

# Respiration Analysis

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## Initial Data Manipulation

```
# Read in data
resp <- read.csv("Fish_Measurement_Data_2.csv")

# Subset dataframe
df.resp <- subset(resp, select = c("Species", "Length_mm", "Weight_g",
                                   "Starting_DO_.ppm", "DO_30min_ppm",
                                   "Experimental_Treatment_C", "Bucket"))

# Remove all rows that have any NA's
df.respiration <- na.omit(df.resp)

# Calculate Respiration Rate
df.respiration$respirationrate <- (df.respiration$Starting_DO_.ppm-
                                   df.respiration$DO_30min_ppm)/30

# Take only positive values
df.respiration_pos <- df.respiration[df.respiration$respirationrate > 0, ]

# Subset data for the two species
copper <- df.respiration_pos[df.respiration_pos$Species=="Copper", ]
black <- df.respiration_pos[df.respiration_pos$Species %in%
                           c("Black", "Yellowtail", "Silver"), ]

# put in experimental treatment temperatures
black$exp_temp <- c(10.33846, 10.33846, 10.33846, 10.45769, 10.45769, 18.48462,
                  18.48462, 18.48462, 20.18269, 20.18269, 20.18269, 13.46111,
                  13.46111, 20.71346, 20.71346, 20.71346, 20.97308, 20.97308,
                  22.61731, 22.61731, 19.35962, 19.35962, 19.35962, 15.23462,
                  15.23462, 15.23462, 19.98462, 19.98462, 17.86923, 17.86923,
                  17.86923, 13.89808, 13.89808, 22.35682, 22.35682, 19.45192,
                  19.45192, 19.45192)

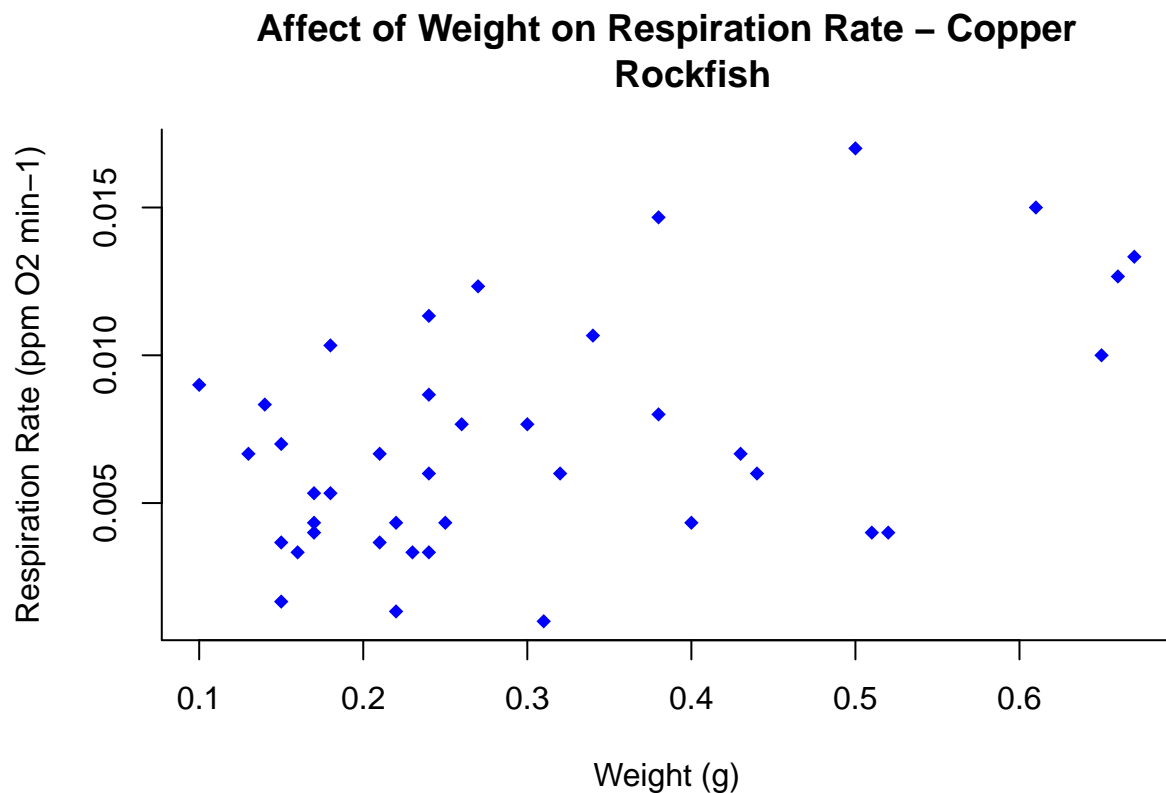
copper$exp_temp <- c(10.58704, 10.58704, 10.51111, 10.51111, 10.51111, 10.51111,
                  19.22222, 19.22222, 19.22222, 19.91852, 19.91852, 19.91852,
                  21.03333, 21.03333, 13.46111, 13.46111, 13.46111, 13.46111,
                  22.01296, 22.01296, 22.01296, 21.40741, 21.40741, 21.40741,
                  22.85417, 17.97037, 17.97037, 17.97037, 17.97037, 15.10000,
                  15.10000, 18.90926, 18.90926, 18.90926, 17.15000, 17.15000,
                  17.15000, 13.71667, 19.98889, 19.98889)
```

