

# 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](https://github.com/RyanLalicker/Data-Analysis-2-STAT-325-825) 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 `Development.Treatment`, and then in the final trimester the each was given one of the three treatments mentioned above. This is recorded in the `Calan.Treatment` column of the dataset.

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

The data contains some missing values. In total 53 rows in the dataset are missing at least one variable. Figure 1 shows which columns have the most missing data. As we can see the values for the variable `DMI`, which according to the USDA represents the dry matter intake for a cow, is missing for two-thirds of the entries. (USDA). Given the number of missing values is this large, it is probably best to not use this variable in our models. Some other variables, including the final body weight of the calf represented by `Final.Calf.BW`, are missing in 19 entries. Of the other four variables the client was most interested in, none have more than ten missing values.

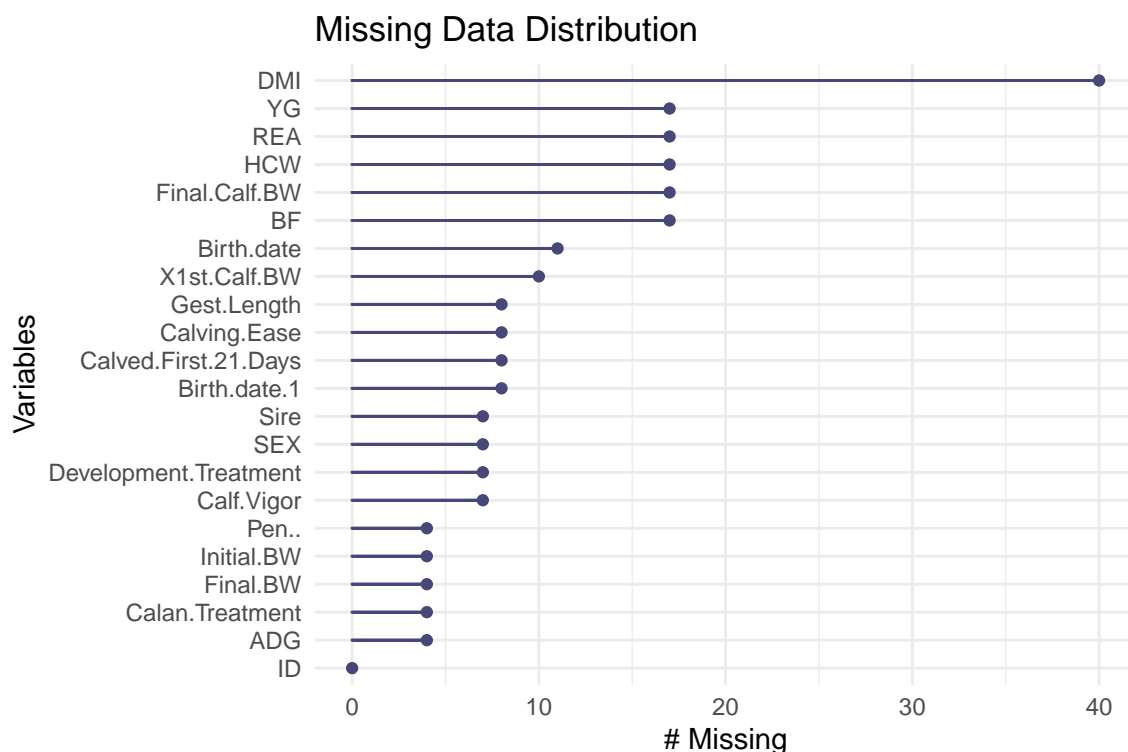


Figure 1: Chart counting the number of missing values for each variable within the data.

## Cleaning the Dataset

Due to the missing values discussed above, we need to clean this dataset before continuing. There are generally two ways to handle missing values. The first is imputing them with some metric like the mean, median, or mode of the variable. The second is to just remove any rows with missing data.

We decided to cut all rows that contained missing values for variables we are interested in. These variables include the five variables the client is interested in, but also the pen number, sire, and the initial weight of the mother. The latter two are **Sire** and **Initial.BW** in the dataset. After removing missing values for these entries the dataset has 101 rows, which we feel is an ample amount for analyzing the data. Note all future figures and models come from this cleaned dataset and not the original.

We initially considered imputing the quantitative variables with the respective median values and using the mode for categorical variables as Memon, Wamala, and Kabano (2023) suggests. This has some issues though. For an example let's consider the third trimester treatment. The MET treatment was used in 40 cases, while the other two treatments were only used 38 times, meaning there are four missing values. If we mode impute this variable there will be 42

instances of the MET treatment. However, it seems very possible that the missing entries were split between the CON and DDG treatments to make an even 40 uses each. While imputing quantitative variables is less risky, we are not fully comfortable with that approach either since we are trying to analyze the data.

## Summary Statistics

Let's take a closer look at what the three dependent variables the client is interested in. Figure 2 shows several summary statistics for each. The calving ease and calf vigor are each scores given. Looking at the minimum and maximum values of each it would seem they are scored in a three-point and five-point system respectively, both only using integers. We can also see from the median and 75th percentiles that both seem very skewed towards the low end of the scale. While the imputing done previously may be exaggerating the curve, Figure 1 shows less than ten values were imputed. This indicates to us the skew was already present before cleaning the data.

