Package 'dearseq'

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Type Package

Title Differential Expression Analysis for RNA-seq data through a robust variance component test

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Imports ggplot2, KernSmooth, matrixStats, methods, patchwork, parallel, pbapply, stats, statmod, survey, viridisLite

Suggests Biobase, BiocManager, BiocSet, edgeR, DESeq2, GEOquery, GSA, knitr, limma, readxl, rmarkdown, S4Vectors, SummarizedExperiment, testthat, covr

Description Differential Expression Analysis RNA-seq data with variance component score test accounting for data heteroscedasticity through precision weights. Perform both gene-wise and gene set analyses, and can deal with repeated or longitudinal data. Methods are detailed in: i) Agniel D & Hejblum BP (2017) Variance component score test for time-course gene set analysis of longitudinal RNA-seq data, Biostatistics, 18(4):589-604 ; and ii) Gauthier M, Agniel D, Thiébaut R & Hejblum BP (2020) dearseq: a variance component score test for RNA-Seq differential analysis that effectively controls the false discovery rate, NAR Genomics and Bioinformatics, 2(4):lqaa093.

LazyData true

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biocViews BiomedicalInformatics, CellBiology, DifferentialExpression, DNASeq, GeneExpression, Genetics, GeneSetEnrichment, ImmunoOncology, KEGG, Regression, RNASeq, Sequencing, SystemsBiology, TimeCourse, Transcription, Transcriptomics

BugReports https://github.com/borishejblum/dearseq/issues

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R topics documented:

`dearseq-package` *dearseq: Differential Expression Analysis for RNA-seq data through a robust variance component test*

Description

Differential Expression Analysis RNA-seq data with variance component score test accounting for data heteroscedasticity through precision weights. Perform both gene-wise and gene set analyses, and can deal with repeated or longitudinal data. Methods are detailed in: i) Agniel D & Hejblum BP (2017) Variance component score test for time-course gene set analysis of longitudinal RNA-seq data, Biostatistics, 18(4):589-604 ; and ii) Gauthier M, Agniel D, Thiébaut R & Hejblum BP (2020) dearseq: a variance component score test for RNA-Seq differential analysis that effectively controls the false discovery rate, NAR Genomics and Bioinformatics, 2(4):lqaa093.

Details

Analysis of RNA-seq data with variance component score test accounting for data heteroscedasticity through precision weights. Performs gene-wise analysis as well as gene set analysis, including for complex experimental designs such as longitudinal data.

Package:	dearseq
Type:	Package
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The two main functions of the `dearseq` package are `dear_seq` and `dgsa_seq`.

Author(s)

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References

Agniel D & Hejblum BP (2017). Variance component score test for time-course gene set analysis of longitudinal RNA-seq data, *Biostatistics*, 18(4):589-604. DOI: 10.1093/biostatistics/kxx005. arXiv:1605.02351.

Gauthier M, Agniel D, Thiébaut R & Hejblum BP (2020). dearseq: a variance component score test for RNA-Seq differential analysis that effectively controls the false discovery rate, *NAR Genomics and Bioinformatics*, 2(4):lqaa093. DOI: 10.1093/nargab/lqaa093. DOI: 10.1101/635714

See Also

Useful links:

- Report bugs at https://github.com/borishejblum/dearseq/issues

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`baduel_5gs` *Small portion of RNA-seq data from plant physiology study.*

Description

A subsample of the RNA-seq data from Baduel *et al.* studying Arabidopsis Arenosa physiology.

Usage

```
data(baduel_5gs)
```

Format

3 objects

- design: a design matrix for the 48 measured samples, containing the following variables:
  - SampleName corresponding column names from expr_norm_corr
  - Intercept an intercept variable
  - Population a factor identifying the plant population
  - Age_weeks numeric age of the plant at sampling time (in weeks)
  - Replicate a purely technical variable as replicates are not from the same individual over weeks. Should not be used in analysis.
  - Vernalized a logical variable indicating whether the plant had undergone vernalization (exposition to cold and short day photoperiods)
  - Vernalized a binary variable indicating whether the plant belonged to the KA population
  - AgeWeeks_Population interaction variable between the AgeWeeks and Population variables
  - AgeWeeks_Vernalized interaction variable between the AgeWeeks and Vernalized variables
  - Vernalized_Population interaction variable between the Vernalized and Population variables
  - AgeWeeks_Vernalized_Population interaction variable between the AgeWeeks, Vernalized and Population variables
- baduel_gmt: a gmt object containing 5 gene sets of interest (see GSA.read.gmt), which is simply a list with the 3 following components:
  - genesets: a list of n gene identifiers vectors composing eachgene set (each gene set is represented as the vector of the gene identifiers composing it)
  - geneset.names: a vector of length n containing the gene set names (i.e. gene sets identifiers)
  - geneset.descriptions: a vector of length n containing gene set descriptions (e.g. textual information on their biological function)
- expr_norm_corr: a numeric matrix containing the normalized batch corrected expression for the 2454 genes included in either of the 5 gene sets of interests

Source

http://www.ncbi.nlm.nih.gov/bioproject/PRJNA312410

References

Baduel P, Arnold B, Weisman CM, Hunter B & Bomblies K (2016). Habitat-Associated Life History and Stress-Tolerance Variation in Arabidopsis Arenosa. *Plant Physiology*, 171(1):437-51. 10.1104/pp.15.01875.

Agniel D & Hejblum BP (2017). Variance component score test for time-course gene set analysis of longitudinal RNA-seq data, *Biostatistics*, 18(4):589-604. 10.1093/biostatistics/kxx005. arXiv:1605.02351.

