DAS Project2 Group18

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```r
library(tidyverse)
library(dplyr)
library(readr)
library(ggplot2)
library(vcd)
library(MASS)
```

```r
#load the data
shelter_01 <- read.csv("dataset18.csv")
```

```r
#Checking for missing value
any_na <- apply(shelter_01, 2, function(x) any(is.na(x)))
any_na
```

```
   animal_type           month            year     intake_type    outcome_type
         FALSE           FALSE           FALSE           FALSE           FALSE
   chip_status time_at_shelter
         FALSE           FALSE
```

```r
total_na <- sum(is.na(shelter_01))
total_na
```

```
[1] 0
```

```r
#Converting a string variable to a factor type and make a summary statistics
shelter_01$animal_type <- as.factor(shelter_01$animal_type)
shelter_01$intake_type <- as.factor(shelter_01$intake_type)
shelter_01$outcome_type <- as.factor(shelter_01$outcome_type)
```

```r
shelter_01$chip_status <- as.factor(shelter_01$chip_status)
summary(shelter_01)
```

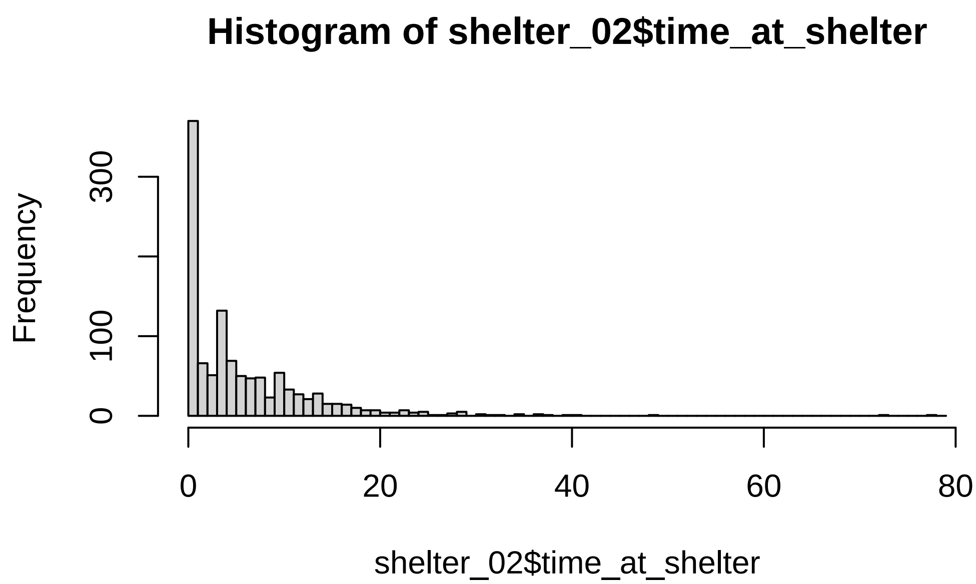
```
   animal_type      month             year                intake_type
BIRD      :  2   Min.   : 1.000   Min.   :2016   CONFISCATED     : 59
CAT       :238   1st Qu.: 4.000   1st Qu.:2017   OWNER SURRENDER:363
DOG       :880   Median : 7.000   Median :2017   STRAY          :713
LIVESTOCK:  1    Mean   : 6.574   Mean   :2017
WILDLIFE : 14    3rd Qu.: 9.000   3rd Qu.:2017
                 Max.   :12.000   Max.   :2017
           outcome_type         chip_status    time_at_shelter
ADOPTION          :474   SCAN CHIP     :214   Min.   : 0.00
DIED              : 14   SCAN NO CHIP  :860   1st Qu.: 1.00
EUTHANIZED        :417   UNABLE TO SCAN: 61   Median : 4.00
FOSTER            : 30                        Mean   : 6.12
RETURNED TO OWNER:200                         3rd Qu.: 9.00
                                              Max.   :78.00
```

```r
#Converting shelter_01 to dataframe
shelter_02 <- as.data.frame(shelter_01)
summary(shelter_02)
```

