Package ‘lmds’

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Type Package

Title Landmark Multi-Dimensional Scaling

Version 0.1.0

Description A fast dimensionality reduction method scaleable to large numbers of samples. Landmark Multi-Dimensional Scaling (LMDS) is an extension of classical Torgerson MDS, but rather than calculating a complete distance matrix between all pairs of samples, only the distances between a set of landmarks and the samples are calculated.

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Encoding UTF-8

LazyData true

Imports assertthat, dynutils (>= 1.0.3), irlba, Matrix

Suggests testthat

RoxygenNote 6.1.1

URL `http://github.com/dynverse/lmds`

BugReports `https://github.com/dynverse/lmds/issues`

Collate 'cmdscale_landmarks.R' 'select_landmarks.R' 'lmds.R' 'package.R'

NeedsCompilation no

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`cmdscale_landmarks` *Perform MDS on landmarks and project other samples to the same space*

Description

Perform MDS on landmarks and project other samples to the same space

Usage

```
cmdscale_landmarks(dist_2lm, ndim = 3, rescale = TRUE, ...)
```

Arguments

`dist_2lm`	Distance matrix between the landmarks and all the samples in original dataset
`ndim`	The number of dimensions
`rescale`	Whether or not to rescale the final dimensionality reduction (recommended)
`...`	Extra params to pass to `irlba::irlba()`

Value

The dimensionality reduction in the form of a `ncol(dist_2lm)` by `ndim` matrix.

Examples

```
library(Matrix)
x <- as.matrix(iris[,1:4])
dist_2lm <- select_landmarks(x)
cmdscale_landmarks(dist_2lm)
```

`lmds` *Landmark MDS*

Description

A fast dimensionality reduction method scaleable to large numbers of samples. Landmark Multi-Dimensional Scaling (LMDS) is an extension of classical 'Torgerson MDS', but rather than calculating a complete distance matrix between all pairs of samples, only the distances between a set of landmarks and the samples are calculated.

A fast dimensionality reduction method scaleable to large numbers of samples. Landmark Multi-Dimensional Scaling (LMDS) is an extension of classical Torgerson MDS´, but rather than calculating a complete distance matrix between all pairs of samples, only the distances between a set of landmarks and the samples are calculated.

Usage

```
lmds(x, ndim = 3, distance_method = c("euclidean", "pearson",
  "spearman", "cosine", "manhattan"), landmark_method = c("sample"),
  num_landmarks = 500)
```

Arguments

`x`	A matrix, optionally sparse.
`ndim`	The number of dimensions
`distance_method`	The distance metric to use. Options are "euclidean" (default), "pearson", "spearman", "cosine", "manhattan".
`landmark_method`	The landmark selection method to use. Options are "sample" (default).
`num_landmarks`	The number of landmarks to use,

Value

The dimensionality reduction in the form of a `nrow(x)` by `ndim` matrix.

Examples

```
library(Matrix)
x <- Matrix::rsparsematrix(1000, 1000, .01)
lmds(x, ndim = 3)
```

`select_landmarks` *Select landmarks from dataset*

Description

In addition, the distances between the landmarks and all samples are calculated.

Usage

```
select_landmarks(x, distance_method = c("euclidean", "pearson",
  "spearman", "cosine", "manhattan"), landmark_method = c("sample"),
  num_landmarks = 500)
```

Arguments

`x`	A matrix, optionally sparse.
`distance_method`	The distance metric to use. Options are "euclidean" (default), "pearson", "spearman", "cosine", "manhattan".
`landmark_method`	The landmark selection method to use. Options are "sample" (default).
`num_landmarks`	The number of landmarks to use,

Value

The distance matrix between the landmarks and all samples. In addition, an attribute `"landmark_ix"` denotes the indices of landmarks that were sampled.

Examples

```
library(Matrix)
x <- Matrix::rsparsematrix(1000, 1000, .01)
select_landmarks(x)
```

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