Package ‘zinbwave’

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Type Package
Title Zero-Inflated Negative Binomial Model for RNA-Seq Data
Version 1.26.0
Description Implements a general and flexible zero-inflated negative binomial model that can be used to provide a low-dimensional representations of single-cell RNA-seq data. The model accounts for zero inflation (dropouts), over-dispersion, and the count nature of the data. The model also accounts for the difference in library sizes and optionally for batch effects and/or other covariates, avoiding the need for pre-normalize the data.
License Artistic-2.0
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computeDevianceResiduals

Deviance residuals of the zero-inflated negative binomial model

Description
Given a matrix of counts, this function computes the deviance residuals under a zero-inflated negative binomial (ZINB) model.

Usage
computeDevianceResiduals(model, x, ignoreW = TRUE)

Arguments
- model: the zinb model
- x: the matrix of counts n cells by J genes
- ignoreW: logical, if true matrix W is ignored. Default is TRUE.

Value
the matrix of deviance residuals of the model.

Examples
se <- SummarizedExperiment(matrix(rpois(60, lambda=5), nrow=10, ncol=6),
colData = data.frame(bio = gl(2, 3)))
m <- zinbFit(se, X=model.matrix(~bio, data=colData(se)),
BPPARAM=BiocParallel::SerialParam())
computeDevianceResiduals(m, t(assay(se)))
**computeObservationalWeights**

*Observational weights of the zero-inflated negative binomial model for each entry in the matrix of counts*

**Description**

Given a matrix of counts, this function computes the observational weights of the counts under a zero-inflated negative binomial (ZINB) model. For each count, the ZINB distribution is parametrized by three parameters: the mean value and the dispersion of the negative binomial distribution, and the probability of the zero component.

**Usage**

```r
computeObservationalWeights(model, x)
```

**Arguments**

- `model`: the zinb model
- `x`: the matrix of counts

**Value**

the matrix of observational weights computed from the model.

**Examples**

```r
se <- SummarizedExperiment(matrix(rpois(60, lambda=1), nrow=10, ncol=6),
colData = data.frame(bio = gl(2, 3)))
m <- zinbFit(se, X=model.matrix(~bio, data=colData(se)),
BPPARAM=BiocParallel::SerialParam())
computeObservationalWeights(m, assay(se))
```

**getAlpha_mu**

*Returns the matrix of parameters alpha_mu*

**Description**

Given an object that describes a matrix of zero-inflated distributions, returns the matrix of parameters associated with W for the mean part (mu)

**Usage**

```r
getAlpha_mu(object, ...)
```
getAlpha_pi

Arguments

object an object that describes a matrix of zero-inflated distributions.

Value

the matrix of alpha mu parameters

Examples

a <- zinbModel(n=5, J=10)
getAlpha_mu(a)

getAlpha_pi

Returns the matrix of parameters alpha_pi

Description

Given an object that describes a matrix of zero-inflated distributions, returns the matrix of parameters associated with W for the zero part (pi)

Usage

getAlpha_pi(object, ...)

Arguments

object an object that describes a matrix of zero-inflated distributions.

Value

the matrix of alpha_pi parameters

Examples

a <- zinbModel(n=5, J=10)
getAlpha_pi(a)
getBeta_pi

Description

Given an object that describes a matrix of zero-inflated distributions, returns the matrix of parameters associated with X_pi

Usage

getBeta_pi(object, ...)

Arguments

object an object that describes a matrix of zero-inflated distributions.
...

Value

the matrix of beta_pi parameters

Examples

a <- zinbModel(n=5, J=10)
getBeta_pi(a)

getBeta_mu

Returns the matrix of parameters beta_mu

Description

Given an object that describes a matrix of zero-inflated distributions, returns the matrix of parameters associated with X_mu

Usage

getBeta_mu(object, ...)

Arguments

object an object that describes a matrix of zero-inflated distributions.
...

Value

the matrix of beta_mu parameters

Examples

a <- zinbModel(n=5, J=10)
getBeta_mu(a)
Examples

```r
a <- zinbModel(n=5, J=10)
getBeta_pi(a)
```

getEpsilon_alpha

Returns the vector of regularization parameter for alpha

Description

Given an object describing a ZINB model, returns a vector of size the number of rows in the parameter alpha with the regularization parameters associated to each row. Here alpha refers to both alpha_mu and alpha_pi, which have the same size and have the same regularization.

Usage

```r
gEpsilon_alpha(object)
```

Arguments

- `object`: an object that describes a matrix of zero-inflated distributions.

Value

the regularization parameters for alpha_mu and alpha_pi.

Examples

```r
a <- zinbModel(n=5, J=10)
getEpsilon_alpha(a)
```

getEpsilon_beta_mu

Returns the vector of regularization parameter for beta_mu

Description

Given an object describing a ZINB model, returns a vector of size the number of rows in the parameter beta_mu with the regularization parameters associated to each row.

Usage

```r
gEpsilon_beta_mu(object)
```

Arguments

- `object`: an object that describes a matrix of zero-inflated distributions.
**Value**

the regularization parameters for \( beta_{\mu} \).

**Examples**

```r
a <- zinbModel(n=5, J=10)
gEpsilon_beta_mu(a)
```

---

**getEpsilon_beta_pi**

*Returns the vector of regularization parameter for beta_{\pi}*

**Description**

Given an object describing a ZINB model, returns a vector of size the number of rows in the parameter \( beta_{\pi} \) with the regularization parameters associated to each row.

**Usage**

```r
gEpsilon_beta_pi(object)
```

**Arguments**

- `object` an object that describes a matrix of zero-inflated distributions.

**Value**

the regularization parameters for \( beta_{\pi} \).

**Examples**

```r
a <- zinbModel(n=5, J=10)
gEpsilon_beta_pi(a)
```

---

**getEpsilon_gamma_mu**

*Returns the vector of regularization parameter for gamma_{\mu}*

**Description**

Given an object describing a ZINB model, returns a vector of size the number of columns in the parameter \( gamma_{\mu} \) with the regularization parameters associated to each row.

**Usage**

```r
gEpsilon_gamma_mu(object)
```

**Arguments**

- `object` an object that describes a matrix of zero-inflated distributions.

**Value**

the regularization parameters for \( gamma_{\mu} \).

**Examples**

```r
a <- zinbModel(n=5, J=10)
gEpsilon_gamma_mu(a)
```
getEpsilon\_gamma\_pi

**Arguments**

- object: an object that describes a matrix of zero-inflated distributions.

**Value**

the regularization parameters for gamma\_mu.

**Examples**

```r
a <- zinbModel(n=5, J=10)
getEpsilon\_gamma\_mu(a)
```

---

getEpsilon\_gamma\_pi 

*Returns the vector of regularization parameter for gamma\_pi*

**Description**

Given an object describing a ZINB model, returns a vector of size the number of columns in the parameter gamma\_pi with the regularization parameters associated to each column.

**Usage**

```r
getEpsilon\_gamma\_pi(object)
```

**Arguments**

- object: an object that describes a matrix of zero-inflated distributions.

**Value**

the regularization parameters for gamma\_pi.

**Examples**

```r
a <- zinbModel(n=5, J=10)
getEpsilon\_gamma\_pi(a)
```
getEpsilon_W  

Returns the vector of regularization parameter for W

Description

Given an object describing a ZINB model, returns a vector of size the number of columns in the parameter W with the regularization parameters associated to each column.

Usage

getEpsilon_W(object)

Arguments

object an object that describes a matrix of zero-inflated distributions.

Value

the regularization parameters for W.

Examples

a <- zinbModel(n=5, J=10)
gEpsilon_W(a)

gEpsilon_zeta  

Returns the regularization parameter for the dispersion parameter

Description

The regularization parameter penalizes the variance of zeta, the log of the dispersion parameters across samples.

Usage

getEpsilon_zeta(object)

Arguments

object an object that describes a matrix of zero-inflated distributions.

Value

the regularization parameters for zeta.

Examples

a <- zinbModel(n=5, J=10)
gEpsilon_zeta(a)
getGamma_mu

Returns the matrix of parameters gamma_mu

Description
Given an object that describes a matrix of zero-inflated distributions, returns the matrix of parameters associated with V_mu

Usage
getGamma_mu(object, ...)

