Report on Malware classification

HarvardX Data Science Capstone Project

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2023-03-15

Contents

Malware

Introduction

Malicious software (Malware) is a software used to harm, damage, access or alter computer systems or networks. There are several types of Malware, including viruses, worms, trojan horses, ransomware and spyware. Most malware access computer systems by internet and emails. They can hide in legitimate applications or are hidden in the system. Static analyses can be effective, but also easily evaded through obfuscation and altering the malware so much, that it is no longer recognized. Therefore additional dynamic features are used to classify malwares.

Dataset

The dataset *Malware static and dynamic features VxHeaven and Virus Total Data Set* [2] from the UCI Machine Learning Repository contains three csv.

- staDynBenignLab.csv: 1086 features extracted from 595 files on MS Windows 7 and 8, obtained Program Files directory.
- staDynVxHeaven2698Lab.csv: 1087 features extracted from 2698 files of VxHeaven dataset.
- staDynVt2955Lab.csv: 1087 features extracted from 2955 provided by Virus Total in 2018.

The staDynBenignLab has all the features of typical non-threatening programs wheare as staDynVx-Heaven2698Lab and staDynVt2955Lab are extracted features of malware programs from the databases of VxHeaven and Virus Total. The dataset provides static features like ASM, compiler version, operating system version, Hex dump and PE header [3] (portable executable) and dynamic features extracted from a cuckoo sandbox [4]. The dataset only contains windows specific programs and malware. The dataset is downloaded from the UCI Machine Learning Repository Dataset and the containing csv files are extracted. The data in each of the csv must be labeled first, describing the class of program identified (e.g. class 0 for benign, class 1 for static malware features and class 2 for dynamic malware features).

Goal

The dataset is used to explore and gain insight on how normal programs and malware differ in static and dynamic structure. Several machine learning algorithms to classify an unseen program as benign or malware (static or dynamic) are developed and compared. Overall, the goal of this project is to improve our understanding of how malware differs from normal programs, and to develop effective techniques for automatically identifying and classifying malware based on its static and dynamic features.

Summary

We are able to correctly identify between benign programs and Malware (static or dynamic) with $> 95\%$ accuracy and also good F1 scores with the Random Forest model.

Analysis

Disclaimer: Not all R code will be shown in this report. For the full code view the R-File on github.

Download

The zipped dataset is downloaded from the UCI archive and unzipped.

This will extract the following files: staDynBenignLab.csv, staDynVt2955Lab.csv, staDynVx-Heaven2698Lab.csv

Where

- *staDynBenignLab.csv*has 1087 features extracted from 595 files on MS Windows 7 and 8, obtained Program Files directory
- *staDynVxHeaven2698Lab.csv* has 1087 features extracted from 2698 files of VxHeaven dataset.
- *staDynVt2955Lab.csv* has 1088 features extracted from 2955 provided by Virus Total in 2018.

Preprocessing

Add classes to each dataset, depending on the origin of their data:

- 0: Normal *benign* programs
- 1: Malware with static features extracted from the *VxHeaven (vxheaven)* dataset
- 2: Malware with dynamic features extracted from the *Virus Total (vt)* dataset

Cleanup

The datasets have

- staDynBenignLab: 0,
- staDynVxHeaven2698Lab: 0 and
- staDynVt2955Lab: 0

missing values.

Check for features that not present in all three datasets, remove unique columns and combine all in one large dataset.

These columns are not present in all datasets:

. . . 1, filename, ___vbaVarIndexLoad, SafeArrayPtrOfIndex

So they are removed and the resulting dataset we now work with has 1086 features for each of the 595 different programs.

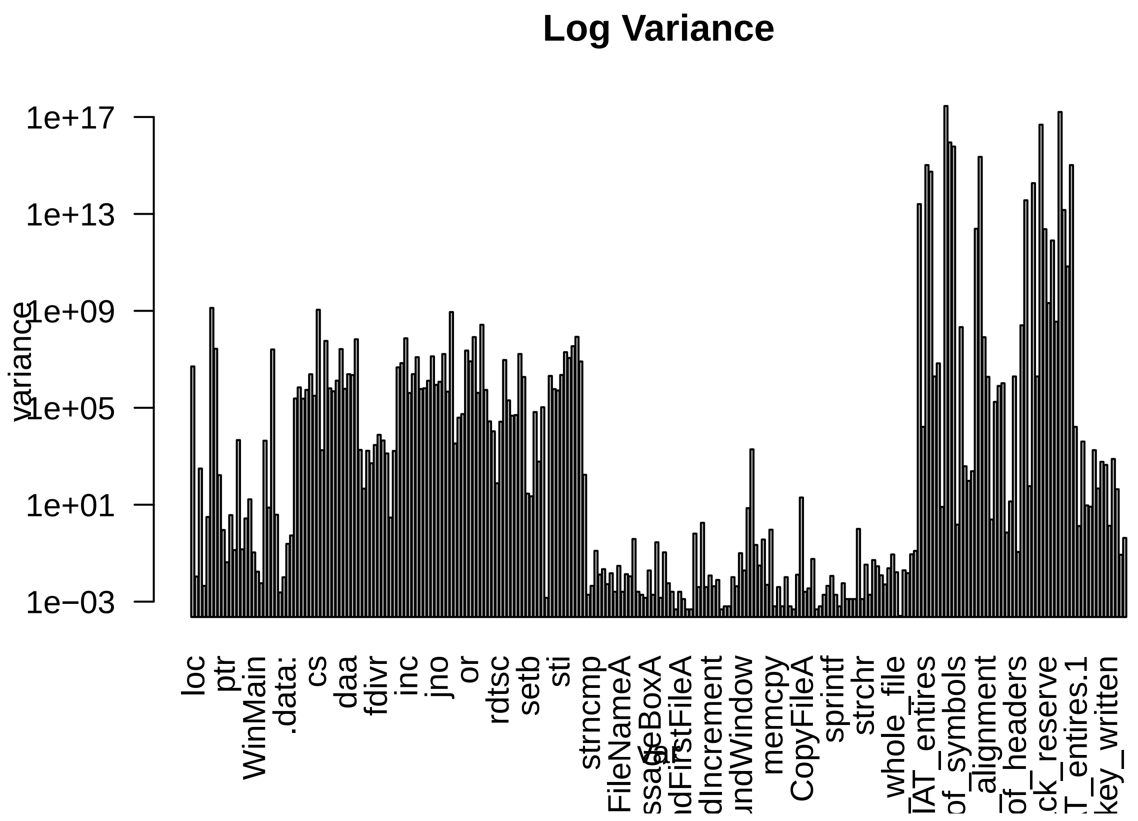
Variance

Check feature variance for features without any relevant information, find all these features where the variation is 0 and remove them from the dataset.

```r
# Calculate the variance of each variable in the dataset
variances <- apply(data, 2, var)

# Find which variances are equal to 0
zero_variances <- which(variances == 0)
```

840 found to have a variance of 0. E.g. all variables of "count_file_renamed" are 0 so there is no benefit for the analysis or training of models. These are removed from the dataset and the remaining variances are plotted here:

```r
# Exclude any variables with 0 variance
nonzero_variances <- variances[variances > 0]
# only 246 variables remain

# Create a bar plot of the variances
barplot(nonzero_variances, main="Log Variance", las=2, log="y", xlab="var", ylab="variance")
```



