

Package ‘MRS’

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Type Package

Title Multi-Resolution Scanning for Cross-Sample Differences

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Description An implementation of the MRS algorithm for comparison across distributions, as described in Jacopo Soriano, Li Ma (2017) <[doi:10.1111/rssb.12180](https://doi.org/10.1111/rssb.12180)>.

The model is based on a nonparametric process taking the form of a Markov model that transitions between a “null” and an “alternative” state on a multi-resolution partition tree of the sample space.

MRS effectively detects and characterizes a variety of underlying differences. These differences can be visualized using several plotting functions.

License GPL (>= 3)

Imports Rcpp (>= 0.11.0), igraph, methods

Suggests KernSmooth

LinkingTo Rcpp, RcppArmadillo

NeedsCompilation yes

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andova *Multi Resolution Scanning for one-way ANDOVA using the multi-scale Beta-Binomial model*

Description

This function executes the Multi Resolution Scanning algorithm to detect differences across the distributions of multiple groups having multiple replicates.

Usage

```
andova(X, G, H, n_groups = length(unique(G)), n_subgroups = NULL,
       Omega = "default", K = 6, init_state = c(0.8, 0.2, 0), beta = 1,
       gamma = 0.07, delta = 0.4, eta = 0, alpha = 0.5,
       nu_vec = 10^(seq(-1, 4)), return_global_null = TRUE, return_tree = TRUE)
```

Arguments

X	Matrix of the data. Each row represents an observation.
G	Numeric vector of the group label of each observation. Labels are integers starting from 1.
H	Numeric vector of the replicate label of each observation. Labels are integers starting from 1.
n_groups	Number of groups.
n_subgroups	Vector indicating the number of replicates for each group.
Omega	Matrix defining the vertices of the sample space. The "default" option defines a hyperrectangle containing all the data points. Otherwise the user can define a matrix where each row represents a dimension, and the two columns contain the associated lower and upper limit.
K	Depth of the tree. Default is K = 6, while the maximum is K = 14.
init_state	Initial state of the hidden Markov process. The three states are <i>null</i> , <i>alternrative</i> and <i>prune</i> , respectively.
beta	Spatial clustering parameter of the transition probability matrix. Default is beta = 1.0.
gamma	Parameter of the transition probability matrix. Default is gamma = 0.07.
delta	Parameter of the transition probability matrix. Default is delta = 0.4.
eta	Parameter of the transition probability matrix. Default is eta = 0.0.
alpha	Pseudo-counts of the Beta random probability assignments.
nu_vec	The support of the discrete uniform prior on nu.
return_global_null	Boolean indicating whether to return the marginal posterior probability of the global null.
return_tree	Boolean indicating whether to return the posterior representative tree.

Value

An mrs object.

References

Ma L. and Soriano J. (2018). Analysis of distributional variation through multi-scale Beta-Binomial modeling. *Journal of Computational and Graphical Statistics*. Vol. 27, No. 3, 529-541.. doi:[10.1080/10618600.2017.1402774](https://doi.org/10.1080/10618600.2017.1402774)

Examples

```
set.seed(1)
n = 1000
M = 5
class_1 = sample(M, n, prob= 1:5, replace=TRUE )
class_2 = sample(M, n, prob = 5:1, replace=TRUE )

Y_1 = rnorm(n, mean=class_1, sd = .2)
Y_2 = rnorm(n, mean=class_2, sd = .2)

X = matrix( c(Y_1, Y_2), ncol = 1)
G = c(rep(1,n),rep(2,n))
H = sample(3,2*n, replace = TRUE )

ans = andova(X, G, H)
ans$PostGlobNull
plot1D(ans)
```

mrs

Multi Resolution Scanning

Description

This function executes the Multi Resolution Scanning algorithm to detect differences across multiple distributions.

Usage

```
mrs(X, G, n_groups = length(unique(G)), Omega = "default", K = 6,
    init_state = NULL, beta = 1, gamma = 0.3, delta = NULL, eta = 0.3,
    alpha = 0.5, return_global_null = TRUE, return_tree = TRUE,
    min_n_node = 0)
```

Arguments

X Matrix of the data. Each row represents an observation.

