Package ‘mixKernel’

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Type    Package
Title   Omics Data Integration Using Kernel Methods
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Imports vegan, phyloseq, corrplot, psych, quadprog, LDRTools, Matrix, methods
Maintainer Jerome Mariette <jerome.mariette@inrae.fr>
Author   Jerome Mariette [aut, cre],
          Celine Brouard [aut],
          Remi Flamary [aut],
          Nathalie Vialaneix [aut]
Description Kernel-based methods are powerful methods for integrating
heterogeneous types of data. mixKernel aims at providing methods to combine
kernel for unsupervised exploratory analysis. Different solutions are
provided to compute a meta-kernel, in a consensus way or in a way that
best preserves the original topology of the data. mixKernel also integrates
kernel PCA to visualize similarities between samples in a non linear space
and from the multiple source point of view. Functions to assess and display
important variables are also provided in the package. Jerome Mariette and
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)
**R topics documented:**

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**Description**

Center and scale a dataset.

**Usage**

`center.scale(X)`

**Arguments**

- `X` a numeric matrix (or data frame) to center and scaled. NAs not allowed.

**Value**

`center.scale` returns a centered and scaled matrix.

**Author(s)**

Celine Brouard <celine.brouard@inrae.fr>
Jerome Mariette <jerome.mariette@inrae.fr>
Nathalie Villa-Vialaneix <nathalie.villa-vialaneix@inrae.fr>

**See Also**

`compute.kernel`, `combine.kernels`
Examples

```r
data("nutrimouse")
## Not run:
nutrimouse.sc <- center.scale(nutrimouse$gene)
## End(Not run)
```

### Description

Compute cosine from Frobenius norm between kernels and display the corresponding correlation plot.

### Usage

```r
cim.kernel(..., scale = TRUE,
method = c("circle", "square", "number", "shade", "color", "pie"))
```

### Arguments

- `...`: list of kernels (called 'blocks') computed on different datasets and measured on the same samples.
- `scale`: boolean. If `scale = TRUE`, each block is standardized to zero mean and unit variance and cosine normalization is performed on the kernel. Default: `TRUE`.
- `method`: character. The visualization method to be used. Currently, seven methods are supported (see Details).

### Details

The displayed similarities are the kernel generalization of the RV-coefficient described in Lavit et al., 1994.

The plot is displayed using the `corrplot` package. Seven visualization methods are implemented: "circle" (default), "square", "number", "pie", "shade" and "color". Circle and square areas are proportional to the absolute value of corresponding similarities coefficients.

### Value

`cim.kernel` returns a matrix containing the cosine from Frobenius norm between kernels.

### Author(s)

Jerome Mariette <jerome.mariette@inrae.fr>

Nathalie Vialaneix <nathalie.vialaneix@inrae.fr>
combine.kernels

Combine multiple kernels into a meta-kernel

Description

Compute multiple kernels into a single meta-kernel

Usage

combine.kernels(..., scale = TRUE,
               method = c("full-UMKL", "STATIS-UMKL", "sparse-UMKL"), knn = 5,
               rho = 20)

Arguments

... list of kernels (called 'blocks') computed on different datasets and measured on
      the same samples.

scale boolean. If scale = TRUE, each block is standardized to zero mean and unit
         variance and cosine normalization is performed on the kernel. Default: TRUE.

method character. Which method should be used to compute the meta-kernel. Default:
           "full-UMKL".

Examples

data(TARAoceans)

# compute one kernel per dataset
phychem.kernel <- compute.kernel(TARAoceans$phychem, kernel.func = "linear")
pro.phylo.kernel <- compute.kernel(TARAoceans$pro.phylo, kernel.func = "abundance")
pro.NOGs.kernel <- compute.kernel(TARAoceans$pro.NOGs, kernel.func = "abundance")

# display similarities between kernels

cim.kernel(phychem = phychem.kernel,
            pro.phylo = pro.phylo.kernel,
            pro.NOGs = pro.NOGs.kernel,
            method = "square")

References


See Also
compute.kernel
**Details**

The arguments method allows to specify the Unsupervised Multiple Kernel Learning (UMKL) method to use:

- "STATIS-UMKL": combines input kernels into the best consensus of all kernels;
- "full-UMKL": computes a kernel that minimizes the distortion between the meta-kernel and the k-NN graphs obtained from all input kernels;
- "sparse-UMKL": a sparse variant of the "full-UMKL" approach.