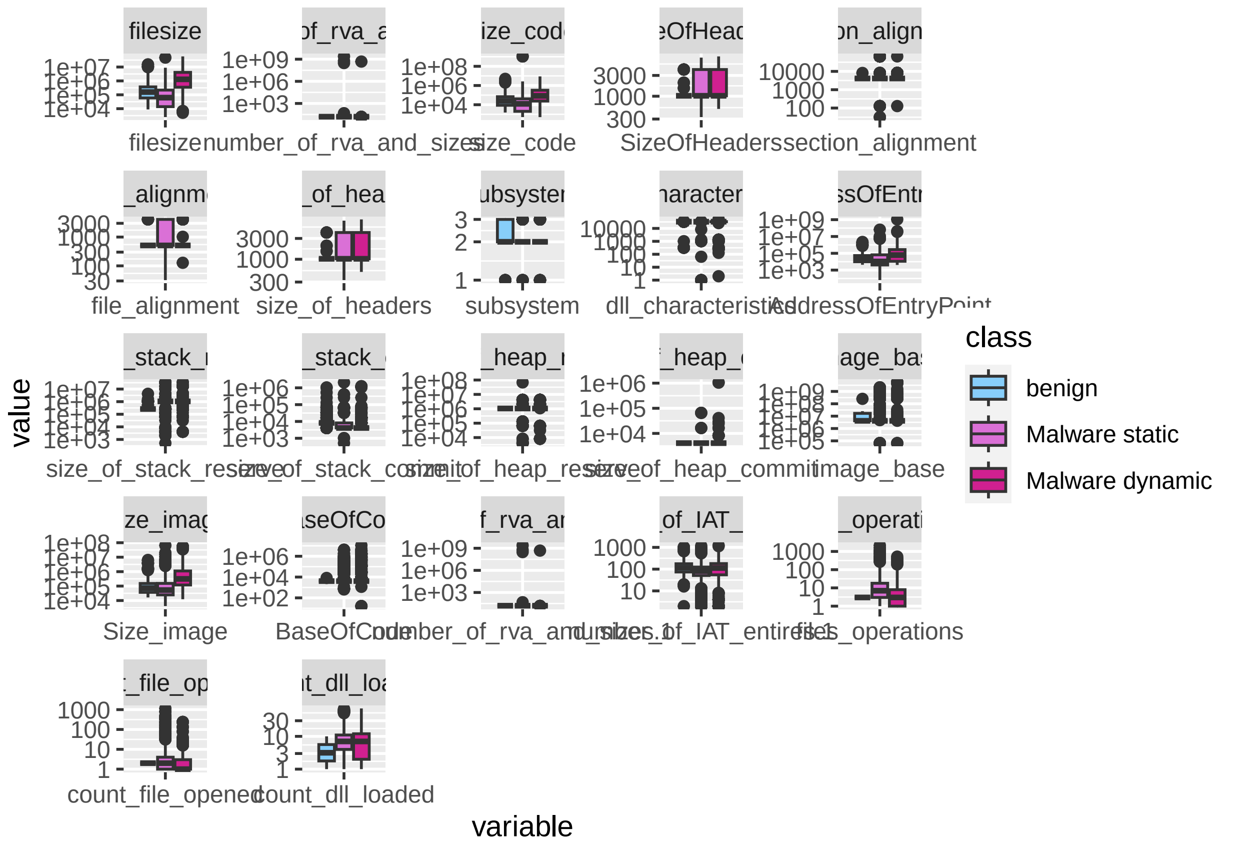
Feature Clusters

Cluster some features that are most likely to be compared against each other like data types (e.g. uint,int,char,word. . .) or File specific characteristics or assembly functions. Some I could not figure out the meaning behind it (like ent_whole_file or ent_var) so these are left out.

File/exe

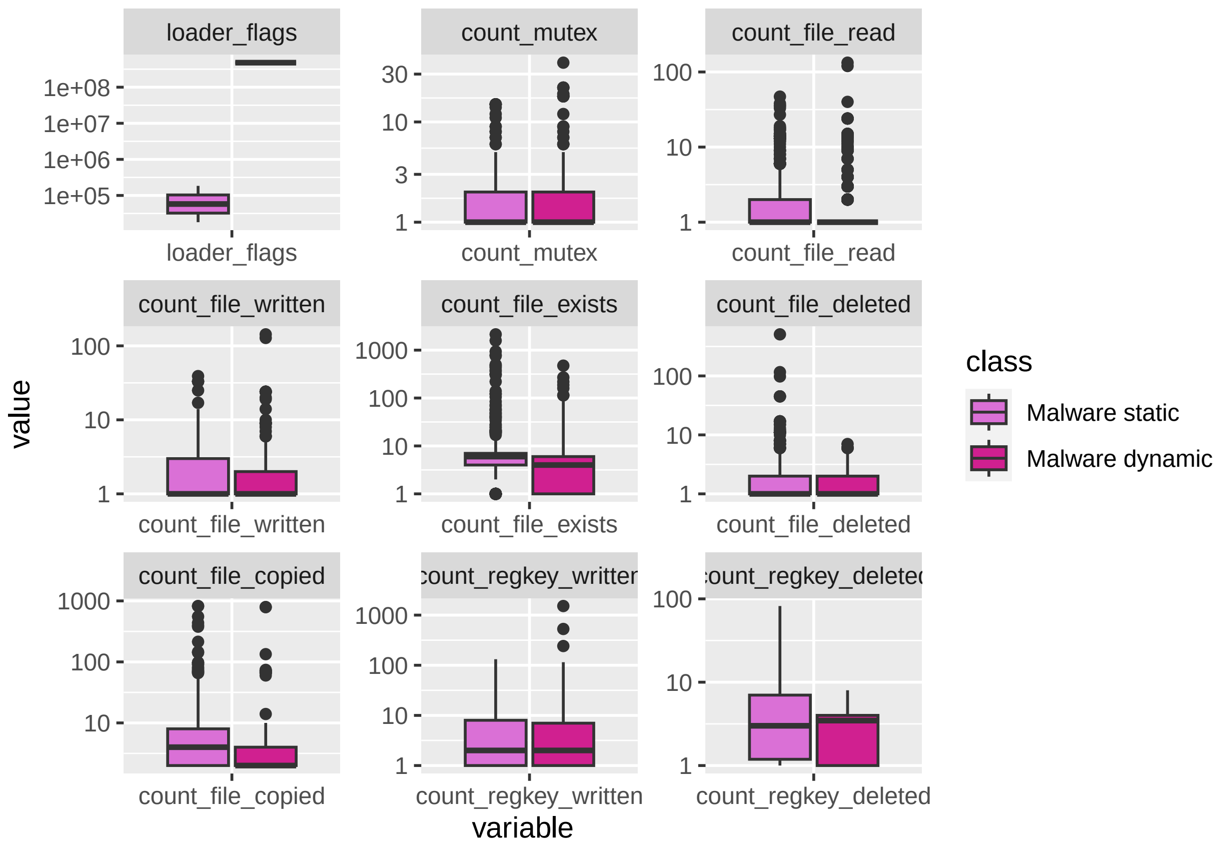
File characteristics like size of number of sections or runtime fingerprints like loaded dll's or stack/heap sizes.

```
#file <- c('.text.','filesize','number_of_rva_and_sizes','size_code','SizeOfHeaders','section_alignment

file <- c('filesize','number_of_rva_and_sizes','size_code','SizeOfHeaders','section_alignment','file_ali


# subset of these types
file_subset <- subset(data_v2, select=file)

# give the classes some better names
file_subset$class <- factor(file_subset$class, levels = c(0, 1, 2), labels = c("benign", "Malware stati

file_subset.m <- melt(file_subset, id.var = "class")

ggplot(data = file_subset.m, aes(x=variable, y=value)) +
  geom_boxplot(aes(fill=class)) +
  scale_fill_manual(values = c("lightskyblue", "orchid", "violetred"),
                    labels = c("benign", "Malware static", "Malware dynamic")) +
  facet_wrap( ~ variable, scales="free") +
  scale_y_log10(limits = c(NA, NA))
```



