Package ‘lmds’

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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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**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**

```r
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

```r
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 \( n_{row(x)} \) by \( ndim \) matrix.

Examples

```r
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

```r
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

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