

Package ‘hypoRF’

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Type Package

Title Random Forest Two-Sample Tests

Version 1.0.1

Description An implementation of Random Forest-based two-sample tests as introduced in Hediger & Michel & Naef (2022).

License GPL-3

Imports stats, ranger

Encoding UTF-8

Suggests testthat

RoxygenNote 7.3.2

NeedsCompilation no

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Contents

hypoRF	2
Index	4

hypoRF

*HypoRF; a Random Forest based Two Sample Test***Description**

Performs a permutation two sample test based on the out-of-bag-error of random forest.

Usage

```
hypoRF(
  data1,
  data2,
  K = 100,
  statistic = "PerClassOOB",
  normalapprox = F,
  seed = NULL,
  alpha = 0.05,
  ...
)
```

Arguments

data1	An object of type "data.frame". The first sample.
data2	An object of type "data.frame". The second sample.
K	A numeric value specifying the number of times the created label is permuted. For K = 1 a binomial test is carried out. The Default is K = 100.
statistic	A character value specifying the statistic for permutation testing. Two options available • PerClassOOB Sum of OOB per class errors. • OverallOOB OOB-error. . Default is statistic = "PerClassOOB".
normalapprox	A logical value asking for the use of a normal approximation. Default is normalapprox = FALSE.
seed	A numeric value for reproducibility.
alpha	The level of the test. Default is alpha = 0.05.
...	Arguments to be passed to ranger

Value

A list with elements

- pvalue: The p-value of the test.
- obs: The OOB-statistic in case of K>1 or the out-of-sample error in case of K=1 (binomial test).

- `val`: The OOB-statistic of the permuted random forests in case of $K > 1$ (otherwise NULL).
- `varest`: The estimated variance of the permuted random forest OOB-statistic in case of $K > 1$ (otherwise NULL).
- `statistic`: The used OOB-statistic
- `importance_ranking`: The variable importance measure, when `importance == "impurity"`.
- `cutoff`: The quantile of the importance distribution at level α .
- `call`: Call to the function.

See Also

[ranger](#)

Examples

```
# Using the default testing procedure (permutation test)
x1 <- data.frame(x=stats::rt(50, df=1.5))
x2 <- data.frame(x=stats::rnorm(50))
hypoRF(x1, x2, num.trees = 50)
# Using the exact binomial test
hypoRF(x1, x2, K=1)
```

Index

hypoRF, [2](#)

ranger, [3](#)