

Business Data Mining (IDS 572)

(source: r-bloggers.com)

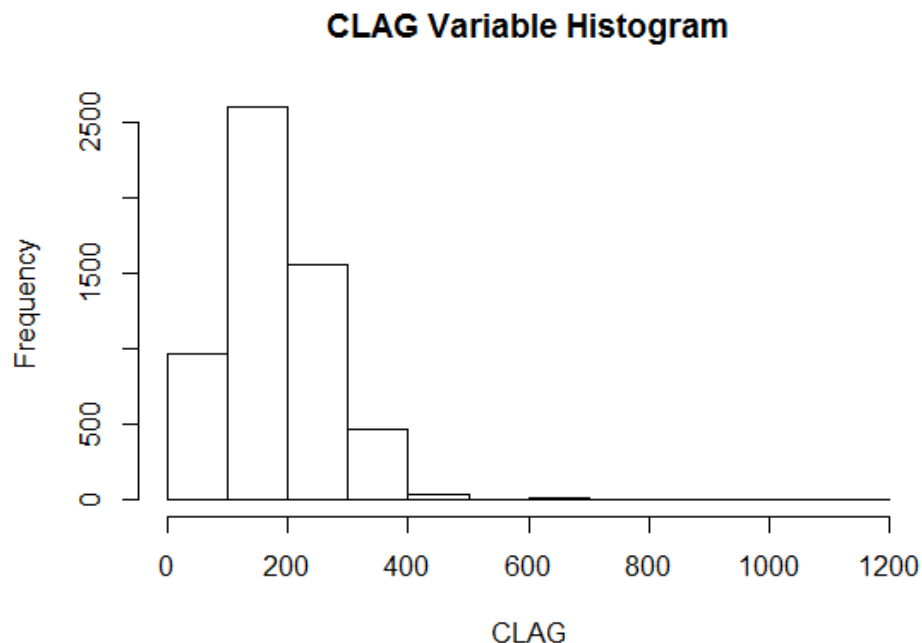
Detecting and removing outliers

In statistics, an outlier is defined as an observation which stands far away from the most of other observations. Often an outlier is present due to the measurement error. Therefore, one of the most important tasks in data analysis is to identify and (if necessary) to remove the outliers.

There are different methods to detect the outliers. Below we provide a few of these methods. To illustrate these methods we use the “hmeq” data set which can be found on blackboard.

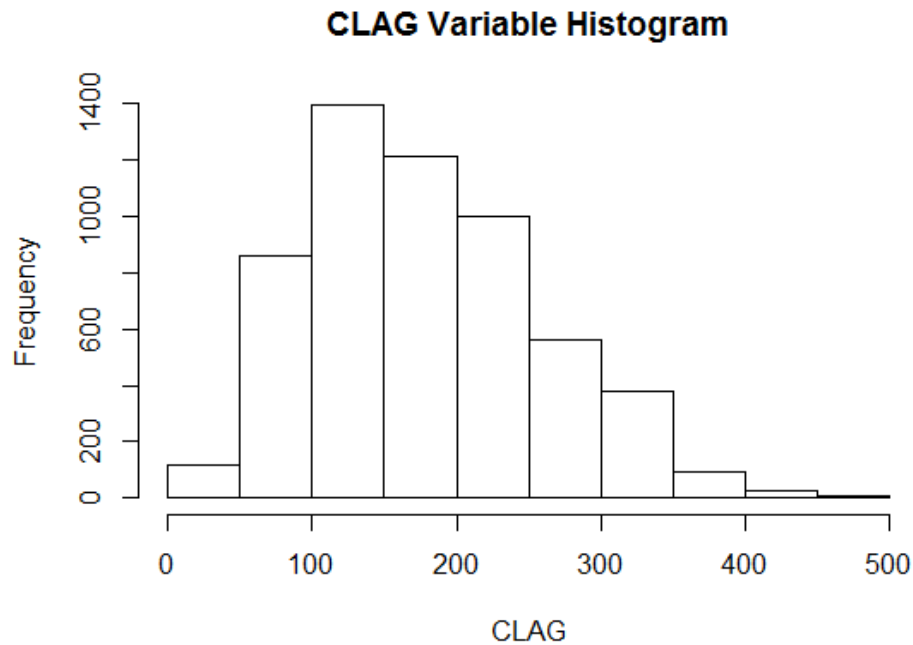
Method 1: To detect the outliers, you can first draw the histogram to determine the range of outliers.

```
> hist(hmeq$CLAG, main = "CLAG Variable Histogram", xlab = "CLAG")
```



