

# Log Journal Project Theme 9

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## EDA of yeast data: Protein Localization

The data has been retrieved from uci. The dataset has been gathered of 1484 yeast sequences from SWISS-PROT using the annotations from YPD.

Attributes information:

- **Sequence Name:** Accession number for the SWISS-PROT database.
- **mcg:** McGeoch's method for signal sequence recognition.
- **gvh:** von Heijne's method for signal sequence recognition.
- **alm:** Score of the ALOM membrane spanning region prediction program.
- **mit:** Score of discriminant analysis of the amino acid content of the N-terminal region (20 residues long) of mitochondrial and non-mitochondrial proteins.
- **erl:** Presence of "HDEL" substring (thought to act as a signal for retention in the endoplasmic reticulum lumen). Binary attribute.
- **pox:** Peroxisomal targeting signal in the C-terminus.
- **vac:** Score of discriminant analysis of the amino acid content of vacuolar and extracellular proteins.
- **nuc:** Score of discriminant analysis of nuclear localization signals of nuclear and non-nuclear proteins.
- **Class Distribution:** The class is the localization site. Consisting of (abbreviation (full name) the amount):

CYT	(cytosolic or cytoskeletal)	463
NUC	(nuclear)	429
MIT	(mitochondrial)	244
ME3	(membrane protein, no N-terminal signal)	163
ME2	(membrane protein, uncleaved signal)	51
ME1	(membrane protein, cleaved signal)	44
EXC	(extracellular)	37
VAC	(vacuolar)	30
POX	(peroxisomal)	20
ERL	(endoplasmic reticulum lumen)	5

## Codebook

Since there is not a codebook. I created my own codebook.

```
# All the attributes name
attr_names <- c("seq.name", "mcg", "gvh", "alm", "mit", "erl",
               "pox", "vac", "nuc", "loc.site" )

data_types <- c("str", "float", "float", "float", "float", "float",
               "bool", "float", "float", "factor")

# The description of the labels
data_labels <- c("Accession number for the SWISS-PROT database",
                 "McGeoch's method for signal sequence recognition",
                 "von Heijne's method for signal sequence recognition",
                 "Score of the ALOM membrane spanning region prediction program",
                 "Score of discriminant analysis of the amino
                 acid content of the N-terminal region",
                 "Presence of 'HDEL' substring",
                 "Peroxisomal targeting signal in the C-terminus",
                 "Score of discriminant analysis of the amino acid content
                 of vacuolar and extracellular proteins",
                 "Score of discriminant analysis of nuclear
                 localization signals of nuclear and non-nuclear proteins",
                 "The class is the localization site")

codebook <- data.frame(Name=attr_names,
                       Fullname=data_labels,
                       Datatypes=data_types)

pander(codebook)
```

Name	Fullname	Datatypes
seq.name	Accession number for the SWISS-PROT database	str
mcg	McGeoch's method for signal sequence recognition	float
gvh	von Heijne's method for signal sequence recognition	float
alm	Score of the ALOM membrane spanning region prediction program	float
mit	Score of discriminant analysis of the amino acid content of the N-terminal region	float
erl	Presence of 'HDEL' substring	float
pox	Peroxisomal targeting signal in the C-terminus	bool
vac	Score of discriminant analysis of the amino acid content of vacuolar and extracellular proteins	float
nuc	Score of discriminant analysis of nuclear localization signals of nuclear and non-nuclear proteins	float
loc.site	The class is the localization site	factor

Here is the codebook. With the attributes abbreviation, explanation and data types. As you can see there are many float datatypes.

## Load the data

Now we need to load in the data. And change the column names to the attributes abbreviation, since these are non-existent. Let's give all the columns a name. And let's take a quick look at the data.

```
# Read the file in as a tibble
data <- as_tibble(read.table("yeast.data", sep = ""))
colnames(data) <- attr_names
head(data)
```

```
# A tibble: 6 x 10
  seq.name      mcg    gvhh    alm    mit    erl    pox    vac    nuc loc.site
  <chr>      <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <chr>
1 ADT1_YEAST  0.58  0.61  0.47  0.13  0.5   0    0.48  0.22 MIT
2 ADT2_YEAST  0.43  0.67  0.48  0.27  0.5   0    0.53  0.22 MIT
3 ADT3_YEAST  0.64  0.62  0.49  0.15  0.5   0    0.53  0.22 MIT
4 AAR2_YEAST  0.58  0.44  0.57  0.13  0.5   0    0.54  0.22 NUC
5 AATM_YEAST  0.42  0.44  0.48  0.54  0.5   0    0.48  0.22 MIT
6 AATC_YEAST  0.51  0.4   0.56  0.17  0.5   0.5   0.49  0.22 CYT
```

The yeast data set contains scores per cellular localization sites.

## Clean the data

We can drop the first columns since it is not necessary. Since the sequence names contribute nothing to create a prediction model.

```
# Drop the first column
data <- data[, -1]
head(data)
```

```
# A tibble: 6 x 9
      mcg    gvhh    alm    mit    erl    pox    vac    nuc loc.site
  <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <chr>
1  0.58  0.61  0.47  0.13  0.5   0    0.48  0.22 MIT
2  0.43  0.67  0.48  0.27  0.5   0    0.53  0.22 MIT
3  0.64  0.62  0.49  0.15  0.5   0    0.53  0.22 MIT
4  0.58  0.44  0.57  0.13  0.5   0    0.54  0.22 NUC
5  0.42  0.44  0.48  0.54  0.5   0    0.48  0.22 MIT
6  0.51  0.4   0.56  0.17  0.5   0.5   0.49  0.22 CYT
```

The first column has been successfully dropped from the data.

Are there any missing values? Let's take a quick look.

```
# Count all the NA values
sum(is.na(data))
```

```
[1] 0
```

There are not any missing values. So nothing needs to be changed for this.

