# Random Forests for Classification Trees and Categorical Dependent Variables: an informal Quick Start R Guide

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Note: random forests work for continuous variables via regression trees, but I have yet to try them for such. Thus, this quick start guide is currently limited to classification trees only.

#### 1. Introduction

#### What are random forests?

Random forests are a type of recursive partitioning method particularly well-suited to small n large p problems (Strobl et al. 2009b: 339). They involve an ensemble (aka: set) of classification (or regression) trees that are calculated on random subsets of the data, using a subset of randomly restricted and selected predictors for each split in each classification tree (Strobl et al. 2008: §2; Strobl et al. 2009b; a.o.). In this way, random forests are able to better examine the contribution and behavior that each predictor has, even when one predictor's effect would usually be overshadowed by more significant competitors in simpler models (e.g., simple or mixed effect regression models) (Strobl et al. 2009b: 337). Furthermore, the results of an ensemble of classification/regression trees have been shown to produce better predictions than the results of one classification tree on its own (Strobl et al. 2008: §2).

Using the random forests, we also have the conditional permutation accuracy variable importance measure available to us. Conditional variable importance is calculated by randomly shuffling the values of a given independent variable thereby "breaking" the variable's bond to the response. Then, the difference of the model accuracy before and after the random permutations, averaged over all trees in the forest, tells us how important that predictor is for determining the outcome (Strobl et al. 2009b: 335).

## ➤ Why the party package?

The party package utilizes conditional inference trees, which ameliorate the bias that random forests otherwise have towards highly correlated variables (see Strobl et al. 2008; 2009a for further discussion).

## > About this quick start guide

This document is meant only as a helpful listing of some R code and random forest guidelines to get you started with the party package and random forest analyses. It is highly recommended that you also read the references listed below in addition to the party package R documentation, all of which have much more detail on the use and interpretation of random

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<u>forest statistics than is included here.</u> This document is also by no means a complete listing of R code for random forest statistics, and it will be continually updated with more code and methods.

All lines of actual R code are listed with a ">" preceding them for readability. Do not copy this arrow when using the code in R.

## 2. A Very Important Note about Random Forests

Random forests are a truly 'random' statistical method in that the model results can vary from run to run. Therefore, it is of utmost importance that you verify the stability of your forests by starting with at least one different seed (see §5) and by increasing the size of your forest (§4) to a sufficiently large number (Strobl 2009a: 17; Strobl 2009b: 343 for a more extensive discussion). Variable importance (§6), as well, should be interpreted and reported as a relative ranking of significant predictors, and "the absolute values of the importance scores should not be interpreted or compared over different studies" (Strobl 2009b: 336).

## 3. Installing and loading R libraries

To download the party package, go to (on the top toolbar in the R console) Packages > Install packages > (select a CRAN mirror nearest to you) > (select packages to download).

For the code included in this document, you'll need at least the Hmisc, lattice, and party libraries. I'd recommend installing languageR, Design, and party instead just to cover all of your bases.

Load the libraries in the R console using the following code.

- > library(languageR)
- > library (Design)
- > library(Party)

For convenience, you can also write this code into your .Rprofile file so that R automatically loads the packages whenever you start the program.

## 4. Model parameters

> Don't forget to report the model parameters used when reporting results of random forest analyses!

Set controls for the random forest.

> data.controls <- cforest unbiased(ntree=1000, mtry=3)</pre>

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Notes on model parameters:

```
ntree (default = 500)
= overall number of trees in the forest
```

The number of trees should be increased as the number of variables or data points increase. A suitably large number of trees will guarantee more stable and robust results. (e.g., having ntree=8000 for a sparse dataset with a large number of predictors is not unheard of.)

```
mtry (default = 5)
= number of randomly preselected predictor variables for each split
Square root of the number of variables (suggested; see Strobl et al. 2009c: 3)
```

## 5. Running the random forest

Set a random seed for your forest run. Any random number will do!

```
> set.seed(47)
```

Running a random forest:

```
> data.cforest <- cforest(Resp ~ x + y + z..., data = mydata,
controls=data.controls)

where "Resp" = dependent variable*;
x, y, z = independent variable;
mydata = name of your dataframe;
data.controls = model parameters set using cforest unbiased()</pre>
```

\*IMPORTANT: When using categorical variables, make sure they are encoded as factors, not as numeric. Use class(data\$Resp) to check the encoding, and use as.factor(data\$Resp) to encode your vector as a factor.)

## 6. Permutation Accuracy Variable Importance

```
> data.cforest.varimp <- varimp(data.cforest, conditional =
TRUE)</pre>
```

(Note: conditional variable importance will take a while and is fairly CPU-intensive, especially for data sets with many variables, observations, and levels to the variables. I would highly recommend running these calculations on a high-powered computer.)

