Package 'qch'

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Version 1.0.0
Description Provides functions for the joint analysis of K sets
of p-values obtained for a same list of items. This joint analysis is
performed by querying a composed hypothesis, i.e. an arbitrary complex
combination of simple hypotheses, as described in Mary-Huard et al.
(2021) <arxiv:2104.14601>. The null distribution corresponding to the</arxiv:2104.14601>
composed hypothesis of interest is obtained by fitting non-parametric
mixtures models (one for each of the simple hypothesis of the complex
combination). Type I error rate control is achieved through Bayesian
False Discovery Rate control. The 3 main functions of the package

GetHinfo(), qch.fit() and qch.test() correspond to the 3 steps for

querying a composed hypothesis (composed H0/H1 formulation, inferring

Title Query Composed Hypotheses

R topics documented:

the null distribution and testing the null hypothesis).
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Description

FastKerFdr

Usage

```
FastKerFdr(Pval, p0 = NULL, plotting = FALSE, NbKnot = 1e+05, tol = 1e-05)
```

Arguments

Pval		(corresponding to a p-value serie)	
PVAI	a vector of p-values	(Corresponding to a p-value serie)	

p0 a priori proportion of H0 hypotheses

plotting boolean, should some diagnostic graphs be plotted. Default is FALSE.

NbKnot The (maximum) number of knot for the kde procedure. Default is 1e5

tol a tolerance value for convergence. Default is 1e-5

Value

A list of 3 objects. Object p0 is an estimate of the proportion of H0 hypotheses., tau is the vector of H1 posteriors. f1 is a numeric vector, each coordinate i corresponding to the evaluation of the H1 density at point pi, where pi is the ith p-value in Pval.

GetHinfo Generate H0/H1 configurations and specify the ones corresponding the composed H1	to
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Description

Generate H0/H1 configurations and specify the ones corresponding to the composed H1

Usage

```
GetHinfo(Q, AtLeast, Consecutive = FALSE)
```

GetHinfoEqual 3

Arguments

Q number of test series to be combined

AtLeast How many H1 hypotheses at least for the item to be of interest?

Consecutive Should the significant test series be consecutive? Default=FALSE

Value

A list of two objects 'Hconfig' and 'Hconfig.H1'. Hconfig is the list of all possible combination of H0 and H1 hypotheses among Q hypotheses tested. Hconfig.H1 is the vector of components of Hconfig that correspond to the 'AtLeast' specification.

See Also

```
GetHinfoEqual()
```

Examples

```
GetHinfo(4,2)
```

GetHinfoEqual Generate H0/H1 configurations and specify the ones corresponding to

the composed H1

Description

Generate H0/H1 configurations and specify the ones corresponding to the composed H1

Usage

```
GetHinfoEqual(Q, Equal, Consecutive = FALSE)
```

Arguments

Q number of test series to be combined

Equal How many H1 hypotheses exactly for the item to be of interest?

Consecutive Should the significant test series be consecutive? Default=FALSE

Value

A list of two objects 'Hconfig' and 'Hconfig.H1'. Hconfig is the list of all possible combination of H0 and H1 hypotheses among Q hypotheses tested. Hconfig.H1 is the vector of components of Hconfig that correspond to the 'Equal' specification.

See Also

```
GetHinfo()
```

qch.fit

Examples

GetHinfoEqual(4,2)

PvalSets

Synthetic example to illustrate the main qch functions

Description

PvalSets is a data.frame with 10,000 rows and 3 columns. Each row corresponds to an item, columns 'Pval1' and 'Pval2' each correspond to a test serie over the items, and column 'Class' provides the truth, i.e. if item i belongs to class 1 then the H0 hypothesis is true for the 2 tests, if item i belongs to class 2 (resp. 3) then the H0 hypothesis is true for the first (resp. second) test only, and if item i belongs to class 4 then both H0 hypotheses are false (for the first and the second test).

Usage

PvalSets

Format

A data.frame

qch.fit

Infer Hconfig posteriors

Description

Infer Hoonfig posteriors

Usage

```
qch.fit(pValMat, Hconfig, plotting = FALSE)
```

Arguments

pValMat a matrix of p-values, each column corresponding to a p-value serie.

Honfig an Honfig list as generated by the GetHinfo() function.

plotting a boolean. Should some diagnostic graphs be plotted? Default is FALSE.

Value

A list of 2 objects 'prior' and 'posterior'. Object 'prior' is a vector of estimated prior probabilities for each of the H-configurations. Object 'posterior' is a matrix providing for each item (in row) its posterior probability to belong to each of the H-configurations (in columns).

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Examples

```
data(PvalSets)
PvalMat <- as.matrix(PvalSets[,-3])
## Build the Hconfig objects
Q <- 2
AtLeast <- 2
Hconfig <- GetHinfo(Q,AtLeast)$Hconfig

## Run the function
res.fit <- qch.fit(PvalMat,Hconfig)

## Display the prior of each class of items
res.fit$prior</pre>
## Display the first posteriors
head(res.fit$posterior)
```

qch.test

Perform composed hypothesis testing with FDR control

Description

Perform composed hypothesis testing with FDR control

Usage

```
qch.test(posterior, Hconfig.H1, Alpha = 0.05)
```

Arguments

posterior a matrix of posterior probabilities for each item to belong the different H-configurations,

as provided by the qch.fit() function.

Hconfig. H1 a list of H1 config, as created by the GetHinfo() function.

Alpha the nominal Type I error rate for FDR control.

Value

A list of 2 objects 'Rejection' and 'IFDR'. Object 'Rejection' is a vector providing for each item the result of the composed hypothesis test, after multiple testing correction. Object 'IFDR' is a vector providing for each item its local FDR estimate.

Examples

```
data(PvalSets)
PvalMat <- as.matrix(PvalSets[,-3])
Truth <- PvalSets[,3]
## Build the Hconfig objects</pre>
```

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```
Q <- 2
AtLeast <- 2
Hconfig <- GetHinfo(Q,AtLeast)$Hconfig
Hconfig.H1 <- GetHinfo(Q,AtLeast)$Hconfig.H1
## Infer the posteriors
res.fit <- qch.fit(PvalMat,Hconfig)
## Run the test procedure with FDR control
res.test <- qch.test(res.fit$posterior,Hconfig.H1)
table(res.test$Rejection,Truth==4)</pre>
```

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