels() to try to match the labels with the positions without overlapping anything else will just stick them on a 45' offset next to the graphed point.
expt_names	Column or character list of preferred sample names.
label_chars	How many characters for sample names before abbreviation.
plot_legend	Print a legend for this plot?
title	Add a title?
...	rawr!

Value

a ggplot2 plot of the number of non-zero genes with respect to each library's CPM.

See Also

[ggplot2]

Examples

```
## Not run:
 nonzero_plot <- plot_nonzero(expt = expt)

## End(Not run)
```

---

plot_num_siggenes *Given a DE table with fold changes and p-values, show how 'significant' changes with changing cutoffs.*

Description

Sometimes one might want to know how many genes are deemed significant while shifting the bars which define significant. This provides that metrics as a set of tables of numbers of significant up/down genes when p-value is held constant, as well as number when fold-change is held constant.

Usage

```
plot_num_siggenes(
  table,
  methods = c("limma", "edger", "deseq", "ebseq"),
  bins = 100,
  constant_p = 0.05,
  constant_fc = 0
)
```

Arguments

table	DE table to examine.
methods	List of methods to use when plotting.
bins	Number of incremental changes in p-value/FC to examine.
constant_p	When plotting changing FC, where should the p-value be held?
constant_fc	When plotting changing p, where should the FC be held?

Value

Plots and dataframes describing the changing definition of 'significant.'

See Also

[ggplot2]

Examples

```
## Not run:
 pairwise_result <- all_pairwise(expt)
 crazy_sigplots <- plot_num_siggenes(pairwise_result)

## End(Not run)
```

---

plot_ontpval *Make a pvalue plot from a df of IDs, scores, and p-values.*

Description

This function seeks to make generating pretty pvalue plots as shown by clusterprofiler easier.

Usage

```
plot_ontpval(
  df,
  ontology = "MF",
  fontsize = 14,
  plot_title = NULL,
  numerator = NULL,
  denominator = NULL
)
```

Arguments

df	Some data from topgo/goseq/clusterprofiler.
ontology	Ontology to plot (MF,BP,CC).
fontsize	Fiddling with the font size may make some plots more readable.
numerator	Column used for printing a ratio of genes/category.
denominator	Column used for printing a ratio of genes/category.

Value

Ggplot2 plot of pvalues vs. ontology.

See Also

[ggplot2]

---

plot_pairwise_ma *Plot all pairwise MA plots in an experiment.*

Description

Use affy's ma.plot() on every pair of columns in a data set to help diagnose problematic samples.

Usage

```
plot_pairwise_ma(data, log = NULL, ...)
```

Arguments

data	Expt expressionset or data frame.
log	Is the data in log format?
...	Options are good and passed to arglist().

Value

List of affy::maplots

See Also

[affy::ma.plot()]

Examples

```
## Not run:
 ma_plots = plot_pairwise_ma(expt = some_expt)

## End(Not run)
```

---

plot_pca *Make a PCA plot describing the samples' clustering.*

Description

Make a PCA plot describing the samples' clustering.

Usage

```
plot_pca(
  data,
  design = NULL,
  plot_colors = NULL,
  plot_title = TRUE,
  plot_size = 5,
  plot_alpha = NULL,
  plot_labels = NULL,
  size_column = NULL,
  pc_method = "fast_svd",
  x_pc = 1,
  y_pc = 2,
  max_overlaps = 20,
  num_pc = NULL,
  expt_names = NULL,
  label_chars = 10,
  ...
)
```

Arguments

data	an expt set of samples.
design	a design matrix and.
plot_colors	a color scheme.
plot_title	a title for the plot.
plot_size	size for the glyphs on the plot.
plot_alpha	Add an alpha channel to the dots?

plot_labels	add labels? Also, what type? FALSE, "default", or "fancy".
size_column	use an experimental factor to size the glyphs of the plot
pc_method	how to extract the components? (svd
x_pc	Component to put on the x axis.
y_pc	Component to put on the y axis.
max_overlaps	Passed to ggrepel.
num_pc	How many components to calculate, default to the number of rows in the metadata.
expt_names	Column or character list of preferred sample names.
label_chars	Maximum number of characters before abbreviating sample names.
...	Arguments passed through to the pca implementations and plotter.

Value

a list containing the following (this is currently wrong)

1. pca = the result of fast.svd()
2. plot = ggplot2 pca_plot describing the principle component analysis of the samples.
3. table = a table of the PCA plot data
4. res = a table of the PCA res data
5. variance = a table of the PCA plot variance

See Also

[corpcor] [Rtsne] [uwot] [fastICA] [pcaMethods] [plot_pcs()]

Examples

```
## Not run:
 pca_plot <- plot_pca(expt = expt)
 pca_plot

## End(Not run)
```

---

plot_pca_genes *Make a PC plot describing the gene' clustering.*

Description

Make a PC plot describing the gene' clustering.

Usage

```
plot_pca_genes(
  data,
  design = NULL,
  plot_colors = NULL,
  plot_title = NULL,
  plot_size = 2,
  plot_alpha = 0.4,
  plot_labels = FALSE,
  size_column = NULL,
  pc_method = "fast_svd",
  x_pc = 1,
  y_pc = 2,
  label_column = "description",
  num_pc = 2,
  expt_names = NULL,
  label_chars = 10,
  ...
)
```

Arguments

data	an expt set of samples.
design	a design matrix and.
plot_colors	a color scheme.
plot_title	a title for the plot.
plot_size	size for the glyphs on the plot.
plot_alpha	Add an alpha channel to the dots?
plot_labels	add labels? Also, what type? FALSE, "default", or "fancy".
size_column	use an experimental factor to size the glyphs of the plot
pc_method	how to extract the components? (svd
x_pc	Component to put on the x axis.
y_pc	Component to put on the y axis.
label_column	Which metadata column to use for labels.
num_pc	How many components to calculate, default to the number of rows in the metadata.
expt_names	Column or character list of preferred sample names.
label_chars	Maximum number of characters before abbreviating sample names.
...	Arguments passed through to the pca implementations and plotter.

Value

a list containing the following (this is currently wrong)

1. pca = the result of fast.svd()
2. plot = ggplot2 pca_plot describing the principle component analysis of the samples.
3. table = a table of the PCA plot data
4. res = a table of the PCA res data
5. variance = a table of the PCA plot variance

See Also

[plot_pcs()]

Examples

```
## Not run:
 pca_plot <- plot_pca(expt = expt)
 pca_plot

## End(Not run)
```

`plot_pcfactor` *make a dotplot of some categorised factors and a set of principle components.*

Description

This should make a quick df of the factors and PCs and plot them.

Usage

```
plot_pcfactor(pc_df, expt, exp_factor = "condition", component = "PC1")
```

Arguments

`pc_df`	Df of principle components.
`expt`	Expt containing counts, metadata, etc.
`exp_factor`	Experimental factor to compare against.
`component`	Which principal component to compare against?

Value

Plot of principle component vs factors in the data

See Also

[ggplot2]

Examples

```
## Not run:
 estimate_vs_pcs <- plot_pcfactor(pcs, times)

## End(Not run)
```

`plot_pcload` *Print a plot of the top-n most PC loaded genes.*

Description

Sometimes it is nice to know what is happening with the genes which have the greatest effect on a given principal component. This function provides that.

Usage

```
plot_pcload(expt, genes = 40, desired_pc = 1, which_scores = "high", ...)
```

Arguments

`expt`	Input expressionset.
`genes`	How many genes to observe?
`desired_pc`	Which component to examine?
`which_scores`	Perhaps one wishes to see the least-important genes, if so set this to low.
`...`	Extra arguments passed, currently to nothing.

Value

List containing an expressionset of the subset and a plot of their expression.

See Also

[plot_sample_heatmap()]

plot_pcs *Plot principle components and make them pretty.*

Description

All the various dimension reduction methods share some of their end-results in common. Most notably a table of putative components which may be plotted against one another so that one may stare at the screen and look for clustering among the samples/genes/whatever. This function attempts to make that process as simple and pretty as possible.

Usage

```
plot_pcs(
  pca_data,
  first = "PC1",
  second = "PC2",
  variances = NULL,
  design = NULL,
  plot_title = TRUE,
  plot_labels = NULL,
  x_label = NULL,
  y_label = NULL,
  plot_size = 5,
  outlines = TRUE,
  plot_alpha = NULL,
  size_column = NULL,
  rug = TRUE,
  max_overlaps = 20,
  cis = c(0.95, 0.9),
  ...
)
```

Arguments

pca_data	Dataframe of principle components PC1 .. PCN with any other arbitrary information.
first	Principle component PCx to put on the x axis.
second	Principle component PCy to put on the y axis.
variances	List of the percent variance explained by each component.
design	Experimental design with condition batch factors.
plot_title	Title for the plot.
plot_labels	Parameter for the labels on the plot.
x_label	Label for the x-axis.
y_label	Label for the y-axis.

plot_size	Size of the dots on the plot
outlines	Add a black outline to the plotted shapes?
plot_alpha	Add an alpha channel to the dots?
size_column	Experimental factor to use for sizing the glyphs
rug	Include the rugs on the sides of the plot?
cis	What (if any) confidence intervals to include.
...	Extra arguments dropped into arglist

Value

gplot2 PCA plot

See Also

[directlabels] [ggplot2] [plot_pca] [pca_information]

Examples

```
## Not run:
 pca_plot = plot_pcs(pca_data, first = "PC2", second = "PC4", design = expt$design)

## End(Not run)
```

---

plot_pct_kept *Make a ggplot graph of the percentage/number of reads kept/removed.*

Description

The function expt_exclude_genes() removes some portion of the original reads. This function will make it possible to see what is left.

Usage

```
plot_pct_kept(
  data,
  row = "pct_kept",
  condition = NULL,
  colors = NULL,
  names = NULL,
  text = TRUE,
  title = NULL,
  yscale = NULL,
  ...
)
```

Arguments

data	Dataframe of the material remaining, usually expt$summary_table
row	Row name to plot.
condition	Vector of sample condition names.
colors	Color scheme if the data is not an expt.
names	Alternate names for the x-axis.
text	Add the numeric values inside the top of the bars of the plot?
title	Title for the plot.
yscale	Whether or not to log10 the y-axis.
...	More parameters for your good time!

Value

a ggplot2 bar plot of every sample's size

See Also

[plot_sample_bars()]

Examples

```
## Not run:
 kept_plot <- plot_pct_kept(expt_removed)
 kept_plot  ## ooo pretty bargraph

## End(Not run)
```

---

plot_peprophet_data *Plot some data from the result of extract_peprophet_data()*

Description

extract_peprophet_data() provides a ridiculously large data table of a comet result after processing by RefreshParser and xinteract/peptideProphet. This table has some 37-ish columns and I am not entirely certain which ones are useful as diagnostics of the data. I chose a few and made options to pull some/most of the rest. Lets play!

Usage

```
plot_peprophet_data(
  table,
  xaxis = "precursor_neutral_mass",
  xscale = NULL,
  yaxis = "num_matched_ions",
  yscale = NULL,
  size_column = "prophet_probability",
  ...
)
```

Arguments

table	Big honking data table from extract_peprophet_data()
xaxis	Column to plot on the x-axis
xscale	Change the scale of the x-axis?
yaxis	guess!
yscale	Change the scale of the y-axis?
size_column	Use a column for scaling the sizes of dots in the plot?
...	extra options which may be used for plotting.

Value

a plot!

---

plot_pyprophet_counts *Count some aspect(s) of the pyprophet data and plot them.*

Description

This function is mostly redundant with the plot_mzxml_boxplot above. Unfortunately, the two data types are subtly different enough that I felt it not worth while to generalize the functions.

Usage

```
plot_pyprophet_counts(
  pyprophet_data,
  type = "count",
  keep_real = TRUE,
  keep_decoys = TRUE,
  expt_names = NULL,
  label_chars = 10,
  title = NULL,
  scale = NULL,
  ...
)
```

Arguments

pyprophet_data	List containing the pyprophet results.
type	What to count/plot?
keep_real	Do we keep the real data when plotting the data? (perhaps we only want the decoys)
keep_decoys	Do we keep the decoys when plotting the data?
expt_names	Names for the x-axis of the plot.

label_chars	Maximum number of characters before abbreviating sample names.
title	Title the plot?
scale	Put the data on a specific scale?
...	Further arguments, presumably for colors or some such.

Value

Boxplot describing the desired column from the data.

`plot_pyprophet_distribution` *Make a boxplot out of some of the various data available in the pyprophet data.*

Description

This function is mostly redundant with the plot_mzxml_boxplot above. Unfortunately, the two data types are subtly different enough that I felt it not worth while to generalize the functions.

Usage

```
plot_pyprophet_distribution(
  pyprophet_data,
  column = "delta_rt",
  keep_real = TRUE,
  keep_decoys = TRUE,
  expt_names = NULL,
  label_chars = 10,
  title = NULL,
  scale = NULL,
  ...
)
```

Arguments

pyprophet_data	List containing the pyprophet results.
column	What column of the pyprophet scored data to plot?
keep_real	Do we keep the real data when plotting the data? (perhaps we only want the decoys)
keep_decoys	Do we keep the decoys when plotting the data?
expt_names	Names for the x-axis of the plot.
label_chars	Maximum number of characters before abbreviating sample names.
title	Title the plot?
scale	Put the data on a specific scale?
...	Further arguments, presumably for colors or some such.

Value

Boxplot describing the desired column from the data.

`plot_pyprophet_points` *Plot some data from the result of extract_pyprophet_data()*

Description

extract_pyprophet_data() provides a ridiculously large data table of a scored openswath data after processing by pyprophet.

Usage

```
plot_pyprophet_points(
  pyprophet_data,
  xaxis = "mass",
  xscale = NULL,
  sample = NULL,
  yaxis = "leftwidth",
  yscale = NULL,
  alpha = 0.4,
  color_by = "sample",
  legend = TRUE,
  size_column = "mscore",
  rug = TRUE,
  ...
)
```

Arguments

`pyprophet_data`	List of pyprophet data, one element for each sample, taken from extract_peprophet_data()
`xaxis`	Column to plot on the x-axis
`xscale`	Change the scale of the x-axis?
`sample`	Which sample(s) to include?
`yaxis`	guess!
`yscale`	Change the scale of the y-axis?
`alpha`	How see-through to make the dots?
`color_by`	Change the colors of the points either by sample or condition?
`legend`	Include a legend of samples?
`size_column`	Use a column for scaling the sizes of dots in the plot?
`rug`	Add a distribution rug to the axes?
`...`	extra options which may be used for plotting.

Value

a plot!

plot_pyprophet_protein *Read data from pyprophet and plot columns from it.*

Description

More proteomics diagnostics! Now that I am looking more closely, I think this should be folded into plot_pyprophet_distribution().