Now we need to take a clearer look at the data set using `str()`.

```
str(data)

tibble [1,484 x 9] (S3: tbl_df/tbl/data.frame)
 $ mcg      : num [1:1484] 0.58 0.43 0.64 0.58 0.42 0.51 0.5 0.48 0.55 0.4 ...
 $ gvh      : num [1:1484] 0.61 0.67 0.62 0.44 0.44 0.4 0.54 0.45 0.5 0.39 ...
 $ alm      : num [1:1484] 0.47 0.48 0.49 0.57 0.48 0.56 0.48 0.59 0.66 0.6 ...
 $ mit      : num [1:1484] 0.13 0.27 0.15 0.13 0.54 0.17 0.65 0.2 0.36 0.15 ...
 $ erl      : num [1:1484] 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 ...
 $ pox      : num [1:1484] 0 0 0 0 0 0.5 0 0 0 0 ...
 $ vac      : num [1:1484] 0.48 0.53 0.53 0.54 0.48 0.49 0.53 0.58 0.49 0.58 ...
 $ nuc      : num [1:1484] 0.22 0.22 0.22 0.22 0.22 0.22 0.22 0.22 0.34 0.22 ...
 $ loc.site: chr [1:1484] "MIT" "MIT" "MIT" "NUC" ...
```

As you can see, the last column, `loc.site`, consists of characters, but this one needs to be converted to factors for clarity and complexity.

```
# Transform the last column to a factor
data$loc.site <- as.factor(data$loc.site)
str(data$loc.site)
```

```
Factor w/ 10 levels "CYT","ERL","EXC",...: 7 7 7 8 7 1 7 8 7 1 ...
```

As you can see the data type of the column `loc.site` has been successfully changed to factors.

There are a lot of rows. Let's visualize the amount of each classification.

```
# A grid to fill in 28x53
df <- expand_grid(y = 1:28, x = 1:53)
# Sort the table
categ_table <- sort(table(data$loc.site), decreasing = T)
df$category <- factor(rep(names(categ_table), categ_table))

ggplot(df, aes(x = x, y = y, fill = category)) +
  geom_tile(color = "black", size = 0.5) +
  scale_x_continuous(expand = c(0, 0)) +
  scale_y_continuous(expand = c(0, 0), trans = 'reverse') +
  scale_fill_brewer(palette = "Set3") +
  labs(title="Waffle Chart", subtitle="'Class' of localization") +
  xlab(NULL) + ylab(NULL)
```

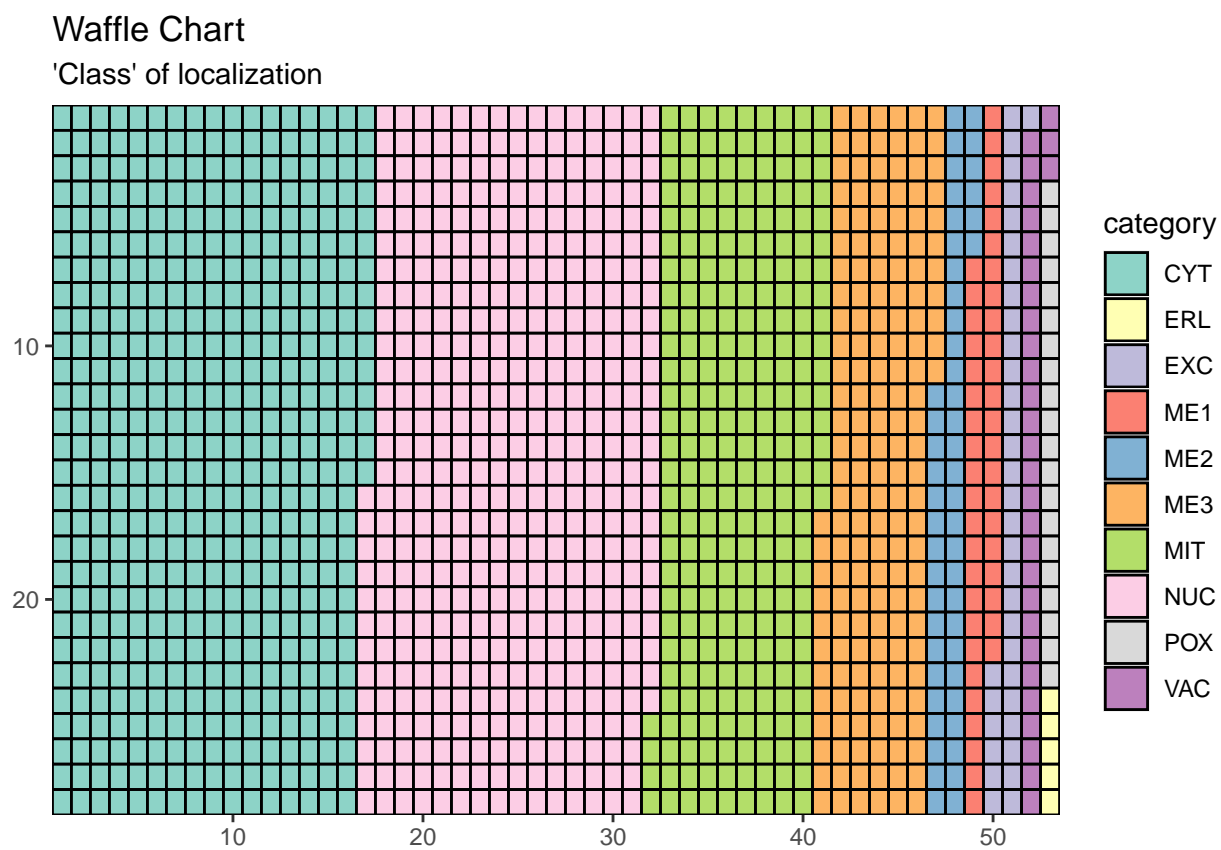


Figure 1: A waffle chart of the categorical composition

There are a lot of CYT and NUC localization. This probably means that CYT has a greater variation in localisation than ERL.

The ERL variable also should be changed. As you can see, it is now a num data type but it needs to be a bool/binary datatype. Let's take a closer look at the ERL column.

```
summary(data$erl)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.5000	0.5000	0.5000	0.5047	0.5000	1.0000

This looks weird because the value should be 0 or 1.

There are a lot of 0.5 values. But should not exist in this column. The variable needs to be a bool, or in other words it must be a 0 or a 1. So all the 0.5 values need to be changed to a 0.

```
table(data[, "erl"])
```

0.5	1
1470	14

Before the data transformation there are 1470 counts of the value 0.5 and 14 of 1.

```
# Change every 0.5 value to a 0
data$erl[data$erl == 0.5] <- 0
table(data[, "erl"])
```

0	1
1470	14

The data has been successfully transformed. Now the datatype has to be changed to a bool.

