Package 'dimRed'

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Title A Framework for Dimensionality Reduction

Version 0.1.0

Description A collection of dimensionality reduction techniques from R packages and provides a common interface for calling the methods.

Depends R (>= 3.0.0), methods, DRR

Suggests MASS, Matrix, RANN, RSpectra, Rtsne, coRanking, diffusionMap, energy, fastICA, ggplot2, graphics, igraph, kernlab, lle, loe, optimx, pcaPP, rgl, scales, scatterplot3d, stats, testthat, tidyr, vegan

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URL https://github.com/gdkrmr/dimRed

LazyData true

Collate 'misc.R' 'dimRedData-class.R' 'dataSets.R' 'dimRedMethod-class.R' 'dimRedResult-class.R' 'diffmap.R' 'dimRed.R' 'drr.R' 'embed.R' 'fastica.R' 'get_info.R' 'graph_embed.R' 'hlle.R' 'isomap.R' 'kpca.R' 'leim.R' 'lle.R' 'loe.R' 'mds.R' 'mixColorSpaces.R' 'nmds.R' 'pca.R' 'plot.R' 'quality.R' 'rotate.R' 'soe.R' 'tsne.R'

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R topics documented:

`dimRed-package` *The dimRed package*

Description

This package simplifies dimensionality reduction in R by providing a framework of S4 classes and methods. dimRed collects dimensionality reduction methods that are implemented in R and implements others. It gives them a common interface and provides plotting functions for visualization and functions for quality assessment.

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References

Lee, J.A., Renard, E., Bernard, G., Dupont, P., Verleysen, M., 2013. Type 1 and 2 mixtures of Kullback-Leibler divergences as cost functions in dimensionality reduction based on similarity preservation. Neurocomputing. 112, 92-107. doi:10.1016/j.neucom.2012.12.036

Lee, J.A., Lee, J.A., Verleysen, M., 2008. Rank-based quality assessment of nonlinear dimensionality reduction. Proceedings of ESANN 2008 49-54.

Chen, L., Buja, A., 2006. Local Multidimensional Scaling for Nonlinear Dimension Reduction, Graph Layout and Proximity Analysis.

See Also

Useful links:

- https://github.com/gdkrmr/dimRed

`as.data.frame` *Converts to data.frame*

Description

General conversions of objects created by `dimRed` to `data.frame`. See class documentations for details (`dimRedData`, `dimRedResult`). For the documentation of this function in base package, see here: `as.data.frame.default`.

Usage

```
as.data.frame(x, row.names, optional, ...)
```

Arguments

x	The object to be converted
row.names	unused in dimRed
optional	unused in dimRed
...	other arguments.

---

as.dimRedData *Converts to dimRedData*

Description

Conversion functions to dimRedData.

Usage

```
as.dimRedData(formula, ...)
```

Arguments

formula	a formula object.
...	other arguments.

AUC_lnK_R_NX,dimRedResult-method *Method AUC_lnK_R_NX*

Description

Calculate the Area under the R_NX(ln K), used in Lee et. al. (2013).

Usage

```
## S4 method for signature 'dimRedResult'
AUC_lnK_R_NX(object)
```

Arguments

object	of class dimRedResult

References

Lee, J.A., Renard, E., Bernard, G., Dupont, P., Verleysen, M., 2013. Type 1 and 2 mixtures of Kullback-Leibler divergences as cost functions in dimensionality reduction based on similarity preservation. Neurocomputing. 112, 92-107. doi:10.1016/j.neucom.2012.12.036

See Also

Other Quality scores for dimensionality reduction: LCMC,dimRedResult-method, Q_NX,dimRedResult-method, Q_global,dimRedResult-method, Q_local,dimRedResult-method, R_NX,dimRedResult-method, cophenetic_correlation,dimRedResult-method, distance_correlation,dimRedResult-method, mean_R_NX,dimRedResult-method, quality,dimRedResult-method, reconstruction_error,dimRedResult-method, reconstruction_rmse,dimRedResult-method, total_correlation,dimRedResult-method

---

cophenetic_correlation,dimRedResult-method

Method cophenetic_correlation

Description

Calculate the correlation between the distance matrices in high and low dimensioal space.

Usage

```
## S4 method for signature 'dimRedResult'
cophenetic_correlation(object, d = stats::dist,
  cor_method = "pearson")
```

Arguments

object	of class dimRedResult
d	the distance function to use.
cor_method	The correlation method.

See Also

Other Quality scores for dimensionality reduction: AUC_lnK_R_NX,dimRedResult-method, LCMC,dimRedResult-method, Q_NX,dimRedResult-method, Q_global,dimRedResult-method, Q_local,dimRedResult-method, R_NX,dimRedResult-method, distance_correlation,dimRedResult-method, mean_R_NX,dimRedResult-method, quality,dimRedResult-method, reconstruction_error,dimRedResult-method, reconstruction_rmse,dimRedResul
total_correlation,dimRedResult-method

dataSets *Example Data Sets for dimensionality reduction*

Description

A compilation of standard data sets that are often being used to showcase dimensionality reduction techniques.

Usage

```
loadDataSet(name = dataSetList(), n = 2000, sigma = 0.05)

dataSetList()
```

Arguments

name	A character vector that specifies the name of the data set.
n	In generated data sets the number of points to be generated, else ignored.
sigma	In generated data sets the standard deviation of the noise added, else ignored.

Details

The argument name should be one of `dataSetList()`. Partial matching is possible, see match.arg. Generated data sets contain the internal coordinates of the manifold in the meta slot. Call `dataSetList()` to see what data sets are available.

Value

`loadDataSet` an object of class dimRedData. `dataSetList()` return a character string with the implemented data sets

Examples

```
## a list of available data sets:
dataSetList()

## Load a data set:
swissRoll <- loadDataSet("Swiss Roll")
plot(swissRoll, type = "3vars")

## Load Iris data set, partial matching:
loadDataSet("I")
```

`DiffusionMaps-class` *Diffusion Maps*

Description

An S4 Class implementing Diffusion Maps

Details

Diffusion Maps uses a diffusion probability matrix to robustly approximate a manifold.

Slots

`fun` A function that does the embedding and returns a dimRedResult object.

`stdpars` The standard parameters for the function.

General usage

Dimensionality reduction methods are S4 Classes that either be used directly, in which case they have to be initialized and a full list with parameters has to be handed to the `@fun()` slot, or the method name be passed to the embed function and parameters can be given to the `...`, in which case missing parameters will be replaced by the ones in the `@stdpars`.

Parameters

Diffusion Maps can take the following parameters:

d a function transforming a matrix row wise into a distance matrix or `dist` object, e.g. `dist`.

ndim The number of dimensions

eps The epsilon parameter that determines the diffusion weight matrix from a distance matrix `d`, $exp(-d^2/eps)$, if set to `"auto"` it will be set to the median distance to the 0.01*n nearest neighbor.

t Time-scale parameter. The recommended value, 0, uses multiscale geometry.

delta Sparsity cut-off for the symmetric graph Laplacian, a higher value results in more sparsity and faster calculation. The predefined value is 10^-5.

Implementation

Wraps around `diffuse`, see there for details. It uses the notation of Richards et al. (2009) which is slightly different from the one in the original paper (Coifman and Lafon, 2006) and there is no α parameter. There is also an out-of-sample extension, see examples.

References

Richards, J.W., Freeman, P.E., Lee, A.B., Schafer, C.M., 2009. Exploiting Low-Dimensional Structure in Astronomical Spectra. ApJ 691, 32. doi:10.1088/0004-637X/691/1/32

Coifman, R.R., Lafon, S., 2006. Diffusion maps. Applied and Computational Harmonic Analysis 21, 5-30. doi:10.1016/j.acha.2006.04.006

See Also

Other dimensionality reduction methods: DRR-class, DrL-class, FastICA-class, FruchtermanReingold-class, HLLE-class, Isomap-class, KamadaKawai-class, LLE-class, MDS-class, PCA-class, dimRedMethod-class, kPCA-class, nMDS-class, tSNE-class

Examples

```
dat <- loadDataSet("3D S Curve")

## use the S4 Class directly:
diffmap <- DiffusionMaps()
emb <- diffmap@fun(dat, diffmap@stdpars)

## simpler, use embed():
emb2 <- embed(dat, "DiffusionMaps")

plot(emb, type = "2vars")

samp <- sample(floor(nrow(dat) / 10))
embsamp <- diffmap@fun(dat[samp], diffmap@stdpars)
embother <- embsamp@apply(dat[-samp])
plot(embsamp, type = "2vars")
points(embother)
```

---

dimRedData-class *Class "dimRedData"*

Description

A class to hold data for dimensionality reduction and methods.