Examples

```
if(interactive()){
data('baduel_5gs')

set.seed(54321)
KAvsTBG <- dgsa_seq(exprmat=log2(expr_norm_corr+1),
                    covariates=apply(as.matrix(design[,
  c('Intercept', 'Vernalized', 'AgeWeeks', 'Vernalized_Population',
  'AgeWeeks_Population'), drop=FALSE]), 2, as.numeric),
                     variables2test =
                         as.matrix(design[, c('PopulationKA'), drop=FALSE]),
                     genesets=baduel_gmt$genesets[c(3,5)],
                     which_test = 'permutation', which_weights = 'loclin',
                     n_perm=1000, preprocessed = TRUE)

set.seed(54321)
Cold <- dgsa_seq(exprmat=log2(expr_norm_corr+1),
                 covariates=apply(as.matrix(design[,
   c('Intercept', 'AgeWeeks', 'PopulationKA', 'AgeWeeks_Population'),
   drop=FALSE]), 2, as.numeric),
                variables2test=as.matrix(design[, c('Vernalized',
                 'Vernalized_Population')]),
                 genesets=baduel_gmt$genesets[c(3,5)],
                 which_test = 'permutation', which_weights = 'loclin',
                 n_perm=1000, preprocessed = TRUE)
}
```

`dear_seq` *Differential expression analyis of RNA-seq data through a variance component test*

Description

Wrapper function for gene-by-gene association testing of RNA-seq data

Usage

```
dear_seq(
  exprmat = NULL,
  object = NULL,
  covariates = NULL,
  variables2test,
  sample_group = NULL,
  weights_var2test_condi = TRUE,
  cov_variables2test_eff = NULL,
  which_test = c("permutation", "asymptotic"),
  which_weights = c("loclin", "voom", "none"),
```

```
  n_perm = 1000,
  progressbar = TRUE,
  parallel_comp = TRUE,
  nb_cores = parallel::detectCores() - 1,
  preprocessed = FALSE,
  gene_based_weights = FALSE,
  bw = "nrd",
 kernel = c("gaussian", "epanechnikov", "rectangular", "triangular", "biweight",
    "tricube", "cosine", "optcosine"),
  exact = FALSE,
  transform = TRUE,
  padjust_methods = c("BH", "BY", "holm", "hochberg", "hommel", "bonferroni"),
  lowess_span = 0.5,
  R = NULL,
  adaptive = TRUE,
  max_adaptive = 64000,
  homogen_traj = FALSE,
  na.rm_dearseq = TRUE
)
```

Arguments

exprmat	a numeric matrix of size G x n containing the raw RNA-seq counts or preprocessed expressions from n samples for G genes. Default is NULL, in which case object must not be NULL.
object	an object that can be either a SummarizedExperiment, an ExpressionSet, a DESeqDataSet, or a DGEList. Default is NULL, in which case exprmat must not be NULL.
covariates	• If exprmat is specified as a matrix: then covariates must be a numeric matrix of size n x p containing the model covariates for n samples (design matrix). Usually, its first column is the intercept (full of 1s). • If object is specified: then covariates must be a character vector of length p containing the colnames of the design matrix given in object. If covariates is NULL (the default), then it is just the intercept.
variables2test	• If exprmat is specified as a matrix: a numeric design matrix of size n x K containing the K variables to be tested. • If object is specified: then variables2test must be a character vector of length K containing the colnames of the design matrix given in object.
sample_group	a vector of length n indicating whether the samples should be grouped (e.g. paired samples or longitudinal data). Coerced to be a factor. Default is NULL in which case no grouping is performed.
weights_var2test_condi	a logical flag indicating whether heteroscedasticity weights computation should be conditional on both the variables to be tested variables2test and on the covariates, or on covariates alone. Default is TRUE in which case conditional means are estimated conditionally on both variables2test and covariates.

cov_variables2test_eff
: a matrix of size K x K containing the covariance matrix of the K random effects. Only used if homogen_traj is FALSE. Default assume diagonal correlation matrix, i.e. independence of random effects.

which_test
: a character string indicating which method to use to approximate the variance component score test, either 'permutation' or 'asymptotic'. Default is 'permutation'.

which_weights
: a character string indicating which method to use to estimate the mean-variance relationship weights. Possibilities are 'loclin', 'voom' or 'none' (in which case no weighting is performed). Default is 'loclin'. See sp_weights and voom_weights for details.

n_perm
: the number of perturbations. Default is 1000

progressbar
: logical indicating wether a progressBar should be displayed when computing permutations (only in interactive mode).

parallel_comp
: a logical flag indicating whether parallel computation should be enabled. Only Linux and MacOS are supported, this is ignored on Windows. Default is TRUE.

nb_cores
: an integer indicating the number of cores to be used when parallel_comp is TRUE. Only Linux and MacOS are supported, this is ignored on Windows. Default is parallel::detectCores() -1.

preprocessed
: a logical flag indicating whether the expression data have already been preprocessed (e.g. log2 transformed). Default is FALSE, in which case y is assumed to contain raw counts and is normalized into log(counts) per million.

gene_based_weights
: a logical flag used for 'loclin' weights, indicating whether to estimate weights at the gene-level, or rather at the observation-level. Default is FALSE, which is what it should be for gene-wise analysis.

bw
: a character string indicating the smoothing bandwidth selection method to use. See bandwidth for details. Possible values are 'ucv', 'SJ', 'bcv', 'nrd' or 'nrd0'.

kernel
: a character string indicating which kernel should be used. Possibilities are 'gaussian', 'epanechnikov', 'rectangular', 'triangular', 'biweight', 'tricube', 'cosine', 'optcosine'. Default is 'gaussian' (NB: 'tricube' kernel corresponds to the loess method).

