Team_Project

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Team Name: i need a </br>

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1) Abstract

Celiotomy, commonly referred to as "colic surgery" is a type of surgery around the abdomin of a horse. According to the American College of Vetinary Surgeons, colic surgery is used to address many issues that affect the longevity of a horse, most commonly used to address issues within the gastrointestinal tract within the intestines. The surgery is also used to address a number of other lesians around the abdominal.

2) Introduction

Horses are regarded as powerful and courageous animal that are highly desired for riding, ranch work, jumping, racing, or dressage. As with any animal, there are always complications that may arise in regards to their health. This is especially true in Horses. Horses can develop health problems at any stage in life and some are more susceptible to health problems than others. Our dataset focuses on horses who suffer from Colic. Colic is defined as having abdominal pains but in horses it is referred to problems in gastro-intestinal tract. Some common causes of Colic are High grain based diets/Low forage diets, Moldy/Tainted feed, Abrupt change in feed, Parasite infestation, Lack of water consumption leading to impaction colics, Sand ingestion, Long term use of NSAIDS, Stress and Dental problems. About 10% of horses die from colic which is why its important to understand variables that can contribute to their outcome given that the horse underwent Colic Surgery.

3) Method(s)

- 1. Data Collection
- 2. Exploratory Data Analysis

4) Data

Our data was sourced from the University of California, Irvine Machine Learning Repository.

This specific dataset was donated August 6, 1989 by Will Taylor. It was created for use by Mary McLeish & Matt Cecile who belong to the Department of Computer Science at the University of Guelph in Guelph, Ontario, Canada.

The data has 299 observations and 27 parameters that range from continuous to discrete and nominal variables. Below you can find an outline of the variables found within the dataset as well as their respective description.

Variable Name	Description		
ID	a row indicator which uniquely identifies each row		
surgery	was the horse treated with or without surgery		
age	identify if the horse in an adult or a child (young identified as under 6 months)		
hospital_number	the case number assigned to the horse (same number if a horse is treated twice)		
rectal_temp	the temperature of the horse's rectum recorded in degrees Celsius		
pulse	a horse's heart rate measured in beats per minute		
respiratory_rate	the number of breaths a horse takes per minute		
temp_of_extremities	a subjective way to measure the condition of outermost circulation by the temperature		
peripheral_pulse	a subjective way to measure the condition of outermost circulation by pulse		
mucous_membrane	a record of the color of the mucous membranes as an indicator of circulation		
capillary_refill_time	measuring the time to refill the capillaries		
pain	a measure of the horse's pain level (not to be taken as a linear variable)		
peristalsis	an indication of the activity in the horse's gut		
abdominal_distention	measure of the amount of air/gas filling the horse's gut as an indicator of a health problem		
nasogastric_tube	amount of gas coming out of the nasogastric tube		
nasogastric_reflux	the amount of reflux within the nasogastric tube		
nasogastric_reflux_ph	ph of the reflux within the nasogastric tube		
rectal_exam_feces	the amount of feces found within the rectal		
abdomen	an indicator to how the abdomen (small and large intestine) is in relation to feces		
packed_cell_volume	number of red cells in the blood by volume		
total_protein	total amount of protein found in the blood		
abdomo_appearance	the color of the fluid taken from the horse's abdominal cavity		
abdomo_protein	total amount of protein found in the gut		
outcome	current status of the horse: alive, dead, or euthanized		
surgical_lesion	could the lesion and/or problem be treated with surgery		
lesion_1	indicator of the site, type, subtype, specific code for lesion 1		
lesion_2	indicator of the site, type, subtype, specific code for lesion 2		
lesion_3	indicator of the site, type, subtype, specific code for lesion 3		
cp_data	indicates if there is pathology data present		

