Package `fastTopics`

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Description Implements fast, scalable optimization algorithms for fitting topic models (``grade of membership'' models) and non-negative matrix factorizations to count data. The methods exploit the special relationship between the multinomial topic model (also, ``probabilistic latent semantic indexing'') and Poisson non-negative matrix factorization. The package provides tools to compare, annotate and visualize model fits, including functions to efficiently create "structure plots" and identify key features in topics. The 'fastTopics' package is a successor to the 'CountClust' package.
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**compare_fits**

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**Description**

Create a table summarizing the results of fitting one or more Poisson non-negative matrix factorizations or multinomial topic models.

**Usage**

```r
compare_fits(fits)
```

**Arguments**

- `fits` An object of class "poisson_nmf_fit" or "multinom_topic_model_fit", or a non-empty, named list in which all list elements are Poisson NMF model fits or all multinomial topic model fits.

**Value**

A data frame with one row per element of `fits`, and with the following columns:

- `k` The rank of the matrix factorization.
- `loglik` The log-likelihood (either Poisson NMF or multinomial topic model likelihood) achieved at the last model fitting update.
- `dev` For Poisson NMF model fits only, the deviance achieved at the last model fitting update.
- `res` The maximum residual of the Karush-Kuhn-Tucker (KKT) system achieved at the last model fitting update; small values indicate that the solution is close to a local maximum, or stationary point, of the likelihood.
- `loglik.diff` The improvement in the log-likelihood relative to the model fit with the smallest log-likelihood.
- `dev.diff` The improvement in the deviance relative to the model fit with the largest deviance.
- `nonzeros.f` The rate of nonzeros in the factors matrix, as determined by `control$zero.threshold`.
- `nonzeros.l` The rate of nonzeros in the loadings matrix, as determined by `control$zero.threshold`.
- `numiter` The number of loadings and/or factor updates performed.
- `runtime` The total runtime (in s) of the model fitting updates.

**See Also**

- `fit_poisson_nmf`, `fit_topic_model`
Differential Expression Analysis using a Topic Model

Description

Implements methods for differential expression analysis using a topic model. These methods are motivated by gene expression studies, but could have other uses, such as identifying “key words” for topics.

Usage

```r
de_analysis(
  fit,
  X,
  s = rowSums(X),
  pseudocount = 0.01,
  fit.method = c("scd", "em", "mu", "ccd", "glm"),
  shrink.method = c("ash", "none"),
  lfc.stat = "le",
  control = list(),
  verbose = TRUE,
  ...
)
```

de_analysis_control_default()

Arguments

- **fit**: An object of class “poisson_nmf_fit” or “multinom_topic_model_fit”. If a Poisson NMF fit is provided as input, the corresponding multinomial topic model fit is automatically recovered using `poisson2multinom`.

- **X**: The n x m counts matrix. It can be a sparse matrix (class "dgCMatrix") or dense matrix (class "matrix").

- **s**: A numeric vector of length n determining how the rates are scaled in the Poisson models. See “Details” for guidance on the choice of s.

- **pseudocount**: Observations with this value are added to the counts matrix to stabilize maximum-likelihood estimation.

- **fit.method**: Method used to fit the Poisson models. Note that `fit.method = "glm"` is the slowest method, and is mainly used for testing.

- **shrink.method**: Method used to stabilize the posterior mean LFC estimates. When `shrink.method = "ash"`, the "adaptive shrinkage" method implemented in the 'ashr' package is used to compute posterior. When `shrink.method = "none"`, no stabilization is performed, and the “raw” posterior mean LFC estimates are returned.
The log-fold change statistics returned: lfc.stat = "vsnull", the log-fold change relative to the null; lfc.stat = "le", the “least extreme” LFC; or a topic name or number, in which case the LFC is defined relative to the selected topic. See “Details” for more detailed explanations of these choices.

A list of parameters controlling behaviour of the optimization and Monte Carlo algorithms. See ‘Details’.

When verbose = TRUE, progress information is printed to the console.

... When shrink.method = "ash", these are additional arguments passed to ash.

**Details**

The methods are based on the Poisson model

\[ x_i \sim \text{Poisson}(\lambda_i), \]

in which the Poisson rates are

\[ \lambda_i = \sum_{j=1}^{k} s_i l_{ij} f_j, \]

the \( l_{ik} \) are the topic proportions and the \( f_j \) are the unknowns to be estimated. This model is applied separately to each column of \( X \). When \( s_i \) (specified by input argument \( s \)) is equal to the total count in row \( i \) (this is the default), the Poisson model will closely approximate a binomial model of the count data, and the unknowns \( f_j \) will approximate binomial probabilities. (The Poisson approximation to the binomial is most accurate when the total counts \( \text{rowSums}(X) \) are large and the unknowns \( f_j \) are small.) Other choices for \( s \) are possible, and implement different normalization schemes.

To allow for some flexibility, de_analysis allows for the log-fold change to be measured in several ways.

One option is to compare against the probability under the null model: \( \text{LFC}(j) = \log_2(f_j/f_0) \), where \( f_0 \) is the single parameter in the Poisson model \( x_i \sim \text{Poisson}(\lambda_i) \) with rates \( \lambda_i = s_i f_0 \). This LFC definition is chosen with \( \text{lfc.stat} = "vsnull" \).

Another option is to compare against a chosen topic, \( k \): \( \text{LFC}(j) = \log_2(f_j/f_k) \). By definition, \( \text{LFC}(k) \) is zero, and statistics such as z-scores and p-values for topic \( k \) are set to \( \text{NA} \). This LFC definition is selected by setting \( \text{lfc.stat} = k \).

A final option (which is the default) computes the “least extreme” LFC, defined as \( \text{LFC}(j) = \log_2(f_j/f_k) \) such that \( k \) is the topic other than \( j \) that gives the ratio \( f_j/f_k \) closest to 1. This option is chosen with \( \text{lfc.stat} = "le" \).

We recommend setting \( \text{shrink.method} = "\text{ash}" \), which uses the “adaptive shrinkage” method (Stephens, 2016) to improve accuracy of the posterior mean estimates and z-scores. We follow the settings used in lfcShrink from the ‘DESeq2’ package, with \( \text{type} = "\text{ashr}" \).

Note that all LFC statistics are defined using the base-2 logarithm following the convention used in differential expression analysis.

The control argument is a list in which any of the following named components will override the default optimization algorithm settings (as they are defined by de_analysis_control_default):

- **numiter** Maximum number of iterations performed in fitting the Poisson models. When fit.method = "glm", this is passed as argument maxit to the glm function.
**minval** A small, positive number. All topic proportions less than this value and greater than $1 - \text{minval}$ are set to this value.

**tol** Controls the convergence tolerance for fitting the Poisson models. When `fit.method = "glm"`, this is passed as argument `epsilon` to function `glm`.

**conf.level** The size of the highest posterior density (HPD) intervals. Should be a number greater than 0 and less than 1.

**ns** Number of Monte Carlo samples simulated by random-walk MCMC for estimating posterior LFC quantities.

**rw** The standard deviation of the normal density used to propose new states in the random-walk MCMC.

**eps** A small, non-negative number added to the terms inside the logarithms to avoid computing logarithms of zero.

**nc** Number of threads used in the multithreaded computations. Note that the multithreading relies on forking hence is not available on Windows; will return an error on Windows unless `nc = 1`. See `mclapply` for details.

**nsplit** The number of data splits used in the multithreaded computations (only relevant when `nc > 1`). More splits increase the granularity of the progress bar, but can also slow down the multithreaded computations by introducing more overhead in the call to `pblapply`.

**Value**

A list with the following elements:

- **est** The log-fold change maximum-likelihood estimates.
- **postmean** Posterior mean LFC estimates.
- **lower** Lower limits of estimated HPD intervals. Note that these are not updated by the shrinkage step.
- **upper** Upper limits of estimated HPD intervals. Note that these are not updated by the shrinkage step.
- **z** z-scores for posterior mean LFC estimates.
- **lpval** $-\log_{10}$ two-tailed p-values obtained from the z-scores. When `shrink.method = "ash"`, this is `NA`, and the s-values are returned instead (see below).
- **svalue** s-values returned by `ash`. s-values are analogous to q-values, but based on the local false sign rate; see Stephens (2016).
- **lfsr** When `shrink.method = "ash"` only, this output contains the estimated local false sign rates.
- **ash** When `shrink.method = "ash"` only, this output contains the `ash` return value (after removing the "data", "result" and "call" list elements).
- **F** Maximum-likelihood estimates of the Poisson model parameters.
- **f0** Maximum-likelihood estimates of the null model parameters.
- **ar** A vector containing the Metropolis acceptance ratios from each MCMC run.
References