```
   animal_type      month             year                intake_type
BIRD      :  2   Min.   : 1.000   Min.   :2016   CONFISCATED     : 59
CAT       :238   1st Qu.: 4.000   1st Qu.:2017   OWNER SURRENDER:363
DOG       :880   Median : 7.000   Median :2017   STRAY          :713
LIVESTOCK:  1    Mean   : 6.574   Mean   :2017
WILDLIFE : 14    3rd Qu.: 9.000   3rd Qu.:2017
                 Max.   :12.000   Max.   :2017
           outcome_type         chip_status    time_at_shelter
ADOPTION          :474   SCAN CHIP     :214   Min.   : 0.00
DIED              : 14   SCAN NO CHIP  :860   1st Qu.: 1.00
EUTHANIZED        :417   UNABLE TO SCAN: 61   Median : 4.00
FOSTER            : 30                        Mean   : 6.12
RETURNED TO OWNER:200                         3rd Qu.: 9.00
                                              Max.   :78.00
```

```r
# Histogram analysis of the dependent variable
hist(shelter_02$time_at_shelter,
```

```r
     breaks = seq(min(shelter_02$time_at_shelter),
                  max(shelter_02$time_at_shelter) + 1, by = 1))
```



The significance of finding out whether the dependent variable is continuous or count is in choosing the appropriate statistical method and model for the analysis. If the histogram shows a continuous and smooth distribution, it usually indicates that the dependent variable is continuous. If the histogram shows a discrete and spaced distribution, it usually indicates that the dependent variable is of the count type.

From the results, it can be known that histogram is showing interval shape and overall is not smooth. Therefore the dependent variable is count type. Count variables are usually analysed using Poisson regression and negative binomial distribution regression. Therefore, we have attempted to use Poisson distribution and negative binomial distribution regression for the subsequent Generalized Linear Model respectively.

```r
glm_model_poi <- glm(time_at_shelter ~ year + month + animal_type + intake_type
                     + outcome_type + chip_status, data = shelter_02,
                   family = poisson())
summary(glm_model_poi)
```

```
Call:
glm(formula = time_at_shelter ~ year + month + animal_type +
    intake_type + outcome_type + chip_status, family = poisson(),
    data = shelter_02)

Coefficients:
                               Estimate Std. Error z value Pr(>|z|)
(Intercept)                  209.563215 219.298918   0.956  0.33927
year                          -0.108790   0.043770  -2.486  0.01294 *
month                         -0.016839   0.005842  -2.882  0.00395 **
animal_typeCAT                13.253664 200.734972   0.066  0.94736
animal_typeDOG                13.354757 200.734971   0.067  0.94696
animal_typeLIVESTOCK          -0.191216 348.317912  -0.001  0.99956
animal_typeWILDLIFE           12.834001 200.735017   0.064  0.94902
intake_typeOWNER SURRENDER    -1.367180   0.049511 -27.614  < 2e-16 ***
intake_typeSTRAY              -0.856870   0.044964 -19.057  < 2e-16 ***
outcome_typeDIED              -0.469573   0.113310  -4.144 3.41e-05 ***
outcome_typeEUTHANIZED        -0.542380   0.027585 -19.662  < 2e-16 ***
outcome_typeFOSTER            -0.576073   0.088272  -6.526 6.75e-11 ***
outcome_typeRETURNED TO OWNER -1.621092   0.050170 -32.312  < 2e-16 ***
chip_statusSCAN NO CHIP       -0.258643   0.031581  -8.190 2.62e-16 ***
chip_statusUNABLE TO SCAN     -0.645688   0.074825  -8.629  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 8495.8  on 1134  degrees of freedom
Residual deviance: 6544.7  on 1120  degrees of freedom
AIC: 9670.3

Number of Fisher Scoring iterations: 10
```

```r
model_poi <- step(glm_model_poi)
```

```
Start:  AIC=9670.31
time_at_shelter ~ year + month + animal_type + intake_type +
    outcome_type + chip_status

               Df Deviance    AIC
<none>              6544.7 9670.3
```

```
- year          1   6550.9  9674.5
- month         1   6553.0  9676.6
- animal_type   4   6587.0  9704.6
- chip_status   2   6651.2  9772.8
- intake_type   2   7270.5 10392.1
- outcome_type  4   8056.1 11173.7
```

The stepwise analysis of the model was carried out while performing the Poisson distribution. The initial model had an AIC value of 9670.31. In further steps, the independent variables such as year, month, animal_type, chip_status, intake_type, and outcome_type were gradually deleted but these deletion operations all lead to an increase in the AIC value, indicating that deleting these variables makes the model worse. Therefore, it can be seen that the best model is when no independent variables are added or removed, which corresponds to an AIC value of 9670.3 and a deviation of 6544.7.