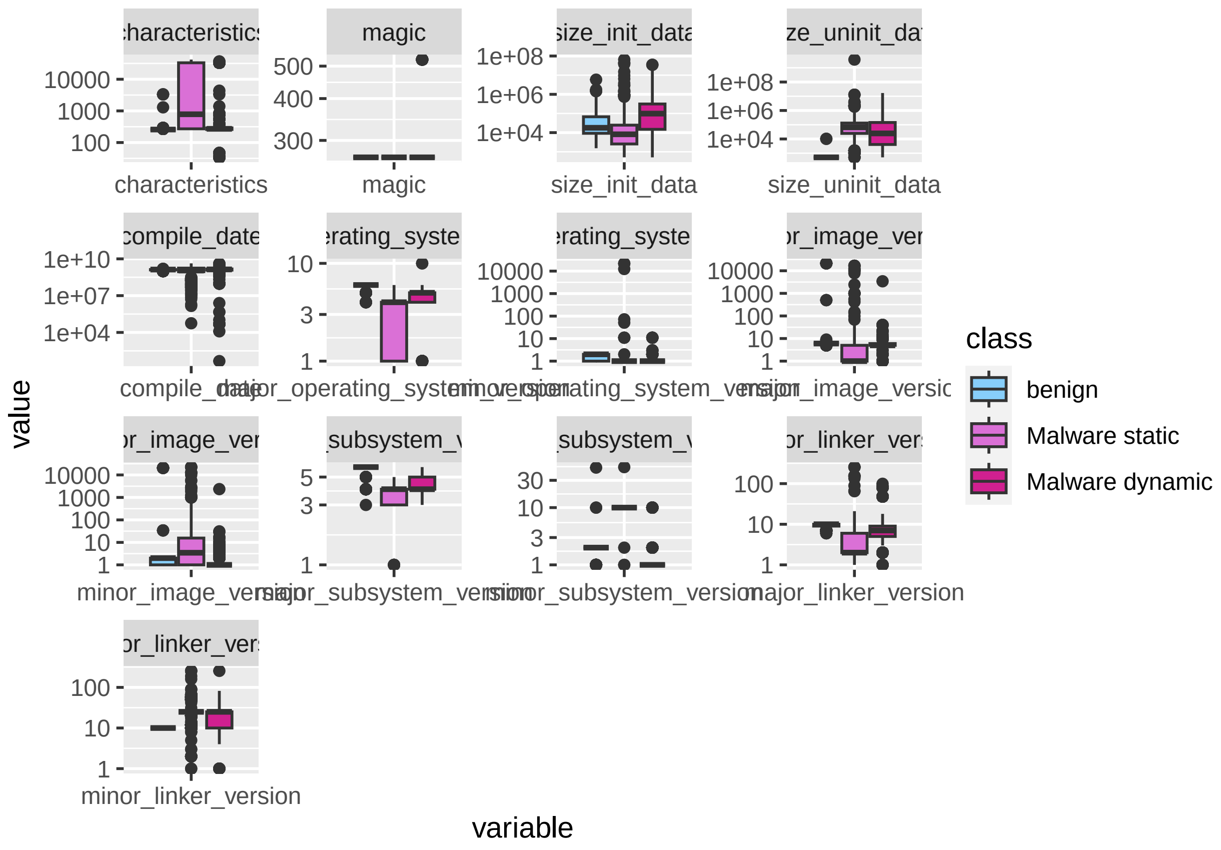
Some do not have characteristic data for all three classes, eg. .rdata, .data, loader_flags, count_mutex, count_file_read, count_file_written, count_file_exists, count_file_deleted, count_file_copied, count_regkey_written and count_regkey_deleted. These are exclusively available for static and dynamic malware. Wile most are quite similar in their distribution, loader_flags is very different between the two classes.

```r
file2 <- c('loader_flags','count_mutex','count_file_read','count_file_written','count_file_exists','cou

# subset of these types
file2_subset <- subset(data_v2, select=file2)

# give the classes some better names
file2_subset$class <- factor(file2_subset$class, levels = c(0, 1, 2), labels = c("benign", "Malware sta

file2_subset.m <- melt(file2_subset, id.var = "class")

ggplot(data = file2_subset.m, aes(x=variable, y=value)) +
  geom_boxplot(aes(fill=class)) +
  scale_fill_manual(values = c("orchid", "violetred"),
                    labels = c("Malware static", "Malware dynamic")) +
  facet_wrap( ~ variable, scales="free") +
  scale_y_log10(limits = c(NA, NA))
```



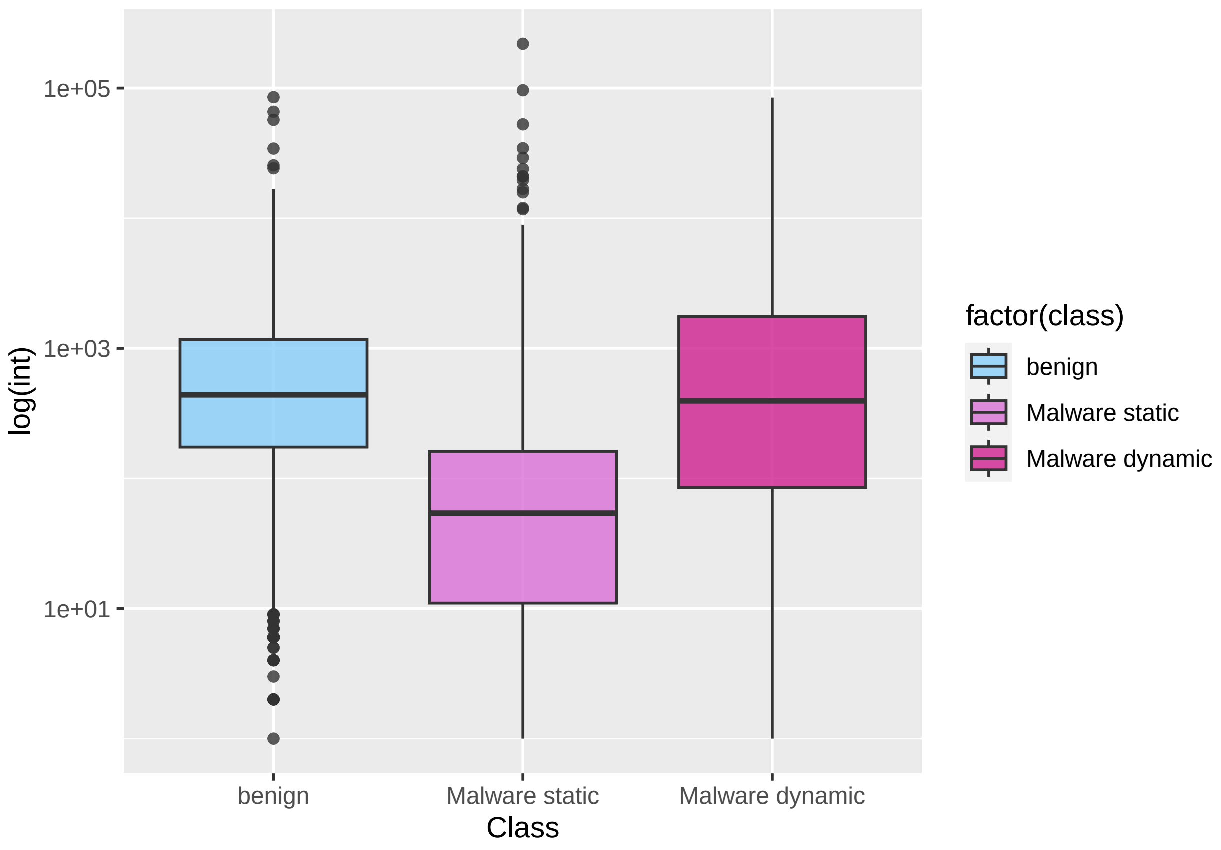
Compiler/Linker

```
compiler <- c('characteristics','magic','size_init_data','size_uninit_data','compile_date','major_opera

# subset of these comiler/linker statistics
compiler_subset <- subset(data_v2, select=compiler)

# give the classes some better names
compiler_subset$class <- factor(compiler_subset$class, levels = c(0, 1, 2), labels = c("benign", "Malwa

compiler_subset.m <- melt(compiler_subset, id.var = "class")

ggplot(data = compiler_subset.m, aes(x=variable, y=value)) +
  geom_boxplot(aes(fill=class)) +
  scale_fill_manual(values = c("lightskyblue", "orchid", "violetred"),
                    labels = c("benign", "Malware static", "Malware dynamic")) +
  facet_wrap( ~ variable, scales="free") +
  scale_y_log10(limits = c(NA, NA))
```