```
# Change the datatype to a logical
data$erl <- as.logical(data$erl)
str(data$erl)
```

```
logi [1:1484] FALSE FALSE FALSE FALSE FALSE FALSE ...
```

Now every column has the right datatype.

## Univariate Analysis

Let's take a quick look at the data using `summary()`. We can drop column 5 and 9 for this. Column 5, ERL, is a logical datatype and column 9, loc.site, is a string datatype.

```
summary(data[, -c(5,9)])
```

mcg	gvh	alm	mit
Min. :0.1100	Min. :0.1300	Min. :0.21	Min. :0.0000
1st Qu.:0.4100	1st Qu.:0.4200	1st Qu.:0.46	1st Qu.:0.1700
Median :0.4900	Median :0.4900	Median :0.51	Median :0.2200
Mean :0.5001	Mean :0.4999	Mean :0.50	Mean :0.2612
3rd Qu.:0.5800	3rd Qu.:0.5700	3rd Qu.:0.55	3rd Qu.:0.3200
Max. :1.0000	Max. :1.0000	Max. :1.00	Max. :1.0000

pox	vac	nuc
Min. :0.0000	Min. :0.0000	Min. :0.0000
1st Qu.:0.0000	1st Qu.:0.4800	1st Qu.:0.2200
Median :0.0000	Median :0.5100	Median :0.2200
Mean :0.0075	Mean :0.4999	Mean :0.2762
3rd Qu.:0.0000	3rd Qu.:0.5300	3rd Qu.:0.3000
Max. :0.8300	Max. :0.7300	Max. :1.0000

As you can see all the datapoints are between 0 and 1. Se the data already has been transformed with a min-max normalization.

Let's visualise this with ggplot. Using jitterpoints and a violing plot.

```
p1 <- ggplot(data, mapping = aes(x = "", y = mcg)) + geom_violin(alpha=0.2) +
  geom_jitter(width = 0.2, alpha = 0.25, height = 0, color = "red") + xlab(NULL)
p2 <- ggplot(data, mapping = aes(x = "", y = gvh)) + geom_violin(alpha=0.2) +
  geom_jitter(width = 0.2, alpha = 0.25, height = 0, color = "blue") + xlab(NULL)
p3 <- ggplot(data, mapping = aes(x = "", y = alm)) + geom_violin(alpha=0.2) +
  geom_jitter(width = 0.2,alpha = 0.25, height = 0, color = "purple") + xlab(NULL)
p4 <- ggplot(data, mapping = aes(x = "", y = mit)) + geom_violin(alpha=0.2) +
  geom_jitter(width = 0.2, alpha = 0.25, height = 0, color = "brown") + xlab(NULL)
p5 <- ggplot(data, mapping = aes(x = "", y = pox)) + geom_violin(alpha=0.2) +
  geom_jitter(width = 0.2,alpha = 0.25, height = 0, color = "orange") + xlab(NULL)
p6 <- ggplot(data, mapping = aes(x = "", y = vac)) + geom_violin(alpha=0.2) +
  geom_jitter(width = 0.2, alpha = 0.25, height = 0, color = "green") + xlab(NULL)
p7 <- ggplot(data, mapping = aes(x = "", y = nuc)) + geom_violin(alpha=0.2) +
  geom_jitter(width = 0.2,alpha = 0.25, height = 0, color = "orange") + xlab(NULL)

plot <- ggarrange(p1, p2, p3, p4, p5, p6, p7, nrow = 4, ncol = 2)
annotate_figure(plot, top = text_grob("Boxplots", face = "bold", size = 14))
```

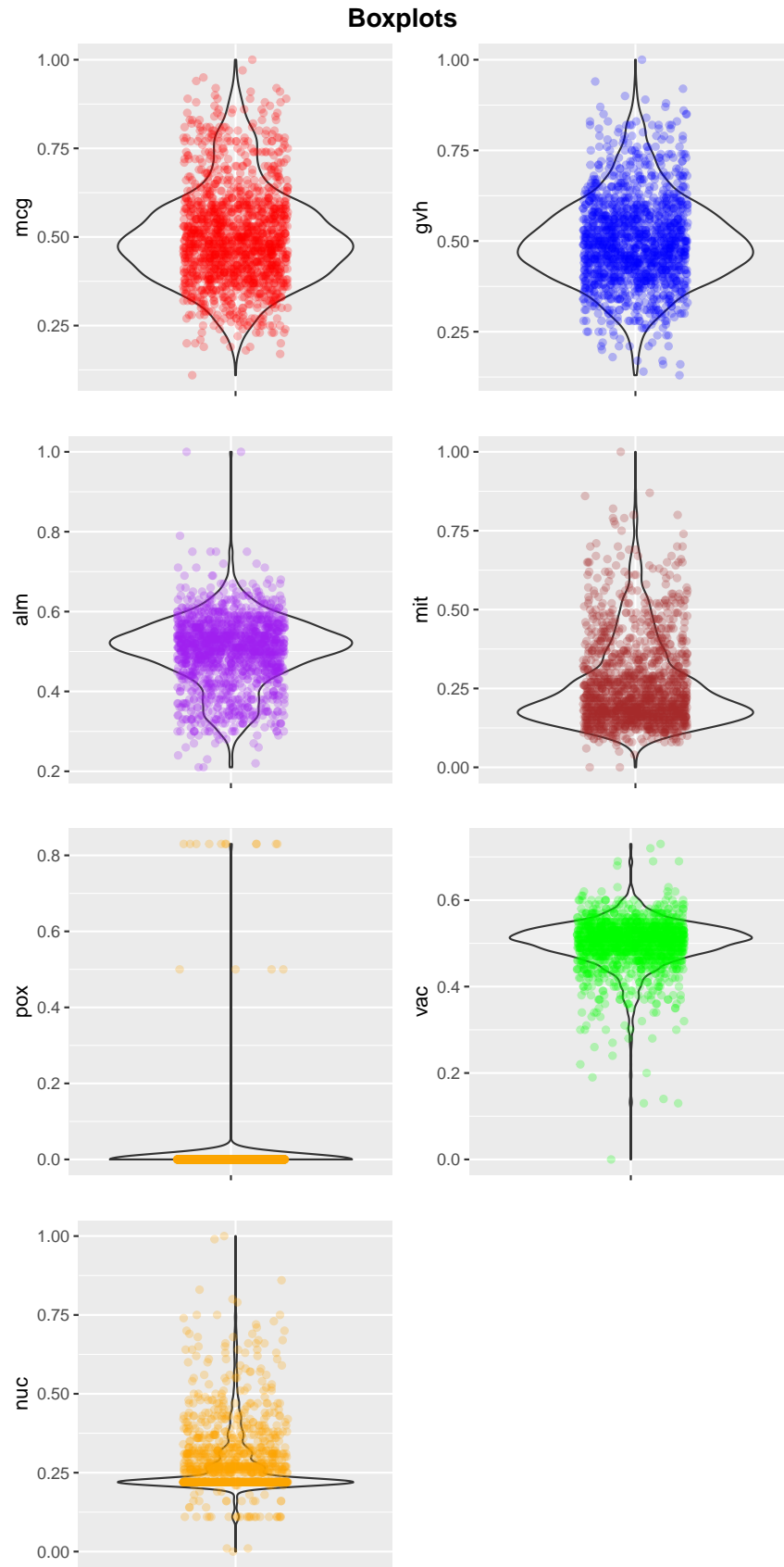


Figure 2: Boxplot comparing basic statistic for all columns



Mcg and gvh are normally distributed. Alm and mit are skewed but nothing crazy to worry about. Vac and nuc are really skewed however, not yet bad enough to worry about it. Pox is looks weird let's take a detailed look at pox.

