### Data Analysis 3

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#### Introduction

In this paper we will be looking at data related to calves. The data comes from an experiment designed to study the impact dietary treatments given to pregnant heifers had on the development of the calves. The study was conducted over a three year period and involved three different dietary treatments given to select groups of heifers in the final trimester. In total the data has 22 variables for 120 entries, though some data points are missing.

For more information on the experiment, the data, or any other files used in this paper see our Github page which can be found at https://github.com/RyanLalicker/Data-Analysis-2-STAT-325-825. The coding languages used in the paper are R and SAS. The corresponding code can be found in  $Appendix\ A-R\ Code$  and  $Appendix\ B-SAS\ Code$  respectively.

### **Exploring the Data**

#### **Variables**

As mentioned above the experiment used three different dietary treatments. These were DDG, CON, and MET. For the first two trimesters the heifers were given one of seven developmental treatments, found in <code>Development.Treatment</code>, and then in the final trimester the each was given one of the three treatments mentioned above. This is recorded in the <code>Calan.Treatment</code> column of the data set.

The heifers were placed into one of four pens by weight, which can be seen in the column Pen #. They were then artificially inseminated from an assigned sire, which we will assume was done randomly since the client says weight was not a factor. The sire is represented by the column of the same name and has six unique entries.

Upon the birth of the calves, several measurements were taken. These include the sex of the calf, weights taken at both birth and slaughter, and scores of both the calf's vigor and the ease of birth. The variable names line up with these descriptions.

Other variables, such as the id of the calf, length of gestation for the heifer, and postmortem scoring such as hot carcass weight (HCW) are included as well. (Saner (2024)). Note two birthdays are included in the data, Birth.date and Birth.date.1. These variables will not be used in the models below so no further investigation was done on our part to determine the differences.

The client's main focus is the effect the third trimester treatment and the sex of a calf have on the calf's vigor score, ease of birth score, and final body weight. Therefore, these are the variables we will place more of an emphasis on, while exploring the effect some of the other variables may have.

#### Missing Values

# UPDATE THIS AFTER SEEING WHAT VARIABLES ARE NEEDED FOR THE MODEL

The data contains some missing values. In regards to the five variables the client is most interested in, 19 entries are missing one or more values. Since that still leaves 101 entries with all five variables

Initially the dataset has missing values in the following columns: Pen #: 4 missing values DMI: 36 missing values SEX: 1 missing value

The heatmap above visualizes the distribution of missing data in the dataset. Columns with missing values (e.g., "Pen #", "DMI", and "SEX") are marked with red line gaps.

```
# Might want this later.
# May need to add more later.
neededvars <- c("Calan.Treatment", "SEX", "Final.Calf.BW", "Calving.Ease", "Calf.Vigor")
data <- data[complete.cases(data[, neededvars]), ]</pre>
```

#### Missing Data Distribution

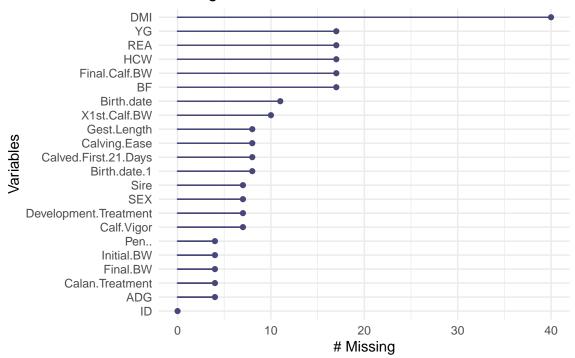


Figure 1: Chart counting the number of missing values for each variable within the data.

#### Cleaning the dataset

This code cleans a data set by replacing all occurrences of . with NA to standardize missing values. It ensures columns are assigned the correct data types, converting numeric-like columns to numeric and others to factor. Missing values are handled by imputing the median for numeric columns and the mode for factor columns. After cleaning, the code verifies that no missing values remain in the dataset.

[1] "Remaining missing values: 0'