As you can see there are outliers for the CLAG variable. To remove the outliers we can use the “subset(DataSet_name, Variable_name < Bound)” function similar to the following code:

```
> DataNew = subset(hmeq, CLAG < 500)
> hist(DataNew$CLAG, main = "CLAD Variable Histogram", xlab = "CLAG")
```



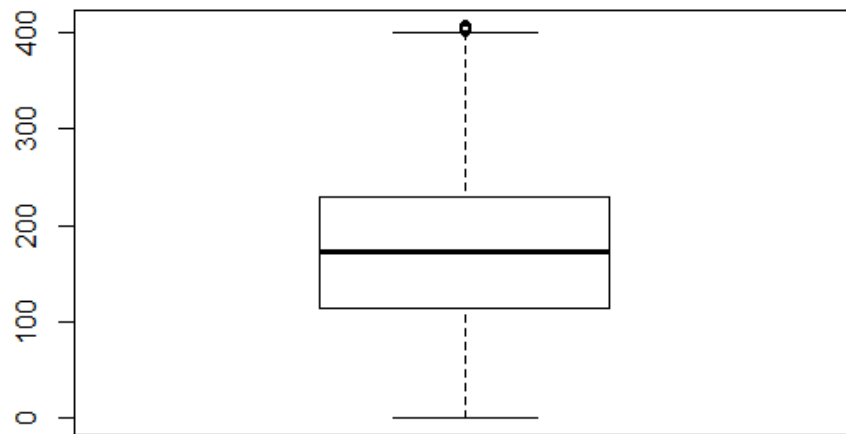
If you have more than one variable with outliers you can use the following formula:

```
> NewData = subset(Data_name, Var1_name < Bound1 & Var2_name < Bound2 & ...)
```

Method 2: To detect the outliers, the command “boxplot.stats()\$out” can be used which uses the Tukey’s method to identify the outliers ranged above and below the $1.5 \times IQR$.

```
> OutLiers = boxplot.stats(hmeq$CLAG)$out # We first save all the outliers in the vector OutLiers
> CLAGnoOut = ifelse(hmeq$CLAG % in % OutLiers, NA, hmeq$CLAG) # if the value of CLAG is in OutLiers then we replace it by NA (or any other value)
> boxplot(CLAGnoOut)
```

Box Plot of CLAG with no outliers



Handling missing values

In R, missing values are represented by the symbol NA (not available) . Impossible values (e.g., dividing by zero) are represented by the symbol NaN (not a number).

To test if there is any missing values in data, we can use the function “is.na()” which returns TRUE for each missing value.

```
> sum(is.na(hmeq$NINQ)) # This give you the number of missing values in the variable NINQ
[1] 510
```

To count the number of rows where one or more columns contain NA (incomplete cases), we can use “sum(!complete.cases())”.

```
> sum(complete.cases(hmeq$NINQ)) # Count of complete cases in the variable NINQ
[1] 5450
> sum(!complete.cases(hmeq$NINQ)) # Count of complete cases in the variable NINQ
[1] 510
> which(!complete.cases(hmeq$NINQ)) # Which cases (row numbers) are incomplete
```

The summary function of a data frame also counts the occurrence of NA in each column.

