

# Package ‘variancePartition’

November 29, 2020

**Type** Package

**Title** Quantify and interpret divers of variation in multilevel gene expression experiments

**Version** 1.20.0

**Date** 2020-10-26

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**Description** Quantify and interpret multiple sources of biological and technical variation in gene expression experiments. Uses a linear mixed model to quantify variation in gene expression attributable to individual, tissue, time point, or technical variables. Includes dream differential expression analysis for repeated measures.

**VignetteBuilder** knitr

**License** GPL (>= 2)

**BugReports** <https://github.com/GabrielHoffman/variancePartition/issues>

**Suggests** BiocStyle, knitr, pander, rmarkdown, edgeR, dendextend, tximport, tximportData, ballgown, DESeq2, RUnit, BiocGenerics, r2glmm, readr

**biocViews** RNASeq, GeneExpression, GeneSetEnrichment, DifferentialExpression, BatchEffect, QualityControl, Regression, Epigenetics, FunctionalGenomics, Transcriptomics, Normalization, Preprocessing, Microarray, ImmunoOncology, Software

**Depends** R (>= 3.6.0), ggplot2, limma, BiocParallel, scales, Biobase, methods

**Imports** MASS, pbkrtest (>= 0.4-4), lmerTest, iterators, splines, foreach, doParallel, colorRamps, gplots, progress, reshape2, lme4 (>= 1.1-10), grDevices, graphics, utils, stats

**RoxygenNote** 7.1.1

**git\_url** <https://git.bioconductor.org/packages/variancePartition>

**git\_branch** RELEASE\_3\_12

**git\_last\_commit** bd06b39

**git\_last\_commit\_date** 2020-10-27

**Date/Publication** 2020-11-28

**R topics documented:**

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---

as.data.frame,varPartResults-method  
*Convert to data.frame*

---

**Description**

Convert varPartResults to data.frame

**Usage**

```
## S4 method for signature 'varPartResults'  
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

**Arguments**

x	varPartResults
row.names	pass thru to generic
optional	pass thru to generic
...	other arguments.

**Value**

data.frame

**Examples**

```
# load library  
# library(variancePartition)  
  
# load simulated data:  
# geneExpr: matrix of gene expression values  
# info: information/metadata about each sample  
data(varPartData)  
  
# Specify variables to consider  
# Age is continuous so we model it as a fixed effect  
# Individual and Tissue are both categorical, so we model them as random effects  
form <- ~ Age + (1|Individual) + (1|Tissue)  
  
# Fit model  
varPart <- fitExtractVarPartModel( geneExpr[1:5,], form, info )  
  
# convert to matrix  
as.data.frame(varPart)
```

---

as.matrix,varPartResults-method

*Convert to matrix*

---

**Description**

Convert varPartResults to matrix

**Usage**

```
## S4 method for signature 'varPartResults'  
as.matrix(x, ...)
```

**Arguments**

x                    varPartResults  
 ...                  other arguments.

**Value**

matrix

**Examples**

```
# load library
# library(variancePartition)

# load simulated data:
# geneExpr: matrix of gene expression values
# info: information/metadata about each sample
data(varPartData)

# Specify variables to consider
# Age is continuous so we model it as a fixed effect
# Individual and Tissue are both categorical, so we model them as random effects
form <- ~ Age + (1|Individual) + (1|Tissue)

# Fit model
varPart <- fitExtractVarPartModel( geneExpr[1:5,], form, info )

# convert to matrix
as.matrix(varPart)
```

---

calcVarPart

*Compute variance statistics*

---

**Description**

For linear model, variance fractions are computed based on the sum of squares explained by each component. For the linear mixed mode, the variance fractions are computed by variance component estimates for random effects and sum of squares for fixed effects.

For a generalized linear model, the variance fraction also includes the contribution of the link function so that fractions are reported on the linear (i.e. link) scale rather than the observed (i.e. response) scale. For linear regression with an identity link, fractions are the same on both scales. But for logit or probit links, the fractions are not well defined on the observed scale due to the transformation imposed by the link function.

The variance implied by the link function is the variance of the corresponding distribution: logit -> logistic distribution -> variance is  $\pi^2/3$  probit -> standard normal distribution -> variance is 1

Reviewed by Nakagawa and Schielzeth. 2012. A general and simple method for obtaining R2 from generalized linear mixed-effects models. <https://doi.org/10.1111/j.2041-210x.2012.00261.x>

Proposed by McKelvey and Zavoina. A statistical model for the analysis of ordinal level dependent variables. The Journal of Mathematical Sociology 4(1) 103-120 <https://doi.org/10.1080/0022250X.1975.9989847>

Also see DeMaris. Explained Variance in Logistic Regression: A Monte Carlo Study of Proposed Measures. Sociological Methods & Research 2002 <https://doi.org/10.1177/0049124102031001002>

We note that Nagelkerke's pseudo  $R^2$  evaluates the variance explained by the full model. Instead, a variance partitioning approach evaluates the variance explained by each term in the model, so that the sum of each systematic plus random term sums to 1 (Hoffman and Schadt, 2016, Nakagawa and Schielzeth, 2012).

### Usage

```
calcVarPart(fit, showWarnings = TRUE, ...)  
  
## S4 method for signature 'lm'  
calcVarPart(fit, showWarnings = TRUE, ...)  
  
## S4 method for signature 'lmerMod'  
calcVarPart(fit, showWarnings = TRUE, ...)  
  
## S4 method for signature 'glm'  
calcVarPart(fit, showWarnings = TRUE, ...)
```

### Arguments

fit	model fit from lm() or lmer()
showWarnings	show warnings about model fit (default TRUE)
...	additional arguments (not currently used)

### Details

Compute fraction of variation attributable to each variable in regression model. Also interpretable as the intra-class correlation after correcting for all other variables in the model.

### Value

fraction of variance explained / ICC for each variable in the linear model

### Examples

```
library(lme4)  
data(varPartData)  
  
# Linear mixed model  
fit <- lmer( geneExpr[1,] ~ (1|Tissue) + Age, info)  
calcVarPart( fit )  
  
# Linear model  
# Note that the two models produce slightly different results  
# This is expected: they are different statistical estimates  
# of the same underlying value  
fit <- lm( geneExpr[1,] ~ Tissue + Age, info)  
calcVarPart( fit )
```

---

`canCorPairs`*canCorPairs*

---

## Description

Assess correlation between all pairs of variables in a formula

## Usage

```
canCorPairs(formula, data, showWarnings = TRUE)
```

## Arguments

<code>formula</code>	standard additive linear model formula (doesn't support random effects currently, so just change the syntax)
<code>data</code>	<code>data.frame</code> with the data for the variables in the formula
<code>showWarnings</code>	default to <code>true</code>

## Details

Canonical Correlation Analysis (CCA) is similar to correlation between two vectors, except that CCA can accommodate matrices as well. For a pair of variables, `canCorPairs` assesses the degree to which they co-vary and contain the same information. Variables in the formula can be a continuous variable or a discrete variable expanded to a matrix (which is done in the backend of a regression model). For a pair of variables, `canCorPairs` uses CCA to compute the correlation between these variables and returns the pairwise correlation matrix.

Statistically, let  $\rho$  be the array of correlation values returned by the standard R function `canCor` to compute CCA. `canCorPairs` returns  $\sqrt{\text{mean}(\rho^2)}$ , which is the fraction of the maximum possible correlation. When comparing a two vectors, or a vector and a matrix, this gives the same value as the absolute correlation. When comparing two sets of categorical variables (i.e. expanded to two matrices), this is equivalent to Cramer's V statistic.

Note that CCA returns correlation values between 0 and 1.

## Value

Matrix of correlation values between all pairs of variables.

## Examples

