Mice Data Analysis

Importing the Data

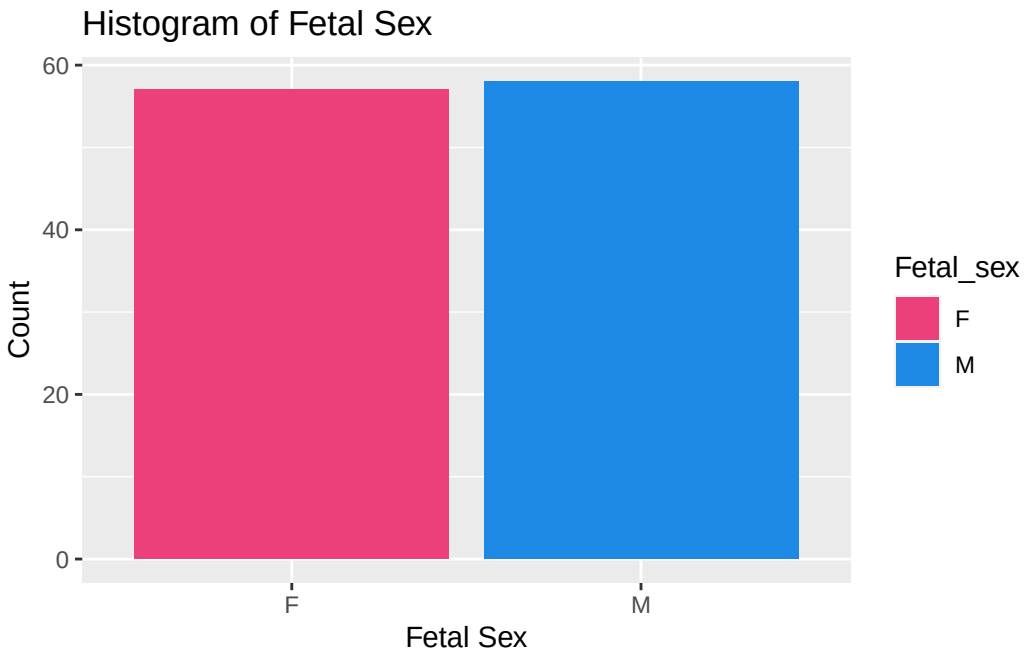
```
fetus_full <- read.csv("data/fetus-cleaned.csv", header=T)

fetus <- fetus_full %>%
  filter(Fetus_genotype != "resorp") %>%
  na.omit() # One empty row. Not sure why...
```

We drop all resorp fetuses. This is because they do not provide information. Of course, the data are not missing at random in this case. However, we can conduct an entirely separate analysis of resorp vs living fetuses later on if that's required.

Assessing Normality of Features and Dependent Variables

First we assess the proportion of male v. female fetuses to make sure our data are not skewed.

```
# Define colors for each sex
color_female <- "#ec407a"  # pink
color_male <- "#1e88e5"    # blue

ggplot(fetus, aes(x = Fetal_sex, fill = Fetal_sex)) +
  geom_bar() +
  scale_fill_manual(values = c(color_female, color_male)) +
  xlab("Fetal Sex") +
  ylab("Count") +
  ggtitle("Histogram of Fetal Sex")
```

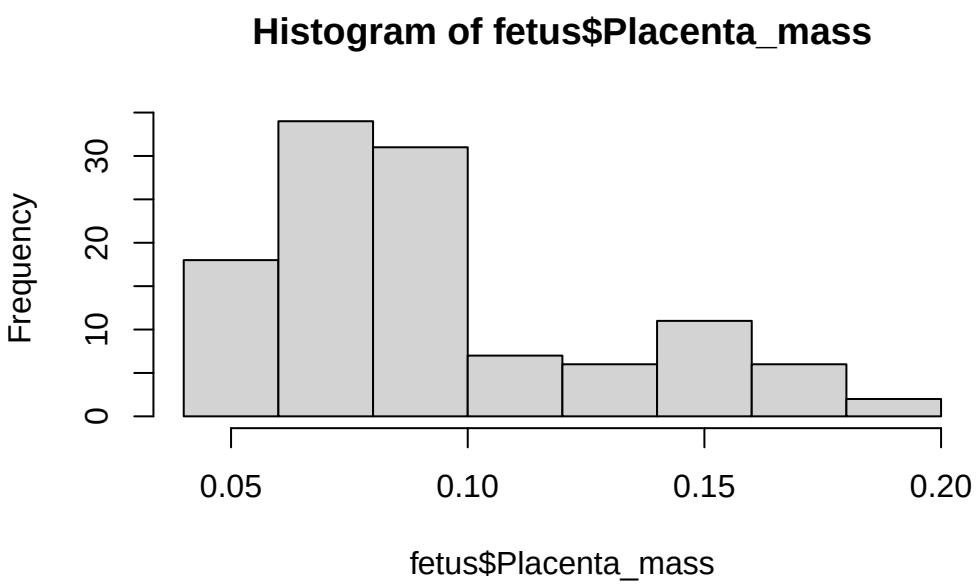



```
mean(fetus$isFemale)
```

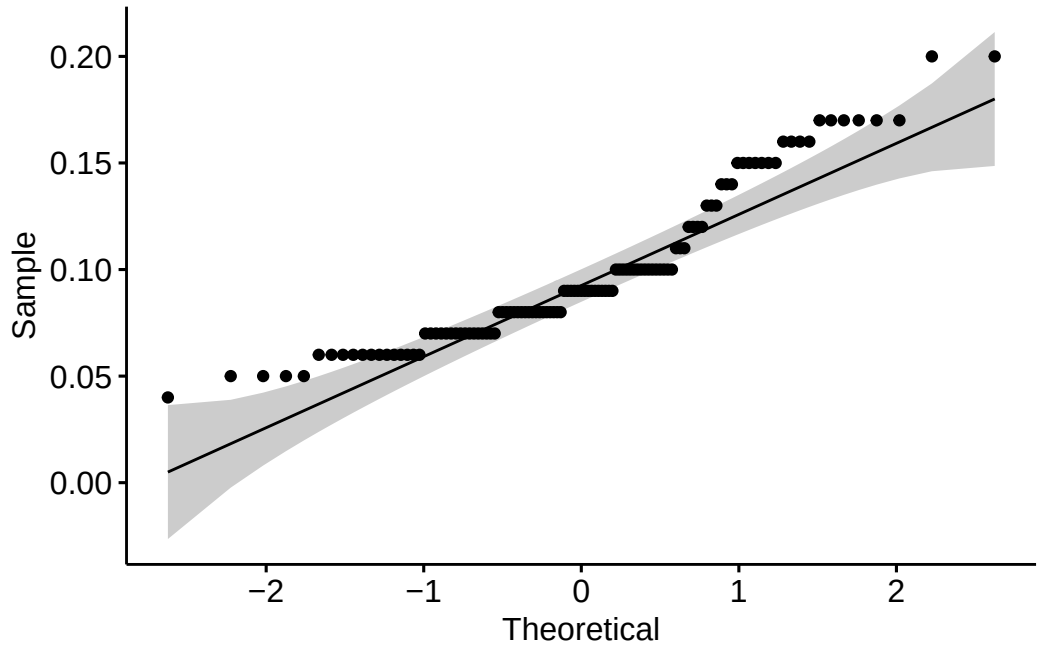
```
[1] 0.4956522
```

Approximately 50% of surviving fetuses are female, so no worries about composition of the data.

```
hist(fetus$Placenta_mass)
```




```
ggqqplot(fetus$Placenta_mass)
```

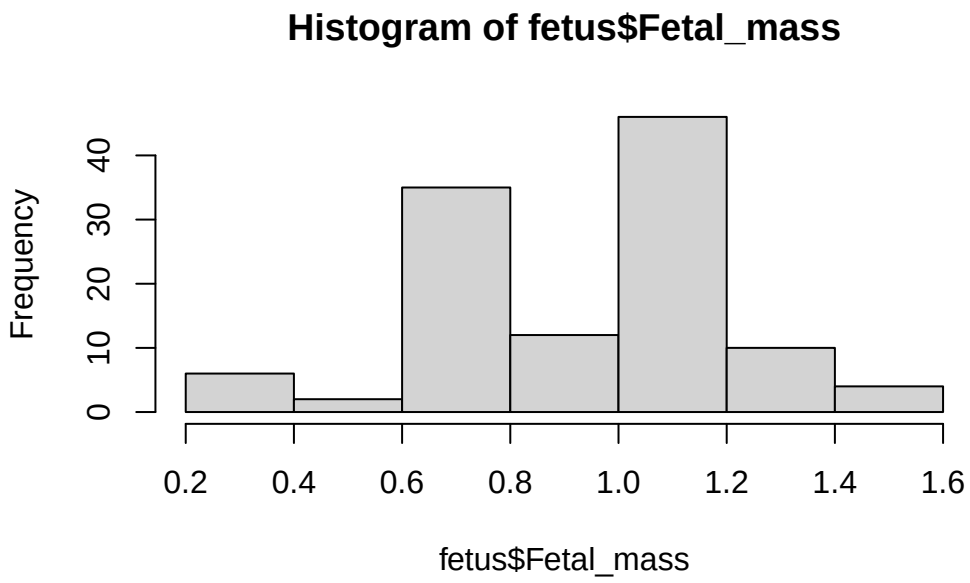


```
shapiro.test(fetus$Placenta_mass)
```

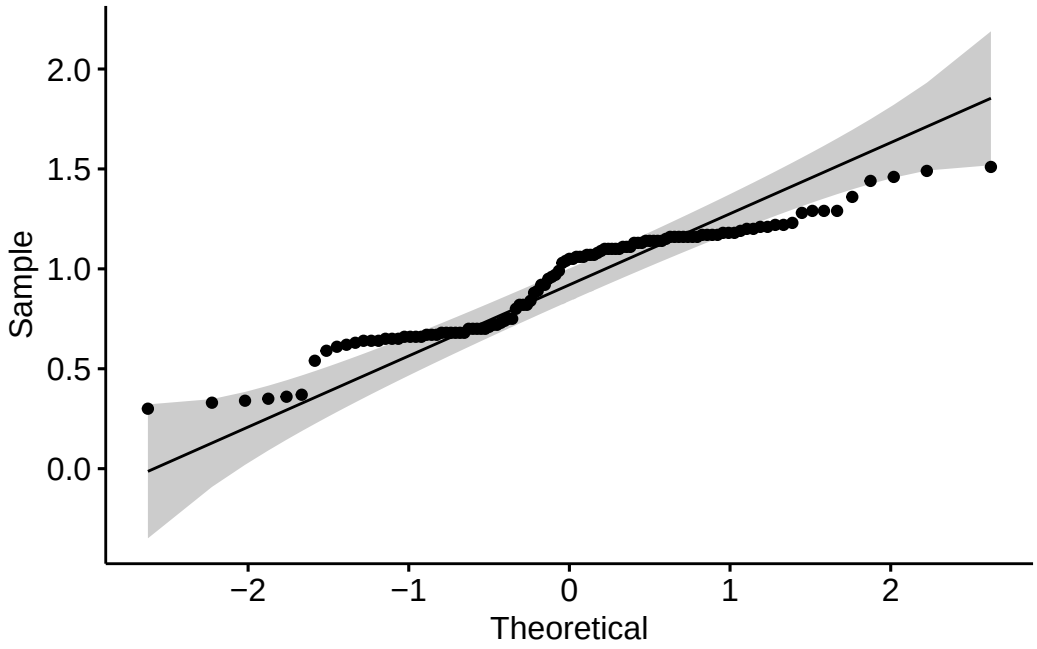
```
    Shapiro-Wilk normality test

data:  fetus$Placenta_mass
W = 0.90156, p-value = 3.798e-07
```

Placenta mass is not normally distributed (right-skewed)

```
hist(fetus$Fetal_mass)
```




```
ggqqplot(fetus$Fetal_mass)
```

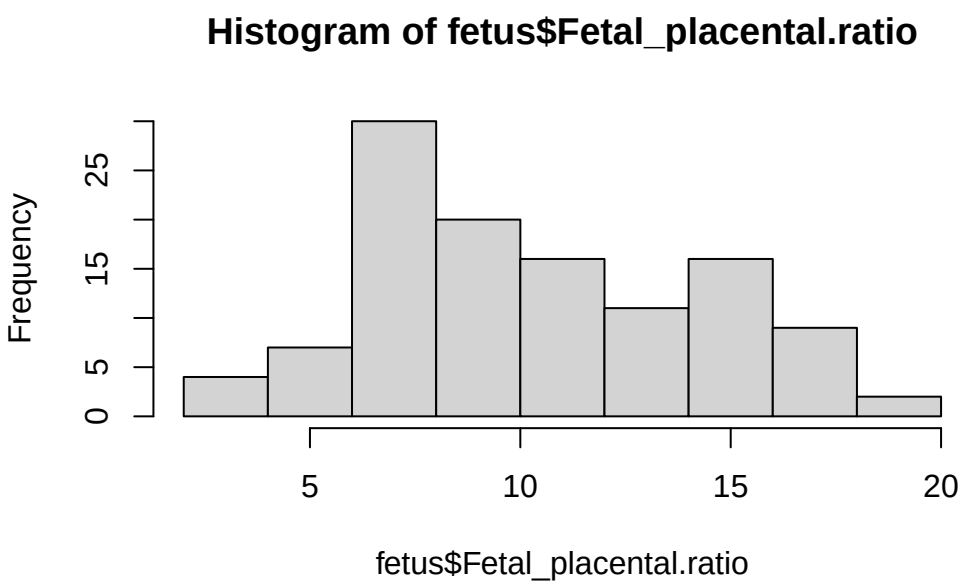



```
shapiro.test(fetus$Fetal_mass)
```