Variable	Mean	Median	SD	25th Percentile	75th Percentile	Min	Max
Calving.Ease	1.118812	1	0.4071149	1	1	1	3
Calf.Vigor	1.257426	1	0.6107940	1	1	1	3
Final.Calf.BW	1291.584158	1292	128.9883148	1219	1365	932	1690

Figure 2: Summary Statistics for Dependent Variables

The final weight of calf is the third variable in Figure 2. The mean and median are relatively similar given the large standard deviation. Going forward we can treat these variables as ordinal, which is just a categorical variable with an order.

While the previous two variables discussed had some concerns on top of being counting variables on a scale, the final weight does not present the same issues. Further investigation into the approximate distribution of the final weight is needed though.

Let's look at a histogram and a Q-Q plot for the final weight of the calves in Figure 3. The bin width for the histogram comes from the Freedman-Diaconis rule. (William (2023)). The histogram appears to follow an approximately normal distribution. The Q-Q plot mostly follows this as most points follow the linear trend represented by the red line.

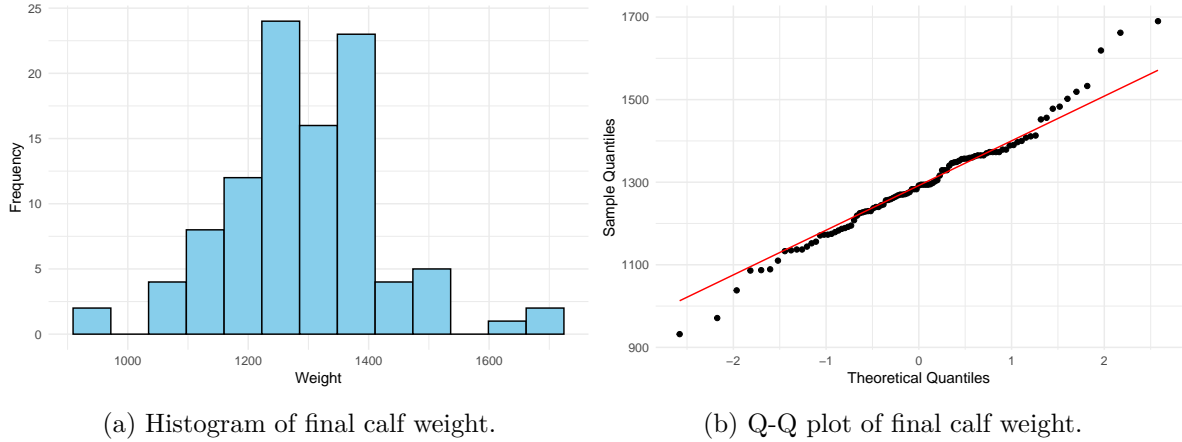


Figure 3: Plots used to check if the distribution of the final calf weight is normal.

Before moving on we want to look at plots of the scoring variables as well. While we suspect a heavy skew for each, the histograms in Figure 4 verify this. It is important to remember that these two variables are not continuous like the weight variable, so the types of models used will vary.

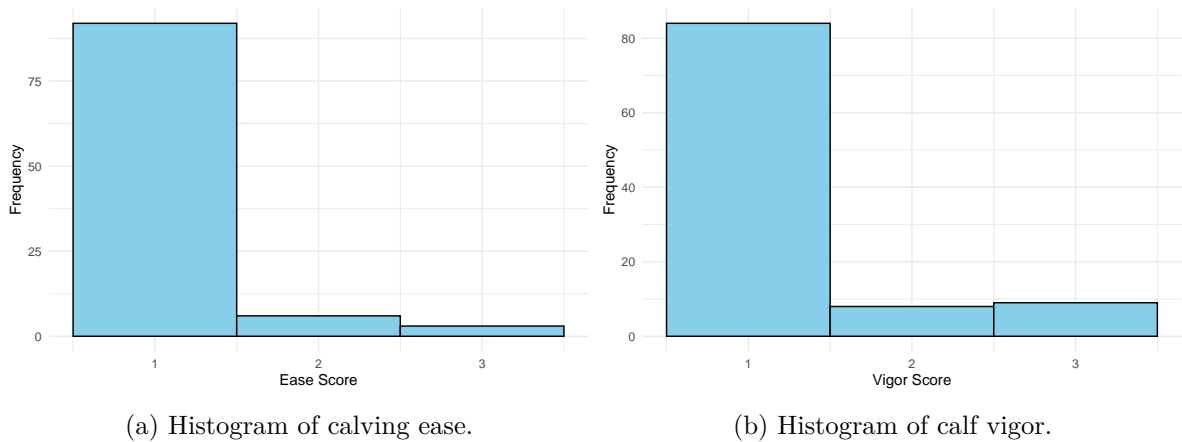


Figure 4: Histograms of scoring variables.