Usage

```
plot_pyprophet_protein(
  pyprophet_data,
  column = "intensity",
  keep_real = TRUE,
  keep_decoys = FALSE,
  expt_names = NULL,
  label_chars = 10,
  protein = NULL,
  title = NULL,
  scale = NULL,
  legend = NULL,
  order_by = "condition",
  show_all = TRUE,
  ...
)
```

Arguments

pyprophet_data	Data from extract_pyprophet_data()
column	Chosen column to plot.
keep_real	FIXME: This should be changed to something like 'data_type' here and in plot_pyprophet_distribution.
keep_decoys	Do we keep the decoys when plotting the data?
expt_names	Names for the x-axis of the plot.
label_chars	Maximum number of characters before abbreviating sample names.
protein	chosen protein(s) to plot.
title	Title the plot?
scale	Put the data on a specific scale?
legend	Include the legend?
order_by	Reorder the samples by some factor, presumably condition.
show_all	Skip samples for which no observations were made.
...	Further arguments, presumably for colors or some such.

Value

Boxplot describing the desired column from the data.

`plot_pyprophet_xy` *Invoked plot_pyprophet_counts() twice, once for the x-axis, and once for the y.*

Description

Then plot the result, hopefully adding some new insights into the state of the post-pyprophet results. By default, this puts the number of identifications (number of rows) on the x-axis for each sample, and the sum of intensities on the y. Currently missing is the ability to change this from sum to mean/median/etc. That should trivially be possible via the addition of arguments for the various functions of interest.

Usage

```
plot_pyprophet_xy(
  pyprophet_data,
  keep_real = TRUE,
  size = 6,
  label_size = 4,
  keep_decoys = TRUE,
  expt_names = NULL,
  label_chars = 10,
  x_type = "count",
  y_type = "intensity",
  title = NULL,
  scale = NULL,
  ...
)
```

Arguments

`pyprophet_data`	List of pyprophet matrices by sample.
`keep_real`	Use the real identifications (as opposed to the decoys)?
`size`	Size of the glyphs used in the plot.
`label_size`	Set the label sizes.
`keep_decoys`	Use the decoy identifications (vs. the real)?
`expt_names`	Manually change the labels to some other column than sample.
`label_chars`	Maximum number of characters in the label before shortening.
`x_type`	Column in the data to put on the x-axis.
`y_type`	Column in the data to put on the y-axis.
`title`	Plot title.

scale	Put the data onto the log scale?
...	Extra arguments passed along.

`plot_qq_all` *Quantile/quantile comparison of the mean of all samples vs. each sample.*

Description

This allows one to visualize all individual data columns against the mean of all columns of data in order to see if any one is significantly different than the cloud.

Usage

```
plot_qq_all(data, labels = "short", ...)
```

Arguments

data	Expressionset, expt, or dataframe of samples.
labels	What kind of labels to print?
...	Arguments passed presumably from graph_metrics().

Value

List containing: logs = a recordPlot() of the pairwise log qq plots. ratios = a recordPlot() of the pairwise ratio qq plots. means = a table of the median values of all the summaries of the qq plots.

See Also

[Biobase]

`plot_rmats` *Given some psi and tpm data from rMATS, make a pretty plot!*

Description

This should take either a dataframe or filename for the psi data from rMATS. This was mostly copy/pasted from plot_suppa().

Usage

```
plot_rmats(
  se = NULL,
  a5ss = NULL,
  a3ss = NULL,
  mxe = NULL,
  ri = NULL,
  sig_threshold = 0.05,
  dpsi_threshold = 0.7,
  label_type = NULL,
  alpha = 0.7
)
```

Arguments

se	Table of skipped exon data from rmats.
a5ss	Table of alternate 5p exons.
a3ss	Table of alternate 3p exons.
mxe	Table of alternate exons.
ri	Table of retained introns.
sig_threshold	Use this significance threshold.
dpsi_threshold	Use a delta threshold.
label_type	Choose a type of event to label.
alpha	How see-through should the points be in the plot?

Value

List containing the plot and some of the requisite data.

See Also

[plot_supps()]

Examples

```
 ## Not run:
 rmats_plot <- plot_rmats(se_table, a5_table, a3_table)

## End(Not run)
```

`plot_rpm` *Make relatively pretty bar plots of coverage in a genome.*

Description

This was written for ribosome profiling coverage / gene. It should however, work for any data with little or no modification, it was also written when I was first learning R and when I look at it now I see a few obvious places which can use improvement.

Usage

```
plot_rpm(
  input,
  workdir = "images",
  output = "01.svg",
  name = "LmjF.01.0010",
  start = 1000,
  end = 2000,
  strand = 1,
  padding = 100
)
```

Arguments

`input`	Coverage / position filename.
`workdir`	Where to put the resulting images.
`output`	Output image filename.
`name`	Gene name to print at the bottom of the plot.
`start`	Relative to 0, where is the gene's start codon.
`end`	Relative to 0, where is the gene's stop codon.
`strand`	Is this on the + or - strand? (+1/-1)
`padding`	How much space to provide on the sides?

Value

coverage plot surrounging the ORF of interest

See Also

[ggplot2]

plot_sample_bars *The actual library size plotter.*

Description

This makes a ggplot2 plot of library sizes.

Usage

```
plot_sample_bars(
  sample_df,
  condition = NULL,
  colors = NULL,
  integerp = FALSE,
  order = NULL,
  text = TRUE,
  title = NULL,
  yscale = NULL,
  ...
)
```

Arguments

sample_df	Expt, dataframe, or expressionset of samples.
condition	Vector of sample condition names.
colors	Color scheme if the data is not an expt.
integerp	Is this comprised of integer values?
order	Explicitly set the order of samples in the plot?
text	Add the numeric values inside the top of the bars of the plot?
title	Title for the plot.
yscale	Whether or not to log10 the y-axis.

plot_sample_cvheatmap *An experiment to see if I can visualize the genes with the highest variance.*

Description

An experiment to see if I can visualize the genes with the highest variance.

Usage

```
plot_sample_cvheatmap(
  expt,
  fun = "mean",
  fact = "condition",
  row_label = NA,
  title = NULL,
  Rowv = TRUE,
  Colv = TRUE,
  label_chars = 10,
  dendrogram = "column",
  min_delta = 0.5,
  x_factor = 1,
  y_factor = 2,
  min_cvsd = NULL,
  cv_min = 1,
  cv_max = Inf,
  remove_equal = TRUE
)
```

Arguments

expt	ExpressionSet
fun	mean or median
fact	Which factor to slice/dice the data?
row_label	Label the rows?
title	Title for the plot
Rowv	Row vs (yeah I forgot what this does.)
Colv	Col vs
label_chars	Maximum number of characters in the sample IDs.
dendrogram	Make a tree of the samples?
min_delta	Minimum delta value for filtering
x_factor	When plotting two factors against each other, which is x?
y_factor	When plotting two factors against each other, which is y?
cv_min	Minimum cv to examine (I think this should be slightly lower)
cv_max	Maximum cV to examine (I think this should be limited to ~ 0.7?)
remove_equal	Filter uninteresting genes.

`plot_sample_heatmap` *Make a heatmap.3 description of the similarity of the genes among samples.*

Description

Sometimes you just want to see how the genes of an experiment are related to each other. This can handle that. These heatmap functions should probably be replaced with neatmaps or heatplus or whatever it is, as the annotation dataframes in them are pretty awesome.

Usage

```
plot_sample_heatmap(
  data,
  colors = NULL,
  design = NULL,
  expt_names = NULL,
  dendrogram = "column",
  row_label = NA,
  title = NULL,
  Rowv = TRUE,
  Colv = TRUE,
  label_chars = 10,
  filter = TRUE,
  ...
)
```

Arguments

`data`	Expt/expressionset/dataframe set of samples.
`colors`	Color scheme of the samples (not needed if input is an expt).
`design`	Design matrix describing the experiment (gotten for free if an expt).
`expt_names`	Alternate samples names.
`dendrogram`	Where to put dendrograms?
`row_label`	Passed through to heatmap.2.
`title`	Title of the plot!
`Rowv`	Reorder the rows by expression?
`Colv`	Reorder the columns by expression?
`label_chars`	Maximum number of characters before abbreviating sample names.
`filter`	Filter the data before performing this plot?
`...`	More parameters for a good time!

Value

a recordPlot() heatmap describing the samples.

See Also

[gplots::heatmap.2()]

`plot_scatter` *Make a pretty scatter plot between two sets of numbers.*

Description

This function tries to supplement a normal scatterplot with some information describing the relationship between the columns of data plotted.

Usage

```
plot_scatter(
  df,
  tooltip_data = NULL,
  color = "black",
  xlab = NULL,
  ylab = NULL,
  alpha = 0.6,
  gvis_filename = NULL,
  size = 2
)
```

Arguments

`df`	Dataframe likely containing two columns.
`tooltip_data`	Df of tooltip information for gvis.
`color`	Color of the dots on the graph.
`xlab`	Alternate x-axis label.
`ylab`	Alternate x-axis label.
`alpha`	Define how see-through the dots are.
`gvis_filename`	Filename to write a fancy html graph.
`size`	Size of the dots on the graph.

Value

Ggplot2 scatter plot.

See Also

[plot_linear_scatter()] [all_pairwise()]

Examples

```
## Not run:
 plot_scatter(lotsofnumbers_intwo_columns, tooltip_data = tooltip_dataframe,
              gvis_filename = "html/fun_scatterplot.html")

## End(Not run)
```

`plot_significant_bar` *Plot significant genes by contrast with different colors for significance levels.*

Description

This is my attempt to recapitulate some plots made in Laura and Najib's mbio paper. The goal of the plot is to show a few ranges of significance as differently colored and stacked bars. The colors are nice because Najib and Laura chose them.

Usage

```
plot_significant_bar(
  ups,
  downs,
  maximum = NULL,
  text = TRUE,
  color_list = c("lightcyan", "lightskyblue", "dodgerblue", "plum1", "orchid",
    "purple4"),
  color_names = c("a_up_inner", "b_up_middle", "c_up_outer", "a_down_inner",
    "b_down_middle", "c_down_outer")
)
```

Arguments

`ups`	Set of up-regulated genes.
`downs`	Set of down-regulated genes.
`maximum`	Maximum/minimum number of genes to display.
`text`	Add text at the ends of the bars describing the number of genes >/< 0 fc.
`color_list`	Set of colors to use for the bars.
`color_names`	Categories associated with aforementioned colors.

Value

weird significance bar plots

See Also

[ggplot2] [extract_significant_genes()]

`plot_single_qq` *Perform a qqplot between two columns of a matrix.*

Description

Given two columns of data, how well do the distributions match one another? The answer to that question may be visualized through a qq plot!

Usage

```
plot_single_qq(data, x = 1, y = 2, labels = TRUE)
```

Arguments

`data`	Data frame/expt/expressionset.
`x`	First column to compare.
`y`	Second column to compare.
`labels`	Include the lables?

Value

a list of the logs, ratios, and mean between the plots as ggplots.

See Also

[Biobase]

`plot_sm` *Make an R plot of the standard median correlation or distance among samples.*

Description

This was written by a mix of Kwame Okrah <kokrah at gmail dot com>, Laura Dillon <dillonl at umd dot edu>, and Hector Corrada Bravo <hcorrada at umd dot edu> I reimplemented it using ggplot2 and tried to make it a little more flexible. The general idea is to take the pairwise correlations/distances of the samples, then take the medians, and plot them. This version of the plot is no longer actually a dotplot, but a point plot, but who is counting?

Usage

```
plot_sm(
  data,
  colors = NULL,
  method = "pearson",
  plot_legend = FALSE,
  expt_names = NULL,
  label_chars = 10,
  title = NULL,
  dot_size = 5,
  ...
)
```

Arguments

data	Expt, expressionset, or data frame.
colors	Color scheme if data is not an expt.
method	Correlation or distance method to use.
plot_legend	Include a legend on the side?
expt_names	Use pretty names for the samples?
label_chars	Maximum number of characters before abbreviating sample names.
title	Title for the graph.
dot_size	How large should the glyphs be?
...	More parameters to make you happy!

Value

ggplot of the standard median something among the samples. This will also write to an open device. The resulting plot measures the median correlation of each sample among its peers. It notes 1.5* the interquartile range among the samples and makes a horizontal line at that correlation coefficient. Any sample which falls below this line is considered for removal because it is much less similar to all of its peers.

See Also

[matrixStats] [ggplot2]

Examples

```
## Not run:
 smc_plot = hpgl_smc(expt = expt)

## End(Not run)
```

`plot_spirograph` *Make spirographs!*

Description

Taken (with modifications) from: http://menugget.blogspot.com/2012/12/spirograph-with-r.html#more A positive value for 'B' will result in a epitrochoid, while a negative value will result in a hypotrochoid.

Usage

```
plot_spirograph(
  radius_a = 1,
  radius_b = -4,
  dist_bc = -2,
  revolutions = 158,
  increments = 3160,
  center_a = list(x = 0, y = 0)
)
```

Arguments

`radius_a`	The radius of the primary circle.
`radius_b`	The radius of the circle travelling around a.
`dist_bc`	A point relative to the center of 'b' which rotates with the turning of 'b'.
`revolutions`	How many revolutions to perform in the plot
`increments`	The number of radial increments to be calculated per revolution
`center_a`	The position of the center of 'a'.

Value

something which I don't yet know.

`plot_suppa` *Given some psi and tpm data, make a pretty plot!*

Description

This should take either a dataframe or filename for the psi data from suppa, along with the same for the average log tpm data (acquired from suppa diffSplice with –save_tpm_events)

Usage

```
plot_suppa(
  dpsi,
  tpm,
  events = NULL,
  psi = NULL,
  sig_threshold = 0.05,
  label_type = NULL,
  alpha = 0.7
)
```

Arguments

dpsi	Table provided by suppa containing all the metrics.
tpm	Table provided by suppa containing all the tpm values.
events	List of event types to include.
psi	Limit the set of included events by psi value?
sig_threshold	Use this significance threshold.
label_type	Choose a type of event to label.
alpha	How see-through should the points be in the plot?

Value

List containing the plot and some of the requisite data.

See Also

[plot_rmats()]

Examples

```
 ## Not run:
 suppa_plot <- plot_suppa(dpsi_file, tmp_file)

## End(Not run)
```

---

plot_svfactor *Make a dotplot of some categorised factors and a set of SVs (for other factors).*

Description

This should make a quick df of the factors and surrogates and plot them.

Usage

```
plot_svfactor(
  expt,
  svest,
  sv = 1,
  chosen_factor = "batch",
  factor_type = "factor"
)
```

Arguments

expt	Experiment from which to acquire the design, counts, etc.
svest	Set of surrogate variable estimations from sva/svg or batch estimates.
sv	Which surrogate to plot?
chosen_factor	Factor to compare against.
factor_type	This may be a factor or range, it is intended to plot a scatterplot if it is a range, a dotplot if a factor.

Value

surrogate variable plot as per Leek's work

See Also

[ggplot2]

Examples

```
## Not run:
 estimate_vs_snps <- plot_svfactor(start, surrogate_estimate, "snpcategory")

## End(Not run)
```

---

plot_topgo_densities *Plot the density of categories vs. the possibilities of all categories.*

Description

This can make a large number of plots.

Usage

```
plot_topgo_densities(godata, table)
```

Arguments

godata	Result from topgo.
table	Table of genes.