Arguments

object an object that describes a matrix of zero-inflated distributions.

... Additional parameters.

Value
the matrix of gamma_mu parameters

Examples
a <- zinbModel(n=5, J=10)
gamma_mu(a)

getGamma_pi

Returns the matrix of parameters gamma_pi

Description
Given an object that describes a matrix of zero-inflated distributions, returns the matrix of parameters associated with V_pi

Usage
gamma_pi(object, ...)

Arguments

object an object that describes a matrix of zero-inflated distributions.

... Additional parameters.

Value
the matrix of gamma_pi parameters
Examples

```r
a <- zinbModel(n=5, J=10)
getGamma_pi(a)
```

---

**getLogitPi**

*Returns the matrix of logit of probabilities of zero*

---

Description

Given an object that describes a matrix of zero-inflated distributions, returns the matrix of logit of probabilities of 0.

Usage

```r
getLogitPi(object)
```

Arguments

- `object` an object that describes a matrix of zero-inflated distributions.

Details

Note that although the user interface of `zinbFit` requires a J x n matrix, internally this is stored as a n x J matrix (i.e., samples in row and genes in column). Hence the parameter matrix returned by this function is of n x J dimensions.

Value

the matrix of logit-probabilities of 0

Examples

```r
a <- zinbModel(n=5, J=10)
getLogitPi(a)
```
getLogMu

Returns the matrix of logarithm of mean parameters

Description
Given an object that describes a matrix of zero-inflated distributions, returns the matrix of logarithm of mean parameters.

Usage
getLogMu(object)

Arguments
object an object that describes a matrix of zero-inflated distributions.

Details
Note that although the user interface of zinbFit requires a J x n matrix, internally this is stored as a n x J matrix (i.e., samples in row and genes in column). Hence the parameter matrix returned by this function is of n x J dimensions.

Value
the matrix of logarithms of mean parameters

Examples
a <- zinbModel(n=5, J=10)
getLogMu(a)

getMu

Returns the matrix of mean parameters

Description
Given an object that describes a matrix of zero-inflated distributions, returns the matrix of mean parameters.

Usage
getMu(object)

Arguments
object an object that describes a matrix of zero-inflated distributions.
getPhi

Details

Note that although the user interface of \texttt{zinbFit} requires a J x n matrix, internally this is stored as a n x J matrix (i.e., samples in row and genes in column). Hence the parameter matrix returned by this function is of n x J dimensions.

Value

the matrix of mean parameters

Examples

a <- zinbModel(n=5, J=10)
getMu(a)

gphi

Returns the vector of dispersion parameters

Description

Given an object that describes a matrix of zero-inflated negative binomial distributions, returns the vector of dispersion parameters \( \phi \).

Usage

gphi(object)

Arguments

object an object that describes a matrix of zero-inflated distributions.

Value

the vector of dispersion parameters

Examples

a <- zinbModel(n=5, J=10)
gphi(a)
getPi

Returns the matrix of probabilities of zero

Description
Given an object that describes a matrix of zero-inflated distributions, returns the matrix of probabilities of 0.

Usage
getPi(object)

Arguments
object an object that describes a matrix of zero-inflated distributions.

Details
Note that although the user interface of zinbFit requires a J x n matrix, internally this is stored as a n x J matrix (i.e., samples in row and genes in column). Hence the parameter matrix returned by this function is of n x J dimensions.

Value
the matrix of probabilities of 0

Examples
a <- zinbModel(n=5, J=10)
getPi(a)

getTheta

Returns the vector of inverse dispersion parameters

Description
Given an object that describes a matrix of zero-inflated negative binomial distributions, returns the vector of inverse dispersion parameters theta.

Usage
getTheta(object)

Arguments
object an object that describes a matrix of zero-inflated distributions.
getV_pi

Value
the vector of inverse dispersion parameters theta

Examples
a <- zinbModel(n=5, J=10)
getTheta(a)

getV_mu

Returns the gene-level design matrix for mu

Description
Given an object that describes a matrix of zero-inflated distributions, returns the gene-level design matrix for mu

Usage
getV_mu(object, ...)

Arguments
object an object that describes a matrix of zero-inflated distributions.
... Additional parameters.

Value
the gene-level design matrix for mu

Examples
a <- zinbModel(n=5, J=10)
getV_mu(a)

getV_pi

Returns the gene-level design matrix for pi

Description
Given an object that describes a matrix of zero-inflated distributions, returns the gene-level design matrix for pi

Usage
getV_pi(object, ...)
getW

Arguments

object an object that describes a matrix of zero-inflated distributions.

... Additional parameters.

Value

the gene-level design matrix for \( \pi \)

Examples

```r
a <- zinbModel(n=5, J=10)
getV_pi(a)
```

---

getW

Returns the low-dimensional matrix of inferred sample-level covariates \( W \)

Description

Given an object that contains the fit of a ZINB-WaVE model, returns the matrix \( W \) of low-dimensional matrix of inferred sample-level covariates.

Usage

```r
getW(object)
```

Arguments

object a ZinbModel object, typically the result of zinbFit.

Value

the matrix \( W \) of inferred sample-level covariates.

Examples

```r
a <- zinbModel(n=5, J=10)
getW(a)
```
**getX_mu**

*Returns the sample-level design matrix for mu*

---

**Description**

Given an object that describes a matrix of zero-inflated distributions, returns the sample-level design matrix for mu.

**Usage**

```r
getX_mu(object, ...)
```

**Arguments**

- `object`: an object that describes a matrix of zero-inflated distributions.
- `...`: Additional parameters.

**Value**

the sample-level design matrix for mu

**Examples**

```r
a <- zinbModel(n=5, J=10)
getX_mu(a)
```

---

**getX_pi**

*Returns the sample-level design matrix for pi*

---

**Description**

Given an object that describes a matrix of zero-inflated distributions, returns the sample-level design matrix for pi.

**Usage**

```r
getX_pi(object, ...)
```

**Arguments**

- `object`: an object that describes a matrix of zero-inflated distributions.
- `...`: Additional parameters.

**Value**

the sample-level design matrix for pi
getZeta

Examples

```r
a <- zinbModel(n=5, J=10)
getX_pi(a)
getZeta(a)
```

getZeta

Returns the vector of log of inverse dispersion parameters

Description

Given an object that describes a matrix of zero-inflated negative binomial distributions, returns the vector zeta of log of inverse dispersion parameters

Usage

```r
getZeta(object)
```

Arguments

- `object`: an object that describes a matrix of zero-inflated distributions.

Value

- the vector zeta of log of inverse dispersion parameters

Examples

```r
a <- zinbModel(n=5, J=10)
getZeta(a)
```

glmWeightedF

Zero-inflation adjusted statistical tests for assessing differential expression.

Description

This function recycles an old version of the `glmLRT` method that allows an F-test with adjusted denominator degrees of freedom to account for the downweighting in the zero-inflation model.

Usage

```r
glmWeightedF(
  glmfit,
  coef = ncol(glmfit$design),
  contrast = NULL,
  ZI = TRUE,
  independentFiltering = TRUE,
  filter = NULL
)
```
Arguments

glmfit  a `DGEGLM-class` object, usually output from `glmFit`.

coef    integer or character vector indicating which coefficients of the linear model are
to be tested equal to zero. Values must be columns or column names of design.
Defaults to the last coefficient. Ignored if `contrast` is specified.

contrast numeric vector or matrix specifying one or more contrasts of the linear model
coefficients to be tested equal to zero. Number of rows must equal to the number
of columns of design. If specified, then takes precedence over `coef`.

ZI       logical, specifying whether the degrees of freedom in the statistical test should
be adjusted according to the weights in the fit object to account for the down-
weighting. Defaults to TRUE and this option is highly recommended.

independentFiltering

logical, specifying whether independent filtering should be performed.

filter   vector of values to perform filtering on. Default is the mean of the fitted values
from glmfit.