```r
glm_model_nb <- glm.nb(time_at_shelter ~ year + month + animal_type + intake_type
                       + outcome_type + chip_status, data = shelter_02)
summary(glm_model_nb)
```

```
Call:
glm.nb(formula = time_at_shelter ~ year + month + animal_type +
    intake_type + outcome_type + chip_status, data = shelter_02,
    init.theta = 0.9633756977, link = log)

Coefficients:
                                Estimate Std. Error z value Pr(>|z|)
(Intercept)                    3.078e+02  1.333e+05   0.002   0.9982
year                          -1.638e-01  1.217e-01  -1.345   0.1785
month                         -2.029e-02  1.613e-02  -1.258   0.2084
animal_typeCAT                 2.619e+01  1.333e+05   0.000   0.9998
animal_typeDOG                 2.631e+01  1.333e+05   0.000   0.9998
animal_typeLIVESTOCK          -3.126e-01  2.315e+05   0.000   1.0000
animal_typeWILDLIFE            2.574e+01  1.333e+05   0.000   0.9998
intake_typeOWNER SURRENDER    -1.703e+00  1.600e-01 -10.640  < 2e-16 ***
intake_typeSTRAY              -1.295e+00  1.506e-01  -8.602  < 2e-16 ***
outcome_typeDIED              -4.871e-01  3.005e-01  -1.621   0.1050
outcome_typeEUTHANIZED        -6.033e-01  7.598e-02  -7.940 2.02e-15 ***
outcome_typeFOSTER            -4.783e-01  2.175e-01  -2.199   0.0279 *
outcome_typeRETURNED TO OWNER -1.843e+00  1.108e-01 -16.638  < 2e-16 ***
chip_statusSCAN NO CHIP       -1.717e-01  9.032e-02  -1.901   0.0573 .
chip_statusUNABLE TO SCAN     -7.708e-01  1.816e-01  -4.244 2.20e-05 ***
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(0.9634) family taken to be 1)

    Null deviance: 1640.1  on 1134  degrees of freedom
Residual deviance: 1312.5  on 1120  degrees of freedom
AIC: 6252.2

Number of Fisher Scoring iterations: 1

              Theta:  0.9634
          Std. Err.:  0.0542

 2 x log-likelihood:  -6220.2480
```

```
model_nb <- step(glm_model_nb)
```

```
Start:  AIC=6250.25
time_at_shelter ~ year + month + animal_type + intake_type +
    outcome_type + chip_status

               Df Deviance    AIC
- month         1   1314.0 6249.7
- year          1   1314.3 6250.1
<none>              1312.5 6250.2
- animal_type   4   1325.0 6254.8
- chip_status   2   1330.3 6264.1
- intake_type   2   1439.1 6372.9
- outcome_type  4   1573.6 6503.4

Step:  AIC=6249.74
time_at_shelter ~ year + animal_type + intake_type + outcome_type +
    chip_status

               Df Deviance    AIC
- year          1   1313.0 6248.2
<none>              1312.6 6249.7
- animal_type   4   1325.5 6254.6
- chip_status   2   1329.9 6263.0
- intake_type   2   1439.1 6372.2
```

```
- outcome_type  4   1574.3 6503.4

Step:  AIC=6248.17
time_at_shelter ~ animal_type + intake_type + outcome_type +
    chip_status

               Df Deviance    AIC
<none>              1312.6 6248.2
- animal_type   4   1325.4 6253.0
- chip_status   2   1330.1 6261.7
- intake_type   2   1439.7 6371.3
- outcome_type  4   1577.9 6505.5
```

We then tried the negative binomial distribution and performed a stepwise analysis of the model. The initial model had an AIC value of 6250.25. In the iteration, the year and month variables were gradually removed and each step resulted in a decrease in the AIC value. The final model contains independent variables such as animal_type, intake_type, outcome_type and chip_status.

By comparing the results of model_poi and model_nb, we can see the difference in the performance of the two models in the stepwise regression analysis. model_nb model obtained a lower AIC value by gradually deleting the year and month variables when selecting the variables, indicating that this model fits the data better, while model_poi model did not find that it could be further optimised during the stepwise regression process. model_poi model did not find any variables that could further optimise the model, so it retained all the independent variables, but with a relatively high AIC value.

By comparing the deviation values of the two models, model_nb has a final deviation value of 1312.6 and model_poi has a final deviation value of 6544.7. We can find that model_nb has a smaller deviation value and fits the data better than model_poi. Therefore, based on the comparison of deviation values, model_nb model is more suitable for interpreting and predicting the data.