Examples

```r
# Perform a differential expression (DE) analysis using the previously 
# fitted multinomial topic model. Note that the de_analysis call could 
# take several minutes to complete.

set.seed(1)
data(pbmcsfacs)
de <- de_analysis(pbmcsfacs$fit,pbmcsfacs$counts)

# Compile the DE analysis results for topic 4 into a table, and 
# rank the genes by the posterior mean log-fold change, limiting to 
# DE genes identified with low lfsr ("local false sign rate").
k <- 4
dat <- data.frame(postmean = de$postmean[,k],
                 z = de$z[,k],
                 lfsr = de$lfsr[,k])
rownames(dat) <- with(pbmcsfacs$genes,paste(symbol,ensembl,sep = "_"))
dat <- subset(dat,lfsr < 0.01)
dat <- dat[order(dat$postmean,decreasing = TRUE),]

# Genes at the top of this ranking are genes that are much more 
# highly expressed in the topic compared to other topics.
head(dat,n = 10)

# The genes at the bottom of the ranking are genes that are much less 
# expressed in the topic.
tail(dat,n = 10)

# Create a volcano plot from the DE results for topic 4.
volcano_plot(de,k = k,ymax = 50,labels = pbmcsfacs$genes$symbol)
```

**PCA, t-SNE and UMAP Plots**

**Description**

Visualize the structure of the Poisson NMF loadings or the multinomial topic model topic proportions by projection onto a 2-d surface. plot_hexbin_plot is most useful for visualizing the PCs of a data set with thousands of samples or more.
Usage

```r
embedding_plot_2d(
  fit,
  Y,
  fill = "loading",
  k,
  fill.label,
  ggplot_call = embedding_plot_2d_ggplot_call,
  plot_grid_call = function(plots) do.call(plot_grid, plots)
)

embedding_plot_2d_ggplot_call(
  Y,
  fill,
  fill.type = c("loading", "numeric", "factor", "none"),
  fill.label,
  font.size = 9
)

pca_plot(
  fit,
  Y,
  pcs = 1:2,
  n = 10000,
  fill = "loading",
  k,
  fill.label,
  ggplot_call = embedding_plot_2d_ggplot_call,
  plot_grid_call = function(plots) do.call(plot_grid, plots),
  ...
)

tsne_plot(
  fit,
  Y,
  n = 2000,
  fill = "loading",
  k,
  fill.label,
  ggplot_call = embedding_plot_2d_ggplot_call,
  plot_grid_call = function(plots) do.call(plot_grid, plots),
  ...
)

umap_plot(
  fit,
  Y,
  n = 2000,
  ...)
fill = "loading",
k,
fill.label,
ggplot_call = embedding_plot_2d_ggplot_call,
plot_grid_call = function(plots) do.call(plot_grid, plots),
...
)

pca_hexbin_plot(
  fit,
  Y,
  pcs = 1:2,
  bins = 40,
  breaks = c(0, 1, 10, 100, 1000, Inf),
  ggplot_call = pca_hexbin_plot_ggplot_call,
  ...
)

pca_hexbin_plot_ggplot_call(Y, bins, breaks, font.size = 9)

Arguments

fit An object of class “poisson_nmf_fit” or “multinom_topic_model_fit”.
Y The n x 2 matrix containing the 2-d embedding, where n is the number of rows in fit$L. If not provided, the embedding will be computed automatically.
fill The quantity to map onto the fill colour of the points in the PCA plot. Set fill = "loading" to vary the fill colour according to the loadings (or topic proportions) of the select topics or topics. Alternatively, fill may be set to a data vector with one entry per row of fit$L, in which case the data are mapped to the fill colour of the points. When fill = "none", the fill colour is not varied.
k The dimensions or topics selected by number or name. When fill = "loading", one plot is created per selected dimension or topic; when fill = "loading" and k is not specified, all dimensions or topics are plotted.
fill.label The label used for the fill colour legend.
ggplot_call The function used to create the plot. Replace embedding_plot_2d_ggplot_call or pca_hexbin_plot_ggplot_call with your own function to customize the appearance of the plot.
plot_grid_call When fill = "loading" and multiple topics (k) are selected, this is the function used to arrange the plots into a grid using plot_grid. It should be a function accepting a single argument, plots, a list of ggplot objects.
fill.type The type of variable mapped to fill colour. The fill colour is not varied when fill.type = "none".
font.size Font size used in plot.
pcs The two principal components (PCs) to be plotted, specified by name or number.
n The maximum number of points to plot. If n is less than the number of rows of fit$L, the rows are subsampled at random. This argument is ignored if Y is provided.
Additional arguments passed to `pca_from_topics`, `tsne_from_topics` or `umap_from_topics`. These additional arguments are only used if Y is not provided.

- **bins**
  Number of bins used to create hexagonal 2-d histogram. Passed as the “bins” argument to `stat_bin_hex`.

- **breaks**
  To produce the hexagonal histogram, the counts are subdivided into intervals based on `breaks`. Passed as the “breaks” argument to `cut`.

**Details**

This is a lightweight interface primarily intended to expedite creation of plots for visualizing the loadings or topic proportions; most of the heavy lifting is done by ‘ggplot2’. The 2-d embedding itself is computed by invoking `pca_from_topics`, `tsne_from_topics` or `umap_from_topics`. For more control over the plot’s appearance, the plot can be customized by modifying the `ggplot_call` and `plot_grid_call` arguments.

An effective 2-d visualization may also require some fine-tuning of the settings, such as the t-SNE “perplexity”, or the number of samples included in the plot. The PCA, UMAP, t-SNE settings can be controlled by the additional arguments (...). Alternatively, a 2-d embedding may be pre-computed, and passed as argument Y.

**Value**

A `ggplot` object.

**See Also**

`pca_from_topics`, `tsne_from_topics`, `umap_from_topics`

**Examples**

```r
set.seed(1)
data(pbmc_facs)

# Get the Poisson NMF and multinomial topic models fitted to the # PBMC data.
fit1 <- multinom2poisson(pbmc_facs$fit)
fit2 <- pbmc_facs$fit

# Plot the first two PCs of the loadings matrix (for the # multinomial topic model, “fit2”, the loadings are the topic # proportions).
subpop <- pbmc_facs$samples$subpop
p1 <- pca_plot(fit1, k = 1)
p2 <- pca_plot(fit2)
p3 <- pca_plot(fit2, fill = "none")
p4 <- pca_plot(fit2, pcs = 3:4, fill = "none")
p5 <- pca_plot(fit2, fill = fit2$L[,1])
p6 <- pca_plot(fit2, fill = subpop)
p7 <- pca_hexbin_plot(fit1)
p8 <- pca_hexbin_plot(fit2)
```
fit_multinom_model

# Plot the loadings using t-SNE.
p1 <- tsne_plot(fit1, k = 1)
p2 <- tsne_plot(fit2)
p3 <- tsne_plot(fit2, fill = subpop)

# Plot the loadings using UMAP.
p1 <- umap_plot(fit1, k = 1)
p2 <- umap_plot(fit2)
p3 <- umap_plot(fit2, fill = subpop)

---

fit_multinom_model  Fit Simple Multinomial Model

Description

Fit a simple multinomial model for count data, in which each sample (i.e., a row of the data matrix \(X\)) is assigned to a cluster. Under this simple multinomial model, \(x_{ij}\) assigned to cluster \(k\) is multinomial with sample size \(s_i = x_{i1} + \ldots + x_{im}\) and multinomial probabilities \(p_{1k}, \ldots, p_{mk}\). This is a special case of the multinomial topic model in which all the mixture proportions are either 0 or 1. The maximum-likelihood estimates (MLEs) of the multinomial probabilities have a closed-form solution; no iterative algorithm is needed to fit this simple model.

Usage