```
# load library
# library(variancePartition)

# load simulated data:
data(varPartData)

# specify formula
form <- ~ Individual + Tissue + Batch + Age + Height

# Compute Canonical Correlation Analysis (CCA)
# between all pairs of variables
```

```
# returns absolute correlation value
C = canCorPairs( form, info)

# Plot correlation matrix
plotCorrMatrix( C )
```

---

classifyTestsF

*Multiple Testing Genewise Across Contrasts*


---

### Description

For each gene, classify a series of related t-statistics as up, down or not significant.

### Usage

```
classifyTestsF(object, ...)
```

### Arguments

object	numeric matrix of t-statistics or an 'MArrayLM2' object from which the t-statistics may be extracted.
...	additional arguments

### Details

Works like `limma::classifyTestsF`, except object can have a list of covariance matrices `object$scov.coefficients.list`, instead of just one in `object$scov.coefficients`

### See Also

`limma::classifyTestsF`

---

classifyTestsF, MArrayLM2-method

*Multiple Testing Genewise Across Contrasts*


---

### Description

For each gene, classify a series of related t-statistics as up, down or not significant.

### Usage

```
## S4 method for signature 'MArrayLM2'
classifyTestsF(
  object,
  cor.matrix = NULL,
  df = Inf,
  p.value = 0.01,
  fstat.only = FALSE
)
```

**Arguments**

object	numeric matrix of t-statistics or an 'MArrayLM2' object from which the t-statistics may be extracted.
cor.matrix	covariance matrix of each row of t-statistics. Defaults to the identity matrix.
df	numeric vector giving the degrees of freedom for the t-statistics. May have length 1 or length equal to the number of rows of tstat.
p.value	numeric value between 0 and 1 giving the desired size of the test
fstat.only	logical, if 'TRUE' then return the overall F-statistic as for 'FStat' instead of classifying the test results

**Details**

Works like `limma::classifyTestsF`, except object can have a list of covariance matrices `object$cov.coefficients.list`, instead of just one in `object$cov.coefficients`

**See Also**

`limma::classifyTestsF`

---

colinearityScore	<i>Collinearity score</i>
------------------	---------------------------

---

**Description**

Collinearity score for a regression model indicating if variables are too highly correlated to give meaningful results

**Usage**

```
colinearityScore(fit)
```

**Arguments**

fit	regression model fit from <code>lm()</code> or <code>lmer()</code>
-----	--

**Value**

Returns the collinearity score between 0 and 1, where a score  $> 0.999$  means the degree of collinearity is too high. This function reports the correlation matrix between coefficient estimates for fixed effects. The collinearity score is the maximum absolute correlation value of this matrix. Note that the values are the correlation between the parameter estimates, and not between the variables themselves.



**Examples**

```

# load library
# library(variancePartition)

# load simulated data:
data(varPartData)
form <- ~ Age + (1|Individual) + (1|Tissue)

res <- fitVarPartModel( geneExpr[1:10,], form, info )

# evaluate the collinearity score on the first model fit
# this reports the correlation matrix between coefficients estimates
# for fixed effects
# the collinearity score is the maximum absolute correlation value
# If the collinearity score > .999 then the variance partition
# estimates may be problematic
# In that case, a least one variable should be omitted
colinearityScore(res[[1]])

```

---

dream

*Differential expression with linear mixed model*


---

**Description**

Fit linear mixed model for differential expression and perform hypothesis test on fixed effects as specified in the contrast matrix L

**Usage**

```

dream(
  exprObj,
  formula,
  data,
  L,
  ddf = c("Satterthwaite", "Kenward-Roger"),
  useWeights = TRUE,
  weightsMatrix = NULL,
  control = lme4::lmerControl(calc.derivs = FALSE, check.rankX = "stop.deficient"),
  suppressWarnings = FALSE,
  quiet = FALSE,
  BPPARAM = bpparam(),
  computeResiduals = TRUE,
  REML = TRUE,
  ...
)

```

**Arguments**

exprObj            matrix of expression data (g genes x n samples), or ExpressionSet, or EList returned by voom() from the limma package

formula	specifies variables for the linear (mixed) model. Must only specify covariates, since the rows of <code>exprObj</code> are automatically used as a response. e.g.: <code>~ a + b + (1 c)</code> Formulas with only fixed effects also work, and <code>lmFit()</code> followed by <code>contrasts.fit()</code> are run.
data	data.frame with columns corresponding to formula
L	contrast matrix specifying a linear combination of fixed effects to test
ddf	Specify "Satterthwaite" or "Kenward-Roger" method to estimate effective degrees of freedom for hypothesis testing in the linear mixed model. Note that Kenward-Roger is more accurate, but is <i>*much*</i> slower. Satterthwaite is a good enough approximation for most datasets.
useWeights	if TRUE, analysis uses heteroskedastic error estimates from <code>voom()</code> . Value is ignored unless <code>exprObj</code> is an <code>EList()</code> from <code>voom()</code> or <code>weightsMatrix</code> is specified
weightsMatrix	matrix the same dimension as <code>exprObj</code> with observation-level weights from <code>voom()</code> . Used only if <code>useWeights</code> is TRUE
control	control settings for <code>lmer()</code>
suppressWarnings	if TRUE, do not stop because of warnings or errors in model fit
quiet	suppress message, default FALSE
BPPARAM	parameters for parallel evaluation
computeResiduals	if TRUE, compute residuals and extract with <code>residuals(fit)</code> . Setting to FALSE saves memory
REML	use restricted maximum likelihood to fit linear mixed model. default is TRUE. See Details.
...	Additional arguments for <code>lmer()</code> or <code>lm()</code>

## Details

A linear (mixed) model is fit for each gene in `exprObj`, using `formula` to specify variables in the regression. If categorical variables are modeled as random effects (as is recommended), then a linear mixed model is used. For example if `formula` is `~ a + b + (1|c)`, then the model is

```
fit <- lmer( exprObj[j,] ~ a + b + (1|c), data=data)
```

`useWeights=TRUE` causes `weightsMatrix[j,]` to be included as weights in the regression model.

Note: Fitting the model for 20,000 genes can be computationally intensive. To accelerate computation, models can be fit in parallel using `BiocParallel` to run code in parallel. Parallel processing must be enabled before calling this function. See below.

The regression model is fit for each gene separately. Samples with missing values in either gene expression or metadata are omitted by the underlying call to `lmer`.

Hypothesis tests and degrees of freedom are produced by `lmerTest` and `pbkrtest` packages

While `REML=TRUE` is required by `lmerTest` when `ddf='Kenward-Roger'`, `ddf='Satterthwaite'` can be used with `REML` as `TRUE` or `FALSE`. Since the Kenward-Roger method gave the best power with an accurate control of false positive rate in our simulations, and since the Satterthwaite method with `REML=TRUE` gives p-values that are slightly closer to the Kenward-Roger p-values, `REML=TRUE` is the default. See Vignette "3) Theory and practice of random effects and REML"

**Value**

MArrayLM2 object (just like MArrayLM from limma), and the directly estimated p-value (without eBayes)

**Examples**

```
# load library
# library(variancePartition)
library(BiocParallel)

# Intialize parallel backend with 4 cores
library(BiocParallel)
register(SnowParam(4))

# load simulated data:
# geneExpr: matrix of gene expression values
# info: information/metadata about each sample
data(varPartData)

form <- ~ Batch + (1|Individual) + (1|Tissue)

