Package: lmds (via r-universe)

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Type Package

Title Landmark Multi-Dimensional Scaling

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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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Imports assertthat, dynutils (>= 1.0.3), irlba (>= 2.0.0)

Suggests Matrix, testthat

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URL https://dynverse.org/lmds/, https://github.com/dynverse/lmds

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

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

Repository https://dynverse.r-universe.dev

RemoteUrl https://github.com/dynverse/lmds

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lmds-package *Landmark Multi-Dimensional Scalng*

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See Also

Useful links:

- https://dynverse.org/lmds/
- https://github.com/dynverse/lmds
- Report bugs at https://github.com/dynverse/lmds/issues

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)
```

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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.

Usage

```
lmds(
  x,
  ndim = 3,
  distance_method = c("euclidean", "pearson", "spearman", "cosine", "chisquared",
    "hamming", "kullback", "manhattan", "maximum", "canberra", "minkowski"),
  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", "chisquared",
    "hamming", "kullback", "manhattan", "maximum", "canberra", "minkowski"),
  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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