##

Parameter 'xdbsock' not found, setting to empty string for general usage

```
library(RMySQL)
## Loading required package: DBI
library(rjson)
drv <- dbDriver("MySQL")</pre>
############
xdbuser <- Sys.getenv("MAS405_AWS_YOLANDA_DB_RO_USER")</pre>
       <- Sys.getenv("MAS405_AWS_YOLANDA_DB_RO_PW")
xdbname <- Sys.getenv("MAS405_AWS_YOLANDA_DB_RO_DBNAME")</pre>
xdbhost <- Sys.getenv("MAS405_AWS_YOLANDA_DB_RO_HOST")</pre>
xdbport <- as.integer( Sys.getenv("MAS405_AWS_YOLANDA_DB_RO_PORT") )</pre>
con <- dbConnect(drv, user=xdbuser, password=xpw, dbname=xdbname, host=xdbhost, port=xdbport, unix.sock
############ get info
dbListTables(con)
## [1] "dataDictionary" "horse"
dbGetInfo(con)
## $host
## [1] "stats405db.cziy0a015m5d.us-east-1.rds.amazonaws.com"
## $user
## [1] "ROuser"
##
## $dbname
## [1] "db1"
##
## [1] "stats405db.cziy0a015m5d.us-east-1.rds.amazonaws.com via TCP/IP"
## $serverVersion
## [1] "8.0.23"
##
## $protocolVersion
## [1] 10
## $threadId
## [1] 18978
##
## $rsId
## list()
qstr <- "SHOW TABLES"</pre>
xx <- dbGetQuery(con, qstr)</pre>
##
      Tables_in_db1
## 1 dataDictionary
```

2

horse

```
xdf_myTables <- xx</pre>
xdf_myTables
##
      Tables_in_db1
## 1 dataDictionary
## 2
               horse
query1 <- "select * from horse"
result1 <- dbGetQuery(con, query1)
head(result1)
##
                   age hospital_number rectal_temp pulse respiratory_rate temp_of_extremities peripheral
     ID surgery
## 1
      1
             no adult
                                 530101
                                                 38.5
                                                          66
                                                                            28
                                                                                                cool
## 2
      2
                                 534817
                                                 39.2
                                                          88
                                                                            20
                                                                                                <NA>
             yes adult
## 3
      3
             no adult
                                 530334
                                                 38.3
                                                          40
                                                                            24
                                                                                              normal
                                                 39.1
                                                        164
                                                                            84
## 4
      4
             yes young
                                5290409
                                                                                                cold
## 5
     5
             no adult
                                 530255
                                                 37.3
                                                        104
                                                                            35
                                                                                                <NA>
                                 528355
## 6
      6
             no adult
                                                   NA
                                                         NA
                                                                            NA
                                                                                                warm
     nasogastric_tube nasogastric_reflux nasogastric_reflux_ph rectal_exam_feces
                                                                                               abdomen packed c
##
## 1
                  <NA>
                                       <NA>
                                                                 NA
                                                                             decreased distend_large
## 2
                  <NA>
                                       <NA>
                                                                                absent
                                                                 NΑ
## 3
                  <NA>
                                       <NA>
                                                                 NΑ
                                                                                normal
                                                                                                normal
## 4
                  none
                              less_1_liter
                                                                  5
                                                                             decreased
                                                                                                  <NA>
## 5
                  <NA>
                                       <NA>
                                                                                   <NA>
                                                                                                  <NA>
                                                                 NA
## 6
                                                                             decreased
                slight
                                       none
                                                                 NA
                                                                                                  firm
     lesion_2 lesion_3 cp_data
##
## 1
             0
                      0
                              no
## 2
             0
                      0
                              no
## 3
             0
                      0
                             yes
## 4
             0
                       0
                             yes
## 5
             0
                       0
                              no
## 6
                       0
                              no
knitr::kable(summary(result1))
```

ID surgegy hospitathantsumpportuntetalerillistikum kuitikataikii kiin kasakii tatututututututa kasakii :35.40 : :23.00 :1.00 : : : 518476 30 8.00 3.30 0.10 0.000.000Quichardreffert Qui. Q7i. SQuite Balled tardrate determinate adterminate after determinate after deter 75.5 528904 48 6.502.00 21120.000.000 :150:Charcheteacte28.20 :25.0Charcheteacheteacheteacheteacheteacteacteacheteacteacheteacteachete :charactæhaæhæætææter : 530301 64 7.50 2.30 23220.000.000 Meana NA Meana Meana Meana NA NA NA NA NA NA NA NA NA Meana Meana