# Fit linear mixed model for each gene
# run on just 10 genes for time
fit = dream( geneExpr[1:10,], form, info)

# view top genes
topTable( fit )

# get contrast matrix testing if the coefficient for Batch2 is
# different from coefficient for Batch3
# The variable of interest must be a fixed effect
L = getContrast( geneExpr, form, info, c("Batch2", "Batch3"))

# plot contrasts
plotContrasts( L )

# Fit linear mixed model for each gene
# run on just 10 genes for time
# Note that that dream() is not compatible with eBayes()
fit2 = dream( geneExpr[1:10,], form, info, L)

# view top genes
topTable( fit2 )

# Parallel processing using multiple cores with reduced memory usage
param = SnowParam(4, "SOCK", progressBar=TRUE)
fit3 = dream( geneExpr[1:10,], form, info, L, BPPARAM = param)

# Fit fixed effect model for each gene
# Use lmFit in the backend
# Need to run eBayes afterward
form <- ~ Batch
fit4 = dream( geneExpr[1:10,], form, info)
fit4 = eBayes( fit4 )
```

```
# view top genes
topTable( fit4 )

# Compute residuals using dream
fit5 = dream( geneExpr[1:10,], form, info, L, BPPARAM = param, computeResiduals=TRUE)

# Return residuals
residuals(fit5)
```

---

eBayes,MArrayLM2-method  
*eBayes for MArrayLM2*

---

### Description

eBayes for MArrayLM2. It simply returns the original input with no change

### Usage

```
## S4 method for signature 'MArrayLM2'
eBayes(
  fit,
  proportion = 0.01,
  stdev.coef.lim = c(0.1, 4),
  trend = FALSE,
  robust = FALSE,
  winsor.tail.p = c(0.05, 0.1)
)
```

### Arguments

fit	fit
proportion	proportion
stdev.coef.lim	stdev.coef.lim
trend	trend
robust	robust
winsor.tail.p	winsor.tail.p

### Details

Note that empirical Bayes is problematic for linear mixed models. This function returns its original input with no change. It is included here just for compatibility.

### Value

results of eBayes

ESS

*Effective sample size***Description**

Compute effective sample size based on correlation structure in linear mixed model

**Usage**

```
ESS(fit, method = "full")
```

```
## S4 method for signature 'lmerMod'
ESS(fit, method = "full")
```

**Arguments**

fit	model fit from lmer()
method	"full" uses the full correlation structure of the model. The "approximate" method makes the simplifying assumption that the study has a mean of m samples in each of k groups, and computes m based on the study design. When the study design is evenly balanced (i.e. the assumption is met), this gives the same results as the "full" method.

**Details**

Effective sample size calculations are based on:

Liu, G., and Liang, K. Y. (1997). Sample size calculations for studies with correlated observations. *Biometrics*, 53(3), 937-47.

"full" method: if

$$V_x = \text{var}(Y; x)$$

is the variance-covariance matrix of Y, the response, based on the covariate x, then the effective sample size corresponding to this covariate is

$$\sum_{i,j} (V_x^{-1})_{i,j}$$

. In R notation, this is: `sum(solve(V_x))`. In practice, this can be evaluated as `sum(w)`, where R

"approximate" method: Letting m be the mean number of samples per group,

$$k$$

be the number of groups, and

$$\rho$$

be the intraclass correlation, the effective sample size is

$$mk / (1 + \rho(m - 1))$$

Note that these values are equal when there are exactly m samples in each group. If m is only an average then this is an approximation.

**Value**

effective sample size for each random effect in the model

**Examples**

```
library(lme4)
data(varPartData)

# Linear mixed model
fit <- lmer( geneExpr[1,] ~ (1|Individual) + (1|Tissue) + Age, info)

# Effective sample size
ESS( fit )
```

---

extractVarPart

*Extract variance statistics*

---

**Description**

Extract variance statistics from list of models fit with `lm()` or `lmer()`

**Usage**

```
extractVarPart(modelList, showWarnings = TRUE, ...)
```

**Arguments**

<code>modelList</code>	list of <code>lmer()</code> model fits
<code>showWarnings</code>	show warnings about model fit (default TRUE)
<code>...</code>	other arguments

**Value**

data.frame of fraction of variance explained by each variable, after correcting for all others.

**Examples**

```
# library(variancePartition)

# Intialize parallel backend with 4 cores
library(BiocParallel)
register(SnowParam(4))

# load simulated data:
# geneExpr: matrix of gene expression values
# info: information/metadata about each sample
data(varPartData)

# Specify variables to consider
# Age is continuous so we model it as a fixed effect
# Individual and Tissue are both categorical, so we model them as random effects
form <- ~ Age + (1|Individual) + (1|Tissue)
```

```

# Step 1: fit linear mixed model on gene expression
# If categorical variables are specified, a linear mixed model is used
# If all variables are modeled as continuous, a linear model is used
# each entry in results is a regression model fit on a single gene
# Step 2: extract variance fractions from each model fit
# for each gene, returns fraction of variation attributable to each variable
# Interpretation: the variance explained by each variable
# after correction for all other variables
varPart <- fitExtractVarPartModel( geneExpr, form, info )

# violin plot of contribution of each variable to total variance
plotVarPart( sortCols( varPart ) )

# Advanced:
# Fit model and extract variance in two separate steps
# Step 1: fit model for each gene, store model fit for each gene in a list
results <- fitVarPartModel( geneExpr, form, info )

# Step 2: extract variance fractions
varPart <- extractVarPart( results )

```

---

```
fitExtractVarPartModel
```

*Fit linear (mixed) model, report variance fractions*

---

## Description

Fit linear (mixed) model to estimate contribution of multiple sources of variation while simultaneously correcting for all other variables. Report fraction of variance attributable to each variable

## Usage

```

fitExtractVarPartModel(
  exprObj,
  formula,
  data,
  REML = FALSE,
  useWeights = TRUE,
  weightsMatrix = NULL,
  showWarnings = TRUE,
  control = lme4::lmerControl(calc.derivs = FALSE, check.rankX = "stop.deficient"),
  quiet = FALSE,
  BPPARAM = bpparam(),
  ...
)

## S4 method for signature 'matrix'
fitExtractVarPartModel(
  exprObj,
  formula,

```

```

    data,
    REML = FALSE,
    useWeights = TRUE,
    weightsMatrix = NULL,
    showWarnings = TRUE,
    control = lme4::lmerControl(calc.derivs = FALSE, check.rankX = "stop.deficient"),
    quiet = FALSE,
    BPPARAM = bpparam(),
    ...
)

## S4 method for signature 'data.frame'
fitExtractVarPartModel(
  exprObj,
  formula,
  data,
  REML = FALSE,
  useWeights = TRUE,
  weightsMatrix = NULL,
  showWarnings = TRUE,
  control = lme4::lmerControl(calc.derivs = FALSE, check.rankX = "stop.deficient"),
  quiet = FALSE,
  BPPARAM = bpparam(),
  ...
)

## S4 method for signature 'EList'
fitExtractVarPartModel(
  exprObj,
  formula,
  data,
  REML = FALSE,
  useWeights = TRUE,
  weightsMatrix = NULL,
  showWarnings = TRUE,
  control = lme4::lmerControl(calc.derivs = FALSE, check.rankX = "stop.deficient"),
  quiet = FALSE,
  BPPARAM = bpparam(),
  ...
)

## S4 method for signature 'ExpressionSet'
fitExtractVarPartModel(
  exprObj,
  formula,
  data,
  REML = FALSE,
  useWeights = TRUE,
  weightsMatrix = NULL,
  showWarnings = TRUE,
  control = lme4::lmerControl(calc.derivs = FALSE, check.rankX = "stop.deficient"),
  quiet = FALSE,

```



```

    BPPARAM = bpparam(),
    ...
)