Details

When ‘independentFiltering=TRUE’ (default) an independent filtering step is applied prior to the
multiple testing procedure, as described in great details in the ‘DESeq2” vignette. The values in the
‘padjFilter’ column refer to this procedure. They are identical to the ‘FDR’ values if the filtering step
does not remove any gene, since the function uses the Benjamini-Hochberg correction by default.
If the procedure filters some genes, the adjusted p-values will typically result in greater power to
detect DE genes. The theory behind independent filtering is described in Bourgon et al. (2010).

Note

This function uses an adapted version of the `glmLRT` function that was originally written by Gordon
Smyth, Davis McCarthy and Yunshun Chen as part of the edgeR package. Koen Van den Berge
wrote code to adjust residual degree of freedoom and added the independent filtering step.

References

McCarthy, DJ, Chen, Y, Smyth, GK (2012). Differential expression analysis of multifactor RNA-
Seq experiments with respect to biological variation. Nucleic Acids Research 40, 4288-4297. Bour-
gon, Richard, Robert Gentleman, and Wolfgang Huber (2010) Independent Filtering Increases De-

See Also

`glmLRT`
**imputeZeros**

Impute the zeros using the estimated parameters from the ZINB model.

**Description**

Given a matrix of counts and a zinb model, this function computes the imputed counts under a zero-inflated negative binomial (ZINB) model.

**Usage**

```r
imputeZeros(model, x)
```

**Arguments**

- `model`: the zinb model
- `x`: the matrix of counts n cells by J genes

**Value**

the matrix of imputed counts.

**Examples**

```r
se <- SummarizedExperiment(matrix(rpois(60, lambda=5), nrow=10, ncol=6),
                           colData = data.frame(bio = gl(2, 3)))
m <- zinbFit(se, X=model.matrix(~bio, data=colData(se)),
             BPPARAM=BiocParallel::SerialParam())
imputeZeros(m, t(assay(se)))
```

---

**independentFiltering**

Perform independent filtering in differential expression analysis.

**Description**

This function uses the DESeq2 independent filtering method to increase detection power in high throughput gene expression studies.

**Usage**

```r
independentFiltering(object, filter, objectType = c("edgeR", "limma"))
```
**Arguments**

- **object** Either a `DGELRT-class` object or a `data.frame` with differential expression results.
- **filter** The characteristic to use for filtering, usually a measure of normalized mean expression for the features.
- **objectType** Either "edgeR" or "limma". If "edgeR", it is assumed that object is of class `DGELRT-class`, the output of `glmLRT`. If "limma", it is assumed that object is a `data.frame` and the output of a limma-voom analysis.

**Author(s)**

Koen Van den Berge

**References**


**See Also**

- `results`

---

**loglik**

*Compute the log-likelihood of a model given some data*

**Description**

Given a statistical model and some data, this function computes the log-likelihood of the model given the data, i.e., the log-probability of the data under the model.

**Usage**

loglik(model, x, ...)

```r
# S4 method for signature 'ZinbModel, matrix'
loglik(model, x)
```

**Arguments**

- **model** an object that describes a statistical model.
- **x** an object that describes data.
- **...** additional arguments.

**Value**

The log-likelihood of the model given the data.
Methods (by class)

- `loglik(model = ZinbModel, x = matrix)`: return the log-likelihood of the ZINB model.

Examples

```r
m <- zinbModel(n=5, J=10)
x <- zinbSim(m)
loglik(m, x$counts)
```

---

### nFactors

Generic function that returns the number of latent factors

**Description**

Given an object that describes a dataset or a model involving latent factors, this function returns the number of latent factors.

**Usage**

```r
nFactors(x)
```

**Arguments**

- `x`: an object that describes a dataset or a model involving latent factors

**Value**

the number of latent factors

**Examples**

```r
a <- zinbModel()
nFactors(a)
```

---

### nFeatures

Generic function that returns the number of features

**Description**

Given an object that describes a dataset or a model, it returns the number of features.

**Usage**

```r
nFeatures(x)
```
Arguments

\(x\)  
an object that describes a dataset or a model.

Value

the number of features.

Examples

\[a <- \text{zinbModel}()\]
\[\text{nFeatures}(a)\]

\[\text{nParams}()\]

\(\text{nParams}(\text{ZinbModel})\): returns the total number of parameters of the model.

Description

Given an object that describes a model or a dataset, it returns total number of parameters of the model.

Usage

\[\text{nParams(model)}\]

## S4 method for signature \'ZinbModel\'

\[\text{nParams(model)}\]

Arguments

model  
an object that describes a dataset or a model.

Value

the total number of parameters of the model.

Functions

- \(\text{nParams(ZinbModel)}\): returns the total number of parameters in the model.

Examples

\[a <- \text{zinbModel}()\]
\[\text{nParams}(a)\]
\begin{verbatim}
**nSamples**

\textit{Generic function that returns the number of samples}

**Description**

Given an object that describes a model or a dataset, it returns the number of samples.

**Usage**

\texttt{nSamples(x)}

**Arguments**

\begin{itemize}
  \item \texttt{x} an object that describes a dataset or a model.
\end{itemize}

**Value**

the number of samples.

**Examples**

\begin{verbatim}
a <- zinbModel()
nSamples(a)
\end{verbatim}

---

**orthogonalizeTraceNorm**

\textit{Orthogonalize matrices to minimize trace norm of their product}

**Description**

Given two matrices \( U \) and \( V \) that can be multiplied, this function finds two new matrices \( U_2 \) and \( V_2 \) such that their product is conserved \((U*V = U_2*V_2)\) and such that \( a\|U\|^2 + b\|V\|^2 \) is minimized.

**Usage**

\texttt{orthogonalizeTraceNorm(U, V, a = 1, b = 1)}

**Arguments**

\begin{itemize}
  \item \texttt{U} left matrix
  \item \texttt{V} right matrix
  \item \texttt{a} weight of the norm of \( U \) (default=1)
  \item \texttt{b} weight of the norm of \( V \) (default=1)
\end{itemize}
\end{verbatim}
Value

A list with the two matrices that solve the problem in the slots U and V.

Examples

U <- matrix(rnorm(15),5,3)
V <- matrix(rnorm(12),3,4)
o <- orthogonalizeTraceNorm(U,V)
norm(U%*%V - o$U%*%o$V) # should be zero
sum(U^2)+sum(V^2)
sum(o$U^2)+sum(o$V^2) # should be smaller

penalty

Compute the penalty of a model

Description

Given a statistical model with regularization parameters, compute the penalty.

Usage

penalty(model)

## S4 method for signature 'ZinbModel'
penalty(model)

Arguments

model an object that describes a statistical model with regularization parameters.

Value

The penalty of the model.

Methods (by class)

• penalty(ZinbModel): return the penalization.

Examples

m <- zinbModel(K=2)
penalty(m)
**pvalueAdjustment**

Perform independent filtering in differential expression analysis.

**Description**

This function performs independent filtering to increase detection power in high throughput gene expression studies.

**Usage**

```r
pvalueAdjustment(
  baseMean,
  filter,
  pValue,
  theta,
  alpha = 0.05,
  pAdjustMethod = "BH"
)
```

**Arguments**

- `baseMean`: A vector of mean values.
- `filter`: A vector of stage-one filter statistics.
- `pValue`: A vector of unadjusted p-values, or a function which is able to compute this vector from the filtered portion of data, if data is supplied. The option to supply a function is useful when the value of the test statistic depends on which hypotheses are filtered out at stage one. (The limma t-statistic is an example.)
- `theta`: A vector with one or more filtering fractions to consider. Actual cutoffs are then computed internally by applying quantile to the filter statistics contained in (or produced by) the filter argument.
- `alpha`: A cutoff to which p-values, possibly adjusted for multiple testing, will be compared. Default is 0.05.
- `pAdjustMethod`: The unadjusted p-values contained in (or produced by) test will be adjusted for multiple testing after filtering. Default is "BH".

**Value**

A list with pvalues, filtering threshold, theta, number of rejections, and alpha.

**Note**

This function is an adapted version of the `pvalueAdjustment` function that was originally written by Michael I. Love as part of the DESeq2 package. Koen Van den Berge adapted the function.
solveRidgeRegression  Solve ridge regression or logistic regression problems

Description

This function solves a regression or logistic regression problem regularized by a L2 or weighted L2 penalty. Contrary to \texttt{lm.ridge} or \texttt{glmnet}, it works for any number of predictors.