## Plotting & Analysis

### Copper Rockfish

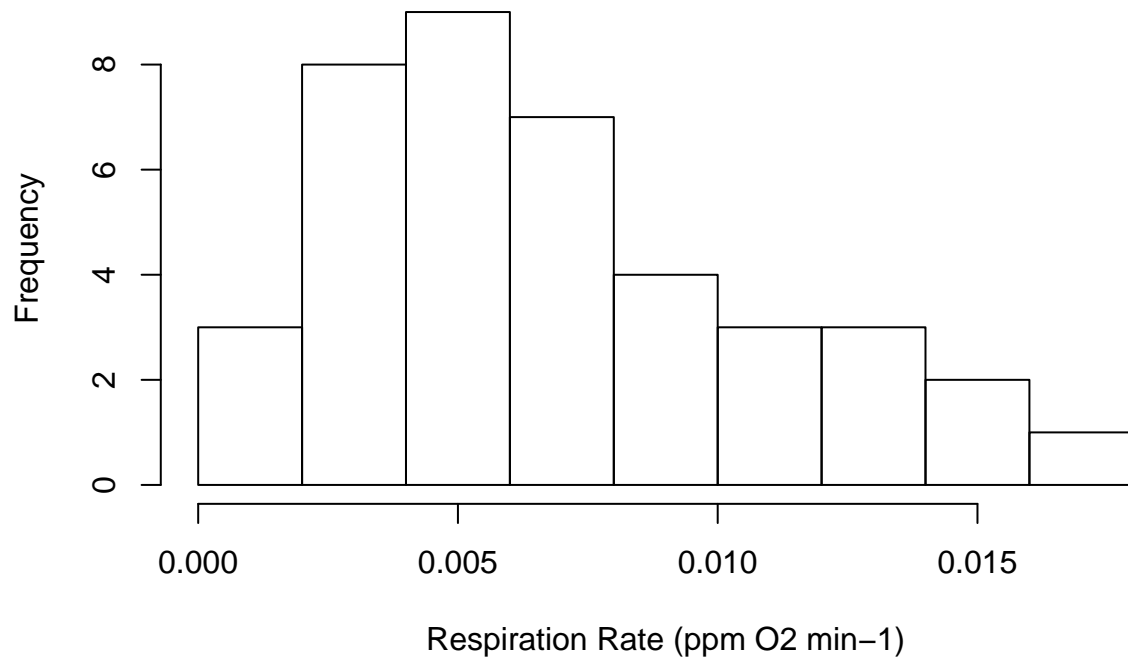
Method 1 - Finding Residuals of Respiration Rate vs Weight first, then plotting against treatment temperature

```
# Do an initial plot to determine the affect of weight on respiration rate  
plot(copper$respirationrate~copper$Weight_g, bty = "l", pch = 18,  
      col = "blue", main = "Affect of Weight on Respiration Rate - Copper  
      Rockfish", xlab = "Weight (g)", ylab = "Respiration Rate (ppm O2 min-1)")
```



```
# Look at distribution of data  
hist(copper$respirationrate, xlab = "Respiration Rate (ppm O2 min-1)")
```

