

Exercise 5

AUTHOR

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8.1 - Recrease simulated data from Exercise 4

```
library(mlbench)
library(tidyverse)
library(base)
library(MASS)
library(earth)
library(AppliedPredictiveModeling)
library(randomForest)
library(caret)
set.seed(200)
simulated <- mlbench.friedman1(200, sd = 1)
simulated <- cbind(simulated$x, simulated$y)
simulated <- as.data.frame(simulated)
colnames(simulated)[ncol(simulated)] <- "y"
```

a. Fit a random forest model to all of the predictors, then estimate the variable importance scores:

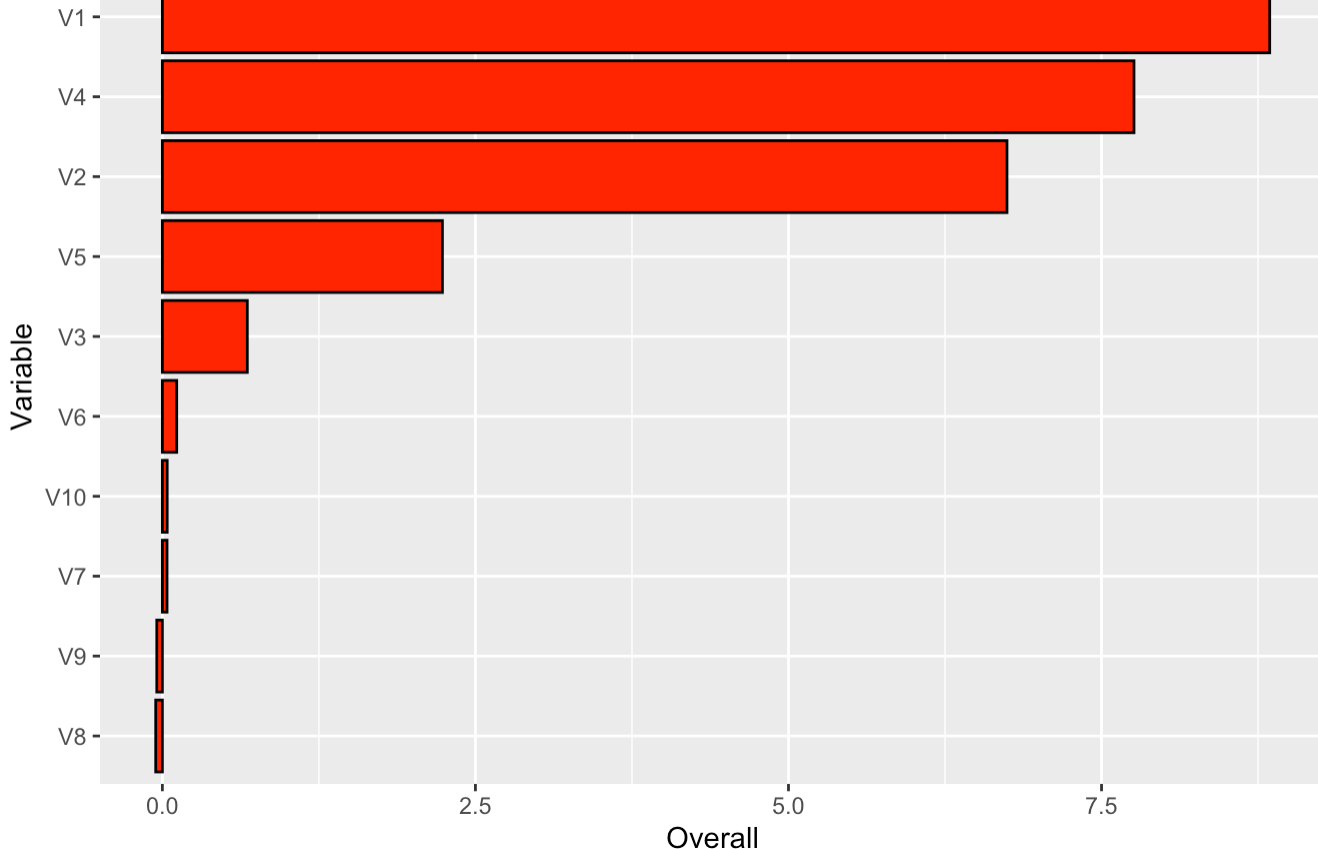
```
model1 <- randomForest(y ~ ., data = simulated, importance = TRUE, ntree = 1000)
rfImp1 <- varImp(model1, scale = FALSE)
print(rfImp1)
```

```
      Overall
V1  8.84289608
V2  6.74508245
V3  0.67830653
V4  7.75934674
V5  2.23628276
V6  0.11429887
V7  0.03724747
V8 -0.05349642
V9 -0.04495617
V10 0.03863205
```