Usage

```
## S4 method for signature 'dimRedData'
as.data.frame(x, meta.prefix = "meta.",
  data.prefix = "")

## S4 method for signature 'formula'
as.dimRedData(formula, data)

## S4 method for signature 'dimRedData'
getData(object)

## S4 method for signature 'dimRedData'
getMeta(object)

## S4 method for signature 'dimRedData'
```

```
nrow(x)

## S4 method for signature 'dimRedData,ANY,ANY,ANY'
x[i]

## S4 method for signature 'dimRedData'
ndims(object)
```

Arguments

x	Of class dimRedData
meta.prefix	Prefix for the columns of the meta data names.
data.prefix	Prefix for the columns of the variable names.
formula	The formula, left hand side is assigned to the meta slot right hand side is assigned to the data slot.
data	A data frame
object	Of class dimRedData.
i	a valid index for subsetting rows.

Details

The class hast two slots, data and meta. The data slot contains a numeric matrix with variables in columns and observations in rows. The meta slot may contain a data.frame with additional information. Both slots need to have the same number of rows or the meta slot needs to contain an empty data.frame.

See examples for easy conversion from and to data.frame.

For plotting functions see plot.dimRedData.

Methods (by generic)

- as.data.frame: convert to data.frame
- as.dimRedData: Convert a data.frame to a dimRedData object using a formula
- getData: Get the data slot.
- getMeta: Get the meta slot.
- nrow: Get the number of observations.
- [: Subset rows.
- ndims: Extract the number of Variables from the data.

Slots

data of class matrix, holds the data, observations in rows, variables in columns

meta of class data.frame, holds meta data such as classes, internal manifold coordinates, or simply additional data of the data set. Must have the same number of rows as the data slot or be an empty data frame.

Examples

```
## Load an example data set:
s3d <- loadDataSet("3D S Curve")

## Create using a constructor:

### without meta information:
dimRedData(iris[, 1:4])

### with meta information:
dimRedData(iris[, 1:4], iris[, 5])

### using slot names:
dimRedData(data = iris[, 1:4], meta = iris[, 5])

## Convert to a dimRedData objects:
Iris <- as(iris[, 1:4], "dimRedData")

## Convert to data.frame:
head(as(s3d, "data.frame"))
head(as.data.frame(s3d))
head(as.data.frame(as(iris[, 1:4], "dimRedData")))

## Extract slots:
head(getData(s3d))
head(getMeta(s3d))

## Get the number of observations:
nrow(s3d)

## Subset:
s3d[1:5, ]

## create a dimRedData object using a formula
as.dimRedData(Species ~ Sepal.Length + Sepal.Width + Petal.Length + Petal.Width,
              iris)[1:5]

## Shuffle data:
s3 <- s3d[nrow(s3d)]

## Get the number of variables:
ndims(s3d)
```

---

dimRedMethod-class *Class "dimRedMethod"*

Description

A virtual class "dimRedMethod" to serve as a template to implement methods for dimensionality reduction.

Details

Implementations of dimensionality reductions should inherit from this class.

The `fun` slot should be a function that takes three arguments

data An object of class `dimRedData`.

pars A list with the standard parameters.

keep.org.data Logical. If the original data should be kept in the output.

and returns an object of class `dimRedResult`.

The `stdpars` slot should take a list that contains standard parameters for the implemented methods.

This way the method can be called by `embed(data,"method-name", ...)`, where `...` can be used to to change single parameters.

Slots

`fun` A function that does the embedding.

`stdpars` A list with the default parameters for the `fun` slot.

See Also

dimRedMethodList

Other dimensionality reduction methods: `DRR-class`, `DiffusionMaps-class`, `DrL-class`, `FastICA-class`, `FruchtermanReingold-class`, `HLLE-class`, `Isomap-class`, `KamadaKawai-class`, `LLE-class`, `MDS-class`, `PCA-class`, `kPCA-class`, `nMDS-class`, `tSNE-class`

`dimRedMethodList` *dimRedMethodList*

Description

Get the names of all methods for dimensionality reduction.

Usage

```
dimRedMethodList()
```

Details

Returns the name of all classes that inherit from `dimRedMethod-class` to use with `embed`.

Value

a character vector with the names of classes that inherit from `dimRedMethod`.

Examples

```
dimRedMethodList()
```

`dimRedResult-class` *Class "dimRedResult"*

Description

A class to hold the results of of a dimensionality reduction.

Usage

```
## S4 method for signature 'dimRedResult'
predict(object, xnew)

## S4 method for signature 'dimRedResult'
inverse(object, ynew)

## S4 method for signature 'dimRedResult'
as.data.frame(x, org.data.prefix = "org.",
  meta.prefix = "meta.", data.prefix = "")

## S4 method for signature 'dimRedResult'
getPars(object)

## S4 method for signature 'dimRedResult'
print(x)

## S4 method for signature 'dimRedResult'
getOrgData(object)

## S4 method for signature 'dimRedResult'
getDimRedData(object)

## S4 method for signature 'dimRedResult'
ndims(object)
```

Arguments

`object`	Of class `dimRedResult`
`xnew`	new data, of type `dimRedData`
`ynew`	embedded data, of type `dimRedData`
`x`	Of class `dimRedResult`
`org.data.prefix`	Prefix for the columns of the org.data slot.
`meta.prefix`	Prefix for the columns of `x@data@meta`.
`data.prefix`	Prefix for the columns of `x@data@data`.

Methods (by generic)

- `predict`: apply a trained method to new data, does not work with all methods, will give an error if there is no `apply`. In some cases the apply function may only be an approximation.
- `inverse`: inverse transformation of embedded data, does not work with all methods, will give an error if there is no `inverse`. In some cases the apply function may only be an approximation.
- `as.data.frame`: convert to `data.frame`
- `getPars`: Get the parameters with which the method was called.
- `print`: Method for printing.
- `getOrgData`: Get the original data and meta.data
- `getDimRedData`: Get the embedded data
- `ndims`: Extract the number of embedding dimensions.

Slots

`data` Output data of class dimRedData.

`org.data` original data, a matrix.

`apply` a function to apply the method to out-of-sampledata, may not exist.

`inverse` a function to calculate the original coordinates from reduced space, may not exist.

`has.org.data` logical, if the original data is included in the object.

`has.apply` logical, if a forward method is exists.

`has.inverse` logical if an inverse method exists.

`method` saves the method used.

`pars` saves the parameters used.

Examples

```
## Create object by embedding data
iris.pca <- embed(loadDataSet("Iris"), "PCA")

## Convert the result to a data.frame
head(as(iris.pca, "data.frame"))
head(as.data.frame(iris.pca))

## There are no nameclashes to avoid here:
head(as.data.frame(iris.pca,
                   org.data.prefix = "",
                   meta.prefix     = "",
                   data.prefix     = ""))

## Print it more or less nicely:
print(iris.pca)

## Get the embedded data as a dimRedData object:
getDimRedData(iris.pca)
```

```
## Get the original data including meta information:
getOrgData(iris.pca)

## Get the number of variables:
ndims(iris.pca)
```

`distance_correlation,dimRedResult-method` *Method distance_correlation*

Description

Calculate the distance correlation between the distance matrices in high and low dimensioal space.

Usage

```
## S4 method for signature 'dimRedResult'
distance_correlation(object)
```

Arguments

`object`	of class dimRedResult

See Also

Other Quality scores for dimensionality reduction: `AUC_lnK_R_NX,dimRedResult-method`, `LCMC,dimRedResult-method`, `Q_NX,dimRedResult-method`, `Q_global,dimRedResult-method`, `Q_local,dimRedResult-method`, `R_NX,dimRedResult-method`, `cophenetic_correlation,dimRedResult-method`, `mean_R_NX,dimRedResult-method`, `quality,dimRedResult-method`, `reconstruction_error,dimRedResult-method`, `reconstruction_rmse,dimRedResul`
`total_correlation,dimRedResult-method`

`DrL-class` *Distributed Recursive Graph Layout*

Description

An S4 Class implementing Distributed recursive Graph Layout.