Usage

\begin{verbatim}
solveRidgeRegression(
  x,  # a matrix of covariates, one sample per row, one covariate per column.
  y,  # a vector of response (continuous for regression, 0/1 binary for logistic regression)
  beta = rep(0, NCOL(x)),  # an initial solution where optimization starts (null vector by default)
  epsilon = 1e-06,  # a scalar or vector of regularization parameters (default 1e-6)
  family = c("gaussian", "binomial"),  # a string to choose the type of regression (default family="gaussian")
  offset = rep(0, NROW(x))  # a vector of offsets (default null vector)
)
\end{verbatim}

Arguments

- \texttt{x}  
a matrix of covariates, one sample per row, one covariate per column.
- \texttt{y}  
a vector of response (continuous for regression, 0/1 binary for logistic regression)
- \texttt{beta}  
an initial solution where optimization starts (null vector by default)
- \texttt{epsilon}  
a scalar or vector of regularization parameters (default 1e-6)
- \texttt{family}  
a string to choose the type of regression (default family="gaussian")
- \texttt{offset}  
a vector of offsets (default null vector)

Details

When family="gaussian", we solve the ridge regression problem that finds the $\beta$ that minimizes:
\begin{equation}
\|y - x\beta\|^2 + \epsilon \|\beta\|^2 / 2.
\end{equation}

When family="binomial" we solve the ridge logistic regression problem
\begin{equation}
\min \sum_i [-y_i (x\beta)_i + \log(1 + \exp(x\beta)_i)] + \epsilon \|\beta\|^2 / 2.
\end{equation}

When epsilon is a vector of size equal to the size of beta, then the penalty is a weighted L2 norm $\sum_i \epsilon_i \beta_i^2 / 2$.

Value

A vector solution of the regression problem.
**toyd ata**

*Toy dataset to check the model*

**Description**

Toy dataset to check the model

**Format**

A matrix of integers (counts) with 96 samples (rows) and 500 genes (columns).

---

**zinb.loglik**

*Log-likelihood of the zero-inflated negative binomial model*

**Description**

Given a vector of counts, this function computes the sum of the log-probabilities of the counts under a zero-inflated negative binomial (ZINB) model. For each count, the ZINB distribution is parametrized by three parameters: the mean value and the dispersion of the negative binomial distribution, and the probability of the zero component.

**Usage**

```
zinb.loglik(Y, mu, theta, logitPi)
```

**Arguments**

- `Y` the vector of counts
- `mu` the vector of mean parameters of the negative binomial
- `theta` the vector of dispersion parameters of the negative binomial, or a single scalar is also possible if the dispersion parameter is constant. Note that theta is sometimes called inverse dispersion parameter (and phi=1/theta is then called the dispersion parameter). We follow the convention that the variance of the NB variable with mean mu and dispersion theta is mu + mu^2/theta.
- `logitPi` the vector of logit of the probabilities of the zero component

**Value**

the log-likelihood of the model.
Examples

```r
n <- 10
mu <- seq(10,50,length.out=n)
logitPi <- rnorm(10)
zeta <- rnorm(10)
Y <- rnbinom(n=n, size=exp(zeta), mu=mu)
zinb.loglik(Y, mu, exp(zeta), logitPi)
zinb.loglik(Y, mu, 1, logitPi)
```

zinb.loglik.dispersion

*Log-likelihood of the zero-inflated negative binomial model, for a fixed dispersion parameter*

Description

Given a unique dispersion parameter and a set of counts, together with a corresponding set of mean parameters and probabilities of zero components, this function computes the sum of the log-probabilities of the counts under the ZINB model. The dispersion parameter is provided to the function through `zeta = log(theta)`, where theta is sometimes called the inverse dispersion parameter. The probabilities of the zero components are provided through their logit, in order to better numerical stability.

Usage

```r
zinb.loglik.dispersion(zeta, Y, mu, logitPi)
```

Arguments

- `zeta` a scalar, the log of the inverse dispersion parameters of the negative binomial model
- `Y` a vector of counts
- `mu` a vector of mean parameters of the negative binomial
- `logitPi` a vector of logit of the probabilities of the zero component

Value

the log-likelihood of the model.

See Also

`zinb.loglik`
**Examples**

```r
mu <- seq(10, 50, length.out = 10)
logitPi <- rnorm(10)
zeta <- rnorm(10)
Y <- rbinom(n = 10, size = exp(zeta), mu = mu)
zinb.loglik.dispersion(zeta, Y, mu, logitPi)
```

**Description**

Derivative of the log-likelihood of the zero-inflated negative binomial model with respect to the log of the inverse dispersion parameter

**Usage**

```r
zinb.loglik.dispersion.gradient(zeta, Y, mu, logitPi)
```

**Arguments**

- `zeta` the log of the inverse dispersion parameters of the negative binomial
- `Y` a vector of counts
- `mu` a vector of mean parameters of the negative binomial
- `logitPi` a vector of the logit of the probability of the zero component

**Value**

the gradient of the inverse dispersion parameters.

**See Also**

`zinb.loglik, zinb.loglik.dispersion`
zinb.loglik.matrix  
Log-likelihood of the zero-inflated negative binomial model for each entry in the matrix of counts

Description

Given a matrix of counts, this function computes the log-probabilities of the counts under a zero-inflated negative binomial (ZINB) model. For each count, the ZINB distribution is parametrized by three parameters: the mean value and the dispersion of the negative binomial distribution, and the probability of the zero component.

Usage

zinb.loglik.matrix(model, x)

Arguments

model  
the zinb model

x  
the matrix of counts

Value

the matrix of log-likelihood of the model.

zinb.loglik.regression  
Penalized log-likelihood of the ZINB regression model

Description

This function computes the penalized log-likelihood of a ZINB regression model given a vector of counts.

Usage

zinb.loglik.regression(
    alpha,
    Y,
    A.mu = matrix(nrow = length(Y), ncol = 0),
    B.mu = matrix(nrow = length(Y), ncol = 0),
    C.mu = matrix(0, nrow = length(Y), ncol = 1),
    A.pi = matrix(nrow = length(Y), ncol = 0),
    B.pi = matrix(nrow = length(Y), ncol = 0),
    C.pi = matrix(0, nrow = length(Y), ncol = 1),
    C.theta = matrix(0, nrow = length(Y), ncol = 1),
    epsilon = 0
)
Arguments

alpha the vectors of parameters c(a.mu, a.pi, b) concatenated
Y the vector of counts
A.mu matrix of the model (see Details, default=empty)
B.mu matrix of the model (see Details, default=empty)
C.mu matrix of the model (see Details, default=zero)
A.pi matrix of the model (see Details, default=empty)
B.pi matrix of the model (see Details, default=empty)
C.pi matrix of the model (see Details, default=zero)
C.theta matrix of the model (see Details, default=zero)
epsilon regularization parameter. A vector of the same length as alpha if each coordinate of alpha has a specific regularization, or just a scalar is the regularization is the same for all coordinates of alpha. Default=0.

details

The regression model is parametrized as follows:

\[
\log(\mu) = A_\mu \ast a_\mu + B_\mu \ast b + C_\mu
\]

\[
\logit(\Pi) = A_\pi \ast a_\pi + B_\pi \ast b
\]

\[
\log(\theta) = C_\theta
\]

where \( \mu, \Pi, \theta \) are respectively the vector of mean parameters of the NB distribution, the vector of probabilities of the zero component, and the vector of inverse dispersion parameters. Note that the \( b \) vector is shared between the mean of the negative binomial and the probability of zero. The log-likelihood of a vector of parameters \( \alpha = (a_\mu; a_\pi; b) \) is penalized by a regularization term \( \epsilon ||\alpha||^2/2 \) is \( \epsilon \) is a scalar, or \( \sum_i \epsilon_i \alpha_i^2/2 \) is \( \epsilon \) is a vector of the same size as \( \alpha \) to allow for differential regularization among the parameters.

value

the penalized log-likelihood.
Usage

zinb.loglik.regression.gradient(
  alpha,
  Y,
  A.mu = matrix(nrow = length(Y), ncol = 0),
  B.mu = matrix(nrow = length(Y), ncol = 0),
  C.mu = matrix(0, nrow = length(Y), ncol = 1),
  A.pi = matrix(nrow = length(Y), ncol = 0),
  B.pi = matrix(nrow = length(Y), ncol = 0),
  C.pi = matrix(0, nrow = length(Y), ncol = 1),
  C.theta = matrix(0, nrow = length(Y), ncol = 1),
  epsilon = 0
)

Arguments

alpha the vectors of parameters c(a.mu, a.pi, b) concatenated
Y the vector of counts
A.mu matrix of the model (see Details, default=empty)
B.mu matrix of the model (see Details, default=empty)
C.mu matrix of the model (see Details, default=zero)
A.pi matrix of the model (see Details, default=empty)
B.pi matrix of the model (see Details, default=empty)
C.pi matrix of the model (see Details, default=zero)
C.theta matrix of the model (see Details, default=zero)
epsilon regularization parameter. A vector of the same length as alpha if each coordinate of alpha has a specific regularization, or just a scalar is the regularization is the same for all coordinates of alpha. Default=0.