Value

density plot as per topgo

See Also

[topGO]

---

plot_topgo_pval *Make a pvalue plot from topgo data.*

Description

The p-value plots from clusterProfiler are pretty, this sets the topgo data into a format suitable for plotting in that fashion and returns the resulting plots of significant ontologies.

Usage

```
plot_topgo_pval(
  topgo,
  wrapped_width = 20,
  cutoff = 0.1,
  n = 30,
  type = "fisher",
  ...
)
```

Arguments

topgo	Some data from topgo!
wrapped_width	Maximum width of the text names.
cutoff	P-value cutoff for the plots.
n	Maximum number of ontologies to include.
type	Type of score to use.
...	arguments passed through presumably from simple_topgo()

Value

List of MF/BP/CC pvalue plots.

See Also

[ggplot2]

plot_topn *Plot the representation of the top-n genes in the total counts / sample.*

Description

One question we might ask is: how much do the most abundant genes in a samples comprise the entire sample? This plot attempts to provide a visual hint toward answering this question. It does so by rank-ordering all the genes in every sample and dividing their counts by the total number of reads in that sample. It then smooths the points to provide the resulting trend. The steeper the resulting line, the more over-represented these top-n genes are. I suspect, but haven't tried yet, that the inflection point of the resulting curve is also a useful diagnostic in this question.

Usage

```
plot_topn(
  data,
  title = NULL,
  num = 100,
  expt_names = NULL,
  plot_labels = "direct",
  label_chars = 10,
  plot_legend = FALSE,
  ...
)
```

Arguments

data	Dataframe/matrix/whatever for performing topn-plot.
title	A title for the plot.
num	The N in top-n genes, if null, do them all.
expt_names	Column or character list of sample names.
plot_labels	Method for labelling the lines.
label_chars	Maximum number of characters before abbreviating samples.
plot_legend	Add a legend to the plot?
...	Extra arguments, currently unused.

Value

List containing the ggplot2

plot_tsne *Shortcut to plot_pca(pc_method = "tsne")*

Description

Shortcut to plot_pca(pc_method = "tsne")

Usage

```
plot_tsne(...)
```

Arguments

...	Arguments for plot_pca()

plot_variance_coefficients *Look at the (biological)coefficient of variation/quartile coefficient of dispersion with respect to an experimental factor.*

Description

I want to look at the (B)CV of some data with respect to condition/batch/whatever. This function should make that possible, with some important caveats. The most appropriate metric is actually the biological coefficient of variation as calculated by DESeq2/EdgeR; but the metrics I am currently taking are the simpler and less appropriate CV(sd/mean) and QCD(q3-q1/q3+q1).

Usage

```
plot_variance_coefficients(
  data,
  x_axis = "condition",
  colors = NULL,
  title = NULL,
  ...
)
```

Arguments

data	Expressionset/epxt to poke at.
x_axis	Factor in the experimental design we may use to group the data and calculate the dispersion metrics.
colors	Set of colors to use when making the violins
title	Optional title to include with the plot.
...	Extra arguments to pass along.

Value

List of plots showing the coefficients vs. genes along with the data.

`plot_volcano_de` *Make a pretty Volcano plot!*

Description

Volcano plots and MA plots provide quick an easy methods to view the set of (in)significantly differentially expressed genes. In the case of a volcano plot, it places the -log10 of the p-value estimate on the y-axis and the fold-change between conditions on the x-axis. Here is a neat snippet from wikipedia: "The concept of volcano plot can be generalized to other applications, where the x-axis is related to a measure of the strength of a statistical signal, and y-axis is related to a measure of the statistical significance of the signal."

Usage

```
plot_volcano_de(
  table,
  alpha = 0.6,
  color_by = "p",
  color_list = c(`FALSE` = "darkblue", `TRUE` = "darkred"),
  fc_col = "logFC",
  fc_name = "log2 fold change",
  gvis_filename = NULL,
  line_color = "black",
  line_position = "bottom",
  logfc = 1,
  p_col = "adj.P.Val",
  p_name = "-log10 p-value",
  p = 0.05,
  shapes_by_state = TRUE,
  size = 2,
  tooltip_data = NULL,
  label = NULL,
  ...
)
```

Arguments

`table`	Dataframe from limma's toptable which includes log(fold change) and an adjusted p-value.
`alpha`	How transparent to make the dots.
`color_by`	By p-value something else?
`color_list`	List of colors for significance.

fc_col	Which column contains the fc data?
fc_name	Name of the fold-change to put on the plot.
gvis_filename	Filename to write a fancy html graph.
line_color	What color for the significance lines?
line_position	Put the significance lines above or below the dots?
logfc	Cutoff defining the minimum/maximum fold change for interesting.
p_col	Which column contains the p-value data?
p_name	Name of the p-value to put on the plot.
p	Cutoff defining significant from not.
shapes_by_state	Add fun shapes for the various significance states?
size	How big are the dots?
tooltip_data	Df of tooltip information for gvis.
label	Label the top/bottom n logFC values?
...	I love parameters!

Value

Ggplot2 volcano scatter plot. This is defined as the -log10(p-value) with respect to log(fold change). The cutoff values are delineated with lines and mark the boundaries between 'significant' and not. This will make a fun clicky googleVis graph if requested.

See Also

[all_pairwise()]

Examples

```
## Not run:
 plot_volcano_de(table, gvis_filename = "html/fun_ma_plot.html")
 ## Currently this assumes that a variant of toptable was used which
 ## gives adjusted p-values.  This is not always the case and I should
 ## check for that, but I have not yet.

## End(Not run)
```

plotly_pca *Plot a PC plot with options suitable for ggplotly.*

Description

Plot a PC plot with options suitable for ggplotly.

Usage

```
plotly_pca(
  data,
  design = NULL,
  plot_colors = NULL,
  plot_title = NULL,
  plot_size = 5,
  plot_alpha = NULL,
  plot_labels = NULL,
  size_column = NULL,
  pc_method = "fast_svd",
  x_pc = 1,
  y_pc = 2,
  outlines = FALSE,
  num_pc = NULL,
  expt_names = NULL,
  label_chars = 10,
  tooltip = c("shape", "fill", "sampleid"),
  ...
)
```

Arguments

data	an expt set of samples.
design	a design matrix and.
plot_colors	a color scheme.
plot_title	a title for the plot.
plot_size	size for the glyphs on the plot.
plot_alpha	Add an alpha channel to the dots?
plot_labels	add labels? Also, what type? FALSE, "default", or "fancy".
size_column	use an experimental factor to size the glyphs of the plot
pc_method	how to extract the components? (svd
x_pc	Component to put on the x axis.
y_pc	Component to put on the y axis.
outlines	Include black outlines around glyphs?

num_pc	How many components to calculate, default to the number of rows in the metadata.
expt_names	Column or character list of preferred sample names.
label_chars	Maximum number of characters before abbreviating sample names.
tooltip	Which columns to include in the tooltip.
...	Arguments passed through to the pca implementations and plotter.

Value

This passes directly to plot_pca(), so its returns should be applicable along with the result from ggplotly.

See Also

[plotly]

---

pp *Plot a picture, with hopefully useful options for most(any) format.*

Description

This calls svg/png/postscript/etc according to the filename provided.

Usage

```
pp(file, image = NULL, width = 9, height = 9, res = 180, ...)
```

Arguments

file	Filename to write
image	Optionally, add the image you wish to plot and this will both print it to file and screen.
width	How wide?
height	How high?
res	The chosen resolution.
...	Arguments passed to the image plotters.

Value

a png/svg/eps/ps/pdf with height = width=9 inches and a high resolution

See Also

[png()] [svg()] [postscript()] [cairo_ps()] [cairo_pdf()] [tiff()] [devEMF::emf()] [jpg()] [bmp()]

print_ups_downs *Reprint the output from extract_significant_genes().*

Description

I found myself needing to reprint these excel sheets because I added some new information. This shortcuts that process for me.

Usage

```
print_ups_downs(
  upsdowns,
  wb,
  excel_basename,
  according = "limma",
  summary_count = 1,
  ma = FALSE
)
```

Arguments

upsdowns	Output from extract_significant_genes().
wb	Workbook object to use for writing, or start a new one.
according	Use limma, deseq, or edger for defining 'significant'.
summary_count	For spacing sequential tables one after another.
ma	Include ma plots?

Value

Return from write_xlsx.

See Also

combine_de_tables

random_ontology *Perform a simple_ontology() on some random data.*

Description

At the very least, the result should be less significant than the actual data!

Usage

```
random_ontology(input, method = "goseq", n = 200, ...)
```

Arguments

input	Some input data
method	goseq, clusterp, topgo, gostats, gprofiler.
n	how many 'genes' to analyse?
...	Arguments passed to the method.

Value

An ontology result

See Also

[simple_goseq()] [simple_clusterprofiler()] [simple_topgo()] [simple_gostats()]

---

rank_order_scatter *Plot the rank order of the data in two tables against each other.*

Description

Steve Christensen has some neat plots showing the relationship between two tables. I thought they were cool, so I co-opted the idea in this function.

Usage

```
rank_order_scatter(
  first,
  second = NULL,
  first_type = "limma",
  second_type = "limma",
  first_table = NULL,
  alpha = 0.5,
  second_table = NULL,
  first_column = "logFC",
  second_column = "logFC",
  first_p_col = "adj.P.Val",
  second_p_col = "adj.P.Val",
  p_limit = 0.05,
  both_color = "red",
  first_color = "green",
  second_color = "blue",
  no_color = "black"
)
```

Arguments

first	First table of values.
second	Second table of values, if null it will use the first.
first_type	Assuming this is from all_pairwise(), use this method.
second_type	Ibid.
first_table	Again, assuming all_pairwise(), use this to choose the table to extract.
alpha	How see-through to make the dots?
second_table	Ibid.
first_column	What column to use to rank-order from the first table?
second_column	What column to use to rank-order from the second table?
first_p_col	Use this column for pretty colors from the first table.
second_p_col	Use this column for pretty colors from the second table.
p_limit	A p-value limit for coloring dots.
both_color	If both columns are 'significant', use this color.
first_color	If only the first column is 'significant', this color.
second_color	If the second column is 'significant', this color.
no_color	If neither column is 'significant', then this color.

Value

a list with a plot and a couple summary statistics.

---

read_counts_expt *Read a bunch of count tables and create a usable data frame from them.*

Description

It is worth noting that this function has some logic intended for the elsayed lab's data storage structure. It shouldn't interfere with other usages, but it attempts to take into account different ways the data might be stored.

Usage

```
read_counts_expt(
  ids,
  files,
  header = FALSE,
  include_summary_rows = FALSE,
  suffix = NULL,
  countdir = NULL,
  ...
)
```

Arguments

ids	List of experimental ids.
files	List of files to read.
header	Whether or not the count tables include a header row.
include_summary_rows	Whether HTSeq summary rows should be included.
suffix	Optional suffix to add to the filenames when reading them.
countdir	Optional count directory to read from.
...	More options for happy time!

Details

Used primarily in create_expt() This is responsible for reading count tables given a list of filenames. It tries to take into account upper/lowercase filenames and uses data.table to speed things along.

Value

Data frame of count tables.

See Also

[data.table] [create_expt()] [tximport]

Examples

```
## Not run:
 count_tables <- hpgl_read_files(as.character(sample_ids), as.character(count_filenames))

## End(Not run)
```

---

read_metadata *Given a table of meta data, read it in for use by create_expt().*

Description

Reads an experimental design in a few different formats in preparation for creating an expt.

Usage

```
read_metadata(file, ...)
```

Arguments

file	Csv/xls file to read.
...	Arguments for arglist, used by sep, header and similar read_csv/read.table parameters.

Value

Df of metadata.

See Also

[openxlsx] [readODS]

`read_snp_columns` *Read the output from bcfutils into a count-table-esque*

Description

Previously, I put all my bcfutils output files into one directory. This function would iterate through every file in that directory and add the contents as columns to this growing data table. Now it works by accepting a list of filenames (presumably kept in the metadata for the experiment) and reading them into the data table. It is worth noting that it can accept either a column name or index – which when you think about it is pretty much always true, but in this context is particularly interesting since I changed the names of all the columns when I rewrote this functionality.

Usage

```
read_snp_columns(samples, file_lst, column = "diff_count")
```

Arguments

`samples`	Sample names to read.
`file_lst`	Set of files to read.
`column`	Column from the bcf file to read.

Value

A big honking data table.

See Also

[readr]

read_thermo_xlsx *Parse the difficult thermo fisher xlsx file.*

Description

The Thermo(TM) workflow has as its default a fascinatingly horrible excel output. This function parses that into a series of data frames.

Usage

```
read_thermo_xlsx(xlsx_file, test_row = NULL)
```

Arguments

xlsx_file	The input xlsx file
test_row	A single row in the xlsx file to use for testing, as I have not yet seen two of these accursed files which had the same headers.

Value

List containing the protein names, group data, protein dataframe, and peptide dataframe.

recolor_points *Quick point-recolorizer given an existing plot, df, list of rownames to recolor, and a color.*

Description

This function should make it easy to color a family of genes in any of the point plots.

Usage

```
recolor_points(plot, df, ids, color = "red", ...)
```

Arguments

plot	Geom_point based plot
df	Data frame used to create the plot
ids	Set of ids which must be in the rownames of df to recolor
color	Chosen color for the new points.
...	Extra arguments are passed to arglist.

Value

prettier plot.

`renderme` *Add a little logic to rmarkdown::render to date the final outputs as per a request from Najib.*

Description

Add a little logic to rmarkdown::render to date the final outputs as per a request from Najib.

Usage

```
renderme(file, format = "html_document")
```

Arguments

`file`	Rmd file to render.
`format`	Chosen file format.

Value

Final filename including the prefix rundate.

See Also

[rmarkdown]

`replot_varpart_percent` *A shortcut for replotting the percent plots from variancePartition.*

Description

In case I wish to look at different numbers of genes from variancePartition and/or different columns to sort from.

Usage

```
replot_varpart_percent(
  varpart_output,
  n = 30,
  column = NULL,
  decreasing = TRUE
)
```

Arguments

varpart_output	List returned by varpart()
n	How many genes to plot.
column	The df column to use for sorting.
decreasing	high->low or vice versa?

Value

The percent variance bar plots from variancePartition!

See Also

[variancePartition]

---

rex *Send the R plotter to the computer of your choice!*

Description

Resets the display and xauthority variables to the new computer I am using so that plot() works.

Usage

```
rex(display = ":0")
```

Arguments

display	DISPLAY variable to use, if NULL it looks in ~/.displays/$(host).last

Value

Fresh plotting window to the display of your choice!

`s2s_all_filters` *Gather together the various SWATH2stats filters into one place.*

Description

There are quite a few filters available in SWATH2stats. Reading the documentation, it seems at least possible, if not appropriate, to use them together when filtering DIA data before passing it to MSstats/etc. This function attempts to formalize and simplify that process.