Details

DrL uses a complex algorithm to avoid local minima in the graph embedding which uses several steps.

Slots

`fun` A function that does the embedding and returns a dimRedResult object.

`stdpars` The standard parameters for the function.

General usage

Dimensionality reduction methods are S4 Classes that either be used directly, in which case they have to be initialized and a full list with parameters has to be handed to the `@fun()` slot, or the method name be passed to the embed function and parameters can be given to the `...`, in which case missing parameters will be replaced by the ones in the `@stdpars`.

Parameters

DrL can take the following parameters:

ndim The number of dimensions, defaults to 2. Can only be 2 or 3

knn Reduce the graph to keep only the neares neighbors. Defaults to 100.

d The distance function to determine the weights of the graph edges. Defaults to euclidean distances.

Implementation

Wraps around `layout_with_drl`. The parameters maxiter, epsilon and kkconst are set to the default values and cannot be set, this may change in a future release. The DimRed Package adds an extra sparsity parameter by constructing a knn graph which also may improve visualization quality.

See Also

Other dimensionality reduction methods: `DRR-class`, `DiffusionMaps-class`, `FastICA-class`, `FruchtermanReingold-class`, `HLLE-class`, `Isomap-class`, `KamadaKawai-class`, `LLE-class`, `MDS-class`, `PCA-class`, `dimRedMethod-class`, `kPCA-class`, `nMDS-class`, `tSNE-class`

Examples

```
## Not run:
dat <- loadDataSet("Swiss Roll", n = 500)

## use the S4 Class directly:
drl <- DrL()
emb <- drl@fun(dat, drl@stdpars)

## simpler, use embed():
emb2 <- embed(dat, "DrL")


plot(emb)

## End(Not run)
```

DRR-class *Dimensionality Reduction via Regression*

Description

An S4 Class implementing Dimensionality Reduction via Regression (DRR).

Details

DRR is a non-linear extension of PCA that uses Kernel Ridge regression.

Slots

`fun` A function that does the embedding and returns a dimRedResult object.

`stdpars` The standard parameters for the function.

General usage

Dimensionality reduction methods are S4 Classes that either be used directly, in which case they have to be initialized and a full list with parameters has to be handed to the `@fun()` slot, or the method name be passed to the embed function and parameters can be given to the `...`, in which case missing parameters will be replaced by the ones in the `@stdpars`.

Parameters

DRR can take the following parameters:

ndim The number of dimensions

lambda The regularization parameter for the ridge regression.

kernel The kernel to use for KRR, defaults to `"rbfdot"`.

kernel.pars A list with kernel parameters, elements depend on the kernel used, `"rbfdot"` uses `"sigma"`.

pca logical, should an initial pca step be performed, defaults to `TRUE`.

pca.center logical, should the data be centered before the pca step. Defaults to `TRUE`.

pca.scale logical, should the data be scaled before the pca ste. Defaults to `FALSE`.

fastcv logical, should `fastCV` from the CVST package be used instead of normal cross-validation.

fastcv.test If `fastcv = TRUE`, separate test data set for fastcv.

cv.folds if `fastcv = FALSE`, specifies the number of folds for crossvalidation.

fastkrr.nblocks integer, higher values sacrifice numerical accuracy for speed and less memory, see below for details.

verbose logical, should the cross-validation results be printed out.

Implementation

Wraps around drr, see there for details. DRR is a non-linear extension of principal components analysis using Kernel Ridge Regression (KRR, details see constructKRRLearner and constructFastKRRLearner). Non-linear regression is used to explain more variance than PCA. DRR provides an out-of-sample extension and a backward projection.

The most expensive computations are matrix inversions therefore the implementation profits a lot from a multithreaded BLAS library. The best parameters for each KRR are determined by cross-validaton over all parameter combinations of `lambda` and `kernel.pars`, using less parameter values will speed up computation time. Calculation of KRR can be accelerated by increasing `fastkrr.nblocks`, it should be smaller than n^1/3 up to sacrificing some accuracy, for details see constructFastKRRLearner. Another way to speed up is to use `pars$fastcv = TRUE` which might provide a more efficient way to search the parameter space but may also miss the global maximum, I have not ran tests on the accuracy of this method.

References

Laparra, V., Malo, J., Camps-Valls, G., 2015. Dimensionality Reduction via Regression in Hyperspectral Imagery. IEEE Journal of Selected Topics in Signal Processing 9, 1026-1036. doi:10.1109/JSTSP.2015.2417833

See Also

Other dimensionality reduction methods: DiffusionMaps-class, DrL-class, FastICA-class, FruchtermanReingold-class, HLLE-class, Isomap-class, KamadaKawai-class, LLE-class, MDS-class, PCA-class, dimRedMethod-class, kPCA-class, nMDS-class, tSNE-class

Examples

```
## Not run:
dat <- loadDataSet("variable Noise Helix", n = 200)[sample(200)]

## use the S4 Class directly:
drr <- DRR()
pars <- drr@stdpars
pars$ndim <- 3
emb <- drr@fun(dat, pars)

## simpler, use embed():
emb2 <- embed(dat, "DRR", ndim = 3)


plot(dat, type = "3vars")
plot(emb, type = "3vars")
plot(emb@inverse(emb@data@data[, 1, drop = FALSE]), type = "3vars")

## End(Not run)
```

embed *dispatches the different methods for dimensionality reduction*

Description

wraps around all dimensionality reduction functions.

Usage

```
embed(.data, ...)

## S4 method for signature 'formula'
embed(.formula, .data, .method = dimRedMethodList(),
  .mute = character(0), .keep.org.data = TRUE, ...)

## S4 method for signature 'ANY'
embed(.data, .method = dimRedMethodList(),
  .mute = character(0), .keep.org.data = TRUE, ...)

## S4 method for signature 'dimRedData'
embed(.data, .method = dimRed::dimRedMethodList(),
  .mute = character(0), .keep.org.data = TRUE, ...)
```

Arguments

.data	object of class dimRedData
...	the pameters, internally passed as a list to the dimensionality reduction method as pars = list(...)
.formula	a formula, see as.dimRedData.
.method	character vector naming one of the dimensionality reduction techniques.
.mute	a character vector containing the elements you want to mute (c("message", "output")), defaults to character(0).
.keep.org.data	TRUE/FALSE keep the original data.

Details

Method must be one of dimRedMethodList(), partial matching is performed. All parameters start with a dot, to avoid clashes with partial argument matching (see the R manual section 4.3.2), if there should ever occur any clashes in the arguments, call the function with all arguments named, e.g. embed(.data = dat,.method = "mymethod", .d = "some parameter").

Value

an object of class dimRedResult

Methods (by class)

- formula: embed a data.frame using a formula.
- ANY: Embed anything as long as it can be coerced to dimRedData.
- dimRedData: Embed a dimRedData object

Examples

```
## Not run:
embed_methods <- dimRedMethodList()
quality_methods <- dimRedQualityList()
dataset <- loadDataSet("Iris")

quality_results <- matrix(NA, length(embed_methods), length(quality_methods),
                          dimnames = list(embed_methods, quality_methods))
embedded_data <- list()

for (e in embed_methods) {
  message("embedding: ", e)
  embedded_data[[e]] <- embed(dataset, e, .mute = c("message", "output"))
  for (q in quality_methods) {
    message("  quality: ", q)
    quality_results[e, q] <- tryCatch(
      quality(embedded_data[[e]], q),
      error = function(e) NA
    )
  }
}

print(quality_results)

## End(Not run)
## embed a data.frame using a formula:
head(as.data.frame(
  embed(Species ~ Sepal.Length + Sepal.Width + Petal.Length + Petal.Width,
        iris, "PCA")
))

head(as.data.frame(
  embed(iris[, 1:4], "PCA")
))
head(as.data.frame(
  embed(as.matrix(iris[, 1:4]), "PCA")
))
```

FastICA-class *Independent Component Analysis*

Description

An S4 Class implementing the FastICA algorithm for Indepentend Component Analysis.