## S4 method for signature 'sparseMatrix'
fitExtractVarPartModel(
  exprObj,
  formula,
  data,
  REML = FALSE,
  useWeights = TRUE,
  weightsMatrix = NULL,
  showWarnings = TRUE,
  control = lme4::lmerControl(calc.derivs = FALSE, check.rankX = "stop.deficient"),
  quiet = FALSE,
  BPPARAM = bpparam(),
  ...
)

```

### Arguments

exprObj	matrix of expression data (g genes x n samples), or ExpressionSet, or EList returned by voom() from the limma package
formula	specifies variables for the linear (mixed) model. Must only specify covariates, since the rows of exprObj are automatically used as a response. e.g.: ~ a + b + (1 c)
data	data.frame with columns corresponding to formula
REML	use restricted maximum likelihood to fit linear mixed model. default is FALSE. See Details.
useWeights	if TRUE, analysis uses heteroskedastic error estimates from voom(). Value is ignored unless exprObj is an EList() from voom() or weightsMatrix is specified
weightsMatrix	matrix the same dimension as exprObj with observation-level weights from voom(). Used only if useWeights is TRUE
showWarnings	show warnings about model fit (default TRUE)
control	control settings for lmer()
quiet	suppress message, default FALSE
BPPARAM	parameters for parallel evaluation
...	Additional arguments for lmer() or lm()

### Details

A linear (mixed) model is fit for each gene in exprObj, using formula to specify variables in the regression. If categorical variables are modeled as random effects (as is recommended), then a linear mixed model is used. For example if formula is ~ a + b + (1|c), then the model is

```
fit <- lmer( exprObj[j,] ~ a + b + (1|c), data=data)
```

If there are no random effects, so formula is ~ a + b + c, a 'standard' linear model is used:

```
fit <- lm( exprObj[j,] ~ a + b + c, data=data)
```

In both cases, `useWeights=TRUE` causes `weightsMatrix[j,]` to be included as weights in the regression model.

Note: Fitting the model for 20,000 genes can be computationally intensive. To accelerate computation, models can be fit in parallel using `BiocParallel` to run in parallel. Parallel processing must be enabled before calling this function. See below.

The regression model is fit for each gene separately. Samples with missing values in either gene expression or metadata are omitted by the underlying call to `lm/lmer`.

`REML=FALSE` uses maximum likelihood to estimate variance fractions. This approach produced unbiased estimates, while `REML=TRUE` can show substantial bias. See Vignette "3) Theory and practice of random effects and REML"

## Value

`list()` of where each entry is a model fit produced by `lmer()` or `lm()`

## Examples

```
# load library
# library(variancePartition)

# Intialize parallel backend with 4 cores
library(BiocParallel)
register(SnowParam(4))

# load simulated data:
# geneExpr: matrix of gene expression values
# info: information/metadata about each sample
data(varPartData)

# Specify variables to consider
# Age is continuous so we model it as a fixed effect
# Individual and Tissue are both categorical, so we model them as random effects
form <- ~ Age + (1|Individual) + (1|Tissue)

# Step 1: fit linear mixed model on gene expression
# If categorical variables are specified, a linear mixed model is used
# If all variables are modeled as continuous, a linear model is used
# each entry in results is a regression model fit on a single gene
# Step 2: extract variance fractions from each model fit
# for each gene, returns fraction of variation attributable to each variable
# Interpretation: the variance explained by each variable
# after correction for all other variables
varPart <- fitExtractVarPartModel( geneExpr, form, info )

# violin plot of contribution of each variable to total variance
plotVarPart( sortCols( varPart ) )

# Note: fitExtractVarPartModel also accepts ExpressionSet
data(sample.ExpressionSet, package="Biobase")

# ExpressionSet example
form <- ~ (1|sex) + (1|type) + score
info2 <- pData(sample.ExpressionSet)
varPart2 <- fitExtractVarPartModel( sample.ExpressionSet, form, info2 )
```

---

fitVarPartModel	<i>Fit linear (mixed) model</i>
-----------------	---------------------------------

---

### Description

Fit linear (mixed) model to estimate contribution of multiple sources of variation while simultaneously correcting for all other variables.

### Usage

```
fitVarPartModel(
  exprObj,
  formula,
  data,
  REML = FALSE,
  useWeights = TRUE,
  weightsMatrix = NULL,
  showWarnings = TRUE,
  fxn = identity,
  control = lme4::lmerControl(calc.derivs = FALSE, check.rankX = "stop.deficient"),
  quiet = FALSE,
  BPPARAM = bpparam(),
  ...
)

## S4 method for signature 'matrix'
fitVarPartModel(
  exprObj,
  formula,
  data,
  REML = FALSE,
  useWeights = TRUE,
  weightsMatrix = NULL,
  showWarnings = TRUE,
  fxn = identity,
  control = lme4::lmerControl(calc.derivs = FALSE, check.rankX = "stop.deficient"),
  quiet = FALSE,
  BPPARAM = bpparam(),
  ...
)

## S4 method for signature 'data.frame'
fitVarPartModel(
  exprObj,
  formula,
  data,
  REML = FALSE,
```

```
    useWeights = TRUE,
    weightsMatrix = NULL,
    showWarnings = TRUE,
    fxn = identity,
    control = lme4::lmerControl(calc.derivs = FALSE, check.rankX = "stop.deficient"),
    quiet = FALSE,
    BPPARAM = bpparam(),
    ...
)

## S4 method for signature 'EList'
fitVarPartModel(
  exprObj,
  formula,
  data,
  REML = FALSE,
  useWeights = TRUE,
  weightsMatrix = NULL,
  showWarnings = TRUE,
  fxn = identity,
  control = lme4::lmerControl(calc.derivs = FALSE, check.rankX = "stop.deficient"),
  quiet = FALSE,
  BPPARAM = bpparam(),
  ...
)

## S4 method for signature 'ExpressionSet'
fitVarPartModel(
  exprObj,
  formula,
  data,
  REML = FALSE,
  useWeights = TRUE,
  weightsMatrix = NULL,
  showWarnings = TRUE,
  fxn = identity,
  control = lme4::lmerControl(calc.derivs = FALSE, check.rankX = "stop.deficient"),
  quiet = FALSE,
  BPPARAM = bpparam(),
  ...
)

## S4 method for signature 'sparseMatrix'
fitVarPartModel(
  exprObj,
  formula,
  data,
  REML = FALSE,
  useWeights = TRUE,
  weightsMatrix = NULL,
  showWarnings = TRUE,
  fxn = identity,
```

```

control = lme4::lmerControl(calc.derivs = FALSE, check.rankX = "stop.deficient"),
quiet = FALSE,
BPPARAM = bpparam(),
...
)

```

### Arguments

exprObj	matrix of expression data (g genes x n samples), or ExpressionSet, or EList returned by voom() from the limma package
formula	specifies variables for the linear (mixed) model. Must only specify covariates, since the rows of exprObj are automatically used as a response. e.g.: ~ a + b + (1 c)
data	data.frame with columns corresponding to formula
REML	use restricted maximum likelihood to fit linear mixed model. default is FALSE. See Details.
useWeights	if TRUE, analysis uses heteroskedastic error estimates from voom(). Value is ignored unless exprObj is an EList() from voom() or weightsMatrix is specified
weightsMatrix	matrix the same dimension as exprObj with observation-level weights from voom(). Used only if useWeights is TRUE
showWarnings	show warnings about model fit (default TRUE)
fxn	apply function to model fit for each gene. Defaults to identify function so it returns the model fit itself
control	control settings for lmer()
quiet	suppress message, default FALSE
BPPARAM	parameters for parallel evaluation
...	Additional arguments for lmer() or lm()

### Details

A linear (mixed) model is fit for each gene in exprObj, using formula to specify variables in the regression. If categorical variables are modeled as random effects (as is recommended), then a linear mixed model is used. For example if formula is ~ a + b + (1|c), then the model is