exact
: a logical flag indicating whether the non-parametric weights accounting for the mean-variance relationship should be computed exactly or extrapolated from the interpolation of local regression of the mean against the variance. Default is FALSE, which uses interpolation (faster computation).

transform
: a logical flag used for 'loclin' weights, indicating whether values should be transformed to uniform for the purpose of local linear smoothing. This may be helpful if tail observations are sparse and the specified bandwidth gives suboptimal performance there. Default is TRUE.

padjust_methods
: multiple testing correction method used if genesets is a list. Default is 'BH', i.e. Benjamini-Hochberg procedure for controlling the FDR. Other possibilities are: 'holm', 'hochberg', 'hommel', 'bonferroni' or 'BY' (for Benjamini-Yekutieli procedure).

lowess_span	smoother span for the lowess function, between 0 and 1. This gives the proportion of points in the plot which influence the smooth at each value. Larger values give more smoothness. Only used if which_weights is 'voom'. Default is 0.5.
R	library.size (optional, important to provide if preprocessed = TRUE). Default is NULL
adaptive	a logical flag indicating whether adaptive permutation should be performed. Default is TRUE
max_adaptive	The maximum number of permutations considered. Default is 64000
homogen_traj	a logical flag indicating whether trajectories should be considered homogeneous. Default is FALSE in which case trajectories are not only tested for trend, but also for heterogeneity.
na.rm_dearseq	logical: should missing values in y (including NA and NaN) be omitted from the calculations? Default is FALSE.

Value

A list with the following elements:

- which_test: a character string carrying forward the value of the 'which_test' argument indicating which test was perform (either 'asymptotic' or 'permutation').
- preprocessed: a logical flag carrying forward the value of the 'preprocessed' argument indicating whether the expression data were already preprocessed, or were provided as raw counts and transformed into log-counts per million.
- n_perm: an integer carrying forward the value of the 'n_perm' argument indicating the number of perturbations performed (NA if asymptotic test was performed).
- genesets: carrying forward the value of the 'genesets' argument defining the gene sets of interest (NULL for gene-wise testing).
- pval: computed p-values. A data.frame with one raw for each each gene set, or for each gene if genesets argument is NULL, and with 2 columns: the first one 'rawPval' contains the raw p-values, the second one contains the FDR adjusted p-values (according to the 'padjust_methods' argument) and is named 'adjPval'.

References

Gauthier M, Agniel D, Thiébaut R & Hejblum BP (2020). dearseq: a variance component score test for RNA-Seq differential analysis that effectivelycontrols the false discovery rate, *NAR Genomics and Bioinformatics*, 2(4):lqaa093. DOI: 10.1093/nargab/lqaa093. DOI: 10.1101/635714

See Also

sp_weights vc_test_perm vc_test_asym p.adjust

Examples

```
#Monte-Carlo estimation of the proportion of DE genes over `nsims` simulations under the null

#number of runs
nsims <- 2 #100
res <- numeric(nsims)
for(i in 1:nsims){
 n <- 1000 #number of genes
 nr=5 #number of measurements per subject (grouped data)
 ni=50 #number of subjects
 r <- nr*ni #number of measurements
 t <- matrix(rep(1:nr), ni, ncol=1, nrow=r) # the variable to be tested
 sigma <- 0.5
 b0 <- 1

 #under the null:
 b1 <- 0

 #create the matrix of gene expression
 y.tilde <- b0 + b1*t + rnorm(r, sd = sigma)
 y <- t(matrix(rnorm(n*r, sd = sqrt(sigma*abs(y.tilde))), ncol=n, nrow=r) +
          matrix(rep(y.tilde, n), ncol=n, nrow=r))

 #no covariates
 x <- matrix(1, ncol=1, nrow=r)

 #run test
 #asymptotic test with preprocessed grouped data
 res_genes <- dear_seq(exprmat=y, covariates=x, variables2test=t,
                       sample_group=rep(1:ni, each=nr),
                       which_test='asymptotic',
                      which_weights='none', preprocessed=TRUE)

 #proportion of raw p-values>0.05
 mean(res_genes$pvals[, 'rawPval']>0.05)

 #quantiles of raw p-values
 quantile(res_genes$pvals[, 'rawPval'])

 #proportion of raw p-values<0.05 i.e. proportion of DE genes
 res[i] <- mean(res_genes$pvals[, 'rawPval']<0.05)
 message(i)
}

#results
mean(res)

if(interactive()){
b0 <- 1
#under the null:
b1 <- 0
```

```
#create the matrix of gene expression
y.tilde <- b0 + b1*t + rnorm(r, sd = sigma)
y <- t(matrix(rnorm(n*r, sd = sqrt(sigma*abs(y.tilde))), ncol=n, nrow=r) +
      matrix(rep(y.tilde, n), ncol=n, nrow=r))

#run test
#asymptotic test with preprocessed grouped data
res_genes <- dear_seq(exprmat=y, covariates=x, variables2test=t,
                  sample_group=rep(1:ni, each=nr),
                  which_weights='none', preprocessed=TRUE)

#results
summary(res_genes$pvals)
}
```

---

dgsa_seq *Time-course Gene Set Analysis*

Description

Wrapper function for performing gene set analysis of (potentially longitudinal) RNA-seq data