Details

ICA is used for blind signal separation of different sources. It is a linear Projection.

Slots

`fun` A function that does the embedding and returns a dimRedResult object.

`stdpars` The standard parameters for the function.

General usage

Dimensionality reduction methods are S4 Classes that either be used directly, in which case they have to be initialized and a full list with parameters has to be handed to the `@fun()` slot, or the method name be passed to the embed function and parameters can be given to the ..., in which case missing parameters will be replaced by the ones in the `@stdpars`.

Parameters

FastICA can take the following parameters:

ndim The number of output dimensions. Defaults to 2

Implementation

Wraps around `fastICA`. FastICA uses a very fast approximation for negentropy to estimate statistical independences between signals. Because it is a simple rotation/projection, forward and backward functions can be given.

See Also

Other dimensionality reduction methods: `DRR-class`, `DiffusionMaps-class`, `DrL-class`, `FruchtermanReingold-class`, `HLLE-class`, `Isomap-class`, `KamadaKawai-class`, `LLE-class`, `MDS-class`, `PCA-class`, `dimRedMethod-class`, `kPCA-class`, `nMDS-class`, `tSNE-class`

Examples

```
dat <- loadDataSet("3D S Curve")

## use the S4 Class directly:
fastica <- FastICA()
emb <- fastica@fun(dat, pars = list(ndim = 2))

## simpler, use embed():
emb2 <- embed(dat, "FastICA", ndim = 2)


plot(emb@data@data)
```

FruchtermanReingold-class

Fruchterman Reingold Graph Layout

Description

An S4 Class implementing the Fruchterman Reingold Graph Layout algorithm.

Slots

`fun` A function that does the embedding and returns a dimRedResult object.

`stdpars` The standard parameters for the function.

General usage

Dimensionality reduction methods are S4 Classes that either be used directly, in which case they have to be initialized and a full list with parameters has to be handed to the `@fun()` slot, or the method name be passed to the embed function and parameters can be given to the `...`, in which case missing parameters will be replaced by the ones in the `@stdpars`.

Parameters

ndim The number of dimensions, defaults to 2. Can only be 2 or 3

knn Reduce the graph to keep only the neares neighbors. Defaults to 100.

d The distance function to determine the weights of the graph edges. Defaults to euclidean distances.

Implementation

Wraps around `layout_with_fr`, see there for details. The Fruchterman Reingold algorithm puts the data into a circle and puts connected points close to each other.

See Also

Other dimensionality reduction methods: `DRR-class`, `DiffusionMaps-class`, `DrL-class`, `FastICA-class`, `HLLE-class`, `Isomap-class`, `KamadaKawai-class`, `LLE-class`, `MDS-class`, `PCA-class`, `dimRedMethod-class`, `kPCA-class`, `nMDS-class`, `tSNE-class`

Examples

```
dat <- loadDataSet("Swiss Roll", n = 100)

## use the S4 Class directly:
fruchterman_reingold <- FruchtermanReingold()
pars <- fruchterman_reingold@stdpars
pars$knn <- 5
emb <- fruchterman_reingold@fun(dat, pars)
```

```
## simpler, use embed():
emb2 <- embed(dat, "FruchtermanReingold", knn = 5)

plot(emb, type = "2vars")
```

`getData` *Method getData*

Description

Extracts the data slot.

Usage

```
getData(object)
```

Arguments

`object`	The object to be converted.

`getDimRedData` *Method getDimRedData*

Description

Extract dimRedData.

Usage

```
getDimRedData(object, ...)
```

Arguments

`object`	The object to extract data from.
`...`	other arguments.

getMeta *Method getMeta*

Description

Extracts the meta slot.

Usage

```
getMeta(object, ...)
```

Arguments

object	The object to be converted.
...	other arguments.

getOrgData *Method getOrgData*

Description

Extract the Original data.

Usage

```
getOrgData(object, ...)
```

Arguments

object	The object to extract data from.
...	other arguments.

getPars *Method getPars*

Description

Extracts the pars slot.

Usage

```
getPars(object, ...)
```

Arguments

object	The object to be converted.
...	other arguments.

getRotationMatrix *getRotationMatrix*

Description

Extract the rotation matrix from dimRedResult objects derived from PCA and FastICA

Usage

```
getRotationMatrix(x)
```

Arguments

x	of type dimRedResult

Details

The data has to be pre-processed the same way as the method does, e.g. centering and/or scaling.

Value

a matrix

Examples

```
dat <- loadDataSet("Iris")

pca <- embed(dat, "PCA")
ica <- embed(dat, "FastICA")

rot_pca <- getRotationMatrix(pca)
rot_ica <- getRotationMatrix(ica)

scale(getData(dat), TRUE, FALSE) %*% rot_pca - getData(getDimRedData(pca))
scale(getData(dat), TRUE, FALSE) %*% rot_ica - getData(getDimRedData(ica))
```

HLLE-class *Hessian Locally Linear Embedding*

Description

An S4 Class implementing Hessian Locally Linear Embedding (HLLE)

Details

HLLE uses local hessians to approximate the curvines and is an extension to non-convex subsets in lowdimensional space.

Slots

`fun` A function that does the embedding and returns a dimRedResult object.

`stdpars` The standard parameters for the function.

General usage

Dimensionality reduction methods are S4 Classes that either be used directly, in which case they have to be initialized and a full list with parameters has to be handed to the `@fun()` slot, or the method name be passed to the embed function and parameters can be given to the `...`, in which case missing parameters will be replaced by the ones in the `@stdpars`.

Parameters

HLLE can take the following parameters:

knn neighborhood size

ndim number of output dimensions

Implementation

Own implementation, sticks to the algorithm in Donoho and Grimes (2003). Makes use of sparsity to speed up final embedding.

References

Donoho, D.L., Grimes, C., 2003. Hessian eigenmaps: Locally linear embedding techniques for high-dimensional data. PNAS 100, 5591-5596. doi:10.1073/pnas.1031596100

See Also

Other dimensionality reduction methods: `DRR-class`, `DiffusionMaps-class`, `DrL-class`, `FastICA-class`, `FruchtermanReingold-class`, `Isomap-class`, `KamadaKawai-class`, `LLE-class`, `MDS-class`, `PCA-class`, `dimRedMethod-class`, `kPCA-class`, `nMDS-class`, `tSNE-class`

Examples

```
dat <- loadDataSet("3D S Curve", n = 1500)

## directy use the S4 class:
hlle <- HLLE()
emb <- hlle@fun(dat, hlle@stdpars)

## using embed():
emb2 <- embed(dat, "HLLE", knn = 45)

plot(emb, type = "2vars")
plot(emb2, type = "2vars")
```

installSuggests *getSuggests*

Description

Install packages wich are suggested by dimRed.

Usage

```
installSuggests()
```

Details

By default dimRed will not install all the dependencies, because there are quite a lot and in case some of them are not available for your platform you will not be able to install dimRed without problems.

To solve this I provide a function which automatically installes all the suggested packages.

Examples

```
## Not run:
installSuggests()

## End(Not run)
```

Isomap-class *Isomap embedding*

Description

An S4 Class implementing the Isomap Algorithm

Details

The Isomap algorithm approximates a manifold using geodesic distances on a k nearest neighbor graph. Then classical scaling is performed on the resulting distance matrix.

Slots

`fun` A function that does the embedding and returns a dimRedResult object.

`stdpars` The standard parameters for the function.

General usage

Dimensionality reduction methods are S4 Classes that either be used directly, in which case they have to be initialized and a full list with parameters has to be handed to the `@fun()` slot, or the method name be passed to the embed function and parameters can be given to the `...`, in which case missing parameters will be replaced by the ones in the `@stdpars`.

Parameters

Isomap can take the following parameters:

knn The number of nearest neighbors in the graph. Defaults to 50.

ndim The number of embedding dimensions, defaults to 2.

Implementation

The dimRed package uses its own implementation of Isomap which also comes with an out of sample extension (known as landmark Isomap). The default Isomap algorithm scales computationally not very well, the implementation here uses `nn2` for a faster search of the neares neighbors. If data are too large it may be useful to fit a subsample of the data and use the out-of-sample extension for the other points.