## Exploring the Data

Before looking at potential models, let's explore how some of the variables interact with each other. While we will be able to include other explanatory variables, the client specifically mentions using the third trimester treatment and the sex of a calf as explanatory variables of interest. The table in Figure 5 shows the breakdown of treatment by sex. Note HFR stands

for heifer and STR stands for steer. Although not every group has an equivalent number of subjects, this is nothing we are concerned about. Please note that the total occurrences per treatment are different than discussed above since rows containing missing values were removed.

	HFR	STR
CON	19	15
DDG	14	20
MET	18	15

Figure 5: Table showing the breakdown of treatment by sex.

One of the key assumptions for some of the models we will be discussing later is that the explanatory variables of the model are not highly correlated with each other. If this assumption is violated, multicollinearity is present. Since both the treatment and the sex of the calf are categorical, we can use the Pearson’s chi-squared on the table in Figure 5 to determine if multicollinearity is a problem for these variables. (Bhalla (2017)). The results of the test, shown in Figure 6, indicate multicollinearity is not a problem since the p-value is well above any commonly used significance level such as 0.05.

Metric	Value
Statistic	1.79
Degrees of Freedom	2
P-Value	0.40811

Figure 6: Chi-squared test for treatment and sex.

Now let’s consider how these variables affect the final body weight. The boxplot shown in Figure 7 allows us to see this relationship graphically. We can see the steers are heavier on average than the heifers. The treatments seem to different variances as well, but their median values are not different by huge quantities. Both the CON and MET treatments had one steer large enough to be an outlier, while the DDG treatment had several outliers for both sexes.

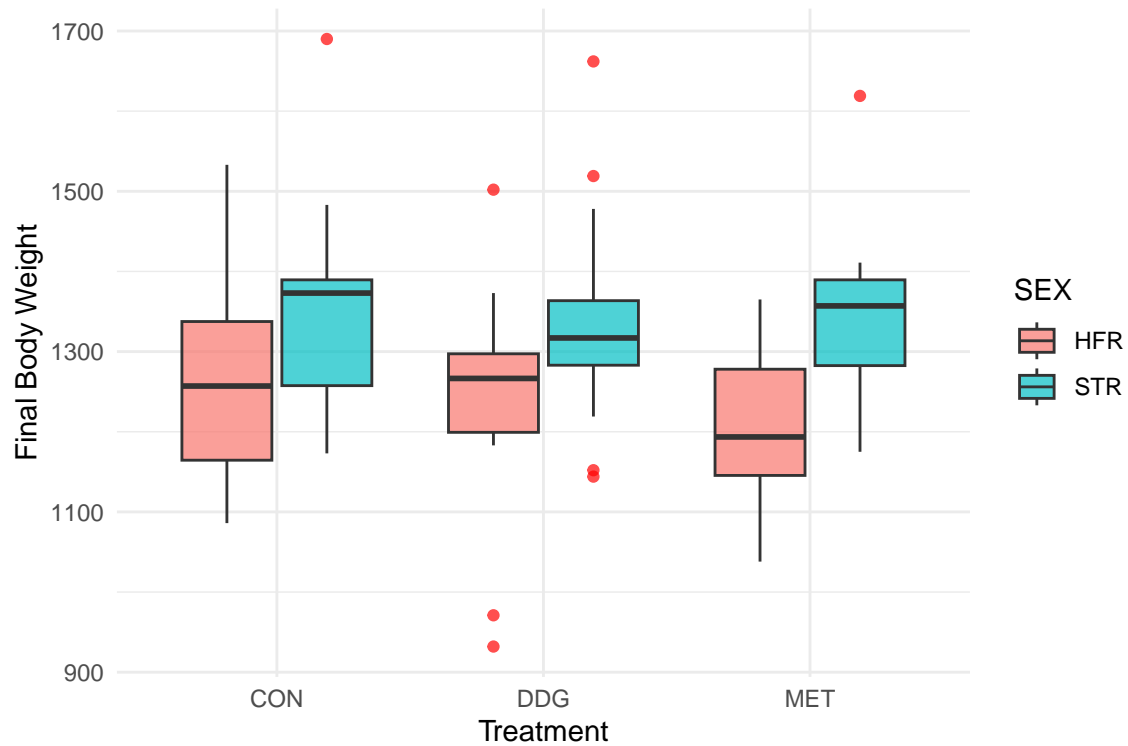


Figure 7: Final body weight by treatment and sex.

Another variable we want to investigate graphically is the initial weight of the heifer that birthed the calf. Let's see how it compares to both the ease and vigor score. In Figure 8 we can see this while also accounting for both the third trimester treatment with the shape of the data point and the sex of the calf with the color of the data point. This allows us to see both how the effect the heifer's initial weight has, but also the trends of both treatment and sex.