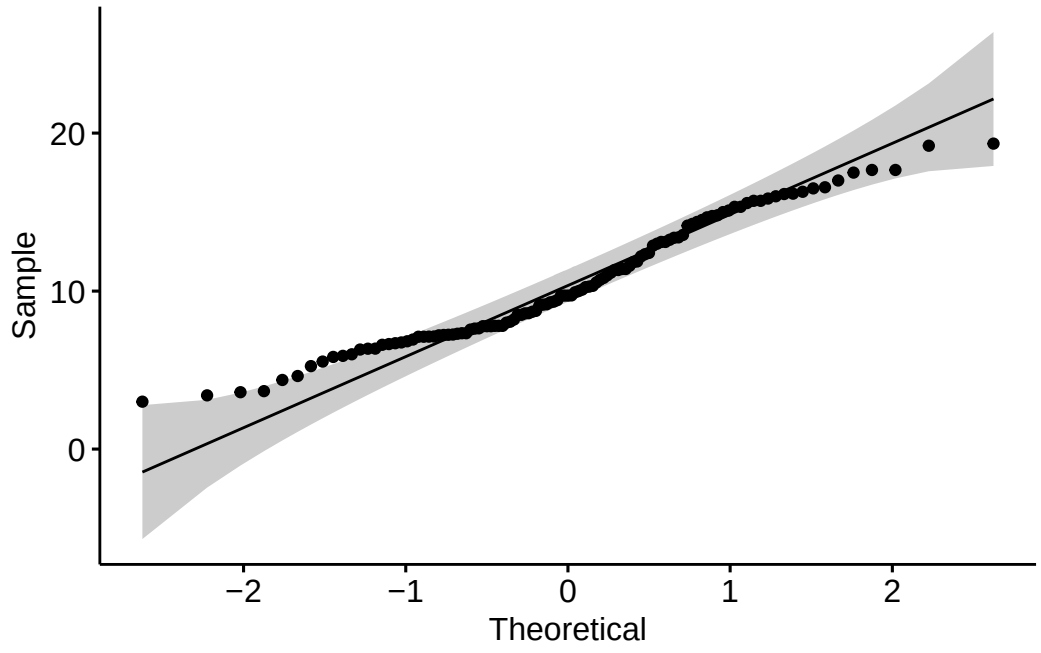
```
    Shapiro-Wilk normality test

data:  fetus$Fetal_mass
W = 0.93942, p-value = 5.661e-05
```

Fetal mass not normally distributed (bimodal). Perhaps bimodality has to do with the sex of the fetus? Worth investigating because, if not, could be related to the genotype.

```
hist(fetus$Fetal_placental.ratio)
```




```
ggqqplot(fetus$Fetal_placental.ratio)
```



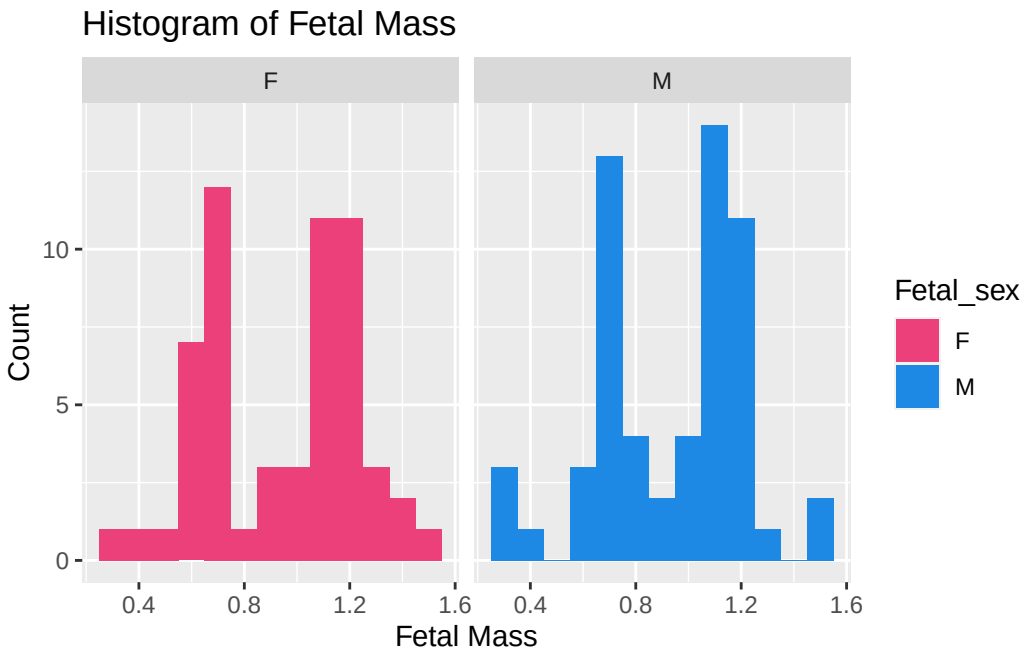
```
shapiro.test(fetus$Fetal_placental.ratio)
```

```
    Shapiro-Wilk normality test

data:  fetus$Fetal_placental.ratio
W = 0.96431, p-value = 0.003709
```

Fetal/placental ratio is not normally distributed (right skew). This makes sense since it's a transformation that is not a sum of two non-normal random variables.

Let's return to assessing fetal mass. Maybe it is related to gender?

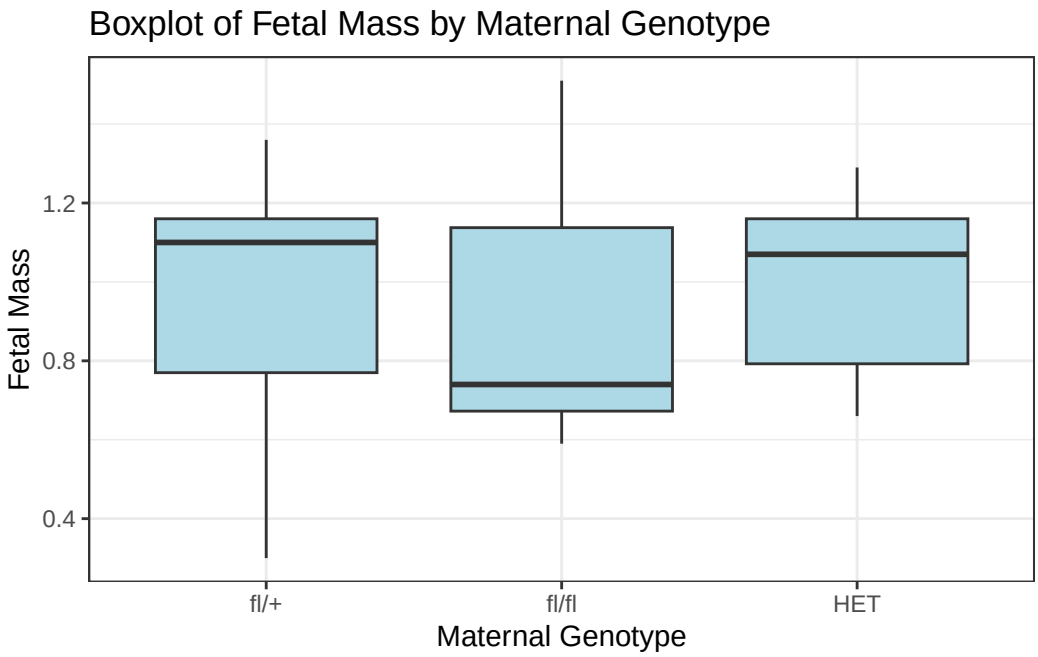
```
# Plot side by side histograms of fetal mass faceted by fetal sex with different colors
ggplot(fetus, aes(x = Fetal_mass, fill = Fetal_sex)) +
  geom_histogram(binwidth = 0.1) +
  scale_fill_manual(values = c(color_female, color_male)) +
  xlab("Fetal Mass") +
  ylab("Count") +
  ggtitle("Histogram of Fetal Mass") +
  facet_wrap(~ Fetal_sex, ncol = 2)
```



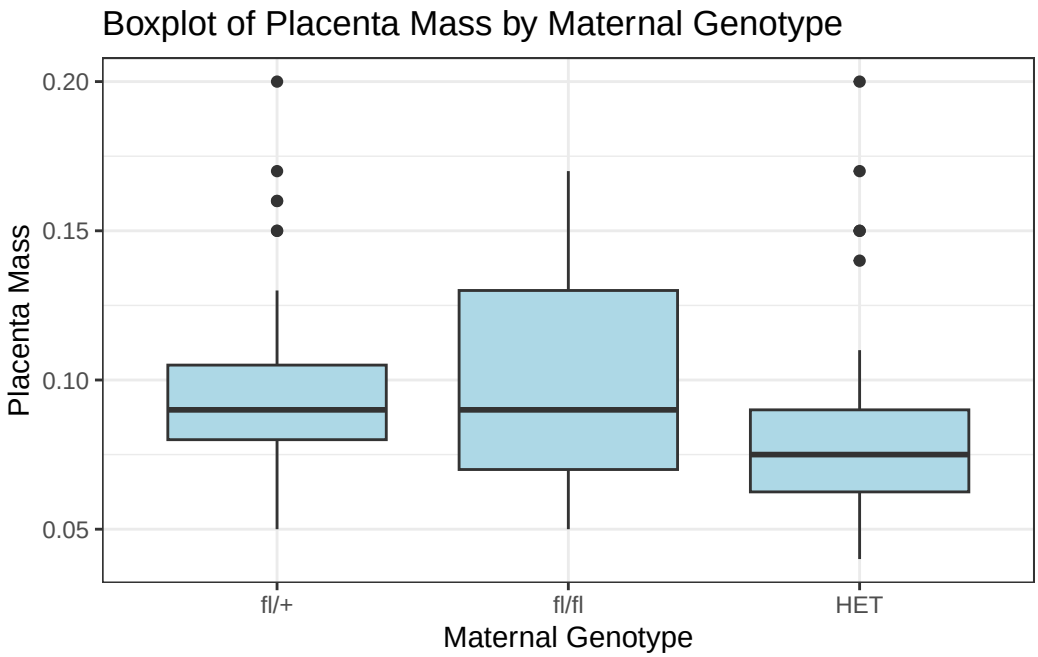
This did not help the bimodality. There is more going on here. Maybe it is related to the genotypes?

Now we visually assess the relationship between our variables of interest and the genotypes using boxplots.

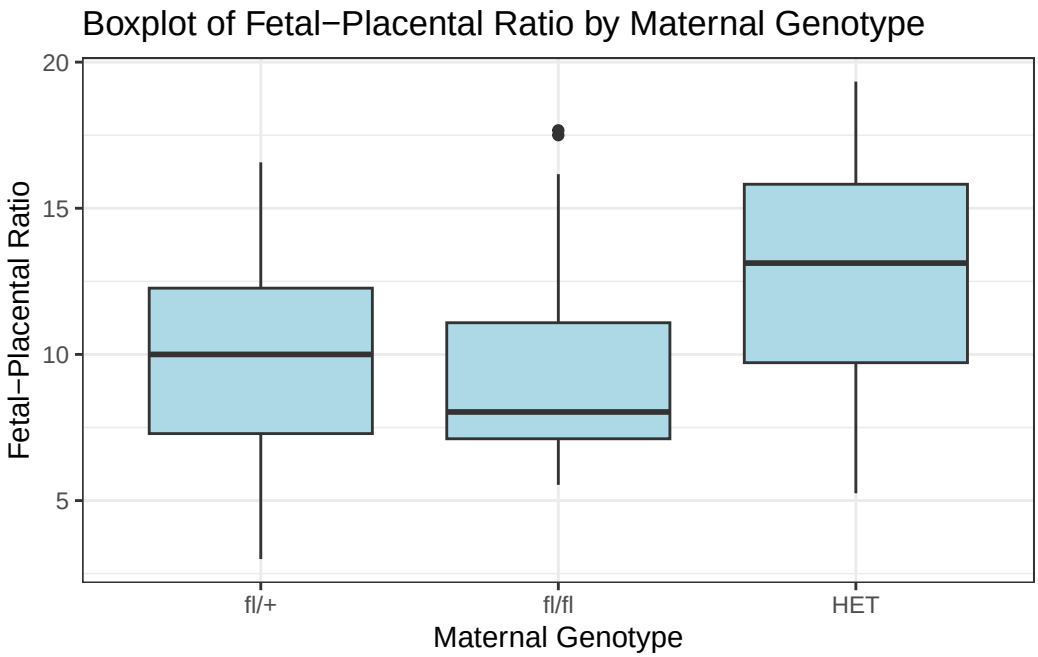
```
# Boxplot of Fetal_mass by Maternal_genotype
ggplot(fetus, aes(x = Maternal_genotype, y = Fetal_mass)) +
  geom_boxplot(fill = "lightblue") +
  xlab("Maternal Genotype") +
  ylab("Fetal Mass") +
  ggtitle("Boxplot of Fetal Mass by Maternal Genotype") +
  theme_bw()
```



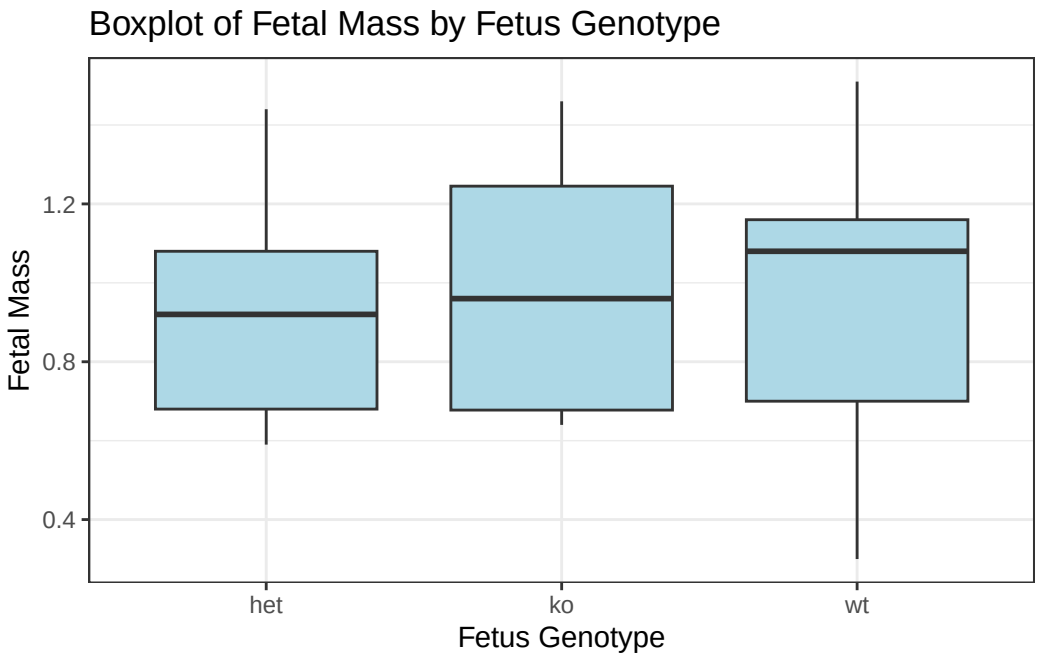

```
# Boxplot of Placenta_mass by Maternal_genotype
ggplot(fetus, aes(x = Maternal_genotype, y = Placenta_mass)) +
  geom_boxplot(fill = "lightblue") +
  xlab("Maternal Genotype") +
  ylab("Placenta Mass") +
  ggtitle("Boxplot of Placenta Mass by Maternal Genotype") +
  theme_bw()
```