```
fit <- lmer( exprObj[j,] ~ a + b + (1|c), data=data)
```

If there are no random effects, so formula is ~ a + b + c, a 'standard' linear model is used:

```
fit <- lm( exprObj[j,] ~ a + b + c, data=data)
```

In both cases, useWeights=TRUE causes weightsMatrix[j,] to be included as weights in the regression model.

Note: Fitting the model for 20,000 genes can be computationally intensive. To accelerate computation, models can be fit in parallel using BiocParallel to run in parallel. Parallel processing must be enabled before calling this function. See below.

The regression model is fit for each gene separately. Samples with missing values in either gene expression or metadata are omitted by the underlying call to lm/lmer.

Since this function returns a list of each model fit, using this function is slower and uses more memory than fitExtractVarPartModel().

REML=FALSE uses maximum likelihood to estimate variance fractions. This approach produced unbiased estimates, while REML=TRUE can show substantial bias. See Vignette "3) Theory and practice of random effects and REML"

**Value**

list() of where each entry is a model fit produced by lmer() or lm()

**Examples**

```
# load library
# library(variancePartition)

# Intialize parallel backend with 4 cores
library(BiocParallel)
register(SnowParam(4))

# load simulated data:
# geneExpr: matrix of gene expression values
# info: information/metadata about each sample
data(varPartData)

# Specify variables to consider
# Age is continuous so we model it as a fixed effect
# Individual and Tissue are both categorical, so we model them as random effects
form <- ~ Age + (1|Individual) + (1|Tissue)

# Step 1: fit linear mixed model on gene expression
# If categorical variables are specified, a linear mixed model is used
# If all variables are modeled as continuous, a linear model is used
# each entry in results is a regression model fit on a single gene
# Step 2: extract variance fractions from each model fit
# for each gene, returns fraction of variation attributable to each variable
# Interpretation: the variance explained by each variable
# after correction for all other variables
varPart <- fitExtractVarPartModel( geneExpr, form, info )

# violin plot of contribution of each variable to total variance
# also sort columns
plotVarPart( sortCols( varPart ) )

# Advanced:
# Fit model and extract variance in two separate steps
# Step 1: fit model for each gene, store model fit for each gene in a list
results <- fitVarPartModel( geneExpr, form, info )

# Step 2: extract variance fractions
varPart <- extractVarPart( results )

# Note: fitVarPartModel also accepts ExpressionSet
data(sample.ExpressionSet, package="Biobase")

# ExpressionSet example
form <- ~ (1|sex) + (1|type) + score
info2 <- pData(sample.ExpressionSet)
results2 <- fitVarPartModel( sample.ExpressionSet, form, info2 )
```

---

getContrast	<i>Extract contrast matrix for linear mixed model</i>
-------------	---

---

### Description

Extract contrast matrix, L, testing a single variable. Contrasts involving more than one variable can be constructed by modifying L directly

### Usage

```
getContrast(exprObj, formula, data, coefficient)
```

### Arguments

exprObj	matrix of expression data (g genes x n samples), or ExpressionSet, or EList returned by voom() from the limma package
formula	specifies variables for the linear (mixed) model. Must only specify covariates, since the rows of exprObj are automatically used as a response. e.g.: ~ a + b + (1 c) Formulas with only fixed effects also work
data	data.frame with columns corresponding to formula
coefficient	the coefficient to use in the hypothesis test

### Value

Contrast matrix testing one variable

### Examples

```
# load simulated data:
# geneExpr: matrix of gene expression values
# info: information/metadata about each sample
data(varPartData)

# get contrast matrix testing if the coefficient for Batch2 is zero
# The variable of interest must be a fixed effect
form <- ~ Batch + (1|Individual) + (1|Tissue)
L = getContrast( geneExpr, form, info, "Batch3")

# get contrast matrix testing if Batch3 - Batch2 = 0
form <- ~ Batch + (1|Individual) + (1|Tissue)
L = getContrast( geneExpr, form, info, c("Batch3", "Batch2"))

# To test against Batch1 use the formula:
# ~ 0 + Batch + (1|Individual) + (1|Tissue)
# to estimate Batch1 directly instead of using it as the baseline
```

---

get_prediction	<i>Compute predicted value of formula for linear (mixed) model</i>
----------------	--

---

## Description

Compute predicted value of formula for linear (mixed) model for with `lm` or `lmer`

## Usage

```
get_prediction(fit, formula)

## S4 method for signature 'lmerMod'
get_prediction(fit, formula)

## S4 method for signature 'lm'
get_prediction(fit, formula)
```

## Arguments

<code>fit</code>	model fit with <code>lm</code> or <code>lmer</code>
<code>formula</code>	formula of fixed and random effects to predict

## Details

Similar motivation as `lme4:::predict.merMod()`, but that function cannot use just a subset of the fixed effects: it either uses none or all. Note that the intercept is included in the formula by default. To exclude it from the prediction use `~ 0 + ...` syntax

## Value

Predicted values from formula using parameter estimates from fit linear (mixed) model

## Examples

```
library(lme4)

# Linear model
fit <- lm(Reaction ~ Days, sleepstudy)

# prediction of intercept
get_prediction(fit, ~ 1)

# prediction of Days without intercept
get_prediction(fit, ~ 0 + Days)

# Linear mixed model

# fit model
fm1 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)

# predict Days, but exclude intercept
get_prediction(fm1, ~ 0 + Days)
```



```
# predict Days and (Days | Subject) random effect, but exclude intercept
get_prediction( fm1, ~ 0 + Days + (Days | Subject))
```

---

ggColorHue

*Default colors for ggplot*

---

### Description

Return an array of n colors the same as the default used by ggplot2

### Usage

```
ggColorHue(n)
```

### Arguments

n                    number of colors

### Value

array of colors of length n

### Examples

```
ggColorHue(4)
```

---

MArrayLM2-class

*Class MArrayLM2*

---

### Description

Class MArrayLM2

---

plotCompareP

*Compare p-values from two analyses*


---

### Description

Plot  $-\log_{10}$  p-values from two analyses and color based on donor component from variancePartition analysis

### Usage

```
plotCompareP(
  p1,
  p2,
  vpDonor,
  dupcorvalue,
  fraction = 0.2,
  xlabel = bquote(duplicateCorrelation ~ (-log[10] ~ p)),
  ylabel = bquote(dream ~ (-log[10] ~ p))
)
```

### Arguments

p1	p-value from first analysis
p2	p-value from second analysis
vpDonor	donor component for each gene from variancePartition analysis
dupcorvalue	scalar donor component from duplicateCorrelation
fraction	fraction of highest/lowest values to use for best fit lines
xlabel	for x-axis
ylabel	label for y-axis

### Value

ggplot2 plot

### Examples

```
# load library
# library(variancePartition)

# Intialize parallel backend with 4 cores
library(BiocParallel)
register(SnowParam(4))

# load simulated data:
# geneExpr: matrix of gene expression values
# info: information/metadata about each sample
data(varPartData)

# Perform very simple analysis for demonstration
```

```
# Analysis 1
form <- ~ Batch
fit = dream( geneExpr, form, info)
fit = eBayes( fit )
res = topTable( fit, number=Inf, coef="Batch3" )

# Analysis 2
form <- ~ Batch + (1|Tissue)
fit2 = dream( geneExpr, form, info)
res2 = topTable( fit2, number=Inf, coef="Batch3" )