Usage

```
s2s_all_filters(
  s2s_exp,
  column = "proteinname",
  pep_column = "fullpeptidename",
  fft = 0.7,
  plot = FALSE,
  target_fdr = 0.02,
  upper_fdr = 0.05,
  mscore = 0.01,
  percentage = 0.75,
  remove_decoys = TRUE,
  max_peptides = 15,
  min_peptides = 2,
  do_mscore = TRUE,
  do_freqobs = TRUE,
  do_fdr = TRUE,
  do_proteotypic = TRUE,
  do_peptide = TRUE,
  do_max = TRUE,
  do_min = TRUE,
  ...
)
```

Arguments

`s2s_exp`	SWHAT2stats result from the sample_annotation() function. (s2s_exp stands for: SWATH2stats experiment)
`column`	What column in the data contains the protein name?
`pep_column`	What column in the data contains the peptide name (not currently used, but it should be.)
`fft`	Ratio of false negatives to true positives, used by assess_by_fdr() and similar functions.
`plot`	Print plots of the various rates by sample?
`target_fdr`	When invoking mscore4assayfdr, choose an mscore which corresponds to this false discovery date.

upper_fdr	Used by filter_mscore_fdr() to choose the minimum threshold of identification confidence.
mscore	Mscore cutoff for the mscore filter.
percentage	Cutoff for the mscore_freqobs filter.
remove_decoys	Get rid of decoys in the final filter, if they were not already removed.
max_peptides	A maximum number of peptides filter.
min_peptides	A minimum number of peptides filter.
do_mscore	Perform the mscore filter? SWATH2stats::filter_mscore()
do_freqobs	Perform the mscore_freqobs filter? SWATH2stats::filter_mscore_freqobs()
do_fdr	Perform the fdr filter? SWATH2stats::filter_mscore_fdr()
do_proteotypic	Perform the proteotypic filter? SWATH2stats::filter_proteotypic_peptides()
do_peptide	Perform the single-peptide filter? SWATH2stats::filter_all_peptides()
do_max	Perform the maximum peptide filter? SWATH2stats::filter_max_peptides()
do_min	Perform the minimum peptide filter? SWATH2stats::filter_min_peptides()
...	Other arguments passed down to the filters.

Value

Smaller SWATH2stats data set.

See Also

[SWATH2stats]

---

samtools_snp_coverage *Use Rsamtools to read alignments and get snp coverage.*

Description

This is horrifyingly slow. I think I might remove this function.

Usage

```
samtools_snp_coverage(
  expt,
  type = "counts",
  input_dir = "preprocessing/outputs",
  tolower = TRUE,
  bam_suffix = ".bam",
  annot_column = annot_column
)
```

Arguments

expt	Expressionset to analyze
type	counts or percent?
input_dir	Directory containing the samtools results.
tolower	lowercase the sample names?
bam_suffix	In case the data came from sam.
annot_column	Passed along to count_expt_snps()

Value

It is so slow I no longer know if it works.

See Also

[count_expt_snps()] [Rsamtools] [GenomicRanges]

---

sanitize_expt *Get rid of characters which will mess up contrast making and such before playing with an expt.*

Description

Get rid of characters which will mess up contrast making and such before playing with an expt.

Usage

```
sanitize_expt(expt)
```

Arguments

expt	An expt object to clean.

saveme *Make a backup rdata file for future reference*

Description

I often use R over a sshfs connection, sometimes with significant latency, and I want to be able to save/load my R sessions relatively quickly. Thus this function uses pxz to compress the R session maximally and relatively fast. This assumes you have pxz installed and >= 4 CPUs.

Usage

```
saveme(
  directory = "savefiles",
  backups = 2,
  cpus = 6,
  filename = "Rdata.rda.xz"
)
```

Arguments

directory	Directory to save the Rdata file.
backups	How many revisions?
cpus	How many cpus to use for the xz call
filename	Choose a filename.

Value

Command string used to save the global environment.

See Also

[loadme()]

Examples

```
## Not run:
 saveme()

## End(Not run)
```

score_gsva_likelihoods *Score the results from simple_gsva().*

Description

Yeah, this is a bit meta, but the scores from gsva seem a bit meaningless to me, so I decided to look at the distribution of observed scores in some of my data; I quickly realized that they follow a nicely normal distribution. Therefore, I thought to calculate some scores of gsva() using that information.

Usage

```
score_gsva_likelihoods(
  gsva_result,
  score = NULL,
  category = NULL,
  factor = NULL,
  sample = NULL,
  factor_column = "condition",
  method = "mean",
  label_size = NULL,
  col_margin = 6,
  row_margin = 12,
  cutoff = 0.95
)
```

Arguments

gsva_result	Input result from simple_gsva()
score	What type of scoring to perform, against a value, column, row?
category	What category to use as baseline?
factor	Which experimental factor to compare against?
sample	Which sample to compare against?
factor_column	When comparing against an experimental factor, which design column to use to find it?
method	mean or median when when bringing together values?
label_size	By default, enlarge the labels to readable at the cost of losing some.
col_margin	Attempt to make heatmaps fit better on the screen with this and...
row_margin	this parameter
cutoff	Highlight only the categories deemed more significant than this.

Details

The nicest thing in this, I think, is that it provides its scoring metric(s) according to a few different possibilities, including: * the mean of samples found in an experimental factor * All provided scores against the distribution of observed scores as z-scores. * A single score against all scores. * Rows (gene sets) against the set of all gene sets.

Value

The scores according to the provided category, factor, sample, or score(s).

See Also

[simple_gsva()]

---

score_mhess *A scoring function for the mh_ess TNSeq method.*

Description

I dunno, I might delete this function, I am not sure if it will ever get use.

Usage

```
score_mhess(expt, ess_column = "essm1")
```

Arguments

expt	Input expressionset with a metadata column with the ess output files.
ess_column	Metadata column containing the mh_ess output files.

Value

List containing the scores along with the genes which have changed using it.

`semantic_copynumber_extract`
Extract multicopy genes from up/down gene expression lists.

Description

The function semantic_copynumber_filter() is the inverse of this.

Usage

```
semantic_copynumber_extract(...)
```

Arguments

...	Arguments for semantic_copynumber_filter()

Details

Currently untested, used for Trypanosome analyses primarily, thus the default strings.

`semantic_copynumber_filter`
Remove multicopy genes from up/down gene expression lists.

Description

In our parasite data, there are a few gene types which are consistently obnoxious. Multi-gene families primarily where the coding sequences are divergent, but the UTRs nearly identical. For these genes, our sequence based removal methods fail and so this just excludes them by name.

Usage

```
semantic_copynumber_filter(
  input,
  max_copies = 2,
  use_files = FALSE,
  invert = TRUE,
  semantic = c("mucin", "sialidase", "RHS", "MASP", "DGF", "GP63"),
  semantic_column = "1.tooltip"
)
```

Arguments

input	List of sets of genes deemed significantly up/down with a column expressing approximate count numbers.
max_copies	Keep only those genes with <= n putative copies.
use_files	Use a set of sequence alignments to define the copy numbers?
invert	Keep these genes rather than drop them?
semantic	Set of strings with gene names to exclude.
semantic_column	Column in the DE table used to find the semantic strings for removal.

Details

Currently untested, used for Trypanosome analyses primarily, thus the default strings.

Value

Smaller list of up/down genes.

See Also

[semantic_copynumber_extract()]

Examples

```
## Not run:
 pruned <- semantic_copynumber_filter(table, semantic = c("ribosomal"))
 ## Get rid of all genes with 'ribosomal' in the annotations.

## End(Not run)
```

---

semantic_expt_filter *Remove/keep specifically named genes from an expt.*

Description

I find subsetting weirdly confusing. Hopefully this function will allow one to include/exclude specific genes/families based on string comparisons.

Usage

```
semantic_expt_filter(
  input,
  invert = FALSE,
  topn = NULL,
  semantic = c("mucin", "sialidase", "RHS", "MASP", "DGF", "GP63"),
  semantic_column = "description"
)
```

Arguments

input	Expt to filter.
invert	The default is to remove the genes with the semantic strings. Keep them when inverted.
topn	Take the topn most abundant genes rather than a text based heuristic.
semantic	Character list of strings to search for in the annotation data.
semantic_column	Column in the annotations to search.

Value

A presumably smaller expt.

See Also

[Biobase]

---

sequence_attributes *Gather some simple sequence attributes.*

Description

This extends the logic of the pattern searching in pattern_count_genome() to search on some other attributes.

Usage

```
sequence_attributes(fasta, gff = NULL, type = "gene", key = NULL)
```

Arguments

fasta	Genome encoded as a fasta file.
gff	Optional gff of annotations (if not provided it will just ask the whole genome).
type	Column of the gff file to use.
key	What type of entry of the gff file to key from?

Value

List of data frames containing gc/at/gt/ac contents.

See Also

[Biostrings] [Rsamtools]

Examples

```
pa_data <- get_paeruginosa_data()
pa_fasta <- pa_data[["fasta"]]
pa_gff <- pa_data[["gff"]]
pa_attribs <- sequence_attributes(pa_fasta, gff = pa_gff)
head(pa_attribs)
```

`set_expt_batches` *Change the batches of an expt.*

Description

When exploring differential analyses, it might be useful to play with the conditions/batches of the experiment. Use this to make that easier.

Usage

```
set_expt_batches(expt, fact, ids = NULL, ...)
```

Arguments

`expt`	Expt to modify.
`fact`	Batches to replace using this factor.
`ids`	Specific samples to change.
`...`	Extra options are like spinach.

Value

The original expt with some new metadata.

See Also

[create_expt()] [set_expt_conditions()] [Biobase]

Examples

```
## Not run:
 expt = set_expt_batches(big_expt, factor = c(some,stuff,here))

## End(Not run)
```

`set_expt_colors` *Change the colors of an expt*

Description

When exploring differential analyses, it might be useful to play with the conditions/batches of the experiment. Use this to make that easier.

Usage

```
set_expt_colors(
  expt,
  colors = TRUE,
  chosen_palette = "Dark2",
  change_by = "condition"
)
```

Arguments

`expt`	Expt to modify
`colors`	colors to replace
`chosen_palette`	I usually use Dark2 as the RColorBrewer palette.
`change_by`	Assuming a list is passed, cross reference by condition or sample?

Value

expt Send back the expt with some new metadata

See Also

[set_expt_conditions()] [set_expt_batches()] [RColorBrewer]

Examples

```
## Not run:
unique(esmer_expt$design$conditions)
chosen_colors <- list(
   "cl14_epi" = "#FF8D59",
   "clbr_epi" = "#962F00",
   "cl14_tryp" = "#D06D7F",
   "clbr_tryp" = "#A4011F",
   "cl14_late" = "#6BD35E",
   "clbr_late" = "#1E7712",
   "cl14_mid" = "#7280FF",
   "clbr_mid" = "#000D7E")
esmer_expt <- set_expt_colors(expt = esmer_expt, colors = chosen_colors)

## End(Not run)
```

set_expt_conditions *Change the condition of an expt*

Description

When exploring differential analyses, it might be useful to play with the conditions/batches of the experiment. Use this to make that easier.

Usage

```
set_expt_conditions(expt, fact = NULL, ids = NULL, null_cell = "null", ...)
```

Arguments

expt	Expt to modify
fact	Conditions to replace
ids	Specific sample IDs to change.
null_cell	How to fill elements of the design which are null?
...	Extra arguments are given to arglist.

Value

expt Send back the expt with some new metadata

See Also

[set_expt_batches()] [create_expt()]

Examples

```
## Not run:
 expt = set_expt_conditions(big_expt, factor = c(some,stuff,here))

## End(Not run)
```

set_expt_factors *Change the factors (condition and batch) of an expt*

Description

When exploring differential analyses, it might be useful to play with the conditions/batches of the experiment. Use this to make that easier.

Usage

```
set_expt_factors(expt, condition = NULL, batch = NULL, ids = NULL, ...)
```

Arguments

expt	Expt to modify
condition	New condition factor
batch	New batch factor
ids	Specific sample IDs to change.
...	Arguments passed along (likely colors)

Value

expt Send back the expt with some new metadata

See Also

[set_expt_conditions()] [set_expt_batches()]

Examples

```
## Not run:
 expt = set_expt_factors(big_expt, condition = "column", batch = "another_column")

## End(Not run)
```

---

set_expt_genenames *Change the gene names of an expt.*

Description

I want to change all the gene names of a big expressionset to the ortholog groups. But I want to also continue using my expts. Ergo this little function.

Usage

```
set_expt_genenames(expt, ids = NULL, ...)
```

Arguments

expt	Expt to modify
ids	Specific sample IDs to change.
...	Extra arguments are given to arglist.

Value

expt Send back the expt with some new metadata

See Also

[set_expt_conditions()] [create_expt()]

Examples

```
## Not run:
 expt = set_expt_conditions(big_expt, factor = c(some,stuff,here))

## End(Not run)
```

`set_expt_samplenames` *Change the sample names of an expt.*

Description

Sometimes one does not like the hpgl identifiers, so provide a way to change them on-the-fly.

Usage

```
set_expt_samplenames(expt, newnames)
```

Arguments

`expt`	Expt to modify
`newnames`	New names, currently only a character vector.

Value

expt Send back the expt with some new metadata

See Also

[set_expt_conditions()] [set_expt_batches()]

Examples

```
## Not run:
 expt = set_expt_samplenames(expt, c("a","b","c","d","e","f"))

## End(Not run)
```

`sig_ontologies` *Take the result from extract_significant_genes() and perform ontology searches.*

Description

It can be annoying/confusing to extract individual sets of 'significant' genes from a differential expression analysis. This function should make that process easier.

Usage

```
sig_ontologies(
  significant_result,
  excel_prefix = "excel/sig_ontologies",
  search_by = "deseq",
  excel_suffix = ".xlsx",
  type = "gprofiler",
  ...
)
```

Arguments

`significant_result`	Result from extract_siggenes()
`excel_prefix`	How to start the output filenames?
`search_by`	Use the definition of 'significant' from which program?
`excel_suffix`	How to end the excel filenames?
`type`	Which specific ontology search to use?
`...`	Arguments passed to the various simple_ontology() function.

Value

A list of the up/down results of the ontology searches.

See Also

[openxlsx] [simple_goseq()] [simple_clusterprofiler()] [simple_topgo()] [simple_gprofiler()] [simple_topgo()] [simple_gostats()]

significant_barplots *Given the set of significant genes from combine_de_tables(), provide a view of how many are significant up/down.*

Description

These plots are pretty annoying, and I am certain that this function is not well written, but it provides a series of bar plots which show the number of genes/contrast which are up and down given a set of fold changes and p-value.

Usage

```
significant_barplots(
  combined,
  lfc_cutoffs = c(0, 1, 2),
  invert = FALSE,
  p = 0.05,
  z = NULL,
  p_type = "adj",
  according_to = "all",
  order = NULL,
  maximum = NULL,
  ...
)
```

Arguments

combined	Result from combine_de_tables and/or extract_significant_genes().
lfc_cutoffs	Choose 3 fold changes to define the queries. 0, 1, 2 mean greater/less than 0 followed by 2 fold and 4 fold cutoffs.
invert	Reverse the order of contrasts for readability?
p	Chosen p-value cutoff.
z	Choose instead a z-score cutoff.
p_type	Adjusted or not?
according_to	limma, deseq, edger, basic, or all of the above.
order	Choose a specific order for the plots.
maximum	Set a specific limit on the number of genes on the x-axis.
...	More arguments are passed to arglist.