Usage

```
dgsa_seq(
  exprmat = NULL,
  object = NULL,
  covariates = NULL,
  variables2test,
  weights_var2test_condi = TRUE,
  genesets,
  sample_group = NULL,
  cov_variables2test_eff = NULL,
  which_test = c("permutation", "asymptotic"),
  which_weights = c("loclin", "voom", "none"),
  n_perm = 1000,
  progressbar = TRUE,
  parallel_comp = TRUE,
  nb_cores = parallel::detectCores() - 1,
  preprocessed = FALSE,
  gene_based_weights = TRUE,
  bw = "nrd",
 kernel = c("gaussian", "epanechnikov", "rectangular", "triangular", "biweight",
    "tricube", "cosine", "optcosine"),
  exact = FALSE,
  transform = TRUE,
  padjust_methods = c("BH", "BY", "holm", "hochberg", "hommel", "bonferroni"),
  lowess_span = 0.5,
```

```
  R = NULL,
  adaptive = TRUE,
  max_adaptive = 64000,
  homogen_traj = FALSE,
  na.rm_gsaseq = TRUE,
  verbose = TRUE
)
```

Arguments

exprmat	a numeric matrix of size G x n containing the raw RNA-seq counts or preprocessed expressions from n samples for G genes. Default is NULL, in which case object must not be NULL.
object	an object that can be either an SummarizedExperiment, an ExpressionSet, a DESeqDataSet, or a DGEList. Default is NULL, in which case exprmat must not be NULL.
covariates	• If exprmat is specified as a matrix: then covariates must be a numeric matrix of size n x p containing the model covariates for n samples (design matrix). Usually, its first column is the intercept (full of 1s). • If object is specified: then covariates must be a character vector of length p containing the colnames of the design matrix given in object. If covariates is NULL (the default), then it is just the intercept.
variables2test	• If exprmat is specified as a matrix: a numeric design matrix of size n x K containing the K variables to be tested. • If object is specified: then variables2test must be a character vector of length K containing the colnames of the design matrix given in object.
weights_var2test_condi	a logical flag indicating whether heteroscedasticity weights computation should be conditional on both the variable(s) to be tested phi and on covariate(s) x, or on x alone. Default is TRUE in which case conditional means are estimated conditionally on both x and phi.
genesets	Can be either: • a vector • a list • a BiocSet object Can be a vector of index or subscripts that defines which rows of y constitute the investigated gene set (when only 1 gene set is being tested). Can also be a list of index (or rownames of y) when several gene sets are tested at once, such as the first element of a gmt object. Finally, can also be a BiocSet object If NULL, then gene-wise p-values are returned.
sample_group	a vector of length n indicating whether the samples should be grouped (e.g. paired samples or longitudinal data). Coerced to be a factor. Default is NULL in which case no grouping is performed.

cov_variables2test_eff
: a matrix of size K x K containing the covariance matrix of the K random effects. Only used if homogen_traj is FALSE. Default assume diagonal correlation matrix, i.e. independence of random effects.

which_test
: a character string indicating which method to use to approximate the variance component score test, either 'permutation' or 'asymptotic'. Default is 'permutation'.

which_weights
: a character string indicating which method to use to estimate the mean-variance relationship weights. Possibilities are 'loclin', 'voom' or 'none' (in which case no weighting is performed). Default is 'loclin'. See sp_weights and voom_weights for details.

n_perm
: the number of perturbations. Default is 1000.

progressbar
: logical indicating wether a progressBar should be displayed when computing permutations (only in interactive mode).

parallel_comp
: a logical flag indicating whether parallel computation should be enabled. Only Linux and MacOS are supported, this is ignored on Windows. Default is TRUE.

nb_cores
: an integer indicating the number of cores to be used when parallel_comp is TRUE. Only Linux and MacOS are supported, this is ignored on Windows. Default is parallel::detectCores() -1.

preprocessed
: a logical flag indicating whether the expression data have already been preprocessed (e.g. log2 transformed). Default is FALSE, in which case y is assumed to contain raw counts and is normalized into log(counts) per million.

gene_based_weights
: a logical flag used for 'loclin' weights, indicating whether to estimate weights at the gene-level, or rather at the observation-level. Default is TRUE, and weights are then estimated at the gene-level.

bw
: a character string indicating the smoothing bandwidth selection method to use. See bandwidth for details. Possible values are 'ucv', 'SJ', 'bcv', 'nrd' or 'nrd0'

kernel
: a character string indicating which kernel should be used. Possibilities are 'gaussian', 'epanechnikov', 'rectangular', 'triangular', 'biweight', 'tricube', 'cosine', 'optcosine'. Default is 'gaussian' (NB: 'tricube' kernel corresponds to the loess method).

exact
: a logical flag indicating whether the non-parametric weights accounting for the mean-variance relationship should be computed exactly or extrapolated from the interpolation of local regression of the mean against the variance. Default is FALSE, which uses interpolation (faster computation).

transform
: a logical flag used for 'loclin' weights, indicating whether values should be transformed to uniform for the purpose of local linear smoothing. This may be helpful if tail observations are sparse and the specified bandwidth gives suboptimal performance there. Default is TRUE.

padjust_methods
: multiple testing correction method used if genesets is a list. Default is 'BH', i.e. Benjamini-Hochberg procedure for controlling the FDR. Other possibilities are: 'holm', 'hochberg', 'hommel', 'bonferroni' or 'BY' (for Benjamini-Yekutieli procedure).

lowess_span	smoother span for the lowess function, between 0 and 1. This gives the proportion of points in the plot which influence the smooth at each value. Larger values give more smoothness. Only used if which_weights is 'voom'. Default is 0.5.
R	library size (optional, important to provide if preprocessed = TRUE). Default is NULL
adaptive	a logical flag indicating whether adaptive permutation should be performed. Default is TRUE
max_adaptive	The maximum number of permutations considered. Default is 64000
homogen_traj	a logical flag indicating whether trajectories should be considered homogeneous. Default is FALSE in which case trajectories are not only tested for trend, but also for heterogeneity.
na.rm_gsaseq	logical: should missing values in y (including NA and NaN) be omitted from the calculations? Default is TRUE.
verbose	logical: should informative messages be printed during the computation? Default is TRUE.