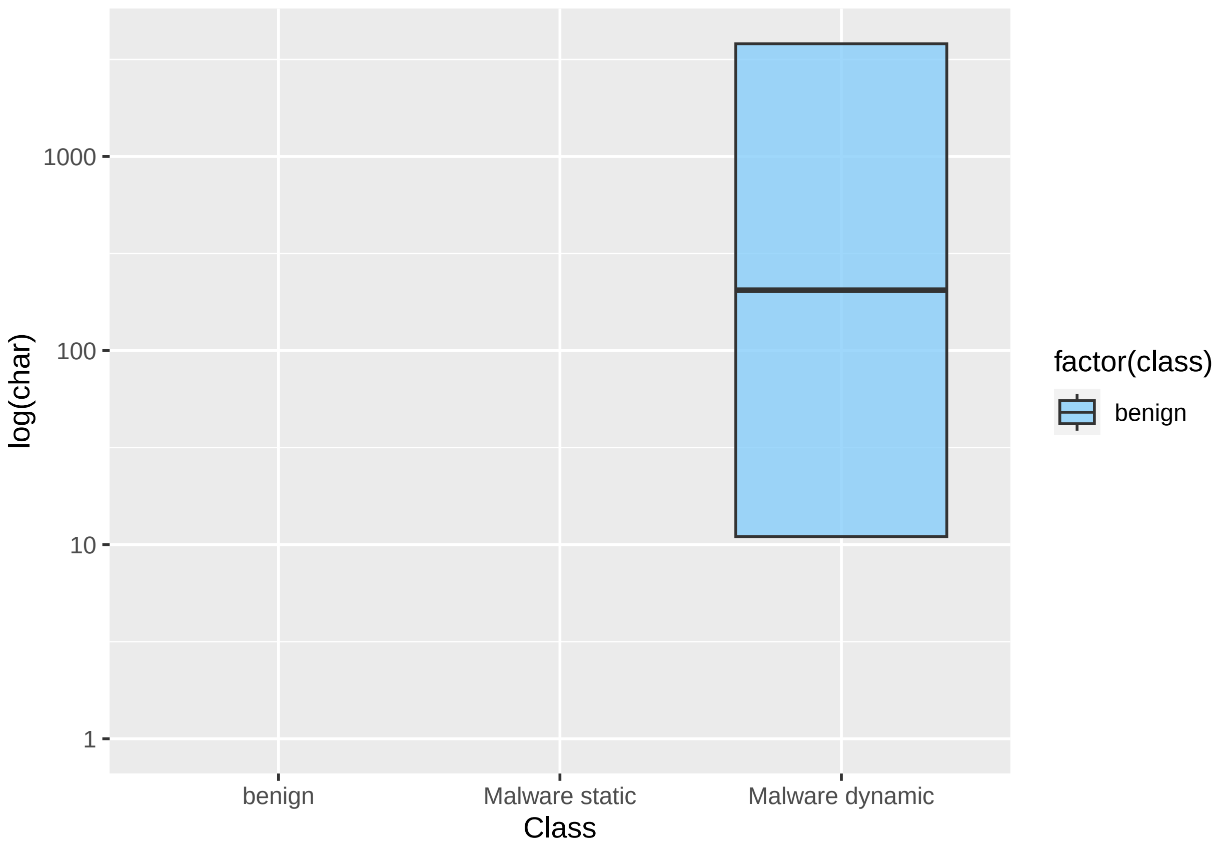
Datatypes

```r
# list datatypes + class
types <- c('UINT', 'LONG', 'BOOL', 'WORD','byte','word','char','int','class')

# subset of these types
types_subset <- subset(data_v2, select=types)
# give the classes some better names
types_subset$class <- factor(types_subset$class, levels = c(0, 1, 2), labels = c("benign", "Malware sta

# boxplot for the type "int"
ggplot(types_subset, aes(x = class, y = int, fill=factor(class))) +
  geom_boxplot(alpha = 0.8) +
  scale_fill_manual(values = c("lightskyblue", "orchid", "violetred"),
                    labels = c("benign", "Malware static", "Malware dynamic")) +
  scale_y_log10(limits = c(1, max(types_subset$int))) +
  labs(x = "Class", y = "log(int)")
```



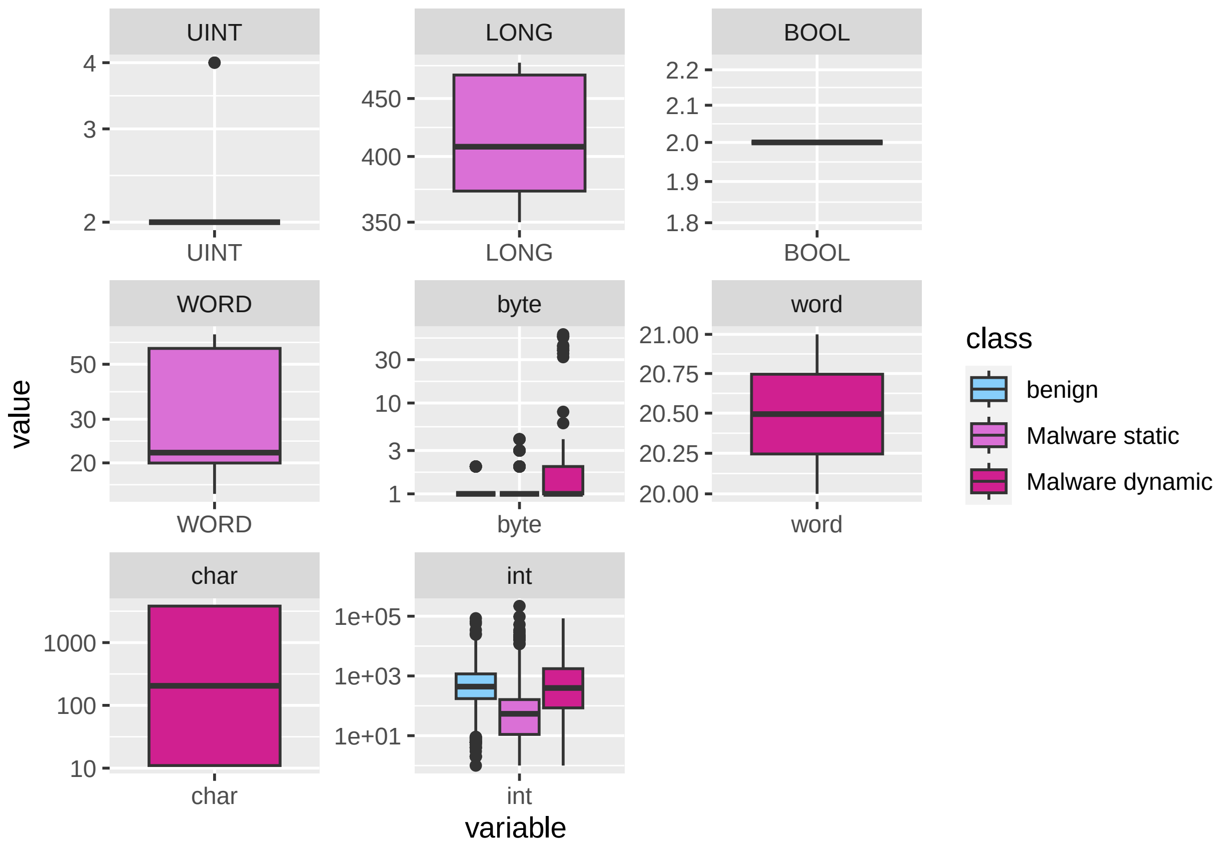
The static malware has generally lower int's than the other classes. But benign and dynamic Malware are quite similar, although bening is a bit denser packet around the mean. There are some types that have data only in one class, e.g. char.

```
ggplot(types_subset, aes(x = class, y = char, fill=factor(class))) +
  geom_boxplot(alpha = 0.8) +
  scale_fill_manual(values = c("lightskyblue", "orchid", "violetred"),
                    labels = c("benign", "Malware static", "Malware dynamic")) +
  scale_y_log10(limits = c(1, max(types_subset$char))) +
  labs(x = "Class", y = "log(char)")
```