Details

The regression model is described in zinb.loglik.regression.

Value

The gradient of the penalized log-likelihood.

See Also

zinb.loglik.regression
zinb.regression.parseModel

Parse ZINB regression model

Description

Given the parameters of a ZINB regression model, this function parses the model and computes the vector of log(mu), logit(pi), and the dimensions of the different components of the vector of parameters. See zinb.loglik.regression for details of the ZINB regression model and its parameters.

Usage

zinb.regression.parseModel(alpha, A.mu, B.mu, C.mu, A.pi, B.pi, C.pi)

Arguments

- **alpha**: the vectors of parameters c(a.mu, a.pi, b) concatenated
- **A.mu**: matrix of the model (see above, default=empty)
- **B.mu**: matrix of the model (see above, default=empty)
- **C.mu**: matrix of the model (see above, default=zero)
- **A.pi**: matrix of the model (see above, default=empty)
- **B.pi**: matrix of the model (see above, default=empty)
- **C.pi**: matrix of the model (see above, default=zero)

Value

A list with slots `logMu`, `logitPi`, `dim.alpha` (a vector of length 3 with the dimension of each of the vectors a.mu, a.pi and b in alpha), and `start.alpha` (a vector of length 3 with the starting indices of the 3 vectors in alpha)

See Also

zinb.loglik.regression

zinbAIC

Compute the AIC or BIC of a model given some data

Description

Given a statistical model and some data, these functions compute the AIC or BIC of the model given the data, i.e., the AIC/BIC of the data under the model.
Usage

zinbAIC(model, x)

zinbBIC(model, x)

## S4 method for signature 'ZinbModel,matrix'
zinbAIC(model, x)

## S4 method for signature 'ZinbModel,matrix'
zinbBIC(model, x)

Arguments

model an object that describes a statistical model.
x an object that describes data.

Value

the AIC/BIC of the model.

Functions

• zinbAIC(model = ZinbModel, x = matrix): returns the AIC of the ZINB model.

• zinbBIC(model = ZinbModel, x = matrix): returns the BIC of the ZINB model.

Examples

se <- SummarizedExperiment(matrix(rpois(60, lambda=5), nrow=10, ncol=6),
colData = data.frame(bio = gl(2, 3)))
m <- zinbFit(se, X=model.matrix(~bio, data=colData(se)),
BPPARAM=BiocParallel::SerialParam())
zinbAIC(m, t(assay(se)))
zinbBIC(m, t(assay(se)))

---

zinbFit Fit a ZINB regression model

Description

Given an object with the data, it fits a ZINB model.
Usage

zinbFit(Y, ...)

## S4 method for signature 'SummarizedExperiment'
zinbFit(
  Y,
  X,
  V,
  K,
  which_assay,
  commondispersion = TRUE,
  zeroinflation = TRUE,
  verbose = FALSE,
  nb.repeat.initialize = 2,
  maxiter.optimize = 25,
  stop.epsilon.optimize = 1e-04,
  BPPARAM = BiocParallel::bpparam(),
  ...
)

## S4 method for signature 'matrix'
zinbFit(
  Y,
  X,
  V,
  K,
  commondispersion = TRUE,
  zeroinflation = TRUE,
  verbose = FALSE,
  nb.repeat.initialize = 2,
  maxiter.optimize = 25,
  stop.epsilon.optimize = 1e-04,
  BPPARAM = BiocParallel::bpparam(),
  ...
)

## S4 method for signature 'dgCMatrix'
zinbFit(Y, ...)

Arguments

Y The data (genes in rows, samples in columns).

... Additional parameters to describe the model, see zinbModel.

X The design matrix containing sample-level covariates, one sample per row. If missing, X will contain only an intercept. If Y is a SummarizedExperiment object, X can be a formula using the variables in the colData slot of Y.

V The design matrix containing gene-level covariates, one gene per row. If missing, V will contain only an intercept. If Y is a SummarizedExperiment object,
V can be a formula using the variables in the rowData slot of Y.

K
integer. Number of latent factors.

which_assay
numeric or character. Which assay of Y to use (only if Y is a SummarizedExperiment).

commondispersion
Whether or not a single dispersion for all features is estimated (default TRUE).

zeroinflation
Whether or not a ZINB model should be fitted. If FALSE, a negative binomial model is fitted instead.

verbose
Print helpful messages.

nb.repeat.initialize
Number of iterations for the initialization of beta_mu and gamma_mu.

maxiter.optimize
maximum number of iterations for the optimization step (default 25).

stop.epsilon.optimize
stopping criterion in the optimization step, when the relative gain in likelihood is below epsilon (default 0.0001).

BPPARAM
object of class bpparamClass that specifies the back-end to be used for computations. See bpparam for details.

Details
By default, i.e., if no arguments other than Y are passed, the model is fitted with an intercept for the regression across-samples and one intercept for the regression across genes, both for mu and for pi.

This means that by default the model is fitted with $X_{mu} = X_{pi} = 1_n$ and $V_{mu} = V_{pi} = 1_J$. If the user explicitly passes the design matrices, this behavior is overwritten, i.e., the user needs to explicitly include the intercept in the design matrices.

If Y is a Summarized experiment, the function uses the assay named "counts", if any, or the first assay.

Currently, if Y is a sparseMatrix, this calls the zinbFit method on as.matrix(Y)

Value
An object of class ZinbModel that has been fitted by penalized maximum likelihood on the data.

Methods (by class)
- zinbFit(SummarizedExperiment): Y is a SummarizedExperiment.
- zinbFit(matrix): Y is a matrix of counts (genes in rows).
- zinbFit(dgCMatrix): Y is a sparse matrix of counts (genes in rows).

See Also
model.matrix.
Examples

```r
se <- SummarizedExperiment(matrix(rpois(60, lambda=5), nrow=10, ncol=6),
  colData = data.frame(bio = gl(2, 3)))

m <- zinbFit(se, X=model.matrix(~bio, data=colData(se)),
  BPPARAM=BiocParallel::SerialParam())

bio <- gl(2, 3)
m <- zinbFit(matrix(rpois(60, lambda=5), nrow=10, ncol=6),
  X=model.matrix(~bio), BPPARAM=BiocParallel::SerialParam())
```

---

**zinbInitialize**

Initialize the parameters of a ZINB regression model

**Description**

The initialization performs quick optimization of the parameters with several simplifying assumptions compared to the true model: non-zero counts are modeled as log-Gaussian, zeros are modeled as dropouts. The dispersion parameter is not modified.

**Usage**

```r
zinbInitialize(
  m,
  Y,
  nb.repeat = 2,
  it.max = 100,
  BPPARAM = BiocParallel::bpparam()
)
```

**Arguments**

- `m` The model of class ZinbModel
- `Y` The matrix of counts.
- `nb.repeat` Number of iterations for the estimation of beta_mu and gamma_mu.
- `it.max` Maximum number of iterations in softImpute.
- `BPPARAM` object of class bpparamClass that specifies the back-end to be used for computations. See bpparam for details.