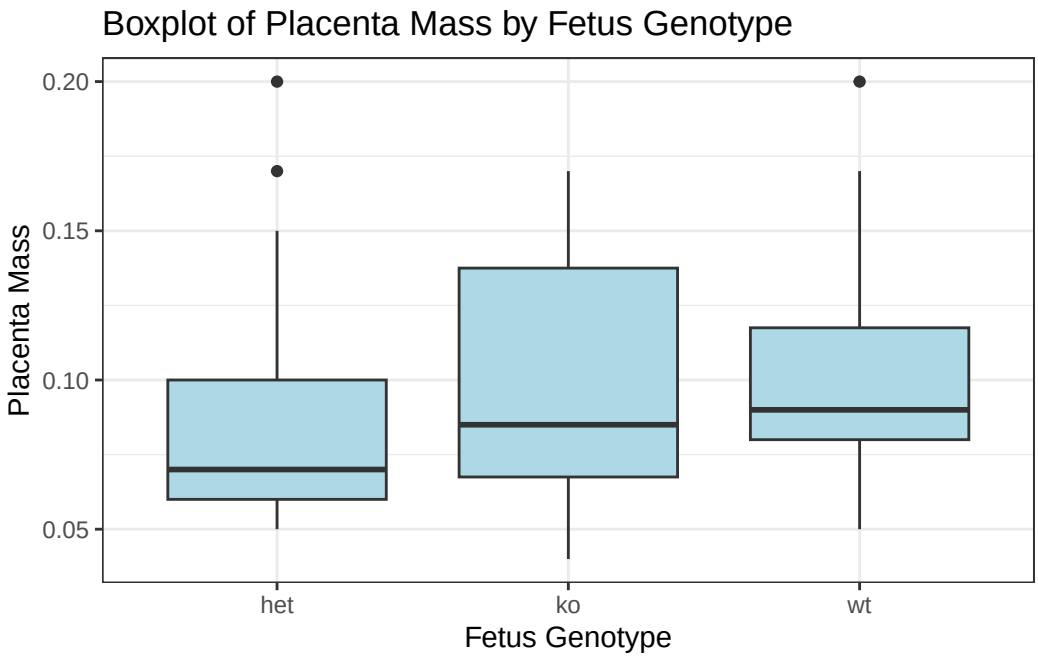

```
# Boxplot of Fetal_placental.ratio by Maternal_genotype
ggplot(fetus, aes(x = Maternal_genotype, y = Fetal_placental.ratio)) +
  geom_boxplot(fill = "lightblue") +
  xlab("Maternal Genotype") +
  ylab("Fetal-Placental Ratio") +
  ggtitle("Boxplot of Fetal-Placental Ratio by Maternal Genotype") +
  theme_bw()
```



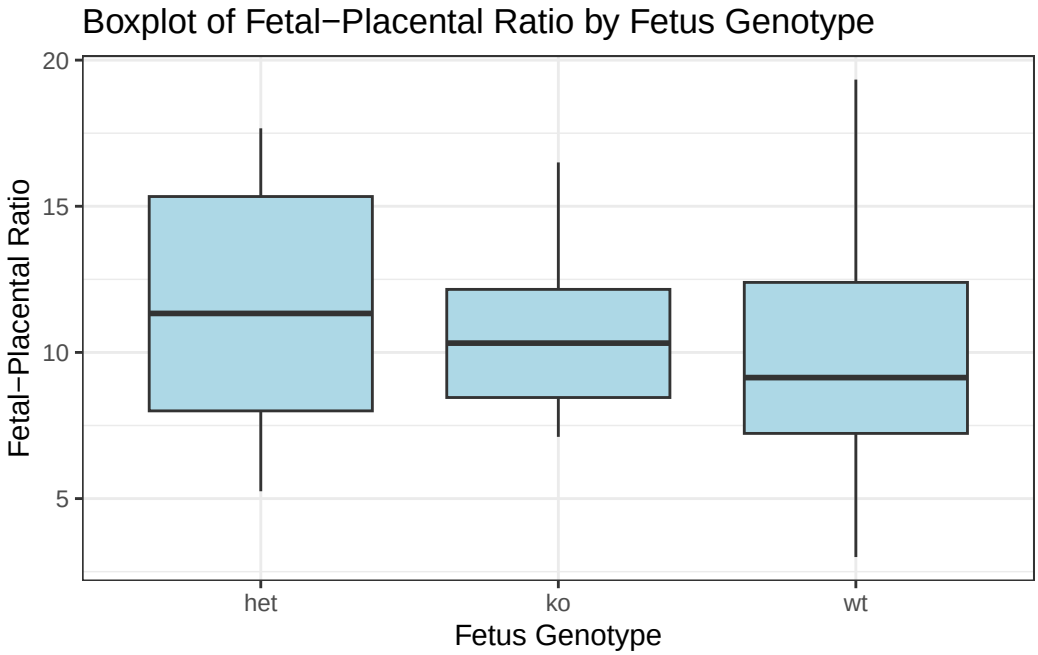

```
# Boxplot of Fetal_mass by Fetus_genotype
ggplot(fetus, aes(x = Fetus_genotype, y = Fetal_mass)) +
  geom_boxplot(fill = "lightblue") +
  xlab("Fetus Genotype") +
  ylab("Fetal Mass") +
  ggtitle("Boxplot of Fetal Mass by Fetus Genotype") +
  theme_bw()
```




```
# Boxplot of Placenta_mass by Fetus_genotype
ggplot(fetus, aes(x = Fetus_genotype, y = Placenta_mass)) +
  geom_boxplot(fill = "lightblue") +
  xlab("Fetus Genotype") +
  ylab("Placenta Mass") +
  ggtitle("Boxplot of Placenta Mass by Fetus Genotype") +
  theme_bw()
```




```
# Boxplot of Fetal_placental.ratio by Fetus_genotype
ggplot(fetus, aes(x = Fetus_genotype, y = Fetal_placental.ratio)) +
  geom_boxplot(fill = "lightblue") +
  xlab("Fetus Genotype") +
  ylab("Fetal-Placental Ratio") +
  ggtitle("Boxplot of Fetal-Placental Ratio by Fetus Genotype") +
  theme_bw()
```

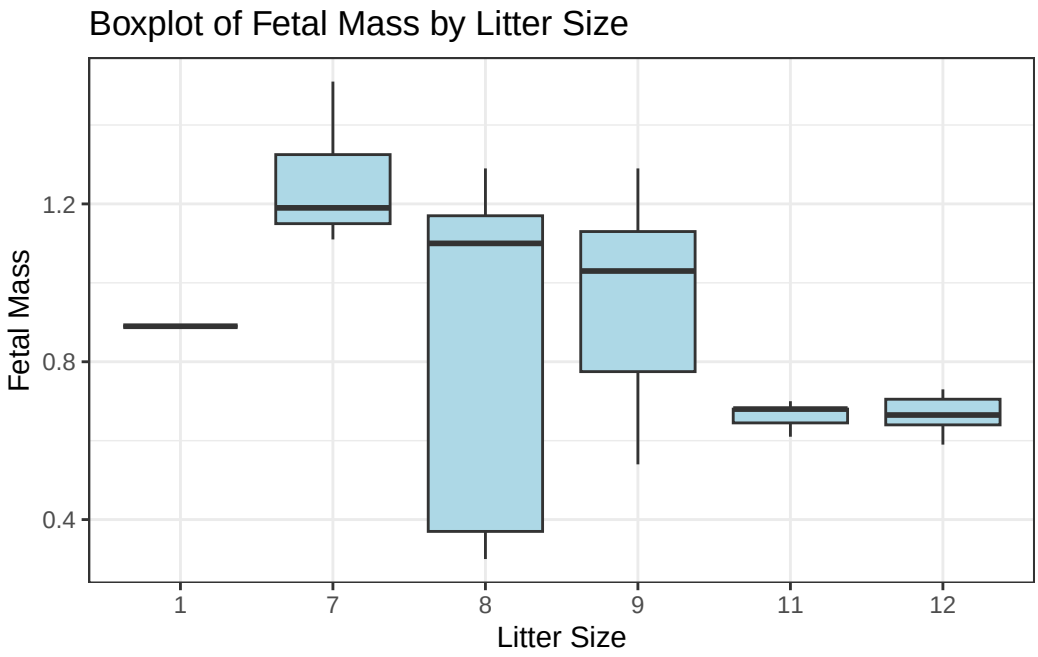


In all cases, it looks like the maternal/fetal genotype has no impact on our dependent variables. In all honesty, it's likely that masses have much more to do with the mass of the mother/father rats since it is genetic. It also might have to do with the day of conception. Presumably, if a fetus is a few days older, it will weigh more on average. I have limited subject expertise though, so I am not sure.

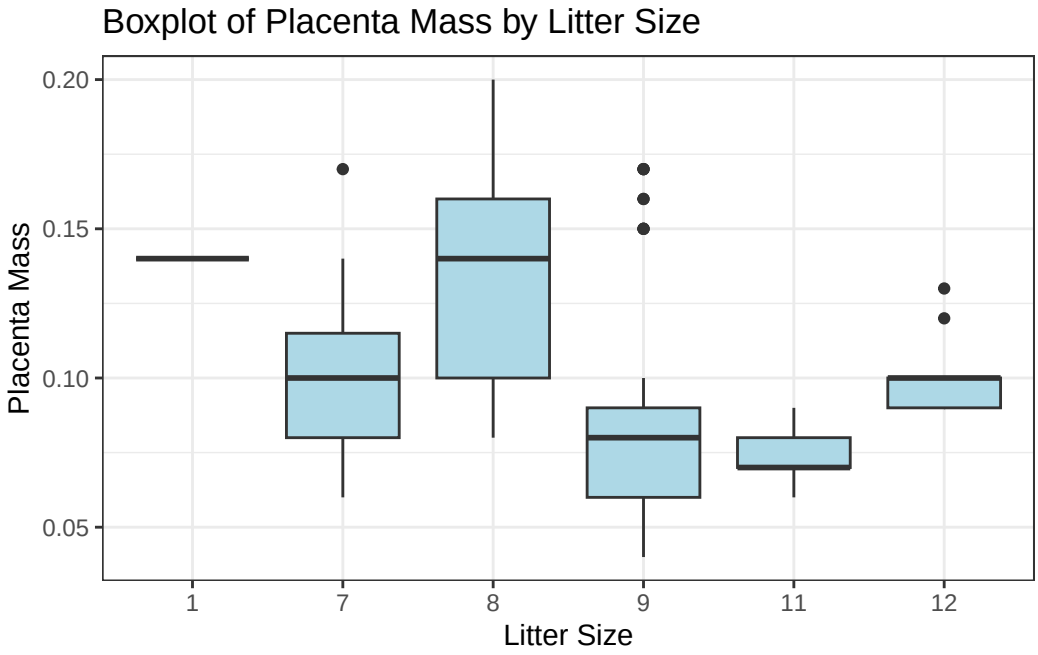
This could be assessed by linking the mother dataset to the fetus dataset, but there is no joining variable (dam id missing from mother dataset?)

Let's look at the last variables of interest for modeling, Litter_size and Fetal_sex.

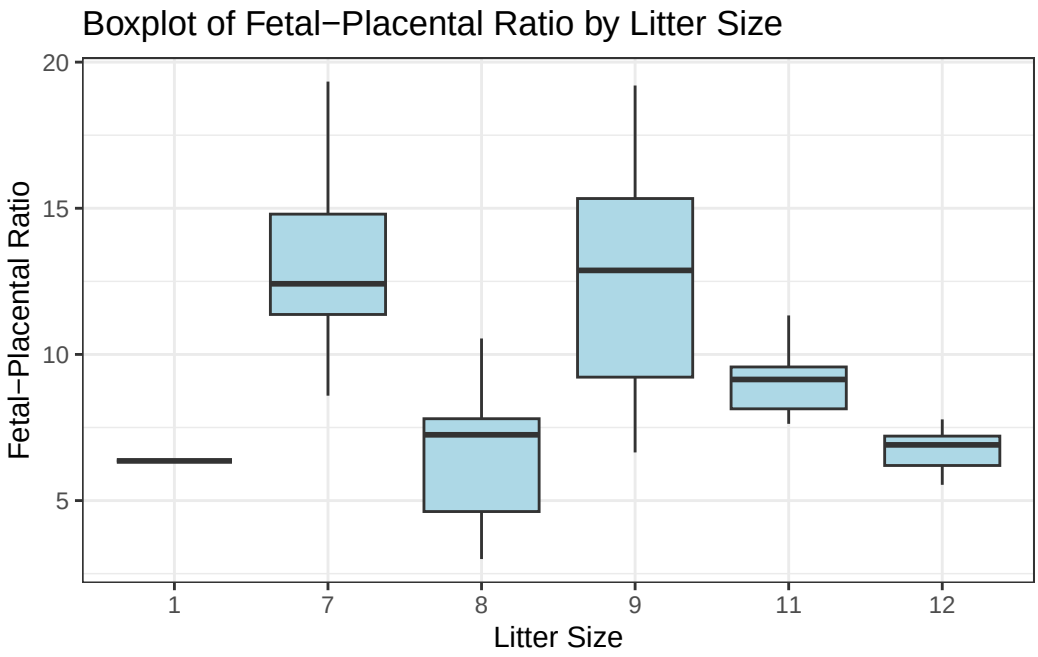
```
# Boxplot of Fetal_mass by Litter_size
ggplot(fetus, aes(x = as.factor(Litter_size), y = Fetal_mass)) +
  geom_boxplot(fill = "lightblue") +
  xlab("Litter Size") +
  ylab("Fetal Mass") +
  ggtitle("Boxplot of Fetal Mass by Litter Size") +
  theme_bw()
```



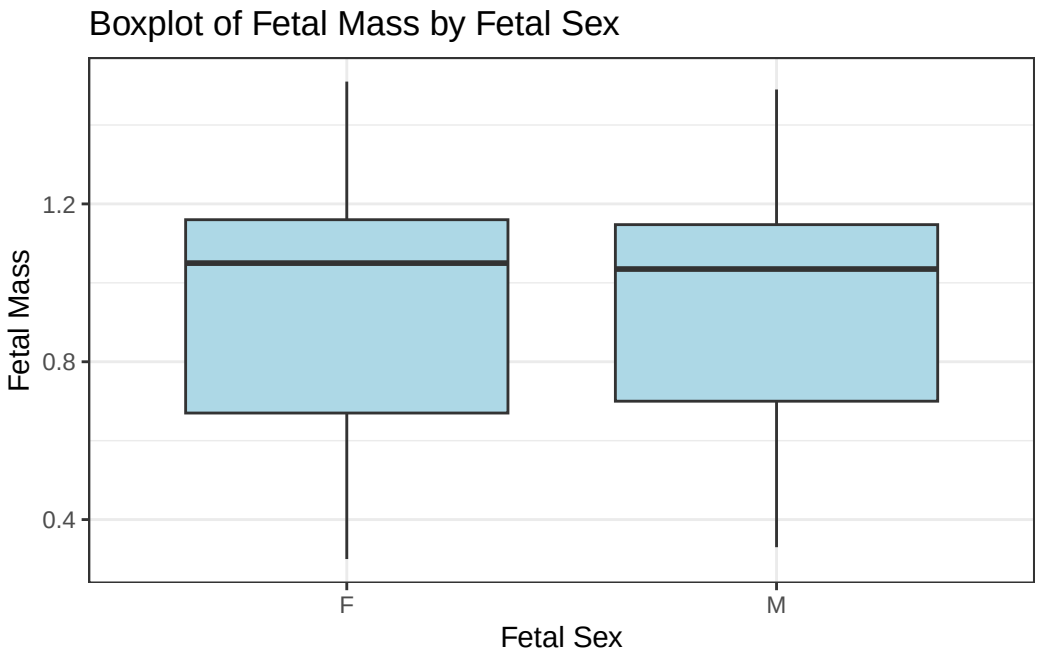

```
# Boxplot of Placenta_mass by Litter_size
ggplot(fetus, aes(x = as.factor(Litter_size), y = Placenta_mass)) +
  geom_boxplot(fill = "lightblue") +
  xlab("Litter Size") +
  ylab("Placenta Mass") +
  ggtitle("Boxplot of Placenta Mass by Litter Size") +
  theme_bw()
```