Value

A list with the following elements:

- which_test: a character string carrying forward the value of the 'which_test' argument indicating which test was perform (either 'asymptotic' or 'permutation').
- preprocessed: a logical flag carrying forward the value of the 'preprocessed' argument indicating whether the expression data were already preprocessed, or were provided as raw counts and transformed into log-counts per million.
- n_perm: an integer carrying forward the value of the 'n_perm' argument indicating the number of perturbations performed (NA if asymptotic test was performed).
- genesets: carrying forward the value of the 'genesets' argument defining the gene sets of interest (NULL for gene-wise t esting).
- pval: computed p-values. A data.frame with one raw for each each gene set, or for each gene if genesets argument is NULL, and with 2 columns: the first one 'rawPval' contains the raw p-values, the second one contains the FDR adjusted p-values (according to the 'padjust_methods' argument) and is named 'adjPval'.

References

Agniel D & Hejblum BP (2017). Variance component score test for time-course gene set analysis of longitudinal RNA-seq data, *Biostatistics*, 18(4):589-604. 10.1093/biostatistics/kxx005. arXiv:1605.02351.

Law, C. W., Chen, Y., Shi, W., & Smyth, G. K. (2014). voom: Precision weights unlock linear model analysis tools for RNA-seq read counts. *Genome Biology*, 15(2), R29.

See Also

sp_weights vc_test_perm vc_test_asym p.adjust

Examples

```
nsims <- 2 #100
res_quant <- list()
for(i in 1:2){
 n <- 2000#0
 nr <- 3
 r <- nr*20 #4*nr#100*nr
 t <- matrix(rep(1:nr), r/nr, ncol=1, nrow=r)
 sigma <- 0.4
 b0 <- 1

 #under the null:
 b1 <- 0

 y.tilde <- b0 + b1*t + rnorm(r, sd = sigma)
 y <- t(matrix(rnorm(n*r, sd = sqrt(sigma*abs(y.tilde))), ncol=n, nrow=r) +
        matrix(rep(y.tilde, n), ncol=n, nrow=r))
 x <- matrix(1, ncol=1, nrow=r)

 #run test
 res <- dgsa_seq(exprmat = y, covariates = x, variables2test = t,
                genesets=lapply(0:9, function(x){x*10+(1:10)}),
                cov_variables2test_eff = matrix(1),
                sample_group = rep(1:(r/nr), each=nr),
                which_test='asymptotic',
                which_weights='none', preprocessed=TRUE)
 res_genes <- dgsa_seq(exprmat = y, covariates = x,
                      variables2test = cbind(t),#, rnorm(r)), #t^2
                      genesets = NULL,
                      cov_variables2test_eff = diag(1),
                      sample_group = rep(1:(r/nr), each=nr),
                      which_test = 'asymptotic',
                      which_weights = 'none', preprocessed = TRUE)
 length(res_genes$pvals[, 'rawPval'])
 quantile(res_genes$pvals[, 'rawPval'])
 res_quant[[i]] <- res_genes$pvals[, 'rawPval']
}


#round(rowMeans(vapply(res_quant, FUN = quantile, FUN.VALUE = rep(1.1, 5)), 3)
#plot(density(unlist(res_quant)))
#mean(unlist(res_quant)<0.05)

if(interactive()){
res_genes <- dgsa_seq(exprmat = y, covariates = x, variables2test = t,
                    genesets = NULL,
                    cov_variables2test_eff = matrix(1),
                    sample_group = rep(1:(r/nr), each=nr),
                    which_test = 'permutation',
                    which_weights = 'none', preprocessed = TRUE,
                    n_perm = 1000, parallel_comp = FALSE)
```

```
mean(res_genes$pvals$rawPval < 0.05)
summary(res_genes$pvals$adjPval)
}
```

PBT_gmt *PBT gene sets related to kidney transplant*

Description

9 Pathogenesis Based Transcripts (PBT) gene sets specifically related to kidney transplant

Usage

```
data(PBT_gmt)
```

Format

a gmt object containing 9 gene sets specific to kidney transplant (see GSA.read.gmt), which is simply a list with the 3 following components:

- genesets: a list of n gene identifiers vectors composing eachgene set (each gene set is represented as the vector of the gene identifiers composing it)
- geneset.names: a vector of length n containing the gene set names (i.e. gene sets identifiers)
- geneset.descriptions: a vector of length n containing gene set descriptions (e.g. textual information on their biological function)

Source

http://atagc.med.ualberta.ca/Research/GeneLists

References

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Sellares J, Reeve J, Loupy A, et al., Molecular diagnosis of antibody-mediated rejection in human kidney transplants, *Am J Transplant*, 13:971-983, 2013.

Broin PO, Hayde N, Bao Y, et al., A pathogenesis-based transcript signature in donor-specific antibody-positive kidney transplant patients with normal biopsies, *Genomics Data* 2: 357-60, 2014.

