DAS Project2 Group18

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

Data Pre-processing

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

```
#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
```

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

```
[1] 0
```

Exploratory Analysis

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

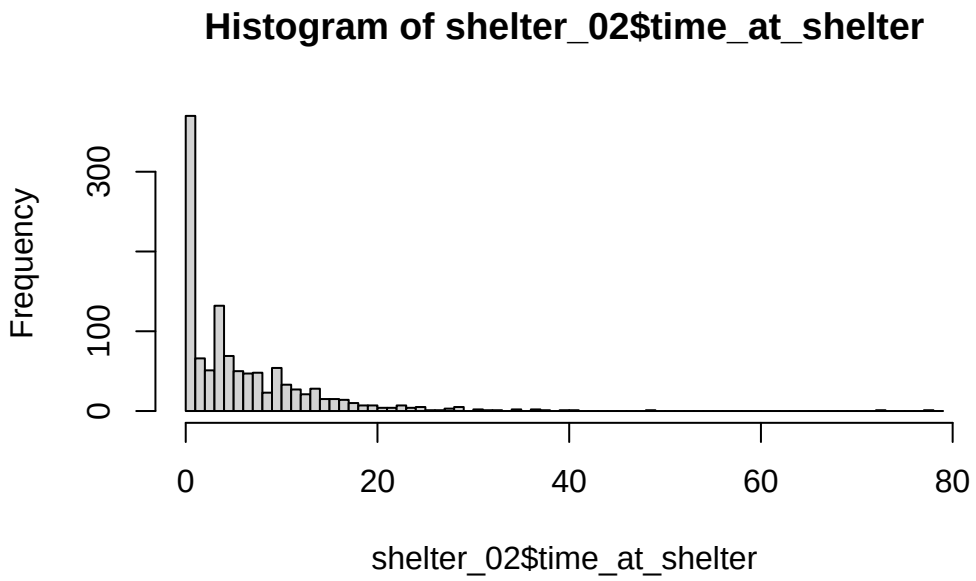
```
   animal_type      month             year               intake_type
BIRD     :  2   Min.   : 1.000   Min.   :2016   CONFISCATED    : 59
CAT      :238   1st Qu.: 4.000   1st Qu.:2017   OWNER SURRENDER:363
DOG      :880   Median : 7.000   Median :2017   STRAY          :713
LIVESTOCK:  1   Mean   : 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
```

```
#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$time_at_shelter,
     breaks = seq(min(shelter_02$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 variables. Count variable is 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
column_variance <- var(shelter_02$time_at_shelter)
column_variance
```

```
[1] 54.57293
```

Formal Analysis

```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
```

```r
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.

Importantly, we choose the Negative Binomial distribution over the Poisson distribution for several reasons. Firstly, the duration of animals staying in shelters is influenced by a series of independent events, such as daily intake and release of animals, leading to uncertainty in trial counts. The Negative Binomial distribution is better suited to describe this uncertainty, as it can model the number of trials required to achieve a specified number of successes. Additionally, factors like animal type and shelter policies may result in unstable rates of stay duration, making the Poisson distribution less appropriate as it assumes a constant rate of event occurrence. Moreover, count data such as the number of days animals spend in a shelter often exhibit a situation where the variance exceeds the mean. This is accommodated by the Negative Binomial distribution, which allows for variance greater than the mean. Therefore, considering these factors, the Negative Binomial distribution provides a more flexible and accurate framework for modeling the duration of animal stays in shelters.

Conclusion

Through this study, we can conclude that several factors significantly affect the length of animals' stay in the shelter and reduce it. The first factor is "automatically sent to the shelter by the original owner", the second factor is "returned by the original owner himself", and the third factor is "no chip was scanned on the animal". There is another factor, animal species, which we are not sure how it affects the length of time an animal spends in the habitat, but in our analysis it is significant. Consider each animal separately, and you will find they are insignificant. This may be due to uneven sample sizes, with some animals such as birds and livestock having too small a sample size. It is also possible that cats and dogs with large sample sizes were collinear in this study.