# Compare p-values
plotCompareP( res$P.Value, res2$P.Value, runif(nrow(res)), .3 )
```

---

plotContrasts

*Plot representation of contrast matrix*

---

## Description

Plot contrast matrix to clarify interpretation of hypothesis tests with linear contrasts

## Usage

```
plotContrasts(L)
```

## Arguments

L                    contrast matrix

## Value

ggplot2 object

## Examples

```
# load library
# library(variancePartition)

# load simulated data:
# geneExpr: matrix of gene expression values
# info: information/metadata about each sample
data(varPartData)

# get contrast matrix testing if the coefficient for Batch2 is zero
form <- ~ Batch + (1|Individual) + (1|Tissue)
L1 = getContrast( geneExpr, form, info, "Batch3" )

# get contrast matrix testing if the coefficient for Batch2 is different from Batch3
form <- ~ Batch + (1|Individual) + (1|Tissue)
L2 = getContrast( geneExpr, form, info, c("Batch2", "Batch3") )
```

```
# combine contrasts into single matrix
L_combined = cbind(L1, L2)

# plot contrasts
plotContrasts( L_combined )
```

---

plotCorrMatrix

*plotCorrMatrix*


---

## Description

Plot correlation matrix

## Usage

```
plotCorrMatrix(
  C,
  dendrogram = "both",
  sort = TRUE,
  margins = c(13, 13),
  key.xlab = "correlation",
  ...
)
```

## Arguments

C	correlation matrix: R or R <sup>2</sup> matrix
dendrogram	character string indicating whether to draw 'both' or none'
sort	sort rows and columns based on clustering
margins	spacing of plot
key.xlab	label of color gradient
...	additional arguments to heatmap.2

## Details

Plots image of correlation matrix using customized call to heatmap.2

## Value

Image of correlation matrix

## Examples

```
# simulate simple matrix of 10 variables
mat = matrix(rnorm(1000), ncol=10)

# compute correlation matrix
C = cor(mat)
```

```
# plot correlations
plotCorrMatrix( C )

# plot squared correlations
plotCorrMatrix( C^2, dendrogram="none" )
```

---

plotCorrStructure      *plotCorrStructure*

---

## Description

Plot correlation structure of a gene based on random effects

## Usage

```
plotCorrStructure(
  fit,
  varNames = names(coef(fit)),
  reorder = TRUE,
  pal = colorRampPalette(c("white", "red", "darkred")),
  hclust.method = "complete"
)
```

## Arguments

fit	linear mixed model fit of a gene produced by lmer() or fitVarPartModel()
varNames	variables in the metadata for which the correlation structure should be shown. Variables must be random effects
reorder	how to reorder the rows/columns of the correlation matrix. reorder=FALSE gives no reorder. reorder=TRUE reorders based on hclust. reorder can also be an array of indices to reorder the samples manually
pal	color palette
hclust.method	clustering methods for hclust

## Value

Image of correlation structure between each pair of experiments for a single gene

## Examples

```
# load library
# library(variancePartition)

# Initialize parallel backend with 4 cores
library(BiocParallel)
register(SnowParam(4))

# load simulated data:
data(varPartData)
```

```

# specify formula
form <- ~ Age + (1|Individual) + (1|Tissue)

# fit and return linear mixed models for each gene
fitList <- fitVarPartModel( geneExpr[1:10,], form, info )

# Focus on the first gene
fit = fitList[[1]]

# plot correlation structure based on Individual, reordering samples with hclust
plotCorrStructure( fit, "Individual" )

# don't reorder
plotCorrStructure( fit, "Individual", reorder=FALSE )

# plot correlation structure based on Tissue, reordering samples with hclust
plotCorrStructure( fit, "Tissue" )

# don't reorder
plotCorrStructure( fit, "Tissue", FALSE )

# plot correlation structure based on all random effects
# reorder manually by Tissue and Individual
idx = order(info$Tissue, info$Individual)
plotCorrStructure( fit, reorder=idx )

# plot correlation structure based on all random effects
# reorder manually by Individual, then Tissue
idx = order(info$Individual, info$Tissue)
plotCorrStructure( fit, reorder=idx )

```

---

plotPercentBars      *Bar plot of variance fractions*

---

### Description

Bar plot of variance fractions for a subset of genes

### Usage

```
plotPercentBars(varPart, col = c(ggColorHue(ncol(varPart) - 1), "grey85"))
```

### Arguments

varPart	object returned by extractVarPart() or fitExtractVarPartModel()
col	color of bars for each variable

### Value

Returns ggplot2 barplot

**Examples**

```
# library(variancePartition)

# Intialize parallel backend with 4 cores
library(BiocParallel)
register(SnowParam(4))

# load simulated data:
# geneExpr: matrix of gene expression values
# info: information/metadata about each sample
data(varPartData)

# Specify variables to consider
form <- ~ Age + (1|Individual) + (1|Tissue)

# Fit model
varPart <- fitExtractVarPartModel( geneExpr, form, info )

# Bar plot for a subset of genes showing variance fractions
plotPercentBars( varPart[1:5,] )

# Move the legend to the top
plotPercentBars( varPart[1:5,] ) + theme(legend.position="top")
```

---

plotStratify

*plotStratify*

---

**Description**

Plot gene expression stratified by another variable

**Usage**

```
plotStratify(
  formula,
  data,
  xlab,
  ylab,
  main,
  sortBy,
  colorBy,
  sort = TRUE,
  text = NULL,
  text.y = 1,
  text.size = 5,
  pts.cex = 1,
  ylim = NULL,
  legend = TRUE,
  x.labels = FALSE
)
```

**Arguments**

formula	specify variables shown in the x- and y-axes. Y-axis should be continuous variable, x-axis should be discrete.
data	data.frame storing continuous and discrete variables specified in formula
xlab	label x-axis. Defaults to value of xval
ylab	label y-axis. Defaults to value of yval
main	main label
sortBy	name of column in geneExpr to sort samples by. Defaults to xval
colorBy	name of column in geneExpr to color box plots. Defaults to xval
sort	if TRUE, sort boxplots by median value, else use default ordering
text	plot text on the top left of the plot
text.y	indicate position of the text on the y-axis as a fraction of the y-axis range
text.size	size of text
pts.cex	size of points
ylim	specify range of y-axis
legend	show legend
x.labels	show x axis labels

**Value**

ggplot2 object

**Examples**

```
# Note: This is a newer, more convient interface to plotStratifyBy()

# load library
# library(variancePartition)

# load simulated data:
data(varPartData)

# Create data.frame with expression and Tissue information for each sample
GE = data.frame( Expression = geneExpr[1,], Tissue = info$Tissue)

# Plot expression stratified by Tissue
plotStratify( Expression ~ Tissue, GE )

# Omit legend and color boxes grey
plotStratify( Expression ~ Tissue, GE, colorBy = NULL)

# Specify colors
col = c( B="green", A="red", C="yellow")
plotStratify( Expression ~ Tissue, GE, colorBy=col, sort=FALSE)
```



---

plotStratifyBy      *plotStratifyBy*

---

### Description

Plot gene expression stratified by another variable

### Usage

