

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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Contents

cmdscale_landmarks	2
lmds	2
select_landmarks	3

Index**5**

cmdscale_landmarks	<i>Perform MDS on landmarks and project other samples to the same space</i>
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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 <code>irlba::irlba()</code>

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	<i>Select landmarks from dataset</i>
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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)
```

Index

`cmdscale_landmarks`, [2](#)

`irlba::irlba()`, [2](#)

`lms`, [2](#)

`lms-package (lms)`, [2](#)

`select_landmarks`, [3](#)