Machine Learning (Random Forest & Linear Regression) With R
Prepared By: Shakil Ahammed

The Parresol tree biomass data

As an example, we'll use a data set of 40 slash pine trees from Louisiana USA presented in Parresol's 2001 paper *Additivity of nonlinear biomass equations*. The data are presented in Table 1 of the paper, which is replicated in this Google Sheet.

We'll read in the data using the read_sheet() function from the **googlesheets4** package. We will also load the **tidyverse** package to use some of its plotting features:

```
library(tidyverse)
library(googlesheets4)
```

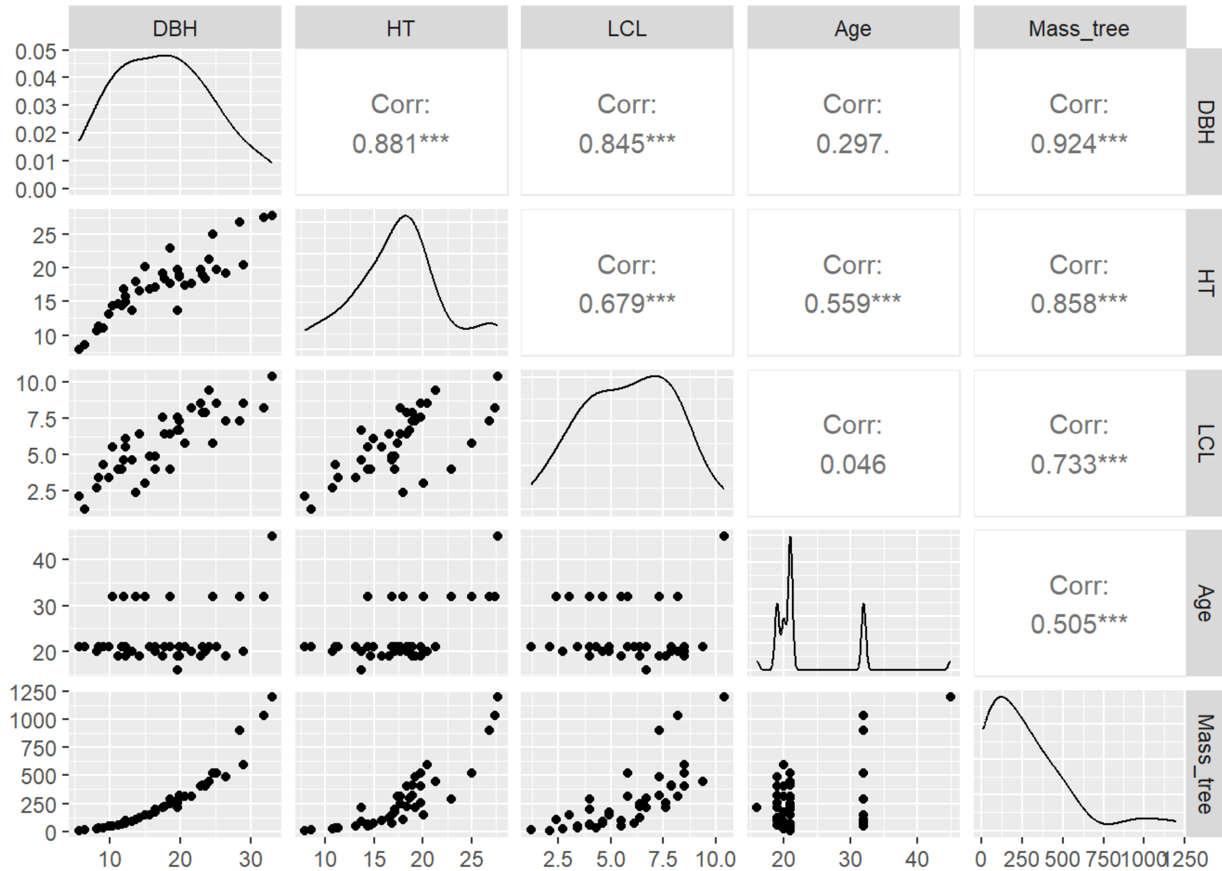
The data contain the following variables:

- TreeID: Tree observation record,
- DBH: Tree diameter at breast height, cm,
- HT: Tree height, m,
- LCL: Tree live crown length, m,
- Age: Age of the tree, years,
- Mass_wood: Green mass of the wood in the tree, kg,
- Mass_bark: Green mass of the bark in the tree, kg,
- Mass_crown: Green mass of the crown of the tree, kg, and
- Mass_tree: Green mass of all tree components, kg.