```
plotStratifyBy(
  geneExpr,
  xval,
  yval,
  xlab = xval,
  ylab = yval,
  main = NULL,
  sortBy = xval,
  colorBy = xval,
  sort = TRUE,
  text = NULL,
  text.y = 1,
  text.size = 5,
  pts.cex = 1,
  ylim = NULL,
  legend = TRUE,
  x.labels = FALSE
)
```

### Arguments

geneExpr	data.frame of gene expression values and another variable for each sample. If there are multiple columns, the user can specify which one to use
xval	name of column in geneExpr to be used along x-axis to stratify gene expression
yval	name of column in geneExpr indicating gene expression
xlab	label x-axis. Defaults to value of xval
ylab	label y-axis. Defaults to value of yval
main	main label
sortBy	name of column in geneExpr to sort samples by. Defaults to xval
colorBy	name of column in geneExpr to color box plots. Defaults to xval
sort	if TRUE, sort boxplots by median value, else use default ordering
text	plot text on the top left of the plot
text.y	indicate position of the text on the y-axis as a fraction of the y-axis range
text.size	size of text
pts.cex	size of points
ylim	specify range of y-axis
legend	show legend
x.labels	show x axis labels

**Value**

ggplot2 object

**Examples**

```
# load library
# library(variancePartition)

# load simulated data:
data(varPartData)

# Create data.frame with expression and Tissue information for each sample
GE = data.frame( Expression = geneExpr[1,], Tissue = info$Tissue)

# Plot expression stratified by Tissue
plotStratifyBy( GE, "Tissue", "Expression")

# Omit legend and color boxes grey
plotStratifyBy( GE, "Tissue", "Expression", colorBy = NULL)

# Specify colors
col = c( B="green", A="red", C="yellow")
plotStratifyBy( GE, "Tissue", "Expression", colorBy=col, sort=FALSE)
```

---

plotVarPart

*Violin plot of variance fractions*

---

**Description**

Violin plot of variance fraction for each gene and each variable

**Usage**

```
plotVarPart(
  obj,
  col = c(ggColorHue(ncol(obj) - 1), "grey85"),
  label.angle = 20,
  main = "",
  ylab = "",
  convertToPercent = TRUE,
  ...
)

## S4 method for signature 'matrix'
plotVarPart(
  obj,
  col = c(ggColorHue(ncol(obj) - 1), "grey85"),
  label.angle = 20,
  main = "",
  ylab = "",
```

```

    convertToPercent = TRUE,
    ...
)

## S4 method for signature 'data.frame'
plotVarPart(
  obj,
  col = c(ggColorHue(ncol(obj) - 1), "grey85"),
  label.angle = 20,
  main = "",
  ylab = "",
  convertToPercent = TRUE,
  ...
)

## S4 method for signature 'varPartResults'
plotVarPart(
  obj,
  col = c(ggColorHue(ncol(obj) - 1), "grey85"),
  label.angle = 20,
  main = "",
  ylab = "",
  convertToPercent = TRUE,
  ...
)

```

### Arguments

obj	varParFrac object returned by fitExtractVarPart or extractVarPart
col	vector of colors
label.angle	angle of labels on x-axis
main	title of plot
ylab	text on y-axis
convertToPercent	multiply fractions by 100 to convert to percent values
...	additional arguments

### Value

Makes violin plots of variance components model. This function uses the graphics interface from ggplot2. Warnings produced by this function usually ggplot2 warning that the window is too small.

### Examples

```

# load library
# library(variancePartition)

# Intialize parallel backend with 4 cores
library(BiocParallel)
register(SnowParam(4))

```

```

# load simulated data:
# geneExpr: matrix of gene expression values
# info: information/metadata about each sample
data(varPartData)

# Specify variables to consider
# Age is continuous so we model it as a fixed effect
# Individual and Tissue are both categorical, so we model them as random effects
form <- ~ Age + (1|Individual) + (1|Tissue)

varPart <- fitExtractVarPartModel( geneExpr, form, info )

# violin plot of contribution of each variable to total variance
plotVarPart( sortCols( varPart ) )

```

---

```

residuals,MArrayLM-method
residuals for MArrayLM

```

---

**Description**

residuals for MArrayLM

**Usage**

```

## S4 method for signature 'MArrayLM'
residuals(object, ...)

```

**Arguments**

object	MArrayLM object from dream
...	other arguments, currently ignored

**Value**

results of residuals

---

```

residuals,MArrayLM2-method
residuals for MArrayLM2

```

---

**Description**

residuals for MArrayLM2

**Usage**

```

## S4 method for signature 'MArrayLM2'
residuals(object, ...)

```

**Arguments**

object            MArrayLM2 object from dream  
 ...                other arguments, currently ignored

**Value**

results of residuals

---

residuals, VarParFitList-method  
*Residuals from model fit*

---

**Description**

Extract residuals for each gene from model fit with fitVarPartModel()

**Usage**

```
## S4 method for signature 'VarParFitList'
residuals(object, ...)
```

**Arguments**

object            object produced by fitVarPartModel()  
 ...                other arguments.

**Details**

If model is fit with missing data, residuals returns NA for entries that were missing in the original data

**Value**

Residuals extracted from model fits stored in object

**Examples**

```
# load library
# library(variancePartition)

# Intialize parallel backend with 4 cores
library(BiocParallel)
register(SnowParam(4))

# load simulated data:
# geneExpr: matrix of gene expression values
# info: information/metadata about each sample
data(varPartData)

# Specify variables to consider
# Age is continuous so we model it as a fixed effect
# Individual and Tissue are both categorical, so we model them as random effects
```

```

form <- ~ Age + (1|Individual) + (1|Tissue)

# Fit model
modelFit <- fitVarPartModel( geneExpr, form, info )

# Extract residuals of model fit
res <- residuals( modelFit )

```

---

sortCols

*Sort variance partition statistics*

---

## Description

Sort columns returned by `extractVarPart()` or `fitExtractVarPartModel()`

## Usage

```

sortCols(
  x,
  FUN = median,
  decreasing = TRUE,
  last = c("Residuals", "Measurement.error"),
  ...
)

## S4 method for signature 'matrix'
sortCols(
  x,
  FUN = median,
  decreasing = TRUE,
  last = c("Residuals", "Measurement.error"),
  ...
)

## S4 method for signature 'data.frame'
sortCols(
  x,
  FUN = median,
  decreasing = TRUE,
  last = c("Residuals", "Measurement.error"),
  ...
)

## S4 method for signature 'varPartResults'
sortCols(
  x,
  FUN = median,
  decreasing = TRUE,
  last = c("Residuals", "Measurement.error"),
  ...
)

```

**Arguments**

x                    object returned by `extractVarPart()` or `fitExtractVarPartModel()`  
 FUN                 function giving summary statistic to sort by. Defaults to `median`  
 decreasing         logical. Should the sorting be increasing or decreasing?  
 last                 columns to be placed on the right, regardless of values in these columns  
 ...                 other arguments to sort

**Value**

data.frame with columns sorted by mean value, with Residuals in last column

**Examples**

```
# library(variancePartition)

# Intialize parallel backend with 4 cores
library(BiocParallel)
register(SnowParam(4))

# load simulated data:
# geneExpr: matrix of gene expression values
# info: information/metadata about each sample
data(varPartData)

# Specify variables to consider
# Age is continuous so we model it as a fixed effect
# Individual and Tissue are both categorical, so we model them as random effects
form <- ~ Age + (1|Individual) + (1|Tissue)

# Step 1: fit linear mixed model on gene expression
# If categorical variables are specified, a linear mixed model is used
# If all variables are modeled as continuous, a linear model is used
# each entry in results is a regression model fit on a single gene
# Step 2: extract variance fractions from each model fit
# for each gene, returns fraction of variation attributable to each variable
# Interpretation: the variance explained by each variable
# after correction for all other variables
varPart <- fitExtractVarPartModel( geneExpr, form, info )