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32090.000.000

3.90

534736 88

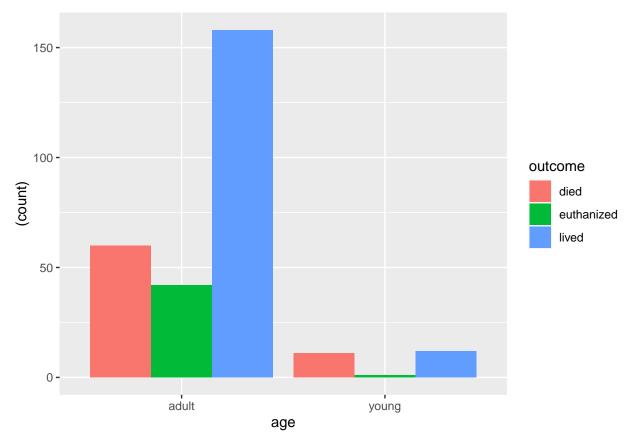
```
str(result1)
```

```
299 obs. of 29 variables:
## 'data.frame':
                         : int 1 2 3 4 5 6 7 8 9 10 ...
## $ surgery
                         : chr "no" "yes" "no" "yes" ...
                         : chr "adult" "adult" "young" ...
## $ age
## $ hospital_number
                         : int 530101 534817 530334 5290409 530255 528355 526802 529607 530051 52996
## $ rectal_temp
                         : num 38.5 39.2 38.3 39.1 37.3 NA 37.9 NA NA 38.3 ...
                         : int 66 88 40 164 104 NA 48 60 80 90 ...
## $ pulse
## $ respiratory_rate
                         : int 28 20 24 84 35 NA 16 NA 36 NA ...
                                "cool" NA "normal" "cold" ...
## $ temp_of_extremities : chr
## $ peripheral_pulse
                         : chr "reduced" NA "normal" "normal" ...
                         : chr NA "pale_cyanotic" "pale_pink" "dark_cyanotic" ...
## $ mucous_membrane
                                "more_3_sec" "less_3_sec" "less_3_sec" "more_3_sec" ...
## $ capillary_refill_time: chr
                                "extreme pain" "mild pain" "mild pain" "depressed" ...
## $ pain
                         : chr
## $ peristalsis
                         : chr "absent" "absent" "hypomotile" "absent" ...
## $ abdominal distention : chr "severe" "slight" "none" "severe" ...
## $ nasogastric_tube
                        : chr NA NA NA "none" ...
## $ nasogastric_reflux
                         : chr NA NA NA "less_1_liter" ...
## $ nasogastric reflux ph: int NA ...
## $ rectal exam feces
                        : chr "decreased" "absent" "normal" "decreased" ...
## $ abdomen
                         : chr "distend large" "other" "normal" NA ...
## $ packed_cell_volume : int 45 50 33 48 74 NA 37 44 38 40 ...
## $ total_protein
                         : num 8.4 85 6.7 7.2 7.4 NA 7 8.3 6.2 6.2 ...
## $ abdomo_appearance
                         : chr NA "cloudy" NA "serosanguious" ...
## $ abdomo_protein
                         : num NA 2 NA 5.3 NA NA NA NA NA 2.2 ...
                         : chr "died" "euthanized" "lived" "died" ...
## $ outcome
## $ surgical_lesion
                         : chr "no" "no" "no" "yes" ...
## $ lesion_1
                         : int 11300 2208 0 2208 4300 0 3124 2208 3205 0 ...
## $ lesion_2
                         : int 0000000000...
## $ lesion_3
                         : int 0000000000...
## $ cp data
                         : chr "no" "no" "yes" "yes" ...
```