Our ultimate interest is in predicting the mass all tree components using common tree measurements such as tree diameter, height, live crown length, and age. Before we start modeling with the data, it is a good practice to first visualize the variables. The ggpairs() function from the **GGally** package is a useful tool that visualizes the distribution and correlation between variables:

```
library(GGally)

ggpairs(tree, columns = c(2:5, 9))
```



You can see a few variables have strong positive correlations with the mass of the tree (e.g., height and diameter) and some more moderate positive correlations (e.g., age).

The randomForest R package

R and Python both have numerous packages that implement random forests. In R alone, there are nearly 400 packages with the word "tree" or "forest" in their name. (Sidebar: This is not ideal if you're a forest analyst of biometrician.) The **Random Forest** R package remains one of the most popular ones in machine learning.

We can install and load the **Random Forest** package:

```
# install.packages("randomForest")
library(randomForest)
```

We will use the randomForest() function to predict total tree mass using several variables in the **tree** data set. A few other key statements to use in the randomForest() function are:

- keep.forest = T: This will save the random forest output, which will be helpful in summarizing the results.
- importance = TRUE: This will assess the importance of each of the predictors, essential output in random forests!
- mtry = 1: This tells the function to randomly sample one variable at each split in the random forest. For applications in regression, the default value is the number of predictor variables divided by three (and rounded down). In the modeling, several small samples of the entire data set are taken. Any observations that are not taken are called "out-of-bag" samples.
- ntree = 500. This tells the function to grow 500 trees. Generally, a larger number of trees will produce more stable estimates. However, increasing the number of trees needs to be done with consideration of time and memory issues when dealing with large data sets.

Our response variable in the random forests model is Mass_tree and predictors are DBH, HT, LCL, and Age.

```
tree.rf <- randomForest(Mass_tree ~ DBH + HT + LCL + Age,
                        data = tree,
                        keep.forest = T,
                        importance = TRUE,
                        mtry = 1,
                        ntree = 500)
tree.rf
```

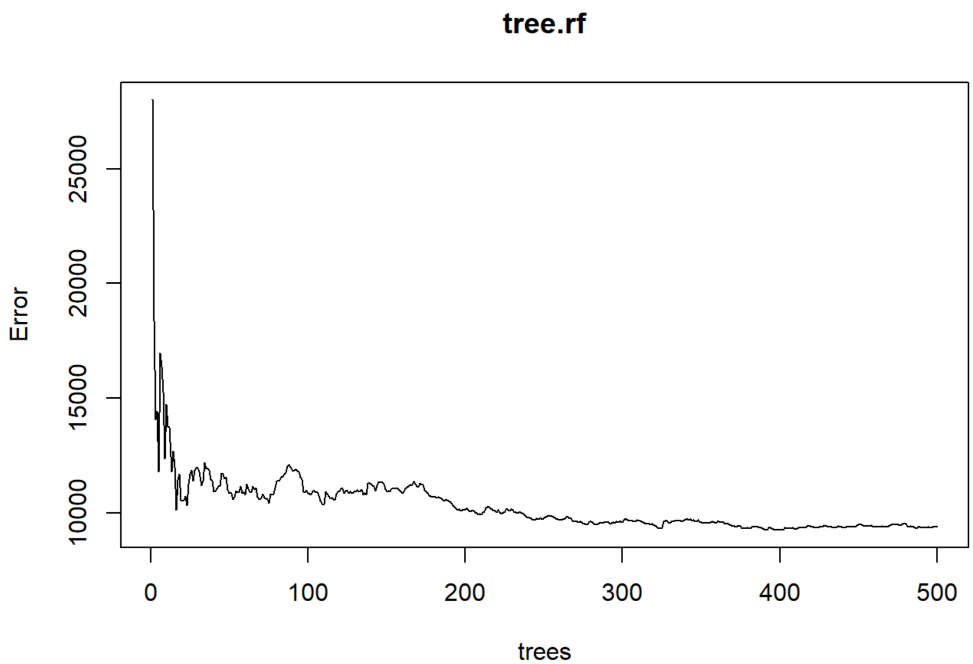
```
Call:
 randomForest(formula = Mass_tree ~ DBH + HT + LCL + Age, data = tree,
keep.forest = T, importance = TRUE, mtry = 1, ntree = 500)
               Type of random forest: regression
                     Number of trees: 500
No. of variables tried at each split: 1

          Mean of squared residuals: 9415.002
                    % Var explained: 87.27
```