Replacing NA values

The function “na.omit()” returns the object with listwise deletion of missing values.

```
> NINQ_Imputed = na.omit(hmeq$NINQ) # Create new variable without missing values
> sum(is.na(NINQ_Imputed))
[1] 0
```

Replacing missing values by a particular value

To replace missing values by a particular value like mean we can use the following code:

```
> hmeq$NINQ[is.na(hmeq$NINQ)] = mean(hmeq$NINQ, na.rm=TRUE) # Recode all NA
in NINQ as the average value
> sum(is.na(hmeq$NINQ))
[1] 0
```

Notice that arithmetic functions on missing values yield missing values. So mean(hmeq\$NINQ) returns NA. To remove the missing values in the computation of mean, we should use “na.rm = TRUE”.

While some quick fixes such as mean-substitution may be fine in some cases, such simple approaches usually introduce bias into the data, for instance, applying mean substitution leaves the mean unchanged (which is desirable) but decreases variance, which may be undesirable. The “mice” package helps you imputing missing values with plausible data values. These plausible values are drawn from a distribution specifically designed for each missing datapoint.

Using mice for looking at missing data pattern

The mice package provides a function “md.pattern()” to get better understanding of the pattern of missing data.

```
> library(mice)
> md.pattern(hmeq)
```

	BAD	LOAN	REASON	JOB	NINQ	VALUE	CLNO	CLAGE	YOJ	MORTDUE	DELINQ	DEROG	DEBTINC	
3551	1	1	1	1	1	1	1	1	1	1	1	1	1	0
176	1	1	1	1	1	1	1	1	1	0	1	1	1	1
15	1	1	1	1	1	0	1	1	1	1	1	1	1	1
188	1	1	1	1	1	1	1	1	0	1	1	1	1	1
158	1	1	1	1	1	1	1	1	1	1	1	0	1	1
29	1	1	1	1	1	1	1	1	1	1	0	1	1	1
28	1	1	1	1	1	1	1	0	1	1	1	1	1	1
932	1	1	1	1	1	1	1	1	1	1	1	1	0	1
4	1	1	1	1	1	0	1	1	1	0	1	1	1	2
53	1	1	1	1	1	1	1	1	0	0	1	1	1	2
1	1	1	1	1	1	0	1	1	0	1	1	1	1	2
2	1	1	1	1	1	0	1	1	1	1	1	0	1	2
12	1	1	1	1	1	1	1	1	1	0	0	1	1	2
1	1	1	1	1	1	0	1	1	1	1	0	1	1	2
10	1	1	1	1	1	1	1	1	0	1	0	1	1	2
178	1	1	1	1	1	1	1	1	1	1	0	0	1	2
19	1	1	1	1	1	1	1	0	1	0	1	1	1	2
16	1	1	1	1	1	1	1	0	0	1	1	1	1	2
55	1	1	1	1	1	1	1	1	1	0	1	1	0	2
54	1	1	1	1	1	0	1	1	1	1	1	1	0	2
40	1	1	1	1	1	1	1	1	0	1	1	1	0	2
33	1	1	1	1	1	1	1	1	1	1	1	0	0	2
8	1	1	1	1	1	1	1	1	1	1	0	1	0	2
17	1	1	1	1	1	1	1	0	1	1	1	1	0	2
6	1	1	1	1	1	1	1	1	0	0	1	0	1	3
12	1	1	1	1	1	1	1	1	0	0	0	1	1	3
23	1	1	1	1	1	1	1	1	1	0	0	0	1	3
7	1	1	1	1	1	1	1	1	0	1	0	0	1	3
6	1	1	1	1	1	0	1	1	1	0	1	1	0	3
13	1	1	1	1	1	1	1	1	0	0	1	1	0	3
1	1	1	1	1	1	0	1	1	0	1	1	1	0	3
3	1	1	1	1	1	0	1	1	1	1	1	0	0	3
1	1	1	1	1	1	1	1	1	0	1	1	0	0	3
1	1	1	1	1	1	1	1	1	1	0	0	1	0	3
1	1	1	1	1	1	0	1	1	1	1	0	1	0	3
2	1	1	1	1	1	1	1	1	0	1	0	1	0	3
22	1	1	1	1	1	1	1	1	1	1	0	0	0	3
4	1	1	1	1	1	1	1	0	1	0	1	1	0	3
1	1	1	1	1	1	1	1	0	0	1	1	1	0	3
40	1	1	1	1	1	1	1	1	0	0	0	0	1	4
62	1	1	1	1	1	1	0	0	1	1	0	0	1	4
1	1	1	1	1	1	0	1	1	1	0	1	0	0	4
1	1	1	1	1	1	1	1	1	0	0	1	0	0	4
1	1	1	1	1	1	1	1	1	0	0	0	1	0	4
2	1	1	1	1	1	1	1	1	1	0	0	0	0	4
1	1	1	1	1	1	0	1	1	1	1	0	0	0	4
1	1	1	1	1	1	1	1	1	0	1	0	0	0	4
1	1	1	1	1	1	0	1	0	1	0	1	1	0	4
4	1	1	1	1	1	1	0	0	1	0	0	0	1	5
2	1	1	1	1	1	0	0	0	1	1	0	0	1	5
43	1	1	1	1	1	1	0	0	0	1	0	0	1	5
3	1	1	1	1	1	0	1	1	1	0	0	0	0	5
4	1	1	1	1	1	1	1	1	0	0	0	0	0	5
22	1	1	1	1	1	1	0	0	1	1	0	0	0	5
47	1	1	1	1	1	1	0	0	0	0	0	0	1	6
9	1	1	1	1	1	1	0	0	1	0	0	0	0	6
4	1	1	1	1	1	0	0	0	1	1	0	0	0	6
8	1	1	1	1	1	1	0	0	0	1	0	0	0	6
6	1	1	1	1	1	0	0	0	0	0	0	0	1	7
2	1	1	1	1	1	0	0	0	1	0	0	0	0	7
9	1	1	1	1	1	1	0	0	0	0	0	0	0	7
4	1	1	1	1	1	0	0	0	0	0	0	0	0	8
	0	0	0	0	0	112	222	308	515	518	580	708	1267	4230