There is no column that represents a unique horse in the table. We tried to retrieve the number of horses by counting the distinct hospital_number which is their case number and they have the same case number when the horses are treated multiple times.

```
library(ggplot2)
query2 <- "select distinct age,outcome, hospital_number from horse"
result2 <- dbGetQuery(con, query2)

ggplot(data=result2,aes(x=age,fill=outcome)) +
   geom_bar(aes(y=(..count..)),position=position_dodge())</pre>
```



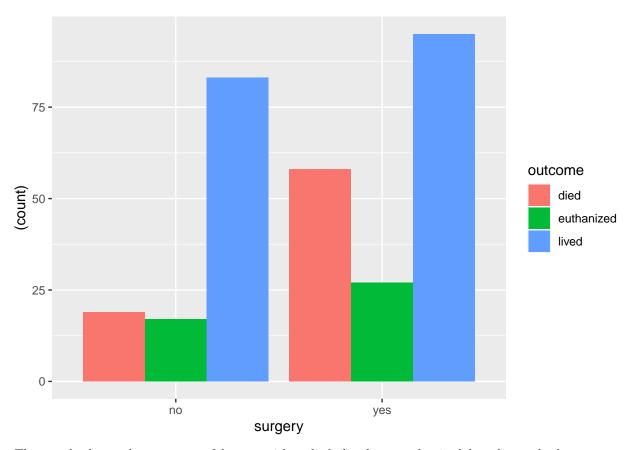
```
query2_1 <- "select age,outcome,count(*) cnt from horse group by age,outcome"
result2_1 <- dbGetQuery(con, query2_1)
knitr::kable(table(result2$age,result2$outcome))</pre>
```

	died	euthanized	lived
adult	60	42	158
young	11	1	12

This graph shows number of horses by age groups and outcome which indicates horses' life status. The number of young horses (24) is very small so that it might not be enought to talk about the pattern. The bar graph shows that adult horses have higher lived proportion than young horses.

```
query3 <- "select surgery,outcome from horse"
result3 <- dbGetQuery(con, query3)

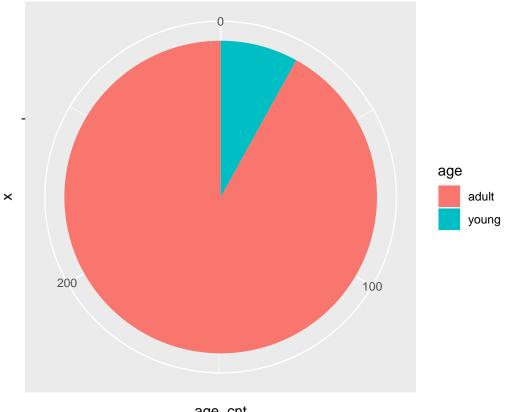
ggplot(data=result3,aes(x=surgery,fill=outcome)) +
   geom_bar(aes(y=(..count..)),position=position_dodge())</pre>
```



The graph shows the outcome of horses, either died, lived, or euthanized based on whether a surgery treatment was applied. There are 119 observations for no surgery, and 180 for surgery. 70% of the horses without surgery survived. For horses who had surgery, around 53% lived, and 32% have died.

```
query4_1 <- "select age,count(age) age_cnt from horse group by age"
result4_1 <- dbGetQuery(con, query4_1)

ggplot(result4_1,aes(x="",y=age_cnt,fill=age)) + geom_bar(stat="identity",width=1) +
    coord_polar("y",start=0)</pre>
```