See Also

Other dimensionality reduction methods: `DRR-class`, `DiffusionMaps-class`, `DrL-class`, `FastICA-class`, `FruchtermanReingold-class`, `HLLE-class`, `KamadaKawai-class`, `LLE-class`, `MDS-class`, `PCA-class`, `dimRedMethod-class`, `kPCA-class`, `nMDS-class`, `tSNE-class`

Examples

```
dat <- loadDataSet("3D S Curve", n = 500)

## use the S4 Class directly:
isomap <- Isomap()
emb <- isomap@fun(dat, isomap@stdpars)

## or simpler, use embed():
samp <- sample(nrow(dat), size = 200)
emb2 <- embed(dat[samp], "Isomap", mute = NULL, knn = 10)
emb3 <- emb2@apply(dat[-samp])

plot(emb2, type = "2vars")
plot(emb3, type = "2vars")
```

KamadaKawai-class *Graph Embedding via the Kamada Kawai Algorithm*

Description

An S4 Class implementing the Kamada Kawai Algorithm for graph embedding.

Details

Graph embedding algorithms se the data as a graph. Between the nodes of the graph exist attracting and repelling forces which can be modeled as electrical fields or springs connecting the nodes. The graph is then forced into a lower dimensional representation that tries to represent the forces betweent he nodes accurately by minimizing the total energy of the attracting and repelling forces.

Slots

`fun` A function that does the embedding and returns a dimRedResult object.

`stdpars` The standard parameters for the function.

General usage

Dimensionality reduction methods are S4 Classes that either be used directly, in which case they have to be initialized and a full list with parameters has to be handed to the `@fun()` slot, or the method name be passed to the embed function and parameters can be given to the `...`, in which case missing parameters will be replaced by the ones in the `@stdpars`.

Parameters

KamadaKawai can take the following parameters:

ndim The number of dimensions, defaults to 2. Can only be 2 or 3

knn Reduce the graph to keep only the neares neighbors. Defaults to 100.

d The distance function to determine the weights of the graph edges. Defaults to euclidean distances.

Implementation

Wraps around `layout_with_kk`. The parameters maxiter, epsilon and kkconst are set to the default values and cannot be set, this may change in a future release. The DimRed Package adds an extra sparsity parameter by constructing a knn graph which also may improve visualization quality.

See Also

Other dimensionality reduction methods: `DRR-class`, `DiffusionMaps-class`, `DrL-class`, `FastICA-class`, `FruchtermanReingold-class`, `HLLE-class`, `Isomap-class`, `LLE-class`, `MDS-class`, `PCA-class`, `dimRedMethod-class`, `kPCA-class`, `nMDS-class`, `tSNE-class`

Examples

```
dat <- loadDataSet("Swiss Roll", n = 500)
kamada_kawai <- KamadaKawai()
kk <- kamada_kawai@fun(dat, kamada_kawai@stdpars)

plot(kk@data@data)
```

---

kPCA-class *Kernel PCA*

Description

An S4 Class implementing Kernel PCA

Details

Kernel PCA is a nonlinear extension of PCA using kernel methods.

Slots

`fun` A function that does the embedding and returns a dimRedResult object.

`stdpars` The standard parameters for the function.

General usage

Dimensionality reduction methods are S4 Classes that either be used directly, in which case they have to be initialized and a full list with parameters has to be handed to the `@fun()` slot, or the method name be passed to the embed function and parameters can be given to the `...`, in which case missing parameters will be replaced by the ones in the `@stdpars`.

Parameters

Kernel PCA can take the following parameters:

ndim the number of output dimensions, defaults to 2

kernel The kernel function, either as a function or a character vector with the name of the kernel. Defaults to `"rbfdot"`

kpar A list with the parameters for the kernel function

Implementation

Wraps around kpca, but provides additionally forward and backward projections.

See Also

Other dimensionality reduction methods: DRR-class, DiffusionMaps-class, DrL-class, FastICA-class, FruchtermanReingold-class, HLLE-class, Isomap-class, KamadaKawai-class, LLE-class, MDS-class, PCA-class, dimRedMethod-class, nMDS-class, tSNE-class

Examples

```
## Not run:
dat <- loadDataSet("3D S Curve")

## use the S4 class directly:
kpca <- kPCA()
emb <- kpca@fun(dat, kpca@stdpars)

## simpler, use embed():
emb2 <- embed(dat, "kPCA")

plot(emb, type = "2vars")

## End(Not run)
```

LaplacianEigenmaps-class

Laplacian Eigenmaps

Description

An S4 Class implementing Laplacian Eigenmaps

Details

Laplacian Eigenmaps use a kernel and were originally developed to separate non-convex clusters under the name spectral clustering.

Slots

`fun` A function that does the embedding and returns a dimRedResult object.

`stdpars` The standard parameters for the function.

General usage

Dimensionality reduction methods are S4 Classes that either be used directly, in which case they have to be initialized and a full list with parameters has to be handed to the `@fun()` slot, or the method name be passed to the embed function and parameters can be given to the ..., in which case missing parameters will be replaced by the ones in the `@stdpars`.

Parameters

`LaplacianEigenmaps` can take the following parameters:

ndim the number of output dimensions.

sparse A character vector specifying hot to make the graph sparse, `"knn"` means that a K-nearest neighbor graph is constructed, `"eps"` an epsilon neighborhood graph is constructed, else a dense distance matrix is used.

knn The number of nearest neighbors to use for the knn graph.

eps The distance for the epsilon neighborhood graph.

t Parameter for the transformation of the distance matrix by $w = exp(-d^2/t)$, larger values give less weight to differences in distance, `t == Inf` treats all distances != 0 equally.

norm logical, should the normed laplacian be used?

Implementation

Wraps around `spec.emb`.

References

Belkin, M., Niyogi, P., 2003. Laplacian Eigenmaps for Dimensionality Reduction and Data Representation. Neural Computation 15, 1373.

Examples

```
dat <- loadDataSet("3D S Curve")
leim <- LaplacianEigenmaps()
emb <- leim@fun(dat, leim@stdpars)


plot(emb@data@data)
```

LCMC,dimRedResult-method

Method LCMC

Description

Calculates the Local Continuity Meta Criterion, which is `Q_NX` adjusted for random overlap inside the K-ary neighborhood.

Usage

```
## S4 method for signature 'dimRedResult'
LCMC(object)
```

Arguments

object	of class dimRedResult

See Also

Other Quality scores for dimensionality reduction: AUC_lnK_R_NX,dimRedResult-method, Q_NX,dimRedResult-method, Q_global,dimRedResult-method, Q_local,dimRedResult-method, R_NX,dimRedResult-method, cophenetic_correlation,dimRedResult-method, distance_correlation,dimRedResult-method, mean_R_NX,dimRedResult-method, quality,dimRedResult-method, reconstruction_error,dimRedResult-method, reconstruction_rmse,dimRedResult-method, total_correlation,dimRedResult-method

---

LLE-class *Locally Linear Embedding*

Description

An S4 Class implementing Locally Linear Embedding (LLE)

Details

LLE approximates the points in the manifold by linear combination of its neighbors. These linear combinations are the same inside the manifold and in highdimensional space.

Slots

`fun` A function that does the embedding and returns a dimRedResult object.

`stdpars` The standard parameters for the function.

General usage

Dimensionality reduction methods are S4 Classes that either be used directly, in which case they have to be initialized and a full list with parameters has to be handed to the `@fun()` slot, or the method name be passed to the embed function and parameters can be given to the `...`, in which case missing parameters will be replaced by the ones in the `@stdpars`.

Parameters

LLE can take the following parameters:

knn the number of neighbors for the knn graph., defaults to 50.

ndim the number of embedding dimensions, defaults to 2.

Implementation

Wraps around `lle`, only exposes the parameters `k` and `m`.