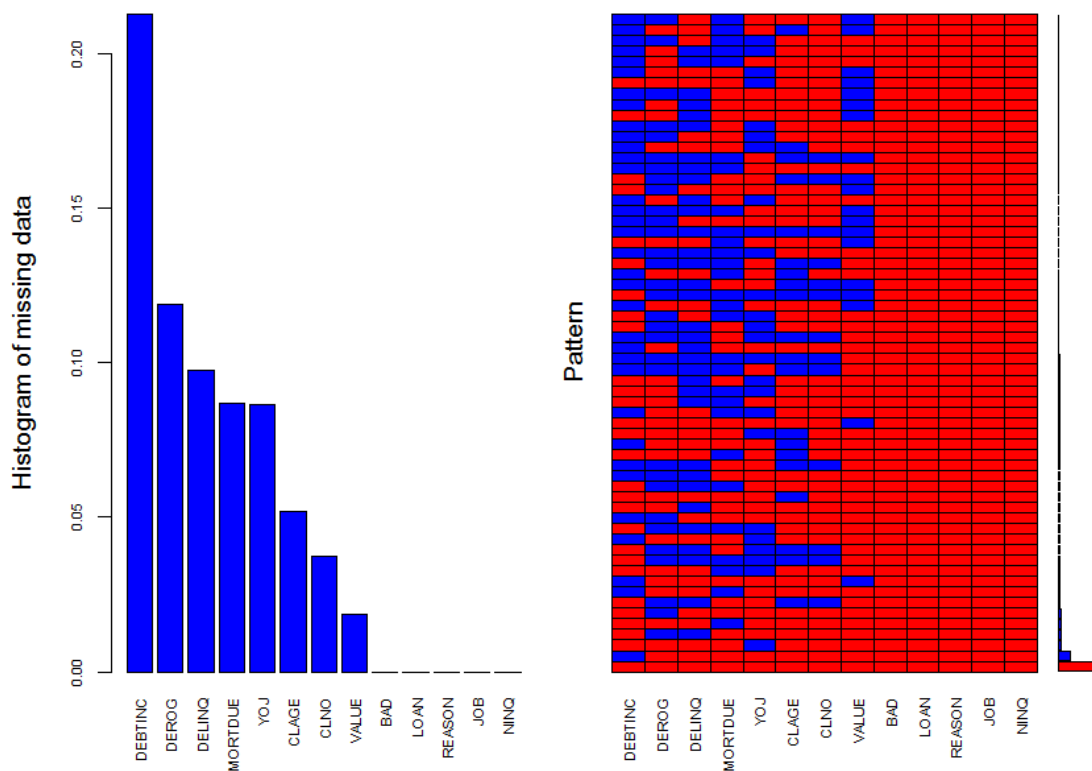
The output tells us that 3551 samples are complete, 176 samples miss only MORTDUE, 15 samples miss only the VALUE and so on.