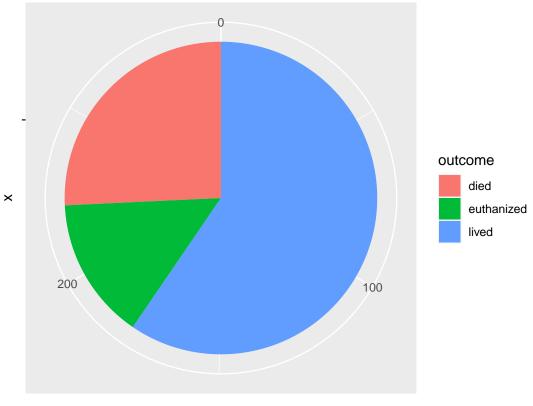


age_cnt

knitr::kable(result4_1)

age	age_cnt
adult	275
young	24

```
query4_2 <- "select outcome,count(outcome) outcome_cnt from horse group by outcome"</pre>
result4_2 <- dbGetQuery(con, query4_2)</pre>
ggplot(result4_2,aes(x="",y=outcome_cnt,fill=outcome )) + geom_bar(stat="identity",width=1) +
 coord_polar("y",start=0)
```



outcome_cnt

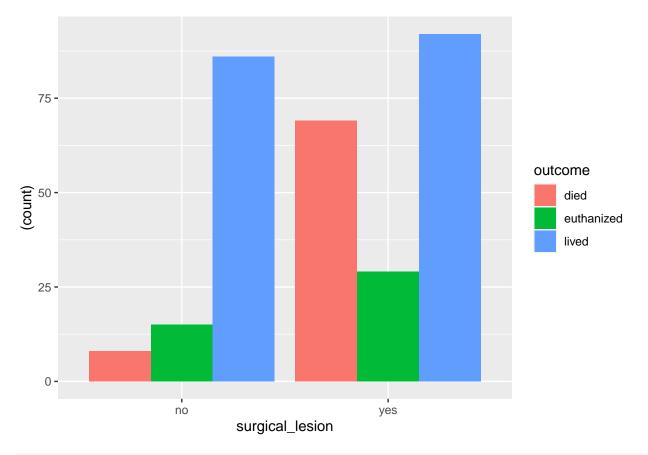
knitr::kable(result4_2)

outcome	$outcome_cnt$
died	77
euthanized	44
lived	178

```
query5 <- "select outcome, surgical_lesion from horse"
result5 <- dbGetQuery(con, query5)
head(result5)</pre>
```

```
##
        outcome surgical_lesion
## 1
           died
## 2 euthanized
                             no
## 3
         lived
                             no
## 4
           died
                            yes
## 5
           died
                             no
## 6
          lived
```

```
ggplot(data=result5,aes(x=surgical_lesion,fill=outcome)) +
  geom_bar(aes(y=(..count..)),position=position_dodge())
```



knitr::kable(table(result5\$outcome,result5\$surgical_lesion))

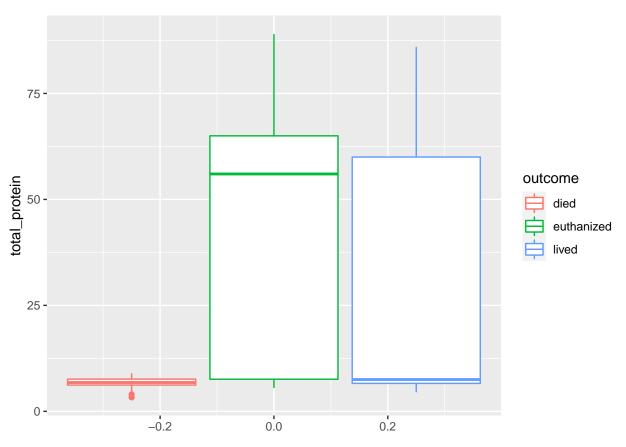
	no	yes
died	8	69
euthanized	15	29
lived	86	92

```
query6 <- "select id,total_protein,outcome from horse"
result6 <- dbGetQuery(con, query6)
head(result6)</pre>
```

```
id total_protein
                        outcome
## 1 1
                 8.4
                           died
## 2 2
                85.0 euthanized
## 3 3
                 6.7
                          lived
                 7.2
                           died
## 5 5
                 7.4
                           died
## 6 6
                  NA
                          lived
```

```
result6$outcome<-as.factor(result6$outcome)
ggplot(data =result6, aes(y=total_protein,color=outcome)) +
  geom_boxplot(notch=F)</pre>
```

Warning: Removed 33 rows containing non-finite values (stat_boxplot).



