Package: impARI (via r-universe)

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Type Package

Title Improving Permutation-Based All-Resolutions Inference ('impARI')

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Description The goal is to improve a permutation-based approach (R package: 'pARI') for simultaneous inference on the true discovery proportion by a branch-and-bound algorithm. It is designed to return a list with a bracketing for the true discovery proportion, rather than a single lower bound from 'pARI'. For more details see Andreella. A (2023) <doi:10.1002/sim.9725>.

License GPL (>= 2)

Imports Rcpp (>= 1.0.12)

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NeedsCompilation yes

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`impARI-package` *Improving Permutation-Based All-Resolutions Inference ('impARI')*

Description

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Arguments

`pmat`	P-value matrix where columns represent the m variables and rows the w permutations.
`set`	Integer vector which expresses the index set of features of interest.
`maxit`	Integer to specify the maximum number of iterations for branch and bound.
`family`	String character. Name of the family confidence envelope to compute the critical vector from `"simes"`, `"aorc"`, `"beta"`, `"higher.criticism"`, and `"power"`. "simes" is with fast computational tricks.
`delta`	Non-negative integer δ value.
`alpha`	Significance level between 0 and 1.
`goleft`	Boolean variable to decide which direction to go in branch and bound algorihtm, the default is go left first, i.e. the subspace to force a feature in.

Details

The main function in the package is impARI:

impARI(pmat, set, maxit, family, delta, alpha)

Value

by default returns a list with the following objects:

`TD`	lower bound for the number of true discoveries in the set selected
`TD_heuristic`	heuristic lower bound for the number of true discoveries in the set selected
`TDP`	lower true discovery proportion of true discoveries in the set selected
`iter`	the number of iterations at the end point, either iter< maxit when the procedure is converged or iter = maxit
`Queue`	queue of non-calculated child spaces in branch and bound algorihtm.

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References

Andreella, A., Hemerik, J., Finos, L., Weeda, W., & Goeman, J. (2023). Permutation-based true discovery proportions for functional magnetic resonance imaging cluster analysis. Statistics in Medicine.

Rosenblatt, J. D., Finos, L., W., W. D., Solari, A., and Goeman, J. J. (2018). All-resolutions inference for brain imaging. NeuroImage, 181:786-796.

Hemerik, J., Solari, A., and Goeman, J. J. (2019). Permutation-based simultaneous confidence bounds for the false discovery proportion. Biometrika, 106(3):635-649.

Examples

```
  #### example
# simulated data ----------------------------------------------------------
m = 10  # features
B = 100 # permutations
set.seed(123)
# create a p-value matrix with m features as columns and B permutations as rows
pmat <- matrix(runif(m * B), nrow = B, ncol = m)
# print(p_value_matrix)

## set of interest
set_interest =  1:m

res = impARI(pmat = pmat, set = set_interest, maxit = 10, family = "simes", delta = 0, alpha=0.05)
res
```

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