### Histogram of copper\$respirationrate

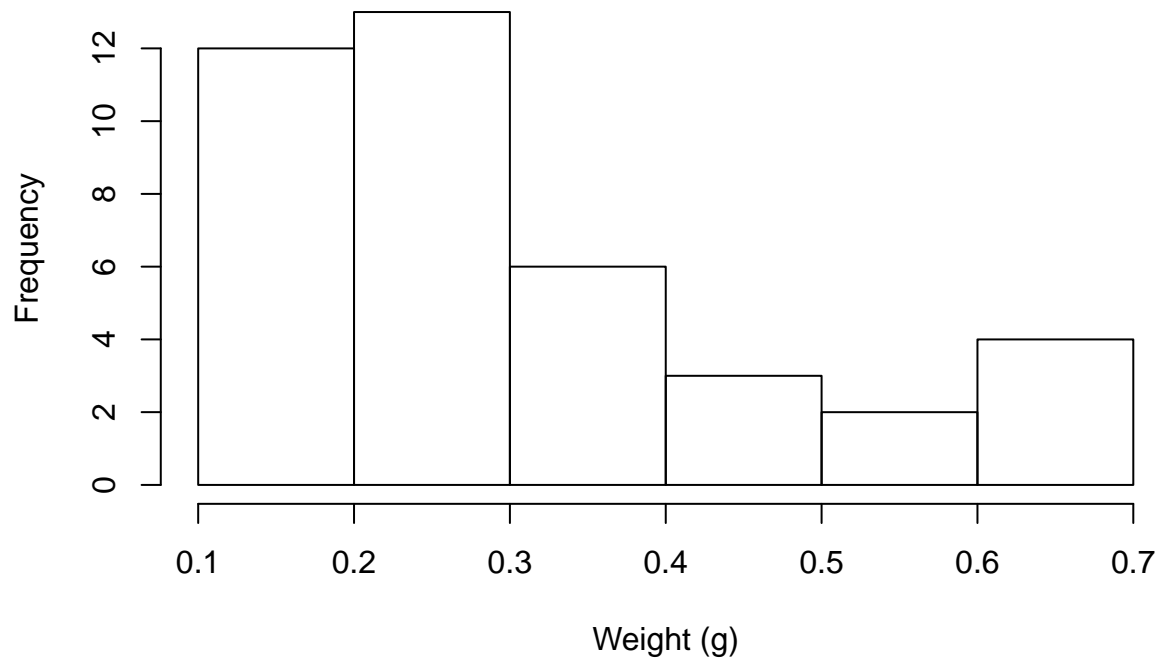


```
## Loading required package: ggplot2
```

```
## Warning: package 'ggplot2' was built under R version 3.2.3
```

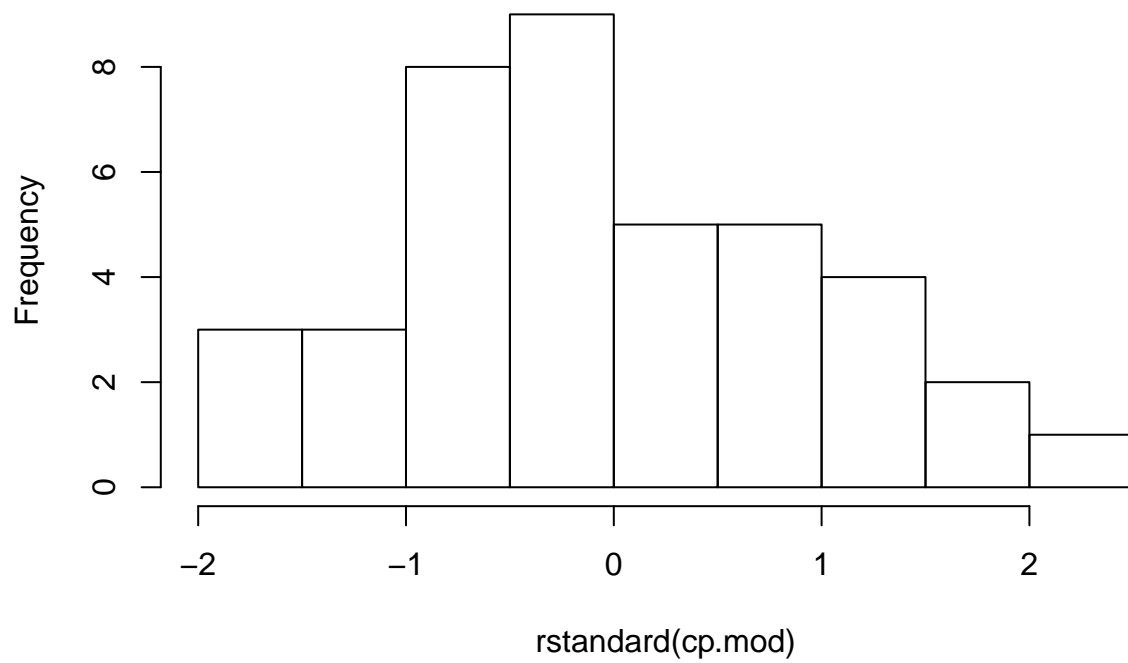
```
hist(copper$Weight_g, xlab = "Weight (g)")
```