Examples

```
data('PBT_gmt')
PBT_gmt
```

perm_pe *Exact permutation p-values*

Description

Calculates exact p-values for permutation tests when permutations are randomly drawn with replacement. This implementation is based on (slightly adapted) the implementation by Belinda Phipson and Gordon Smyth from the R package `statmod`

Usage

```
perm_pe(nperm_supobs, nperm_eff, total_possible_nperm)
```

Arguments

`nperm_supobs`	number of permutations that yielded test statistics at least as extreme as the observed data. Can be a vector or an array of values.
`nperm_eff`	number of permutations effectively computed.
`total_possible_nperm`	total number of permutations possible.

Value

a vector (or an array, similar to `nperm_supobs`) of exact p-values

Author(s)

Belinda Phipson and Gordon Smyth (adapted by Boris Hejblum)

References

Phipson B, and Smyth GK (2010). Permutation p-values should never be zero: calculating exact p-values when permutations are randomly drawn. *Statistical Applications in Genetics and Molecular Biology*, Volume 9, Issue 1, Article 39. http://www.statsci.org/smyth/pubs/PermPValuesPreprint.pdf

See Also

statmod::permp

Examples

```
perm_pe(10, 100, 1000)
```

plot.dearseq *Plot method for dearseq objects*

Description

Plot method for dearseq objects

Usage

```
## S3 method for class 'dearseq'
plot(x, signif_threshold = 0.05, ...)
```

Arguments

x	an object of class dear_seq
signif_threshold	a value between 0 and 1 specifying the nominal significance threshold. Default is 0.05.
...	further arguments

Value

a ggplot object

Author(s)

Boris Hejblum

plot_hist_pvals *Plotting raw p-values histogram*

Description

Display the histogram of raw p-values for diagnostic plots

Usage

```
plot_hist_pvals(pvals, binwidth = 0.02)
```

Arguments

pvals	a vector of raw p-values
binwidth	a value specifying the width of the histogram bins. Default is 0.02.

Value

a ggplot object

Author(s)

Boris Hejblum

`plot_ord_pvals` *Plot of gene-wise p-values*

Description

This function prints the sorted exact p-values along with the Benjamini-Hochberg limit and the 5

Usage

```
plot_ord_pvals(pvals, signif_threshold = 0.05)
```

Arguments

`pvals`	a vector of length `n` containing the raw p-values for each gene
`signif_threshold`	a value between `0` and 1 specifying the nominal significance threshold. Default is `0.05`.

Value

a plot of sorted gene-wise p-values

`plot_weights` *Plotting mean-variance fit for precision weights estimation*

Description

Display the variability with respect to the level of expression and the associated smoothed estimation of precision weights accounting for heteroscedasticity.

Usage

```
plot_weights(x)
```

Arguments

x	a list (such as outputed by the functions sp_weights or voom_weights) containing the following components: • weights: a matrix n x G containing the estimated precision weights • plot_utilities: a list containing the following elements: – reverse_trans: a function encoding the reverse function used for smoothing the observations before computing the weights – method: the weight computation method (either "voom" or "loclin") – smth: the vector of the smoothed values computed – gene_based: a logical indicating whether the computed weights are based on average at the gene level or on individual observations – mu: the transformed observed counts or averages – v: the observed variability estimates

Value

a ggplot object

Author(s)

Boris Hejblum

Examples

```
G <- 10000
n <- 12
p <- 2
y <- sapply(1:n, FUN = function(x){rnbinom(n = G, size = 0.07, mu = 200)})
x <- sapply(1:p, FUN = function(x){rnorm(n = n, mean = n, sd = 1)})

if(interactive()){
 w <- sp_weights(y, x, use_phi=FALSE, na.rm = TRUE, gene_based=TRUE)
 plot_weights(w)

 vw <-  voom_weights(y, x)
 plot_weights(vw)
}
```

---

sp_weights *Non parametric local heteroscedasticity weights*

Description

Computes precision weights that account for heteroscedasticity in RNA-seq count data based on non-parametric local linear regression estimates.

Usage

```
sp_weights(
  y,
  x,
  phi = NULL,
  use_phi = TRUE,
  preprocessed = FALSE,
  gene_based = FALSE,
  bw = c("nrd", "ucv", "SJ", "nrd0", "bcv"),
 kernel = c("gaussian", "epanechnikov", "rectangular", "triangular", "biweight",
    "tricube", "cosine", "optcosine"),
  exact = FALSE,
  transform = TRUE,
  verbose = TRUE,
  na.rm = FALSE
)
```

Arguments

y	a numeric matrix of size G x n containing the raw RNA-seq counts or preprocessed expression from n samples for G genes.
x	a numeric matrix of size n x p containing the model covariate(s) from n samples (design matrix).
phi	a numeric design matrix of size n x K containing the K variable(s) of interest(e.g. bases of time).
use_phi	a logical flag indicating whether conditional means should be conditioned on phi and on covariate(s) x, or on x alone. Default is TRUE in which case conditional means are estimated conditionally on both x and phi.
preprocessed	a logical flag indicating whether the expression data have already been preprocessed (e.g. log2 transformed). Default is FALSE, in which case y is assumed to contain raw counts and is normalized into log(counts) per million.
gene_based	a logical flag indicating whether to estimate weights at the gene-level. Default is FALSE, when weights will be estimated at the observation-level.
bw	a character string indicating the smoothing bandwidth selection method to use. See bandwidth for details. Possible values are 'ucv', 'SJ', 'bcv', 'nrd' or 'nrd0'. Default is 'nrd'.
kernel	a character string indicating which kernel should be used. Possibilities are 'gaussian', 'epanechnikov', 'rectangular', 'triangular', 'biweight', 'tricube', 'cosine', 'optcosine'. Default is 'gaussian' (NB: 'tricube' kernel corresponds to the loess method).
exact	a logical flag indicating whether the non-parametric weights accounting for the mean-variance relationship should be computed exactly or extrapolated from the interpolation of local regression of the mean against the variance. Default is FALSE, which uses interpolation (faster).
transform	a logical flag indicating whether values should be transformed to uniform for the purpose of local linear smoothing. This may be helpful if tail observations are

	sparse and the specified bandwidth gives suboptimal performance there. Default is TRUE.
verbose	a logical flag indicating whether informative messages are printed during the computation. Default is TRUE.
na.rm	logical: should missing values (including NA and NaN) be omitted from the calculations? Default is FALSE.