Did the random forest model significantly use the uninformative predictors (V6 - V10)?

```
rfImp1 %>%
  mutate (var = rownames(rfImp1)) %>%
  ggplot(aes(Overall, reorder(var, Overall, sum), var)) +
  geom_col(fill = 'red', colour = 'black') +
  labs(title = 'Model 1 Variable Importance' , y = 'Variable')
```

Model 1 Variable Importance



**** The cumulative bar graph above shows that V6-10 were not significantly used in our random forest model.****

b. Now add an additional predictor that is highly correlated with one of the informative predictors. For example:

```
simulated$duplicate1 <- simulated$V1 + rnorm(200) * .1
cor(simulated$duplicate1, simulated$V1)
```

```
[1] 0.9396216
```

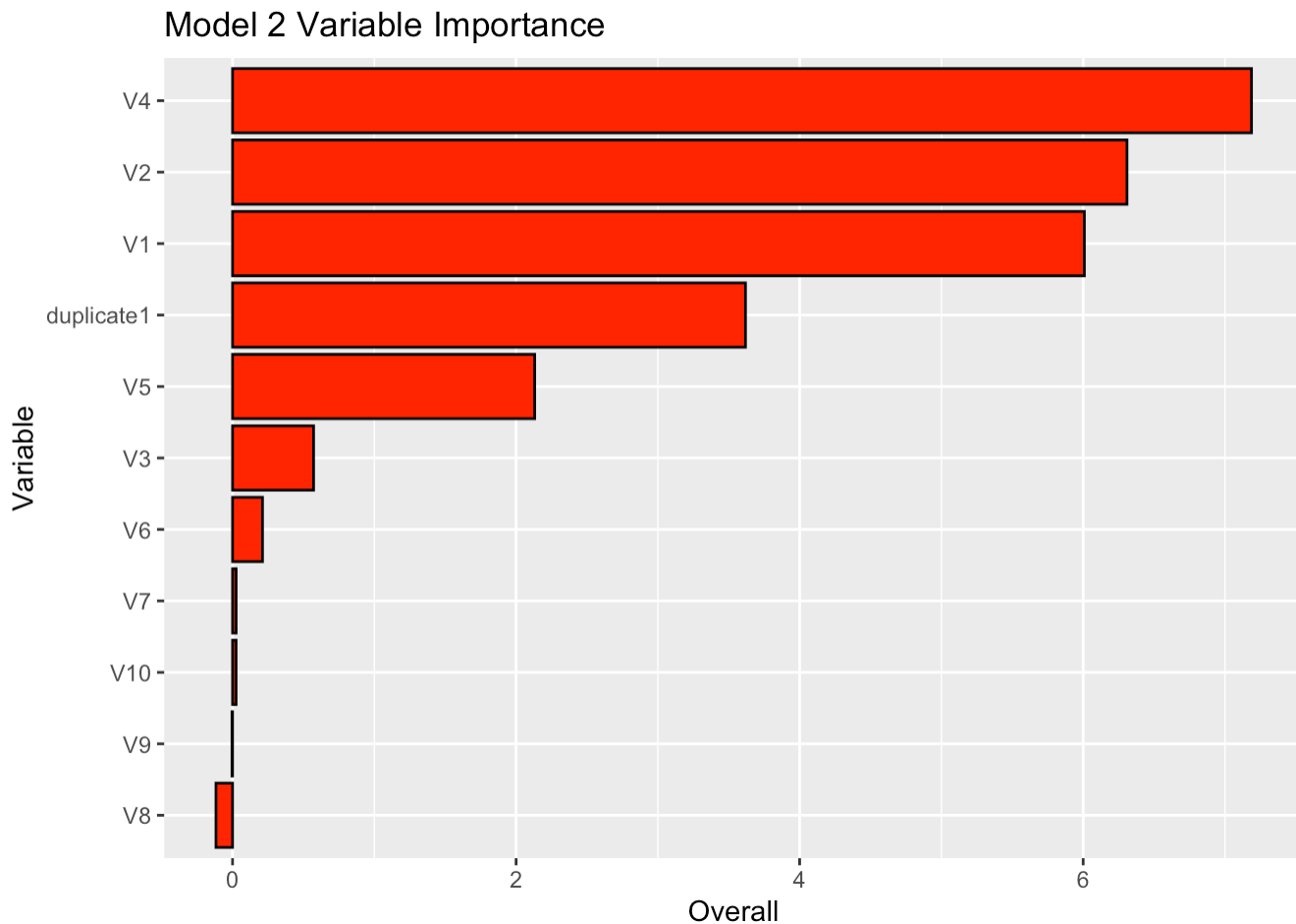
Fit another random forest model to these data. Did the importance score for V1 change? What happens when you add another predictor that is also highly correlated with V1?

```
rf_model2 <- randomForest(y ~ ., data = simulated, importance = TRUE, ntree = 1000)
rfImp2 <- varImp(rf_model2, scale = FALSE)
print(rfImp2)
```

```

      Overall
V1      6.008319352
V2      6.308908170
V3      0.571604465
V4      7.187015958
V5      2.131040245
V6      0.211304611
V7      0.025100355
V8     -0.116980037
V9     -0.003679481
V10     0.024878337
duplicate1 3.618101735
```

```
rfImp2 %>%
  mutate (var = rownames(rfImp2)) %>%
  ggplot(aes(Overall, reorder(var, Overall, sum), var)) +
  geom_col(fill = 'red', colour = 'black') +
  labs(title = 'Model 2 Variable Importance' , y = 'Variable')
```