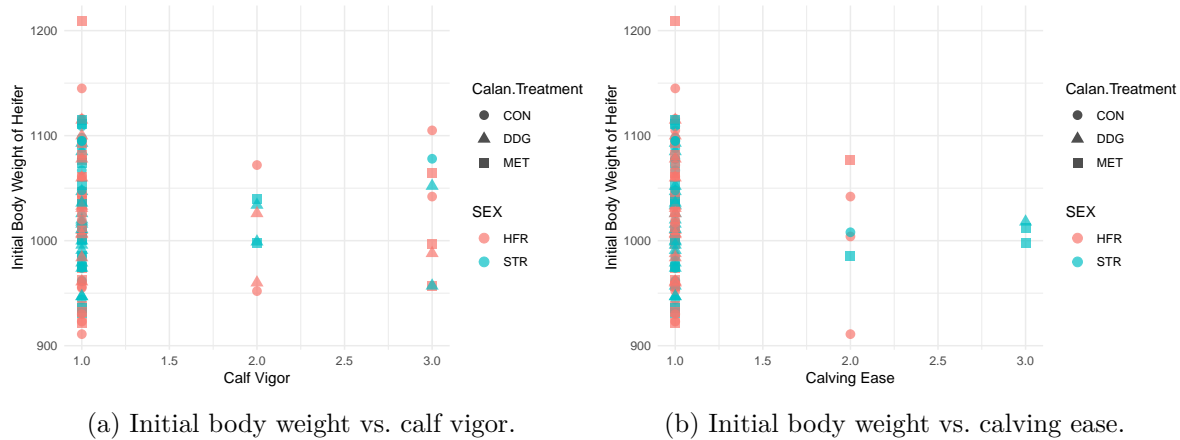


Figure 8: Scatterplot of heifer's initial body weight versus scoring variables, controlling for third trimester treatment and sex of the calf.

Summarize and consider more plots

## Models for Calving Ease

Since the client is interested in three different dependent variables we will need to handle one variable at a time. For the next two models we will be focused on calving ease.

### Ordinal Logistic Regression Model

Since calving ease is a score from one to three it can be considered an ordinal variable. This means instead of treating it as a quantitative variable as we did previously, it could be considered an ordered categorical variable. One method of modeling ordinal variables is with ordinal logistic regression, or OLS. This uses one or more independent variables to predict the ordinal value of the dependent variable. A key assumption of OLS, outside of the dependent variable being ordinal, is no multicollinearity between independent variables. (“Ordinal Regression” (n.d.)).

Let's attempt to apply an OLS to the calving ease variable. In this simple case we will use the third trimester treatment and the calf's sex as the independent variables. As we saw in Figure 6, multicollinearity is not a problem with these variables, so we may proceed.

**START BACK HERE**



```
Call:
polr(formula = Calving.Ease ~ Calan.Treatment * SEX, data = data2,
      Hess = TRUE)
```

Coefficients:

	Value	Std. Error	t value
Calan.TreatmentDDG	-16.8625	0.7285	-23.1471
Calan.TreatmentMET	-1.1165	1.2030	-0.9281
SEXSTR	-0.9264	1.2079	-0.7669
Calan.TreatmentDDG:SEXSTR	16.6163	0.7285	22.8091
Calan.TreatmentMET:SEXSTR	2.4732	1.7137	1.4432

Intercepts:

	Value	Std. Error	t value
1 2	1.7349	0.6250	2.7759
2 3	2.9393	0.7811	3.7632

Residual Deviance: 65.95121

AIC: 79.95121

	Value	Std. Error	t value	p-value
Calan.TreatmentDDG	-16.8625201	0.7284933	-23.1471161	1.554309e-118
Calan.TreatmentMET	-1.1164610	1.2030046	-0.9280604	3.533762e-01
SEXSTR	-0.9263778	1.2078743	-0.7669488	4.431119e-01
Calan.TreatmentDDG:SEXSTR	16.6162838	0.7284931	22.8091163	3.722994e-115
Calan.TreatmentMET:SEXSTR	2.4732157	1.7136521	1.4432426	1.489521e-01
1 2	1.7348982	0.6249873	2.7758935	5.505025e-03
2 3	2.9392992	0.7810718	3.7631615	1.677788e-04

## CUT THIS - Multinomial Logistic Regression

```
# weights: 21 (12 variable)
initial value 110.959841
iter 10 value 29.432881
iter 20 value 29.222854
iter 30 value 29.215412
iter 40 value 29.209442
iter 50 value 29.208986
final value 29.208984
converged
```

Call:

```
multinom(formula = Calving.Ease ~ Calan.Treatment * SEX, data = data2)
```

Coefficients:

	(Intercept)	Calan.TreatmentDDG	Calan.TreatmentMET	SEXSTR
2	-1.673984	-89.53191	-1.159207	-0.9650507
3	-21.595074	4.64936	4.446292	1.2808117
	Calan.TreatmentDDG:SEXSTR	Calan.TreatmentMET:SEXSTR		
2	-6.615244	1.313325		
3	12.720477	14.076217		

Std. Errors:

	(Intercept)	Calan.TreatmentDDG	Calan.TreatmentMET	SEXSTR
2	0.6291544	6.210743e-07	1.206083	1.211298
3	604.7136553	9.531250e+02	955.622215	603.218409
	Calan.TreatmentDDG:SEXSTR	Calan.TreatmentMET:SEXSTR		
2	7.567627e-08	1.899839		
3	9.535708e+02	956.119462		

