

Package ‘forestControl’

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Type Package

Title Approximate False Positive Rate Control in Selection Frequency
for Random Forest

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Description Approximate false positive rate control in selection frequency for
random forest using the methods described by En-
der Konukoglu and Melanie Ganz (2014) <arXiv:1410.2838>.
Methods for calculating the selection frequency threshold at false positive rates
and selection frequency false positive rate feature selection.

Imports Rcpp, purrr, tibble, magrittr, dplyr

Suggests testthat, randomForest, ranger, parsnip

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Encoding UTF-8

LazyData true

URL <https://github.com/aberHRML/forestControl>

BugReports <https://github.com/aberHRML/forestControl/issues>

RoxygenNote 6.0.1

LinkingTo Rcpp

Roxygen list(markdown = TRUE)

NeedsCompilation yes

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R topics documented:

forestControl-package	2
extract_params	2

fpr_fs	3
selection_freqs	4
sft	4
Index	6

forestControl-package	<i>False Positive Rate Control in Selection Frequency for Random Forest</i>
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Description

This package is an implementation of the methods described by Ender Konukoglu and Melanie Ganz in *Konukoglu, E. and Ganz, M., 2014. Approximate false positive rate control in selection frequency for random forest. arXiv preprint arXiv:1410.2838 <https://arxiv.org/abs/1410.2838>.*

extract_params	<i>Extract forest parameters</i>
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Description

For a randomForest or ranger classification object, extract the parameters needed to calculate an approximate selection frequency threshold

Usage

extract_params(x)

Arguments

x a randomForest or ranger object

Value

- a list of four elements
- **Fn** The number of features considered at each internal node (mtry)
 - **Ft** The total number of features in the data set
 - **K** The average number of binary tests/internal nodes across the entire forest
 - **Tr** The total number of trees in the forest

Author(s)

Tom Wilson <tpw2@aber.ac.uk>

Examples

```
library(randomForest)
data(iris)
iris.rf <- randomForest(iris[,-5], iris[,5], forest = TRUE)

iris.params <- extract_params(iris.rf)
print(iris.params)
```

fpr_fs*False Postivie Rate Feature Selection*

Description

Calculate the False Positive Rate (FPR) for each feature using it's selection frequency

Usage

```
fpr_fs(x)
```

Arguments

x a randomForest or ranger object

Value

a tibble of selection frequencies and their false positive rate

Author(s)

Jasen Finch <jsf9@aber.ac.uk>

Examples

```
library(randomForest)
data(iris)
iris.rf <- randomForest(iris[,-5], iris[,5], forest = TRUE)

iris.features <- fpr_fs(iris.rf)
print(iris.features)
```

selection_freqs	<i>Variable Selection Frequencies</i>
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Description

Extract variable selection frequencies from randomForest and ranger model objects

Usage

```
selection_freqs(x)
```

Arguments

x a randomForest or ranger object

Value

tibble of variable selection frequencies

Examples

```
library(randomForest)
data(iris)
iris.rf <- randomForest(iris[,-5], iris[,5], forest = TRUE)

iris.freqs <- selection_freqs(iris.rf)
print(iris.freqs)
```

sft	<i>Selection Frequency Threshold</i>
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Description

Determine the selecton frequency threshold of a model at a specified false positive rate

Usage

```
sft(x, alpha)
```

Arguments

x a randomForest or ranger object
alpha a false positive rate (ie, 0.01)

Value

a list of two elements

- **sft** The selection frequency threshold
- **probs_atsft** The estimated false positive rate

Author(s)

Tom Wilson <tpw2@aber.ac.uk>

Examples

```
library(randomForest)
data(iris)
iris.rf <- randomForest(iris[, -5], iris[, 5], forest = TRUE)

# For a false positive rate of 1%
iris.sft <- sft(iris.rf, 0.01)
print(iris.sft)

# To iterate through a range of alpha values

alpha <- c(0.01, 0.05, 0.1, 0.15, 0.2, 0.25)
threshold <- NULL
for(i in seq_along(alpha)){
  threshold[i] <- sft(iris.rf, alpha[i])$sft
}

plot(alpha, threshold, type = 'b')
```

Index

`extract_params`, [2](#)
`forestControl-package`, [2](#)
`fpr_fs`, [3](#)
`selection_freqs`, [4](#)
`sft`, [4](#)