The importance score for V1 decreased, but increased for the other variables when another highly correlated variable with V1 is added.

c. Use the `cforest` function in the `party` package to fit a random forest model using conditional inference trees. The `party` package function `varimp` can calculate predictor importance. The `conditional` argument of that function toggles between the traditional importance measure and the modified version. Do these importances show the same pattern as the traditional random forest model?

```
library(partykit)
library(party)

# Fit cforest model
set.seed(123)
cf_model <- cforest(y ~ ., data = simulated, controls = cforest_unbiased(ntree = 1000))

# Calculate variable importance
cf_varimp <- varimp(cf_model, conditional = FALSE)
print(cf_varimp)
```

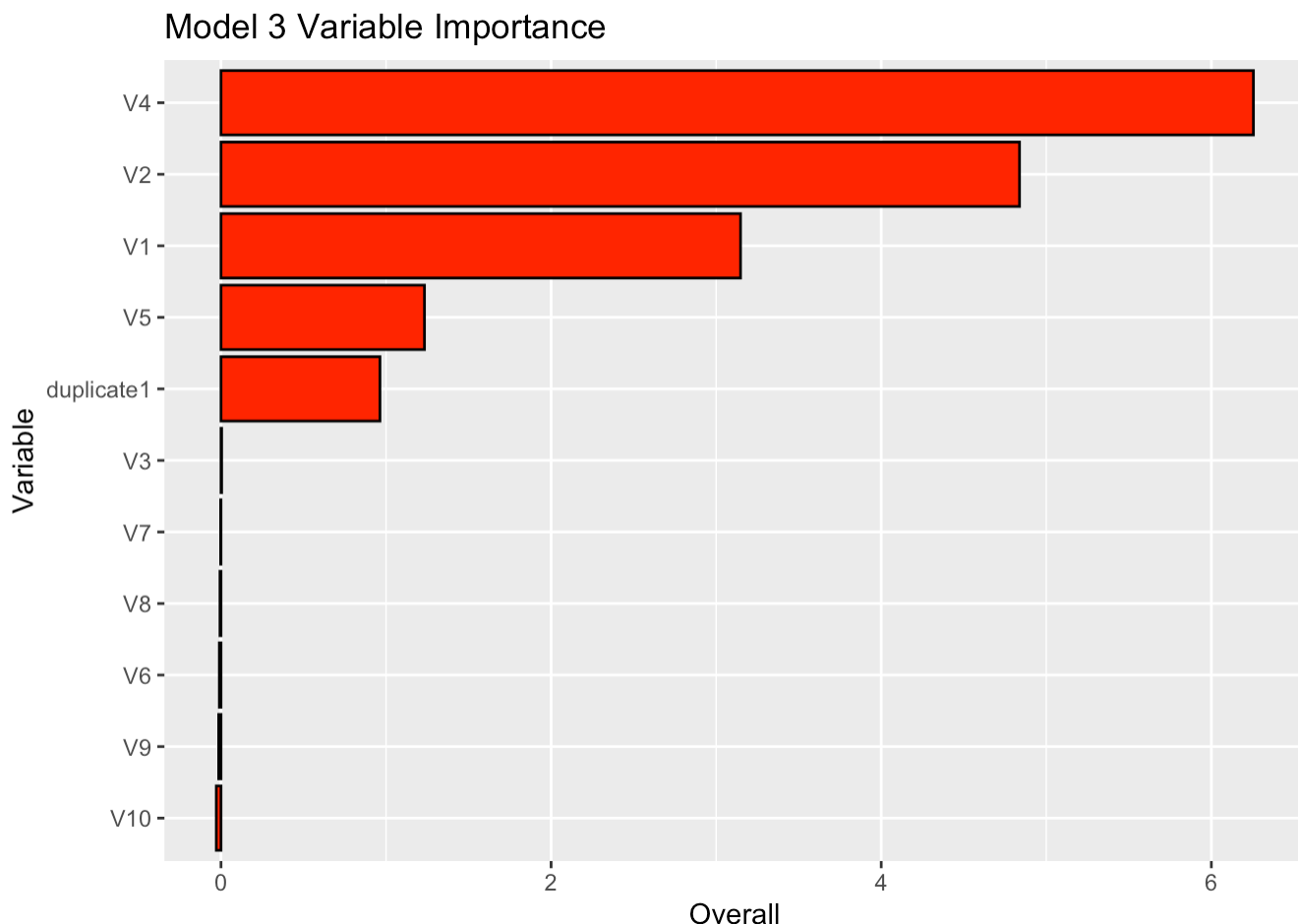
V1 V2 V3 V4 V5 V6

6.762175680	6.011214623	-0.002809259	7.857594235	2.053362995	0.007422406
V7	V8	V9	V10	duplicate1	
0.033006890	-0.025242264	0.008089810	-0.057880930	2.773897304	

```
# Calculate conditional variable importance
cf_cond_varimp <- varimp(cf_model, conditional = TRUE)
print(cf_cond_varimp)
```

V1	V2	V3	V4	V5	V6
3.186416009	4.786623908	0.004089477	6.277869376	1.186573199	0.009167534
V7	V8	V9	V10	duplicate1	