**Value**

combine.kernels returns an object of classes "kernel" and "metaKernel", a list that contains the following components:

- kernel: the computed meta-kernel matrix;
- X: the dataset from which the kernel has been computed, as given by the function compute.kernel. Can be NULL if a kernel matrix was passed to this function;
- weights: a vector containing the weights used to combine the kernels.

**References**


**Author(s)**

Jerome Mariette <jerome.mariette@inrae.fr>
Nathalie Vialaneix <nathalie.vialaneix@inrae.fr>

**See Also**

compute.kernel, kernel.pca

**Examples**

data(TARAoceans)

# compute one kernel per dataset
phychem.kernel <- compute.kernel(TARAoceans$phychem, kernel.func = "linear")
pro.phylo.kernel <- compute.kernel(TARAoceans$pro.phylo, kernel.func = "abundance")
pro.NOGs.kernel <- compute.kernel(TARAoceans$pro.NOGs, kernel.func = "abundance")

# compute the meta kernel
compute.kernel <- combine.kernels(phychem = phychem.kernel,  
                            pro.phylo = pro.phylo.kernel,  
                            pro.NOGs = pro.NOGs.kernel,  
                            method = "full-UMKL")

compute.kernel Compute a kernel

Description
Compute a kernel from a given data matrix.

Usage

compute.kernel(X, kernel.func = "linear", ..., test.pos.semidef = FALSE)

Arguments

   X           a numeric matrix (or data frame) used to compute the kernel. NAs not allowed.
   kernel.func the kernel function to use. This parameter can be set to any user defined kernel function. Widely used kernel functions are pre-implemented, that can be used by setting kernel.func to one of the following strings: "kidentity", "abundance", "linear", "gaussian.radial.basis", "poisson" or "phylogenetic". Default: "linear".
   ...         the kernel function arguments. Valid parameters for pre-implemented kernels are:
   • phylogenetic.tree ("phylogenetic"): an instance of phylo-class that contains a phylogenetic tree (required).
   • scale ("linear" or "gaussian.radial.basis"): logical. Should the variables be scaled to unit variance prior the kernel computation? Default: TRUE.
   • sigma ("gaussian.radial.basis"): double. The inverse kernel width used by "gaussian.radial.basis".
   • method ("phylogenetic" or "abundance"): character. Can be "unifrac" or "wunifrac" for "phylogenetic". Which dissimilarity to use for "abundance": one of "bray", "euclidean", "canberra", "manhattan", "kulczynski", "jaccard", "gower", "altGower", "morisita", "horn", "mountford", "raup", "binomial", "chao" and "cao".
   • normalization ("poisson"): character. Can be "deseq" (more robust), "mle" (less robust) or "quantile".

   test.pos.semidef boolean. If test.pos.semidef = TRUE, the resulting matrix is tested to be positive-semidefinite.
kernel.pca

Value
compute.kernel returns an object of classes "kernel", a list that contains the following components:

kernel : the computed kernel matrix.
X : the original dataset. If "kidentity", X is set to NULL.
kernel.func : the kernel function used.
kernel.args : the arguments used to compute the kernel.

Author(s)
Jerome Mariette <jerome.mariette@inrae.fr>
Nathalie Vialaneix <nathalie.vialaneix@inrae.fr>

References

See Also
combine.kernels, kernel.pca

Examples
data(TARAoceans)
pro.NOGs.kernel <- compute.kernel(TARAoceans$pro.NOGs, kernel.func = "abundance")

kernel.pca

Kernel Principal Components Analysis

Description
Performs a kernel PCA.

Usage
kernel.pca(K, ncomp = nrow(K$kernel))
kernel.pca

Arguments

K a kernel object obtained using either compute.kernel or combine.kernels.
ncomp integer. Indicates the number of components to return.

Value

kernel.pca returns an object of classes "kernel.pca" and "pca", which is a list containing the following entries:

- ncomp: the number of principal components;
- X: the input kernel matrix;
- kernel: the input kernel object provided by the user;
- sdev: the singular values (square root of the eigenvalues);
- rotation: the matrix of variable loadings (i.e., a matrix whose columns contain the eigenvectors);
- loadings: same as 'rotation' to keep the mixOmics spirit;
- x: same as 'rotation' to keep the mixOmics spirit;

References


Author(s)

Jerome Mariette <jerome.mariette@inrae.fr>
Nathalie Vialaneix <nathalie.vialaneix@inrae.fr>

See Also

compute.kernel, combine.kernels

Examples

data(TARAoceans)
phychem.kernel <- compute.kernel(TARAoceans$phychem, kernel.func = "linear")
kernel.pca.result <- kernel.pca(phychem.kernel, ncomp = 3)
**kernel.pca.permute**

Assess variable importance

---

**Description**

Assess importance of variables on a given PC component by computing the Crone-Crosby distance between original sample positions and sample positions obtained by a random permutation of the variables.

