

# Package ‘impARI’

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**Type** Package

**Title** Improving Permutation-Based All-Resolutions Inference (‘impARI’)

**Version** 0.0.3

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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](https://doi.org/10.1002/sim.9725)>.

**License** GPL (>= 2)

**Imports** Rcpp (>= 1.0.12)

**LinkingTo** Rcpp,RcppArmadillo

**NeedsCompilation** yes

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**Repository** CRAN

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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, et.al (2023) <[doi:10.1002/sim.9725](https://doi.org/10.1002/sim.9725)>.

**Arguments**

<code>pmat</code>	P-value matrix where columns represent the $m$ variables and rows the $w$ permutations.
<code>set</code>	Integer vector which expresses the index set of features of interest.
<code>maxit</code>	Integer to specify the maximum number of iterations for branch and bound.
<code>family</code>	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.
<code>delta</code>	Non-negative integer $\delta$ value.
<code>alpha</code>	Significance level between 0 and 1.
<code>goleft</code>	Boolean variable to decide which direction to go in branch and bound algorithm, 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:

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

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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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