0.007945494	-0.019904985	-0.002481725	-0.021467387	1.006965608	

```
rf_model3 <- cforest(y ~ ., data = simulated)
rfImp3 <- varimp(rf_model3, conditional = TRUE) %>% as.data.frame()
rfImp3 %>%
  rename(Overall = '.') %>%
  mutate (var = rownames(rfImp3)) %>%
  ggplot(aes(Overall, reorder(var, Overall, sum), var)) +
  geom_col(fill = 'red', colour = 'black') +
  labs(title = 'Model 3 Variable Importance' , y = 'Variable')
```



**** The pattern of importance remains the same and V6-V10 remain unimportant.****

d. Repeat this process with different tree models, such as boosted trees and Cubist. Does the same pattern occur?

```
library(gbm)

# Fit gbm model
set.seed(123)
gbm_model <- train(y ~ ., data = simulated, method = "gbm", trControl = trainControl(method =

# Calculate variable importance
gbm_varimp <- varImp(gbm_model, scale = FALSE)
print(gbm_varimp)
```

gbm variable importance

	Overall
V4	4896.32
V2	3865.06
V1	3516.32
V5	1781.39
V3	1276.47
duplicate1	609.03
V7	170.98
V9	124.41
V6	101.75
V10	100.11
V8	76.49

```
library(Cubist)

# Fit Cubist model
set.seed(123)
cubist_model <- train(y ~ ., data = simulated, method = "cubist", trControl = trainControl(me

# Calculate variable importance
cubist_varimp <- varImp(cubist_model, scale = FALSE)
print(cubist_varimp)
```