**Value**

An object of class ZinbModel similar to the one given as argument with modified parameters alpha_mu, alpha_pi, beta_mu, beta_pi, gamma_mu, gamma_pi, W.
Examples

Y <- matrix(rpois(60, lambda=2), 6, 10)
bio <- gl(2, 3)
time <- rnorm(6)
gc <- rnorm(10)
m <- zinbModel(Y, X=model.matrix(~bio + time), V=model.matrix(~gc),
    which_X_pi=1L, which_V_mu=1L, K=1)
m <- zinbInitialize(m, Y, BPPARAM=BiocParallel::SerialParam())

zinbModel

Initialize an object of class ZinbModel

Description

Initialize an object of class ZinbModel

Usage

zinbModel(
  X,
  V,
  O_mu,
  O_pi,
  which_X_mu,
  which_X_pi,
  which_V_mu,
  which_V_pi,
  W,
  beta_mu,
  beta_pi,
  gamma_mu,
  gamma_pi,
  alpha_mu,
  alpha_pi,
  zeta,
  epsilon,
  epsilon_beta_mu,
  epsilon_gamma_mu,
  epsilon_beta_pi,
  epsilon_gamma_pi,
  epsilon_W,
  epsilon_alpha,
  epsilon_zeta,
  epsilon_min_logit,
  n,
  J,
  K
)
Arguments

\(X\) matrix. The design matrix containing sample-level covariates, one sample per row.

\(V\) matrix. The design matrix containing gene-level covariates, one gene per row.

\(O_{\text{mu}}\) matrix. The offset matrix for \(\mu\).

\(O_{\text{pi}}\) matrix. The offset matrix for \(\pi\).

which\_X\_mu integer. Indeces of which columns of \(X\) to use in the regression of \(\mu\).

which\_X\_pi integer. Indeces of which columns of \(X\) to use in the regression of \(\pi\).

which\_V\_mu integer. Indeces of which columns of \(V\) to use in the regression of \(\mu\).

which\_V\_pi integer. Indeces of which columns of \(V\) to use in the regression of \(\pi\).

\(W\) matrix. The factors of sample-level latent factors.

\(\beta_{\text{mu}}\) matrix or NULL. The coefficients of \(X\) in the regression of \(\mu\).

\(\beta_{\text{pi}}\) matrix or NULL. The coefficients of \(X\) in the regression of \(\pi\).

\(\gamma_{\text{mu}}\) matrix or NULL. The coefficients of \(V\) in the regression of \(\mu\).

\(\gamma_{\text{pi}}\) matrix or NULL. The coefficients of \(V\) in the regression of \(\pi\).

\(\alpha_{\text{mu}}\) matrix or NULL. The coefficients of \(W\) in the regression of \(\mu\).

\(\alpha_{\text{pi}}\) matrix or NULL. The coefficients of \(W\) in the regression of \(\pi\).

\(\zeta\) numeric. A vector of log of inverse dispersion parameters.

\(\epsilon\) nonnegative scalar. Regularization parameter.

\(\epsilon_{\beta_{\text{mu}}}\) nonnegative scalar. Regularization parameter for \(\beta_{\text{mu}}\).

\(\epsilon_{\beta_{\text{pi}}}\) nonnegative scalar. Regularization parameter for \(\beta_{\text{pi}}\).

\(\epsilon_{\gamma_{\text{mu}}}\) nonnegative scalar. Regularization parameter for \(\gamma_{\text{mu}}\).

\(\epsilon_{\gamma_{\text{pi}}}\) nonnegative scalar. Regularization parameter for \(\gamma_{\text{pi}}\).

\(\epsilon_{\alpha}\) nonnegative scalar. Regularization parameter for \(\alpha\) (both \(\alpha_{\text{mu}}\) and \(\alpha_{\text{pi}}\)).

\(\epsilon_{\zeta}\) nonnegative scalar. Regularization parameter for \(\zeta\).

\(\epsilon_{\text{min\_logit}}\) scalar. Minimum regularization parameter for parameters of the logit model, including the intercept.

\(n\) integer. Number of samples.

\(J\) integer. Number of genes.

\(K\) integer. Number of latent factors.
Details

This is a wrapper around the new() function to create an instance of class ZinbModel. Rarely, the user will need to create a ZinbModel object from scratch, as typically this is the result of zinbFit.

If any of X, V, W matrices are passed, n, J, and K are inferred. Alternatively, the user can specify one or more of n, J, and K.

The regularization parameters can be set by a unique parameter epsilon or specific values for the different regularization parameters can also be provided. If only epsilon is specified, the other parameters take the following values:

- epsilon_beta = epsilon/J
- epsilon_gamma = epsilon/n
- epsilon_W = epsilon/n
- epsilon_alpha = epsilon/J
- epsilon_zeta = epsilon

We empirically found that large values of epsilon provide a more stable estimation of W.

A call with no argument has the following default values: n = 50, J = 100, K = 0, epsilon=J.

Although it is possible to create new instances of the class by calling this function, this is not the most common way of creating ZinbModel objects. The main use of the class is within the zinbFit function.

Value

an object of class ZinbModel.

Examples

```r
a <- zinbModel()
nSamples(a)
nFeatures(a)
nFactors(a)
nParams(a)
```

Description

Objects of this class store all the values needed to work with a zero-inflated negative binomial (ZINB) model, as described in the vignette. They contain all information to fit a model by penalized maximum likelihood or simulate data from a model.
Usage

## S4 method for signature 'ZinbModel'
show(object)

## S4 method for signature 'ZinbModel'
nSamples(x)

## S4 method for signature 'ZinbModel'
nFeatures(x)

## S4 method for signature 'ZinbModel'
nFactors(x)

## S4 method for signature 'ZinbModel'
getX_mu(object, intercept = TRUE)

## S4 method for signature 'ZinbModel'
getX_pi(object, intercept = TRUE)

## S4 method for signature 'ZinbModel'
getV_mu(object, intercept = TRUE)

## S4 method for signature 'ZinbModel'
getV_pi(object, intercept = TRUE)

## S4 method for signature 'ZinbModel'
getLogMu(object)

## S4 method for signature 'ZinbModel'
getMu(object)

## S4 method for signature 'ZinbModel'
getLogitPi(object)

## S4 method for signature 'ZinbModel'
getPi(object)

## S4 method for signature 'ZinbModel'
getZeta(object)

## S4 method for signature 'ZinbModel'
getPhi(object)

## S4 method for signature 'ZinbModel'
getTheta(object)

## S4 method for signature 'ZinbModel'
getEpsilon_beta_mu(object)
## S4 method for signature 'ZinbModel'
getEpsilon_gamma_mu(object)

## S4 method for signature 'ZinbModel'
getEpsilon_beta_pi(object)

## S4 method for signature 'ZinbModel'
getEpsilon_gamma_pi(object)

## S4 method for signature 'ZinbModel'
getEpsilon_W(object)

## S4 method for signature 'ZinbModel'
getEpsilon_alpha(object)

## S4 method for signature 'ZinbModel'
getEpsilon_zeta(object)

## S4 method for signature 'ZinbModel'
getW(object)

## S4 method for signature 'ZinbModel'
getBeta_mu(object)

## S4 method for signature 'ZinbModel'
getBeta_pi(object)

## S4 method for signature 'ZinbModel'
getGamma_mu(object)

## S4 method for signature 'ZinbModel'
getGamma_pi(object)

## S4 method for signature 'ZinbModel'
getAlpha_mu(object)

## S4 method for signature 'ZinbModel'
getAlpha_pi(object)

### Arguments

- **object**
  - an object of class `ZinbModel`.

- **x**
  - an object of class `ZinbModel`.

- **intercept**
  - logical. Whether to return the intercept (ignored if the design matrix has no intercept). Default `TRUE`
Details

For the full description of the model see the model vignette. Internally, the slots are checked so that the matrices are of the appropriate dimensions: in particular, \( X, O_{\mu}, O_{\pi}, \) and \( W \) need to have \( n \) rows, \( V \) needs to have \( J \) rows, \( zeta \) must be of length \( J \).

Value

\( nSamples \) returns the number of samples; \( nFeatures \) returns the number of features; \( nFactors \) returns the number of latent factors.