**Histogram of copper\$Weight\_g**



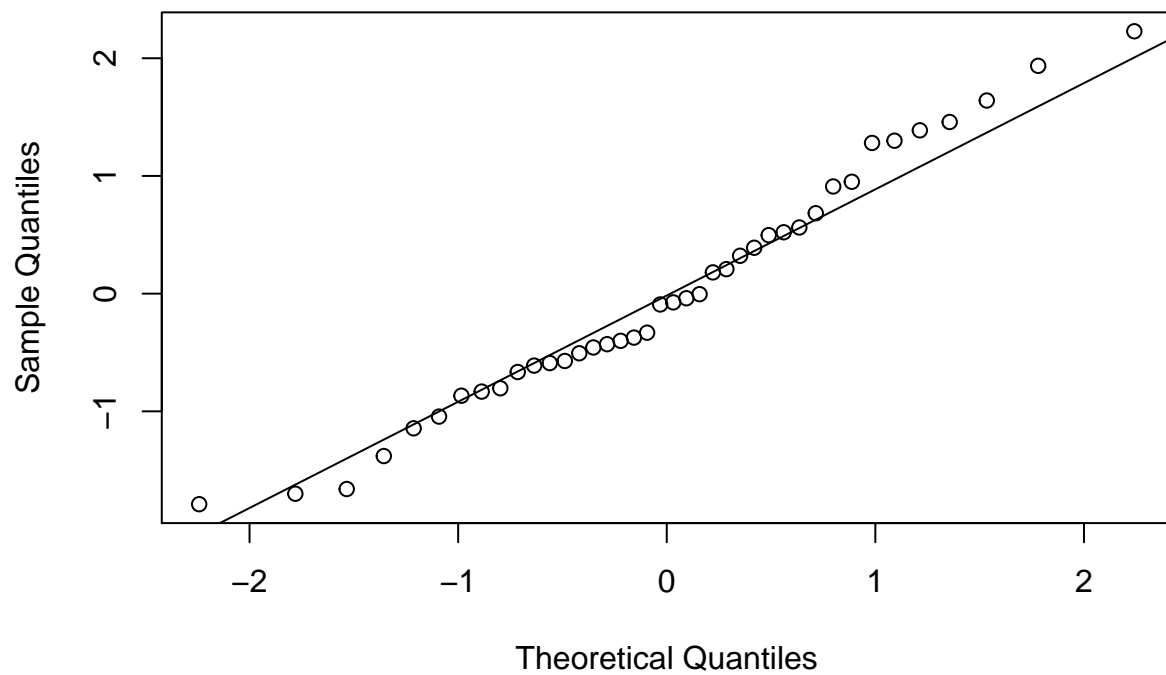
```
# Data has a right-skew - use logarithmic transformation??  
cp.mod <- lm(copper$respirationrate~copper$Weight_g)  
#Histogram of residuals  
hist(rstandard(cp.mod))
```

**Histogram of rstandard(cp.mod)**



```
#qqplot to test for normality in residuals  
qqnorm(rstandard(cp.mod))  
qqline(rstandard(cp.mod))
```