**Usage**

```r
kernel.pca.permute(kpca.result, ncomp = 1, ..., directory = NULL)
```

**Arguments**

- `kpca.result`: a kernel.pca object returned by the `kernel.pca` function.
- `ncomp`: integer. Number of KPCA components used to compute the importance. Default: 1.
- `...`: list of character vectors. The parameter name must be the kernel name to be considered for permutation of variables. Provided vectors length has to be equal to the number of variables of the input dataset. A kernel is performed on each unique variables values. Crone-Crosby distances are computed on each KPCA performed on resulted kernels or meta-kernels and can be displayed using the `plotVar.kernel.pca`.
- `directory`: character. To limit computational burden, this argument allows to store / read temporary computed kernels.

**Value**

`kernel.pca.permute` returns a copy of the input `kpca.result` results and add values in the three entries: `cc.distances`, `cc.variables` and `cc.blocks`.

**References**


**Author(s)**

Jerome Mariette <jerome.mariette@inrae.fr>
Nathalie Vialaneix <nathalie.vialaneix@inrae.fr>

**See Also**

`compute.kernel`, `kernel.pca`, `plotVar.kernel.pca`
Examples

```r
data(TARAoceans)

# compute one kernel for the psychem dataset
phychem.kernel <- compute.kernel(TARAoceans$phychem, kernel.func = "linear")
# perform a KPCA
kernel.pca.result <- kernel.pca(phychem.kernel)

# compute importance for all variables in this kernel
kernel.pca.result <- kernel.pca.permute(kernel.pca.result, phychem = colnames(TARAoceans$phychem))
```

mixKernel.users.guide  View mixKernel User’s Guide

Description

Find the location of the mixKernel User’s Guide and optionally opens it

Usage

```r
mixKernel.users.guide(html = TRUE, view = html)
```

Arguments

- `html` logical. Should the document returned by the function be the compiled PDF or the Rmd source. Default to `TRUE`
- `view` logical. Should the document be opened using the default HTML viewer? Default to `html`. It has no effect if `html = FALSE`

Details

If the operating system is not Windows, then the HTML viewer used is that given by `Sys.getenv("R_BROWSER")`. The HTML viewer can be changed using `Sys.setenv(R_BROWSER = )`.

Value

Character string giving the file location. If `html = TRUE` and `view = TRUE`, the HTML document reader is started and the User’s Guide is opened in it.

Author(s)

Jerome Mariette <jerome.mariette@inrae.fr>
Nathalie Vialaneix <nathalie.vialaneix@inrae.fr>

Examples

```r
mixKernel.users.guide(view = FALSE)
mixKernel.users.guide(html = FALSE)
## Not run: mixKernel.users.guide()
```
Description

Provides a representation of variable importance in kernel PCA.

Usage

plotVar.kernel.pca(object, blocks = unique(object$cc.blocks), ndisplay = 5, ncol = 2, ...)

Arguments

object : a kernel.pca object returned by kernel.pca.
blocks a numerical vector indicating the block variables to display.
ndisplay integer. The number of important variables per blocks shown in the representation. Default: 5.
ncol integer. Each block of variables is displayed in a separate subfigure. ncol sets the number of columns for the global figure. Default: 2.
... external arguments.

Details

plotVar.kernel.pca produces a barplot for each block. The variables for which the importance has been computed with kernel.pca.permute are displayed. The representation is limited to the ndisplay most important variables.

References


Author(s)

Jerome Mariette <jerome.mariette@inrae.fr>
Nathalie Vialaneix <nathalie.vialaneix@inrae.fr>

See Also

kernel.pca, kernel.pca.permute
Examples

```r
data(TARAoceans)

# compute one kernel for the phychem dataset
phychem.kernel <- compute.kernel(TARAoceans$phychem, kernel.func = "linear")
# perform a KPCA
kernel.pca.result <- kernel.pca(phychem.kernel)
# compute importance for all variables in this kernel
kernel.pca.result <- kernel.pca.permute(kernel.pca.result, phychem = colnames(TARAoceans$phychem))

## Not run: plotVar.kernel.pca(kernel.pca.result, ndisplay = 10)
```

---

**select.features**

Select features using supervised or unsupervised kernel method. A supervised features selection method is computed if Y is provided.

**Description**

Select features using supervised or unsupervised kernel method. A supervised features selection method is computed if Y is provided.

