Package ‘TreeBH’

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Type Package

Title Error Control for Tree-Structured Hypotheses

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Description This package implements a multiple testing procedure which addresses the challenge of controlling error rates at multiple levels of resolution. We frame this problem as the selection of hypotheses which are organized in a tree structure. The procedure controls relevant error rates (in particular, the selective FDR in each level of the tree) given certain assumptions on the dependence among the hypotheses.

Depends qvalue (>= 2.0.0)

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Description

This package implements a multiple testing procedure which addresses the challenge of controlling error rates at multiple levels of resolution. We frame this problem as the selection of hypotheses which are organized in a tree structure. The procedure controls relevant error rates (in particular, the selective FDR in each level of the tree) given certain assumptions on the dependence among the hypotheses. For code designed specifically for error control in the context of single and multi-tissue eQTL analysis, see the TreeQTL package.

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Details

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Author(s)

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References


Examples

# This example follows the simulation set-up in Section 5.2 of Bogomolov et al. (2021)
# [https://doi.org/10.1093/biomet/asaa086] and Section 6.2 of Barber and Ramdas (2017)
# [http://dx.doi.org/10.1111/rssb.12218]. Specifically, there are a total of 100 x 100
# hypotheses, with the non-null hypotheses (true signals) arranged into 2 blocks of size
# 15 x 15 with 15 additional non-null hypotheses along the diagonal.

# Set up matrix with 0 for true null hypotheses and 1 for non-nulls
truth <- matrix(0, nrow = 100, ncol = 100)
truth[1:15, 1:15] <- 1
truth[16:30, 16:30] <- 1
for (i in 31:45) {
  truth[i, i] <- 1
}

# Generate p-values following known structure
mu <- truth * 3
X <- mu + matrix(rnorm(100 * 100), nrow = 100, ncol = 100)
pval_table <- 1 - pnorm(X)

# Define a three-level hierarchy, with hypotheses grouped
# 1. By row
# 2. In blocks of size 15 (with a final block of size 10) within each row
# 3. Individually within each block
level1_grouping <- as.vector(matrix(rep(1:100, 100), ncol = 100, byrow = FALSE))
level2_grouping <- as.vector(matrix(c(rep(1, 15), rep(2, 15), rep(3, 15),
                                      rep(4, 15), rep(5, 15), rep(6, 15),
                                      rep(7, 10)), ncol = 100, nrow = 100, byrow = TRUE) +
                           t(matrix(c(rep(1, 15), rep(2, 15), rep(3, 15),
                                      rep(4, 15), rep(5, 15), rep(6, 15),
                                      rep(7, 10), rep(8, 10)), ncol = 100, nrow = 100, byrow = TRUE)) +
                           matrix(0:99 * 7, ncol = 100, nrow = 100, byrow = TRUE))
levels3_grouping <- 1:10000

groups <- cbind(level1_grouping, level2_grouping, levels3_grouping)
# Apply TreeBH procedure, targeting a selective FDR of 0.2 in each level

target_level <- 0.2

treeBH_results <- get_TreeBH_selections(pvals = as.vector(pval_table),
                   groups = groups,
                   q = rep(target_level, 3))

get_fisher_p

Compute Fisher p-value given a list of p-values

Description

Compute Fisher p-value given a list of p-values, assuming that NAs do not count toward the total number of tests

Usage

get_fisher_p(pvals)

Arguments

pvals Vector of p-values (which may include NAs)

Value

Value of the Fisher p-value

Author(s)

Christine B. Peterson

References


get_simes_p

Compute Simes p-value given a list of p-values

Description

Compute Simes p-value given a list of p-values, assuming that NAs do not count toward the total number of tests

Usage

get_simes_p(pvals)

Arguments

pvals Vector of p-values (which may include NAs)
Value

Value of the Simes p-value

Author(s)

Christine B. Peterson

References


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**get_TreeBH_selections**

*Performs multi-level hierarchical selection*

Description

This function identifies hypotheses of interest, where the hypotheses are organized within a hierarchical tree structure. Given p-values for the leaf nodes and a definition of the tree structure, this procedure identifies selected hypotheses, controlling the targeted selective false discovery rate at each level in the tree.

Usage

```
get_TreeBH_selections(pvals, groups, q, test = "simes")
```

Arguments

- `pvals` Vector of N p-values (some of which may be NA) corresponding to the individual hypotheses in the most granular level of the tree
- `groups` Matrix defining how hypotheses are grouped within each level of the tree. Specifically, an N x L matrix where if hypothesis n belongs to the kth group in level l, `groups[n,l]` should be set to k. The final column should just be 1:N since the most granular grouping is by individual hypothesis
- `q` Vector of L error rates (e.g. 0.05) to be targeted for each level in the tree
- `test` Vector of L-1 combination methods to obtain level l-1 p-values from level l p-values. Options are "simes" and "fisher". Default is "simes" at each level.

Value

N x L binary matrix. This matrix matches up with the input argument `groups`. If the kth group in level 1 was selected, the first matrix element corresponding to this group will be set to 1 to indicate the group was selected. The remaining entries will be 0s.

Author(s)

Christine B. Peterson
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