G Numeric vector of the group label of each observation. Labels are integers starting from 1.

n_groups	Number of groups.
Omega	Matrix defining the vertices of the sample space. The "default" option defines a hyperrectangle containing all the data points. Otherwise the user can define a matrix where each row represents a dimension, and the two columns contain the associated lower and upper limits for each dimension.
K	Depth of the tree. Default is $K = 6$, while the maximum is $K = 14$.
init_state	Initial state of the hidden Markov process. The three states are <i>null</i> , <i>altenrative</i> and <i>prune</i> , respectively.
beta	Spatial clustering parameter of the transition probability matrix. Default is $\beta = 1$.
gamma	Parameter of the transition probability matrix. Default is $\gamma = 0.3$.
delta	Optional parameter of the transition probability matrix. Default is $\delta = \text{NULL}$.
eta	Parameter of the transition probability matrix. Default is $\eta = 0.3$.
alpha	Pseudo-counts of the Beta random probability assignments. Default is $\alpha = 0.5$.
return_global_null	Boolean indicating whether to return the posterior probability of the global null hypothesis.
return_tree	Boolean indicating whether to return the posterior representative tree.
min_n_node	Node in the tree is returned if there are more than <code>min_n_node</code> data-points in it.

Value

An mrs object.

References

Soriano J. and Ma L. (2017). Probabilistic multi-resolution scanning for two-sample differences. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*. doi:10.1111/rssb.12180

Examples

```
set.seed(1)
n = 20
p = 2
X = matrix(c(runif(p*n/2),rbeta(p*n/2, 1, 4)), nrow=n, byrow=TRUE)
G = c(rep(1,n/2), rep(2,n/2))
ans = mrs(X=X, G=G)
```

plot1D *Plot regions of the representative tree in 1D*

Description

This function visualizes the regions of the representative tree of the output of the `mrs` function. For each region the posterior probability of difference (PMAP) or the effect size is plotted.

Usage

```
plot1D(ans, type = "prob", group = 1, dim = 1, regions = rep(1,
  length(ans$RepresentativeTree$Levels)), legend = FALSE, main = "default",
  abs = TRUE)
```

Arguments

<code>ans</code>	An <code>mrs</code> object.
<code>type</code>	What is represented at each node. The options are <code>type = c("eff", "prob")</code> . Default is <code>type = "prob"</code> .
<code>group</code>	If <code>type = "eff"</code> , which group effect size is used. Default is <code>group = 1</code> .
<code>dim</code>	If the data are multivariate, <code>dim</code> is the dimension plotted. Default is <code>dim = 1</code> .
<code>regions</code>	Binary vector indicating the regions to plot. The default is to plot all regions.
<code>legend</code>	Color legend for type. Default is <code>legend = FALSE</code> .
<code>main</code>	Overall title for the plot.
<code>abs</code>	If TRUE, plot the absolute value of the effect size. Only used when <code>type = "eff"</code> .

References

Soriano J. and Ma L. (2017). Probabilistic multi-resolution scanning for two-sample differences. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*. doi:[10.1111/rssb.12180](https://doi.org/10.1111/rssb.12180)

Ma L. and Soriano J. (2018). Analysis of distributional variation through multi-scale Beta-Binomial modeling. *Journal of Computational and Graphical Statistics. Vol. 27, No. 3, 529-541.* doi:[10.1080/10618600.2017.1402774](https://doi.org/10.1080/10618600.2017.1402774)

Examples

```
set.seed(1)
p = 1
n1 = 200
n2 = 200
mu1 = matrix( c(0,10), nrow = 2, byrow = TRUE)
mu2 = mu1; mu2[2] = mu1[2] + .01
sigma = c(1,.1)

Z1 = sample(2, n1, replace=TRUE, prob=c(0.9, 0.1))
Z2 = sample(2, n2, replace=TRUE, prob=c(0.9, 0.1))
```

```

X1 = mu1[Z1] + matrix(rnorm(n1*p), ncol=p)*sigma[Z1]
X2 = mu2[Z2] + matrix(rnorm(n2*p), ncol=p)*sigma[Z1]
X = rbind(X1, X2)
G = c(rep(1, n1), rep(2,n2))

ans = mrs(X, G, K=10)
plot1D(ans, type = "prob")
plot1D(ans, type = "eff")

```

plot2D

Plot regions of the representative tree in 2D

Description

This function visualizes the regions of the representative tree of the output of the `mrs` function.