# violin plot of contribution of each variable to total variance
# sort columns by median value
plotVarPart( sortCols( varPart ) )
```

---

VarParCIList-class      *Class VarParCIList*

---

**Description**

Class VarParCIList

---

VarParFitList-class    *Class VarParFitList*

---

### Description

Class VarParFitList

---

varParFrac-class    *Class varParFrac*

---

### Description

Class varParFrac

---

varPartConfInf    *Linear mixed model confidence intervals*

---

### Description

Fit linear mixed model to estimate contribution of multiple sources of variation while simultaneously correcting for all other variables. Then perform parametric bootstrap sampling to get a 95% confidence intervals for each variable for each gene.

### Usage

```
varPartConfInf(
  exprObj,
  formula,
  data,
  REML = FALSE,
  useWeights = TRUE,
  weightsMatrix = NULL,
  showWarnings = TRUE,
  colinearityCutoff = 0.999,
  control = lme4::lmerControl(calc.derivs = FALSE, check.rankX = "stop.deficient"),
  nsim = 1000,
  ...
)
```

### Arguments

exprObj	matrix of expression data (g genes x n samples), or ExpressionSet, or EList returned by voom() from the limma package
formula	specifies variables for the linear (mixed) model. Must only specify covariates, since the rows of exprObj are automatically used as a response. e.g.: ~ a + b + (1 c)
data	data.frame with columns corresponding to formula



REML	use restricted maximum likelihood to fit linear mixed model. default is FALSE. Strongly discourage against changing this option, but here for compatibility.
useWeights	if TRUE, analysis uses heteroskedastic error estimates from voom(). Value is ignored unless exprObj is an EList from voom() or weightsMatrix is specified
weightsMatrix	matrix the same dimension as exprObj with observation-level weights from voom(). Used only if useWeights is TRUE
showWarnings	show warnings about model fit (default TRUE)
colinearityCutoff	cutoff used to determine if model is computationally singular
control	control settings for lmer()
nsim	number of bootstrap datasets
...	Additional arguments for lmer() or lm()

### Details

A linear mixed model is fit for each gene, and bootMer() is used to generate parametric bootstrap confidence intervals. use.u=TRUE is used so that the

$$\hat{u}$$

values from the random effects are used as estimated and are not re-sampled. This gives confidence intervals as if additional data were generated from these same current samples. Conversely, use.u=FALSE assumes that this dataset is a sample from a larger population. Thus it simulates

$$\hat{u}$$

based on the estimated variance parameter. This approach gives confidence intervals as if additional data were collected from the larger population from which this dataset is sampled. Overall, use.u=TRUE gives smaller confidence intervals that are appropriate in this case.

### Value

list() of where each entry is the result for a gene. Each entry is a matrix of the 95% confidence interval of the variance fraction for each variable

### Examples

```
# load library
# library(variancePartition)

# Intialize parallel backend with 4 cores
library(BiocParallel)
register(SnowParam(4))

# load simulated data:
# geneExpr: matrix of gene expression values
# info: information/metadata about each sample
data(varPartData)

# Specify variables to consider
# Age is continuous so we model it as a fixed effect
# Individual and Tissue are both categorical, so we model them as random effects
```

```

form <- ~ Age + (1|Individual) + (1|Tissue)

# Compute bootstrap confidence intervals for each variable for each gene
resCI <- varPartConfInf( geneExpr[1:5,], form, info, nsim=100 )

```

---

varPartData	<i>Simulation dataset for examples</i>
-------------	--

---

### Description

A simulated dataset of gene expression and metadata

A simulated dataset of gene counts

info about study design

Normalized expression data

### Usage

```
data(varPartData)
```

```
data(varPartData)
```

```
data(varPartData)
```

```
data(varPartData)
```

### Format

A dataset of 100 samples and 200 genes

A dataset of 100 samples and 200 genes

A dataset of 100 samples and 200 genes

A dataset of 100 samples and 200 genes

### Details

- geneCounts gene expression in the form of RNA-seq counts
- geneExpr gene expression on a continuous scale
- info metadata about the study design
- geneCounts gene expression in the form of RNA-seq counts
- geneExpr gene expression on a continuous scale
- info metadata about the study design
- geneCounts gene expression in the form of RNA-seq counts
- geneExpr gene expression on a continuous scale
- info metadata about the study design
- geneCounts gene expression in the form of RNA-seq counts
- geneExpr gene expression on a continuous scale
- info metadata about the study design

---

varPartDEdata	<i>Simulation dataset for dream example</i>
---------------	---

---

**Description**

Gene counts from RNA-seq  
metadata matrix of sample information

**Usage**

```
data(varPartDEdata)  
data(varPartDEdata)
```

**Format**

A dataset of 24 samples and 19,364 genes  
A dataset of 24 samples and 19,364 genes

**Details**

- countMatrix gene expression in the form of RNA-seq counts
- metadata metadata about the study design
- countMatrix gene expression in the form of RNA-seq counts
- metadata metadata about the study design

---

varPartResults-class	<i>Class varPartResults</i>
----------------------	-----------------------------

---

**Description**

Class varPartResults

---

voomWithDreamWeights *Transform RNA-Seq Data Ready for Linear Mixed Modelling with dream()*

---

### Description

Transform count data to log<sub>2</sub>-counts per million (logCPM), estimate the mean-variance relationship and use this to compute appropriate observation-level weights. The data are then ready for linear mixed modelling with `dream()`. This method is the same as `limma::voom()`, except that it allows random effects in the formula

### Usage

```
voomWithDreamWeights(
  counts,
  formula,
  data,
  lib.size = NULL,
  normalize.method = "none",
  span = 0.5,
  plot = FALSE,
  save.plot = FALSE,
  quiet = FALSE,
  BPPARAM = bpparam(),
  ...
)
```

### Arguments

<code>counts</code>	a numeric matrix containing raw counts, or an <code>ExpressionSet</code> containing raw counts, or a <code>DGEList</code> object. Counts must be non-negative and NAs are not permitted.
<code>formula</code>	specifies variables for the linear (mixed) model. Must only specify covariates, since the rows of <code>exprObj</code> are automatically used as a response. e.g.: <code>~ a + b + (1 c)</code> Formulas with only fixed effects also work, and <code>lmFit()</code> followed by <code>contrasts.fit()</code> are run.
<code>data</code>	<code>data.frame</code> with columns corresponding to formula
<code>lib.size</code>	numeric vector containing total library sizes for each sample. Defaults to the normalized (effective) library sizes in counts if <code>counts</code> is a <code>DGEList</code> or to the columnwise count totals if <code>counts</code> is a matrix.
<code>normalize.method</code>	the microarray-style normalization method to be applied to the logCPM values (if any). Choices are as for the <code>method</code> argument of <code>normalizeBetweenArrays</code> when the data is single-channel. Any normalization factors found in counts will still be used even if <code>normalize.method="none"</code> .
<code>span</code>	width of the lowess smoothing window as a proportion.
<code>plot</code>	logical, should a plot of the mean-variance trend be displayed?
<code>save.plot</code>	logical, should the coordinates and line of the plot be saved in the output?
<code>quiet</code>	suppress message, default FALSE

BPPARAM            parameters for parallel evaluation  
...                other arguments are passed to lmer.

### Details

Adapted from vomm() in limma v3.40.2

### Value

An EList object just like the result of limma::voom()

### See Also

limma::voom()

### Examples

```
# library(variancePartition)
library(edgeR)
library(BiocParallel)

data(varPartDEdata)

# normalize RNA-seq counts
dge = DGEList(counts = countMatrix)
dge = calcNormFactors(dge)

# specify formula with random effect for Individual
form <- ~ Disease + (1|Individual)

# compute observation weights
vobj = voomWithDreamWeights( dge[1:20,], form, metadata)

# fit dream model
res = dream( vobj, form, metadata)

# extract results
topTable(res, coef="Disease1")
```

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