Here a plot for all datatypes. Only byte and int have variables in all classes. WORD and word are probably the same and can be compared but there is no word for the benign class.

```
types_subset.m <- melt(types_subset, id.var = "class")

ggplot(data = types_subset.m, aes(x=variable, y=value)) +
  geom_boxplot(aes(fill=class)) +
  scale_fill_manual(values = c("lightskyblue", "orchid", "violetred"),
                    labels = c("benign", "Malware static", "Malware dynamic")) +
  facet_wrap( ~ variable, scales="free") +
  scale_y_log10(limits = c(NA, NA))
```

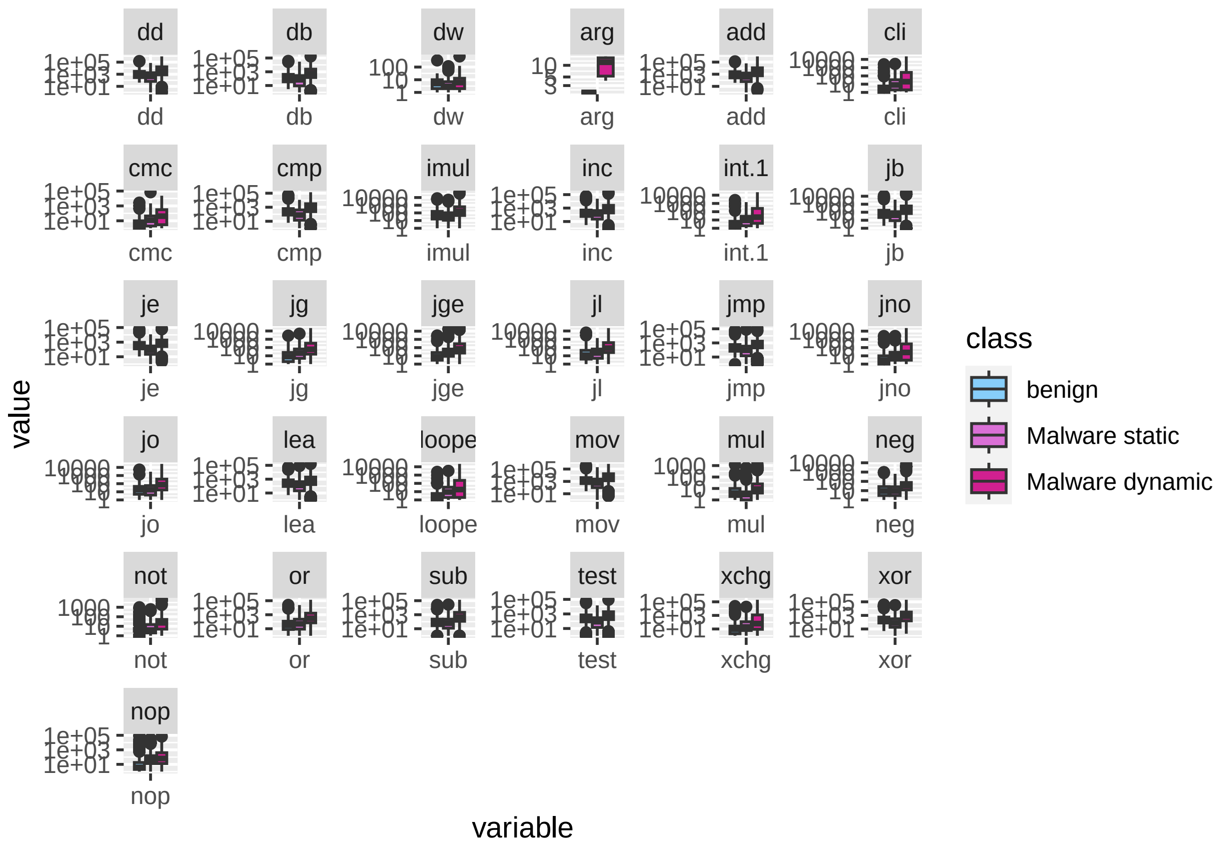


```
#  scale_y_log10(limits = c(1, max(types_subset.m$value)), expand = c(0, 0))
```

ASM/Functions

There are way to many assembly functions listed for plotting. so some are selected.