Value

list containing the significance bar plots and some information to hopefully help interpret them.

Examples

```
## Not run:
 expt <- create_expt(metadata = "some_metadata.xlsx", gene_info = annotations)
 pairwise_result <- all_pairwise(expt)
 combined_result <- combine_de_tables(pairwise_result)
 ## Damn I wish I were smrt enough to make this elegant, but I cannot.
 barplots <- significant_barplots(combined_result)

## End(Not run)
```

---

sillydist *Calculate a simplistic distance function of a point against two axes.*

Description

Sillydist provides a distance of any point vs. the axes of a plot. This just takes the abs(distances) of each point to the axes, normalizes them against the largest point on the axes, multiplies the result, and normalizes against the max of all point.

Usage

```
sillydist(firstterm, secondterm, firstaxis = 0, secondaxis = 0)
```

Arguments

firstterm	X-values of the points.
secondterm	Y-values of the points.
firstaxis	X-value of the vertical axis.
secondaxis	Y-value of the second axis.

Value

Dataframe of the distances.

See Also

[ggplot2]

Examples

```
## Not run:
 mydist <- sillydist(df[,1], df[,2], first_median, second_median)
 first_vs_second <- ggplot2::ggplot(df, ggplot2::aes_string(x = "first", y = "second"),
                                    environment = hpgl_env) +
   ggplot2::xlab(paste("Expression of", df_x_axis)) +
   ggplot2::ylab(paste("Expression of", df_y_axis)) +
  ggplot2::geom_vline(color = "grey", xintercept=(first_median - first_mad), size = line_size) +
  ggplot2::geom_vline(color = "grey", xintercept=(first_median + first_mad), size = line_size) +
```

```
   ggplot2::geom_vline(color = "darkgrey", xintercept = first_median, size = line_size) +
  ggplot2::geom_hline(color = "grey", yintercept=(second_median - second_mad), size = line_size) +
  ggplot2::geom_hline(color = "grey", yintercept=(second_median + second_mad), size = line_size) +
   ggplot2::geom_hline(color = "darkgrey", yintercept = second_median, size = line_size) +
    ggplot2::geom_point(colour = grDevices::hsv(mydist$dist, 1, mydist$dist),
                        alpha = 0.6, size = size) +
    ggplot2::theme(legend.position = "none")
 first_vs_second  ## dots get colored according to how far they are from the medians
 ## replace first_median, second_median with 0,0 for the axes

## End(Not run)
```

`simple_clusterprofiler` *Perform the array of analyses in the 2016-04 version of clusterProfiler*

Description

The new version of clusterProfiler has a bunch of new toys. However, it is more stringent in terms of input in that it now explicitly expects to receive annotation data in terms of a orgdb object. This is mostly advantageous, but will probably cause some changes in the other ontology functions in the near future. This function is an initial pass at making something similar to my previous 'simple_clusterprofiler()' but using these new toys.

Usage

```
simple_clusterprofiler(
  sig_genes,
  de_table = NULL,
  orgdb = "org.Dm.eg.db",
  orgdb_from = NULL,
  orgdb_to = "ENTREZID",
  go_level = 3,
  pcutoff = 0.05,
  qcutoff = 0.1,
  fc_column = "logFC",
  second_fc_column = "limma_logfc",
  updown = "up",
  permutations = 1000,
  min_groupsize = 5,
  kegg_prefix = NULL,
  kegg_organism = NULL,
  do_gsea = TRUE,
  categories = 12,
  excel = NULL,
  do_david = FALSE,
  david_id = "ENTREZ_GENE_ID",
  david_user = "unknown@unknown.org"
)
```

Arguments

sig_genes	Dataframe of genes deemed 'significant.'
de_table	Dataframe of all genes in the analysis, primarily for gse analyses.
orgdb	Name of the orgDb used for gathering annotation data.
orgdb_from	Name of a key in the orgdb used to cross reference to entrez IDs.
orgdb_to	List of keys to grab from the orgdb for cross referencing ontologies.
go_level	How deep into the ontology tree should this dive for over expressed categories.
pcutoff	P-value cutoff for 'significant' analyses.
qcutoff	Q-value cutoff for 'significant' analyses.
fc_column	When extracting vectors of all genes, what column should be used?
second_fc_column	When extracting vectors of all genes, what column should be tried the second time around?
updown	Include the less than expected ontologies?
permutations	How many permutations for GSEA-ish analyses?
min_groupsize	Minimum size of an ontology before it is included.
kegg_prefix	Many KEGG ids need a prefix before they will cross reference.
kegg_organism	Choose the 3 letter KEGG organism name here.
do_gsea	Perform gsea searches?
categories	How many categories should be plotted in bar/dot plots?
excel	Print the results to an excel file?
do_david	Attempt to use the DAVID database for a search?
david_id	Which column to use for cross-referencing to DAVID?
david_user	Default registered username to use.

Value

a list

See Also

[clusterProfiler] [AnnotationDbi] [KEGGREST]

Examples

```
## Not run:
 holyasscrackers <- simple_clusterprofiler(gene_list, all_genes, "org.Dm.eg.db")

## End(Not run)
```

simple_cp_enricher *Generic enrichment using clusterProfiler.*

Description

culsterProfiler::enricher provides a quick and easy enrichment analysis given a set of siginficant' genes and a data frame which connects each gene to a category.

Usage

```
simple_cp_enricher(sig_genes, de_table, go_db = NULL)
```

Arguments

sig_genes	Set of 'significant' genes as a table.
de_table	All genes from the original analysis.
go_db	Dataframe of GO->ID matching the gene names of sig_genes to GO categories.

Value

Table of 'enriched' categories.

simple_filter_counts *Filter low-count genes from a data set only using a simple threshold and number of samples.*

Description

This was a function written by Kwame Okrah and perhaps also Laura Dillon to remove low-count genes. It drops genes based on a threshold and number of samples.

Usage

```
simple_filter_counts(count_table, threshold = 2)
```

Arguments

count_table	Data frame of (pseudo)counts by sample.
threshold	Lower threshold of counts for each gene.

Value

Dataframe of counts without the low-count genes.

See Also

[edgeR]

Examples

```
## Not run:
 filtered_table <- simple_filter_counts(count_table)

## End(Not run)
```

`simple_gadem` *run the rGADEM suite*

Description

This should provide a set of rGADEM results given an input file of sequences and a genome.

Usage

```
simple_gadem(
  inputfile,
  genome = "BSgenome.Hsapiens.UCSC.hs19",
  p = 0.1,
  e = 0,
  ...
)
```

Arguments

`inputfile`	Fasta or bed file containing sequences to search.
`genome`	BSgenome to read.
`...`	Parameters for plotting the gadem result.

Value

A list containing slots for plots, the stdout output from gadem, the gadem result, set of occurences of motif, and the returned set of motifs.

See Also

[IRanges] [Biostrings] [rGADEM]

simple_goseq *Perform a simplified goseq analysis.*

Description

goseq can be pretty difficult to get set up for non-supported organisms. This attempts to make that process a bit simpler as well as give some standard outputs which should be similar to those returned by clusterprofiler/topgo/gostats/gprofiler.

Usage

```
simple_goseq(
  sig_genes,
  go_db = NULL,
  length_db = NULL,
  doplot = TRUE,
  adjust = 0.1,
  pvalue = 0.1,
  plot_title = NULL,
  length_keytype = "transcripts",
  go_keytype = "entrezid",
  goseq_method = "Wallenius",
  padjust_method = "BH",
  bioc_length_db = "ensGene",
  expand_categories = TRUE,
  excel = NULL,
  ...
)
```

Arguments

sig_genes	Data frame of differentially expressed genes, containing IDs etc.
go_db	Database of go to gene mappings (OrgDb/OrganismDb)
length_db	Database of gene lengths (gff/TxDb)
doplot	Include pwf plots?
adjust	Minimum adjusted pvalue for 'significant.'
pvalue	Minimum pvalue for 'significant.'
length_keytype	Keytype to provide to extract lengths
go_keytype	Keytype to provide to extract go IDs
goseq_method	Statistical test for goseq to use.
padjust_method	Which method to use to adjust the pvalues.
bioc_length_db	Source of gene lengths?
expand_categories	Expand the GO categories to make the results more readable?

excel	Print the results to an excel file?
...	Extra parameters which I do not recall

Value

Big list including: the pwd:pwf function, alldata:the godata dataframe, pvalue_histogram:p-value histograms, godata_interesting:the ontology information of the enhanced groups, term_table:the goterms with some information about them, mf_subset:a plot of the MF enhanced groups, mfp_plot:the pvalues of the MF group, bp_subset:a plot of the BP enhanced groups, bpp_plot, cc_subset, and ccp_plot

See Also

[goseq] [GO.db] [GenomicFeatures] [stats::p.adjust()]

Examples

```
## Not run:
 lotsotables <- simple_goseq(gene_list, godb, lengthdb)

## End(Not run)
```

---

simple_gostats *Simplification function for gostats, in the same vein as those written for clusterProfiler, goseq, and topGO.*

Description

GOstats has a couple interesting peculiarities: Chief among them: the gene IDs must be integers. As a result, I am going to have this function take a gff file in order to get the go ids and gene ids on the same page.

Usage

```
simple_gostats(
  sig_genes,
  go_db = NULL,
  gff = NULL,
  gff_df = NULL,
  universe_merge = "id",
  second_merge_try = "locus_tag",
  species = "fun",
  pcutoff = 0.1,
  conditional = FALSE,
  categorysize = NULL,
  gff_id = "ID",
  gff_type = "cds",
  excel = NULL,
```

```
  ...
)
```

Arguments

sig_genes	Input list of differentially expressed genes.
go_db	Set of GOids, as before in the format ID/GO.
gff	Annotation information for this genome.
gff_df	I do not remember what this is for.
universe_merge	Column from which to create the universe of genes.
second_merge_try	If the first universe merge fails, try this.
species	Genbank organism to use.
pcutoff	Pvalue cutoff for deciding significant.
conditional	Perform a conditional search?
categorysize	Category size below which to not include groups.
gff_id	key in the gff file containing the unique IDs.
gff_type	Gff column to use for creating the universe.
excel	Print the results to an excel file?
...	More parameters!

Value

List of returns from GSEABase, Category, etc.

See Also

[GSEABase] [Category] [load_gff_annotations()] [GOstats]

Examples

```
## Not run:
 knickerbockers <- simple_gostats(sig_genes, gff_file, goids)

## End(Not run)
```

simple_gprofiler *Run searches against the web service g:Profiler.*

Description

Thank you Ginger for showing me your thesis, gProfiler is pretty cool!

Usage

```
simple_gprofiler(
  sig_genes,
  species = "hsapiens",
  convert = TRUE,
  first_col = "logFC",
  second_col = "limma_logfc",
  do_go = TRUE,
  do_kegg = TRUE,
  do_reactome = TRUE,
  do_mi = TRUE,
  do_tf = TRUE,
  do_corum = TRUE,
  do_hp = TRUE,
  significant = TRUE,
  pseudo_gsea = TRUE,
  id_col = "row.names",
  excel = NULL
)
```

Arguments

sig_genes	Guess! The set of differentially expressed/interesting genes.
species	Organism supported by gprofiler.
convert	Use gProfileR's conversion utility?
first_col	First place used to define the order of 'significant'.
second_col	If that fails, try a second column.
do_go	Perform GO search?
do_kegg	Perform KEGG search?
do_reactome	Perform reactome search?
do_mi	Do miRNA search?
do_tf	Search for transcription factors?
do_corum	Do corum search?
do_hp	Do the hp search?
significant	Only return the statistically significant hits?

pseudo_gsea	Is the data in a ranked order by significance?
id_col	Which column in the table should be used for gene ID crossreferencing? gProfiler uses Ensembl ids. So if you have a table of entrez or whatever, translate it!
excel	Print the results to an excel file?

Value

List of results for go, kegg, reactome, and a few more.

See Also

[gProfiler]

Examples

```
## Not run:
 gprofiler_is_nice_and_easy <- simple_gprofiler(genes, species='mmusculus')

## End(Not run)
```

---

simple_gprofiler2 *Run searches against the web service g:Profiler.*

Description

This is the beginning of a reimplementation to use gprofiler2. However, AFAICT gprofiler2 does not yet actually work for anything other than their GO data.

Usage

```
simple_gprofiler2(
  sig_genes,
  species = "hsapiens",
  convert = TRUE,
  first_col = "logFC",
  second_col = "deseq_logfc",
  do_go = TRUE,
  do_kegg = TRUE,
  do_reactome = TRUE,
  do_mi = TRUE,
  do_tf = TRUE,
  do_corum = TRUE,
  do_hp = TRUE,
  do_hpa = TRUE,
  do_wp = TRUE,
  significant = FALSE,
```

```
  exclude_iea = FALSE,
  do_under = FALSE,
  evcodes = TRUE,
  threshold = 0.05,
  adjp = "fdr",
  domain_scope = "annotated",
  bg = NULL,
  pseudo_gsea = TRUE,
  id_col = "row.names",
  excel = NULL
)
```

Arguments

sig_genes	Guess! The set of differentially expressed/interesting genes.
species	Organism supported by gprofiler.
convert	Use gProfileR's conversion utility?
first_col	First place used to define the order of 'significant'.
second_col	If that fails, try a second column.
do_go	Perform GO search?
do_kegg	Perform KEGG search?
do_reactome	Perform reactome search?
do_mi	Do miRNA search?
do_tf	Search for transcription factors?
do_corum	Do corum search?
do_hp	Do the hp search?
do_hpa	Do the hpa search?
do_wp	Do the wp search?
significant	Only return the statistically significant hits?
exclude_iea	Passed directly to gprofiler2.
do_under	Perform under-representation search?
evcodes	Get the set of evcodes in the data? This makes it take longer.
threshold	p-value 'significance' threshold.
adjp	Method to adjust p-values.
domain_scope	Passed to gprofiler2.
bg	Background genes.
pseudo_gsea	Is the data in a ranked order by significance?
id_col	Which column in the table should be used for gene ID crossreferencing? gProfiler uses Ensembl ids. So if you have a table of entrez or whatever, translate it!
excel	Print the results to an excel file?

Value

a list of results for go, kegg, reactome, and a few more.

See Also

[gProfiler]

Examples

```
## Not run:
 gprofiler_is_nice_and_easy <- simple_gprofiler(genes, species='mmusculus')

## End(Not run)
```

`simple_gsva` *Provide some defaults and guidance when attempting to use gsva.*

Description

gsva seems to hold a tremendous amount of potential. Unfortunately, it is somewhat opaque and its requirements are difficult to pin down. This function will hopefully provide some of the requisite defaults and do some sanity checking to make it more likely that a gsva analysis will succeed.