References

Roweis, S.T., Saul, L.K., 2000. Nonlinear Dimensionality Reduction by Locally Linear Embedding. Science 290, 2323-2326. doi:10.1126/science.290.5500.2323

See Also

Other dimensionality reduction methods: DRR-class, DiffusionMaps-class, DrL-class, FastICA-class, FruchtermanReingold-class, HLLE-class, Isomap-class, KamadaKawai-class, MDS-class, PCA-class, dimRedMethod-class, kPCA-class, nMDS-class, tSNE-class

Examples

```
dat <- loadDataSet("3D S Curve", n = 500)

## directy use the S4 class:
lle <- LLE()
emb <- lle@fun(dat, lle@stdpars)

## using embed():
emb2 <- embed(dat, "LLE", knn = 45)

plot(emb, type = "2vars")
plot(emb2, type = "2vars")
```

---

makeKNNgraph *makeKNNgraph*

Description

Create a K-nearest neighbor graph from data x. Uses nn2 as a fast way to find the neares neighbors.

Usage

```
makeKNNgraph(x, k, eps = 0, diag = FALSE)
```

Arguments

x	data, a matrix, observations in rows, dimensions in columns
k	the number of nearest neighbors.
eps	number, if `eps > 0` the KNN search is approximate, see nn2
diag	logical, if TRUE every edge of the returned graph will have an edge with weight 0 to itself.

Value

an object of type igraph with edge weight being the distances.

maximize_correlation,dimRedResult-method *Maximize Correlation with the Axes*

Description

Rotates the data in such a way that the correlation with the first naxes axes is maximized.

Usage

```
## S4 method for signature 'dimRedResult'
maximize_correlation(object,
  naxes = ncol(object@data@data), cor_method = "pearson")
```

Arguments

object	A dimRedResult object
naxes	the number of axes to optimize for.
cor_method	which correlation method to use

Details

Methods that do not use eigenvector decomposition, like t-SNE often do not align the data with axes according to the correlation of variables with the data. maximize_correlation uses the optimx package to rotate the data in such a way that the original variables have maximum correlation with the embedding axes.

MDS-class *Metric Dimensional Scaling*

Description

An S4 Class implementing classical scaling (MDS).

Details

MDS tries to maintain distances in high- and low-dimensional space, it has the advantage over PCA that arbitrary distance functions can be used, but it is computationally more demanding.

Slots

fun A function that does the embedding and returns a dimRedResult object.

stdpars The standard parameters for the function.

General usage

Dimensionality reduction methods are S4 Classes that either be used directly, in which case they have to be initialized and a full list with parameters has to be handed to the `@fun()` slot, or the method name be passed to the embed function and parameters can be given to the `...`, in which case missing parameters will be replaced by the ones in the `@stdpars`.

Parameters

MDS can take the following parameters:

ndim The number of dimensions.

d The function to calculate the distance matrix from the input coordinates, defaults to euclidean distances.

Implementation

Wraps around `cmdscale`. The implementation also provides an out-of-sample extension which is not completely optimized yet.

See Also

Other dimensionality reduction methods: `DRR-class`, `DiffusionMaps-class`, `DrL-class`, `FastICA-class`, `FruchtermanReingold-class`, `HLLE-class`, `Isomap-class`, `KamadaKawai-class`, `LLE-class`, `PCA-class`, `dimRedMethod-class`, `kPCA-class`, `nMDS-class`, `tSNE-class`

Examples

```
## Not run:
dat <- loadDataSet("3D S Curve")

## Use the S4 Class directly:
mds <- MDS()
emb <- mds@fun(dat, mds@stdpars)

## use embed():
emb2 <- embed(dat, "MDS", d = function(x) exp(stats::dist(x)))


plot(emb, type = "2vars")
plot(emb2, type = "2vars")

## End(Not run)
```

mean_R_NX,dimRedResult-method *Method mean_R_NX*

Description

Calculate the mean_R_NX score to assess the quality of a dimensionality reduction.

Usage

```
## S4 method for signature 'dimRedResult'
mean_R_NX(object)
```

Arguments

object	of class dimRedResult

See Also

Other Quality scores for dimensionality reduction: AUC_lnK_R_NX,dimRedResult-method, LCMC,dimRedResult-method, Q_NX,dimRedResult-method, Q_global,dimRedResult-method, Q_local,dimRedResult-method, R_NX,dimRedResult-method, cophenetic_correlation,dimRedResult-method, distance_correlation,dimRedResul quality,dimRedResult-method, reconstruction_error,dimRedResult-method, reconstruction_rmse,dimRedResul total_correlation,dimRedResult-method

mixColorRamps *Mixing color ramps*

Description

mix different color ramps

Usage

```
mixColorRamps(vars, ramps)

mixColor1Ramps(vars, ramps = colorRamp(c("blue", "black", "red")))

mixColor2Ramps(vars, ramps = list(colorRamp(c("blue", "green")),
  colorRamp(c("blue", "red"))))

mixColor3Ramps(vars, ramps = list(colorRamp(c("#001A00", "#00E600")),
  colorRamp(c("#00001A", "#0000E6")), colorRamp(c("#1A0000", "#E60000"))))
```

Arguments

vars	a list of variables
ramps	a list of color ramps, one for each variable.

Details

automatically create colors to represent a varying number of dimensions.

Examples

```
cols <- expand.grid(x = seq(0, 1, length.out = 10),
                    y = seq(0, 1, length.out = 10),
                    z = seq(0, 1, length.out = 10))
mixed <- mixColor3Ramps(cols)

## Not run:
library(rgl)
plot3d(cols$x, cols$y, cols$z, col = mixed, pch = 15)

cols <- expand.grid(x = seq(0, 1, length.out = 10),
                    y = seq(0, 1, length.out = 10))
mixed <- mixColor2Ramps(cols)

## End(Not run)

plot(cols$x, cols$y, col = mixed, pch = 15)
```

---

ndims *Method ndims*

Description

Extract the number of dimensions.

Usage

```
ndims(object, ...)
```

Arguments

object	To extract the number of dimensions from.
...	Arguments for further methods

nMDS-class *Non-Metric Dimensional Scaling*

Description

An S4 Class implementing Non-Metric Dimensional Scaling.

Details

A non-linear extension of MDS using monotonic regression

Slots

`fun` A function that does the embedding and returns a dimRedResult object.

`stdpars` The standard parameters for the function.

General usage

Dimensionality reduction methods are S4 Classes that either be used directly, in which case they have to be initialized and a full list with parameters has to be handed to the `@fun()` slot, or the method name be passed to the embed function and parameters can be given to the `...`, in which case missing parameters will be replaced by the ones in the `@stdpars`.

Parameters

nMDS can take the following parameters:

d A distance function.

ndim The number of embedding dimensions.

Implementation

Wraps around the `monoMDS`. For parameters that are not available here, the standard configuration is used.

See Also

Other dimensionality reduction methods: `DRR-class`, `DiffusionMaps-class`, `DrL-class`, `FastICA-class`, `FruchtermanReingold-class`, `HLLE-class`, `Isomap-class`, `KamadaKawai-class`, `LLE-class`, `MDS-class`, `PCA-class`, `dimRedMethod-class`, `kPCA-class`, `tSNE-class`

Examples

```
dat <- loadDataSet("3D S Curve", n = 1000)

## using the S4 classes:
nmds <- nMDS()
emb <- nmds@fun(dat, nmds@stdpars)


## using embed()
emb2 <- embed(dat, "nMDS", d = function(x) exp(dist(x)))


plot(emb, type = "2vars")
plot(emb2, type = "2vars")
```

`PCA-class` *Principal Component Analysis*

Description

S4 Class implementing PCA.

Details

PCA transforms the data in orthogonal components so that the first axis accounts for the larges variance in the data, all the following axes account for the highest variance under the constraint that they are orthogonal to the preceding axes. PCA is sensitive to the scaling of the variables. PCA is by far the fastest and simples method of dimensionality reduction and should probably always be applied as a baseline if other methods are tested.

Slots

`fun` A function that does the embedding and returns a dimRedResult object.

`stdpars` The standard parameters for the function.

General usage

Dimensionality reduction methods are S4 Classes that either be used directly, in which case they have to be initialized and a full list with parameters has to be handed to the `@fun()` slot, or the method name be passed to the embed function and parameters can be given to the ..., in which case missing parameters will be replaced by the ones in the `@stdpars`.

Parameters

PCA can take the following parameters:

ndim The number of output dimensions.

center logical, should the data be centered, defaults to TRUE.

scale. logical, should the data be scaled, defaults to FALSE.

Implementation

Wraps around prcomp. Because PCA can be reduced to a simple rotation, forward and backward projection functions are supplied. .