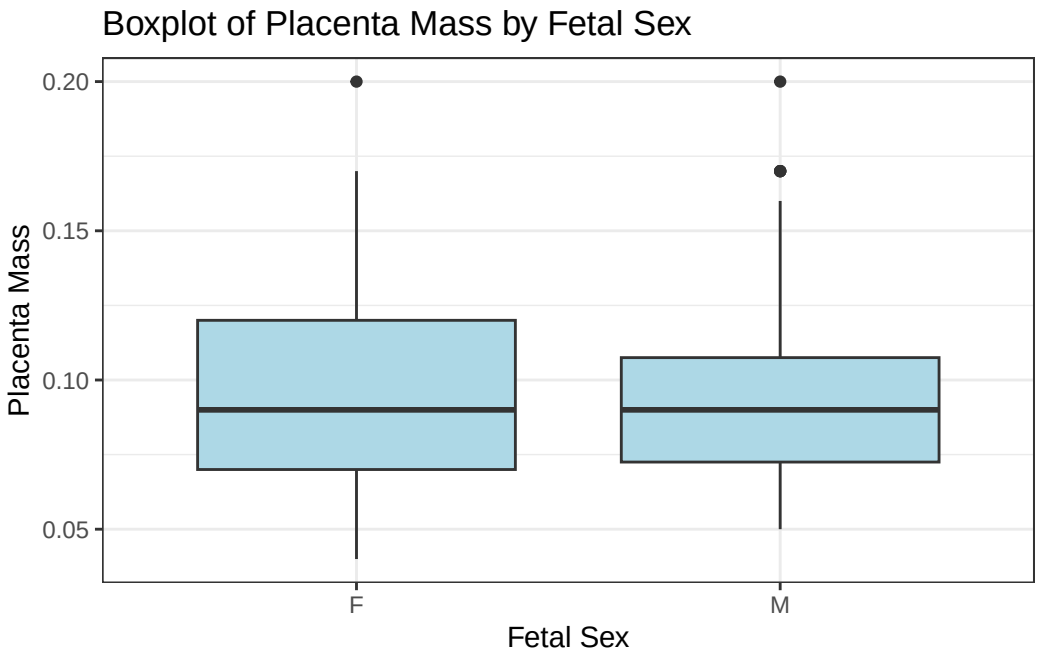

```
# Boxplot of Fetal_placental_ratio by Litter_size
ggplot(fetus, aes(x = as.factor(Litter_size), y = Fetal_placental.ratio)) +
  geom_boxplot(fill = "lightblue") +
  xlab("Litter Size") +
  ylab("Fetal-Placental Ratio") +
  ggtitle("Boxplot of Fetal-Placental Ratio by Litter Size") +
  theme_bw()
```



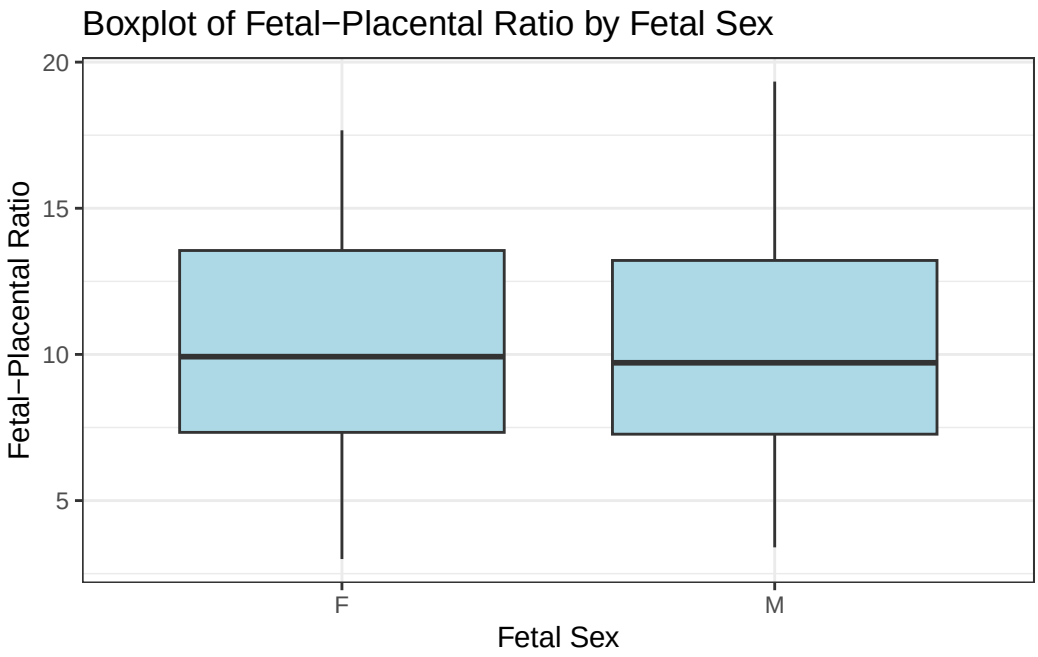

```
# Boxplot of Fetal_mass by Fetal_sex
ggplot(fetus, aes(x = Fetal_sex, y = Fetal_mass)) +
  geom_boxplot(fill = "lightblue") +
  xlab("Fetal Sex") +
  ylab("Fetal Mass") +
  ggtitle("Boxplot of Fetal Mass by Fetal Sex") +
  theme_bw()
```




```
# Boxplot of Placenta_mass by Fetal_sex
ggplot(fetus, aes(x = Fetal_sex, y = Placenta_mass)) +
  geom_boxplot(fill = "lightblue") +
  xlab("Fetal Sex") +
  ylab("Placenta Mass") +
  ggtitle("Boxplot of Placenta Mass by Fetal Sex") +
  theme_bw()
```

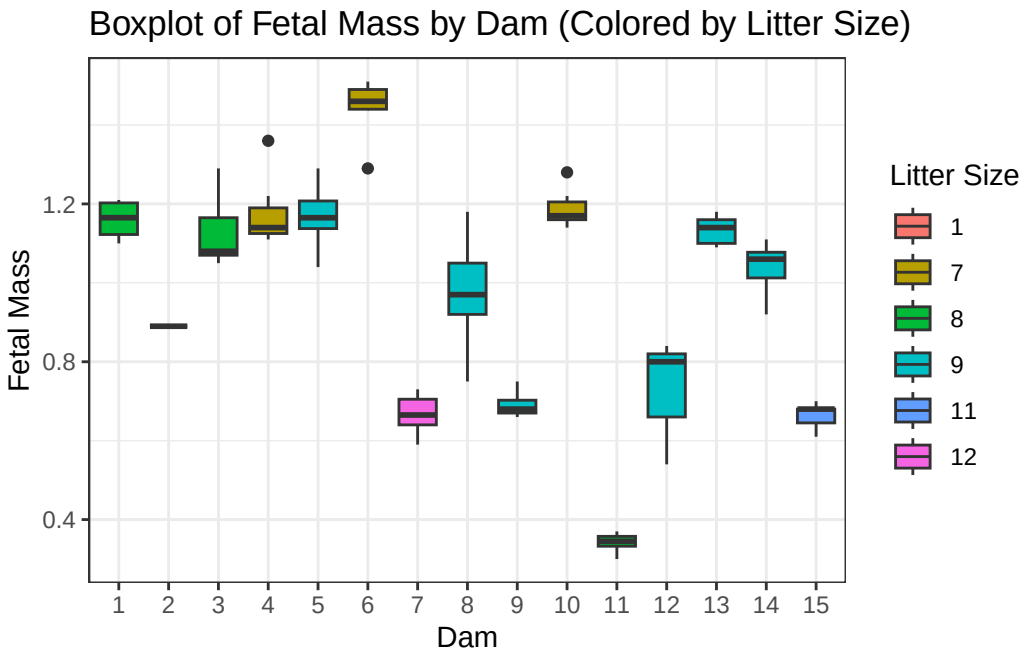



```
# Boxplot of Fetal_placental_ratio by Fetal_sex
ggplot(fetus, aes(x = Fetal_sex, y = Fetal_placental.ratio)) +
  geom_boxplot(fill = "lightblue") +
  xlab("Fetal Sex") +
  ylab("Fetal-Placental Ratio") +
  ggtitle("Boxplot of Fetal-Placental Ratio by Fetal Sex") +
  theme_bw()
```

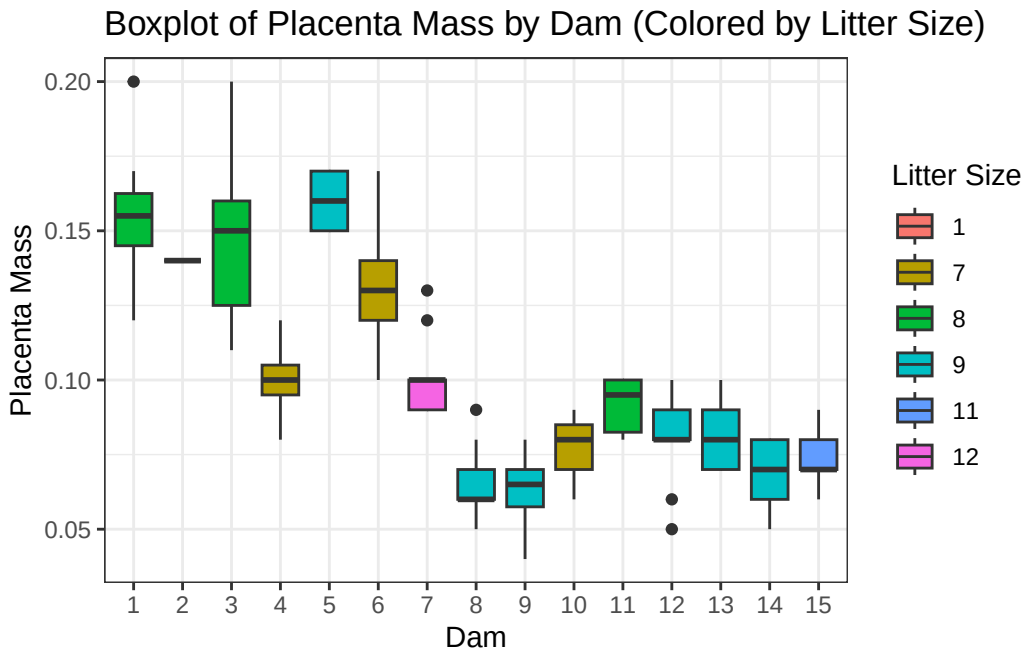


Litter size could have an effect. But, what is far more likely, is that litter size captures the variance of Dam.

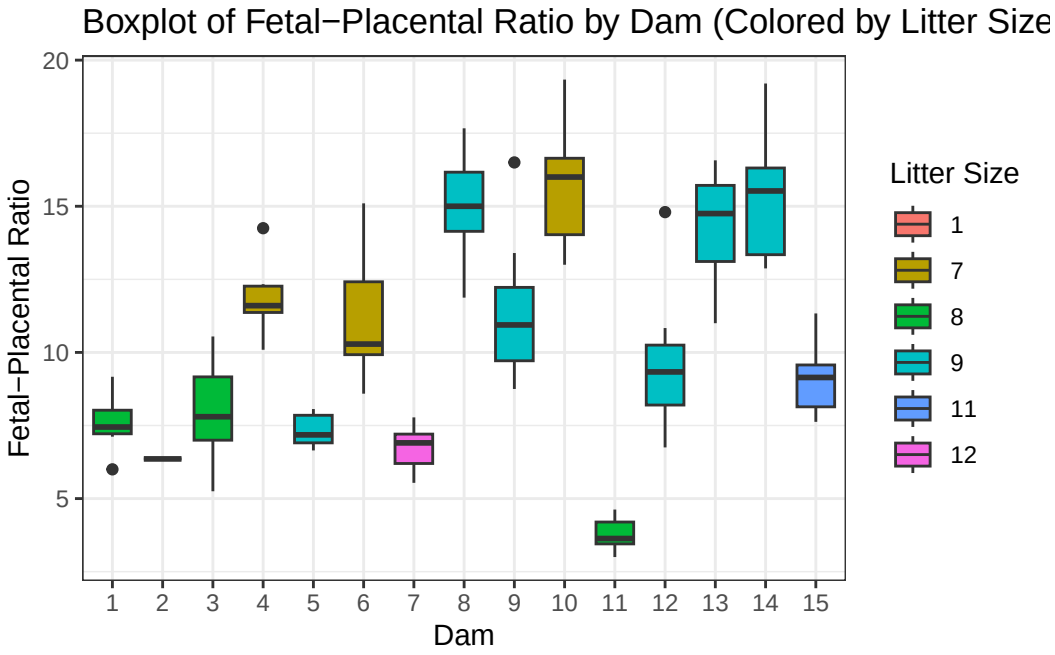
```
# Boxplot of Fetal_mass by Dam with box color by Litter_size
ggplot(fetus, aes(x = as.factor(Dam), y = Fetal_mass, fill = as.factor(Litter_size))) +
  geom_boxplot() +
  xlab("Dam") +
  ylab("Fetal Mass") +
  labs(fill = "Litter Size") +
  ggtitle("Boxplot of Fetal Mass by Dam (Colored by Litter Size)") +
  theme_bw()
```




```
# Boxplot of Placenta_mass by Dam with box color by Litter_size
ggplot(fetus, aes(x = as.factor(Dam), y = Placenta_mass, fill = as.factor(Litter_size))) +
  geom_boxplot() +
  xlab("Dam") +
  ylab("Placenta Mass") +
  labs(fill = "Litter Size") +
  ggtitle("Boxplot of Placenta Mass by Dam (Colored by Litter Size)") +
  theme_bw()
```




```r
# Boxplot of Fetal_placental_ratio by Dam with box color by Litter_size
ggplot(fetus, aes(x = as.factor(Dam), y = Fetal_placental.ratio, fill = as.factor(Litter_s
  geom_boxplot() +
  xlab("Dam") +
  ylab("Fetal-Placental Ratio") +
  labs(fill = "Litter Size") +
  ggtitle("Boxplot of Fetal-Placental Ratio by Dam (Colored by Litter Size)") +
  theme_bw()
```



While these plots are a bit cluttered, what they do show is that there is little correlation between litter size and any of our variables of interest. It also shows that these variables are highly dependent on Dam. Babies from the same mother looks similar (hence why the boxes are not tall and have short tails on average).