```r
fit_multinom_model(cluster, X, verbose = c("none", "detailed"), ...)
```

Arguments

- `cluster` A factor specifying a grouping, or clustering, of the rows of \(X\); e.g., the “cluster” output from `kmeans`.
- `X` The \(n \times m\) matrix of counts; all entries of \(X\) should be non-negative. It can be a sparse matrix (class "dgCMatrix") or dense matrix (class "matrix"), with some exceptions (see ‘Details’).
- `verbose` This is passed as the “verbose” argument in the call to `init_poisson_nmf`.
- `...` Additional arguments passed to `init_poisson_nmf`.

Value

A multinomial topic model fit.

See Also

- `fit_topic_model`
fit_poisson_nmf

Fit Non-negative Matrix Factorization to Count Data

Description
Approximate the input matrix \( X \) by the non-negative matrix factorization \( \text{tcrossprod}(L,F) \), in which the quality of the approximation is measured by a “divergence” criterion; equivalently, optimize the likelihood under a Poisson model of the count data, \( X \), in which the Poisson rates are given by \( \text{tcrossprod}(L,F) \). Function \text{fit_poisson_nmf} runs a specified number of coordinate-wise updates to fit the \( L \) and \( F \) matrices.

Usage

\[
\text{fit_poisson_nmf}(X, k, \text{fit0}, \text{numiter} = 100, \text{update.factors} = \text{seq}(1, \text{nrow}(X)), \text{update.loadings} = \text{seq}(1, \text{ncol}(X)), \text{method} = \text{c("scd", "em", "mu", "ccd")}, \text{init.method} = \text{c("topicscore", "random")}, \text{control} = \text{list()}, \text{verbose} = \text{c("progressbar", "detailed", "none")})
\]

\text{fit_poisson_nmf\_control\_default()}

\text{init_poisson_nmf}(X, F, L, k, \text{init.method} = \text{c("topicscore", "random")}, \beta = 0.5, \beta_{\text{max}} = 0.99, \text{control} = \text{list()}, \text{verbose} = \text{c("detailed", "none")})

\text{init_poisson_nmf\_from\_clustering}(X, \text{clusters}, \ldots)

Arguments

\( X \) The \( n \times m \) matrix of counts; all entries of \( X \) should be non-negative. It can be a sparse matrix (class "dgCMatrix") or dense matrix (class "matrix"), with some exceptions (see ‘Details’).
An integer 2 or greater giving the matrix rank. This argument should only be
specified if the initial fit (fit0 or F, L) is not provided.

The initial model fit. It should be an object of class "poisson_nmf_fit", such as
an output from init_poisson_nmf, or from a previous call to fit_poisson_nmf.

The number of updates of the factors and loadings to perform.

A numeric vector specifying which factors (rows of F) to update. By default, all
factors are updated. Note that the rows that are not updated may still change by
rescaling. When NULL, all factors are fixed. This option is only implemented for
method = "em" and method = "scd". If another method is selected, the default
setting of update.factors must be used.

A numeric vector specifying which loadings (rows of L) to update. By default,
all loadings are updated. Note that the rows that are not updated may still change by
rescaling. When NULL, all loadings are fixed. This option is only imple-
mented for method = "em" and method = "scd". If another method is selected,
the default setting of update.loadings must be used.

The method to use for updating the factors and loadings. Four methods are im-
plemented: multiplicative updates, method = "mu"; expectation maximization
(EM), method = "em"; sequential co-ordinate descent (SCD), method = "scd";
and cyclic co-ordinate descent (CCD), method = "ccd". See 'Details' for a de-
tailed description of these methods.

The method used to initialize the factors and loadings. When init.method = "random", the factors and loadings are initialized uniformly at random; when
init.method = "topicscore", the factors are initialized using the (very fast)
Topic SCORE algorithm (Ke & Wang, 2017), and the loadings are initialized by running a small number of SCD updates. This input argument is ignored if initial estimates of the factors and loadings are already provided via input fit0,
or inputs F and L.

A list of parameters controlling the behaviour of the optimization algorithm (and
the Topic SCORE algorithm if it is used to initialize the model parameters). See 'Details'.

When verbose = "detailed", information about the algorithm's progress is
printed to the console at each iteration; when verbose = "progressbar", a
progress bar is shown; and when verbose = "none", no progress information
is printed. See the description of the "progress" return value for an explana-
tion of verbose = "detailed" console output. (Note that some columns of the
"progress" data frame are not shown in the console output.)

An optional argument giving the initial estimate of the factors (also known as "basis vectors"). It should be an m x k matrix, where m is the number of
columns in the counts matrix X, and k > 1 is the rank of the matrix factorization
(equivalently, the number of "topics"). All entries of F should be non-negative.
When F and L are not provided, input argument k should be specified instead.

An optional argument giving the initial estimate of the loadings (also known as
"activations"). It should be an n x k matrix, where n is the number of rows in the
counts matrix X, and k > 1 is the rank of the matrix factorization (equivalently,
the number of “topics”). All entries of \(L\) should be non-negative. When \(F\) and \(L\) are not provided, input argument \(k\) should be specified instead.

**beta**
Initial setting of the extrapolation parameter. This is \(beta\) in Algorithm 3 of Ang & Gillis (2019).

**betamax**
Initial setting for the upper bound on the extrapolation parameter. This is \(\bar{\gamma}\) in Algorithm 3 of Ang & Gillis (2019).

**clusters**
A factor specifying a grouping, or clustering, of the rows of \(X\).

**...**
Additional arguments passed to `init_poisson_nmf`.

### Details

In Poisson non-negative matrix factorization (Lee & Seung, 2001), counts \(x_{ij}\) in the \(n \times m\) matrix, \(X\), are modeled by the Poisson distribution:

\[ x_{ij} \sim \text{Poisson}(\lambda_{ij}). \]

Each Poisson rate, \(\lambda_{ij}\), is a linear combination of parameters \(f_{jk} \geq 0, l_{ik} \geq 0\) to be fitted to the data:

\[ \lambda_{ij} = \sum_{k=1}^{K} l_{ik} f_{jk}, \]

in which \(K\) is a user-specified tuning parameter specifying the rank of the matrix factorization. Function `fit_poisson_nmf` computes maximum-likelihood estimates (MLEs) of the parameters. For additional mathematical background, and an explanation of how Poisson NMF is connected to topic modeling, see the vignette: vignette(topic = "relationship", package = "fastTopics").

Using this function requires some care; only minimal argument checking is performed, and error messages may not be helpful.

The EM and multiplicative updates are simple and fast, but can be slow to converge to a stationary point. When control$numiter = 1$, the EM and multiplicative updates are mathematically equivalent to the multiplicative updates, and therefore share the same convergence properties. However, the implementation of the EM updates is quite different; in particular, the EM updates are more suitable for sparse counts matrices. The implementation of the multiplicative updates is adapted from the MATLAB code by Daichi Kitamura [http://d-kitamura.net](http://d-kitamura.net).

Since the multiplicative updates are implemented using standard matrix operations, the speed is heavily dependent on the BLAS/LAPACK numerical libraries used. In particular, using optimized implementations such as OpenBLAS or Intel MKL can result in much improved performance of the multiplicative updates.

The cyclic co-ordinate descent (CCD) and sequential co-ordinate descent (SCD) updates adopt the same optimization strategy, but differ in the implementation details. In practice, we have found that the CCD and SCD updates arrive at the same solution when initialized “sufficiently close” to a stationary point. The CCD implementation is adapted from the C++ code developed by Cho-Jui Hsieh and Inderjit Dhillon, which is available for download at [https://www.cs.utexas.edu/~cjhsieh/nmf/](https://www.cs.utexas.edu/~cjhsieh/nmf/). The SCD implementation is based on version 0.4-3 of the ‘NNLM’ package.

An additional re-scaling step is performed after each update to promote numerical stability.

We use three measures of progress for the model fitting: (1) improvement in the log-likelihood (or deviance), (2) change in the model parameters, and (3) the residuals of the Karush-Kuhn-Tucker
(KKT) first-order conditions. As the iterates approach a stationary point of the loss function, the change in the model parameters should be small, and the residuals of the KKT system should vanish. Use plot_progress to plot the improvement in the solution over time.

See fit_topic_model for additional guidance on model fitting, particularly for large or complex data sets.

The control argument is a list in which any of the following named components will override the default optimization algorithm settings (as they are defined by fit_poisson_nmf_control_default):

- **numiter**: Number of “inner loop” iterations to run when performing and update of the factors or loadings. This must be set to 1 for method = "mu" and method = "ccd".
- **nc**: Number of RcppParallel threads to use for the updates. When nc is NA, the number of threads is determined by calling defaultNumThreads. This setting is ignored for the multiplicative updates (method = "mu").
- **minval**: A small, positive constant used to safeguard the multiplicative updates. The safeguarded updates are implemented as $F \leftarrow \text{pmax}(F1, \text{minval})$ and $L \leftarrow \text{pmax}(L1, \text{minval})$, where $F1$ and $L1$ are the factors and loadings matrices obtained by applying an update. This is motivated by Theorem 1 of Gillis & Glineur (2012). Setting minval = 0 is allowed, but some methods are not guaranteed to converge to a stationary point without this safeguard, and a warning will be given in this case.
- **extrapolate**: When extrapolate = TRUE, the extrapolation scheme of Ang & Gillis (2019) is used.
- **extrapolate.reset**: To promote better numerical stability of the extrapolated updates, they are “reset” every so often. This parameter determines the number of iterations to wait before resetting.
- **beta.increase**: When the extrapolated update improves the solution, scale the extrapolation parameter by this amount.
- **beta.reduce**: When the extrapolated update does not improve the solution, scale the extrapolation parameter by this amount.
- **betamax.increase**: When the extrapolated update improves the solution, scale the extrapolation parameter by this amount.
- **eps**: A small, non-negative number that is added to the terms inside the logarithms to sidestep computing logarithms of zero. This prevents numerical problems at the cost of introducing a small inaccuracy in the solution. Increasing this number may lead to faster convergence but possibly a less accurate solution.
- **zero.threshold**: A small, non-negative number used to determine which entries of the solution are exactly zero. Any entries that are less than or equal to zero.threshold are considered to be exactly zero.

An additional setting, control$init.numiter, controls the number of sequential co-ordinate descent (SCD) updates that are performed to initialize the loadings matrix when init.method = "topicscore".

**Value**

init_poisson_nmf and fit_poisson_nmf both return an object capturing the optimization algorithm state (for init_poisson_nmf, this is the initial state). It is a list with the following elements:
fit_poisson_nmf

F  A matrix containing the current best estimates of the factors.
L  A matrix containing the current best estimates of the loadings.
Fn A matrix containing the non-extrapolated factor estimates. If extrapolation is not used, Fn and F will be the same.
Ln A matrix containing the non-extrapolated estimates of the loadings. If extrapolation is not used, Ln and L will be the same.
Fy A matrix containing the extrapolated factor estimates. If the extrapolation scheme is not used, Fy and F will be the same.
Ly A matrix containing the extrapolated estimates of the loadings. If extrapolation is not used, Ly and L will be the same.
loss Value of the objective (“loss”) function computed at the current best estimates of the factors and loadings.
loss.fnly Value of the objective (“loss”) function computed at the extrapolated solution for the loadings (Ly) and the non-extrapolated solution for the factors (Fn). This is used internally to implement the extrapolated updates.
iter The number of the most recently completed iteration.
beta The extrapolation parameter; beta in Algorithm 3 of Ang & Gillis (2019).
betamax Upper bound on the extrapolation parameter. This is \( \bar{\gamma} \) in Algorithm 3 of Ang & Gillis (2019).
beta0 The setting of the extrapolation parameter at the last iteration that improved the solution.
progress A data frame containing detailed information about the algorithm’s progress. The data frame should have numiter rows. The columns of the data frame are: “iter”, the iteration number; “loglik”, the Poisson NMF log-likelihood at the current best factor and loading estimates; “loglik.multinom”, the multinomial topic model log-likelihood at the current best factor and loading estimates; “dev”, the deviance at the current best factor and loading estimates; “res”, the maximum residual of the Karush-Kuhn-Tucker (KKT) first-order optimality conditions at the current best factor and loading estimates; “delta.f”, the largest change in the factors matrix; “delta.l”, the largest change in the loadings matrix; “nonzeros.f”, the proportion of entries in the factors matrix that are nonzero; “nonzeros.l”, the proportion of entries in the loadings matrix that are nonzero; “extrapolate”, which is 1 if extrapolation is used, otherwise it is 0; “beta”, the setting of the extrapolation parameter; “betamax”, the setting of the extrapolation parameter upper bound; and “timing”, the elapsed time in seconds (recorded using proc.time).

References


See Also

`fit_topic_model`, `plot_progress`

Examples