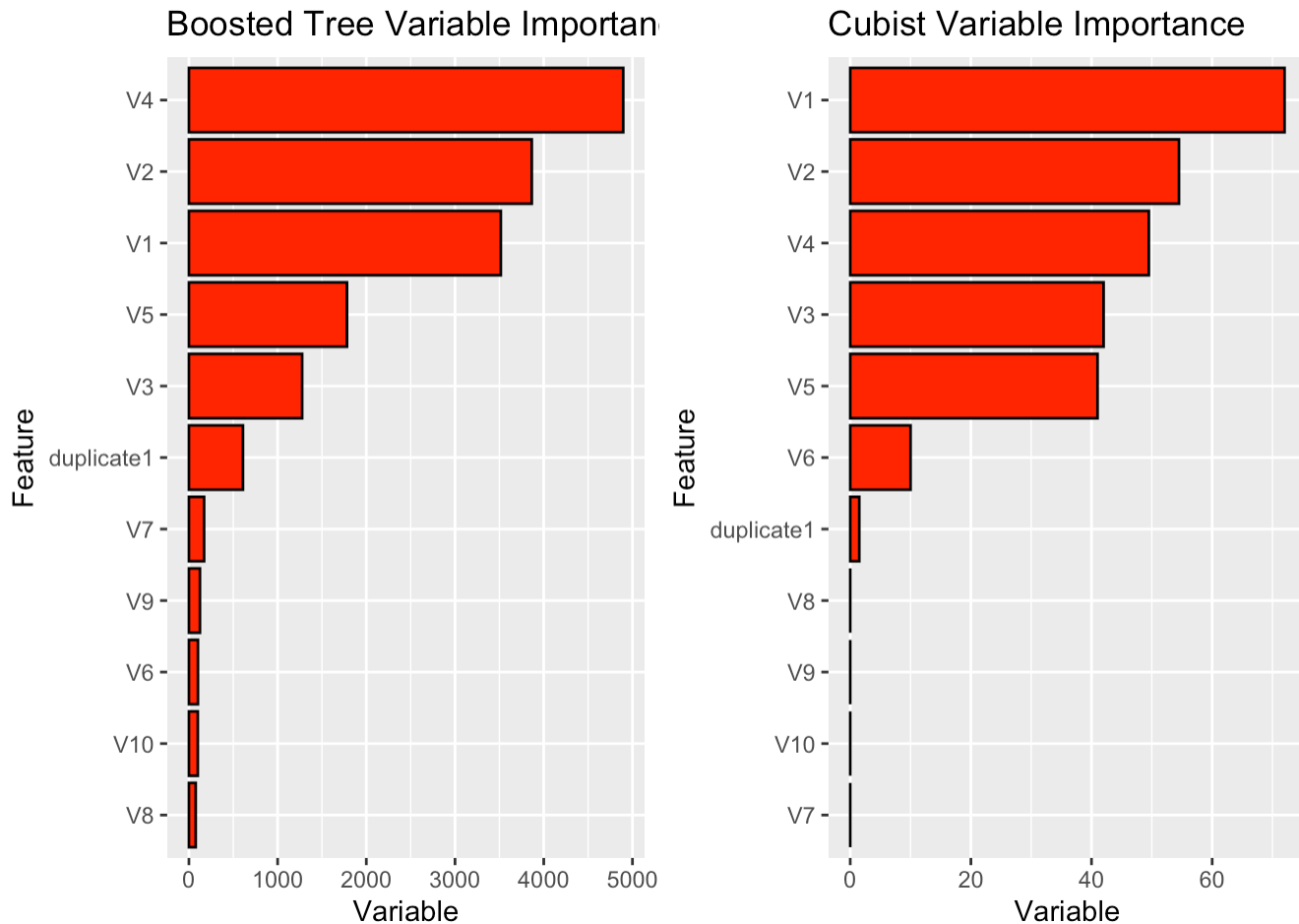
cubist variable importance

	Overall
V1	72.0
V2	54.5
V4	49.5
V3	42.0
V5	41.0
V6	10.0
duplicate1	1.5
V9	0.0
V7	0.0
V8	0.0
V10	0.0

```
gbm_plot <- gbm_varimp %>%
  ggplot(aes(Overall, reorder(var, Overall, sum), var)) +
  geom_col(fill = 'red', colour = 'black') +
  labs(title = 'Boosted Tree Variable Importance' , y = 'Variable')
```

```
cubist_plot <- cubist_varimp %>%
  ggplot(aes(Overall, reorder(var, Overall, sum), var)) +
  geom_col(fill = 'red', colour = 'black') +
  labs(title = 'Cubist Variable Importance' , y = 'Variable')
```

```
library(ggpubr)
ggarrange(gbm_plot, cubist_plot)
```



V1-V5 are both significant predictors in the boosted tree and cubist models, but their patterns of importance differ. The ranked order (most -> least important) for the boosted tree model is V4, V2, V1, V5, and V3. The ranked order for the Cubist model is V1, V2, V4, V3, and V5.