Usage

```
simple_gsva(
  expt,
  signatures = "c2BroadSets",
  data_pkg = "GSVAdata",
  signature_category = "c2",
  cores = NULL,
  current_id = "ENSEMBL",
  required_id = "ENTREZID",
  min_catsize = 5,
  orgdb = "org.Hs.eg.db",
  method = "ssgsea",
  kcdf = NULL,
  ranking = FALSE,
  msig_xml = NULL,
  wanted_meta = c("ORGANISM", "DESCRIPTION_BRIEF", "AUTHORS", "PMID")
)
```

Arguments

`expt`	Expt object to be analyzed.
`signatures`	Provide an alternate set of signatures (GeneSetCollections)
`data_pkg`	What package contains the requisite dataset?

signature_category
: Specify a subset category to extract from the signatures database.

cores
: How many CPUs to use?

current_id
: Where did the IDs of the genes come from?

required_id
: gsva (I assume) always requires ENTREZ IDs, but just in case this is a parameter.

min_catsize
: Minimum category size to consider interesting (passed to gsva()).

orgdb
: What is the data source for the rownames()?

method
: Which gsva method to use? Changed this from gsva to ssgsea because it was throwing segmentation faults.

kcdf
: Options for the gsva methods.

ranking
: another gsva option.

msig_xml
: XML file contining msigdb annotations.

wanted_meta
: Desired metadata elements from the mxig_xml file.

Value

List containing three elements: first a modified expressionset using the result of gsva in place of the original expression data; second the result from gsva, and third a data frame of the annotation data for the gene sets in the expressionset. This seems a bit redundant, perhaps I should revisit it?

See Also

[GSEABase] [load_gmt_signatures()] [create_expt()] [GSVA]

---

simple_motifRG *Run motifRG on a fasta file.*

Description

Run motifRG on a fasta file.

Usage

```
simple_motifRG(
  input_fasta,
  control_fasta,
  maximum = 3,
  title = "Motifs of XXX",
  prefix = "motif",
  genome = "BSgenome.Hsapiens.UCSC.hg19"
)
```

Arguments

input_fasta	Input file.
control_fasta	control file.
maximum	3
title	Output image title.
prefix	Prefix for the output files.
genome	Package containing the full genome.

See Also

[motifRG]

---

simple_pathview *Print some data onto KEGG pathways.*

Description

KEGGREST and pathview provide neat functions for coloring molecular pathways with arbitrary data. Unfortunately they are somewhat evil to use. This attempts to alleviate that.

Usage

```
simple_pathview(
  path_data,
  indir = "pathview_in",
  outdir = "pathview",
  pathway = "all",
  species = "lma",
  from_list = NULL,
  to_list = NULL,
  suffix = "_colored",
  filenames = "id",
  fc_column = "limma_logfc",
  format = "png",
  verbose = TRUE
)
```

Arguments

path_data	Some differentially expressed genes.
indir	Directory into which the unmodified kegg images will be downloaded (or already exist).
outdir	Directory which will contain the colored images.
pathway	Perform the coloring for a specific pathway?

species	Kegg identifier for the species of interest.
from_list	Regex to help in renaming KEGG categories/gene names from one format to another.
to_list	Regex to help in renaming KEGG categories/gene names from one format to another.
suffix	Add a suffix to the completed, colored files.
filenames	Name the final files by id or name?
fc_column	What is the name of the fold-change column to extract?
format	Format of the resulting images, I think only png really works well.
verbose	When on, this function is quite chatty.

Value

A list of some information for every KEGG pathway downloaded/examined. This information includes: a. The filename of the final image for each pathway. b. The number of genes which were found in each pathway image. c. The number of genes in the 'up' category d. The number of genes in the 'down' category

See Also

[pathview] [KEGGREST]

Examples

```
## Not run:
 thy_el_comp2_path = hpgl_pathview(thy_el_comp2_kegg, species = "spz", indir = "pathview_in",
                                   outdir = "kegg_thy_el_comp2", string_from = "_Spy",
                                   string_to = "_Spy_", filenames = "pathname")

## End(Not run)
```

---

simple_proper *Invoke PROPER and replace its default data set with data of interest.*

Description

Recent reviewers of Najib's grants have taken an increased interest in knowing the statistical power of the various experiments. He queried Dr. Corrada-Bravo who suggested PROPER. I spent some time looking through it and, with some revervations, modified its workflow to (at least in theory) be able to examine any dataset. The workflow in question is particularly odd and warrants further discussion/analysis. This function is a modified version of 'default_proper()' above and invokes PROPER after re-formatting a given dataset in the way expected by PROPER.

Usage

```
simple_proper(
  de_tables,
  p = 0.05,
  experiment = "cheung",
  nsims = 20,
  reps = c(3, 5, 7, 10),
  de_method = "edger",
  alpha_type = "fdr",
  alpha = 0.1,
  stratify = "expr",
  target = "lfc",
  mean_or_median = "mean",
  filter = "none",
  delta = 0.5
)
```

Arguments

de_tables	A set of differential expression results, presumably from EdgeR or DESeq2.
p	Cutoff
experiment	The default data set in PROPER is entitled 'cheung'.
nsims	Number of simulations to perform.
reps	Simulate these number of experimental replicates.
de_method	There are a couple choices here for tools which are pretty old, my version of this only accepts deseq or edger.
alpha_type	I assume p-adjust type.
alpha	Accepted fdr rate.
stratify	There are a few options here, I don't fully understand them.
target	Cutoff.
mean_or_median	Use mean or median values?
filter	Apply a filter?
delta	Not epsilon! (E.g. I forget what this does).

Value

List containin the various tables and plots returned by PROPER.

See Also

[PROPER]

simple_topgo *Perform a simplified topgo analysis.*

Description

This will attempt to make it easier to run topgo on a set of genes.

Usage

```
simple_topgo(
  sig_genes,
  goid_map = "id2go.map",
  go_db = NULL,
  pvals = NULL,
  limitby = "fisher",
  limit = 0.1,
  signodes = 100,
  sigforall = TRUE,
  numchar = 300,
  selector = "topDiffGenes",
  pval_column = "adj.P.Val",
  overwrite = FALSE,
  densities = FALSE,
  pval_plots = TRUE,
  excel = NULL,
  ...
)
```

Arguments

sig_genes	Data frame of differentially expressed genes, containing IDs any other columns.
goid_map	File containing mappings of genes to goids in the format expected by topgo.
go_db	Data frame of the goids which may be used to make the goid_map.
pvals	Set of pvalues in the DE data which may be used to improve the topgo results.
limitby	Test to index the results by.
limit	Ontology pvalue to use as the lower limit.
signodes	I don't remember right now.
sigforall	Provide the significance for all nodes?
numchar	Character limit for the table of results.
selector	Function name for choosing genes to include.
pval_column	Column from which to acquire scores.
overwrite	Yeah I do not remember this one either.
densities	Densities, yeah, the densities...

pval_plots	Include pvalue plots of the results a la clusterprofiler?
excel	Print the results to an excel file?
...	Other options which I do not remember right now!

Value

Big list including the various outputs from topgo

See Also

[topGO]

`simple_varpart` *Use variancePartition to try and understand where the variance lies in a data set.*

Description

The arguments and usage of variancePartition are a bit opaque. This function attempts to fill in reasonable values and simplify its invocation.

Usage

```
simple_varpart(
  expt,
  predictor = NULL,
  factors = c("condition", "batch"),
  chosen_factor = "batch",
  do_fit = FALSE,
  cor_gene = 1,
  cpus = NULL,
  genes = 40,
  parallel = TRUE,
  mixed = FALSE,
  modify_expt = TRUE
)
```

Arguments

expt	Some data
predictor	Non-categorical predictor factor with which to begin the model.
factors	Character list of columns in the experiment design to query
chosen_factor	When checking for sane 'batches', what column to extract from the design?
do_fit	Perform a fitting using variancePartition?
cor_gene	Provide a set of genes to look at the correlations, defaults to the first gene.

cpus	Number cpus to use
genes	Number of genes to count.
parallel	Use doParallel?
modify_expt	Add annotation columns with the variance/factor?

Value

List of plots and variance data frames

See Also

[variancePartition]

`simple_xcell` *Invoke xCell and pretty-ify the result.*

Description

I initially thought xCell might prove the best tool/method for exploring cell deconvolution. I slowly figured out its limitations, but still think it seems pretty nifty for its use case. Thus this function is intended to make invoking it easier/faster.

Usage

```
simple_xcell(
  expt,
  signatures = NULL,
  genes = NULL,
  spill = NULL,
  expected_types = NULL,
  label_size = NULL,
  col_margin = 6,
  row_margin = 12,
  sig_cutoff = 0.2,
  verbose = TRUE,
  cores = 4,
  ...
)
```

Arguments

expt	Expressionset to query.
signatures	Alternate set of signatures to use.
genes	Subset of genes to query.
spill	The xCell spill parameter.

expected_types	Set of assumed types in the data.
label_size	How large to make labels when printing the final heatmap.
col_margin	Used by par() when printing the final heatmap.
row_margin	Ibid.
cores	How many CPUs to use?
...	Extra arguments when normalizing the data for use with xCell.

Value

Small list providing the output from xCell, the set of signatures, and heatmap.

See Also

[xCell]

---

sm *Silence*

Description

Some libraries/functions just won't shut up. Ergo, silence, peasant! This is a simpler silence peasant.

Usage

```
sm(..., wrap = TRUE)
```

Arguments

...	Some code to shut up.
wrap	Wrap the invocation and try again if it failed?

Value

Whatever the code would have returned.

`snp_by_chr` *The real worker. This extracts positions for a single chromosome and puts them into a parallelizable data structure.*

Description

The real worker. This extracts positions for a single chromosome and puts them into a parallelizable data structure.

Usage

```
snp_by_chr(medians, chr_name = "01", limit = 1)
```

Arguments

`medians`	A set of medians by position to look through
`chr_name`	Chromosome name to search
`limit`	Minimum number of median hits/position to count as a snp.

Value

A list of variant positions where each element is one chromosome.

See Also

[Vennerable]

`snp_subset_genes` *Look for only the variant positions in a subset of genes.*

Description

This was written in response to a query from Nancy and Maria Adelaida who wanted to look only at the variant positions in a few specific genes.

Usage

```
snp_subset_genes(
  expt,
  snp_expt,
  start_col = "start",
  end_col = "end",
  expt_name_col = "chromosome",
  snp_name_col = "chromosome",
  snp_start_col = "position",
```

```
  expt_gid_column = "gid",
  genes = c("LPAL13_120010900", "LPAL13_340013000", "LPAL13_000054100",
    "LPAL13_140006100", "LPAL13_180018500", "LPAL13_320022300")
)
```

Arguments

expt	Initial expressionset.
snp_expt	Variant position expressionset.
start_col	Metadata column with the start positions for each gene.
end_col	Metadata column with the end of the genes.
expt_name_col	Metadata column with the chromosome names.
snp_name_col	Ditto for the snp_expressionset.
snp_start_col	Metadata column containing the variant positions.
expt_gid_column	ID column for the genes.
genes	Set of genes to cross reference.

Value

New expressionset with only the variants for the genes of interest.

See Also

[GenomicRanges::makeGRangesFromDataFrame()] [IRanges::subsetByOverlaps()]

---

snps_intersections *Cross reference observed variants against the transcriptome annotation.*

Description

This function should provide counts of how many variant positions were observed with respect to each chromosome and with respect to each annotated sequence (currently this is limited to CDS, but that is negotiable).

Usage

```
snps_intersections(
  expt,
  snp_result,
  start_column = "start",
  end_column = "end",
  chr_column = "seqnames"
)
```

Arguments

expt	The original expressionset. This provides the annotation data.
snp_result	The result from get_snp_sets or count_expt_snps.
chr_column	Column in the annotation with the chromosome names.

Value

List containing the set of intersections in the conditions contained in snp_result, the summary of numbers of variants per chromosome, and

See Also

[snps_vs_genes()] [GenomicRanges::makeGRangesFromDataFrame()] [IRanges::subsetByOverlaps()] [IRanges::countOverlaps()]

Examples

```
 ## Not run:
 expt <- create_expt(metadata, gene_information)
 snp_expt <- count_expt_snps(expt)
 snp_result <- get_snp_sets(snp_expt)
 intersections <- snps_vs_intersections(expt, snp_result)

## End(Not run)
```

---

snps_vs_genes *Make a summary of the observed snps by gene ID.*

Description

Instead of cross referencing variant positions against experimental condition, one might be interested in seeing what variants are observed per gene. This function attempts to answer that question.

Usage

```
snps_vs_genes(
  expt,
  snp_result,
  start_col = "start",
  end_col = "end",
  snp_name_col = "seqnames",
  expt_name_col = "chromosome"
)
```

Arguments

expt	The original expressionset.
snp_result	The result from get_snp_sets().
start_col	Which column provides the start of each gene?
end_col	and the end column of each gene?
snp_name_col	Name of the column in the metadata with the sequence names.
expt_name_col	Name of the metadata column with the chromosome names.

Value

List with some information by gene.

See Also

[GenomicRanges::makeGRangesFromDataFrame()] [IRanges::subsetByOverlaps()] [IRanges::mergeByOverlaps()] [IRanges::countOverlaps()]

Examples

```
 ## Not run:
 expt <- create_expt(metadata, gene_information)
 snp_expt <- count_expt_snps(expt)
 snp_result <- get_snp_sets(snp_expt)
 gene_intersections <- snps_vs_genes(expt, snp_result)

## End(Not run)
```

---

subset_expt *Extract a subset of samples following some rule(s) from an experiment class.*

Description

Sometimes an experiment has too many parts to work with conveniently, this operation allows one to break it into smaller pieces.

Usage

```
subset_expt(expt, subset = NULL, ids = NULL, nonzero = NULL, coverage = NULL)
```

Arguments

expt	Expt chosen to extract a subset of data.
subset	Valid R expression which defines a subset of the design to keep.
ids	List of sample IDs to extract.
coverage	Request a minimum coverage/sample rather than text-based subset.

Value

metadata Expt class which contains the smaller set of data.

See Also

[Biobase] [pData()] [exprs()] [fData()]

Examples

```
## Not run:
 smaller_expt <- expt_subset(big_expt, "condition=='control'")
 all_expt <- expt_subset(expressionset, "")  ## extracts everything

## End(Not run)
```

---

subset_ontology_search

Perform ontology searches on up/down subsets of differential expression data.

Description

In the same way all_pairwise() attempts to simplify using multiple DE tools, this function seeks to make it easier to extract subsets of differentially expressed data and pass them to goseq, clusterProfiler, topGO, GOstats, and gProfiler.

Usage

```
subset_ontology_search(
  changed_counts,
  doplot = TRUE,
  do_goseq = TRUE,
  do_cluster = TRUE,
  do_topgo = TRUE,
  do_gostats = TRUE,
  do_gprofiler = TRUE,
  according_to = "limma",
  ...
)
```

Arguments

changed_counts	List of changed counts as ups and downs.
doplot	Include plots in the results?
do_goseq	Perform goseq search?
do_cluster	Perform clusterprofiler search?

do_topgo	Perform topgo search?
do_gostats	Perform gostats search?
do_gprofiler	Do a gprofiler search?
according_to	If results from multiple DE tools were passed, which one defines 'significant'?
...	Extra arguments!