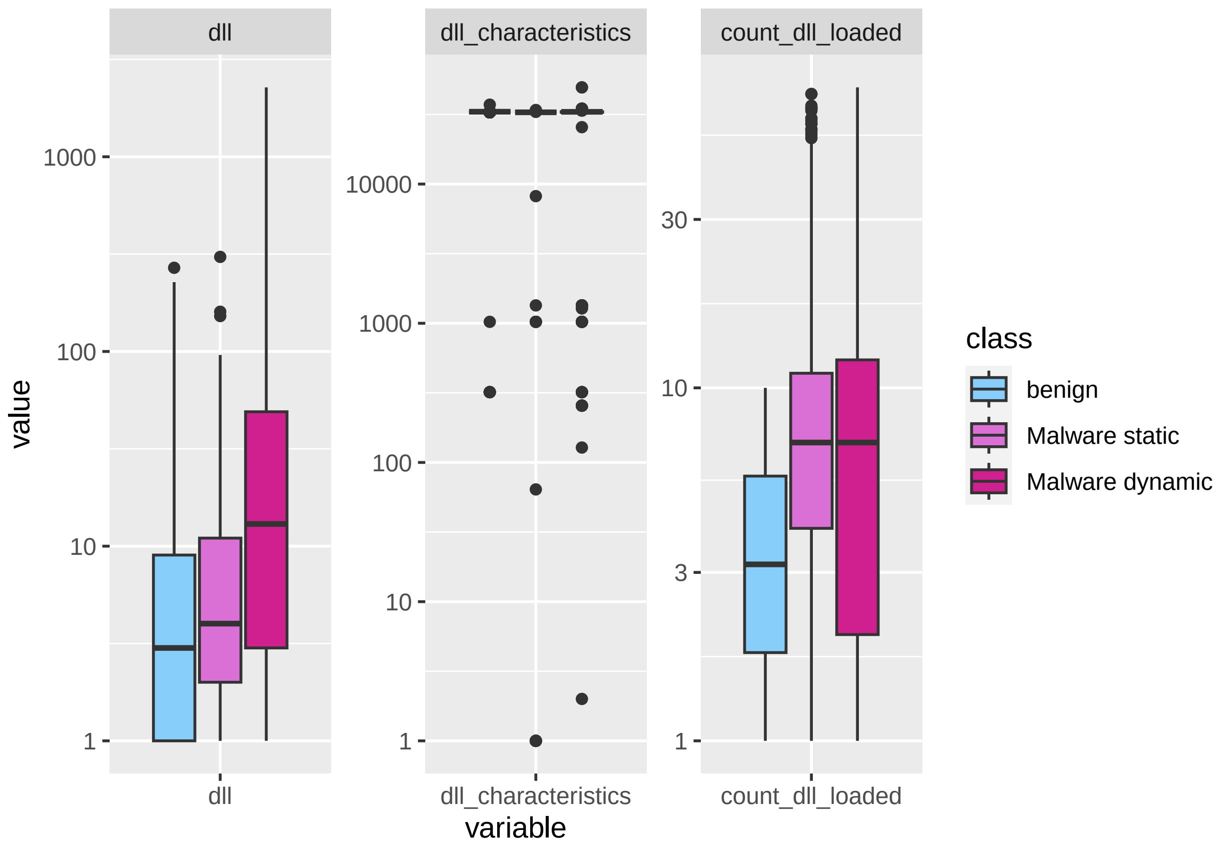
```
#c('dd','db','dw','stdcall','arg','edx','esi','es','fs','ds','ss','gs','cs','ah','al','ax','bh','bl','b
#c('dl','dx','eax','ebp','ebx','ecx','edi','esp','add','al.1','bt','call','cdq')
#c('cld','cli','cmc','cmp','const','cwd','daa','db.1','dd.1','dec','dw.1','enp','ends')
#c('faddp','fchs','fdiv','fdivp','fdivr','fild','fistp','fld','fstcw','fstcwimul','fstp','fword','fxch',
#c('imul','in','inc','ins','int.1','jb','je','jg','jge','jl','jmp','jnb','jno','jnz')
#c('jo','jz','lea','loope','mov','movzx','mul','near','neg','not','or','out','outs','pop','popf','proc.
#c('rcr','rdtsc','rep','ret','retn','rol','ror','sal','sar','sbb','scas','setb','setle','setnle','setnz

asms <- c('dd','db','dw','arg','add','cli','cmc','cmp','imul','inc','int.1','jb','je','jg','jge','jl','

# subset of these comiler/linker statistics
asm_subset <- subset(data_v2, select=asms)

# give the classes some better names
asm_subset$class <- factor(asm_subset$class, levels = c(0, 1, 2), labels = c("benign", "Malware static"

asm_subset.m <- melt(asm_subset, id.var = "class")

ggplot(data = asm_subset.m, aes(x=variable, y=value)) +
  geom_boxplot(aes(fill=class)) +
  scale_fill_manual(values = c("lightskyblue", "orchid", "violetred"),
                    labels = c("benign", "Malware static", "Malware dynamic")) +
  facet_wrap( ~ variable, scales="free") +
  scale_y_log10(limits = c(NA, NA))
```



There we probably see the most significant difference between the three classes.

DLL

```
dlls <- c('dll','dll_characteristics','count_dll_loaded','class')

# subset of these comiler/linker statistics
dll_subset <- subset(data_v2, select=dlls)

# give the classes some better names
dll_subset$class <- factor(dll_subset$class, levels = c(0, 1, 2), labels = c("benign", "Malware static"

dll_subset.m <- melt(dll_subset, id.var = "class")

ggplot(data = dll_subset.m, aes(x=variable, y=value)) +
  geom_boxplot(aes(fill=class)) +
  scale_fill_manual(values = c("lightskyblue", "orchid", "violetred"),
                    labels = c("benign", "Malware static", "Malware dynamic")) +
  facet_wrap( ~ variable, scales="free") +
  scale_y_log10(limits = c(NA, NA))
```



Malware generally loads more dll's than legit programs. Maybe due to the fact, that in hiding in a legitimate program it must provide the functionality of the application and some harmful code.

Models

Test several machine learning approaches to classify unseen programs (according to their static and dynamic features) as benign or possibly malicious, differenciate between identified according to static or dynamic features. The dataset is split into two parts, one for training and anoter for testing the model. The proportion of the data allocated to the test set is 30% of the complete data, the other 70% are used for the training set.

The goal is to achieve a high accuracy (>90%) with balanced precision and recall (F1) over all classes.

Guessing

The simplest approach, though not very usefull, would be by simply guessing the classification of a program. It is expected that the accuracy would be 33.3%.

The achieved accuracy is 0.3312, close to the expected 33.3%.

Model	Accuracy	F1 Class0	F1 Class1	F1 Class2
Guessing	0.3312	0.1502463	0.3640138	0.3978567

Naive Bayes

Naive Bayes is a simple and fast algorithm often used for classifications. The algorithm is based on the Bayes' theorem, that the probability of an event might be related to the event based on knowledge of conditions.

$P(A|B) = P(B|A) * P(A)/P(B)$

Naive means that the features are mutually independent, so a the probability of one feature does not affect the probability of another feature. There are several Naive Bayes variants:

- Gaussian Naive Bayes where the features are normally distributed
- Bernoulli Naive Bayes where the features are binary
- Multinomial Naive Bayes where frequency of occurences of features is calculated

Once the likelihood and prior probabilities have been calculated, Naive Bayes uses Bayes' theorem to compute the probability of each class label for a given set of feature values. The class label with the highest probability is then selected as the predicted label for these set of input data. The algorithm can be effective for classifications when lots of features are involved, but performance may suffer when features are not independent or unbalanced distributed.

```r
# Train the Naive Bayes model
nb_model <- naiveBayes(class ~ ., data=train_set)
nb_pred <- predict(nb_model, newdata=test_set)

# creater confusion matrix
nb_cm <- confusionMatrix(table(factor(test_set$class), nb_pred))

# Get overall accuracy and F1 scores
nb_acc <- nb_cm$overall['Accuracy']
nb_f1_c0 <- nb_cm$byClass[, 'F1'][1]
nb_f1_c1 <- nb_cm$byClass[, 'F1'][2]
nb_f1_c2 <- nb_cm$byClass[, 'F1'][3]

ml_results <- ml_results %>%
  bind_rows(tibble(Model="Naive Bayes", Accuracy=nb_acc, "F1 Class0"=nb_f1_c0, "F1 Class1"=nb_f1_c1, "F
```

The Naive Bayes is not a route to follow further, we get a very low overall accuracy 0.2112, lower than guessing.

Model	Accuracy	F1 Class0	F1 Class1	F1 Class2
Guessing	0.3312	0.1502463	0.3640138	0.3978567
Naive Bayes	0.2112	0.1910112	0.0142857	0.3893805

SVM

Support Vector Machine (SVM) is a supervised machine learning algorithm used for regression or classification tasks. The algorithm tries to fit hyperplanes that separates the data into different classes. In the training finding the hyperplane with the largest margin (distance between the hyperplane and the closest data points from each class).
In 2-D the hyperplane is basically a line, that separates the classes. Non-binary classification can be done by transforming the input features in higher dimensional space where it can be separated by hyperplanes.

SVM are powerfull if the data is clearly separated, but must be used carefully with noisy data or imbalanced classes.

```r
# train SVM model
svm_model <- svm(class ~ ., data=train_set)
svm_pred <- factor(round(predict(svm_model, newdata=test_set)), levels=c(0,1,2))

# creater confusion matrix
svm_cm <- confusionMatrix(table(factor(test_set$class), svm_pred))

# Get overall accuracy and F1 scores
svm_acc <- svm_cm$overall['Accuracy']
svm_f1_c0 <- svm_cm$byClass[, 'F1'][1]
svm_f1_c1 <- svm_cm$byClass[, 'F1'][2]
svm_f1_c2 <- svm_cm$byClass[, 'F1'][3]

ml_results <- ml_results %>%
  bind_rows(tibble(Model="SVM", Accuracy=svm_acc, "F1 Class0"=svm_f1_c0, "F1 Class1"=svm_f1_c1, "F1 Cla
```

With 0.522157 we are now better than guessing, but the F1 scores are still a bit low.