Methods (by generic)

- \( \text{show}(\text{ZinbModel}) \): show useful info on the object.
- \( \text{nSamples}(\text{ZinbModel}) \): returns the number of samples.
- \( \text{nFeatures}(\text{ZinbModel}) \): returns the number of features.
- \( \text{nFactors}(\text{ZinbModel}) \): returns the number of latent factors.
- \( \text{getX}_\mu(\text{ZinbModel}) \): returns the sample-level design matrix for \( \mu \).
- \( \text{getX}_\pi(\text{ZinbModel}) \): returns the sample-level design matrix for \( \pi \).
- \( \text{getV}_\mu(\text{ZinbModel}) \): returns the gene-level design matrix for \( \mu \).
- \( \text{getV}_\pi(\text{ZinbModel}) \): returns the sample-level design matrix for \( \pi \).
- \( \text{getLogMu}(\text{ZinbModel}) \): returns the logarithm of the mean of the non-zero component.
- \( \text{getMu}(\text{ZinbModel}) \): returns the mean of the non-zero component.
- \( \text{getLogitPi}(\text{ZinbModel}) \): returns the logit-probability of zero.
- \( \text{getPi}(\text{ZinbModel}) \): returns the probability of zero.
- \( \text{getZeta}(\text{ZinbModel}) \): returns the log of the inverse of the dispersion parameter.
- \( \text{getPhi}(\text{ZinbModel}) \): returns the dispersion parameter.
- \( \text{getTheta}(\text{ZinbModel}) \): returns the inverse of the dispersion parameter.
- \( \text{getEpsilon}_\beta_\mu(\text{ZinbModel}) \): returns the regularization parameters for \( \beta_\mu \).
- \( \text{getEpsilon}_\gamma_\mu(\text{ZinbModel}) \): returns the regularization parameters for \( \gamma_\mu \).
- \( \text{getEpsilon}_\beta_\pi(\text{ZinbModel}) \): returns the regularization parameters for \( \beta_\pi \).
- \( \text{getEpsilon}_\gamma_\pi(\text{ZinbModel}) \): returns the regularization parameters for \( \gamma_\pi \).
- \( \text{getEpsilon}_W(\text{ZinbModel}) \): returns the regularization parameters for \( W \).
- \( \text{getEpsilon}_\alpha(\text{ZinbModel}) \): returns the regularization parameters for \( \alpha \).
- \( \text{getEpsilon}_\zeta(\text{ZinbModel}) \): returns the regularization parameters for \( \zeta \).
- \( \text{getW}(\text{ZinbModel}) \): returns the matrix \( W \) of inferred sample-level covariates.
- \( \text{getBeta}_\mu(\text{ZinbModel}) \): returns the matrix \( \beta_\mu \) of inferred parameters.
- \( \text{getBeta}_\pi(\text{ZinbModel}) \): returns the matrix \( \beta_\pi \) of inferred parameters.
- \( \text{getGamma}_\mu(\text{ZinbModel}) \): returns the matrix \( \gamma_\mu \) of inferred parameters.
- \( \text{getGamma}_\pi(\text{ZinbModel}) \): returns the matrix \( \gamma_\pi \) of inferred parameters.
- \( \text{getAlpha}_\mu(\text{ZinbModel}) \): returns the matrix \( \alpha_\mu \) of inferred parameters.
- \( \text{getAlpha}_\pi(\text{ZinbModel}) \): returns the matrix \( \alpha_\pi \) of inferred parameters.
Slots

- **X** matrix. The design matrix containing sample-level covariates, one sample per row.
- **V** matrix. The design matrix containing gene-level covariates, one gene per row.
- **O_mu** matrix. The offset matrix for mu.
- **O_pi** matrix. The offset matrix for pi.
- **which_X_mu** integer. Indeces of which columns of X to use in the regression of mu.
- **which_V_mu** integer. Indeces of which columns of V to use in the regression of mu.
- **which_X_pi** integer. Indeces of which columns of X to use in the regression of pi.
- **which_V_pi** integer. Indeces of which columns of V to use in the regression of pi.
- **X_mu_intercept** logical. TRUE if X_mu contains an intercept.
- **X_pi_intercept** logical. TRUE if X_pi contains an intercept.
- **V_mu_intercept** logical. TRUE if V_mu contains an intercept.
- **V_pi_intercept** logical. TRUE if V_pi contains an intercept.
- **W** matrix. The factors of sample-level latent factors.
- **beta_mu** matrix or NULL. The coefficients of X in the regression of mu.
- **gamma_mu** matrix or NULL. The coefficients of V in the regression of mu.
- **alpha_mu** matrix or NULL. The coefficients of W in the regression of mu.
- **beta_pi** matrix or NULL. The coefficients of X in the regression of pi.
- **gamma_pi** matrix or NULL. The coefficients of V in the regression of pi.
- **alpha_pi** matrix or NULL. The coefficients of W in the regression of pi.
- **zeta** numeric. A vector of log of inverse dispersion parameters.
- **epsilon_beta_mu** nonnegative scalar. Regularization parameter for beta_mu.
- **epsilon_gamma_mu** nonnegative scalar. Regularization parameter for gamma_mu.
- **epsilon_beta_pi** nonnegative scalar. Regularization parameter for beta_pi.
- **epsilon_gamma_pi** nonnegative scalar. Regularization parameter for gamma_pi.
- **epsilon_W** nonnegative scalar. Regularization parameter for W.
- **epsilon_alpha** nonnegative scalar. Regularization parameter for alpha (both alpha_mu and alpha_pi).
- **epsilon_zeta** nonnegative scalar. Regularization parameter for zeta.
- **epsilon_min_logit** scalar. Minimum regularization parameter for parameters of the logit model, including the intercept.
zinbOptimize

Optimize the parameters of a ZINB regression model

Description

The parameters of the model given as argument are optimized by penalized maximum likelihood on the count matrix given as argument. It is recommended to call zinb_initialize before this function to have good starting point for optimization, since the optimization problem is not convex and can only converge to a local minimum.

Usage

zinbOptimize(
  m,
  Y,
  commondispersion = TRUE,
  maxiter = 25,
  stop.epsilon = 1e-04,
  verbose = FALSE,
  BPPARAM = BiocParallel::bpparam()
)

Arguments

m
  The model of class ZinbModel
Y
  The matrix of counts.
commondispersion
  Whether the dispersion is the same for all features (default=TRUE)
maxiter
  maximum number of iterations (default 25)
stop.epsilon
  stopping criterion, when the relative gain in likelihood is below epsilon (default 0.0001)
verbose
  print information (default FALSE)
BPPARAM
  object of class bpparamClass that specifies the back-end to be used for computations. See bpparam for details.

Value

An object of class ZinbModel similar to the one given as argument with modified parameters alpha_mu, alpha_pi, beta_mu, beta_pi, gamma_mu, gamma_pi, W.

Examples

Y = matrix(10, 3, 5)
m = zinbModel(n=NROW(Y), J=NCOL(Y))
m = zinbInitialize(m, Y, BPPARAM=BiocParallel::SerialParam())
m = zinbOptimize(m, Y, BPPARAM=BiocParallel::SerialParam())
zinbOptimizeDispersion

Optimize the dispersion parameters of a ZINB regression model

Description

The dispersion parameters of the model are optimized by penalized maximum likelihood on the count matrix given as argument.

Usage

```r
zinbOptimizeDispersion(
  J,
  mu,
  logitPi,
  epsilon,
  Y,
  commondispersion = TRUE,
  BPPARAM = BiocParallel::bpparam()
)
```

Arguments

- `J` The number of genes.
- `mu` the matrix containing the mean of the negative binomial.
- `logitPi` the matrix containing the logit of the probability parameter of the zero-inflation part of the model.
- `epsilon` the regularization parameter.
- `Y` The matrix of counts.
- `commondispersion` Whether or not a single dispersion for all features is estimated (default TRUE).
- `BPPARAM` object of class bpparamClass that specifies the back-end to be used for computations. See bpparam for details.

Value

An object of class ZinbModel similar to the one given as argument with modified parameters zeta.

Examples

```r
Y = matrix(10, 3, 5)
m = zinbModel(n=NROW(Y), J=NCOL(Y))
m = zinbInitialize(m, Y, BPPARAM=BiocParallel::SerialParam())
m = zinbOptimizeDispersion(NROW(Y), getMu(m), getLogitPi(m),
  getEpsilon_zeta(m), Y, BPPARAM=BiocParallel::SerialParam())
```
zinbSim

Simulate counts from a zero-inflated negative binomial model

Description

Given an object that describes zero-inflated negative binomial distribution, simulate counts from the distribution.