Residual Deviance: 58.41797

AIC: 82.41797

## Pairwise Comparisons

SEX = HFR:

contrast	estimate	SE	df	t.ratio	p.value
CON - DDG	-9.39e-18	1.90e-10	12	0.000	1.0000
CON - MET	-4.49e-17	NaN	12	NaN	NaN
DDG - MET	-3.55e-17	NaN	12	NaN	NaN

SEX = STR:

contrast	estimate	SE	df	t.ratio	p.value
CON - DDG	-4.84e-17	3.09e-10	12	0.000	1.0000
CON - MET	-1.72e-17	NaN	12	NaN	NaN
DDG - MET	3.12e-17	NaN	12	NaN	NaN

Results are averaged over the levels of: Calving.Ease

P value adjustment: tukey method for varying family sizes

## Models for Calf Vigor

### Ordinal Logistic Regression Model

Call:

```
polr(formula = Calf.Vigor ~ Calan.Treatment * SEX, data = data2,  
      Hess = TRUE)
```

Coefficients:

	Value	Std. Error	t value
Calan.TreatmentDDG	-0.02146	0.8519	-0.02519
Calan.TreatmentMET	-0.17876	0.8454	-0.21145
SEXSTR	-1.27076	1.1768	-1.07981
Calan.TreatmentDDG:SEXSTR	1.22910	1.4516	0.84673
Calan.TreatmentMET:SEXSTR	0.83354	1.5350	0.54301

Intercepts:

	Value	Std. Error	t value
1 2	1.3316	0.5592	2.3812
2 3	2.0682	0.6012	3.4399

Residual Deviance: 113.059

AIC: 127.059

	Value	Std. Error	t value	p-value
Calan.TreatmentDDG	-0.02146293	0.8519098	-0.02519389	0.9799003072
Calan.TreatmentMET	-0.17875927	0.8453950	-0.21145059	0.8325356827
SEXSTR	-1.27076073	1.1768363	-1.07981095	0.2802263761
Calan.TreatmentDDG:SEXSTR	1.22909789	1.4515849	0.84672823	0.3971466190
Calan.TreatmentMET:SEXSTR	0.83353681	1.5350294	0.54301033	0.5871226874
1 2	1.33164741	0.5592312	2.38121078	0.0172558351
2 3	2.06823750	0.6012463	3.43991700	0.0005818926

### Pairwise comparisons

SEX = HFR:

contrast	estimate	SE	df	z.ratio	p.value
CON - DDG	0.0215	0.852	Inf	0.025	0.9997
CON - MET	0.1788	0.845	Inf	0.211	0.9757
DDG - MET	0.1573	0.904	Inf	0.174	0.9834

```
SEX = STR:
  contrast estimate    SE df z.ratio p.value
CON - DDG  -1.2076 1.175 Inf  -1.028  0.5594
CON - MET   -0.6548 1.281 Inf  -0.511  0.8660
DDG - MET    0.5529 0.937 Inf   0.590  0.8253
```

P value adjustment: tukey method for comparing a family of 3 estimates

## CUT THIS - Multinomial Logistic Regression

```
# weights:  21 (12 variable)
initial value 110.959841
iter  10 value 53.136150
iter  20 value 52.192910
iter  30 value 52.189566
final value 52.189559
converged
```

Call:

```
multinom(formula = Calf.Vigor ~ Calan.Treatment * SEX, data = data2)
```

Coefficients:

```
(Intercept) Calan.TreatmentDDG Calan.TreatmentMET    SEXSTR
2  -2.014703          0.3098633          -10.204618 -11.653191
3  -2.014924          -0.3829679           0.405398  -0.624152
Calan.TreatmentDDG:SEXSTR Calan.TreatmentMET:SEXSTR
2              11.2786344              22.00063
3              0.9425919              -12.94747
```

Std. Errors:

```
(Intercept) Calan.TreatmentDDG Calan.TreatmentMET    SEXSTR
2  0.7527132          1.075883          116.2395818 248.246686
3  0.7527868          1.287470           0.9832157  1.279897
Calan.TreatmentDDG:SEXSTR Calan.TreatmentMET:SEXSTR
2              248.249009              274.1132
3              1.814259              548.9998
```

Residual Deviance: 104.3791

AIC: 128.3791

## Models for Final Calf Weight

### Linear Model

Call:

```
lm(formula = Final.Calf.BW ~ Calan.Treatment * SEX, data = data2)
```

Residuals:

Min	1Q	Median	3Q	Max
-308.36	-76.44	8.13	46.27	336.27

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	1259.842	27.319	46.116	<2e-16 ***
Calan.TreatmentDDG	-19.485	41.943	-0.465	0.6433
Calan.TreatmentMET	-46.398	39.168	-1.185	0.2391
SEXSTR	93.891	41.130	2.283	0.0247 *
Calan.TreatmentDDG:SEXSTR	4.102	58.426	0.070	0.9442
Calan.TreatmentMET:SEXSTR	41.531	58.522	0.710	0.4796

---

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

Residual standard error: 119.1 on 95 degrees of freedom

Multiple R-squared: 0.1903, Adjusted R-squared: 0.1477

F-statistic: 4.467 on 5 and 95 DF, p-value: 0.001066

### Tukey comparison

Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

Fit: `lm(formula = Final.Calf.BW ~ Calan.Treatment * SEX, data = data2)`

Linear Hypotheses:

	Estimate	Std. Error	t value	Pr(> t )
DDG - CON == 0	-19.48	41.94	-0.465	0.888
MET - CON == 0	-46.40	39.17	-1.185	0.465
MET - DDG == 0	-26.91	42.43	-0.634	0.801

(Adjusted p values reported -- single-step method)

## Linear Mixed Model

This will need to be redone in SAS if we stick with it.

```
Linear mixed model fit by REML ['lmerMod']
Formula: Final.Calf.BW ~ Calan.Treatment * SEX + (1 | Pen..) + (1 | Sire)
Data: data2
```

REML criterion at convergence: 1189.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.73730	-0.58693	-0.00815	0.55733	2.55789

Random effects:

Groups	Name	Variance	Std.Dev.
Sire	(Intercept)	2374	48.72
Pen..	(Intercept)	0	0.00
Residual		12484	111.73

Number of obs: 101, groups: Sire, 6; Pen.., 4

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	1270.84	33.12	38.367
Calan.TreatmentDDG	-33.97	40.43	-0.840
Calan.TreatmentMET	-40.09	37.29	-1.075
SEXSTR	93.05	38.93	2.390
Calan.TreatmentDDG:SEXSTR	23.75	55.50	0.428
Calan.TreatmentMET:SEXSTR	37.75	55.84	0.676

Correlation of Fixed Effects:

```
(Intr) Cl.TDDG Cl.TMET SEXSTR C.TDDG:
Cln.TrtmDDG -0.528
Cln.TrtmMET -0.551  0.464
SEXSTR      -0.527  0.441  0.469
C.TDDG:SEXS 0.385 -0.724 -0.331 -0.704
C.TMET:SEXS 0.383 -0.323 -0.677 -0.705 0.500
optimizer (nloptwrap) convergence code: 0 (OK)
boundary (singular) fit: see help('isSingular')
```

Tukey comparison

## Simultaneous Tests for General Linear Hypotheses

### Multiple Comparisons of Means: Tukey Contrasts

```
Fit: lmer(formula = Final.Calf.BW ~ Calan.Treatment * SEX + (1 | Pen..) +  
      (1 | Sire), data = data2)
```

#### Linear Hypotheses:

	Estimate	Std. Error	z value	Pr(> z )
DDG - CON == 0	-33.973	40.426	-0.840	0.678
MET - CON == 0	-40.087	37.286	-1.075	0.529
MET - DDG == 0	-6.114	40.318	-0.152	0.987

(Adjusted p values reported -- single-step method)

### Pariwise comparison

SEX = HFR:

contrast	estimate	SE	df	t.ratio	p.value
CON - DDG	33.97	41.1	92.5	0.826	0.6881
CON - MET	40.09	37.9	91.9	1.056	0.5435
DDG - MET	6.11	41.6	91.2	0.147	0.9882

SEX = STR:

contrast	estimate	SE	df	t.ratio	p.value
CON - DDG	10.23	38.7	89.8	0.264	0.9623
CON - MET	2.34	41.6	90.0	0.056	0.9983
DDG - MET	-7.89	39.8	91.4	-0.198	0.9786

Degrees-of-freedom method: kenward-roger

P value adjustment: tukey method for comparing a family of 3 estimates

## ANCOVA Model

This includes initial weight.

Call:

```
lm(formula = Final.Calf.BW ~ Calan.Treatment * SEX + Initial.BW,  
    data = data2)
```

Residuals:

Min	1Q	Median	3Q	Max
-291.13	-71.63	-2.30	68.94	319.47

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	618.7117	205.4833	3.011	0.00334 **
Calan.TreatmentDDG	-28.2295	40.2033	-0.702	0.48431
Calan.TreatmentMET	-54.0660	37.5328	-1.441	0.15305
SEXSTR	75.6272	39.7561	1.902	0.06020 .
Initial.BW	0.6336	0.2014	3.146	0.00222 **
Calan.TreatmentDDG:SEXSTR	31.3903	56.5380	0.555	0.58007
Calan.TreatmentMET:SEXSTR	63.2236	56.3838	1.121	0.26501

---

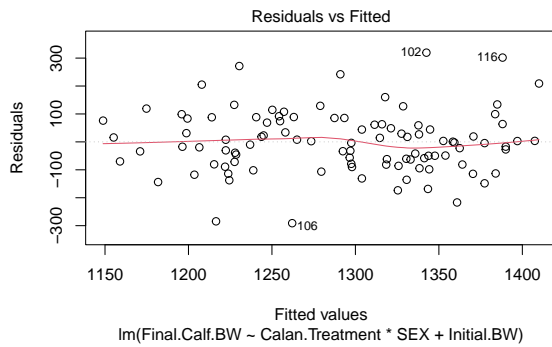
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 113.9 on 94 degrees of freedom