**Normal Q-Q Plot**

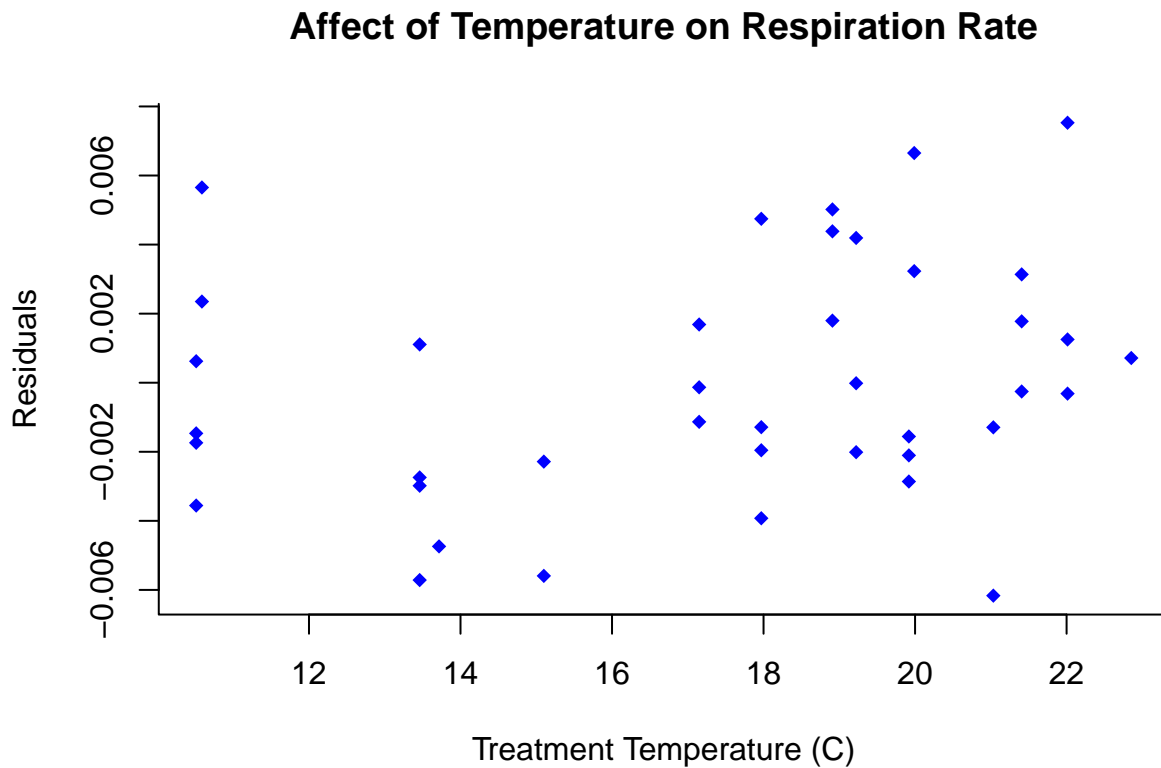


```
#Residuals of the model are normally distributed
```

```
# Get Residuals
```

```
copper$residuals <- resid(cp.mod)
```

```
plot(copper$residuals~copper$exp_temp, bty = "l", pch = 18, col = "blue",  
     main = "Affect of Temperature on Respiration Rate", xlab = "Treatment Temperature (C)",  
     ylab = "Residuals")
```



```
ggplot(copper, aes(x=exp_temp, y=residuals)) + labs(x = "Treatment Temperature (Celcius)", y = "Residuals")
```

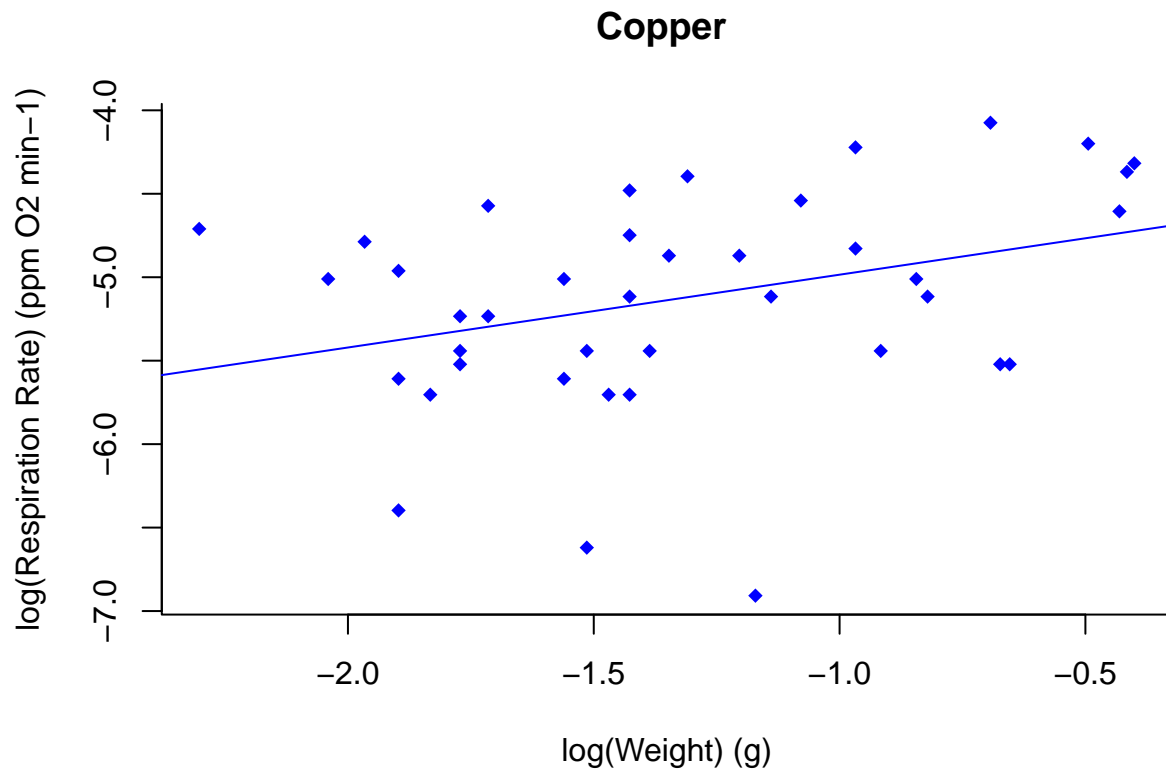


```

# Just to look at it: Plot log of each variable
plot(log(copper$respirationrate)~log(copper$Weight_g), bty = "l", pch = 18,
     col = "blue", main = "Copper ", xlab = "log(Weight) (g)",
     ylab = "log(Respiration Rate) (ppm O2 min-1)")

# Create linear model
cp.mod.1 <- lm(log(copper$respirationrate)~log(copper$Weight_g))
abline(lm(log(copper$respirationrate)~log(copper$Weight_g)), col = "blue")