```
table(data[, "pox"])
```

```

  0  0.5 0.83
1469   4   11

```

As you can see almost all the numbers are 0. This does not mean that we just discard this column. Maybe it is very significant if the number is not 0.

```
# Subset the data where pox is larger than 0
subset(data, pox > 0, select=loc.site)
```

```

# A tibble: 15 x 1
  loc.site
  <fct>
1 CYT
2 MIT
3 POX
4 POX
5 POX
6 POX
7 POX
8 POX
9 POX
10 MIT
11 POX
12 MIT
13 POX
14 POX
15 POX

```

If the number is non-zero then the probability is very high that the protein is localised in peroxisomal region.

## Bivariate Analysis

With a heatmap, you can easily see where there are correlations between variables. First let's create a correlation matrix

```

# Create a cor matrix
cor_matrix <- cor(data[, -c(5,9)])
cor_matrix <- as_tibble(cor_matrix)
# Add a column with the variable names
(cor_matrix <- cor_matrix %>% mutate(varnames = all_of(attr_names)[-c(1,6,10)]))

```

```

# A tibble: 7 x 8
  mcg      gvh      alm      mit      pox      vac      nuc varnames
  <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl> <chr>

```

1	1	0.582	-0.164	0.158	0.00560	0.0750	-0.125	mcg
2	0.582	1	-0.272	0.140	0.000392	0.0888	-0.103	gvh
3	-0.164	-0.272	1	0.0597	0.00938	-0.186	-0.0220	alm
4	0.158	0.140	0.0597	1	-0.00904	-0.104	-0.0548	mit
5	0.00560	0.000392	0.00938	-0.00904	1	0.0209	-0.0357	pox
6	0.0750	0.0888	-0.186	-0.104	0.0209	1	0.0897	vac
7	-0.125	-0.103	-0.0220	-0.0548	-0.0357	0.0897	1	nuc

The calculated correlation matrix. This needs to be tranformed to a long matrix.

```
# Create a long matrix
(cor_matrix_long <- pivot_longer(data = cor_matrix,
                                cols = all_of(attr_names)[-c(1,6,10)],
                                names_to = "variable", values_to = "cor"))
```

```
# A tibble: 49 x 3
  varnames variable    cor
  <chr>      <chr>    <dbl>
1 mcg      mcg      1
2 mcg      gvh      0.582
3 mcg      alm     -0.164
4 mcg      mit      0.158
5 mcg      pox      0.00560
6 mcg      vac      0.0750
7 mcg      nuc     -0.125
8 gvh      mcg      0.582
9 gvh      gvh      1
10 gvh     alm     -0.272
# ... with 39 more rows
```

The long calculated correlation matrix.

```
ggplot(data = cor_matrix_long, aes(x=varnames, y=variable, fill=cor)) +
  geom_tile() +
  labs(x=NULL, y=NULL, title="Heatmap Correlation") +
  scale_fill_gradient(high = "purple", low = "white" )
```

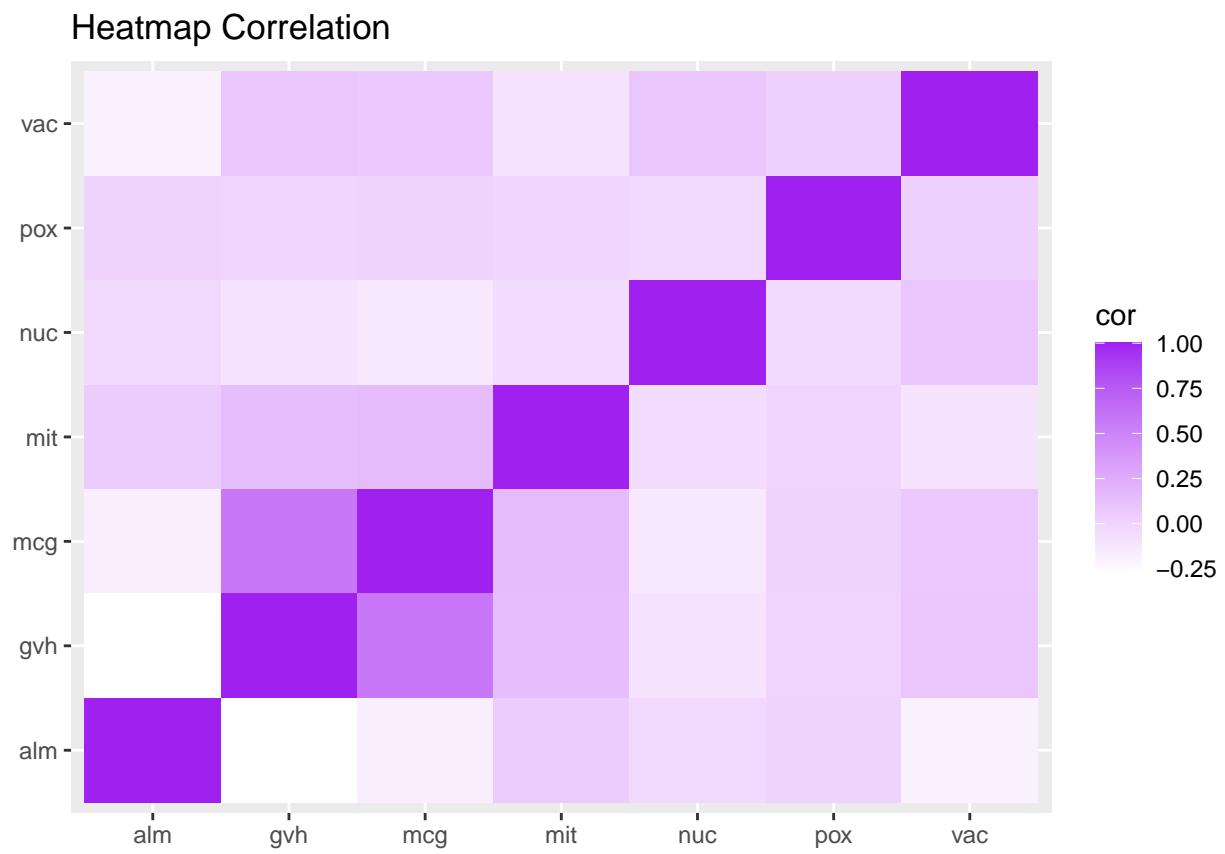


Figure 3: A heatmap pairwise correlation of selected numeric variables

As seen from the heatmap there is some correlation between mcg and gvh. Let's visualise this.