Value

a list containing the following components:

- weights: a matrix n x G containing the computed precision weights
- plot_utilities: a list containing the following elements:
  - reverse_trans: a function encoding the reverse function used for smoothing the observations before computing the weights
  - method: the weight computation method ("loclin")
  - smth: the vector of the smoothed values computed
  - gene_based: a logical indicating whether the computed weights are based on average at the gene level or on individual observations
  - mu: the transformed observed counts or averages
  - v: the observed variability estimates

Author(s)

Boris Hejblum

See Also

bandwidth density

Examples

```
set.seed(123)

G <- 10000
n <- 12
p <- 2
y <- sapply(1:n, FUN = function(x){rnbinom(n = G, size = 0.07, mu = 200)})

x <- sapply(1:p, FUN = function(x){rnorm(n = n, mean = n, sd = 1)})

w <- sp_weights(y, x, use_phi=FALSE, na.rm = TRUE)
```

summary.dearseq *Summary method for dearseq objects*

Description

Summary method for dearseq objects

Usage

```
## S3 method for class 'dearseq'
summary(object, signif_threshold = 0.05, ...)

## S3 method for class 'summary.dearseq'
print(x, ...)
```

Arguments

object	an object of class dear_seq
signif_threshold	a value between 0 and 1 specifying the nominal significance threshold. Default is 0.05.
...	further arguments
x	an object of class 'summary.dearseq'.

Value

a list

Author(s)

Boris Hejblum

vc_test_asym *Asymptotic variance component test statistic and p-value*

Description

This function computes an approximation of the variance component test based on the asymptotic distribution of a mixture of χ^2s using the saddlepoint method from pchisqsum, as per Chen & Lumley 20219 CSDA.

Usage

```
vc_test_asym(
  y,
  x,
  indiv = rep(1, nrow(x)),
  phi,
  w,
  Sigma_xi = diag(ncol(phi)),
  genewise_pvals = FALSE,
  homogen_traj = FALSE,
  na.rm = FALSE
)
```

Arguments

y	a numeric matrix of dim g x n containing the raw or normalized RNA-seq counts for g genes from n samples.
x	a numeric design matrix of dim n x p containing the p covariates to be adjusted for
indiv	a vector of length n containing the information for attributing each sample to one of the studied individuals. Coerced to be a factor.
phi	a numeric design matrix of size n x K containing the K longitudinal variables to be tested (typically a vector of time points or functions of time)
w	a vector of length n containing the weights for the n samples, corresponding to the inverse of the diagonal of the estimated covariance matrix of y.
Sigma_xi	a matrix of size K x K containing the covariance matrix of the K random effects corresponding to phi.
genewise_pvals	a logical flag indicating whether gene-wise p-values should be returned. Default is FALSE in which case gene set p-value is computed and returned instead.
homogen_traj	a logical flag indicating whether trajectories should be considered homogeneous. Default is FALSE in which case trajectories are not only tested for trend, but also for heterogeneity.
na.rm	logical: should missing values (including NA and NaN) be omitted from the calculations? Default is FALSE.

Value

A list with the following elements when the set p-value is computed:

- set_score_obs: the approximation of the observed set score
- set_pval: the associated set p-value

or a list with the following elements when gene-wise p-values are computed:

- gene_scores_obs: vector of approximating the observed gene-wise scores
- gene_pvals: vector of associated gene-wise p-values

References

Chen T & Lumley T (2019), Numerical evaluation of methods approximating the distribution of a large quadratic form in normal variables, Computational Statistics & Data Analysis, 139:75-81.

See Also

pchisqsum

Examples

```
set.seed(123)

##generate some fake data
########################
n <- 100
r <- 12
t <- matrix(rep(1:(r/4)), 4, ncol=1, nrow=r)
sigma <- 0.4
b0 <- 1

#under the null:
b1 <- 0
#under the alternative:
#b1 <- 0.5
y.tilde <- b0 + b1*t + rnorm(r, sd = sigma)
y <- t(matrix(rnorm(n*r, sd = sqrt(sigma*abs(y.tilde))), ncol=n, nrow=r) +
      matrix(rep(y.tilde, n), ncol=n, nrow=r))
x <- matrix(1, ncol=1, nrow=r)

#run test
asymTestRes <- vc_test_asym(y, x, phi=cbind(t, t^2),
                            w=matrix(1, ncol=ncol(y), nrow=nrow(y)),
                            Sigma_xi=diag(2), indiv=1:r, genewise_pvals=TRUE)
plot(density(asymTestRes$gene_pvals))
quantile(asymTestRes$gene_pvals)
```

---

vc_test_perm *Permutation-based variance component test statistic and p-value*

Description

This function computes an approximation of the Variance Component test for a mixture of χ^2s using permutations. This is preferable to the asymptotic approximation for small sample sizes. We rely on exact p-values following Phipson and Smyth, 2010 (see References).