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A sample read-out of the conditional variable importance results:

> data.cforest.varimp

## ➤ How to interpret variable importance results

Variables can be considered informative and important if their variable importance value is above the absolute value of the lowest negative-scoring variable. "The rationale for this rule of thumb is that the importance of irrelevant variables varies randomly around zero" (Strobl et al. 2009b: 342). As mentioned in §2, results from random forests and conditional variable importance should always be verified via multiple random forest runs starting with different seeds and sufficiently large ntree values to insure the robustness and stability of results (Strobl et al. 2009b: 343).

To export your variable importance results as a table for later data visualization:

```
> write.table(data.cforest.varimp, file="FILEPATH.txt")
```

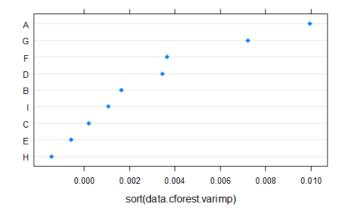
(This is especially useful if you are running your random forest variable importance calculations on a remote server without a graphical interface.)

## 7. Visualizing variable importance

## Dot plots

A simple dotplot of the variable importance results

> dotplot(sort(data.cforest.varimp))



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To aid the interpretation of variable importance results, you can add a line on the plot at the absolute value of the lowest ranking predictor (see §6 for explanation).

```
> dotplot(sort(data.cforest.varimp), xlab="Variable Importance
in DATA\n (predictors to right of dashed vertical line are
significant)", panel = function(x,y){
  panel.dotplot(x, y, col='darkblue', pch=16, cex=1.1)
  panel.abline(v=abs(min(data.cforest.varimp)), col='red',
  lty='longdash', lwd=2)
  )
              G
              F
              D
              В
              С
              Е
              Н
                     0.000
                           0.002
                                  0.004
                                        0.006
                                              0.008
                                                     0.010
```

Notes on graphical parameters:

```
сех
```

changes the size of the dots in the dotplot. .5 = 50% of default size, 1.5 = 150% of default size.

Variable Importance in mydata (predictors to right of dashed vertical line are significant)

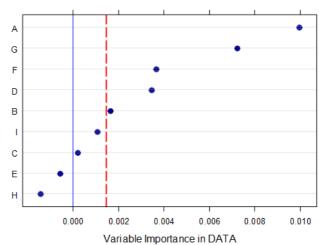
## pch

changes dot type. See <a href="http://www.statmethods.net/advgraphs/parameters.html">http://www.statmethods.net/advgraphs/parameters.html</a> for a list as well as additional information on graphical parameters.

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You can also insert a blue line at 0 on the x-axis. Before the closing "}" in the code above, insert this following line.

panel.abline(v=0, col='blue')

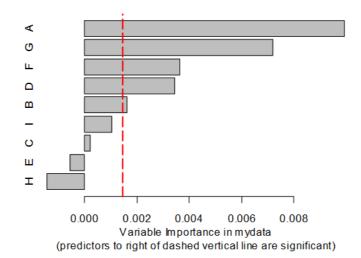


(predictors to right of dashed vertical line are significant)

# Barplots

> barplot(sort(data.cforest.varimp), horiz=TRUE, xlab="Variable
Importance in mydata\n(predictors to right of dashed vertical
line are significant)")

> abline(v=abs(min(data.cforest.varimp)), col='red',
lty='longdash', lwd=2)

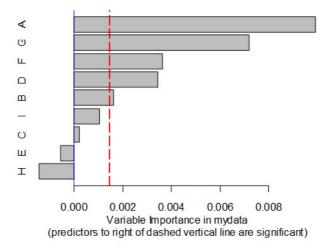


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To insert a blue line at 0 on the x-axis:

> abline(v=0, col="blue")



# Saving plots

To save plots for use in Microsoft Office, use .emf filetypes.

```
> savePlot(filename="FILEPATH/filename", type=c("emf"))
```

The type argument also supports .png, .jpeg, .jpg, .bmp, .ps, .eps, and .pdf file types. You'll want .ps or .eps files for LaTeX use:

# 8. Model statistics and predictions

Obtaining the C statistic and Somers' Dxy

- > data.trp <- treeresponse(data.cforest)</pre>
- > data.predforest <- sapply(data.trp, FUN = function(v)
  return(v[1]))</pre>
- > somers2(data.predforest, mydata\$Resp)

С	Dxy	n	Missing
0.8447197	0.6894393	410.0000000	0.0000000

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#### **Select References**

Hothron, Torsten; Kurt Hornik; and Achim Zeileis. 2006. Unbiased recursive partitioning: A conditional framework. *Journal of Computational and Graphical Statistics*. 15(3): 651-674.

Hothorn, Torsten; Kurt Hornik; Carolin Strobl; and Achim Zeileis. 2010. A Laboratory for Recursive Partytioning. < <a href="http://cran.r-project.org/web/packages/party/party.pdf">http://cran.r-project.org/web/packages/party/party.pdf</a>>

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Questions? Comments? Mistakes? Suggestions?

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Quick guide download: http://www.stanford.edu/~stephsus/R-randomforest-guide.pdf

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