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**Working Paper**

## Bias in random forest variable importance measures: illustrations, sources and a solution

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```
#####
# To start the analysis the following packages must be loaded.      #
# (Please install the latest versions of the packages before use.) #
#####

require("randomForest")

require("party")

#####
# Prepare the data set:                                             #
#####

# Download the data:

arabidopsis_url <-
  "http://www.biomedcentral.com/content/supplementary/1471-2105-5-132-S1.txt"

arabidopsis <- read.table(arabidopsis_url, header = TRUE,
  sep = " ", na.string = "X")

# Remove cases with missing values and variables without variation:

arabidopsis <- subset(arabidopsis, complete.cases(arabidopsis))

arabidopsis <- arabidopsis[, !(names(arabidopsis) %in% c("X0", "loc"))]

#####
#
#           randomForest                                           #
#
#####

# Function call to create a random forest:

my_randomForest <- randomForest(edit ~ ., data = arabidopsis,
  importance = TRUE, ntree = 50,
  mtry = 3, replace = TRUE)

#####
# Options:                                                         #
#
# importance = TRUE                                               #
# calculate the variable importance                               #
#
# ntree = 50                                                       #
# number of individual classification trees grown                 #
# in the random forest                                           #
#
# mtry = 3                                                         #
# size of the random subset of predictor variables provided as   #
# splitting variables in each split of each classification tree  #
#
# replace = TRUE                                                  #
# bootstrap samples are drawn with replacement (default)         #
#####

# Function call to return variable importance:

my_varimp <- importance(my_randomForest, scale=TRUE)[,3]
```

```
#####
# Options:
#
# scale = TRUE
# return scaled measure incorporating standard error (default)
#
# Usage:
# Elements importance()[,1] and importance()[,2] return separate
# variable importance measures for response class $Y = 0$ and
# $Y = 1$.
# importance()[,4] returns the overall improvement in the
# ``Gini gain'' splitting criterion.
# Note that the ``Gini gain'' splitting criterion is strongly
# biased in favor of predictor variables with a high number of
# categories!
#####
```

```
#####
#
# cforest
#
#####
```

```
# Function call to create a random forest:
```

```
my_cforest_control <- cforest_control(teststat = "quad",
  testtype = "Univ", mincriterion = 0, ntree = 50, mtry = 3,
  replace = TRUE)
```

```
my_cforest <- cforest(edit ~ ., data = arabidopsis,
  controls = my_cforest_control)
```

```
#####
# Options:
#
# teststat = "quad"
# type of the test statistic is quadratic
#
# testtype = "Univ"
# computation of the distribution of the test statistic, where
# the default values for teststat and testtype produce result
# more similar to randomForest
#
# mincriterion = 0
# the threshold criterion value that must be exceeded for
# splitting is set to zero to guarantee that a split is
# conducted in each tree
#
# ntree = 50
# same as in randomForest
#
# mtry = 3
# same as in randomForest
#
# replace = TRUE
# same as in randomForest
#####
```

```
# Function call to return variable importance:
```

```
varimp_cforest <- varimp(my_cforest)
```

```
varimp_cforest_unscaled <- varimp_cforest[,1]  
varimp_cforest_scaled <- varimp_cforest[,1]/varimp_cforest[,2]
```