Modeling of the Dependent Variables

Dam is obviously the most important factor here. If we were to train a regression without it, we'd certainly get awful results. In fact, we can see this here. We only do this for Fetal_mass.

```
model <- lm(Fetal_mass ~ Litter_size + isFemale + Maternal_genotype + Fetus_genotype, data

summary(model)
```

```
Call:
lm(formula = Fetal_mass ~ Litter_size + isFemale + Maternal_genotype +
    Fetus_genotype, data = fetus)

Residuals:
     Min       1Q   Median       3Q      Max
```

```
-0.90129 -0.10817  0.02673  0.15308  0.31921

Coefficients:
                         Estimate Std. Error t value Pr(>|t|)
(Intercept)              1.727050   0.151470  11.402  < 2e-16 ***
Litter_size             -0.098878   0.015497  -6.380 4.51e-09 ***
isFemale                -0.011653   0.045971  -0.253   0.8004
Maternal_genotypefl/fl   0.142784   0.065461   2.181   0.0313 *
Maternal_genotypeHET     0.086907   0.066400   1.309   0.1934
Fetus_genotypeko         0.002518   0.083843   0.030   0.9761
Fetus_genotypewt         0.031989   0.060187   0.531   0.5962
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.2392 on 108 degrees of freedom
Multiple R-squared:  0.2931,    Adjusted R-squared:  0.2539
F-statistic: 7.465 on 6 and 108 DF,  p-value: 1.055e-06
```

Notice that nothing except for the intercept and Litter_size (which before we proposed might just indirectly be capturing the variance of Dam ID) are significant. With Bayesian model selection, we can confirm this is the case.

```r
y<-fetus$Fetal_mass
fetus_encoded <- fetus %>%
  mutate(
    Maternal_genotype = as.factor(Maternal_genotype),
    Fetus_genotype = as.factor(Fetus_genotype)
  )

# Create the design matrix X
X <- model.matrix(Fetal_mass ~ isFemale + Litter_size + Maternal_genotype + Fetus_genotype

lmratio.gprior<-function(z0,z1,y,X,g=dim(X)[1],nu0=1,
                 s200=mean( lm(y~-1+X[,z0==1])$res^2),
                 s201=mean( lm(y~-1+X[,z1==1])$res^2) )
{
  n<-dim(X)[1]

  X0<-X[,z0==1]
  X1<-X[,z1==1]

  H0<- (g/(g+1)) * X0%*%solve(t(X0)%*%X0)%*%t(X0)
```

```
  SS0<- t(y)%*%( diag(1,nrow=n)  - H0 ) %*%y
  p0<-sum(z0==1)

  H1<- (g/(g+1)) * X1%*%solve(t(X1)%*%X1)%*%t(X1)
  SS1<- t(y)%*%( diag(1,nrow=n)  - H1 ) %*%y
  p1<-sum(z1==1)

   -.5*(p1-p0)*log( 2*pi*(1+g))  +
    .5*nu0*log(s201/s200) + .5*(nu0+n)*log( (nu0*s200+SS0)/(nu0+s201+SS1) )
}

lpy.X<-function(y,X,g=length(y),nu0=1,s20=try(summary(lm(y~-1+X))$sigma^2,silent=TRUE))
{
  n<-dim(X)[1] ; p<-dim(X)[2]
  if(p==0) { s20<-mean(y^2) }
  H0<-0 ; if(p>0) { H0<- (g/(g+1)) * X%*%solve(t(X)%*%X)%*%t(X) }
  SS0<- t(y)%*%( diag(1,nrow=n)  - H0 ) %*%y

  -.5*n*log(2*pi) +lgamma(.5*(nu0+n)) - lgamma(.5*nu0)  - .5*p*log(1+g) +
   .5*nu0*log(.5*nu0*s20) -.5*(nu0+n)*log(.5*(nu0*s20+SS0))
}
```

```
#### Bayesian model selection
p<-dim(X)[2]
S<-1000
z<-rep(1,p)
Z<-matrix(NA,S,p)
lpy.c<-lpy.X(y,X[,z==1,drop=FALSE])
for(s in 1:S)
{
  for(j in sample(1:p))
  {
    zp<-z ; zp[j]<-1-zp[j]
    lpy.p<-lpy.X(y,X[,zp==1,drop=FALSE])
    r<- (lpy.p - lpy.c)*(-1)^(zp[j]==0)
    z[j]<-rbinom(1,1,1/(1+exp(-r)))
    if(z[j]==zp[j]) {lpy.c<-lpy.p}
  }
  Z[s,]<-z
}
```

```
means <- colMeans(Z)
matrix(means, nrow = 1, ncol = ncol(Z), dimnames = list(NULL, colnames(X)))
```

```
     (Intercept) isFemale Litter_size Maternal_genotypefl/fl
[1,]           1    0.079           1                   0.3
     Maternal_genotypeHET Fetus_genotypeko Fetus_genotypewt
[1,]                0.106            0.085            0.084
```

Only the intercept and Litter Size are probably features. We will thus switch over to a mixed model to see if there is any value to the genotypes.

```
fetal_mass_model<-lmer(Fetal_mass ~ Litter_size + isFemale*Fetus_genotype + (1|Dam) + (1|M
```

```
boundary (singular) fit: see help('isSingular')
```

```
summary(fetal_mass_model)
```

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: Fetal_mass ~ Litter_size + isFemale * Fetus_genotype + (1 | Dam) +
    (1 | Maternal_genotype)
   Data: fetus

REML criterion at convergence: -189.1

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.81303 -0.48478 -0.05347  0.56638  2.72874

Random effects:
 Groups            Name        Variance Std.Dev.
 Dam               (Intercept) 0.082115 0.28656
 Maternal_genotype (Intercept) 0.000000 0.00000
 Residual                      0.004689 0.06848
Number of obs: 115, groups:  Dam, 15; Maternal_genotype, 3

Fixed effects:
                          Estimate Std. Error       df t value Pr(>|t|)
(Intercept)                1.16725    0.27595 13.97137   4.230 0.000844 ***
```

```
Litter_size               -0.03086    0.03217 13.65742  -0.959 0.354159
isFemale                   0.03554    0.02693 94.99296   1.320 0.190007
Fetus_genotypeko           0.03493    0.03413 95.14271   1.023 0.308707
Fetus_genotypewt           0.06588    0.02709 95.43547   2.432 0.016887 *
isFemale:Fetus_genotypeko -0.01959    0.05207 95.06774  -0.376 0.707546
isFemale:Fetus_genotypewt -0.05356    0.03322 95.20069  -1.612 0.110204
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
                 (Intr) Lttr_s isFeml Fts_gntypk Fts_gntypw isFml:Fts_gntypk
Litter_size      -0.960
isFemale         -0.061  0.000
Fets_gntypk      -0.051  0.002  0.508
Fts_gntypwt      -0.077  0.006  0.638  0.487
isFml:Fts_gntypk  0.025  0.002 -0.502 -0.602     -0.252
isFml:Fts_gntypw  0.040  0.013 -0.838 -0.421     -0.741       0.396
optimizer (nloptwrap) convergence code: 0 (OK)
boundary (singular) fit: see help('isSingular')
```

```
placenta_mass_model<-lmer(Placenta_mass ~ Litter_size + isFemale*Fetus_genotype + (1|Dam)
```

```
boundary (singular) fit: see help('isSingular')
```

```
summary(placenta_mass_model)
```

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: Placenta_mass ~ Litter_size + isFemale * Fetus_genotype + (1 |
    Dam) + (1 | Maternal_genotype)
   Data: fetus

REML criterion at convergence: -522.4

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.29513 -0.58310 -0.01651  0.52652  3.05477

Random effects:
 Groups            Name        Variance  Std.Dev.
```

```
 Dam               (Intercept) 0.0011418 0.03379
 Maternal_genotype (Intercept) 0.0000000 0.00000
 Residual                      0.0002511 0.01584
Number of obs: 115, groups:  Dam, 15; Maternal_genotype, 3

Fixed effects:
                            Estimate Std. Error        df t value Pr(>|t|)
(Intercept)                 0.149157   0.034623 16.993231   4.308 0.000477 ***
Litter_size                -0.005834   0.003981 15.749549  -1.466 0.162446
isFemale                    0.005232   0.006227 95.410430   0.840 0.402842
Fetus_genotypeko            0.010757   0.007885 95.954771   1.364 0.175679
Fetus_genotypewt            0.001410   0.006244 97.004093   0.226 0.821820
isFemale:Fetus_genotypeko -0.016641   0.012034 95.687772  -1.383 0.169936
isFemale:Fetus_genotypewt -0.009003   0.007670 96.161517  -1.174 0.243413
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
                (Intr) Lttr_s isFeml Fts_gntypk Fts_gntypw isFml:Fts_gntypk
Litter_size     -0.956
isFemale        -0.113  0.000
Fets_gntypk     -0.096  0.005  0.508
Fts_gntypwt     -0.144  0.011  0.639  0.489
isFml:Fts_gntypk  0.046  0.004 -0.502 -0.603     -0.255
isFml:Fts_gntypw  0.076  0.023 -0.838 -0.421     -0.741       0.397
optimizer (nloptwrap) convergence code: 0 (OK)
boundary (singular) fit: see help('isSingular')
```

```
fpratio_model<-lmer(Fetal_placental.ratio ~ Litter_size + isFemale*Fetus_genotype + (1|Dam
summary(fpratio_model)
```

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: Fetal_placental.ratio ~ Litter_size + isFemale * Fetus_genotype +
    (1 | Dam) + (1 | Maternal_genotype)
   Data: fetus

REML criterion at convergence: 489.6

Scaled residuals:
    Min      1Q  Median      3Q     Max
```

```
-1.9672 -0.5152 -0.1121  0.4116  3.0492

Random effects:
 Groups            Name        Variance Std.Dev.
 Dam               (Intercept) 15.0830  3.8837
 Maternal_genotype (Intercept)  0.1468  0.3832
 Residual                       2.8984  1.7025
Number of obs: 115, groups:  Dam, 15; Maternal_genotype, 3

Fixed effects:
                          Estimate Std. Error       df t value Pr(>|t|)
(Intercept)                8.71167    3.94680 15.49467   2.207   0.0428 *
Litter_size                0.14759    0.45407 12.39835   0.325   0.7506
isFemale                   0.15960    0.66913 95.17382   0.239   0.8120
Fetus_genotypeko          -1.15735    0.84746 95.65656  -1.366   0.1752
Fetus_genotypewt           0.47085    0.67146 96.45555   0.701   0.4848
isFemale:Fetus_genotypeko  2.45928    1.29330 95.41909   1.902   0.0602 .
isFemale:Fetus_genotypewt -0.06081    0.82446 95.84057  -0.074   0.9414
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
                 (Intr) Lttr_s isFeml Fts_gntypk Fts_gntypw isFml:Fts_gntypk
Litter_size      -0.955
isFemale         -0.107  0.000
Fets_gntypk      -0.090  0.005  0.508
Fts_gntypwt      -0.135  0.011  0.639  0.489
isFml:Fts_gntypk  0.043  0.003 -0.502 -0.603     -0.254
isFml:Fts_gntypw  0.071  0.022 -0.838 -0.421     -0.741       0.397
```

We've noticed that a fetus of genotype WT might have, on average, higher fetal mass. We investigate this claim on 4 mothers with the largest litter sizes.

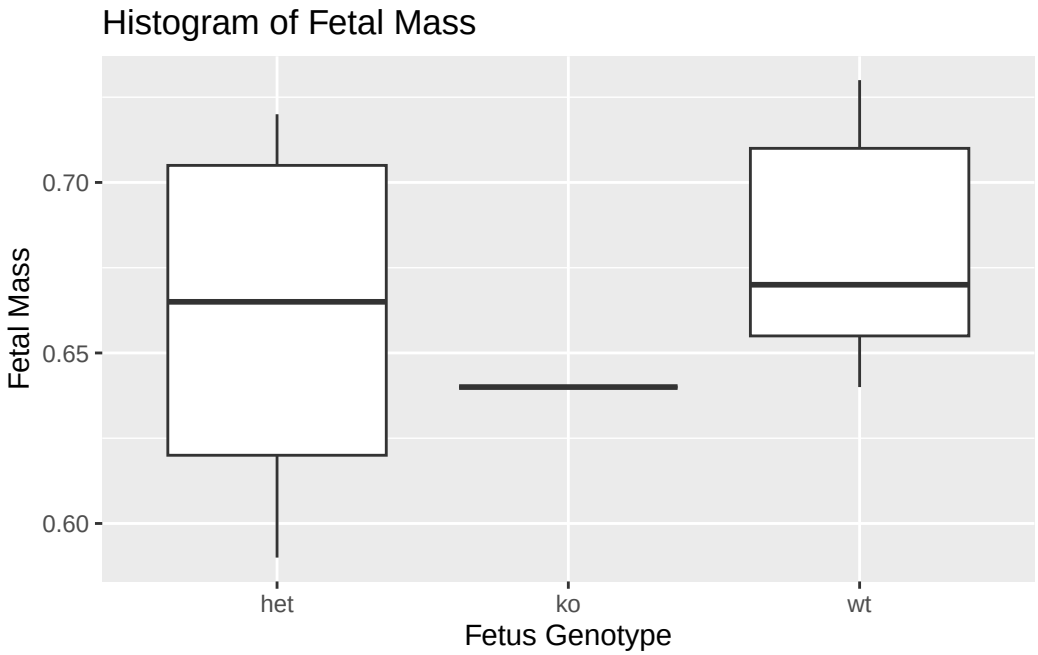
filtered_fetus

```r
# Filter the dataset to include observations from the four Dams with the largest litter si
dam_values <- unique(fetus %>%
  group_by(Dam) %>%
  arrange(desc(Litter_size)) %>%
  top_n(4, Dam) %>%
  pull(Dam)
)[1:4]
```

```
# Filter the dataset to include observations where Dam is one of the specified values
dam1 <- fetus %>%
  filter(Dam == dam_values[1])
dam2 <- fetus %>%
  filter(Dam == dam_values[2])
dam3 <- fetus %>%
  filter(Dam == dam_values[3])
dam4 <- fetus %>%
  filter(Dam == dam_values[4])
```

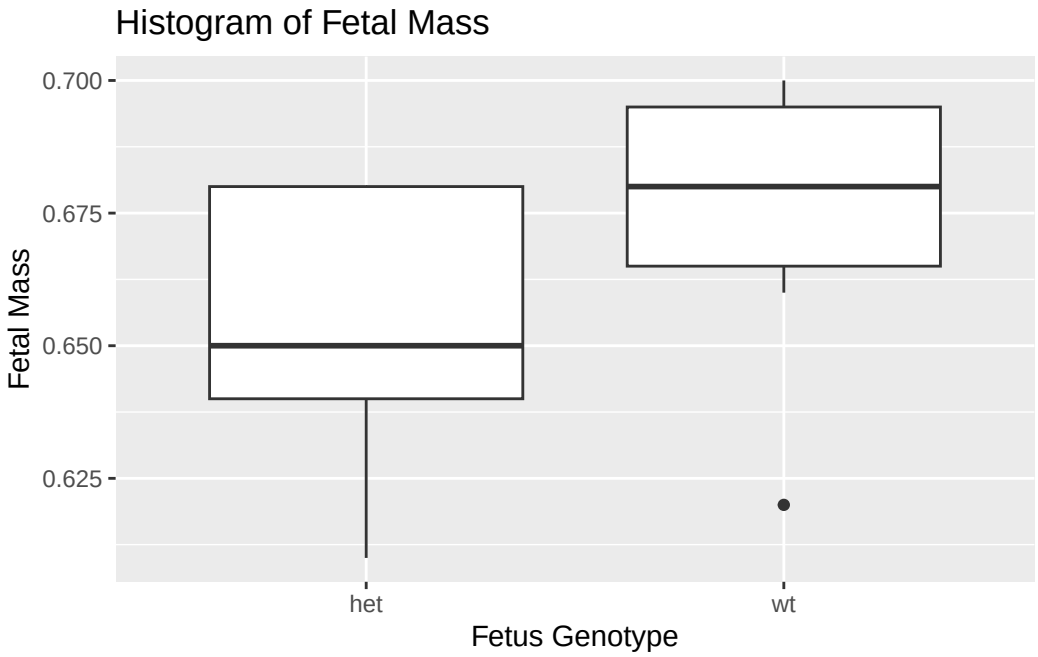
The plots below show the actual values.