Usage

```

plot2D(ans, type = "prob", data.points = "all", background = "none",
  group = 1, dim = c(1, 2),
  levels = sort(unique(ans$RepresentativeTree$Levels)), regions = rep(1,
  length(ans$RepresentativeTree$Levels)), legend = FALSE, main = "default",
  abs = TRUE)

```

Arguments

<code>ans</code>	An <code>mrs</code> object.
<code>type</code>	Different options on how to visualize the rectangular regions. The options are <code>type = c("eff", "prob", "empty", "none")</code> . Default is <code>type = "prob"</code> .
<code>data.points</code>	Different options on how to plot the data points. The options are <code>data.points = c("all", "differential", "none")</code> . Default is <code>data.points = "all"</code> .
<code>background</code>	Different options on the background. The options are <code>background = c("smeared", "none")</code> .
<code>group</code>	If <code>type = "eff"</code> , which group effect size is used. Default is <code>group = 1</code> .
<code>dim</code>	If the data are multivariate, <code>dim</code> are the two dimensions plotted. Default is <code>dim = c(1, 2)</code> .
<code>levels</code>	Vector with the level of the regions to plot. The default is to plot regions at all levels.
<code>regions</code>	Binary vector indicating the regions to plot. The default is to plot all regions.
<code>legend</code>	Color legend for type. Default is <code>legend = FALSE</code> .
<code>main</code>	Overall title for the legend.
<code>abs</code>	If TRUE, plot the absolute value of the effect size. Only used when <code>type = "eff"</code> .

References

- Soriano J. and Ma L. (2017). Probabilistic multi-resolution scanning for two-sample differences. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*. doi:10.1111/rssb.12180
- Ma L. and Soriano J. (2018). Analysis of distributional variation through multi-scale Beta-Binomial modeling. *Journal of Computational and Graphical Statistics. Vol. 27, No. 3, 529-541..* doi:10.1080/10618600.2017.1402774

Examples

```
set.seed(1)
p = 2
n1 = 200
n2 = 200
mu1 = matrix( c(9,9,0,4,-2,-10,3,6,6,-10), nrow = 5, byrow=TRUE)
mu2 = mu1; mu2[2,] = mu1[2,] + 1

Z1 = sample(5, n1, replace=TRUE)
Z2 = sample(5, n2, replace=TRUE)
X1 = mu1[Z1,] + matrix(rnorm(n1*p), ncol=p)
X2 = mu2[Z2,] + matrix(rnorm(n2*p), ncol=p)
X = rbind(X1, X2)
colnames(X) = c(1,2)
G = c(rep(1, n1), rep(2,n2))

ans = mrs(X, G, K=8)
plot2D(ans, type = "prob", legend = TRUE)

plot2D(ans, type="empty", data.points = "differential",
        background = "none")

plot2D(ans, type="none", data.points = "differential",
        background = "smeared", levels = 4)
```

plotTree

Plot nodes of the representative tree

Description

This function visualizes the representative tree of the output of the `mrs` function. For each node of the representative tree, the posterior probability of difference (PMAP) or the effect size is plotted. Each node in the tree is associated to a region of the sample space. All non-terminal nodes have two children nodes obtained by partitioning the parent region with a dyadic cut along a given direction. The numbers under the vertices represent the cutting direction.

Usage

```
plotTree(ans, type = "prob", group = 1, legend = FALSE, main = "",
        node.size = 5, abs = TRUE)
```

Arguments

ans	A mrs object.
type	What is represented at each node. The options are type = c("eff", "prob").
group	If type = "eff", which group effect size is used.
legend	Color legend for type. Default is legend = FALSE.
main	Main title. Default is main = "".
node.size	Size of the nodes. Default is node.size = 5.
abs	If TRUE, plot the absolute value of the effect size. Only used when type = "eff".