```
ggplot(data, aes(x=mcg, y=gvh, color=loc.site)) +
  labs(x="MCG", y="GVH") +
  geom_jitter(mapping = aes(color=loc.site),
             na.rm=T, width=0.2, height=0.2,
             alpha=0.5, shape=16, size=0.8) +
  ylim(0,1) + labs(title="Scatterplot and trendline") +
  geom_smooth(formula = y ~ x, method = "loess")
```

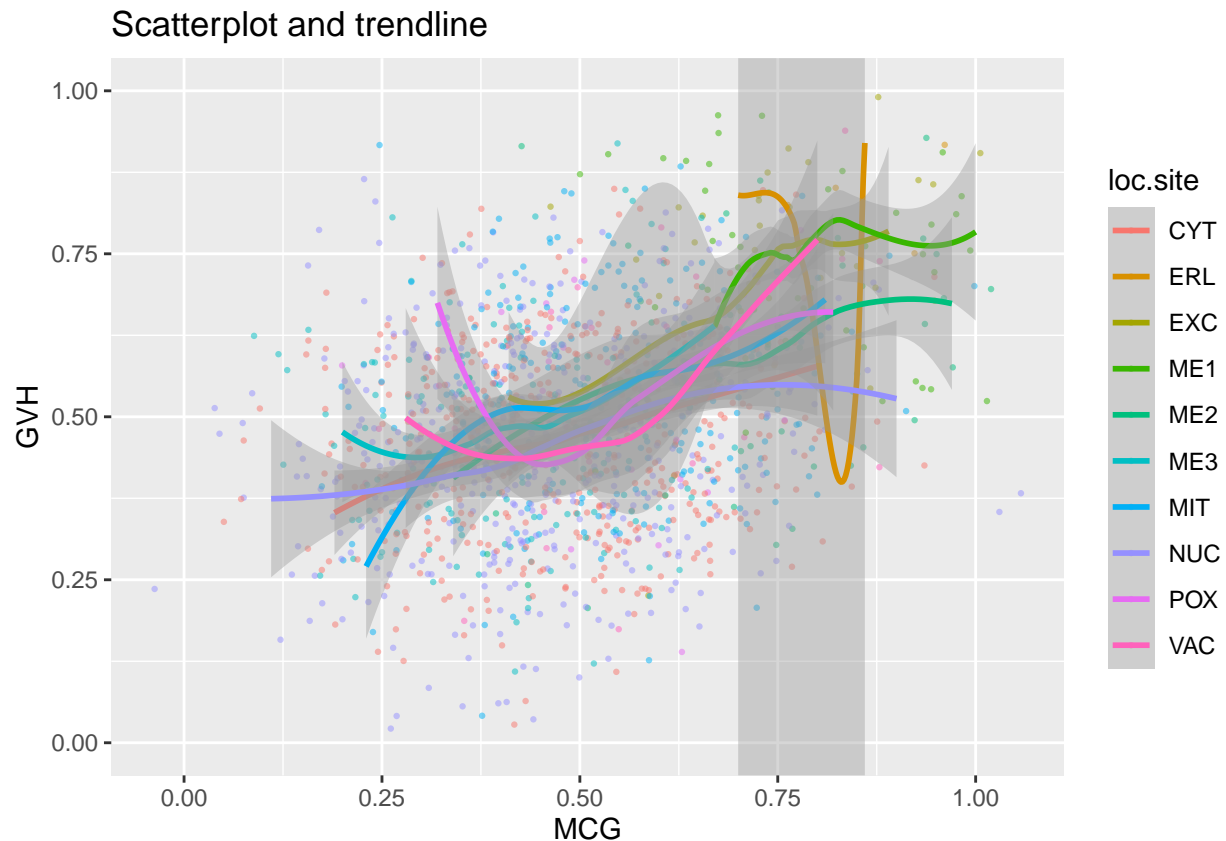


Figure 4: Scatterplot with trendline with the dependent variables

Every variable goes with a slow upward trend except erl this one has a weird curve.

## Class labels

Now we need to look at how the data correlates with the classes. The height of the peak doesn't matter much, shifted peaks do.

```
p1 <- ggplot(data, aes(x=mcg)) + geom_density(aes(color=loc.site))
p2 <- ggplot(data, aes(x=gvh)) + geom_density(aes(color=loc.site))
p3 <- ggplot(data, aes(x=alm)) + geom_density(aes(color=loc.site))
p4 <- ggplot(data, aes(x=mit)) + geom_density(aes(color=loc.site))
p5 <- ggplot(data, aes(x=pox)) + geom_density(aes(color=loc.site))
```