```r
# Simulate a (sparse) 80 x 100 counts matrix.
library(Matrix)
set.seed(1)
X <- simulate_count_data(80,100,k = 3,sparse = TRUE)$X

# Remove columns (words) that do not appear in any row (document).
X <- X[,colSums(X > 0) > 0]

# Run 10 EM updates to find a good initialization.
fit0 <- fit_poisson_nmf(X,k = 3,numiter = 10,method = "em")

# Fit the Poisson NMF model by running 50 EM updates.
fit_em <- fit_poisson_nmf(X,fit0 = fit0,numiter = 50,method = "em")

# Fit the Poisson NMF model by running 50 extrapolated SCD updates.
fit_scd <- fit_poisson_nmf(X,fit0 = fit0,numiter = 50,method = "scd",
                          control = list(extrapolate = TRUE))

# Compare the two fits.
fits <- list(em = fit_em,scd = fit_scd)
compare_fits(fits)
plot_progress(fits,y = "loglik")
plot_progress(fits,y = "res")

# Recover the topic model. After this step, the L matrix contains the
# mixture proportions ("loadings"), and the F matrix contains the
# word frequencies ("factors").
fit_multinom <- poisson2multinom(fit_scd)
```

Description

Fits a multinomial topic model to the count data, hiding most of the complexities of model fitting. The default optimization settings used here are intended to work well in a wide range of data sets, although some fine-tuning may be needed for more difficult cases. For full control, use `fit_poisson_nmf`.

Usage

```r
fit_topic_model(
  X,
  k,
  numiter.main = 100,
  numiter.refine = 100,
  method.main = "em",
  method.refine = "scd",
  init.method = c("topicscore", "random"),
  control.init = list(),
  control.main = list(numiter = 4),
  control.refine = list(numiter = 4, extrapolate = TRUE),
  verbose = c("progressbar", "detailed", "none")
)
```

Arguments

- **X**: The n x m matrix of counts; all entries of X should be non-negative. It can be a sparse matrix (class "dgCMatrix") or dense matrix (class "matrix").
- **k**: The number of topics. Must be 2 or greater.
- **numiter.main**: Number of updates of the factors and loadings to perform in the main model fitting step. Should be 1 or more.
- **numiter.refine**: Number of updates of the factors in the model refinement step.
- **method.main**: The method to use for updating the factors and loadings in the main model fitting step. Passed as argument "method" to `fit_poisson_nmf`.
- **method.refine**: The method to use for updating the factors in the model refinement step. Passed as argument "method" to `fit_poisson_nmf`.
- **init.method**: The method used to initialize the factors and loadings. See `init_poisson_nmf` for details.
- **control.init**: A list of parameters controlling the behaviour of the optimization and TopicSCORE method in the call to `init_poisson_nmf`. This is passed as argument "control" to `init_poisson_nmf`.
control.main  A list of parameters controlling the behaviour of the optimization in the main model fitting step. This is passed as argument "control" to `fit_poisson_nmf`.

control.refine  A list of parameters controlling the behaviour of the of the optimization algorithm in the model refinement step. This is passed as argument "control" to `fit_poisson_nmf`.

verbose  When verbose = "progressbar" or verbose = "detailed", information about the progress of the model fitting is printed to the console. See `fit_poisson_nmf` for more information.

Details

With the default settings, the model fitting is accomplished in four steps: (1) initialize the Poisson NMF model fit (`init_poisson_nmf`); (2) perform the main model fitting step by running 100 EM updates using `fit_poisson_nmf`; (3) refine the fit by running 100 extrapolated SCD updates, again using `fit_poisson_nmf`; and (4) recover the multinomial topic model by calling `poisson2multinom`.

This two-stage fitting approach is based on our findings that the EM algorithm initially makes rapid progress toward a solution, but its convergence slows considerably as the iterates approach a solution. Close to a solution, we have found that other algorithms make much more rapid progress than EM; in particularly, we found that the extrapolated SCD updates usually performed best). For larger data sets, more updates in the main model fitting and refinement steps may be needed to obtain a good fit.

For larger data sets, more than 200 updates may be needed to obtain a good fit.

Value

A multinomial topic model fit; see `poisson2multinom` and `fit_poisson_nmf` for details. Note that outputted likelihoods and deviances in progress are evaluated with respect to the equivalent Poisson NMF model.

References


See Also

`init_poisson_nmf`, `fit_poisson_nmf`, `poisson2multinom`, `fit_multinom_model`

Examples

```r
library(Matrix)
set.seed(1)
X <- simulate_count_data(80,100,k = 3,sparse = TRUE)$X
```
```r
fit <- fit_topic_model(X, k = 3)
print(summary(fit))
```

---

**Description**

Generate one or more barcharts to visualize the relationship between the loadings or mixture proportions and a selected categorical variable (a factor).

**Usage**

```r
loadings_plot(
  fit,
  x,
  k,
  ggplot_call = loadings_plot_ggplot_call,
  plot_grid_call = function(plots) do.call(plot_grid, plots)
)
```

```r
loadings_plot_ggplot_call(dat, topic.label, font.size = 9)
```

**Arguments**

- `fit`: An object of class “poisson_nmf_fit” or “multinom_topic_model_fit”.
- `x`: A categorical variable represented as a `factor`. It should have the same number of elements as the number of rows in `fit$L`.
- `k`: The topic, or topics, selected by number or name. When not specified, all topics are plotted.
- `ggplot_call`: The function used to create the plot. Replace `loadings_plot_ggplot_call` with your own function to customize the appearance of the plot.
- `plot_grid_call`: When multiple topics are selected, this is the function used to arrange the plots into a grid using `plot_grid`. It should be a function accepting a single argument, `plots`, a list of ggplot objects.
- `dat`: A data frame passed as input to `ggplot`, containing, at a minimum, columns “x” and “loading”.
- `topic.label`: The name or number of the topic being plotted. Only used to determine the plot title.
- `font.size`: Font size used in plot.
Details

This is a lightweight interface primarily intended to expedite creation of boxplots for investigating relationships between topics and a categorical variables of interest without having to spend a great deal of time worrying about the plotting settings; most of the “heavy lifting” is done by ‘ggplot2’ (specifically, function `geom_boxplot` in the ‘ggplot2’ package). For more control over the plot’s appearance, the plot can be customized by modifying the `ggplot_call` and `plot_grid_call` arguments.

Value

A ggplot object.

Description

Compute log-likelihoods and deviances for assessing fit of a topic model or a non-negative matrix factorization (NMF).

Usage