Model	Accuracy	F1 Class0	F1 Class1	F1 Class2
Guessing	0.331200	0.1502463	0.3640138	0.3978567
Naive Bayes	0.211200	0.1910112	0.0142857	0.3893805
SVM	0.522157	NA	0.6452636	0.3126787

KNN

K-Nearest Neighbors (KNN) is a supervised machine learning algorithm used for regression or classification tasks. It uses the proximity to grouping to make predictions of an individual point, assuming similar points can be found close to another.

Small k values can lead to overfitting and the model becomes to sensitive to noise and outliers, whereas a large k may result in underfitting and the model does not capture patterns in the data.

The KNN algorithm will perform best with a small number of features. Therefore we don't expect have high hopes for this approach.

```r
knn_model <- knn(train_set[, -ncol(train_set)], test_set[, -ncol(test_set)], train_set$class, k = 3)

# creater confusion matrix
knn_cm <- confusionMatrix(table(factor(test_set$class), knn_model))

# Get overall accuracy and F1 scores
knn_acc <- knn_cm$overall['Accuracy']
```

```r
knn_f1_c0 <- knn_cm$byClass[, 'F1'][1]
knn_f1_c1 <- knn_cm$byClass[, 'F1'][2]
knn_f1_c2 <- knn_cm$byClass[, 'F1'][3]

ml_results <- ml_results %>%
  bind_rows(tibble(Model="KNN", Accuracy=knn_acc, "F1 Class0"=knn_f1_c0, "F1 Class1"=knn_f1_c1, "F1 Cla
```

Accuracy is now very good 0.9162667, and also the F1 scores around 0.9.

Model	Accuracy	F1 Class0	F1 Class1	F1 Class2
Guessing	0.3312000	0.1502463	0.3640138	0.3978567
Naive Bayes	0.2112000	0.1910112	0.0142857	0.3893805
SVM	0.5221570	NA	0.6452636	0.3126787
KNN	0.9162667	0.8664688	0.9292308	0.9138702

Decision Trees

Decision Trees can be used for regression and classification models. Each node in the tree represents a decision on feature which are followed until a leaf node is reached, which represents a class. These trees are easy to visualize and interpret. But if a tree is too complex, it is prone to overfitting and must be used carefully with noisy data. For improved performance other variants might be considered like Random Forest and Gradient Boosted Trees.

```r
dt_model <- rpart(class ~ ., data=train_set)
dt_pred <- round(predict(dt_model, newdata=test_set))
dt_acc <- sum(dt_pred == test_set$class) / nrow(test_set)

# create confusion matrix
dt_cm <- confusionMatrix(table(factor(test_set$class), dt_pred))

# Get overall accuracy and F1 scores
dt_acc <- dt_cm$overall['Accuracy']
dt_f1_c0 <- dt_cm$byClass[, 'F1'][1]
dt_f1_c1 <- dt_cm$byClass[, 'F1'][2]
dt_f1_c2 <- dt_cm$byClass[, 'F1'][3]

ml_results <- ml_results %>%
  bind_rows(tibble(Model="Decision Tree", Accuracy=dt_acc, "F1 Class0"=dt_f1_c0, "F1 Class1"=dt_f1_c1,
```

Even better accuracy 0.9237333 than with KNN, and the F1 scores are overall better and all > 0.916.

Model	Accuracy	F1 Class0	F1 Class1	F1 Class2
Guessing	0.3312000	0.1502463	0.3640138	0.3978567
Naive Bayes	0.2112000	0.1910112	0.0142857	0.3893805
SVM	0.5221570	NA	0.6452636	0.3126787
KNN	0.9162667	0.8664688	0.9292308	0.9138702
Decision Tree	0.9237333	1.0000000	0.9155346	0.9163253

Random Forest

Random Forest combine multiple Decision Trees into a single model by randomly selecting a subset of data and features for each tree and combining the predictions (majority voting).

Random Forest corrects the habit of Decision Trees to ovefitting and are more robust with noisy data. They generally perform better than Decision Trees but with lower accuracy than Gradient Boosted Trees. But the additional complexity comes at the cost of more computational power required. They also don't perform well where the feature correlation is high or unbalanced.

```r
rf_model <- ranger(class ~ ., data=train_set, num.trees=480)
rf_pred <- factor(round(predict(rf_model, data = test_set)$predictions), levels = c(0, 1, 2))
rf_acc <- sum(rf_pred == test_set$class) / nrow(test_set)

# Calculate F1 score
rf_cm <- confusionMatrix(table(factor(test_set$class), rf_pred))

# Get overall accuracy and F1 scores
rf_acc <- rf_cm$overall['Accuracy']
rf_f1_c0 <- rf_cm$byClass[, 'F1'][1]
rf_f1_c1 <- rf_cm$byClass[, 'F1'][2]
rf_f1_c2 <- rf_cm$byClass[, 'F1'][3]

ml_results <- ml_results %>%
  bind_rows(tibble(Model="Random Forest", Accuracy=rf_acc, "F1 Class0"=rf_f1_c0, "F1 Class1"=rf_f1_c1,
```

Increasing the number of trees (to about 500) increases the model performance slightly but too high and the accuracy and F1 scores will come down again. While accuracy has gone up to 0.9541333, the average F1 score has come down slightly but still > 0.95.

Model	Accuracy	F1 Class0	F1 Class1	F1 Class2
Guessing	0.3312000	0.1502463	0.3640138	0.3978567
Naive Bayes	0.2112000	0.1910112	0.0142857	0.3893805
SVM	0.5221570	NA	0.6452636	0.3126787
KNN	0.9162667	0.8664688	0.9292308	0.9138702
Decision Tree	0.9237333	1.0000000	0.9155346	0.9163253
Random Forest	0.9541333	0.9422492	0.9480676	0.9620397

Gradient Boosting

Gradient Boosting iteratively new weak learners (Decision Trees) to correct errors made by previous ones. Each iteration the negative gradient of the loss function is calculated. A new weak learner (Decision Tree) is fitted.
Several tuning parameters are available like learning rate (determines the step size), number of weak learners and depth of the Decision Trees. Gradient Boosting can be computationally expensive and prone to overfitting if the number of weak learners or the complexity of the individual trees is too high. Early stopping, regularization, and subsampling can be used to improve the performance and stability of the algorithm.

```r
gb_model <- xgboost(data = as.matrix(train_set[, -1]),
                    label = train_set$class,
                    nrounds = 3,
                    objective = "multi:softmax",
                    num_class = 3,
                    eval_metric = "merror",
                    verbose = 0)

# convert predictions to integer class labels
gb_pred <- factor(predict(gb_model, as.matrix(test_set[, -1])), levels=c(0,1,2))

# Confusion matrix
gb_cm <- confusionMatrix(table(factor(test_set$class), gb_pred))

# Get overall accuracy and F1 scores
```

```
gb_acc <- gb_cm$overall['Accuracy']
gb_f1_c0 <- gb_cm$byClass[, 'F1'][1]
gb_f1_c1 <- gb_cm$byClass[, 'F1'][2]
gb_f1_c2 <- gb_cm$byClass[, 'F1'][3]

ml_results <- ml_results %>%
  bind_rows(tibble(Model="Gradient Boost", Accuracy=gb_acc, "F1 Class0"=gb_f1_c0, "F1 Class1"=gb_f1_c1,
```

Well we got the "ultimate" accuracy of 1 and all the F1 scores also at the maximum.