```

p6 <- ggplot(data, aes(x=vac)) + geom_density(aes(color=loc.site))
p7 <- ggplot(data, aes(x=nuc)) + geom_density(aes(color=loc.site))
plot <- ggarrange(p1, p2, p3, p4, p5, p6, p7, ncol=4, nrow=2,
  common.legend=TRUE, legend="right")
annotate_figure(plot, top = text_grob("Density plots", face = "bold", size = 14))

```

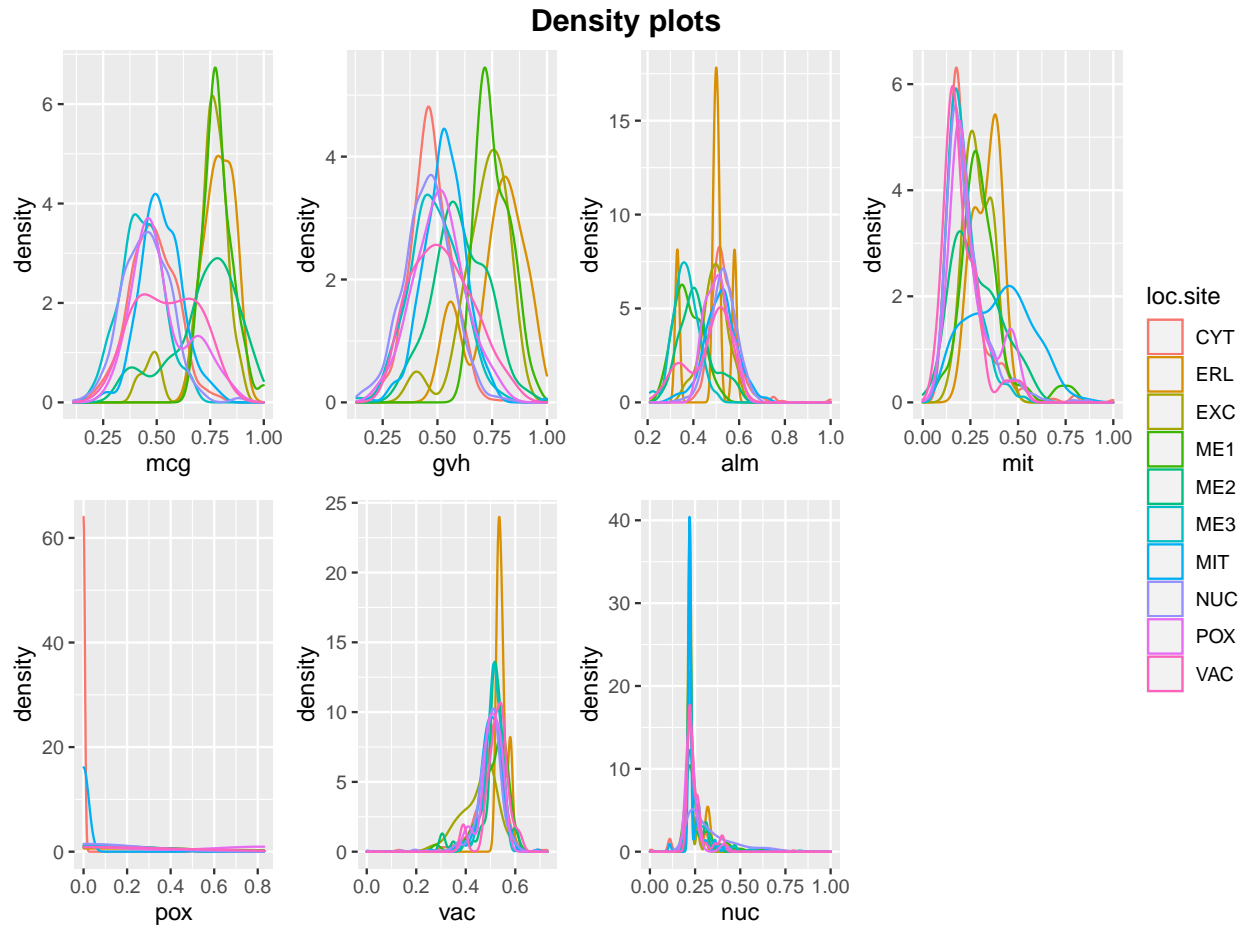


Figure 5: Density plots shows class distinction

At pox, vac and nuc, you don't see shifted peaks. At mcg and gvh you really see shifted peaks this shows a distribution of the different classes. There are small shifted peaks at alm and mit, this shows that there is difference but not so much. Let's look at mcg and gvh using ridge lines plot.

```

p1 <- ggplot(data, aes(x=mcg, y=loc.site, fill = loc.site)) +
  geom_density_ridges2(rel_min_height = 0.005) + theme_minimal() +
  coord_cartesian(clip = "off")
p2 <- ggplot(data, aes(x=gvh, y=loc.site, fill = loc.site)) +
  geom_density_ridges2(rel_min_height = 0.005) + theme_minimal() +
  coord_cartesian(clip = "off")
plot <- ggarrange(p1, p2, common.legend = TRUE)
annotate_figure(plot, top = text_grob("Ridge line plot", face = "bold", size = 14))

```

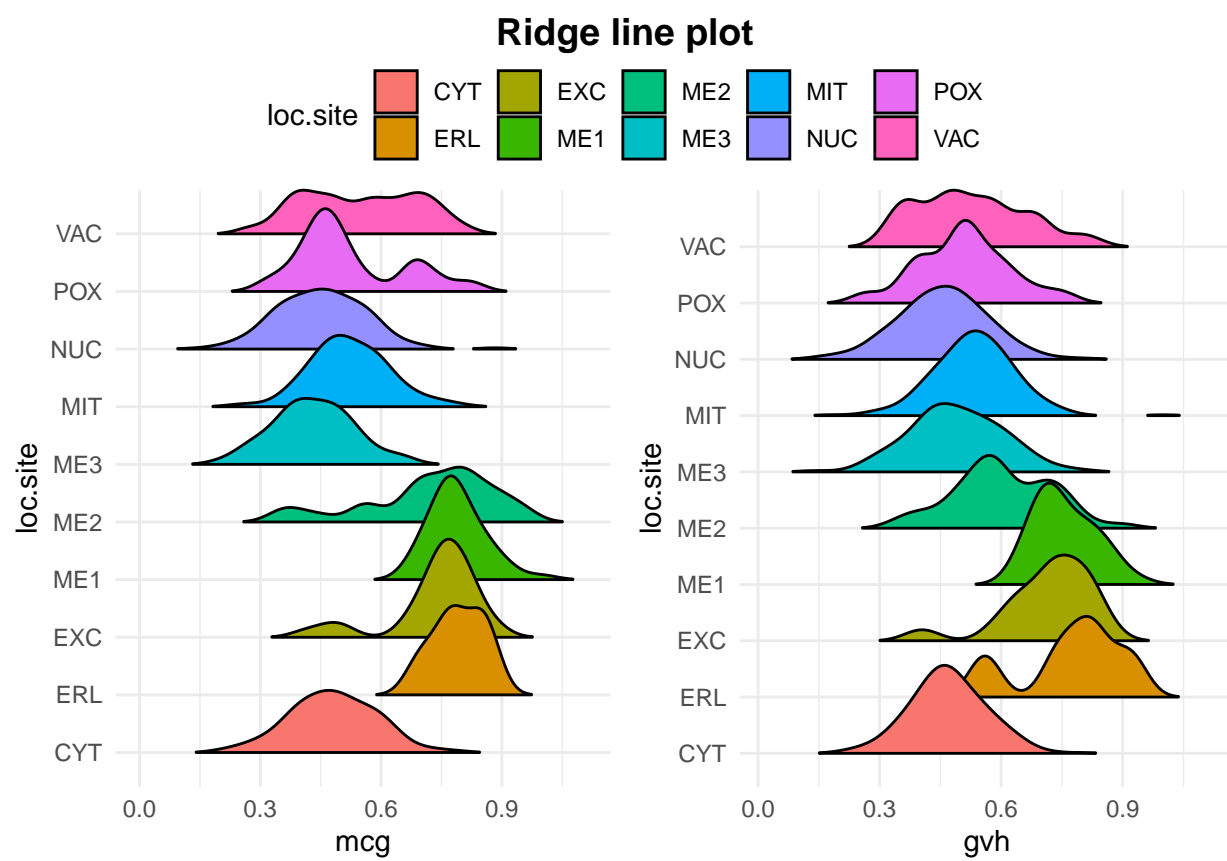


Figure 6: Ridge line plot between mcg and gvh

Now you can really see that the peaks are shifted.

We need to test the data to see if there is significant difference between it. Using a 1-way ANOVA test.