```
loglik_poisson_nmf(X, fit, e = 1e-08)
loglik_multinom_topic_model(X, fit, e = 1e-08)
deviance_poisson_nmf(X, fit, e = 1e-08)
cost(X, A, B, e = 1e-08, family = c("poisson", "multinom"), version)
```

Arguments

- `X`: The n x m matrix of counts or pseudocounts. It can be a sparse matrix (class "dgCMatrix") or dense matrix (class "matrix").
- `fit`: A Poisson NMF or multinomial topic model fit, such as an output from `fit_poisson_nmf` or `fit_topic_model`.
- `e`: A small, non-negative number added to the terms inside the logarithms to avoid computing logarithms of zero. This prevents numerical problems at the cost of introducing a very small inaccuracy in the computation.
- `A`: The n x k matrix of loadings. It should be a dense matrix.
- `B`: The k x m matrix of factors. It should be a dense matrix.
- `family`: If `model = "poisson"`, the loss function values corresponding to the Poisson non-negative matrix factorization are computed; if `model = "multinom"`, the multinomial topic model loss function values are returned.
version

When version == "R", the computations are performed entirely in R; when version == "Rcpp", an Rcpp implementation is used. The R version is typically faster when X is a dense matrix, whereas the Rcpp version is faster and more memory-efficient when X is a large, sparse matrix. When not specified, the most suitable version is called depending on whether X is dense or sparse.

Details

Function cost computes loss functions proportional to the negative log-likelihoods, and is mainly for internal use to quickly compute log-likelihoods and deviances; it should not be used directly unless you know what you are doing. In particular, little argument checking is performed by cost.

Value

A numeric vector with one entry per row of X.

Examples

# Generate a small counts matrix.
set.seed(1)
out <- simulate_count_data(10,20,3)
X <- out$X
fit <- out[c("F","L")]
class(fit) <- c("poisson_nmf_fit","list")

# Compute the Poisson log-likelihoods and deviances.
data.frame(loglik = loglik_poisson_nmf(X,fit),
            deviance = deviance_poisson_nmf(X,fit))

# Compute multinomial log-likelihoods.
loglik_multinom_topic_model(X,fit)

merge_topics

Combine Topics in Multinomial Topic Model

Description

Combine two or more topics in a multinomial topic model fit.

Usage

merge_topics(fit, k)

Arguments

fit A multinomial topic model fit.
k The names or numbers of the topics to be combined. Two or more topics should be chosen.
multinom2poisson

Details
Mixture proportions are combined by summation, and factors are combined by averaging.

Value
A multinomial topic model fit.

multinom2poisson Recover Poisson NMF Fit from Multinomial Topic Model Fit

Description
This function recovers parameter estimates of the Poisson non-negative matrix factorization (NMF) given parameter estimates for a multinomial topic model.

Usage
multinom2poisson(fit, X)

Arguments
fit An object of class “multinom_topic_model_fit”, such as an output from poisson2multinom. If a Poisson NMF fit is provided (that is, an object of class “poisson_nmf_fit”), the fit object is immediately returned “as is”.

X Optional n x m matrix of counts, or pseudocounts. It can be a sparse matrix (class “dgCMatrix”) or dense matrix (class “matrix”). This only needs to be provided if the document sizes fit$s are not available.

Value
The return value is the list fit, in which matrices fit$F and fit$L specify the factors and loadings in the Poisson non-negative matrix factorization; specifically, the counts matrix is modeled by the low-rank matrix product tcrossprod(fit$L,fit$F).

pbmc_facs Mixture of 10 FACS-purified PBMC Single-Cell RNA-seq data

Description
These data are a selection of the reference transcriptome profiles generated via single-cell RNA sequencing (RNA-seq) of 10 bead-enriched subpopulations of PBMCs (Donor A), described in Zheng et al (2017). The data are unique molecular identifier (UMI) counts for 16,791 genes in 3,774 cells. (Genes with no expression in any of the cells were removed.) Since the majority of the UMI counts are zero, they are efficiently stored as a 3,774 x 16,791 sparse matrix. These data are used in the vignette illustrating how `fastTopics` can be used to analyze single-cell RNA-seq data. Data for a separate set of 1,000 cells is provided as a “test set” to evaluate out-of-sample predictions.
Format

pbmc_facs is a list with the following elements:

- **counts**: 3,774 x 16,791 sparse matrix of UMI counts, with rows corresponding to samples (cells) and columns corresponding to genes. It is an object of class "dgCMatrix".

- **counts_test**: UMI counts for an additional test set of 100 cells.

- **samples**: Data frame containing information about the samples, including cell barcode and source FACS population (“celltype” and “facs_subpop”).

- **samples_test**: Sample information for the additional test set of 100 cells.

- **genes**: Data frame containing information and the genes, including gene symbol and Ensembl identifier.

- **fit**: Poisson non-negative matrix factorization (NMF) fitted to the UMI count data counts, with rank k = 6. See the vignette how the Poisson NMF model fitting was performed.

Source

https://www.10xgenomics.com/resources/datasets

References


Examples

```r
library(Matrix)
data(pbmc_facs)
cat(sprintf("Number of cells: %d\n",nrow(pbmc_facs$counts)))
cat(sprintf("Number of genes: %d\n",ncol(pbmc_facs$counts)))
cat(sprintf("Proportion of counts that are non-zero: %0.1f%%.\n",100*mean(pbmc_facs$counts > 0)))
```

**pca_from_topics**  
*Low-dimensional Embeddings from Poisson NMF or Multinomial Topic Model*

Description

Lightweight interface for rapidly producing low-dimensional embeddings from matrix factorizations or multinomial topic models. The defaults used are more suitable for producing embeddings from matrix factorizations or topic models.
**Usage**

```r
pca_from_topics(fit, dims = 2, center = TRUE, scale. = FALSE, ...)
```

```r
tsn_from_topics(
  fit,
  dims = 2,
  pca = FALSE,
  normalize = FALSE,
  perplexity = 100,
  theta = 0.1,
  max_iter = 1000,
  eta = 200,
  check_duplicates = FALSE,
  verbose = TRUE,
  ...
)
```

```r
umap_from_topics(
  fit,
  dims = 2,
  n_neighbors = 30,
  metric = "euclidean",
  scale = "none",
  pca = NULL,
  verbose = TRUE,
  ...
)
```

**Arguments**

- **fit**
  An object of class “poisson_nmf_fit” or “multinom_topic_model_fit”.

- **dims**
  The number of dimensions in the embedding. In `tsn_from_topics`, this is passed as argument “dims” to `Rtsne`. In `umap_from_topics`, this is passed as argument “n_components” to `umap`.

- **center**
  A logical value indicating whether columns of `fit$L` should be zero-centered before performing PCA; passed as argument “center” to `prcomp`.

- **scale.**
  A logical value indicating whether columns of `fit$L` should be scaled to have unit variance prior to performing PCA; passed as argument “scale.” to `prcomp`.

... Additional arguments passed to `prcomp`, `Rtsne` or `umap`.

- **pca**
  Whether to perform a PCA processing step in t-SNE or UMAP; passed as argument “pca” to `Rtsne` or `umap`.

- **normalize**
  Whether to normalize the data prior to running t-SNE; passed as argument “normalize” to `Rtsne`.

- **perplexity**
  t-SNE perplexity parameter, passed as argument “perplexity” to `Rtsne`. The perplexity is automatically revised if it is too large; see `Rtsne` for more information.

- **theta**
  t-SNE speed/accuracy trade-off parameter; passed as argument “theta” to `Rtsne`. 
max_iter  Maximum number of t-SNE iterations; passed as argument “max_iter” to Rtsne.
eta t-SNE learning rate parameter; passed as argument “eta” to Rtsne.
check_duplicates When check_duplicates = TRUE, checks whether there are duplicate rows in fit$L; passed as argument “check_duplicates” to Rtsne.
verbose If verbose = TRUE, progress updates are printed; passed as argument “verbose” to Rtsne or umap.
n_neighbors Number of nearest neighbours in manifold approximation; passed as argument “n_neighbors” to umap.
metric Distance matrix used to find nearest neighbors; passed as argument “metric” to umap.
scale Scaling to apply to fit$L; passed as argument “scale” to umap.

Details
Note that since tsne_from_topics and umap_from_topics use nonlinear transformations of the data, distances between points are generally less interpretable than a linear transformation obtained by, say, PCA.

Value
An n x d matrix containing the embedding, where n is the number of rows of fit$L, and d = dims.

References

See Also
pca_plot, tsne_plot, umap_plot, prcomp, Rtsne, umap

Examples
library(ggplot2)
library(cowplot)
set.seed(1)
data(pbmc_facs)

# Get the Poisson NMF and multinomial topic model fit to the PBMC data.
fit1 <- multinom2poisson(pbmc_facs$fit)
fit2 <- pbmc_facs$fit
fit2 <- poisson2multinom(fit1)

# Compute the first two PCs of the loadings matrix (for the topic model, fit2, the loadings are the topic proportions).
Y1 <- pca_from_topics(fit1)
Y2 <- pca_from_topics(fit2)
subpop <- pbmc_facs$samples$subpop
**plot_loglik_vs_rank**  

```
quickplot(Y1[,1],Y1[,2],color = subpop) + theme_cowplot()
quickplot(Y2[,1],Y2[,2],color = subpop) + theme_cowplot()

# Compute a 2-d embedding of the loadings using t-SNE.
Y1 <- tsne_from_topics(fit1)
Y2 <- tsne_from_topics(fit2)
quickplot(Y1[,1],Y1[,2],color = subpop) + theme_cowplot()
quickplot(Y2[,1],Y2[,2],color = subpop) + theme_cowplot()

# Compute a 2-d embedding of the loadings using UMAP.
Y1 <- umap_from_topics(fit1)
Y2 <- umap_from_topics(fit2)
quickplot(Y1[,1],Y1[,2],color = subpop) + theme_cowplot()
quickplot(Y2[,1],Y2[,2],color = subpop) + theme_cowplot()
```

---

**plot_loglik_vs_rank**  

*Plot Log-Likelihood Versus Rank*

**Description**

Create a plot showing the improvement in the log-likelihood as the rank of the matrix factorization or the number of topics (“k”) increases.

**Usage**