Model	Accuracy	F1 Class0	F1 Class1	F1 Class2
Guessing	0.3312000	0.1502463	0.3640138	0.3978567
Naive Bayes	0.2112000	0.1910112	0.0142857	0.3893805
SVM	0.5221570	NA	0.6452636	0.3126787
KNN	0.9162667	0.8664688	0.9292308	0.9138702
Decision Tree	0.9237333	1.0000000	0.9155346	0.9163253
Random Forest	0.9541333	0.9422492	0.9480676	0.9620397
Gradient Boost	1.0000000	1.0000000	1.0000000	1.0000000

This is extremely unlikely to happen in practice, so there might be some problems:

- Overfitting
- Dataset is too small
- Dataset is too simple
- Data leakage (training data is used in verification)

At the moment the Gradient Boosting results must be excluded until the underlying problem is identified and fixed.

Conclusion

While some models perform not or only slightly better than guessing, like Naive Bayes and SVM. Others achieve very good performance while stay balanced, like KNN, Decision Tree and Random Forest. For some of the models some additional tuning of parameters might be beneficial. We are able to correctly identify between benign programs and Malware (static or dynamic) with > 95% accuracy and also good F1 scores:

Model	Accuracy	F1 Class0	F1 Class1	F1 Class2
Random Forest	0.9541333	0.9422492	0.9480676	0.9620397

Future Improvements

Bigger datasets like the one from Microsoft used for the (Ronen et al. 2018) "Microsoft Malware Classification Challenge" with more than 20'000 malware samples. The malwares are also finer classified into 9 different families and types (e.g. Worm, Adware, Backdoor, Trojan, TrojanDownloader, . . .). Since the Microsoft dataset includes the file contents in hex format, lots of work would have been allocated to preprocessing the files. Also the dataset is quite popular in the cybersecurity research community with over 50 research papers and thesis works citing the dataset, this would violate the Capstone rules.

The models are not very refined and some tuning might increase the Accuracy (or F1 Score for the matter).

The goal might be to only identify two classes, benign and Malware. For now it was interessting to see if we can classify the Malware even further into dynamic and static, but in real world applications, this might not be of interesst.

Extracting other features from the original hex-files could provide more unique features. For this a more in-depth look at the dissassembly of these malwares is required. Also some feature combination or "pools" could be interessting, like the GUI or Menu relations or Events the program is using/triggering.

Some model approaches were not tested or lead to faulty results:

- Neuronal Network
- Gradient Descent
- Gradient Boosting

System

Hardware

All above computations are done with an Intel(R) Core(TM) i7-7500U CPU @ 2.70GHz CPU with 4 and 7.49 GB of RAM.

Software

This report is compiled using R markdown with RStudio.

```
sessionInfo()
```

```
## R version 4.2.2 (2022-10-31)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Arch Linux
##
## Matrix products: default
## BLAS:   /usr/lib/libblas.so.3.11.0
## LAPACK: /usr/lib/liblapack.so.3.11.0
##
## locale:
##  [1] LC_CTYPE=en_GB.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=en_GB.UTF-8        LC_COLLATE=en_GB.UTF-8
##  [5] LC_MONETARY=en_GB.UTF-8    LC_MESSAGES=en_GB.UTF-8
##  [7] LC_PAPER=en_GB.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_GB.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] parallel  stats     graphics  grDevices utils     datasets  methods
## [8] base
##
## other attached packages:
##  [1] reshape2_1.4.4    GGally_2.1.2      glmnet_4.1-6      Matrix_1.5-1
##  [5] nnet_7.3-18       xgboost_1.7.3.1   rpart_4.1.19      ranger_0.14.1
##  [9] class_7.3-20      e1071_1.7-12      httr_1.4.5        caret_6.0-93
## [13] lattice_0.20-45   forcats_0.5.2     dplyr_1.0.10      purrr_0.3.5
## [17] readr_2.1.3       tidyr_1.2.1       tibble_3.2.0      tidyverse_1.3.2
## [21] kableExtra_1.3.4  stringr_1.4.1     scales_1.2.1      lubridate_1.9.0
## [25] timechange_0.1.1  rmarkdown_2.18    benchmarkme_1.0.8 ggplot2_3.4.0
## [29] pacman_0.5.1
##
## loaded via a namespace (and not attached):
##  [1] googledrive_2.0.0     colorspace_2.0-3      ellipsis_0.3.2
##  [4] fs_1.5.2              rstudioapi_0.14       proxy_0.4-27
##  [7] farver_2.1.1          listenv_0.8.0         bit64_4.0.5
## [10] prodlim_2019.11.13    fansi_1.0.4           xml2_1.3.3
## [13] codetools_0.2-18      splines_4.2.2         doParallel_1.0.17
## [16] knitr_1.41            jsonlite_1.8.4        pROC_1.18.0
## [19] broom_1.0.1           dbplyr_2.2.1          compiler_4.2.2
## [22] backports_1.4.1       assertthat_0.2.1      fastmap_1.1.0
## [25] gargle_1.2.1          cli_3.6.0             htmltools_0.5.4
## [28] tools_4.2.2           gtable_0.3.1          glue_1.6.2
## [31] Rcpp_1.0.9            cellranger_1.1.0      vctrs_0.5.2
## [34] svglite_2.1.1          nlme_3.1-160          iterators_1.0.14
## [37] timeDate_4021.106      gower_1.0.0           xfun_0.35
## [40] globals_0.16.2         rvest_1.0.3           lifecycle_1.0.3
## [43] googlesheets4_1.0.1    future_1.29.0         MASS_7.3-58.1
## [46] ipred_0.9-13           vroom_1.6.0           hms_1.1.2
## [49] RColorBrewer_1.1-3     yaml_2.3.6            reshape_0.8.9
## [52] stringi_1.7.8          highr_0.9             foreach_1.5.2
## [55] hardhat_1.2.0          lava_1.7.0            shape_1.4.6
## [58] benchmarkmeData_1.0.4 rlang_1.0.6            pkgconfig_2.0.3
## [61] systemfonts_1.0.4      archive_1.1.5         evaluate_0.18
## [64] labeling_0.4.2         recipes_1.0.3         bit_4.0.5
## [67] tidyselect_1.2.0       parallelly_1.32.1     plyr_1.8.8
## [70] magrittr_2.0.3         R6_2.5.1              generics_0.1.3
## [73] DBI_1.1.3              pillar_1.8.1          haven_2.5.1
## [76] withr_2.5.0            survival_3.4-0        future.apply_1.10.0
## [79] modelr_0.1.10          crayon_1.5.2          utf8_1.2.3
## [82] tzdb_0.3.0             grid_4.2.2            readxl_1.4.1
## [85] data.table_1.14.6      ModelMetrics_1.2.2.2  reprex_2.0.2
## [88] digest_0.6.30          webshot_0.5.4         stats4_4.2.2
## [91] munsell_0.5.0          viridisLite_0.4.1
```

Resources

[1] Rafael Irizarry. 2018. Introduction to Data Science.https://rafalab.dfci.harvard.edu/dsbook/

[2] Malware static and dynamic features VxHeaven and Virus Total Data Set https://archive.ics.uci.edu/ml /datasets/Malware+static+and+dynamic+features+VxHeaven+and+Virus+Total#

[3] PE Format https://learn.microsoft.com/en-us/windows/win32/debug/pe-format

[4] cuckoo sandbox https://cuckoosandbox.org/

Ronen, Royi, Marian Radu, Corina Feuerstein, Elad Yom-Tov, and Mansour Ahmadi. 2018. "Microsoft Malware Classification Challenge." arXiv. https://doi.org/10.48550/ARXIV.1802.10135.