```
# Perform a one way anova test
res.aov <- summary(aov(mcg ~ loc.site, data = data))
res.aov[[1]]$`Pr(>F)`[1]
```

```
[1] 1.203676e-146
```

The P-value is  $< 0.05$ . So there is a significant difference.

## Multivariate analysis

One way to see if groups are clustered is to MDS plot the groups and calculated the distance matrix.

```
# Create a matrix
matrix <- with(data, rbind(mcg, gvh, alm, mit, pox, vac, nuc))
(distmat <- dist(matrix))
```

	mcg	gvh	alm	mit	pox	vac
gvh	4.623700					
alm	6.699455	6.524822				
mit	11.476977	11.321051	11.025910			
pox	19.910020	19.776585	19.479594	11.495734		
vac	5.580672	5.083611	4.342165	10.946100	19.312255	
nuc	11.161711	10.858508	10.144550	6.884693	11.545921	9.715282

Here is the distance matrix.

```
autoplot(cmdscale(distmat, eig = TRUE), shape = FALSE, label = TRUE, label.size = 4)
```

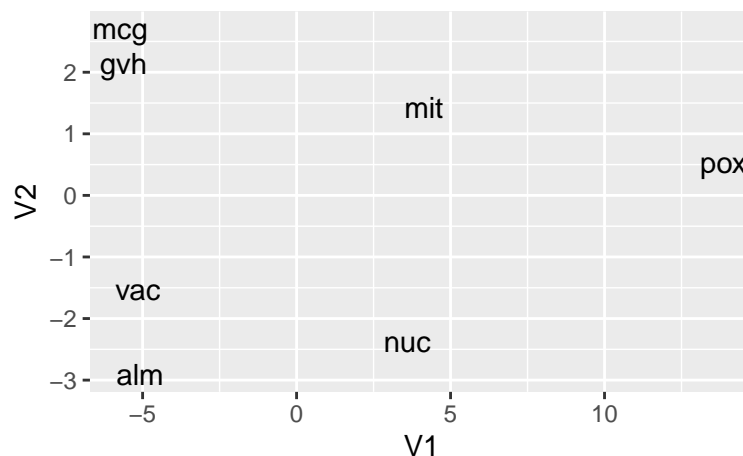


Figure 7: Classical (Metric) Multidimensional Scaling

As seen from above mcg and gvh are the clustered group.

A other plot to show is using PCA.

```
df <- data[-c(5,9)]
pca_res <- prcomp(df, scale. = TRUE)
autoplot(pca_res, data = data, colour = 'loc.site', loadings = TRUE, loadings.label = TRUE)
```

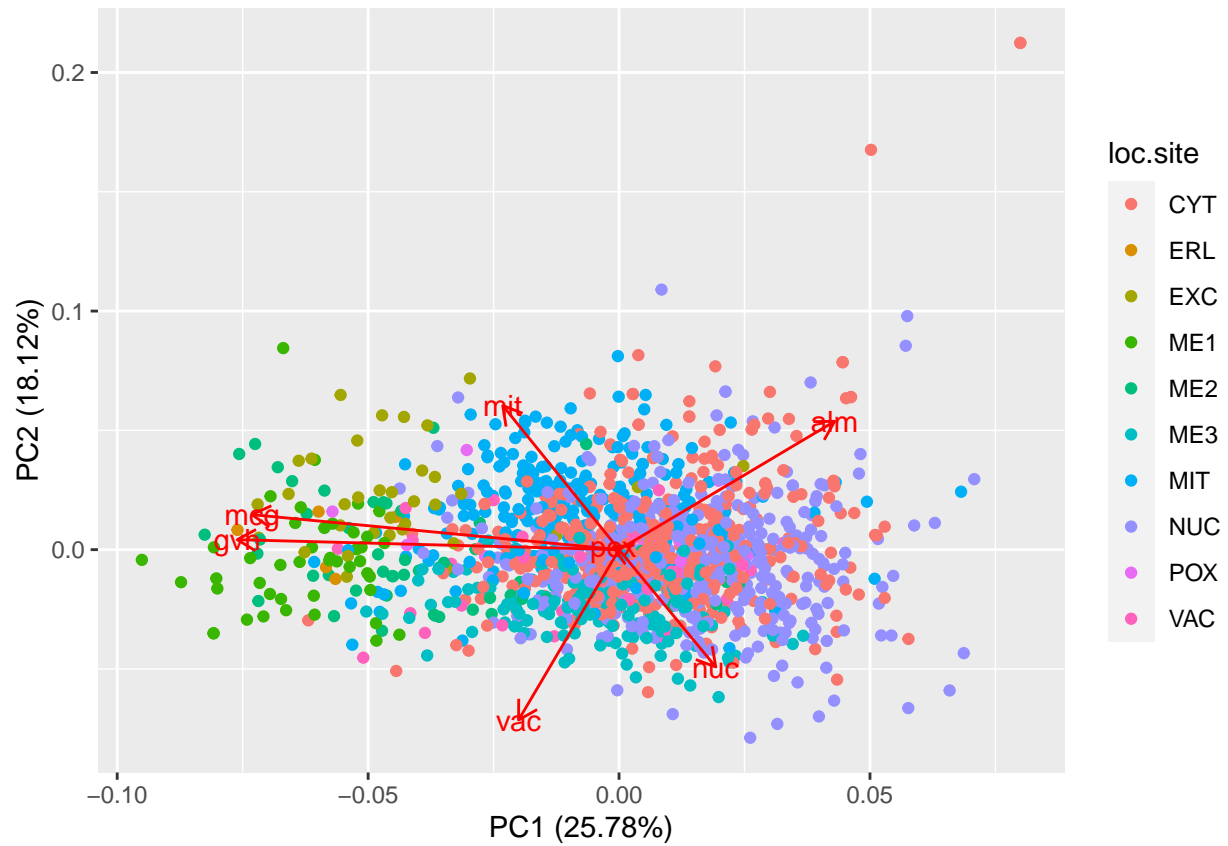


Figure 8: PCA plot showing the groups

As earlier shown mcg and gvh are grouped together.



## MIL algorithms

First we need to investigate which standard ML algorithms is the best to use for this dataset using Weka.

Weka accepts .arff files. You can convert a .csv to a .arff file in Weka. So we need to export the clean dataset to a .csv file.