Note

The package **igraph** is required.

References

Soriano J. and Ma L. (2017). Probabilistic multi-resolution scanning for two-sample differences. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*. doi:10.1111/rssb.12180

Ma L. and Soriano J. (2018). Analysis of distributional variation through multi-scale Beta-Binomial modeling. *Journal of Computational and Graphical Statistics. Vol. 27, No. 3, 529-541..* doi:10.1080/10618600.2017.1402774

Examples

```
set.seed(1)
p = 2
n1 = 200
n2 = 200
mu1 = matrix( c(9,9,0,4,-2,-10,3,6,6,-10), nrow = 5, byrow=TRUE)
mu2 = mu1; mu2[2,] = mu1[2,] + 1

Z1 = sample(5, n1, replace=TRUE)
Z2 = sample(5, n2, replace=TRUE)
X1 = mu1[Z1,] + matrix(rnorm(n1*p), ncol=p)
X2 = mu2[Z2,] + matrix(rnorm(n2*p), ncol=p)
X = rbind(X1, X2)
colnames(X) = c(1,2)
G = c(rep(1, n1), rep(2,n2))

ans = mrs(X, G, K=8)
plotTree(ans, type = "prob", legend = TRUE)
```

print.summary.mrs *Print summary of a mrs object*

Description

This function print the summary the output of the `mrs` function. It provides the marginal prior and posterior of the null and the top regions of the representative tree.

Usage

```
## S3 method for class 'summary.mrs'  
print(x, ...)
```

Arguments

`x` A `summary.mrs` object
`...` Additional print parameters.

References

Soriano J. and Ma L. (2017). Probabilistic multi-resolution scanning for two-sample differences. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*. doi:10.1111/rssb.12180

Ma L. and Soriano J. (2018). Analysis of distributional variation through multi-scale Beta-Binomial modeling. *Journal of Computational and Graphical Statistics. Vol. 27, No. 3, 529-541..* doi:10.1080/10618600.2017.1402774

Examples

```
set.seed(1)  
n = 100  
p = 2  
X = matrix(c(runif(p*n/2),rbeta(p*n/2, 1, 4)), nrow=n, byrow=TRUE)  
G = c(rep(1,n/2), rep(2,n/2))  
x = mrs(X=X, G=G)  
fit = summary(x, rho = 0.95, abs_eff = 1)  
print(fit)
```

summary.mrs *Summary of a mrs object*

Description

This function summarizes the output of the `mrs` function. It provides the marginal prior and posterior null and the top regions of the representative tree.

Usage

```
## S3 method for class 'mrs'
summary(object, rho = 0.5, abs_eff = 0, sort_by = "eff",
  ...)
```

Arguments

object	A mrs object
rho	Threshold for the posterior alternative probability. All regions with posterior alternative probability larger than rho are reported. Default is rho = 0.5.
abs_eff	Threshold for the effect size. All regions with effect size larger than abs_eff in absolute value are reported. Default is abs_eff = 0.
sort_by	Define in which order the regions are reported. The options are sort_by = c("eff", "prob") and the default is sort_by = "eff".
...	Additional summary parameters.

Value

A list with information about the top regions.

References

Soriano J. and Ma L. (2017). Probabilistic multi-resolution scanning for two-sample differences. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*. doi:10.1111/rssb.12180

Ma L. and Soriano J. (2018). Analysis of distributional variation through multi-scale Beta-Binomial modeling. *Journal of Computational and Graphical Statistics. Vol. 27, No. 3, 529-541..* doi:10.1080/10618600.2017.1402774

Examples

```
set.seed(1)
n = 100
p = 2
X = matrix(c(runif(p*n/2),rbeta(p*n/2, 1, 4)), nrow=n, byrow=TRUE)
G = c(rep(1,n/2), rep(2,n/2))
object = mrs(X=X, G=G)
fit = summary(object, rho = 0.5, abs_eff = 0.1)
```

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