Note: the mean of squared residuals and the percent variation explained (analogous to R-squared) provided in the output. (We'll revisit them later.)

Another way to visualize the out-of-bag error rates of the random forests models is to use the plot() function. In this application, although we specified 500 trees, the out-of-bag error generally stabilizes after 100 trees:

```
plot(tree.rf)
```



Some of the most helpful output in random forests is the importance of each of the predictor variables. The importance score is calculated by evaluating the regression tree with and without that variable. When evaluating the regression tree, the mean square error (MSE) will go up, down, or stay the same.

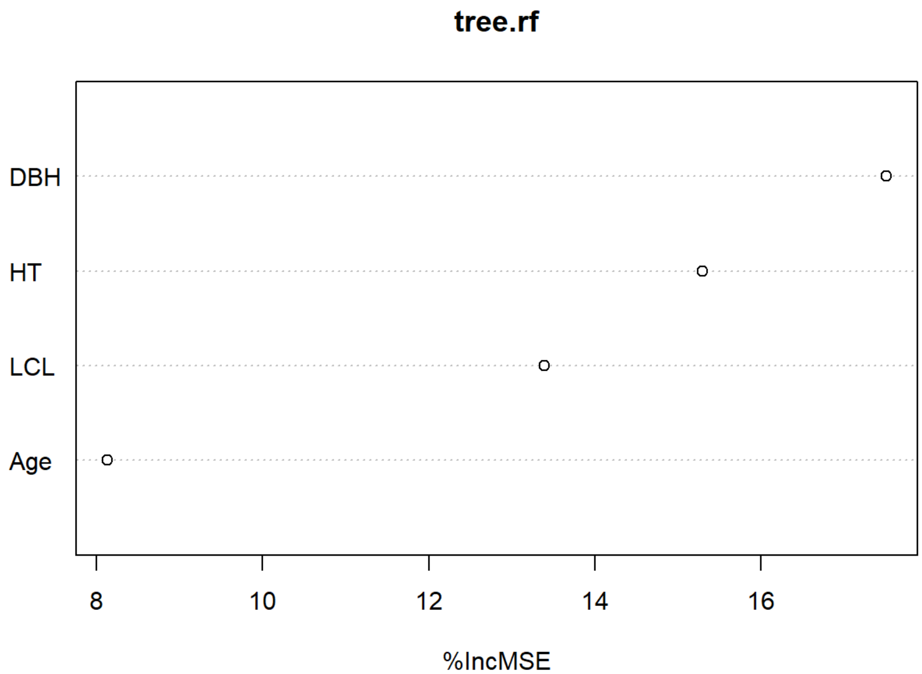
If the percent increase in MSE after removing the variable is large, it indicates an important variable. If the percent increase in MSE after removing the variable is small, it's less important.

The importance() function prints the importance scores for each variable and the varImpPlot() function plots them:

```
importance(tree.rf)
```

```
    %IncMSE IncNodePurity
DBH 17.507804      880292.7
HT  15.296300      807963.8
LCL 13.388462      639453.3
```

```
Age  8.131857      408963.7
varImpPlot(tree.rf,type=1)
```



The output indicates that DBH is the most important variable for predicting Mass_tree and age the least important.

Comparing random forests and regression models

Forest analysts often compare multiple models and determine which one has a better predictive ability. In this case, we can fit a multiple linear regression model to the data and compare it to the random forests model.