```
plot_loglik_vs_rank(fits, ggplot_call = loglik_vs_rank_ggplot_call)

loglik_vs_rank_ggplot_call(dat, font.size = 9)
```

**Arguments**

- **fits**  
  A list with 2 more list elements, in which each list element is an object of class "poisson_nmf_fit" or "multinom_topic_model_fit". If two or more fits share the same rank, or number of topics, the largest log-likelihood is plotted.

- **ggplot_call**  
  The function used to create the plot. Replace loglik_vs_rank_ggplot_call with your own function to customize the appearance of the plot.

- **dat**  
  A data frame passed as input to `ggplot`, containing, at a minimum, columns “x” and “y”.

- **font.size**  
  Font size used in plot.

**Value**

A ggplot object.
plot_progress

Plot Progress of Model Fitting Over Time

Description

Create a plot showing improvement in one or more Poisson NMF or multinomial topic model fits over time.

Usage

plot_progress(
  fits,
  x = c("timing", "iter"),
  y = c("loglik", "dev", "res"),
  add.point.every = 20,
  colors = c("#E69F00", "#56B4E9", "#009E73", "#F0E442", "#0072B2", "#D55E00",
              "#CC79A7"),
  linetypes = "solid",
  linesizes = 0.5,
  shapes = 19,
  fills = "white",
  e = 0.01,
  theme = function() theme_cowplot(12)
)

Arguments

fits An object of class "poisson_nmf_fit" or "multinom_topic_model_fit", or a non-empty, named list in which each all list elements are objects of class "poisson_nmf_fit" or all objects of class "multinom_topic_model_fit".

x Choose "timing" to plot improvement in the solution over time, or choose "iter" to plot improvement in the solution per iteration.

y Column of the "progress" data frame used to assess progress of the Poisson NMF optimization method(s). Should be one of "loglik" (Poisson NMF or multinomial topic model log-likelihood), "dev" (deviance) or "res" (maximum residual of KKT conditions). The deviance is only valid for Poisson NMF model fits.

add.point.every A positive integer giving the iteration interval for drawing points on the progress curves. Set to Inf to prevent points from being drawn on the plot.

colors Colours used to draw progress curves; passed as the values input to scale_color_manual. If fewer colours than "fits" are given, the colours are recycled.

linetypes Line types used to draw progress curves; passed as the values input to scale_linetype_manual. If fewer line types than “fits” are given, the line types are recycled.

linesizes Line sizes used to draw progress curves; passed as the values input to scale_size_manual. If fewer line sizes than “fits” are given, the line sizes are recycled.
Shapes used to draw points at the selected iterations; passed as the values input to `scale_shape_manual`. If fewer shapes than “fits” are given, the shapes are recycled.

**fills**

Fill colours used to draw points at the selected iterations; passed as the values input to `scale_fill_manual`. If fewer fill colours than “fits” are given, the fill colours are recycled.

**e**

A small, positive number added to the vertical axis (for y = "loglik" and y = "dev" only) so that the logarithmic scale does not over-emphasize very small differences.

**theme**

The ‘ggplot2’ “theme”.

**Details**

The horizontal axis shows the recorded runtime (in s), and the vertical axis shows some quantity measuring the quality of the fit: the log-likelihood, deviance or maximum residual of the Karush-Kuhn-Tucker (KKT) first-order optimality conditions. To better visualize log-likelihoods and deviances, log-likelihood and deviance differences are shown on the logarithmic scale. Differences are calculated with respect to the best value achieved over all the fits compared.

Note that only minimal argument checking is performed.

**Value**

A ggplot object.

**See Also**

`fit_poisson_nmf`

---

**Description**

This function recovers parameter estimates of the multinomial topic model given parameter estimates for a Poisson non-negative matrix factorization (NMF).

**Usage**

`poisson2multinom(fit)`

**Arguments**

- **fit**
  
  An object of class “poisson_nmf_fit”, such as an output from `fit_poisson_nmf`. It does not make sense for a multinomial topic model to have less than two topics, so an error will be reported when k < 2, where k is the rank of the matrix factorization. If a multinomial topic model fit is provided (that is, an object of class “multinom_topic_model_fit”), the fit object is immediately returned “as is”.

---

**Recover Multinomial Topic Model Fit from Poisson NMF fit**

---

**Description**

This function recovers parameter estimates of the multinomial topic model given parameter estimates for a Poisson non-negative matrix factorization (NMF).
Value

The return value is the list \( \text{fit} \), in which \( \text{fit}\$F \) and \( \text{fit}\$L \) are the parameters of the multinomial topic model; specifically, \( \text{fit}\$L[i,] \) gives the topic probabilities for sample or document \( i \), and \( \text{fit}\$F[k] \) gives the term probabilities for topic \( k \). An additional vector \( \text{fit}\$s \) of length \( n \) is returned giving the "size factors".

predict.poisson_nmf_fit

Predict Methods for Poisson NMF and Multinomial Topic Model

Description

Predict loadings based on previously fit Poisson NMF, or predict topic proportions based on previously fit multinomial topic model. This can be thought of as projecting data points onto a previously estimated set of factors \( \text{fit}\$F \).

Usage

```r
## S3 method for class 'poisson_nmf_fit'
predict(object, newdata, numiter = 20, ...)
## S3 method for class 'multinom_topic_model_fit'
predict(object, newdata, numiter = 20, ...)
```

Arguments

- `object` An object of class "poisson_nmf_fit" or "multinom_topic_model_fit".
- `newdata` An optional counts matrix. If omitted, the loadings estimated in the original data are returned.
- `numiter` The number of updates to perform.
- `...` Additional arguments passed to `fit_poisson_nmf`.

Value

A loadings matrix with one row for each data point and one column for each topic or factor. For `predict.multinom_topic_model_fit`, the output can also be interpreted as a matrix of estimated topic proportions, in which \( L[i,j] \) is the proportional contribution of topic \( j \) to data point \( i \).

See Also

`fit_poisson_nmf`
Examples

# Simulate a 175 x 1,200 counts matrix.
set.seed(1)
dat <- simulate_count_data(175,1200,k = 3)

# Split the data into training and test sets.
train <- dat$X[1:100,]
test <- dat$X[101:175,]

# Fit a Poisson non-negative matrix factorization using the
# training data.
fit <- init_poisson_nmf(train,F = dat$F,init.method = "random")
fit <- fit_poisson_nmf(train,fit0 = fit)

# Compare the estimated loadings in the training data against the
# loadings used to simulate these data.
Ltrain <- predict(fit)
plot(dat$L[1:100,],Ltrain,pch = 20,col = "darkblue")
abline(a = 0,b = 1,col = "magenta",lty = "dotted",
xlab = "true",ylab = "estimated")

# Next, predict loadings in unseen (test) data points, and compare
# these predictions against the loadings that were used to simulate
# the test data.
Ltest <- predict(fit,test)
plot(dat$L[101:175,],Ltest,pch = 20,col = "darkblue",
xlab = "true",ylab = "estimated")
abline(a = 0,b = 1,col = "magenta",lty = "dotted")

# Simulate a 175 x 1,200 counts matrix.
set.seed(1)
dat <- simulate_multinom_gene_data(175,1200,k = 3)

# Split the data into training and test sets.
train <- dat$X[1:100,]
test <- dat$X[101:175,]

# Fit a topic model using the training data.
fit <- init_poisson_nmf(train,F = dat$F,init.method = "random")
fit <- fit_poisson_nmf(train,fit0 = fit)
fit <- poisson2multinom(fit)

# Compare the estimated topic proportions in the training data against
# the topic proportions used to simulate these data.
Ltrain <- predict(fit)
plot(dat$L[1:100,],Ltrain,pch = 20,col = "darkblue")
abline(a = 0,b = 1,col = "magenta",lty = "dotted",
xlab = "true",ylab = "estimated")

# Next, predict loadings in unseen (test) data points, and compare
# these predictions against the loadings that were used to simulate
# the test data.
Ltest <- predict(fit,test)
plot(dat$L[101:175,],Ltest,pch = 20,col = "darkblue",
     xlab = "true",ylab = "estimated")
abline(a = 0,b = 1,col = "magenta",lty = "dotted")

---

**run_homer**

**Perform HOMER Motif Enrichment Analysis using DE Genomic Positions**

### Description

Run HOMER motif finding algorithm (*findMotifsGenome.pl*) to identify motifs enriched for differentially expressed (DE) genomic positions. See [http://homer.ucsd.edu](http://homer.ucsd.edu) for more information.

### Usage