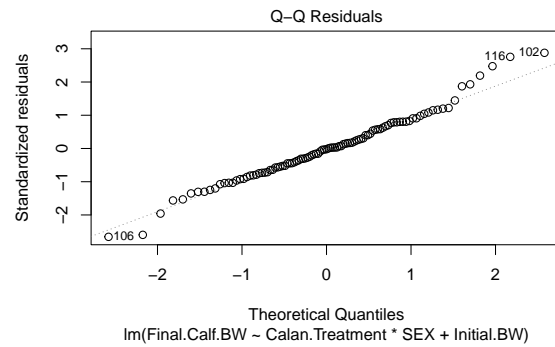
Multiple R-squared: 0.2675, Adjusted R-squared: 0.2207

F-statistic: 5.72 on 6 and 94 DF, p-value: 4.184e-05

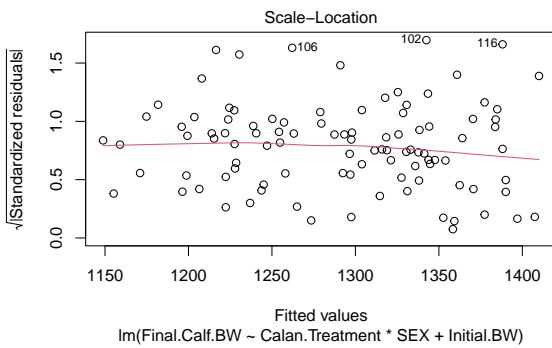




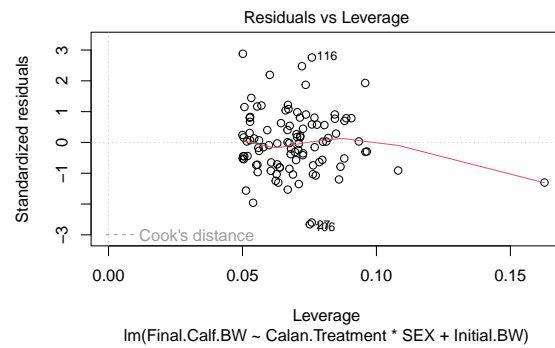
(a)



(b)



(c)



(d)

## Post Hoc Test

SEX = HFR:

contrast	estimate	SE	df	t.ratio	p.value
CON - DDG	28.23	40.2	94	0.702	0.7628
CON - MET	54.07	37.5	94	1.441	0.3245
DDG - MET	25.84	40.6	94	0.637	0.8003

SEX = STR:

contrast	estimate	SE	df	t.ratio	p.value
CON - DDG	-3.16	39.3	94	-0.080	0.9964
CON - MET	-9.16	41.8	94	-0.219	0.9739
DDG - MET	-6.00	38.9	94	-0.154	0.9870