Value

List of ontology search results, up and down for each contrast.

See Also

[goseq] [clusterProfiler] [topGO] [goStats] [gProfiler]

---

subtract_expt *Try a very literal subtraction*

Description

Try a very literal subtraction

Usage

```
subtract_expt(
  expt,
  new_meta,
  sample_column = "sample",
  convert_state = "cpm",
  transform_state = "raw",
  handle_negative = "zero",
  savefile = "subtracted.rda",
  ...
)
```

Arguments

expt	Input expressionset.
new_meta	dataframe containing the new metadata.
sample_column	Column in the sample sheet to use to acquire the sample IDs given the subtractions.
convert_state	Expected state of the input data vis a vis conversion (rpkm/cpm).
transform_state	Expected state of the input data vis a vis transformation (log/linear).
savefile	Save the new expt data to this file.
...	Parameters to pass to normalize_expt()
negative_to_zero	Set negative subtracted values to zero?

Value

New expt

`sum_eupath_exon_counts` *I want an easy way to sum counts in eupathdb-derived data sets. These have a few things which should make this relatively easy. Notably: The gene IDs look like: "exon_ID-1 exon_ID-2 exon_ID-3" Therefore we should be able to quickly merge these.*

Description

I want an easy way to sum counts in eupathdb-derived data sets. These have a few things which should make this relatively easy. Notably: The gene IDs look like: "exon_ID-1 exon_ID-2 exon_ID-3" Therefore we should be able to quickly merge these.

Usage

```
sum_eupath_exon_counts(counts)
```

Arguments

`counts`	Matrix/df/dt of count data.

Value

The same data type but with the exons summed.

`sum_exon_widths` *Given a data frame of exon counts and annotation information, sum the exons.*

Description

This function will merge a count table to an annotation table by the child column. It will then sum all rows of exons by parent gene and sum the widths of the exons. Finally it will return a list containing a df of gene lengths and summed counts.

Usage

```
sum_exon_widths(
  data = NULL,
  gff = NULL,
  annotdf = NULL,
  parent = "Parent",
  child = "row.names"
)
```

Arguments

data	Count tables of exons.
gff	Gff filename.
annotdf	Dataframe of annotations (probably from load_gff_annotations).
parent	Column from the annotations with the gene names.
child	Column from the annotations with the exon names.

Value

List of 2 data frames, counts and lengths by summed exons.

Author(s)

Keith Hughitt with some modifications by atb.

See Also

[rtracklayer] [load_gff_annotations()]

Examples

```
## Not run:
 summed <- sum_exon_widths(counts, gff = "reference/xenopus_laevis.gff.xz")

## End(Not run)
```

---

sva_modify_pvalues *Use sva's f.pvalue to adjust p-values for data adjusted by combat.*

Description

This is from section 5 of the sva manual: "Adjusting for surrogate values using the f.pvalue function." The following chunk of code is longer and more complex than I would like. This is because f.pvalue() assumes a pairwise comparison of a data set containing only two experimental factors. As a way to provide an example of _how_ to calculate appropriately corrected p-values for surrogate factor adjusted models, this is great; but when dealing with actual data, it falls a bit short.

Usage

```
sva_modify_pvalues(results)
```

Arguments

results	Table of differential expression results.

See Also

[sva]

table_style *Set the xlsx table style*

Description

Set the xlsx table style

Usage

```
table_style
```

Format

An object of class `character` of length 1.

tnseq_multi_saturation *Plot the saturation of multiple libraries simultaneously.*

Description

Plot the saturation of multiple libraries simultaneously.

Usage

```
tnseq_multi_saturation(
  meta,
  meta_column,
  ylimit = 100,
  column = "Reads",
  adjust = 1,
  ggstatsplot = FALSE
)
```

Arguments

`meta`	Experimental metadata
`meta_column`	Metadata column containing the filenames to query.
`ylimit`	Maximum y axis
`column`	Data file column to use for density calculation.
`adjust`	Density adjustment.
`ggstatsplot`	Include pretty ggstatsplot plot?

Value

a plot and table of the saturation for all samples.

`tnseq_saturation` *Make a plot and some simple numbers about tnseq saturation*

Description

This function takes as input a tab separated file from essentiality_tas.pl This is a perl script written to read a bam alignment of tnseq reads against a genome and count how many hits were observed on every TA in the given genome. It furthermore has some logic to tell the difference between reads which were observed on the forward vs. reverse strand as well as reads which appear to be on both strands (eg. they start and end with 'TA').

Usage

```
tnseq_saturation(data, column = "Reads", ylimit = 100, adjust = 2)
```

Arguments

`data`	data to plot
`column`	which column to use for plotting
`ylimit`	Define the y axis?
`adjust`	Prettification parameter from ggplot2.

Value

A plot and some numbers:

1. maximum_reads = The maximum number of reads observed in a single position.
2. hits_by_position = The full table of hits / position
3. num_hit_table = A table of how many times every number of hits was observed.
4. eq_0 = How many times were 0 hits observed?
5. gt_1 = How many positions have > 1 hit?
6. gt_2 = How many positions have > 2 hits?
7. gt_4 = How many positions have > 4 hits?
8. gt_8 = How many positions have > 8 hits?
9. gt_16 = How many positions have > 16 hits?
10. gt_32 = How many positions have > 32 hits?
11. ratios = Character vector of the ratios of each number of hits vs. 0 hits.
12. hit_positions = 2 column data frame of positions and the number of observed hits.
13. hits_summary = summary(hit_positions)
14. plot = Histogram of the number of hits observed.

See Also

[ggplot2]

Examples

```
 ## Not run:
 input <- "preprocessing/hpgl0837/essentiality/hpgl0837-trimmed_ca_ta-v0M1.wig"
 saturation <- tnseq_saturation(file = input)

## End(Not run)
```

`topDiffGenes` *A very simple selector of strong scoring genes (by p-value)*

Description

This function was provided in the topGO documentation, but not defined. It was copied/pasted here. I have ideas for including up/down expression but have so far deemed them not needed because I am feeding topGO already explicit lists of genes which are up/down/whatever. But it still is likely to be useful to be able to further subset the data.

Usage

```
topDiffGenes(allScore)
```

Arguments

`allScore`	The scores of the genes

`topgo_tables` *Make pretty tables out of topGO data*

Description

The topgo function GenTable is neat, but it needs some simplification to not be obnoxious.

Usage

```
topgo_tables(
  result,
  limit = 0.1,
  limitby = "fisher",
  numchar = 300,
  orderby = "fisher",
  ranksof = "fisher"
)
```

Arguments

result	Topgo result.
limit	Pvalue limit defining 'significant'.
limitby	Type of test to perform.
numchar	How many characters to allow in the description?
orderby	Which of the available columns to order the table by?
ranksof	Which of the available columns are used to rank the data?

Value

prettier tables

See Also

[topGO]

---

topgo_trees *Print trees from topGO.*

Description

The tree printing functionality of topGO is pretty cool, but difficult to get set correctly.

Usage

```
topgo_trees(
  tg,
  score_limit = 0.01,
  sigforall = TRUE,
  do_mf_fisher_tree = TRUE,
  do_bp_fisher_tree = TRUE,
  do_cc_fisher_tree = TRUE,
  do_mf_ks_tree = FALSE,
  do_bp_ks_tree = FALSE,
  do_cc_ks_tree = FALSE,
  do_mf_el_tree = FALSE,
  do_bp_el_tree = FALSE,
  do_cc_el_tree = FALSE,
  do_mf_weight_tree = FALSE,
  do_bp_weight_tree = FALSE,
  do_cc_weight_tree = FALSE,
  parallel = FALSE
)
```

Arguments

tg	Data from simple_topgo().
score_limit	Score limit to decide whether to add to the tree.
sigforall	Add scores to the tree?
do_mf_fisher_tree	Add the fisher score molecular function tree?
do_bp_fisher_tree	Add the fisher biological process tree?
do_cc_fisher_tree	Add the fisher cellular component tree?
do_mf_ks_tree	Add the ks molecular function tree?
do_bp_ks_tree	Add the ks biological process tree?
do_cc_ks_tree	Add the ks cellular component tree?
do_mf_el_tree	Add the el molecular function tree?
do_bp_el_tree	Add the el biological process tree?
do_cc_el_tree	Add the el cellular component tree?
do_mf_weight_tree	Add the weight mf tree?
do_bp_weight_tree	Add the bp weighted tree?
do_cc_weight_tree	Add the guess
parallel	Perform operations in parallel to speed this up?

Value

Big list including the various outputs from topgo.

See Also

[topGO]

---

transform_counts *Perform a simple transformation of a count table (log2)*

Description

the add argument is only important if the data was previously cpm'd because that does a +1, thus this will avoid a double+1 on the data.

Usage

```
transform_counts(count_table, design = NULL, method = "raw", base = NULL, ...)
```

Arguments

count_table	Matrix of count data
design	Sometimes the experimental design is also required.
method	Type of transformation to perform: log2/log10/log.
base	Other log scales?
...	Options I might pass from other functions are dropped into arglist.

Value

dataframe of transformed counts.

See Also

[limma]

Examples

```
## Not run:
 filtered_table = transform_counts(count_table, transform='log2', converted='cpm')

## End(Not run)
```

---

u_plot *Plot the rank order svd$u elements to get a view of how much the first genes contribute to the total variance by PC.*

Description

Plot the rank order svd$u elements to get a view of how much the first genes contribute to the total variance by PC.

Usage

```
u_plot(plotted_us)
```

Arguments

plotted_us	a list of svd$u elements

Value

a recordPlot() plot showing the first 3 PCs by rank-order svd$u.

unAsIs *Remove the AsIs attribute from some data structure.*

Description

Notably, when using some gene ontology libraries, the returned data structures include information which is set to type 'AsIs' which turns out to be more than slightly difficult to work with.

Usage

```
unAsIs(stuff)
```

Arguments

stuff	The data from which to remove the AsIs classification.

varpart_summaries *Attempt to use variancePartition's fitVarPartModel() function.*

Description

Note the word 'attempt'. This function is so ungodly slow that it probably will never be used.

Usage

```
varpart_summaries(expt, factors = c("condition", "batch"), cpus = 6)
```

Arguments

expt	Input expressionset.
factors	Set of factors to query
cpus	Number of cpus to use in doParallel.

Value

Summaries of the new model, in theory this would be a nicely batch-corrected data set.

See Also

[variancePartition]

`verbose` *Set a default verbosity, for now this just queries if this is an interactive session.*

Description

Set a default verbosity, for now this just queries if this is an interactive session.

Usage

```
verbose
```

Format

An object of class `logical` of length 1.

`what_happened` *Print a string describing what happened to this data.*

Description

Sometimes it is nice to have a string like: log2(cpm(data)) describing what happened to the data.

Usage

```
what_happened(
  expt = NULL,
  transform = "raw",
  convert = "raw",
  norm = "raw",
  filter = "raw",
  batch = "raw"
)
```

Arguments

`expt`	The expressionset.
`transform`	How was it transformed?
`convert`	How was it converted?
`norm`	How was it normalized?
`filter`	How was it filtered?
`batch`	How was it batch-corrected?

Value

An expression describing what has been done to this data.

See Also

[create_expt()] [normalize_expt()]

`write_basic` *Writes out the results of a basic search using write_de_table()*

Description

Looking to provide a single interface for writing tables from basic and friends.

Usage

```
write_basic(data, ...)
```

Arguments

`data`	Output from basic_pairwise()
`...`	Options for writing the xlsx file.

Details

Tested in test_26basic.R

See Also

[basic_pairwise()] [write_de_table()]

Examples

```
## Not run:
 finished_comparison <- basic_pairwise(expressionset)
 data_list <- write_basic(finished_comparison)

## End(Not run)
```

write_combined_legend *Write the legend of an excel file for combine_de_tables()*

Description

Write the legend of an excel file for combine_de_tables()

Usage

```
write_combined_legend(
  wb,
  excel_basename,
  plot_dim,
  apr,
  limma,
  include_limma,
  deseq,
  include_deseq,
  edger,
  include_edger,
  ebseq,
  include_ebseq,
  basic,
  include_basic,
  padj_type
)
```

Arguments

wb	Workbook to write
excel_basename	Where to write it
plot_dim	Default plot size.
apr	The all_pairwise() result.
limma	The limma result, which is redundant.
include_limma	Include the limma result?
deseq	The deseq result, which is redundant.
include_deseq	Include the deseq result?
edger	The edger result, which is redundant.
include_edger	Include the edger result?
ebseq	The ebseq result, which is redundant.
include_ebseq	Include the ebseq result?
basic	Basic data
include_basic	Include the basic result?
padj_type	P-adjustment employed.

write_combined_summary *Internal function to write a summary of some combined data*

Description

Internal function to write a summary of some combined data

Usage

```
write_combined_summary(
  wb,
  excel_basename,
  apr,
  extracted,
  compare_plots,
  lfc_cutoff = 1,
  p_cutoff = 0.05
)
```

Arguments

wb	xlsx workbook to which to write.
excel_basename	basename for printing plots.
apr	a pairwise result
extracted	table extracted from the pairwise result
compare_plots	series of plots to print out.

write_cp_data *Make a pretty table of clusterprofiler data in excel.*

Description

It is my intention to make a function like this for each ontology tool in my repetoire

Usage

```
write_cp_data(
  cp_result,
  excel = "excel/clusterprofiler.xlsx",
  wb = NULL,
  add_trees = TRUE,
  order_by = "qvalue",
  pval = 0.1,
```

```
  add_plots = TRUE,
  height = 15,
  width = 10,
  decreasing = FALSE,
  ...
)
```

Arguments

cp_result	A set of results from simple_clusterprofiler().
excel	An excel file to which to write some pretty results.
wb	Workbook object to write to.
add_trees	Include topgoish ontology trees?
order_by	What column to order the data by?
pval	Choose a cutoff for reporting by p-value.
add_plots	Include some pvalue plots in the excel output?
height	Height of included plots.
width	and their width.
decreasing	which direction?
...	Extra arguments are passed to arglist.

Value

The result from openxlsx in a prettyified xlsx file.

See Also

[openxlsx]

---

write_de_table *Writes out the results of a single pairwise comparison.*

Description

However, this will do a couple of things to make one's life easier: 1. Make a list of the output, one element for each comparison of the contrast matrix. 2. Write out the results() output for them in separate sheets in excel. 3. Since I have been using qvalues a lot for other stuff, add a column.

Usage

```
write_de_table(data, type = "limma", excel = "de_table.xlsx", ...)
```

Arguments

data	Output from results().
type	Which DE tool to write.
excel	Filename into which to save the xlsx data.
...	Parameters passed downstream, dumped into arglist and passed, notably the number of genes (n), the coefficient column (coef)

Details

Tested in test_24deseq.R Rewritten in 2016-12 looking to simplify combine_de_tables(). That function is far too big, this should become a template for that.

Value

List of data frames comprising the toptable output for each coefficient, I also added a qvalue entry to these toptable() outputs.