The lm() function can be used to develop a parametric model for Mass_tree:

```
tree.reg <- lm(Mass_tree ~ DBH + HT + LCL + Age, data = tree)
summary(tree.reg)
```

```
Call:
lm(formula = Mass_tree ~ DBH + HT + LCL + Age, data = tree)

Residuals:
     Min       1Q   Median       3Q      Max 
-136.285  -57.177   -9.399   43.822  189.758 
```

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -545.374     67.916  -8.030 1.89e-09 ***
DBH           40.523      5.778   7.013 3.68e-08 ***
HT           -15.048      8.079  -1.862   0.0709 .
LCL            2.490     12.259   0.203   0.8402
Age           15.431      3.198   4.825 2.72e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 82.33 on 35 degrees of freedom
Multiple R-squared:  0.9198,    Adjusted R-squared:  0.9106
F-statistic: 100.4 on 4 and 35 DF,  p-value: < 2.2e-16
```

Note: the residual standard error of 82.33 kg and the adjusted R-squared of 0.91. The residual standard error is slightly lower and the R-squared value slightly higher for the multiple regression model compared to the random forest output. In addition, further work may be conducted on the multiple regression model by removing the non-significant variables and refitting the model.

Another aspect of model evaluation is comparing predictions. Although random forests models are often considered a “black box” method because their results are not easily interpreted, the predict() function provides predictions of total tree mass:

```
Mass_pred_rf <- predict(tree.rf, tree, predict.all = F)
Mass_pred_reg <- predict(tree.reg, tree, predict.all = F)
```

In an ideal setting we might test our model on an independent data set not used in model fitting. However, we can combine the predicted tree weights from both models to the **tree** data set:

```
tree2 <- as.data.frame(cbind(tree, Mass_pred_rf, Mass_pred_reg))
```

Note that some predictions from the linear regression model on the 40 trees provide negative values for predicted total tree mass, an undesirable feature that may need to be addressed before implementing the model:

```
tree2 %>%
  summarize(Mass_tree, Mass_pred_rf, Mass_pred_reg)
```

	Mass_tree	Mass_pred_rf	Mass_pred_reg
1	9.8	25.21493	-108.051811
2	12.1	25.05643	-86.903051
3	24.4	40.88979	-62.814807
4	27.0	34.52743	-42.513067
5	33.6	43.41506	-7.391764
6	43.5	45.98330	-8.814627
7	46.0	99.98358	168.354603
8	56.1	77.63545	-8.073626
9	64.4	65.60557	47.563293
10	70.8	108.85428	64.024945
11	75.9	111.52683	189.278688
12	88.7	84.93915	103.439719
13	95.7	102.76580	18.126885
14	102.4	143.41118	238.684823
15	123.7	145.36054	90.880242
16	147.6	176.06111	261.258307
17	148.5	143.53247	174.276553
18	174.8	170.33346	186.750002
19	193.0	169.30845	199.939638
20	211.7	207.50296	306.293014
21	214.6	269.89235	186.964881
22	225.3	245.55534	240.537957
23	244.7	247.63206	277.932654
24	258.2	289.27981	263.034375
25	285.8	259.22561	363.444771
26	297.6	285.91326	317.816460
27	309.8	270.94465	366.051168
28	316.2	342.13331	392.605018
29	318.0	314.38717	283.934957
30	401.1	424.69591	399.000959
31	402.2	389.01151	463.875242
32	411.9	401.71263	450.015697
33	446.3	467.22418	458.158909
34	490.3	419.49775	546.871939
35	522.6	519.87912	583.516204
36	522.7	472.62866	519.012527
37	593.6	580.70856	652.592720
38	900.3	788.07493	714.152257
39	1034.9	892.33950	845.142484

40 1198.5 1006.03689 1095.330861

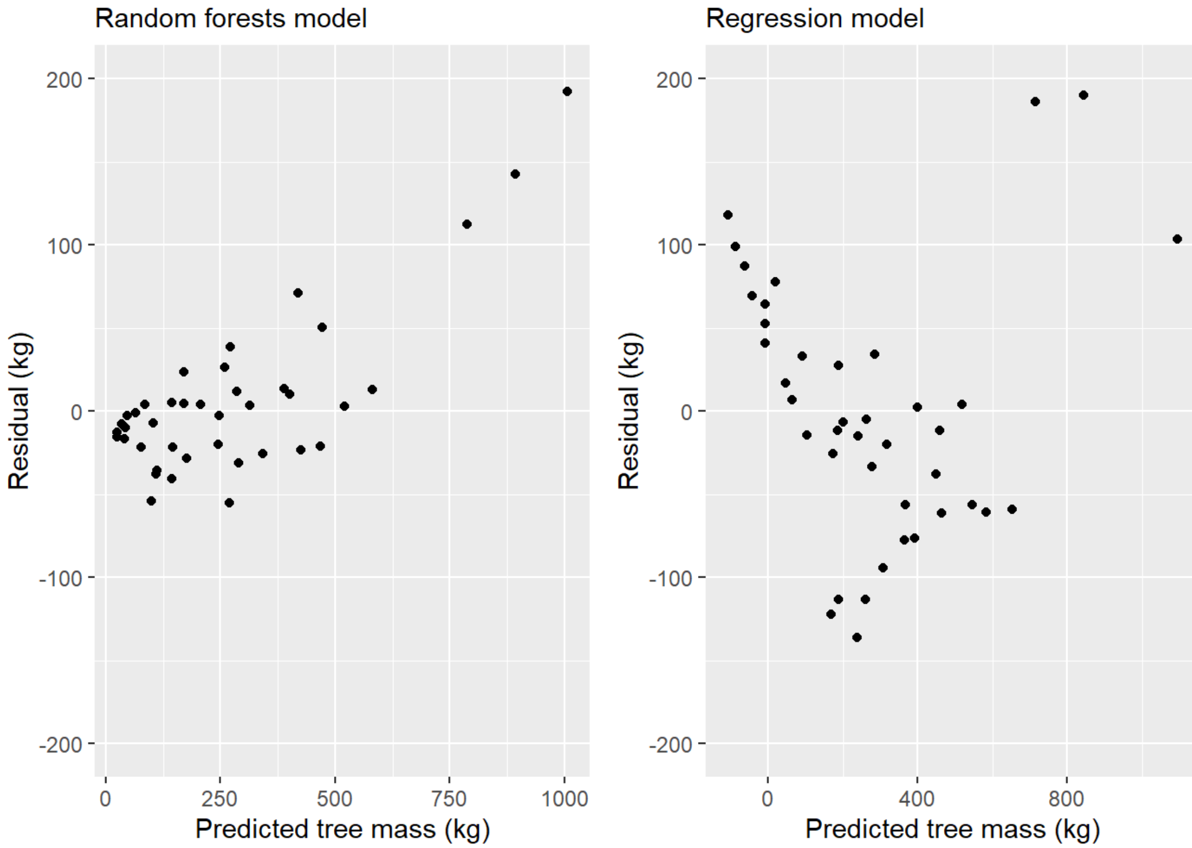
We may also be interested in plotting residual values from both model types to compare their performance:

```
p.rf <- ggplot(tree2, (aes(x = Mass_pred_rf, y = Mass_tree - Mass_pred_rf))) +
  geom_point() +
  scale_y_continuous(limits = c(-200, 200)) +
  labs(x = "Predicted tree mass (kg)",
       y = "Residual (kg)",
       subtitle = "Random forests model")

p.reg <- ggplot(tree2, (aes(x = Mass_pred_reg, y = Mass_tree - Mass_pred_reg)))
+
  geom_point() +
  scale_y_continuous(limits = c(-200, 200)) +
  labs(x = "Predicted tree mass (kg)",
       y = "Residual (kg)",
       subtitle = "Regression model")

library(patchwork)

p.rf + p.reg
```



With the heteroscedastic residuals in the models, we'd likely want to explore transforming the data prior to model fitting, or to explore other modeling techniques.

Summary

Random forests techniques are flexible and can perform comparably with other regression or classification methods. Random forests can handle all types of data (e.g., categorical, continuous) and are advantageous because they work well with data sets containing many predictor variables. The **Random Forest** package has seen a lot of development and can be used to help solve modeling problems in your future forest analytics work.