```r
run_homer(
  de,
  k,
  positions,
  genome = "hg19",
  subset = function(postmean, lpval, lfsr, rank, quantile) lfsr < 0.05,
  homer.exec = "findMotifsGenome.pl",
  out.dir = tempdir(),
  homer.options = "-len 8,10,12 -size 200 -mis 2 -S 25 -p 1 -h",
  verbose = TRUE
)
```

### Arguments

- **de**
  - An object of class “topic_model_de_analysis”, usually the result of running `de_analysis`.

- **k**
  - Use the DE analysis results for this topic.

- **positions**
  - A table of genomic positions corresponding to rows of the `de_analysis` results. Specifically, it should be a data frame with four columns: “chr”, chromosome name or number; “start”, start position of genomic feature; “end”, end position of genomic feature; and “name”, the name of the genomic feature. If not specified, the genomic positions will be extracted from the row names of `de$postmean`, in which the row names are expected to be of the form `chr_start_end`. The genomic positions will be written to a BED file (see [https://genome.ucsc.edu/FAQ/FAQformat.html](https://genome.ucsc.edu/FAQ/FAQformat.html) for more information about BED files).

- **genome**
  - The genome parameter passed to `findMotifsGenome.pl`.

- **subset**
  - Describe input argument "subset" here.
select.poisson_nmf_fit

The name or file path of the HOMER findMotifsGenome.pl executable.

out.dir

The positions BED file and HOMER results are written to this directory.

homer.options

Character string used to override default findMotifsGenome.pl options.

verbose

When verbose = TRUE, progress information is printed to the console.

Value

A data frame containing the motif enrichment results. It is created from the knownResults.txt HOMER output.

References


select.poisson_nmf_fit

Extract or Re-order Data Rows in Poisson NMF or Multinomial Topic Model Fit

Description

This function can be used to extract estimates for a subset of the count data, or to re-order the rows of the loadings matrix.

Usage

## S3 method for class 'poisson_nmf_fit'
select(.data, loadings, ...)

## S3 method for class 'multinom_topic_model_fit'
select(.data, loadings, ...)

select_loadings(.data, loadings, ...)

Arguments

.data

Poisson NMF or Multinomial Topic Model fit; that is, an object of class “poisson_nmf_fit” or “multinom_topic_model_fit”, such as an output from fit_poisson_nmf or fit_topic_model.

loadings

Indices (names or numbers) giving data rows to keep. If not specified, all rows are kept.

... Other arguments passed to the generic select function.

Value

A Poisson NMF or multinomial topic model fit containing the selected data rows only.
Simulate Count Data from Poisson NMF Model

Description

Simulate a counts matrix $X$ such that $X[i,j]$ is Poisson with rate (mean) $Y[i,j]$, where $Y = \text{tcrossprod}(L,F)$, $L$ is an $n \times k$ loadings (“activations”) matrix, and $F$ is an $m \times k$ factors (“basis vectors”) matrix. The entries of matrix $L$ are drawn uniformly at random between zero and $l_{max}$, and the entries of matrix $F$ are drawn uniformly at random between 0 and $f_{max}$.

Usage

simulate_count_data(n, m, k, fmax = 1, lmax = 1, sparse = FALSE)

Arguments

- **n**: Number of rows in simulated count matrix. The number of rows should be at least 2.
- **m**: Number of columns in simulated count matrix. The number of columns should be at least 2.
- **k**: Number of factors, or “topics”, used to determine Poisson rates. The number of topics should be 1 or more.
- **fmax**: Factors are drawn uniformly at random between zero and $f_{max}$.
- **lmax**: Loadings are drawn uniformly at random between zero and $l_{max}$.
- **sparse**: If $\text{sparse} = \text{TRUE}$, convert the counts matrix to a sparse matrix in compressed, column-oriented format; see $\text{sparseMatrix}$.

Details

Note that only minimal argument checking is performed. This function is mainly used to simulate small data sets for the examples and package tests.

Value

The return value is a list containing the counts matrix $X$ and the factorization, $F$ and $L$, used to generate the counts.
simulate_poisson_gene_data

Simulate Gene Expression Data from Poisson NMF or Multinomial Topic Model

Description

Simulate count data from a Poisson NMF model or multinomial topic model, in which topics represent “gene expression programs”, and gene expression programs are characterized by different rates of expression. The way in which the counts are simulated is modeled after gene expression studies in which expression is measured by single-cell RNA sequencing (“RNA-seq”) techniques: each row of the counts matrix corresponds a gene expression profile, each column corresponds to a gene, and each matrix element is a “read count”, or “UMI count”, measuring expression level. Factors are simulated so as to capture realistic changes in gene expression across different cell types. See “Details” for the procedure used to simulate factors, loadings and counts.

Usage

simulate_poisson_gene_data(n, m, k, s, p = 1, sparse = FALSE)
simulate_multinom_gene_data(n, m, k, sparse = FALSE)

Arguments

n  Number of rows in the simulated count matrix. Should be at least 2.
m  Number of columns in the simulated count matrix. Should be at least 2.
k  Number of factors, or “topics”, used to generate the data. Should be 2 or more.
s  Vector of “size factors”; each row of the loadings matrix \(L\) is scaled by the entries of \(s\) before generating the counts. This should be a vector of length \(n\) containing only positive values.
p  Probability that \(F[i,j]\) is equal to the mean rate. Smaller values of \(p\) will result in more factors that are the same across topics.
sparse  If sparse = TRUE, convert the counts matrix to a sparse matrix in compressed, column-oriented format; see sparseMatrix.

Details

Here we describe the process for generating the \(n \times k\) loadings matrix \(L\) and the \(m \times k\) factors matrix \(F\).

Each row of the \(L\) matrix is generated in the following manner: (1) the number of nonzero mixture proportions is \(1 \leq n \leq k\), with probability proportional to \(2^{-n}\); (2) the indices of the nonzero mixture proportions are sampled uniformly at random; and (3) the nonzero mixture proportions are sampled from the Dirichlet distribution with \(\alpha = 1\) (so that all topics are equally likely).

Each row of the factors matrix are generated according to the following procedure: (1) generate \(u = |r| - 5\), where \(r \sim N(0, 2)\); (2) for each topic \(k\), generate the Poisson rates as \(exp(max(t, -5))\),
simulate_toy_gene_data

Simulate Toy Gene Expression Data

Description

Simulate gene expression data (UMI counts) under a toy expression model. Samples (expression profiles) are drawn from a multinomial topic model in which topics are "gene programs".

Usage

simulate_toy_gene_data(n, m, k, s)

Arguments

n
The number of samples (gene expression profiles) to simulate.

m
The number of counts (genes) to simulate.

k
The number of topics ("gene programs") used to simulate the data.

s
A scalar specifying the total expression of each sample; it specifies the "size" parameter in the calls to rmultinom.

Details

The mixture proportions are generated as follows. With probability 0.9, one proportion is one, or close to one, and the remaining are zero, or close to zero; that is, the counts are primarily generated from a single gene program. Otherwise (with probability 0.1), the mixture proportions are roughly equal.

Gene frequencies are drawn uniformly at random from [0,1].
Structure Plot

Description

Create a “Structure plot” from a multinomial topic model fit. The Structure plot represents the estimated topic proportions of each sample in a stacked bar chart, with bars of different colors representing different topics. Consequently, samples that have similar topic proportions have similar amounts of each color.

Usage

structure_plot(
  fit,
  topics,
  grouping,
  loadings_order = "embed",
  n = 2000,
  colors = c("#e41a1c", "#377eb8", "#4daf4a", "#984ea3", "#ff7f00", "#ffff33",
            "#a65628", "#f781bf", "#999999"),
  gap = 1,
  embed_method = structure_plot_default_embed_method,
  ggplot_call = structure_plot_ggplot_call,
  ...
)

structure_plot_default_embed_method(fit, ...)

## S3 method for class 'poisson_nmf_fit'
plot(x, ...)

## S3 method for class 'multinom_topic_model_fit'
plot(x, ...)

structure_plot_ggplot_call(dat, colors, ticks = NULL, font.size = 9)

Arguments

- **fit**: An object of class “poisson_nmf_fit” or “multinom_topic_model_fit”. If a Poisson NMF fit is provided as input, the corresponding multinomial topic model fit is automatically recovered using poisson2multinom.
topics Top-to-bottom ordering of the topics in the Structure plot; topics[1] is shown on the top, topics[2] is shown next, and so on. If the ordering of the topics is not specified, the topics are automatically ordered so that the topics with the greatest total “mass” are at shown at the bottom of the plot. The topics may be specified by number or by name.

grouping Optional categorical variable (a factor) with one entry for each row of the loadings matrix fit$L defining a grouping of the samples (rows). The samples (rows) are arranged along the horizontal axis according to this grouping, then within each group according to loadings_order. If grouping is not a factor, an attempt is made to convert it to a factor using as.factor. Note that if loadings_order is specified manually, grouping should be the groups for the rows of fit$L before reordering.

loadings_order Ordering of the rows of the loadings matrix fit$L along the horizontal axis the Structure plot (after they have been grouped). If loadings_order = "embed", the ordering is generated automatically from a 1-d embedding, separately for each group. The rows may be specified by number or by name. Note that loadings_order may include all the rows of fit$L, or a subset.

n The maximum number of samples (rows of the loadings matrix fit$L) to include in the plot. Typically there is little to no benefit in including large number of samples in the Structure plot due to screen resolution limits. Ignored if loadings_order is provided.