See Also

Other dimensionality reduction methods: DRR-class, DiffusionMaps-class, DrL-class, FastICA-class, FruchtermanReingold-class, HLLE-class, Isomap-class, KamadaKawai-class, LLE-class, MDS-class, dimRedMethod-class, kPCA-class, nMDS-class, tSNE-class

Examples

```
dat <- loadDataSet("Iris")

## using the S4 Class
pca <- PCA()
emb <- pca@fun(dat, pca@stdpars)

## using embed()
emb2 <- embed(dat, "PCA")

plot(emb, type = "2vars")
plot(emb@inverse(emb@data), type = "3vars")
```

---

plot *Plotting of dimRed* objects*

Description

Plots a object of class dimRedResult and dimRedData. For the documentation of the plotting function in base see here: plot.default.

Usage

```
plot(x, y, ...)

## S4 method for signature 'dimRedData,ANY'
plot(x, type = "pairs",
  vars = seq_len(ncol(x@data)), col = seq_len(min(3, ncol(x@meta))), ...)
```

```
## S4 method for signature 'dimRedResult,ANY'
plot(x, type = "pairs",
  vars = seq_len(ncol(x@data@data)), col = seq_len(min(3,
  ncol(x@data@meta))), ...)
```

Arguments

x	dimRedResult/dimRedData class, e.g. output of embedded/loadDataSet
y	Ignored
...	handed over to the underlying plotting function.
type	plot type, one of c("pairs", "parallel", "2vars","3vars", "3varsrgl")
vars	the axes of the embedding to use for plotting
col	the columns of the meta slot to use for coloring, can be referenced as the column names or number of x@data

Details

Plotting functions for the classes usind in dimRed. they are intended to give a quick overview over the results, so they are somewhat inflexible, e.g. it is hard to modify color scales or plotting parameters.

If you require more control over plotting, it is better to convert the object to a data.frame first and use the standard functions for plotting.

Methods (by class)

- x = dimRedData,y = ANY: Ploting of dimRedData objects
- x = dimRedResult,y = ANY: Ploting of dimRedResult objects.

Examples

```
scurve = loadDataSet("3D S Curve")
plot(scurve, type = "pairs", main = "pairs plot of S curve")
plot(scurve, type = "parpl")
plot(scurve, type = "2vars", vars = c("y", "z"))
plot(scurve, type = "3vars")
```

---

plot_R_NX *plot_R_NX*

Description

Plot the R_NX curve for different embeddings. Takes a list of dimRedResult objects as input. Also the Area under the curve values are computed for logarithmic K (AUC_lnK) and appear in the legend.

Usage

```
plot_R_NX(x)
```

Arguments

x	a list of dimRedResult objects. The names of the list will appear in the legend with the AUC_lnK value.

Value

A ggplot object, the design can be changed by appending `theme(...)`

Examples

```
## define which methods to apply
embed_methods <- c("Isomap", "PCA")
## load test data set
data_set <- loadDataSet("3D S Curve", n = 1000)
## apply dimensionality reduction
data_emb <- lapply(embed_methods, function(x) embed(data_set, x))
names(data_emb) <- embed_methods
## plot the R_NX curves:
plot_R_NX(data_emb) +
    ggplot2::theme(legend.title = ggplot2::element_blank(),
                   legend.position = c(0.5, 0.1),
                   legend.justification = c(0.5, 0.1))
```

---

print *Method print*

Description

Imports the print method into the package namespace.

Usage

```
print(x, ...)
```

Arguments

x	The object to be printed.
...	Other arguments for printing.

quality,dimRedResult-method
Quality Criteria for dimensionality reduction.

Description

A collection of functions to compute quality measures on dimRedResult objects.

Usage

```
## S4 method for signature 'dimRedResult'
quality(.data, .method = dimRedQualityList(),
  .mute = character(0), ...)

dimRedQualityList()
```

Arguments

.data	object of class dimRedResult
.method	character vector naming one of the methods
.mute	what output from the embedding method should be muted.
...	the pameters, internally passed as a list to the quality method as pars = list(...)

Value

a number

Methods (by class)

- dimRedResult: Calculate a quality index from a dimRedResult object.

Implemented methods

Method must be one of "Q_local", "Q_global","mean_R_NX", "total_correlation","cophenetic_correlation",

Rank based criteria

Q_local, Q_global, and mean_R_nx are quality criteria based on the Co-ranking matrix. Q_local and Q_global determine the local/global quality of the embedding, while mean_R_nx determines the quality of the overall embedding. They are parameter free and return a single number. The object must include the original data. The number returns is in the range [0, 1], higher values mean a better local/global embedding.

Correlation based criteria

`total_correlation` calculates the sum of the mean squared correlations of the original axes with the axes in reduced dimensions, because some methods do not care about correlations with axes, there is an option to rotate data in reduced space to maximize this criterium. The number may be greater than one if more dimensions are summed up.

`cophenetic_correlation` calculate the correlation between the lower triangles of distance matrices, the correlation and distance methods may be specified. The result is in range [-1, 1].

`distance_correlation` measures the independes of samples by calculating the correlation of distances. For details see `dcor`.

Reconstruction error

`reconstruction_rmse` calculates the root mean squared error of the reconstrucion. `object` requires an inverse function.

Author(s)

Guido Kraemer

References

Lueks, W., Mokbel, B., Biehl, M., Hammer, B., 2011. How to Evaluate Dimensionality Reduction? - Improving the Co-ranking Matrix. arXiv:1110.3917 [cs].

Szekely, G.J., Rizzo, M.L., Bakirov, N.K., 2007. Measuring and testing dependence by correlation of distances. Ann. Statist. 35, 2769-2794. doi:10.1214/009053607000000505

Lee, J.A., Peluffo-Ordonez, D.H., Verleysen, M., 2015. Multi-scale similarities in stochastic neighbour embedding: Reducing dimensionality while preserving both local and global structure. Neurocomputing, 169, 246-261. doi:10.1016/j.neucom.2014.12.095

See Also

Other Quality scores for dimensionality reduction: `AUC_lnK_R_NX,dimRedResult-method`, `LCMC,dimRedResult-method`, `Q_NX,dimRedResult-method`, `Q_global,dimRedResult-method`, `Q_local,dimRedResult-method`, `R_NX,dimRedResult-method`, `cophenetic_correlation,dimRedResult-method`, `distance_correlation,dimRedResul`
`mean_R_NX,dimRedResult-method`, `reconstruction_error,dimRedResult-method`, `reconstruction_rmse,dimRedRes`
`total_correlation,dimRedResult-method`

Examples

```
## Not run:
embed_methods <- dimRedMethodList()
quality_methods <- dimRedQualityList()
scurve <- loadDataSet("3D S Curve", n = 500)

quality_results <- matrix(NA, length(embed_methods), length(quality_methods),
                          dimnames = list(embed_methods, quality_methods))
embedded_data <- list()

for (e in embed_methods) {
```

```
  message("embedding: ", e)
  embedded_data[[e]] <- embed(scurve, e, .mute = c("message", "output"))
  for (q in quality_methods) {
    message("  quality: ", q)
    quality_results[e, q] <- tryCatch(
      quality(embedded_data[[e]], q),
      error = function (e) NA
    )
  }
}

print(quality_results)

## End(Not run)
```

`Q_global,dimRedResult-method`
Method Q_global

Description

Calculate the Q_global score to assess the quality of a dimensionality reduction.

Usage

```
## S4 method for signature 'dimRedResult'
Q_global(object)
```

Arguments

`object`	of class dimRedResult

See Also

Other Quality scores for dimensionality reduction: `AUC_lnK_R_NX,dimRedResult-method`, `LCMC,dimRedResult-method`, `Q_NX,dimRedResult-method`, `Q_local,dimRedResult-method`, `R_NX,dimRedResult-method`, `cophenetic_correlation`, `distance_correlation,dimRedResult-method`, `mean_R_NX,dimRedResult-method`, `quality,dimRedResult-method`, `reconstruction_error,dimRedResult-method`, `reconstruction_rmse,dimRedResult-method`, `total_correlation,dimRedResult-method`

`Q_local,dimRedResult-method`
Method Q_local

Description

Calculate the Q_local score to assess the quality of a dimensionality reduction.