#### **Summary Statistics**

[1] "Summary Statistics for Numerical Variables"

```
Birth.date_min Birth.date_max Birth.date_median Development.Treatment_mean
                          50
                                         22.5
 Development.Treatment_sd Development.Treatment_min Development.Treatment_max
                1.842522
 Development.Treatment median Calan.Treatment mean Calan.Treatment sd
                                           2.05
 Calan.Treatment min Calan.Treatment max Calan.Treatment median Pen.. mean
                                                              2.508333
 Pen.._sd Pen.._min Pen.._max Pen.._median Initial.BW_mean Initial.BW_sd
                                               50.79167
                          4
                                3
 Initial.BW min Initial.BW max Initial.BW median Final.BW mean Final.BW sd
                          99
                                         49.5
                                                   48.16667
 Final.BW min Final.BW max Final.BW median DMI mean DMI sd DMI min DMI max
                      94
                            49.5 40.66667 18.57681
                    ADG_sd ADG_min ADG_max ADG_median Gest.Length_mean
 DMI_median ADG_mean
         46 51.675 27.73378 1 95
                                                   55
 Gest.Length_sd Gest.Length_min Gest.Length_max Gest.Length_median
       3.775158
                                          21
 Calved.First.21.Days_mean Calved.First.21.Days_sd Calved.First.21.Days_min
                 1.966667
                                      0.1802581
 Calved.First.21.Days_max Calved.First.21.Days_median X1st.Calf.BW_mean
 X1st.Calf.BW_max X1st.Calf.BW_median
                              1
                                            35
 Calving.Ease_mean Calving.Ease_sd Calving.Ease_min Calving.Ease_max
            1.125
                       0.4213324
 Calving. Ease median Calf. Vigor mean Calf. Vigor sd Calf. Vigor min
                          1.341667 0.8043561
 Calf.Vigor_max Calf.Vigor_median Birth.date.1_mean Birth.date.1_sd
                             1
                                         21.775
 Birth.date.1 min Birth.date.1 max Birth.date.1 median Sire mean Sire sd
                             43
                                                 23 2.883333 1.768935
 Sire min Sire max Sire median SEX mean SEX sd SEX min SEX max SEX median
                      3 1.55 0.4995797
 Final.Calf.BW mean Final.Calf.BW sd Final.Calf.BW min Final.Calf.BW max
           42.68333
                          21.14217
                              HCW_sd HCW_min HCW_max HCW_median REA_mean
 Final.Calf.BW_median HCW_mean
                                        1 83
                  44
                      44.225 21.38069
  REA_sd REA_min REA_max REA_median YG_mean YG_sd YG_min YG_max YG_median
                               45 32.93333 18.45036 1
1 26.7777
                    100
                                                           70
         BF_sd BF_min BF_max BF_median
 BF_mean
1 44.9 22.85556 1
                           88
```

[1] "Summary Statistics for Categorical Variables"

data frame with 0 columns and 1 row

#### **Exploring the Data**

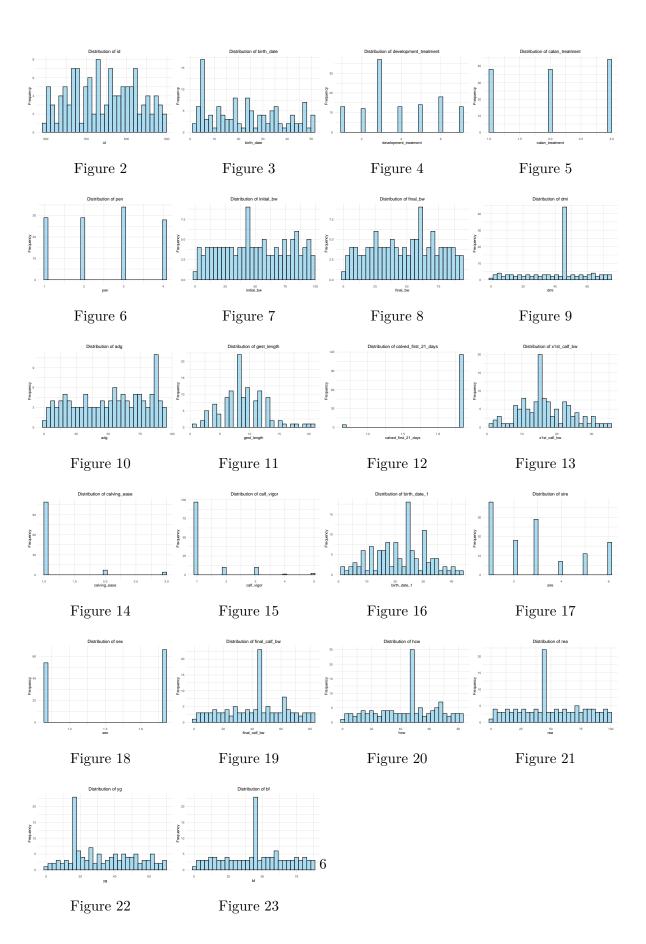
#### Relationships among variables

#### Potential models

#### Model 1

```
Df Sum Sq Mean Sq F value Pr(>F)
calan_treatment
                          1840
                                   920
                                         2.347 0.100267
                         4802
                                  4802 12.254 0.000666 ***
sex
                      1
initial_bw
                      1
                           800
                                   800 2.041 0.155884
calan_treatment:sex
                      2
                         1472
                                   736 1.879 0.157560
Residuals
                    113 44279
                                   392
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
  Tukey multiple comparisons of means
    95% family-wise confidence level
Fit: aov(formula = final_calf_bw ~ calan_treatment * sex + initial_bw, data = data_cleaned)
$calan_treatment
         diff
                     lwr
                               upr
                                        p adj
2-1 5.210526 -5.575086 15.9961383 0.4871443
3-1 -4.287081 -14.698511 6.1243487 0.5922780
3-2 -9.497608 -19.909038 0.9138223 0.0814415
$sex
        diff
                  lwr
                           upr
                                   p adj
```

2-1 12.63931 5.443081 19.83554 0.0007141



```
calan_treatment:sex 2 1472 736 1.879 0.157560
Residuals 113 44279 392
```

---

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

$$y_{ijklmn} = ENTER - MODEL - HERE$$

where  $y_{ijklm}$  represents the  $dependent\ variable,$  ...

![Picture of SAS Output](filename.png){width="3in"}

### Conclusion

#### Recomendation

### References

Saner, Brianna, Randy & Buseman. 2024. "How Many Pounds of Meat Can We Expect from a Beef Animal?" 2024. https://beef.unl.edu/beefwatch/2020/how-many-pounds-meat-can-we-expect-beef-animal.

# Appendix A - R Code

# Appendix B - SAS Code

# Appendix C - Additional SAS Output

![](filename.png)