Package: scStability (via r-universe)

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Title Measuring the Stability of Dimension Reduction and Cluster Assignment in scRNA-Seq Experiments

Version 1.0.3

Description Provides functions for evaluating the stability of low-dimensional embeddings and cluster assignments in single-cell RNA sequencing (scRNA-seq) datasets. Starting from a principal component analysis (PCA) object, users can generate multiple replicates of t-Distributed Stochastic Neighbor Embedding (t-SNE) or Uniform Manifold Approximation and Projection (UMAP) embeddings. Embedding stability is quantified by computing pairwise Kendall's Tau correlations across replicates and summarizing the distribution of correlation coefficients. In addition to dimensionality reduction, 'scStability' assesses clustering consistency using either Louvain or Leiden algorithms and calculating the Normalized Mutual Information (NMI) between all pairs of cluster assignments. For background on UMAP and t-SNE algorithms, see McInnes et al. (2020, <doi:10.21105/joss.00861>) and van der Maaten & Hinton (2008, <`https://github.com/lvdmaaten/bhtsne`>), respectively.

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Author Ben Abrahams [aut, cre]

Maintainer Ben Abrahams <ben.abrahams.de@gmail.com>

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Contents

`clustStable` *Create and compare multiple clustering runs on scRNA-seq data*

Description

Generate multiple clustering iterations on a Seurat object containing scRNA-seq data using the provided dimensionality reduction. The function creates a shared nearest neighbor (SNN) graph and assigns clusters using the specified algorithm, then calculates stability metrics across iterations.

Usage

```
clustStable(
  n_runs,
  seurat_obj,
  method = c("louvain", "leiden"),
  resolution = 0.8,
  dims = 1:10,
  n_cores = 1,
  verbose = TRUE,
  print_plot = TRUE,
  seeds = NULL
)
```

Arguments

`n_runs`	Integer specifying the number of cluster assignments to generate (default: 100)
`seurat_obj`	A Seurat object containing scRNA-seq data with a PCA reduction
`method`	Character string specifying the clustering algorithm to use: either "louvain" or "leiden"
`resolution`	Numeric value specifying the clustering resolution parameter (default: 0.8)
`dims`	Integer vector specifying which PCA dimensions to use (default: 1:10)
`n_cores`	Integer specifying the number of CPU cores to use for parallelization (default: 1)
`verbose`	Whether the function should print summary statistics as it calculates them
`print_plot`	Whether the final violin plot should be automatically printed
`seeds`	A set of seeds of length n_runs for creating clusters

Value

A list containing the following components:

`per_index_means`	Numeric vector of NMI values for each clustering iteration
`ci`	Numeric vector containing the lower and upper bounds of the 95% confidence interval
`cluster_labels`	List of cluster assignments for each iteration

`compareEmb` *Compare dimensional reduction embeddings and calculate stability statistics*

Description

Evaluates the stability of a set of dimension reduction embeddings by performing pairwise Procrustes alignment and calculating Kendall's Tau correlation between each pair. This function quantifies the consistency of embeddings generated with the same algorithm but different random initializations.

Usage

```
compareEmb(emb_list, n_cores = 1, verbose = TRUE, print_plot = TRUE)
```

Arguments

`emb_list`	A list of 2D embeddings (each typically containing coordinates for UMAP or t-SNE) created by the `createEmb` function
`n_cores`	Integer specifying the number of CPU cores to use for parallelization (default: 1)
`verbose`	Whether the function should print summary statistics as it calculates them
`print_plot`	Whether the final violin plot should be automatically printed

Value

A list containing the following components:

`mean`	Numeric value representing the overall mean correlation across all pairwise comparisons
`mean_per_embedding`	Numeric vector of mean correlation values for each embedding
`all_pairwise_correlations`	Numeric vector containing all pairwise correlation values
`range`	Numeric vector with minimum and maximum of mean correlation per embedding
`ci`	Numeric vector containing the lower and upper bounds of the 95% confidence interval

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`createEmb` *Create multiple dimension reduction embeddings*

Description

Generates multiple dimension reduction embeddings using either UMAP or t-SNE algorithms. Each embedding is created with different random initializations to assess stability. The function returns a list of embeddings, each represented as a data frame or matrix.

Usage

```
createEmb(
  dr_input,
  n_runs = 100,
  method = c("umap", "tsne"),
  n_neighbors = 15,
  min_dist = 0.1,
  perplexity = 30,
  theta = 0.5,
  n_cores = 1,
  seeds = NULL
)
```

Arguments

`dr_input`	A numeric matrix or data frame containing the input data for dimension reduction, with rows representing observations (cells) and columns representing PCA components
`n_runs`	Integer specifying the number of embeddings to generate (default: 100)
`method`	Character string specifying the dimension reduction method to use: either "umap" or "tsne"

`n_neighbors`	Integer specifying the number of neighbors to consider when constructing the initial graph (used for UMAP only, default: 30)
`min_dist`	Numeric value specifying the minimum distance between points in the embedding (used for UMAP only, default: 0.1)
`perplexity`	Numeric value controlling the effective number of neighbors (used for t-SNE only, default: 30)
`theta`	Numeric value between 0 and 1 controlling the speed/accuracy trade-off (used for t-SNE only, default: 0.5)
`n_cores`	Integer specifying the number of CPU cores to use for parallelization (default: 1)
`seeds`	A set of seeds of length n_runs to be used for each embedding

Value

A list of dimension reduction embeddings, each represented as a data frame with rows corresponding to observations (cells) and two columns representing the x and y coordinates in the reduced space.

`scStability` *A user friendly wrapper function that runs the entire scRNA-seq stability workflow and shows statistics for each step*

Description

A wrapper function that runs all other stability analysis functions in order. Statistics for each step are printed accordingly and a final DR and cluster plot is shown which represents the medoid embeddings and cluster assignments that were generated.

Usage

```
scStability(
  seurat_obj,
  n_runs = 100,
  dr_method = "umap",
  clust_method = "louvain",
  n_cores = 1,
  verbose = TRUE,
  print_plot = TRUE,
  seeds = NULL
)
```

Arguments

`seurat_obj`	A Seurat object containing scRNA-seq data and a PCA
`n_runs`	Number of DR embeddings and number of cluster assignments to be generated (< 250 recommended)
`dr_method`	Method to use for dimension reduction, either "umap" or "tsne"
`clust_method`	Algorithm used for clustering, either "louvain" or "leiden"
`n_cores`	Number of CPU cores to use for parallelising functions
`verbose`	Whether the function should print summary statistics as it calculates them
`print_plot`	Whether the final medoid plot should be printed
`seeds`	A set of seeds of length n_runs used for generating embeddings and clusters

Value

A list containing:

`mean_emb`	Data frame containing the mean embedding coordinates
`mean_clust`	Vector of the mean cluster assignments
`plot`	ggplot2 object with the medoid embedding plot and cluster assignments
`embedding_stats`	List of embedding statistics
`cluster_stats`	List of clustering statistics
`seurat_object`	Seurat object now containing mean embeddings and mean clusters

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