Usage

```
vc_test_perm(
  y,
  x,
  indiv = rep(1, nrow(x)),
  phi,
  w,
  Sigma_xi = diag(ncol(phi)),
  n_perm = 1000,
  progressbar = TRUE,
  parallel_comp = TRUE,
  nb_cores = parallel::detectCores() - 1,
  genewise_pvals = FALSE,
  adaptive = TRUE,
  max_adaptive = 64000,
  homogen_traj = FALSE,
  na.rm = FALSE
)
```

Arguments

y	a numeric matrix of dim G x n containing the raw RNA-seq counts for G genes from n samples.
x	a numeric design matrix of dim n x p containing the p covariates to be adjusted for.
indiv	a vector of length n containing the information for attributing each sample to one of the studied individuals. Coerced to be a factor.
phi	a numeric design matrix of size n x K containing the K variables to be tested
w	a vector of length n containing the weights for the n samples.
Sigma_xi	a matrix of size K x K containing the covariance matrix of the K random effects.
n_perm	the number of perturbations. Default is 1000.
progressbar	logical indicating wether a progressBar should be displayed when computing permutations (only in interactive mode).
parallel_comp	a logical flag indicating whether parallel computation should be enabled. Only Linux and MacOS are supported, this is ignored on Windows. Default is TRUE.
nb_cores	an integer indicating the number of cores to be used when parallel_comp is TRUE. Only Linux and MacOS are supported, this is ignored on Windows. Default is parallel::detectCores() -1.
genewise_pvals	a logical flag indicating whether gene-wise p-values should be returned. Default is FALSE in which case gene-set p-value is computed and returned instead.
adaptive	a logical flag indicating whether adaptive permutation should be performed. Default is TRUE
max_adaptive	The maximum number of permutations considered. Default is 64000

homogen_traj	a logical flag indicating whether trajectories should be considered homogeneous. Default is FALSE in which case trajectories are not only tested for trend, but also for heterogeneity.
na.rm	logical: should missing values (including NA and NaN) be omitted from the calculations? Default is FALSE.

Value

A list with the following elements when the set p-value is computed:

- set_score_obs: the approximation of the observed set score
- set_pval: the associated set p-value

or a list with the following elements when gene-wise p-values are computed:

- gene_scores_obs: vector of approximating the observed gene-wise scores
- gene_pvals: vector of associated gene-wise p-values
- ds_fdr: vector of associated gene-wise discrete false discovery rates

References

Phipson B, and Smyth GK (2010). Permutation p-values should never be zero: calculating exact p-values when permutations are randomly drawn. *Statistical Applications in Genetics and Molecular Biology*, Volume 9, Issue 1, Article 39. http://www.statsci.org/smyth/pubs/PermPValuesPreprint.pdf

Examples

```
set.seed(123)

##generate some fake data
########################
n <- 100
r <- 12
t <- matrix(rep(1:3), 4, ncol=1, nrow=r)
sigma <- 0.4
b0 <- 1

#under the null:
b1 <- 0
#under the alternative:
b1 <- 0.5
y.tilde <- b0 + b1*t + rnorm(r, sd = sigma)
y <- t(matrix(rnorm(n*r, sd = sqrt(sigma*abs(y.tilde))), ncol=n, nrow=r) +
      matrix(rep(y.tilde, n), ncol=n, nrow=r))
x <- matrix(1, ncol=1, nrow=r)

#run test
permTestRes <- vc_test_perm(y, x, phi=t,
                            w=matrix(1, ncol=ncol(y), nrow=nrow(y)),
                            indiv=rep(1:4, each=3), n_perm=50, #1000,
```

```
                              parallel_comp = FALSE)
permTestRes$set_pval
```

`voom_weights` *Precision weights accounting for heteroscedasticity in RNA-seq count data*

Description

Implementation of the procedure described in Law *et al.* for estimating precision weights from RNA-seq data.

Usage

```
voom_weights(y, x, preprocessed = FALSE, lowess_span = 0.5, R = NULL)
```

Arguments

`y`	a matrix of size `G` x `n` containing the raw RNA-seq counts or preprocessed expressions from `n` samples for `G` genes.
`x`	a matrix of size `n` x `p` containing the model covariates from `n` samples (design matrix).
`preprocessed`	a logical flag indicating whether the expression data have already been preprocessed (e.g. log2 transformed). Default is `FALSE`, in which case `y` is assumed to contain raw counts and is normalized into log(counts) per million.
`lowess_span`	smoother span for the lowess function, between 0 and 1. This gives the proportion of points in the plot which influence the smooth at each value. Larger values give more smoothness. Default is `0.5`.
`R`	library.size (optional, important to provide if `preprocessed = TRUE`). Default is `NULL`

Value

a vector of length `n` containing the computed precision weights

Author(s)

Boris Hejblum

References

Law, C. W., Chen, Y., Shi, W., & Smyth, G. K. (2014). voom: Precision weights unlock linear model analysis tools for RNA-seq read counts. *Genome Biology*, 15(2), R29.

See Also

`lowess` `approxfun` `voom`

Examples

```
set.seed(123)

G <- 10000
n <- 12
p <- 2

y <- sapply(1:n, FUN=function(x){rnbinom(n=G, size=0.07, mu=200)})
x <- sapply(1:p, FUN=function(x){rnorm(n=n, mean=n, sd=1)})

my_w <-  voom_weights(y, x)
plot_weights(my_w)
if (requireNamespace('limma', quietly = TRUE)) {
 w_voom <- limma::voom(counts=y, design=x, plot=TRUE)
 #slightly faster, same results
 all.equal(my_w$weights, w_voom$weights)
}

if(interactive()){
#microbenchmark::microbenchmark(limma::voom(counts=t(y), design=x,
#                               plot=FALSE), voom_weights(x, y),
#                               times=30)
}
```

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