Usage

```
## S4 method for signature 'dimRedResult'
Q_local(object)
```

Arguments

`object`	of class dimRedResult

See Also

Other Quality scores for dimensionality reduction: `AUC_lnK_R_NX,dimRedResult-method`, `LCMC,dimRedResult-method`, `Q_NX,dimRedResult-method`, `Q_global,dimRedResult-method`, `R_NX,dimRedResult-method`, `cophenetic_correlation,dimRedResult-method`, `distance_correlation,dimRedResult-method`, `mean_R_NX,dimRedResult-method`, `quality,dimRedResult-method`, `reconstruction_error,dimRedResult-method`, `reconstruction_rmse,dimRedResult-method`, `total_correlation,dimRedResult-method`

`Q_NX,dimRedResult-method`
Method Q_NX

Description

Calculate the Q_NX score (Chen & Buja 2006, the notation in the publication is M_k). Which is the fraction of points that remain inside the same K-ary neighborhood in high and low dimensional space.

Usage

```
## S4 method for signature 'dimRedResult'
Q_NX(object)
```

Arguments

`object`	of class dimRedResult

See Also

Other Quality scores for dimensionality reduction: AUC_lnK_R_NX,dimRedResult-method, LCMC,dimRedResult-method, Q_global,dimRedResult-method, Q_local,dimRedResult-method, R_NX,dimRedResult-method, cophenetic_correlation,dimRedResult-method, distance_correlation,dimRedResult-method, mean_R_NX,dimRedResult-method, quality,dimRedResult-method, reconstruction_error,dimRedResult-method, reconstruction_rmse,dimRedResult-method, total_correlation,dimRedResult-method

---

reconstruction_error,dimRedResult-method

Method reconstruction_error

Description

Calculate the error using only the first n dimensions of the embedded data. error_fun can either be one of c("rmse", "mae") to calculate the root mean square error or the mean absolute error respectively, or a function that takes to equally sized vectors as input and returns a single number as output.

Usage

```
## S4 method for signature 'dimRedResult'
reconstruction_error(object,
  n = seq_len(ndims(object)), error_fun = "rmse")
```

Arguments

object	of class dimRedResult
n	a positive integer or vector of integers <= ndims(object)
error_fun	a function or string indicating an error function.

Value

a vector of number with the same length as n with the

Author(s)

Guido Kraemer

See Also

Other Quality scores for dimensionality reduction: AUC_lnK_R_NX,dimRedResult-method, LCMC,dimRedResult-method, Q_NX,dimRedResult-method, Q_global,dimRedResult-method, Q_local,dimRedResult-method, R_NX,dimRedResult-method, cophenetic_correlation,dimRedResult-method, distance_correlation,dimRedResul mean_R_NX,dimRedResult-method, quality,dimRedResult-method, reconstruction_rmse,dimRedResult-method, total_correlation,dimRedResult-method

Examples

```
## Not run:
ir <- loadDataSet("Iris")
ir.drr <- embed(ir, "DRR", ndim = ndims(ir))
ir.pca <- embed(ir, "PCA", ndim = ndims(ir))

rmse <- data.frame(
  rmse_drr = reconstruction_error(ir.drr),
  rmse_pca = reconstruction_error(ir.pca)
)

matplot(rmse, type = "l")
plot(ir)
plot(ir.drr)
plot(ir.pca)

## End(Not run)
```

---

reconstruction_rmse,dimRedResult-method

Method reconstruction_rmse

Description

Calculate the reconstruction root mean squared error a dimensionality reduction, the method must have an inverse mapping.

Usage

```
## S4 method for signature 'dimRedResult'
reconstruction_rmse(object)
```

Arguments

object	of class dimRedResult

See Also

Other Quality scores for dimensionality reduction: AUC_lnK_R_NX,dimRedResult-method, LCMC,dimRedResult-method, Q_NX,dimRedResult-method, Q_global,dimRedResult-method, Q_local,dimRedResult-method, R_NX,dimRedResult-method, cophenetic_correlation,dimRedResult-method, distance_correlation,dimRedResul mean_R_NX,dimRedResult-method, quality,dimRedResult-method, reconstruction_error,dimRedResult-method, total_correlation,dimRedResult-method

R_NX,dimRedResult-method

Method R_NX

Description

Calculate the R_NX score from Lee et. al. (2013) which shows the neighborhood preservation for the Kth nearest neighbors, corrected for random point distributions and scaled to range [0, 1].

Usage

```
## S4 method for signature 'dimRedResult'
R_NX(object)
```

Arguments

object	of class dimRedResult

See Also

Other Quality scores for dimensionality reduction: AUC_lnK_R_NX,dimRedResult-method, LCMC,dimRedResult-method, Q_NX,dimRedResult-method, Q_global,dimRedResult-method, Q_local,dimRedResult-method, cophenetic_correlation,dimRedResult-method, distance_correlation,dimRedResult-method, mean_R_NX,dimRedResult-method, quality,dimRedResult-method, reconstruction_error,dimRedResult-method, reconstruction_rmse,dimRedResult-method, total_correlation,dimRedResult-method

total_correlation,dimRedResult-method

Method total_correlation

Description

Calculate the total correlation of the variables with the axes to assess the quality of a dimensionality reduction.

Usage

```
## S4 method for signature 'dimRedResult'
total_correlation(object, naxes = ndims(object),
  cor_method = "pearson", is.rotated = FALSE)
```

Arguments

object	of class dimRedResult
naxes	the number of axes to use for optimization.
cor_method	the correlation method to use.
is.rotated	if FALSE the object is rotated.

See Also

Other Quality scores for dimensionality reduction: AUC_lnK_R_NX,dimRedResult-method, LCMC,dimRedResult-method, Q_NX,dimRedResult-method, Q_global,dimRedResult-method, Q_local,dimRedResult-method, R_NX,dimRedResult-method, cophenetic_correlation,dimRedResult-method, distance_correlation,dimRedResu mean_R_NX,dimRedResult-method, quality,dimRedResult-method, reconstruction_error,dimRedResult-method, reconstruction_rmse,dimRedResult-method

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tSNE-class *t-Distributed Stochastic Neighborhood Embedding*

Description

An S4 Class for t-SNE.

Details

t-SNE is a method that uses Kullback-Leibler divergence between the distance matrices in high and low-dimensional space to embed the data. The method is very well suited to visualize complex structures in low dimensions.

Slots

`fun` A function that does the embedding and returns a dimRedResult object.

`stdpars` The standard parameters for the function.

General usage

Dimensionality reduction methods are S4 Classes that either be used directly, in which case they have to be initialized and a full list with parameters has to be handed to the `@fun()` slot, or the method name be passed to the embed function and parameters can be given to the `...`, in which case missing parameters will be replaced by the ones in the `@stdpars`.

Parameters

t-SNE can take the following parameters:

d A distance function, defaults to euclidean distances

perplexity The perplexity parameter, roughly equivalent to neighborhood size.

theta Approximation for the nearest neighbour search, large values are more inaccurate.

ndim The number of embedding dimensions.

Implementation

Wraps around Rtsne, which is very well documented. Setting `theta = 0` does a normal t-SNE, larger values for `theta < 1` use the Barnes-Hut algorithm which scales much nicer with data size. Larger values for perplexity take larger neighborhoods into account.

References

Maaten, L. van der, 2014. Accelerating t-SNE using Tree-Based Algorithms. Journal of Machine Learning Research 15, 3221-3245.

van der Maaten, L., Hinton, G., 2008. Visualizing Data using t-SNE. J. Mach. Learn. Res. 9, 2579-2605.

See Also

Other dimensionality reduction methods: DRR-class, DiffusionMaps-class, DrL-class, FastICA-class, FruchtermanReingold-class, HLLE-class, Isomap-class, KamadaKawai-class, LLE-class, MDS-class, PCA-class, dimRedMethod-class, kPCA-class, nMDS-class

Examples

```
## Not run:
dat <- loadDataSet("3D S Curve", n = 500)

## using the S4 class directly:
tsne <- tSNE()
emb <- tsne@fun(dat, tsne@stdpars)

## using embed()
emb2 <- embed(dat, "tSNE", perplexity = 80)

plot(emb, type = "2vars")
plot(emb2, type = "2vars")

## End(Not run)
```

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