**Usage**

```r
select.features(X, Y=NULL, kx.func=c("linear", "gaussian.radial.basis", "bray"),
    ky.func=c("linear", "gaussian.radial.basis"), keepX=NULL,
    method=c("kernel", "kpca", "graph"),
    lambda=NULL, n_components=2, Lg=NULL,
    mu=1, max_iter=100, nstep=50, ...)
```

**Arguments**

- **X**
  
a numeric matrix (or data frame) used to select variables. NAs not allowed.

- **Y**
  
a numeric matrix (or data frame) used to select variables. NAs not allowed.

- **kx.func**
  
the kernel function name to use on X. Widely used kernel functions are pre- implemented, and can be directly used by setting kx.func to one of the following strings: "linear", "gaussian.radial.basis" or "bray". Default: "linear". If Y is provided, the kernel "bray" is not allowed.

- **ky.func**
  
the kernel function name to use on Y. Available kernels are: "linear", and "gaussian.radial.basis". Default: "linear". This value is ignored when Y is not provided.

- **keepX**
  
the number of variables to select.

- **method**
  
the method to use. Either an unsupervised variable selection method ("kernel"), a kernel PCA oriented variable selection method ("kpca") or a structure driven variable selection selection ("graph"). Default: "kernel".

- **lambda**
  
the penalization parameter that controls the trade-off between the minimization of the distorsion and the sparsity of the solution parameter.
select.features

n_components  how many principal components should be used with method "kpca". Required with method "kpca". Default: 2.

Lg  the Laplacian matrix of the graph representing relations between the input dataset variables. Required with method "graph".

mu  the penalization parameter that controls the trade-off between the the distorsion and the influence of the graph. Default: 1.

max_iter  the maximum number of iterations. Default: 100.

nstep  the number of values used for the regularization path. Default: 50.

...  the kernel function arguments. In particular sigma("gaussian.radial.basis"): double. The inverse kernel width used by "gaussian.radial.basis".

Value

ukfs returns a vector of sorted selected features indexes.

Author(s)

Celine Brouard <celine.brouard@inrae.fr>
Jerome Mariette <jerome.mariette@inrae.fr>
Nathalie Villa-Vialaneix <nathalie.villa-vialaneix@inrae.fr>

References


See Also

compute.kernel

Examples

data("Koren.16S")
## Not run:
sf.res <- select.features(Koren.16S$data.raw, kx.func = "bray", lambda=1,
 keepX=40, nstep=1)
colnames(Koren.16S$data.raw)[sf.res]
## End(Not run)
data("nutrimouse")
## Not run:
grb.func = "gaussian.radial.basis"
genes = center.scale(nutrimouse$gene)
lipids = center.scale(nutrimouse$lipid)
sf.res <- select.features(genes, lipids, kx.func = grb.func, ky.func = grb.func,
 keepX = 40)
colnames(nutrimouse$gene)[sf.res]
## End(Not run)
Description

The TARA Oceans expedition facilitated the study of plankton communities by providing oceans metagenomic data combined with environmental measures to the scientific community. This dataset focuses on 139 prokaryotic-enriched samples collected from 68 stations and spread across three depth layers: the surface (SRF), the deep chlorophyll maximum (DCM) layer and the mesopelagic (MES) zones. Samples were located in height different oceans or seas: Indian Ocean (IO), Mediterranean Sea (MS), North Atlantic Ocean (NAO), North Pacific Ocean (NPO), Red Sea (RS), South Atlantic Ocean (SAO), South Pacific Ocean (SPO) and South Ocean (SO). Here, only a subset of the original data is provided (1% of the 35,650 prokaryotic operational taxonomic units (OTUs) and of the 39,246 bacterial genes (NOGs) (selected at random).

Usage

data(TARAoceans)

Format

A list containing the following components:

- **phychem** data matrix with 139 rows and 22 columns. Each row represents a sample and each column an environmental variable.
- **pro.phylo** data matrix with 139 rows (samples) and 356 columns (prokaryotic OTUs).
- **taxonomy** data matrix with 356 rows (prokaryotic OTUs) and 6 columns indicating the taxonomy of each OTU.
- **phylogenetic.tree** a phylo object (see package 'ape') representing the prokaryotic OTUs phylogenetic tree.
- **pro.NOGs** data matrix with 139 rows (samples) and 638 columns (NOGs).
- **sample** a list containing three following entries (all three are character vectors): name (sample name), ocean (oceanic region of the sample) and depth (sample depth).

References


Source

The raw data were downloaded from [http://ocean-microbiome.embl.de/companion.html](http://ocean-microbiome.embl.de/companion.html).
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