See Also

write_xlsx

Examples

```
## Not run:
 finished_comparison <- eBayes(deseq_output)
 data_list <- write_deseq(finished_comparison, workbook = "excel/deseq_output.xls")

## End(Not run)
```

---

write_deseq *Writes out the results of a deseq search using write_de_table()*

Description

Looking to provide a single interface for writing tables from deseq and friends.

Usage

```
write_deseq(data, ...)
```

Arguments

data	Output from deseq_pairwise()
...	Options for writing the xlsx file.

Details

Tested in test_24deseq.R

See Also

[write_de_table()]

Examples

```
## Not run:
 finished_comparison <- deseq2_pairwise(expressionset)
 data_list <- write_deseq(finished_comparison)

## End(Not run)
```

`write_edger` *Writes out the results of a edger search using write_de_table()*

Description

Looking to provide a single interface for writing tables from edger and friends.

Usage

```
write_edger(data, ...)
```

Arguments

`data`	Output from deseq_pairwise()
`...`	Options for writing the xlsx file.

Details

Tested in test_26edger.R

See Also

[write_de_Table()]

Examples

```
## Not run:
 finished_comparison <- edger_pairwise(expressionset)
 data_list <- write_edger(finished_comparison, excel = "edger_result.xlsx")

## End(Not run)
```

write_expt *Make pretty xlsx files of count data.*

Description

Some folks love excel for looking at this data. ok.

Usage

```
write_expt(
  expt,
  excel = "excel/pretty_counts.xlsx",
  norm = "quant",
  violin = TRUE,
  sample_heat = TRUE,
  convert = "cpm",
  transform = "log2",
  batch = "svaseq",
  filter = TRUE,
  med_or_mean = "mean",
  color_na = "#DD0000",
  merge_order = "counts_first",
  ...
)
```

Arguments

expt	An expressionset to print.
excel	Filename to write.
norm	Normalization to perform.
violin	Include violin plots?
sample_heat	Include sample heatmaps?
convert	Conversion to perform.
transform	Transformation used.
batch	Batch correction applied.
filter	Filtering method used.
med_or_mean	When printing mean by condition, one may want median.
merge_order	Used to decide whether to put the counts or annotations first when printing count tables.
...	Parameters passed down to methods called here (graph_metrics, etc).

Details

Tested in test_03graph_metrics.R This performs the following: Writes the raw data, graphs the raw data, normalizes the data, writes it, graphs it, and does a median-by-condition and prints that. I replaced the openxlsx function which writes images into xlsx files with one which does not require an opening of a pre-existing plotter. Instead it (optionally)opens a pdf device, prints the plot to it, opens a png device, prints to that, and inserts the resulting png file. Thus it sacrifices some flexibility for a hopefully more consistent behaivor. In addition, one may use the pdfs as a set of images importable into illustrator or whatever.

Value

A big honking excel file and a list including the dataframes and images created.

See Also

[openxlsx] [Biobase] [normalize_expt()] [graph_metrics()]

Examples

```
## Not run:
 excel_sucks <- write_expt(expt)

## End(Not run)
```

`write_go_xls` *Write gene ontology tables for excel*

Description

Combine the results from goseq, cluster profiler, topgo, and gostats and drop them into excel. Hopefully with a relatively consistent look.

Usage

```
write_go_xls(
  goseq,
  cluster,
  topgo,
  gostats,
  gprofiler,
  file = "excel/merged_go",
  dated = TRUE,
  n = 30,
  overwritefile = TRUE
)
```

Arguments

goseq	The goseq result from simple_goseq()
cluster	The result from simple_clusterprofiler()
topgo	Guess
gostats	Yep, ditto
gprofiler	woo hoo!
file	the file to save the results.
dated	date the excel file
n	the number of ontology categories to include in each table.
overwritefile	overwrite an existing excel file

Value

the list of ontology information

See Also

[openxlsx] [simple_goseq()] [simple_clusterprofiler()] [simple_gostats()] [simple_topgo()] [simple_gprofiler()]

---

write_goseq_data *Make a pretty table of goseq data in excel.*

Description

It is my intention to make a function like this for each ontology tool in my repetoire

Usage

```
write_goseq_data(
  goseq_result,
  excel = "excel/goseq.xlsx",
  wb = NULL,
  add_trees = TRUE,
  gather_genes = TRUE,
  order_by = "qvalue",
  pval = 0.1,
  add_plots = TRUE,
  height = 15,
  width = 10,
  decreasing = FALSE,
  ...
)
```

Arguments

goseq_result	A set of results from simple_goseq().
excel	An excel file to which to write some pretty results.
wb	Workbook object to write to.
add_trees	Include topgoish ontology trees?
gather_genes	Make a table of the genes in each category? (This may be slow)
order_by	What column to order the data by?
pval	Choose a cutoff for reporting by p-value.
add_plots	Include some pvalue plots in the excel output?
height	Height of included plots.
width	and their width.
decreasing	In forward or reverse order?
...	Extra arguments are passed to arglist.

Value

The result from openxlsx in a prettyified xlsx file.

See Also

[openxlsx] [simple_goseq()]

---

write_gostats_data *Make a pretty table of gostats data in excel.*

Description

It is my intention to make a function like this for each ontology tool in my repetoire

Usage

```
write_gostats_data(
  gostats_result,
  excel = "excel/gostats.xlsx",
  wb = NULL,
  add_trees = TRUE,
  order_by = "qvalue",
  pval = 0.1,
  add_plots = TRUE,
  height = 15,
  width = 10,
  decreasing = FALSE,
  ...
)
```

Arguments

gostats_result	A set of results from simple_gostats().
excel	An excel file to which to write some pretty results.
wb	Workbook object to write to.
add_trees	Include topgoish ontology trees?
order_by	Which column to order the data by?
pval	Choose a cutoff for reporting by p-value.
add_plots	Include some pvalue plots in the excel output?
height	Height of included plots.
width	and their width.
decreasing	Which order?
...	Extra arguments are passed to arglist.

Value

The result from openxlsx in a prettyified xlsx file.

See Also

[openxlsx] [simple_gostats()]

---

write_gprofiler_data *Write some excel results from a gprofiler search.*

Description

Gprofiler is pretty awesome. This function will attempt to write its results to an excel file.

Usage

```
write_gprofiler_data(
  gprofiler_result,
  wb = NULL,
  excel = "excel/gprofiler_result.xlsx",
  order_by = "recall",
  add_plots = TRUE,
  height = 15,
  width = 10,
  decreasing = FALSE,
  ...
)
```

Arguments

gprofiler_result	The result from simple_gprofiler().
wb	Optional workbook object, if you wish to append to an existing workbook.
excel	Excel file to which to write.
order_by	Which column to order the data by?
add_plots	Add some pvalue plots?
height	Height of included plots?
width	And their width.
decreasing	Which order?
...	More options, not currently used I think.

Value

A prettyified table in an xlsx document.

See Also

[openxlsx] [simple_gprofiler()]

---

write_gsva *Write out my various attempts at making sense of gsva.*

Description

While I am trying to make sense of gsva, I will use this function to write out the results I get so I can pass them to Najib/Maria Adelaida/Theresa to see if I am making sense.

Usage

```
write_gsva(retlist, excel, plot_dim = 6)
```

Arguments

retlist	Result from running get_sig_gsva
excel	Excel file to write
plot_dim	Plot dimensions, likely needs adjustment.

See Also

[simple_gsva()] [score_gsva_likelihoods()] [get_sig_gsva_categories()]

write_limma *Writes out the results of a limma search using write_de_table()*

Description

Looking to provide a single interface for writing tables from limma and friends.

Usage

```
write_limma(data, ...)
```

Arguments

data	Output from limma_pairwise()
...	Options for writing the xlsx file.

See Also

[write_de_table()]

Examples

```
## Not run:
 finished_comparison = limma_pairwise(expressionset)
 data_list = write_limma(finished_comparison)

## End(Not run)
```

write_sample_design *Put the metadata at the end of combined_de_tables()*

Description

For the moment this is a stupidly short function. I am betting we will elaborate on this over time.

Usage

```
write_sample_design(wb, apr)
```

Arguments

wb	workbook object.
apr	Pairwise result.

write_sig_legend *Internal function to write a legend for significant gene tables.*

Description

Internal function to write a legend for significant gene tables.

Usage

```
write_sig_legend(wb)
```

Arguments

wb	xlsx workbook object from openxlsx.

write_subset_ontologies *Write gene ontology tables for data subsets*

Description

Given a set of ontology results, this attempts to write them to an excel workbook in a consistent and relatively easy-to-read fashion.

Usage

```
write_subset_ontologies(
  kept_ontology,
  outfile = "excel/subset_go",
  dated = TRUE,
  n = NULL,
  overwritefile = TRUE,
  add_plots = TRUE,
  ...
)
```

Arguments

kept_ontology	A result from subset_ontology_search()
outfile	Workbook to which to write.
dated	Append the year-month-day-hour to the workbook.
n	How many ontology categories to write for each search
overwritefile	Overwrite an existing workbook?
add_plots	Add the various p-value plots to the end of each sheet?
...	some extra parameters

Value

a set of excel sheet/coordinates

See Also

[openxlsx]

Examples

```
## Not run:
 all_contrasts <- all_pairwise(expt, model_batch = TRUE)
 keepers <- list(bob = ('numerator','denominator'))
 kept <- combine_de_tables(all_contrasts, keepers = keepers)
 changed <- extract_significant_genes(kept)
 kept_ontologies <- subset_ontology_search(changed, lengths = gene_lengths,
                                           goids = goids, gff = gff, gff_type='gene')
 go_writer <- write_subset_ontologies(kept_ontologies)

## End(Not run)
```

`write_suppa_table` *Take a set of results from suppa and attempt to write it to a pretty xlsx file.*

Description

Suppa provides a tremendous amount of output, this attempts to standardize those results and print them to an excel sheet.

Usage

```
write_suppa_table(
  table,
  annotations = NULL,
  by_table = "gene_name",
  by_annot = "ensembl_gene_id",
  columns = "default",
  excel = "excel/suppa_table.xlsx"
)
```

Arguments

`table`	Result table from suppa.
`annotations`	Set of annotation data to include with the suppa result.
`by_table`	Use this column to merge the annotations and data tables from the perspective of the data table.

by_annot	Use this column to merge the annotations and data tables from the perspective of the annotations.
columns	Choose a subset of columns to include, or leave the defaults.
excel	Provide an excel file to write.

Value

Data frame of the merged data.

See Also

[write_xlsx()]

Examples

```
 ## Not run:
 prettier_table <- write_suppa_table(suppa_result_file,
                                     annotations = gene_info,
                                     excel = "excel/pretty_suppa_table.xlsx")

## End(Not run)
```

---

write_topgo_data *Make a pretty table of topgo data in excel.*

Description

It is my intention to make a function like this for each ontology tool in my repetoire

Usage

```
write_topgo_data(
  topgo_result,
  excel = "excel/topgo.xlsx",
  wb = NULL,
  order_by = "fisher",
  decreasing = FALSE,
  pval = 0.1,
  add_plots = TRUE,
  height = 15,
  width = 10,
  ...
)
```

Arguments

topgo_result	A set of results from simple_topgo().
excel	An excel file to which to write some pretty results.
wb	Workbook object to write to.
order_by	Which column to order the results by?
decreasing	In forward or reverse order?
pval	Choose a cutoff for reporting by p-value.
add_plots	Include some pvalue plots in the excel output?
height	Height of included plots.
width	and their width.
...	Extra arguments are passed to arglist.

Value

The result from openxlsx in a prettyified xlsx file.

See Also

[openxlsx] [simple_topgo()]

---

write_xlsx *Write a dataframe to an excel spreadsheet sheet.*

Description

I like to give folks data in any format they prefer, even though I sort of hate excel. Most people I work with use it, so therefore I do too. This function has been through many iterations, first using XLConnect, then xlsx, and now openxlsx. Hopefully this will not change again.

Usage

```
write_xlsx(
  data = "undef",
  wb = NULL,
  sheet = "first",
  excel = NULL,
  rownames = TRUE,
  start_row = 1,
  start_col = 1,
  title = NULL,
  ...
)
```

Arguments

data	Data frame to print.
wb	Workbook to which to write.
sheet	Name of the sheet to write.
excel	Filename of final excel workbook to write
rownames	Include row names in the output?
start_row	First row of the sheet to write. Useful if writing multiple tables.
start_col	First column to write.
title	Title for this xlsx table.
...	Set of extra arguments given to openxlsx.

Value

List containing the sheet and workbook written as well as the bottom-right coordinates of the last row/column written to the worksheet.

See Also

[openxlsx] [openxlsx::createWorkbook()] [openxlsx::writeData()] [openxlsx::writeDataTable()] [openxlsx::saveWorkbook()]

Examples

```
 ## Not run:
  xls_coords <- write_xlsx(dataframe, sheet = "hpgl_data", excel = "testing.xlsx")
  xls_coords <- write_xlsx(another_df, wb = xls_coords$workbook,
                           sheet = "hpgl_data", start_row = xls_coords$end_col)

## End(Not run)
```

---

xlsx_plot_png *An attempt to improve the behaivor of openxlsx's plot inserter.*

Description

The functions provided by openxlsx for adding plots to xlsx files are quite nice, but they can be a little annoying. This attempt to catch some corner cases and potentially save an extra svg-version of each plot inserted.

Usage

```
xlsx_plot_png(
  a_plot,
  wb = NULL,
  sheet = 1,
  width = 6,
  height = 6,
  res = 90,
  plotname = "plot",
  savedir = "saved_plots",
  fancy_type = "pdf",
  start_row = 1,
  start_col = 1,
  file_type = "png",
  units = "in",
  ...
)
```

Arguments

a_plot	The plot provided
wb	Workbook to which to write.
sheet	Name or number of the sheet to which to add the plot.
width	Plot width in the sheet.
height	Plot height in the sheet.
res	Resolution of the png image inserted into the sheet.
plotname	Prefix of the pdf file created.
savedir	Directory to which to save pdf copies of the plots.
fancy_type	Plot publication quality images in this format.
start_row	Row on which to place the plot in the sheet.
start_col	Column on which to place the plot in the sheet.
file_type	Currently this only does pngs, but perhaps I will parameterize this.
units	Units for the png plotter.
...	Extra arguments are passed to arglist (Primarily for vennerable plots which are odd)

Value

List containing the result of the tryCatch used to invoke the plot prints.

See Also

[openxlsx::insertImage()]

Examples

```
 ## Not run:
  fun_plot <- plot_pca(stuff)$plot
  df <- some_data_frame
  wb <- write_xlsx(df, excel = "funkytown.xlsx")$workbook
  try_results <- xlsx_plot_png(fun_plot, wb = wb)

## End(Not run)
```

---

ymxb_print *Print a model as y = mx + b just like in grade school!*

Description

Because, why not!?

Usage

```
ymxb_print(lm_model, as = "glue")
```

Arguments

lm_model	Model to print from glm/lm/robustbase.
as	Type to return.

Value

a string representation of that model.

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