```



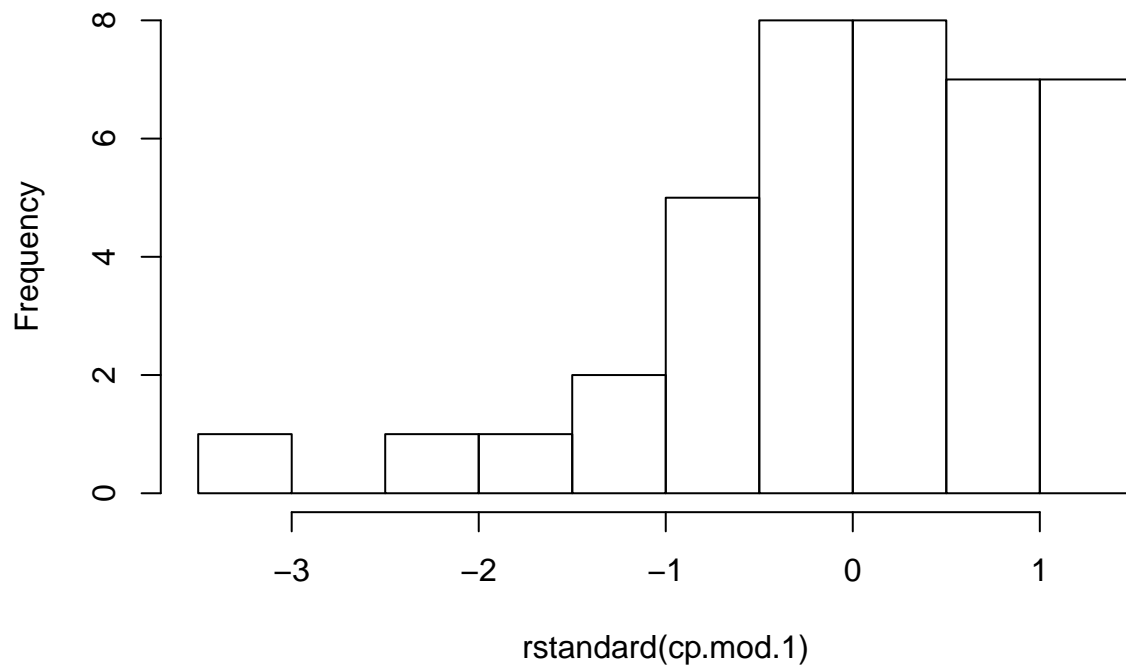
```

#Histogram of residuals
hist(rstandard(cp.mod.1))