P value adjustment: tukey method for comparing a family of 3 estimates

## Binary Logistic Regression with GLM

Call:

```
glm(formula = Calf.Vigor.Binary ~ Calan.Treatment * SEX + Initial.BW,  
     family = binomial(link = "logit"), data = data)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-2.459e+01	1.283e+05	0	1
Calan.TreatmentDDG	-7.795e+00	2.634e+06	0	1
Calan.TreatmentMET	1.519e+00	1.043e+05	0	1
SEXSTR	1.414e+01	2.635e+06	0	1
Initial.BW1001	7.404e+00	2.641e+06	0	1
Initial.BW1002	7.404e+00	2.641e+06	0	1
Initial.BW1003	1.024e+00	1.509e+05	0	1
Initial.BW1004	1.024e+00	1.509e+05	0	1
Initial.BW1006	8.819e+00	2.639e+06	0	1
Initial.BW1007	8.819e+00	2.639e+06	0	1
Initial.BW1008	-1.312e+01	2.639e+06	0	1
Initial.BW1009	1.024e+00	1.509e+05	0	1
Initial.BW1010	7.919e+00	2.639e+06	0	1
Initial.BW1011	-1.011e-10	1.124e+05	0	1
Initial.BW1012	7.404e+00	2.641e+06	0	1
Initial.BW1013	-4.955e-01	1.352e+05	0	1
Initial.BW1016	-1.032e-10	1.124e+05	0	1
Initial.BW1017	1.024e+00	1.509e+05	0	1
Initial.BW1018	-1.029e-10	1.124e+05	0	1
Initial.BW1020	3.981e-01	1.007e+05	0	1
Initial.BW1023	8.819e+00	2.639e+06	0	1
Initial.BW1026	8.115e-01	9.549e+04	0	1
Initial.BW1027	-4.955e-01	1.352e+05	0	1
Initial.BW1031	8.819e+00	2.639e+06	0	1
Initial.BW1033	8.819e+00	2.639e+06	0	1
Initial.BW1034	-9.604e-11	1.124e+05	0	1
Initial.BW1035	7.404e+00	2.641e+06	0	1
Initial.BW1036	-1.059e-10	1.124e+05	0	1
Initial.BW1038	-4.955e-01	1.230e+05	0	1
Initial.BW1040	7.404e+00	2.641e+06	0	1
Initial.BW1042	4.816e+01	1.509e+05	0	1
Initial.BW1043	1.024e+00	1.509e+05	0	1
Initial.BW1045	7.404e+00	2.641e+06	0	1

Initial.BW1046	-4.955e-01	1.352e+05	0	1
Initial.BW1047	-1.041e-10	1.124e+05	0	1
Initial.BW1048	-1.312e+01	2.639e+06	0	1
Initial.BW1052	4.713e+01	1.124e+05	0	1
Initial.BW1053	7.404e+00	2.641e+06	0	1
Initial.BW1060	8.819e+00	2.639e+06	0	1
Initial.BW1061	2.521e-02	1.194e+05	0	1
Initial.BW1064	4.664e+01	1.352e+05	0	1
Initial.BW1065	4.664e+01	1.352e+05	0	1
Initial.BW1067	-1.312e+01	2.639e+06	0	1
Initial.BW1072	1.024e+00	1.509e+05	0	1
Initial.BW1074	7.404e+00	2.641e+06	0	1
Initial.BW1077	-4.955e-01	1.352e+05	0	1
Initial.BW1078	1.045e+01	2.638e+06	0	1
Initial.BW1079	7.404e+00	2.641e+06	0	1
Initial.BW1082	-4.955e-01	1.352e+05	0	1
Initial.BW1085	-1.020e-10	1.124e+05	0	1
Initial.BW1088	-1.312e+01	2.639e+06	0	1
Initial.BW1090	-1.012e-10	1.124e+05	0	1
Initial.BW1092	4.816e+01	1.509e+05	0	1
Initial.BW1093	-2.749e-01	1.079e+05	0	1
Initial.BW1095	-1.312e+01	2.638e+06	0	1
Initial.BW1098	-1.312e+01	2.639e+06	0	1
Initial.BW1100	8.819e+00	2.639e+06	0	1
Initial.BW1105	4.816e+01	1.509e+05	0	1
Initial.BW1109	-1.312e+01	2.639e+06	0	1
Initial.BW1111	7.404e+00	2.641e+06	0	1
Initial.BW1115	7.919e+00	2.639e+06	0	1
Initial.BW1116	1.024e+00	1.509e+05	0	1
Initial.BW1133	5.454e+01	2.641e+06	0	1
Initial.BW1145	1.024e+00	1.509e+05	0	1
Initial.BW1209	-4.955e-01	1.352e+05	0	1
Initial.BW893	-1.312e+01	2.639e+06	0	1
Initial.BW911	1.024e+00	1.509e+05	0	1
Initial.BW921	5.454e+01	2.641e+06	0	1
Initial.BW922	-4.955e-01	1.352e+05	0	1
Initial.BW923	1.024e+00	1.509e+05	0	1
Initial.BW928	3.401e+01	2.639e+06	0	1
Initial.BW930	1.024e+00	1.509e+05	0	1
Initial.BW931	7.404e+00	2.641e+06	0	1
Initial.BW932	-4.955e-01	1.352e+05	0	1
Initial.BW936	7.404e+00	2.641e+06	0	1
Initial.BW938	-4.955e-01	1.352e+05	0	1

Initial.BW944	-1.312e+01	2.639e+06	0	1
Initial.BW947	4.733e-09	9.732e+04	0	1
Initial.BW952	1.024e+00	1.509e+05	0	1
Initial.BW955	1.024e+00	1.509e+05	0	1
Initial.BW956	1.024e+00	1.509e+05	0	1
Initial.BW957	4.691e+01	1.014e+05	0	1
Initial.BW960	8.819e+00	2.639e+06	0	1
Initial.BW961	1.809e+00	1.391e+05	0	1
Initial.BW962	-1.312e+01	2.639e+06	0	1
Initial.BW963	-4.955e-01	1.352e+05	0	1
Initial.BW974	-1.186e+01	2.638e+06	0	1
Initial.BW975	7.404e+00	2.641e+06	0	1
Initial.BW978	4.713e+01	1.124e+05	0	1
Initial.BW979	-9.563e-11	1.124e+05	0	1
Initial.BW981	-1.312e+01	2.639e+06	0	1
Initial.BW984	8.819e+00	2.639e+06	0	1
Initial.BW985	-1.225e+01	2.638e+06	0	1
Initial.BW988	5.595e+01	2.639e+06	0	1
Initial.BW989	-9.994e-11	1.124e+05	0	1
Initial.BW991	-8.333e-11	1.124e+05	0	1
Initial.BW996	-1.052e-10	1.124e+05	0	1
Initial.BW997	4.664e+01	1.352e+05	0	1
Initial.BW998	7.404e+00	2.641e+06	0	1
Initial.BW999	-9.982e-11	1.124e+05	0	1
Calan.TreatmentDDG:SEXSTR	-5.325e+00	5.270e+06	0	1
Calan.TreatmentMET:SEXSTR	-2.204e+01	1.476e+05	0	1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 88.4945 on 112 degrees of freedom  
Residual deviance: 2.7726 on 11 degrees of freedom  
(7 observations deleted due to missingness)  
AIC: 206.77

Number of Fisher Scoring iterations: 22

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

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

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

**Conclusion**

**Recomendation**

## References

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## Appendix A - R Code

## Appendix B - SAS Code

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## Appendix C - Additional SAS Output