To visualize these information, the package VIM can be used.

```
> library(VIM)
> aggr_plot = aggr(hmeq, col = c('red', 'blue'), numbers = TRUE, prop = TRUE, sortVars
= TRUE, labels = names(hmeq), cex.axis = 1, gap = 0, ylab = c("Histogram of missing
data", "Pattern"))
```

The color red indicates observed values and the color blue indicates missing values.

```
variables sorted by number of missings:
Variable      Count
DEBTINC 0.21258389
DEROG 0.11879195
DELINQ 0.09731544
MORTDUE 0.08691275
YOJ 0.08640940
CLAGE 0.05167785
CLNO 0.03724832
VALUE 0.01879195
BAD 0.00000000
LOAN 0.00000000
REASON 0.00000000
JOB 0.00000000
NINQ 0.00000000
```



The plot helps us to understand which variables has the largest number of missing values. In addition, this plot shows that almost 21% of data are missing the DEBTINC value, 11% are missing DEROG value and so on.

To know more about the details of arguments in `aggr()` function you can use the help option in R.

Imputing the missing values using mice

The “`mice()`” function takes care of imputing process.

```
> NewData = mice(hmeq, m=5, maxit=50, meth='pmm', seed=500)
> summary(NewData)
```

A couple of notes on the parameters:

- `m=5` refers to the number of imputed datasets. Five is the default value.
- `meth='pmm'` refers to the imputation method. In this case we are using predictive mean matching as imputation method. Other imputation methods can be used, type `methods(mice)` for a list of the available imputation methods.

To check the imputed data, for example for CLAGE, we can use the following code”

```
> NewData$imp$CLAGE
```

	1	2	3	4	5
4	276.841935	308.75918	114.461955	105.530376	101.82614
11	186.633333	146.93333	217.786841	84.837250	125.76667
18	100.616421	62.05011	134.000074	122.766667	89.43649
22	147.100000	115.60000	177.566667	62.900000	288.16667
52	138.164705	230.06728	297.001608	102.500000	196.55422
64	321.633333	115.90000	55.358803	297.482505	199.73871
74	289.545673	135.57298	310.366757	246.754666	55.55805
93	17.200000	85.25084	17.460750	91.715293	228.03600

The output shows the imputed data for each observation (first column left) within each imputed dataset (first row at the top).

To check the imputation method used for each variable, we can use “`NewData$meth`”.

```
> NewData$meth
```

BAD	LOAN	MORTDUE	VALUE	REASON	JOB	YOJ	DEROG	DELINQ	CLAGE	NINQ
"pmm"	"pmm"	"pmm"	"pmm"	"pmm"	"pmm"	"pmm"	"pmm"	"pmm"	"pmm"	"pmm"
CLNO	DEBTINC									
"pmm"	"pmm"									

We can get back the completed dataset using the `complete()` function.

```
> complete(NewData, 1)
```

As far as categorical variables are concerned, replacing categorical variables is usually not advisable. Some common practice include replacing missing categorical variables with the mode of the observed ones, however, it is questionable whether it is a good choice. Even though in this case no data points are missing from the categorical variables, we remove them from our dataset (we can add them back later if needed) and take a look at the data using `summary()`.