#knitr::kable(result6\$total_protein,result6\$outcome)
library(dplyr)

##

##

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

```
## filter, lag

## The following objects are masked from 'package:base':
##

## intersect, setdiff, setequal, union

query6_1 <- "select outcome,avg(total_protein) mean_protein,STDDEV_SAMP(total_protein) sd, count(distin result6_1 <- dbGetQuery(con, query6_1)

#Protein in the guts
# query6_2 <- "select id,abdomo_protein,outcome from horse"
# result6_2 <- dbGetQuery(con, query6_2)
#</pre>
```

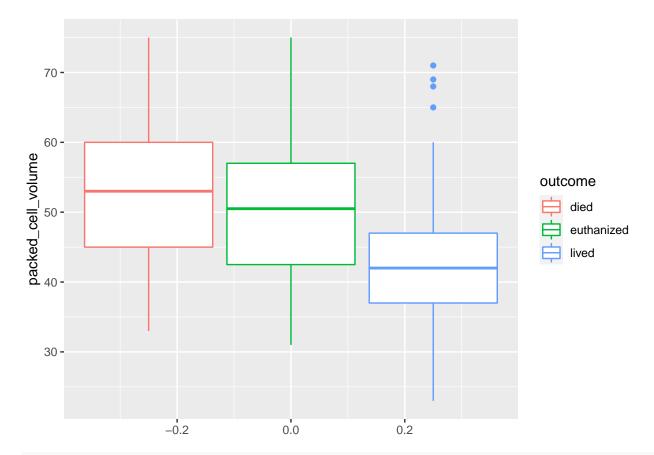
```
# ggplot(data =result6_2, aes(y=abdomo_protein,color=outcome)) +
# geom_boxplot(notch=F)
knitr::kable(as.data.frame(result6_1))
```

outcome	mean_protein	sd	horse_cnt
died	6.844615	1.177661	77
euthanized	42.038889	30.705228	44
lived	27.264848	28.452084	178

```
query7 <- "select id,packed_cell_volume,outcome from horse"
result7 <- dbGetQuery(con, query7)

ggplot(data =result7, aes(y=packed_cell_volume,color=outcome)) +
    geom_boxplot()</pre>
```

Warning: Removed 29 rows containing non-finite values (stat_boxplot).



A tibble: 3 x 4

mean

sd count

outcome

	died	euthanized	lived
alert	2	1	35
$\operatorname{depressed}$	14	12	33
$extreme_pain$	24	6	12
mild _pain	8	5	54
severe_pain	17	11	10

```
# Display two-way table for abdominal distention and Outcome
query10 <- "SELECT * FROM db1.horse;"
result10 <- dbGetQuery(con, query10)
twoWay_abdominal_distention_Outcome <- pander(table(result10$abdominal_distention, result10$outcome))
twoWay_abdominal_distention_Outcome</pre>
```

	died	euthanized	lived
moderate	27	12	26
none	7	7	61
severe	15	10	13
slight	14	4	47

```
# Display two-way table for nasogastric reflux and Outcome
query11 <- "SELECT * FROM db1.horse;"
result11 <- dbGetQuery(con, query11)
twoWay_nasogastric_reflux_Outcome <- pander(table(result11$nasogastric_reflux, result10$outcome))
twoWay_nasogastric_reflux_Outcome</pre>
```

	died	euthanized	lived
less_1_liter	14	5	16
${f more_1_liter}$	14	10	15
none	22	17	80

5) Conclusions

Bibliography and References

 $\label{lem:colic_emergencies} \begin{tabular}{ll} College of veterinary medicine "University of Florida.~(n.d.). Retrieved May 28, 2021, from https://largeanimal.vethospitals.ufl.edu/hospital-services/surgery/colic/$

 $\label{lem:colic-surgery} \mbox{Colic-Surgery in Horses. (n.d.)}. \mbox{ Retrieved from https://www.acvs.org/surgical-procedures/colic-surgery-horses}$