```
ggplot(dam1, aes(y = Fetal_mass, x = Fetus_genotype)) +
  geom_boxplot() +
  ylab("Fetal Mass") +
  xlab("Fetus Genotype") +
  ggtitle("Histogram of Fetal Mass")
```

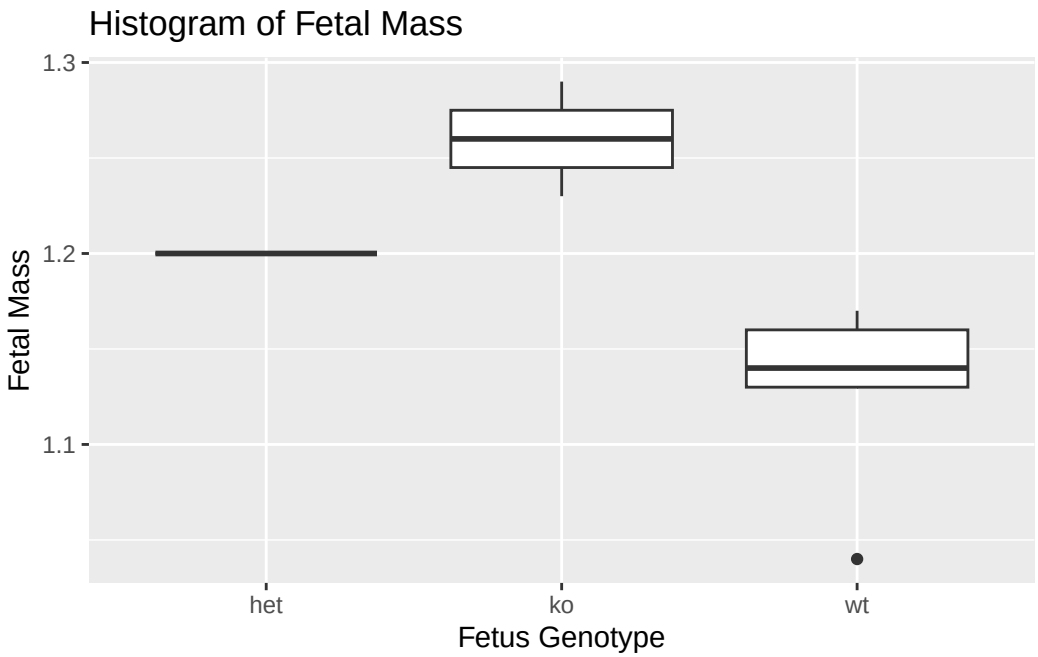



```
ggplot(dam2, aes(y = Fetal_mass, x = Fetus_genotype)) +
  geom_boxplot() +
  ylab("Fetal Mass") +
```

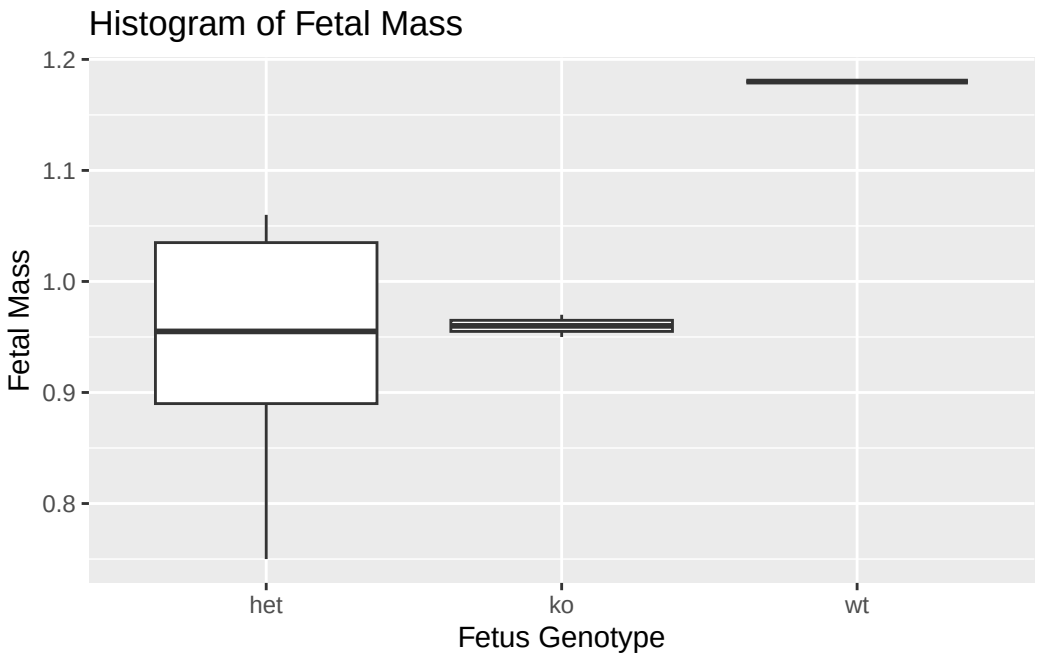
```
  xlab("Fetus Genotype") +
  ggtitle("Histogram of Fetal Mass")
```



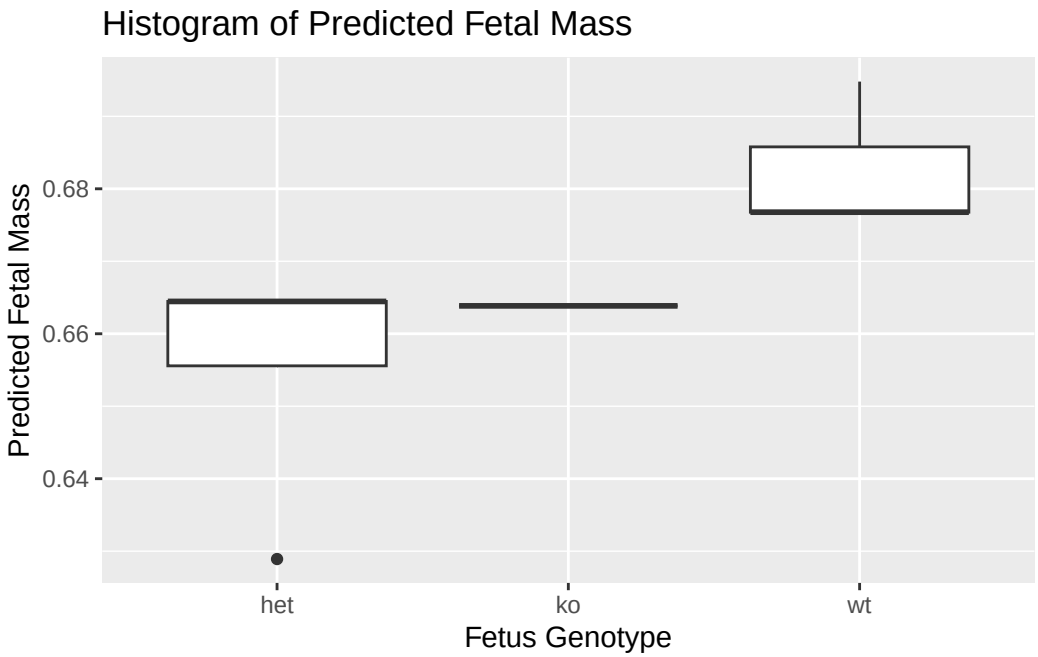

```
ggplot(dam3, aes(y = Fetal_mass, x = Fetus_genotype)) +
  geom_boxplot() +
  ylab("Fetal Mass") +
  xlab("Fetus Genotype") +
  ggtitle("Histogram of Fetal Mass")
```



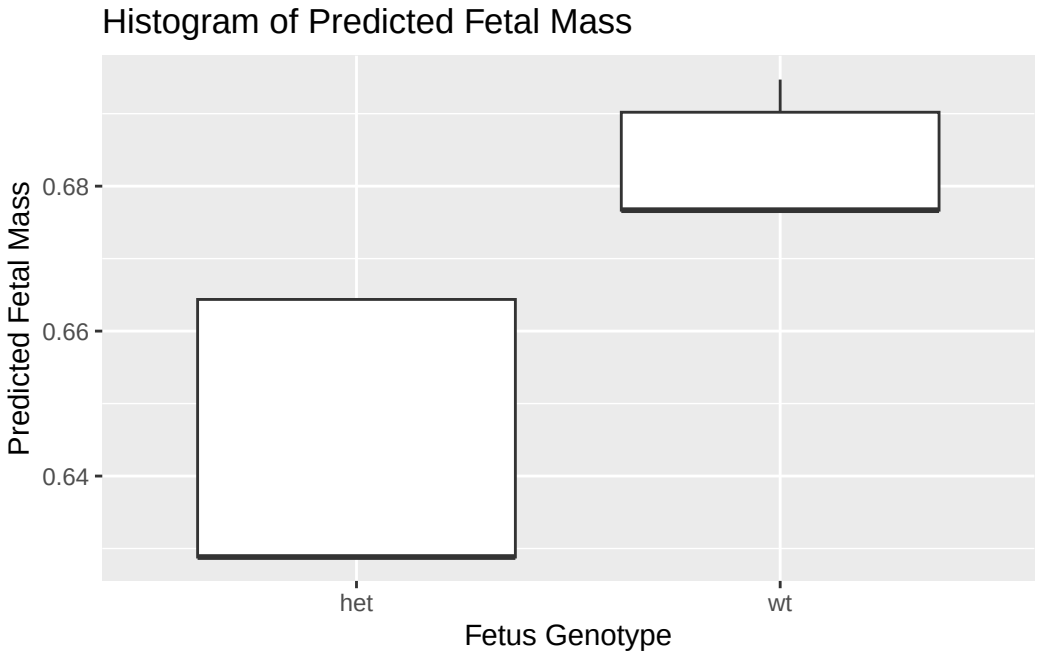

```
ggplot(dam4, aes(y = Fetal_mass, x = Fetus_genotype)) +
  geom_boxplot() +
  ylab("Fetal Mass") +
  xlab("Fetus Genotype") +
  ggtitle("Histogram of Fetal Mass")
```



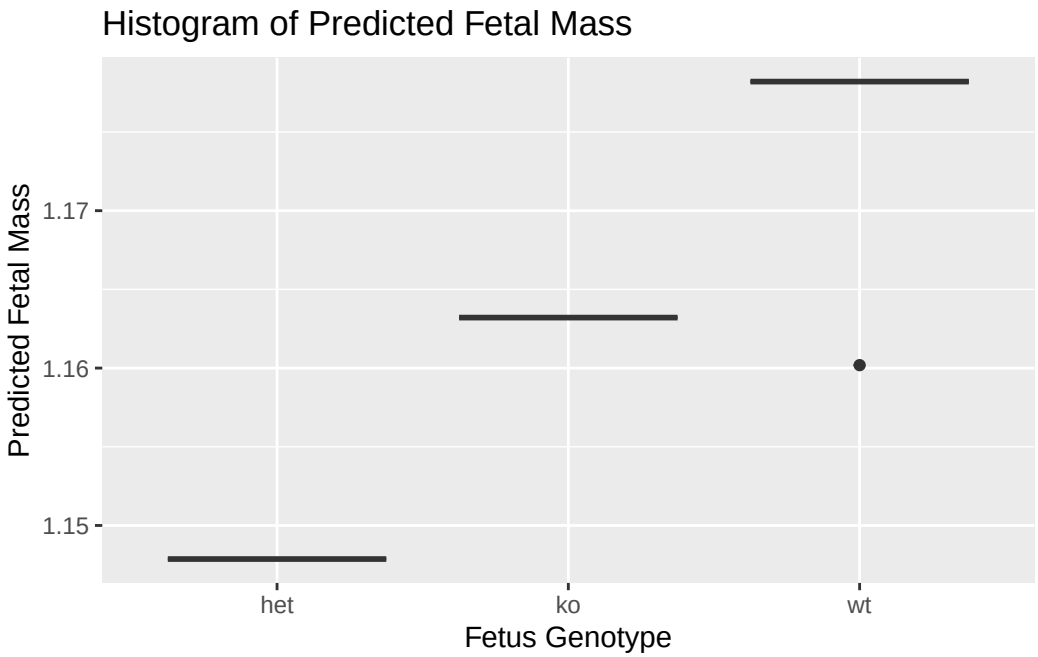