Usage

zinbSim(object, seed, ...)

## S4 method for signature 'ZinbModel'
zinbSim(object, seed)

Arguments

object an object that describes a matrix of zero-inflated negative binomial.
seed an optional integer to specify how the random number generator should be initialized with a call to set.seed. If missing, the random generator state is not changed.
... additional arguments.

Value

A list with the following elements.

- counts the matrix with the simulated counts.
- dataNB the data simulated from the negative binomial.
- dataDropout the data simulated from the binomial process.
- zeroFraction the fraction of zeros.

Methods (by class)

- zinbSim(ZinbModel): simulate from a ZINB distribution.

Examples

a <- zinbModel(n=5, J=10)
zinbSim(a)
Perform dimensionality reduction using a ZINB regression model for large datasets.

Description

Given an object with the data, it performs dimensionality reduction using a ZINB regression model with gene and cell-level covariates on a random subset of the data. It then projects the remaining data onto the lower dimensional space.

Usage

```
zinbsurf(Y, ...)
```

## S4 method for signature 'SummarizedExperiment'

```
zinbsurf(
  Y,
  X,
  V,
  K,
  which_assay,
  which_genes,
  zeroinflation = TRUE,
  prop_fit = 0.1,
  BPPARAM = BiocParallel::bpparam(),
  verbose = FALSE,
  ...
)
```

Arguments

- `Y`  
The data (genes in rows, samples in columns). Currently implemented only for `SummarizedExperiment`.

- `...` 
Additional parameters to describe the model, see `zinbModel`.

- `X`  
The design matrix containing sample-level covariates, one sample per row. If missing, X will contain only an intercept. If Y is a `SummarizedExperiment` object, X can be a formula using the variables in the `colData` slot of Y.

- `V`  
The design matrix containing gene-level covariates, one gene per row. If missing, V will contain only an intercept. If Y is a `SummarizedExperiment` object, V can be a formula using the variables in the `rowData` slot of Y.

- `K`  
integer. Number of latent factors. Specify K = 0 if only computing observational weights.

- `which_assay`  
numeric or character. Which assay of Y to use. If missing, if `assayNames(Y)` contains "counts" then that is used. Otherwise, the first assay is used.
which_genes character. Which genes to use to estimate W (see details). Ignored if fitted_model is provided.
zeroinflation Whether or not a ZINB model should be fitted. If FALSE, a negative binomial model is fitted instead.
prop_fit numeric between 0 and 1. The proportion of cells to use for the zinbwave fit.
BPPARAM object of class bpparamClass that specifies the back-end to be used for computations. See bpparam for details.
verbose Print helpful messages.

Details

This function implements an approximate strategy, in which the full zinbwave model is fit only on a random subset of the data (controlled by the prop_fit parameter). The rest of the samples are subsequently projected onto the low-rank space. This strategy is much faster and uses less memory than the full zinbwave method. It is recommended with extremely large datasets.

By default zinbsurf uses all genes to estimate W. However, we recommend to use the top 1,000 most variable genes for this step. In general, a user can specify any custom set of genes to be used to estimate W, by specifying either a vector of gene names, or a single character string corresponding to a column of the rowData.

Value

An object of class SingleCellExperiment; the dimensionality reduced matrix is stored in the reducedDims slot.

Methods (by class)

- zinbsurf(SummarizedExperiment): Y is a SummarizedExperiment.

Examples

```r
se <- SingleCellExperiment(assays = list(counts = matrix(rpois(60, lambda=5),
nrow=10, ncol=6)),
colData = data.frame(bio = gl(2, 3)))
colnames(se) <- paste0("sample", 1:6)
m <- zinbsurf(se, X="~bio", K = 1, prop_fit = .5, which_assay = 1,
BPPARAM=BiocParallel::SerialParam())
```

zinbwave Perform dimensionality reduction using a ZINB regression model with gene and cell-level covariates.

Description

Given an object with the data, it performs dimensionality reduction using a ZINB regression model with gene and cell-level covariates.
Usage

zinbwave(Y, ...)

## S4 method for signature 'SummarizedExperiment'
zinbwave(
  Y,
  X,
  V,
  K = 2,
  fitted_model,
  which_assay,
  which_genes,
  commondispersion = TRUE,
  zeroinflation = TRUE,
  verbose = FALSE,
  nb.repeat.initialize = 2,
  maxiter.optimize = 25,
  stop.epsilon.optimize = 1e-04,
  BPPARAM = BiocParallel::bpparam(),
  normalizedValues = FALSE,
  residuals = FALSE,
  imputedValues = FALSE,
  observationalWeights = FALSE,
  ...
)

Arguments

Y  The data (genes in rows, samples in columns). Currently implemented only for SummarizedExperiment.

...  Additional parameters to describe the model, see zinbModel.

X  The design matrix containing sample-level covariates, one sample per row. If missing, X will contain only an intercept. If Y is a SummarizedExperiment object, X can be a formula using the variables in the colData slot of Y.

V  The design matrix containing gene-level covariates, one gene per row. If missing, V will contain only an intercept. If Y is a SummarizedExperiment object, V can be a formula using the variables in the rowData slot of Y.

K  integer. Number of latent factors. Specify K = 0 if only computing observational weights.

fitted_model  a ZinbModel object.

which_assay  numeric or character. Which assay of Y to use. If missing, if ‘assayNames(Y)’ contains “counts” then that is used. Otherwise, the first assay is used.

which_genes  character. Which genes to use to estimate W (see details). Ignored if fitted_model is provided.

commondispersion  Whether or not a single dispersion for all features is estimated (default TRUE).
zero_inflation: Whether or not a ZINB model should be fitted. If FALSE, a negative binomial model is fitted instead.

verbose: Print helpful messages.

nb.repeat.initialize: Number of iterations for the initialization of beta_mu and gamma_mu.

max.iter.optimize: maximum number of iterations for the optimization step (default 25).

stop.epsilon.optimize: stopping criterion in the optimization step, when the relative gain in likelihood is below epsilon (default 0.0001).

BPPARAM: object of class bpparamClass that specifies the back-end to be used for computations. See bpparam for details.

normalizedValues: indicates whether or not you want to compute normalized values for the counts after adjusting for gene and cell-level covariates.

residuals: indicates whether or not you want to compute the residuals of the ZINB model. Deviance residuals are computed.

imputedValues: indicates whether or not you want to compute the imputed counts of the ZINB model.

observationalWeights: indicates whether to compute the observational weights for differential expression (see vignette).

Details

For visualization (heatmaps, ...), please use the normalized values. It corresponds to the deviance residuals when the W is not included in the model but the gene and cell-level covariates are. As a result, when W is not included in the model, the deviance residuals should capture the biology. Note that we do not recommend to use the normalized values for any downstream analysis (such as clustering, or differential expression), but only for visualization.

If one has already fitted a model using ZinbModel, the object containing such model can be used as input of zinbwave to save the resulting W into a SummarizedExperiment and optionally compute residuals and normalized values, without the need for re-fitting the model.

By default zinbwave uses all genes to estimate W. However, we recommend to use the top 1,000 most variable genes for this step. In general, a user can specify any custom set of genes to be used to estimate W, by specifying either a vector of gene names, or a single character string corresponding to a column of the rowData.

Note that if both which_genes is specified and at least one among observationalWeights, imputedValues, residuals, and normalizedValues is TRUE, the model needs to be fit twice.

Value

An object of class SingleCellExperiment; the dimensionality reduced matrix is stored in the reducedDims slot and optionally normalized values and residuals are added in the list of assays.
Methods (by class)

* zinbwave(SummarizedExperiment): Y is a SummarizedExperiment.

Examples

```r
se <- SingleCellExperiment(assays = list(counts = matrix(rpois(60, lambda=5),
    nrow=10, ncol=6)),
    colData = data.frame(bio = gl(2, 3)))

m <- zinbwave(se, X="bio", BPPARAM=BiocParallel::SerialParam())
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