```

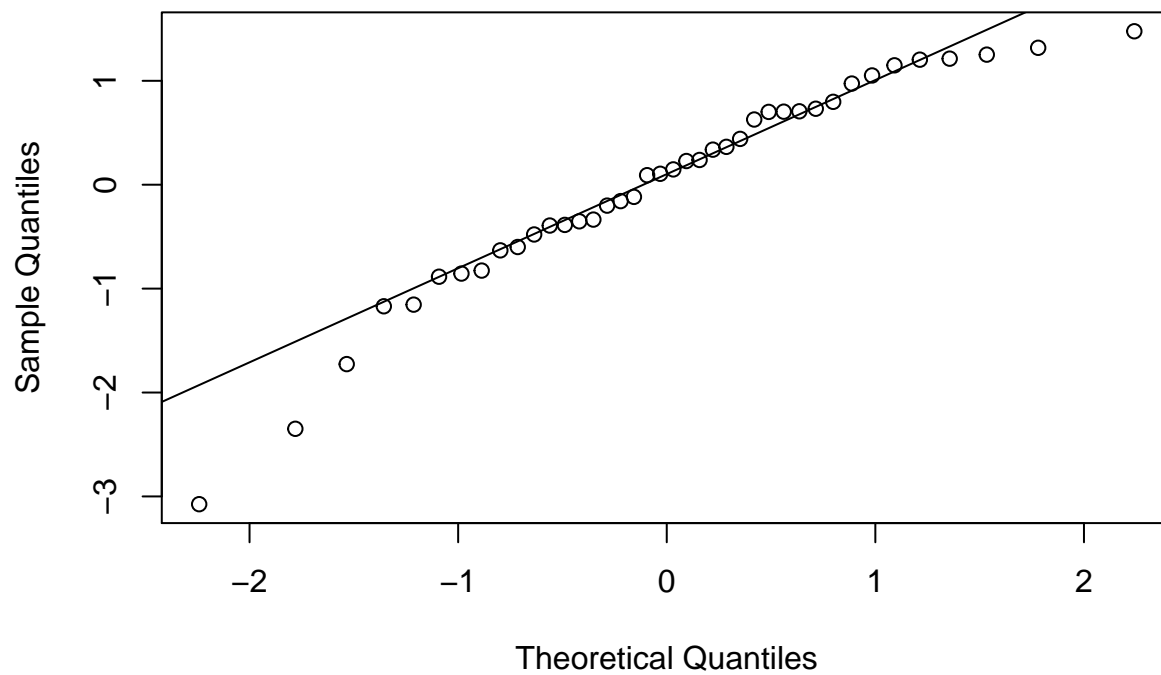


### Histogram of rstandard(cp.mod.1)



```
#qqplot to test for normality in residuals  
qqnorm(rstandard(cp.mod.1))  
qqline(rstandard(cp.mod.1))
```

### Normal Q-Q Plot



```
#Residuals of the model are not quite normally distributed
```

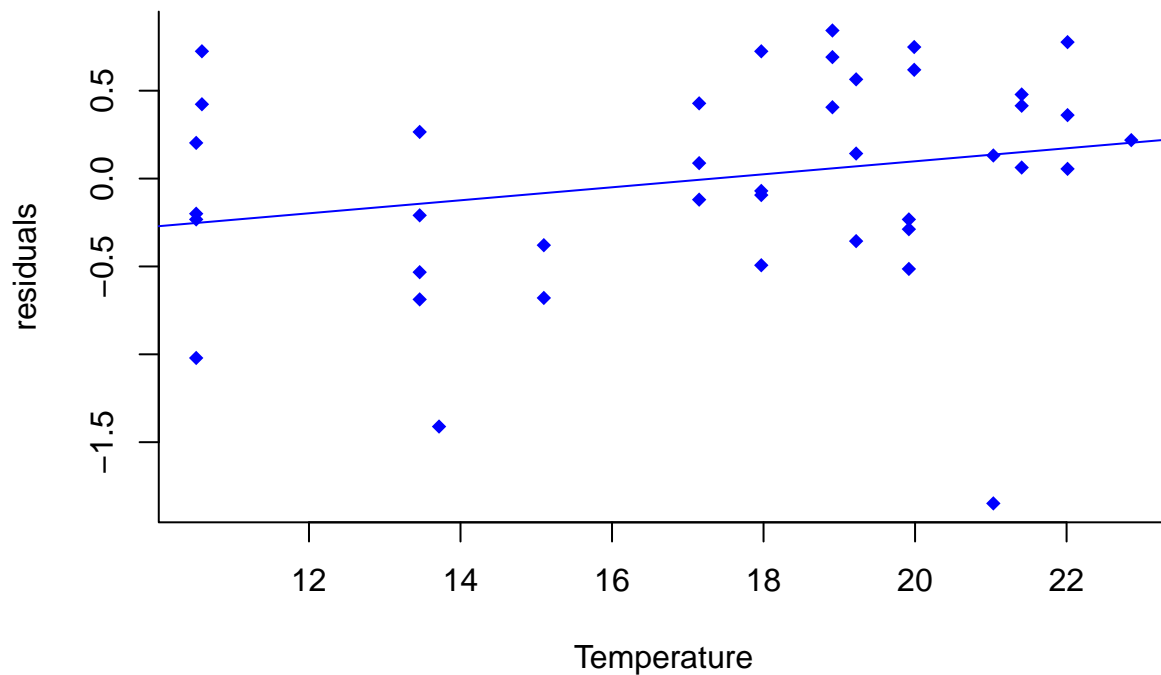
```
# Get the residuals of the model
```

```
copper$residuals <- resid(cp.mod.1)
```