```
dam1$predicted = predict(fetal_mass_model, newdata=dam1)
dam2$predicted = predict(fetal_mass_model, newdata=dam2)
dam3$predicted = predict(fetal_mass_model, newdata=dam3)
dam4$predicted = predict(fetal_mass_model, newdata=dam4)

ggplot(dam1, aes(y = predicted, x = Fetus_genotype)) +
  geom_boxplot() +
  ylab("Predicted Fetal Mass") +
  xlab("Fetus Genotype") +
  ggtitle("Histogram of Predicted Fetal Mass")
```



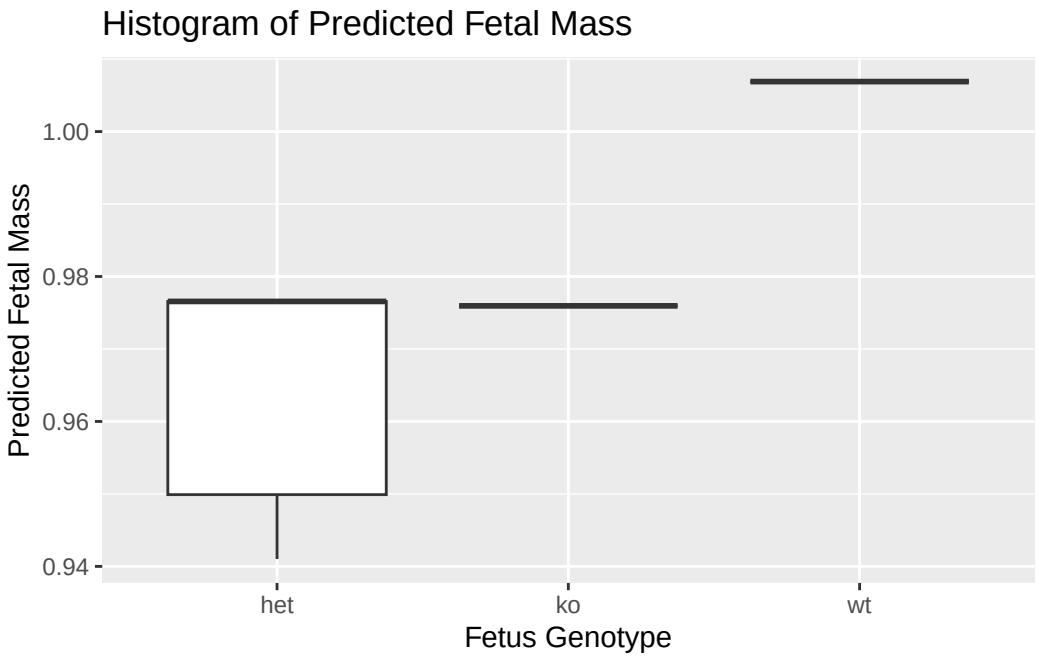

```
ggplot(dam2, aes(y = predicted, x = Fetus_genotype)) +
  geom_boxplot() +
  ylab("Predicted Fetal Mass") +
  xlab("Fetus Genotype") +
  ggtitle("Histogram of Predicted Fetal Mass")
```




```
ggplot(dam3, aes(y = predicted, x = Fetus_genotype)) +
  geom_boxplot() +
  ylab("Predicted Fetal Mass") +
  xlab("Fetus Genotype") +
  ggtitle("Histogram of Predicted Fetal Mass")
```




```
ggplot(dam4, aes(y = predicted, x = Fetus_genotype)) +
  geom_boxplot() +
  ylab("Predicted Fetal Mass") +
  xlab("Fetus Genotype") +
  ggtitle("Histogram of Predicted Fetal Mass")
```

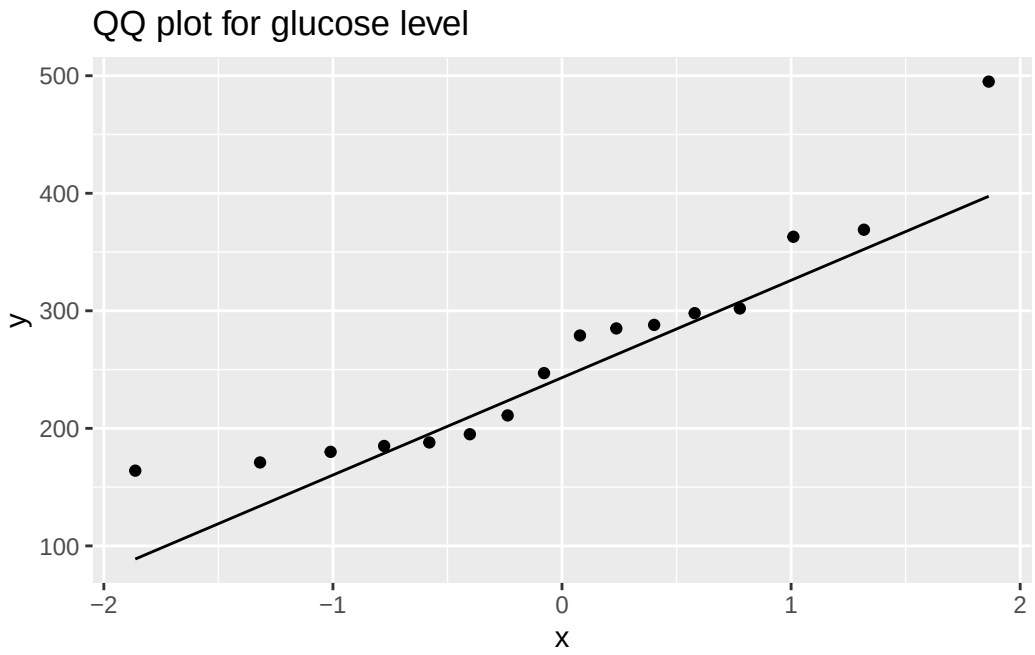


Mother Data

```
mother <- read.csv("data/mother-data.csv", header=T)
```

Now we'd like to assess the differences in mean blood glucose levels between maternal genotypes. For each time period, we will check if there is normality and constant variance, then conduct an ANCOVA analysis to see if the genotype makes a difference.

```
# Checking visually
ggplot(mother, aes(sample=gluc_60)) +
  stat_qq() +
  stat_qq_line() +
  ggtitle("QQ plot for glucose level")
```




```
# Checking mathematically
shapiro.test(mother$gluc_60)
```

```
    Shapiro-Wilk normality test

data:  mother$gluc_60
W = 0.88957, p-value = 0.05483
```

Normality is satisfied.

```
mother %>%
  group_by(Maternal_genotype) %>%
  summarise(n = n(), mean = mean(gluc_60), sd = sd(gluc_60))
```

```
# A tibble: 3 x 4
  Maternal_genotype     n  mean    sd
  <chr>             <int> <dbl> <dbl>
1 fl/+                  5  223.  60.7
2 fl/fl                 7  327.  95.3
3 HET                   4  204.  34.5
```

Constant variance is satisfied ($95/34 \approx 2.8$ and sample size is small, so this is fine).

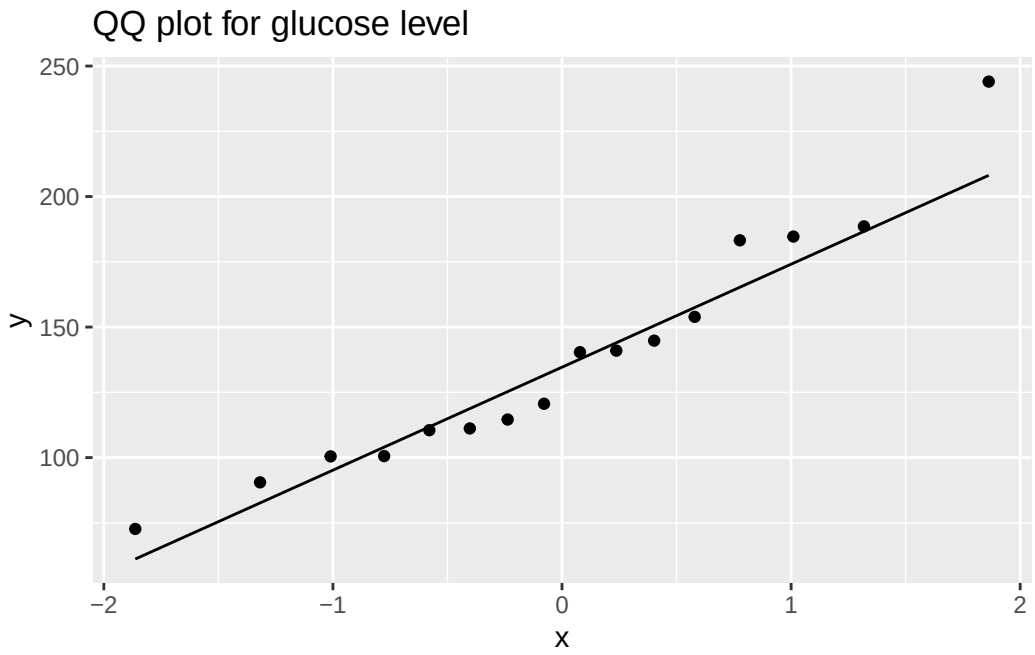
```
# First, construct a model including covariates
model <- lm(gluc_60 ~ Maternal_genotype + num_fetus + percent_body_weight_gain, data = mot

# Then perform ANCOVA using the model
anova(model)
```

```
Analysis of Variance Table

Response: gluc_60
                         Df Sum Sq Mean Sq F value  Pr(>F)
Maternal_genotype         2  50758 25379.1  6.2132 0.01564 *
num_fetus                 1  27732 27732.4  6.7894 0.02445 *
percent_body_weight_gain  1    187   186.8  0.0457 0.83456
Residuals                11  44932  4084.7
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

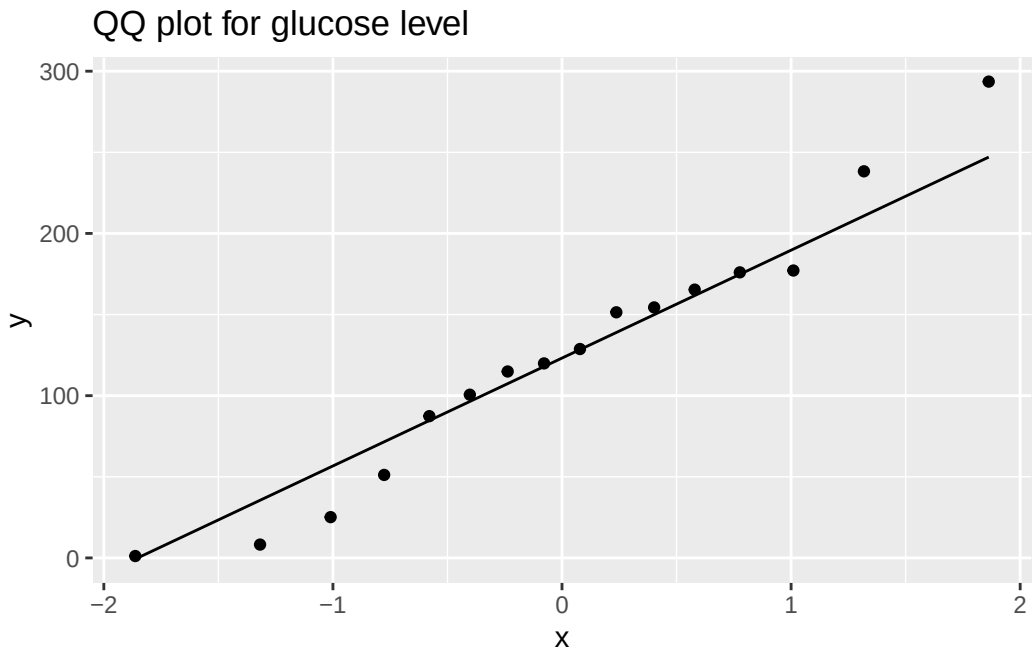
We find that only at 60 minutes are we 95% confident that there is a difference in average blood glucose level.

Now we repeat this for % change in blood glucose levels

```
# Checking visually
ggplot(mother, aes(sample=chng_base_15)) +
  stat_qq() +
  stat_qq_line() +
  ggtitle("QQ plot for glucose level")
```




```
ggplot(mother, aes(sample=chng_base_30)) +
  stat_qq() +
  stat_qq_line() +
  ggtitle("QQ plot for glucose level")
```




```
ggplot(mother, aes(sample=chng_base_60)) +
  stat_qq() +
  stat_qq_line() +
  ggtitle("QQ plot for glucose level")
```


```
# Checking mathematically
shapiro.test(mother$chng_base_15)
```

```
    Shapiro-Wilk normality test

data:  mother$chng_base_15
W = 0.93838, p-value = 0.3297
```

```
shapiro.test(mother$chng_base_30)
```

```
    Shapiro-Wilk normality test

data:  mother$chng_base_30
W = 0.96662, p-value = 0.7814
```

```
shapiro.test(mother$chng_base_60)
```

```
    Shapiro-Wilk normality test

data:  mother$chng_base_60
W = 0.88822, p-value = 0.0522
```

Normality is satisfied.

```
mother %>%
  group_by(Maternal_genotype) %>%
  summarise(n = n(), mean = mean(chng_base_15), sd = sd(chng_base_15))
```

```
# A tibble: 3 x 4
  Maternal_genotype     n  mean    sd
  <chr>             <int> <dbl> <dbl>
1 fl/+                  5  116.  42.7
2 fl/fl                 7  163.  46.8
3 HET                   4  121.  23.2
```

```
mother %>%
  group_by(Maternal_genotype) %>%
  summarise(n = n(), mean = mean(chng_base_30), sd = sd(chng_base_30))
```

```
# A tibble: 3 x 4
  Maternal_genotype     n  mean    sd
  <chr>             <int> <dbl> <dbl>
1 fl/+                  5  85.1  70.1
2 fl/fl                 7 186.   59.7
3 HET                   4  67.0  51.7
```

```
mother %>%
  group_by(Maternal_genotype) %>%
  summarise(n = n(), mean = mean(chng_base_60), sd = sd(chng_base_60))
```

```
# A tibble: 3 x 4
  Maternal_genotype     n  mean    sd
  <chr>             <int> <dbl> <dbl>
1 fl/+                  5  33.9  49.3
2 fl/fl                 7 131.   59.8
3 HET                   4  16.3  29.8
```

Constant variance is satisfied.

```r
# First, construct a model including covariates
model_15_30 <- lm(chng_15_30 ~ Maternal_genotype + num_fetus + percent_body_weight_gain, d
model_base_30 <- lm(chng_base_30 ~ Maternal_genotype + num_fetus + percent_body_weight_gai
model_base_60 <- lm(chng_base_60 ~ Maternal_genotype + num_fetus + percent_body_weight_gai

# Then perform ANCOVA using the model
anova(model_15_30)
```

```
Analysis of Variance Table

Response: chng_15_30
                         Df Sum Sq Mean Sq F value  Pr(>F)
Maternal_genotype         2 3565.2 1782.60  5.9329 0.01787 *
num_fetus                 1  153.8  153.83  0.5120 0.48918
percent_body_weight_gain  1    1.0    0.99  0.0033 0.95521
Residuals                11 3305.0  300.46
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
anova(model_base_30)
```

```
Analysis of Variance Table

Response: chng_base_30
                         Df Sum Sq Mean Sq F value  Pr(>F)
Maternal_genotype         2  47244 23621.9  5.4670 0.02247 *
num_fetus                 1     38    37.9  0.0088 0.92709
percent_body_weight_gain  1   1499  1499.2  0.3470 0.56773
Residuals                11  47529  4320.8
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
anova(model_base_60)
```

```
Analysis of Variance Table

Response: chng_base_60
```