colors Colors used to draw topics in Structure plot. The default colour setting is the from https://colorbrewer2.org (qualitative data, “9-class Set1”).

gap The horizontal spacing between groups. Ignored if grouping is not provided.

embed_method The function used to compute an 1-d embedding from a loadings matrix fit$L; only used if loadings_order = "embed". The function must accept the multinomial topic model fit as its first input (“fit”) and additional arguments may be passed (…). The output should be a named numeric vector with one entry per row of fit$L, and the names of the entries should be the same as the row names of fit$L.

ggplot_call The function used to create the plot. Replace structure_plot_ggplot_call with your own function to customize the appearance of the plot.

... Additional arguments passed to structure_plot (for the plot method) or embed_method (for function structure_plot).

x An object of class “poisson_nmf_fit” or “multinom_topic_model_fit”. If a Poisson NMF fit is provided as input, the corresponding multinomial topic model fit is automatically recovered using poisson2multinom.

dat A data frame passed as input to ggplot, containing, at a minimum, columns “sample”, “topic” and “prop”: the “sample” column contains the positions of the samples (rows of the L matrix) along the horizontal axis; the “topic” column is a topic (a column of L); and the “prop” column is the topic proportion for the respective sample.

ticks The placement of the group labels along the horizontal axis, and their names. For data that are not grouped, use ticks = NULL.

font.size Font size used in plot.
Details

The name “Structure plot” comes from its widespread use in population genetics to visualize the results of the Structure software (Rosenberg et al, 2002).

For most uses of the Structure plot in population genetics, there is usually some grouping of the samples (e.g., assignment to pre-defined populations) that guides arrangement of the samples along the horizontal axis in the bar chart. In other applications, such as analysis of gene expression data, a pre-defined grouping may not always be available. Therefore, a “smart” arrangement of the samples is, by default, generated automatically by performing a 1-d embedding of the samples.

Value

A ggplot object.

References


Examples

set.seed(1)
data(pbmc_facs)

# Get the multinomial topic model fitted to the
# PBMC data.
fit <- pbmc_facs$fit

# Create a Structure plot without labels. The samples (rows of L) are
# automatically arranged along the x-axis using t-SNE to highlight the
# structure in the data.
p1 <- structure_plot(fit)

# Create a Structure plot with the FACS cell-type labels. Within each
# group (cell-type), the cells (rows of L) are automatically arranged
# using t-SNE.
subpop <- pbmc_facs$samples$subpop
p2 <- structure_plot(fit, grouping = subpop)

# Next, we apply some customizations to improve the plot: (1) use the
# "topics" argument to specify the order in which the topic
# proportions are stacked on top of each other; (2) use the "gap"
# argument to increase the whitespace between the groups; (3) use "n"
# to decrease the number of rows of L included in the Structure plot;
# and (4) use "colors" to change the colors used to draw the topic
# proportions.
topic_colors <- c("skyblue","forestgreen","darkmagenta",
                   "dodgerblue","gold","darkorange")
p3 <- structure_plot(fit, grouping = pbmc_facs$samples$subpop, gap = 20, n = 1500, topics = c(5, 6, 1, 4, 2, 3), colors = topic_colors)

# In this example, we use UMAP instead of t-SNE to arrange the cells in the Structure plot. Note that this can be accomplished in a different way by overriding the default setting of "embed_method".
y <- drop(umap_from_topics(fit, dims = 1))
p4 <- structure_plot(fit, loadings_order = order(y), grouping = subpop, gap = 40, colors = topic_colors)

# We can also use PCA to arrange the cells.
y <- drop(pca_from_topics(fit, dims = 1))
p5 <- structure_plot(fit, loadings_order = order(y), grouping = subpop, gap = 40, colors = topic_colors)

# In this final example, we plot a random subset of 400 cells, and arrange the cells randomly along the horizontal axis of the Structure plot.
p6 <- structure_plot(fit, loadings_order = sample(3744, 400), gap = 10, grouping = subpop, colors = topic_colors)

summary.poisson_nmf_fit

Summarize Poisson NMF or Multinomial Topic Model Fit

Description

summary method for the “poisson_nmf_fit” and “multinom_topic_model_fit” classes.

Usage

## S3 method for class 'poisson_nmf_fit'
summary(object, ...)

## S3 method for class 'multinom_topic_model_fit'
summary(object, ...)

## S3 method for class 'summary.poisson_nmf_fit'
print(x, show.mixprops = FALSE, show.topic.reps = FALSE, ...)

## S3 method for class 'summary.multinom_topic_model_fit'
print(
x, show.size.factors = FALSE, show.mixprops = FALSE, show.topic.reps = FALSE,
Arguments

object

An object of class "poisson_nmf_fit" or "multinom_topic_model_fit". The former is usually the result of calling fit_poisson_nmf; the latter is usually the result of calling fit_topic_model or poisson2multinom.

Arguments

... Additional arguments passed to the generic summary or print.summary method.

x

An object of class "summary.poisson_nmf_fit", usually a result of a call to summary.poisson_nmf_fit.

show.mixprops

If TRUE, print a summary of the mixture proportions.

show.topic.reps

If TRUE, print a summary of the topic representatives.

show.size.factors

If TRUE, print a summary of the size factors.

Value

The functions summary.poisson_nmf_fit and summary.multinom_topic_model_fit compute and return a list of statistics summarizing the model fit. The returned list includes some or all of the following elements:

n
The number of rows in the counts matrix, typically the number of samples.

m
The number of columns in the counts matrix, typically the number of observed counts per sample.

k
The rank of the Poisson NMF or the number of topics.

s
A vector of length n giving the "size factor" estimates; these estimates should be equal, or close to, the total counts in each row of the counts matrix.

numiter
The number of loadings and/or factor updates performed.

loglik
The Poisson NMF log-likelihood.

loglik.multinom
The multinomial topic model log-likelihood.

devid
The Poisson NMF deviance.

res
The maximum residual of the Karush-Kuhn-Tucker (KKT) first-order optimality conditions. This can be used to assess convergence of the updates to a (local) solution.

mixprops
Matrix giving a high-level summary of the mixture proportions, in which rows correspond to topics, and columns are ranges of mixture proportions.

topic.reps
A matrix in which the ith row gives the mixture proportions for the sample "most representative" of topic i; by "most representative", we mean the row (or sample) with the highest proportion of counts drawn from the topic i.
Volcano Plots for Visualizing Results of Differential Expression Analysis

Description

Create a “volcano” plot to visualize the results of a differential count analysis using a topic model. Here, the volcano plot is a scatterplot in which the posterior mean log-fold change (LFC), estimated by running the methods implemented in \texttt{de\_analysis}, is plotted against the estimated \textit{z}-score. Use \texttt{volcano\_plotly} to create an interactive volcano plot.

Usage

\begin{verbatim}
volcano_plot(de, k, labels, do.label = volcano_plot_do_label_default, ymax = Inf, max.overlaps = Inf, plot.title = paste("topic", k), ggplot_call = volcano_plot_ggplot_call )

## S3 method for class 'topic_model_de_analysis'
plot(x, ...)

volcano_plotly(de, k, file, labels, ymax = Inf, width = 500, height = 500, plot.title = paste("topic", k), plot_ly_call = volcano_plot_ly_call )

volcano_plot_do_label_default(lfc, z)

volcano_plot_ggplot_call(dat, plot.title, max.overlaps = Inf, font.size = 9)

volcano_plot_ly_call(dat, plot.title, width, height)
\end{verbatim}
Arguments

de An object of class “topic_model_de_analysis”, usually an output from `de_analysis`. It is better to run `de_analysis` with `shrink.method = "ash"` so that the points in the volcano plot can be coloured by their local false sign rate (lfsr).
k The topic, selected by number or name.
labels Character vector specifying how the points in the volcano plot are labeled. This should be a character vector with one entry per LFC estimate (row of `de$postmean`). When not specified, the row names of `de$postmean` are used. When available, labels are added to the plot using `geom_text_repel`.
do.label The function used to determine which LFC estimates to label. Replace `volcano_plot_do_label_default` with your own function to customize the labeling of points in the volcano plot.
ymax z-scores greater than `ymax` (in magnitude) are shown as `max`. Setting `ymax` to a finite value can improve the volcano plot when some z-scores are much larger (in magnitude) than others.
max.overlaps Argument passed to `geom_text_repel`.
plot.title The title of the plot.
ggplot_call The function used to create the plot. Replace `volcano_plot_ggplot_call` with your own function to customize the appearance of the plot.
x An object of class “topic_model_de_analysis”, usually an output from `de_analysis`.
... Additional arguments passed to `volcano_plot`.
file Save the interactive volcano plot to this HTML file using `saveWidget`.
width Width of the plot in pixels. Passed as argument “width” to `plot_ly`.
height Height of the plot in pixels. Passed as argument “height” to `plot_ly`.
plot_ly_call The function used to create the plot. Replace `volcano_plot_ly_call` with your own function to customize the appearance of the interactive plot.
lfc A vector of log-fold change estimates.
z A vector of z-scores of the same length as `lfc`.
dat A data frame passed as input to `ggplot`, containing, at a minimum, columns “f0”, “postmean”, “z”, “zabs”, “lfsr” and “label”.
font.size Font size used in plot.

Details

Interactive volcano plots can be created using the ‘plotly’ package. The “hover text” shows the label and detailed LFC statistics.

Value

A ggplot object or a plotly object.

See Also

`de_analysis`
Examples

# See help(de_analysis) for examples.
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