```
write.table(data,"data.csv", quote = FALSE, sep = ",", row.names=FALSE)
```

Open the .csv in Weka under tools -> ArffViewer. And saved the file as .arff. The first 15 lines of the .arff file needs to look like this.

```
cat(readLines("data.arff", n = 15), sep = "\n")
```

```
@relation data
```

```
@attribute mcg numeric
```

```
@attribute gvh numeric
```

```
@attribute alm numeric
```

```
@attribute mit numeric
```

```
@attribute erl {FALSE,TRUE}
```

```
@attribute pox numeric
```

```
@attribute vac numeric
```

```
@attribute nuc numeric
```

```
@attribute loc.site {MIT,NUC,CYT,ME1,EXC,ME2,ME3,VAC,POX,ERL}
```

```
@data
```

```
0.58,0.61,0.47,0.13,FALSE,0,0.48,0.22,MIT
```

```
0.43,0.67,0.48,0.27,FALSE,0,0.53,0.22,MIT
```

### *Criteria for MIL algorithms*

An accurate algorithm is needed that accurately predicts the dataset. It needs a high percentage of correct classifications on the dataset. An algorithm that is fast. What if there is a dataset of 1 million observations. And it should also not contain too many false negatives and false positives.

Research has been done on which algorithm is the best. From every representatives of all classifier categories. And ZeroR and OneR for a baseline performance. Eg: Decision Trees (C4.5, J48, RandomForest), Nearest Neighbor (IBk), SVM (SMO), NaiveBayes (Naïve Bayes) and Linear Logistic (SimpleLogistic). And carried out classifications 10-fold cross validation.

```
wekaResult <- read.table("ResultWeka.txt", header = TRUE)
colnames(wekaResult) <- c("Classifier", "TP Rate Avg.", "FP Rate Avg.",
                          "Precision", "VAC Precision")
pander(wekaResult)
```

Classifier	TP Rate Avg.	FP Rate Avg.	Precision	VAC Precision
ZeroR	0.312	0.312	?	?
OneR	0.394	0.228	?	?
C4.5	0.537	0.153	0.531	0.000
J48	0.559	0.144	0.550	0.000
RandomForest	0.611	0.132	0.603	0.000

Classifier	TP Rate Avg.	FP Rate Avg.	Precision	VAC Precision
IBk	0.523	0.149	0.524	0.077
SMO	0.57	0.159	?	?
NaiveBayes	0.576	0.137	0.584	0.000
SimpleLogistic	0.59	0.143	?	?

Several algorithms cannot make a prediction for the classification VAC (0.000) and for some they get an error (?). 1 algorithm IBk has a very low prediction for VAC. All the algorithm above in table NUMBER except for ZeroR, OneR, SMO and SimpleLogistic were used in the Weka Experimenter to compare.

```
>-< > < Resultset
4 4 0 trees.RandomForest '-P 100 -I 100 -num-slots 1 -K 0 -M 1.0 -V 0.001 -S 1' 1116839470751428698
1 2 1 bayes.NaiveBayes '' 5995231201785697655
0 1 1 trees.J48 '-C 0.25 -M 2' -217733168393644444
-2 0 2 rules.PART '-C 0.25 -M 2' 8121455039782598361
-3 0 3 lazy.IBk '-K 1 -W 0 -A \"weka.core.neighboursearch.LinearNNSearch -A \"weka.core.EuclideanDistance -R first-last\"' -3080186098777067172
```

Figure 9: Ranking of chosen algorithms

This shows the ranking of the algorithms by the number of times a given algorithm beat the other algorithms. And RandomForest beat all 4 algorithms.

Dataset	(1) trees.Ra	(2) rules	(3) trees	(4) lazy.	(5) bayes
data	(100) 61.25	54.70 *	56.38 *	52.61 *	57.88 *
	(v/ /*)	(0/0/1)	(0/0/1)	(0/0/1)	(0/0/1)

Figure 10: Ranking of chosen algorithms by SD

RandomForest has a 'v' next to their result. This means that the difference in the accuracy for these algorithms compared to all the other algorithms is significant.

After testing multiple algorithms in Weka, the algorithm RandomForest was chosen. It has the highest average precision of 0.611. And this was one of the few algorithms where the precision for VAC was not a '?'.

But for the ratings, no algorithm could make a prediction except 1 for VAC, however, it was also very low. So we looked at whether there is significant difference if we remove this classifier.

Dataset	(1) trees.Rand
data	(100) 61.25
data-weka.filters.unsuper(100)	62.66
(v/ /*)	

Figure 11: Removed class difference

And by the looks of it, there is no significant difference. So VAC is not removed from the dataset.