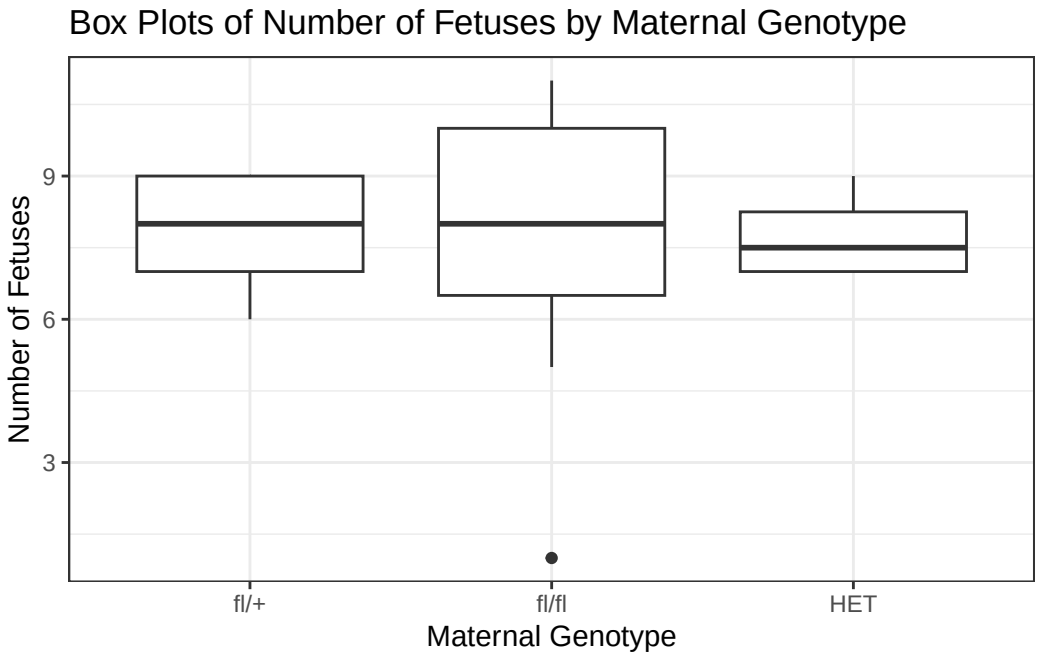
```
                          Df Sum Sq Mean Sq F value   Pr(>F)
Maternal_genotype          2  43659 21829.3  9.7512 0.003663 **
num_fetus                  1   7821  7821.0  3.4937 0.088443 .
percent_body_weight_gain   1   1396  1396.3  0.6237 0.446353
Residuals                 11  24625  2238.6
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

15-30, base-30, base-60 all have significant p-values to suggest a difference among maternal genotype groups.

Now we are interested in assessing the impact of Maternal Genotype on the # of fetuses, # of absorptions, body weight gain, and % body weight gain.

We first do this visually and with linear models.

```
# Num Fetuses
ggplot(data = mother, aes(x = Maternal_genotype, y = num_fetus)) +
  geom_boxplot() +
  xlab("Maternal Genotype") +
  ylab("Number of Fetuses") +
  ggtitle("Box Plots of Number of Fetuses by Maternal Genotype") +
  theme_bw()
```

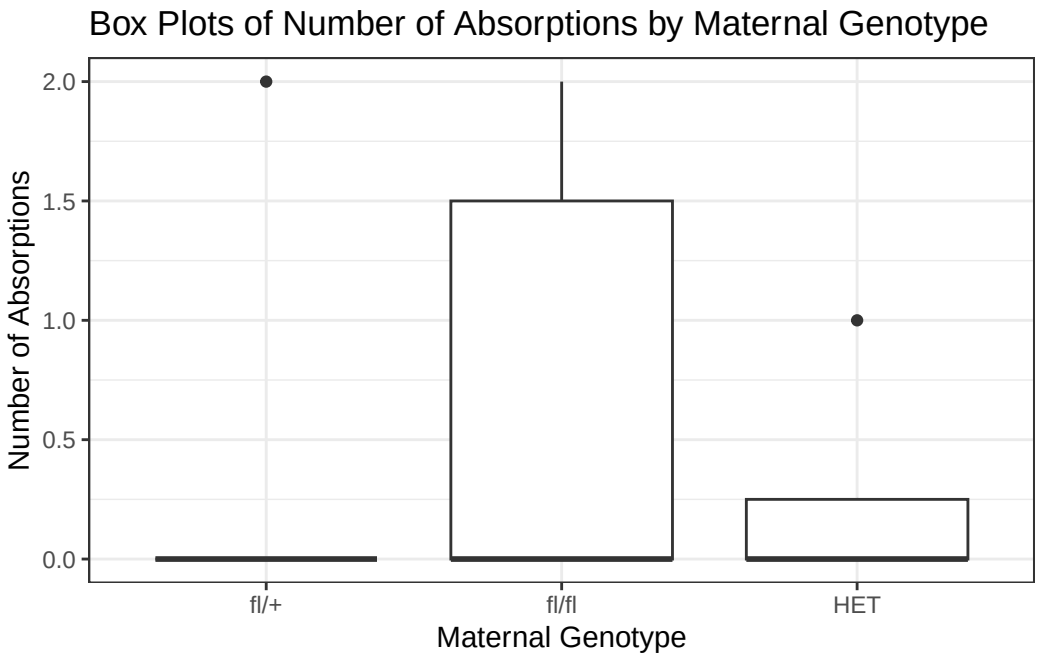


```r
model <- lm(num_fetus ~ Maternal_genotype, data=mother)

summary(model)
```

```
Call:
lm(formula = num_fetus ~ Maternal_genotype, data = mother)

Residuals:
    Min      1Q  Median      3Q     Max
-6.5714 -0.7625  0.3393  1.2125  3.4286

Coefficients:
                      Estimate Std. Error t value Pr(>|t|)
(Intercept)             7.8000     1.1453   6.810 1.24e-05 ***
Maternal_genotypefl/fl -0.2286     1.4996  -0.152    0.881
Maternal_genotypeHET   -0.0500     1.7180  -0.029    0.977
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.561 on 13 degrees of freedom
Multiple R-squared:  0.002027,  Adjusted R-squared:  -0.1515
F-statistic: 0.0132 on 2 and 13 DF,  p-value: 0.9869
```

No impact of maternal genotype on the # of fetus

```r
# Num Absorptions
ggplot(data = mother, aes(x = Maternal_genotype, y = absorptions)) +
  geom_boxplot() +
  xlab("Maternal Genotype") +
  ylab("Number of Absorptions") +
  ggtitle("Box Plots of Number of Absorptions by Maternal Genotype") +
  theme_bw()
```




```r
# Use poisson regression for count data
model <- glm(absorptions ~ Maternal_genotype, data=mother, family="poisson")

summary(model)
```

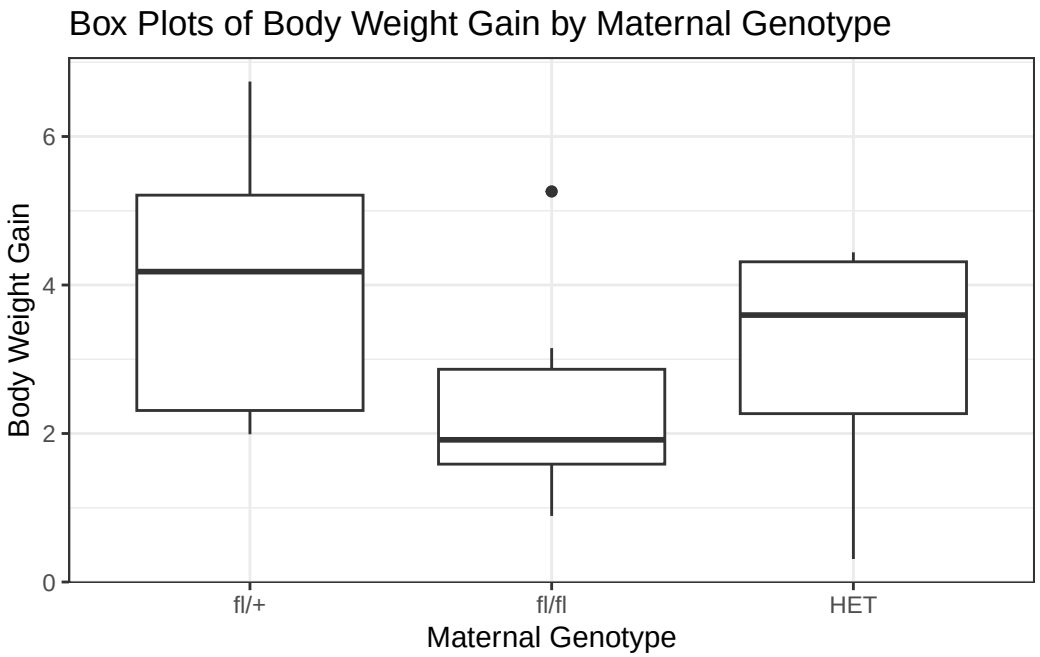
```
Call:
glm(formula = absorptions ~ Maternal_genotype, family = "poisson",
    data = mother)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.1952  -0.9696  -0.8008   0.5210   1.7994

Coefficients:
                      Estimate Std. Error z value Pr(>|z|)
(Intercept)            -0.9163     0.7071  -1.296    0.195
Maternal_genotypefl/fl  0.5798     0.8367   0.693    0.488
Maternal_genotypeHET   -0.4700     1.2247  -0.384    0.701

(Dispersion parameter for poisson family taken to be 1)
```

```
    Null deviance: 19.408  on 15  degrees of freedom
Residual deviance: 18.120  on 13  degrees of freedom
AIC: 35.961

Number of Fisher Scoring iterations: 6
```

No attributable effect of maternal genotype on number of absorptions, almost meaningless analysis though since there's very little data

```
# Body weight gain
ggplot(data = mother, aes(x = Maternal_genotype, y = body_weight_gain)) +
  geom_boxplot() +
  xlab("Maternal Genotype") +
  ylab("Body Weight Gain") +
  ggtitle("Box Plots of Body Weight Gain by Maternal Genotype") +
  theme_bw()
```

```
Warning: Removed 1 rows containing non-finite values (`stat_boxplot()`).
```

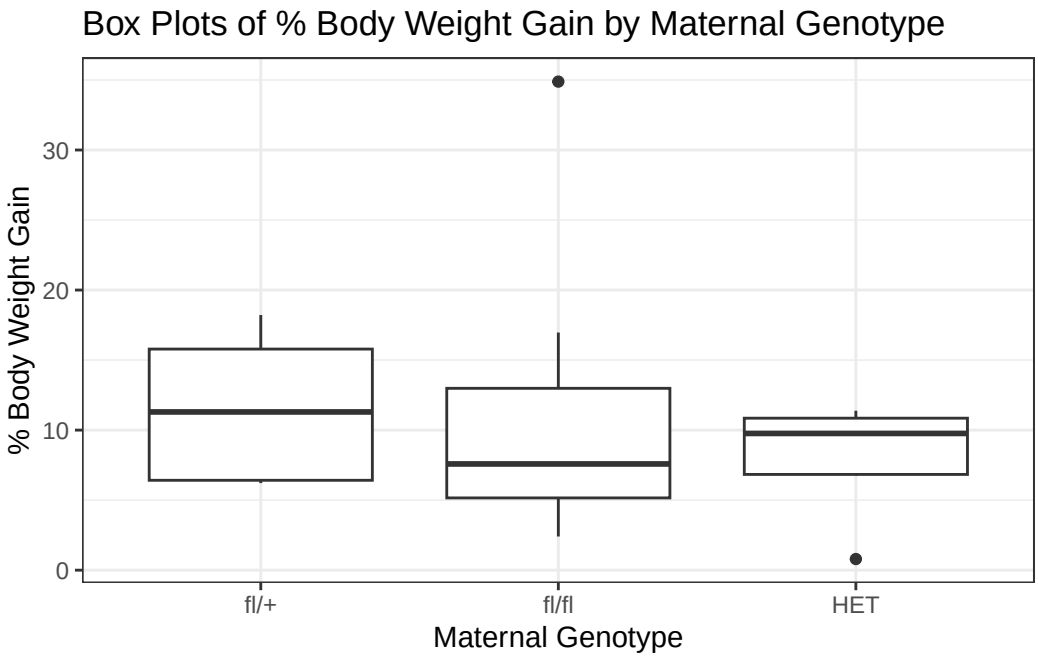


```r
model <- lm(body_weight_gain ~ Maternal_genotype, data=mother)

summary(model)
```

```
Call:
lm(formula = body_weight_gain ~ Maternal_genotype, data = mother)

Residuals:
   Min     1Q Median     3Q    Max
-2.675 -1.240 -0.065  1.204  2.820

Coefficients:
                      Estimate Std. Error t value Pr(>|t|)
(Intercept)             4.0860     0.8071   5.063 0.000279 ***
Maternal_genotypefl/fl -1.6460     1.0928  -1.506 0.157879
Maternal_genotypeHET   -1.1010     1.2106  -0.909 0.381027
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.805 on 12 degrees of freedom
  (1 observation deleted due to missingness)
Multiple R-squared:  0.1612,    Adjusted R-squared:  0.02138
F-statistic: 1.153 on 2 and 12 DF,  p-value: 0.3483
```

No significant effect of maternal genotype on body weight gain.

```r
# % body weight gain
ggplot(data = mother, aes(x = Maternal_genotype, y = percent_body_weight_gain)) +
  geom_boxplot() +
  xlab("Maternal Genotype") +
  ylab("% Body Weight Gain") +
  ggtitle("Box Plots of % Body Weight Gain by Maternal Genotype") +
  theme_bw()
```




```r
model <- lm(percent_body_weight_gain ~ Maternal_genotype, data=mother)

summary(model)
```

```
Call:
lm(formula = percent_body_weight_gain ~ Maternal_genotype, data = mother)

Residuals:
   Min     1Q Median     3Q    Max
-9.189 -5.489 -1.442  3.644 23.290

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)
(Intercept)           11.587362   3.823964   3.030  0.00966 **
Maternal_genotypefl/fl  0.006755   5.006744   0.001  0.99894
Maternal_genotypeHET   -3.661619   5.735946  -0.638  0.53432
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.551 on 13 degrees of freedom
Multiple R-squared:  0.04068,   Adjusted R-squared:  -0.1069
```

```
F-statistic: 0.2757 on 2 and 13 DF,  p-value: 0.7634
```

No significant effect of % bw gain.