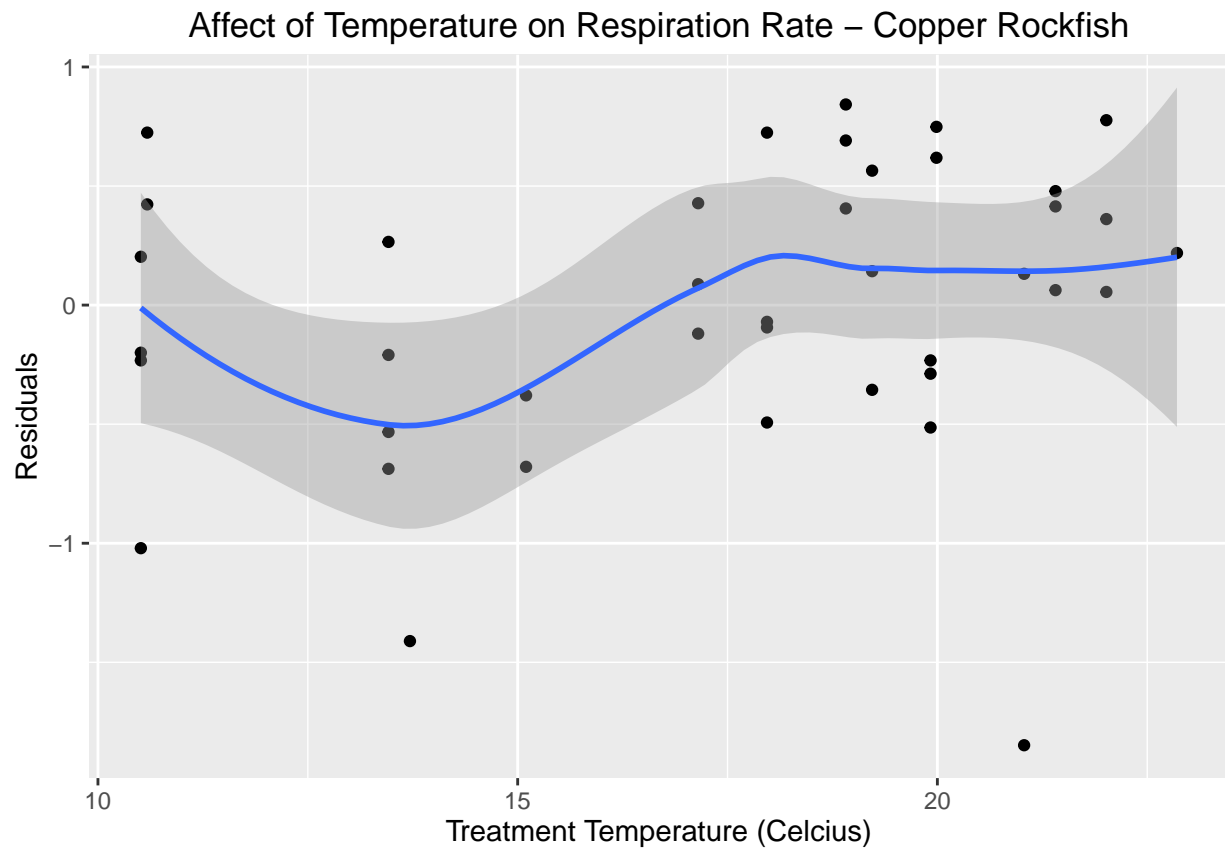
```
plot(copper$residuals~copper$exp_temp, bty = "l", pch = 18,  
     col = "blue", main = "Affect of Temperature on Respiration Rate - Copper",  
     xlab = "Temperature", ylab = "residuals")
```

```
abline(lm(copper$residuals~copper$exp_temp), col = "blue")
```

## Affect of Temperature on Respiration Rate – Copper



```
ggplot(copper, aes(x=exp_temp, y=residuals)) + labs(x = "Treatment Temperature (Celcius)", y = "Residuals")
```



## Models - AIC model selection

```
# Create full model
```

```
full.med1.cp.mod1 <- lm(copper$respirationrate~copper$exp_temp + I(copper$exp_temp^2) + copper$Weight_g  
summary(full.med1.cp.mod1)
```

```
##  
## Call:  
## lm(formula = copper$respirationrate ~ copper$exp_temp + I(copper$exp_temp^2) +  
##     copper$Weight_g)  
##  
## Residuals:  
##      Min       1Q   Median       3Q      Max   
## -0.0073647 -0.0021809 -0.0008446  0.0023816  0.0062611  
##  
## Coefficients:  
##              Estimate Std. Error t value Pr(>|t|)      
## (Intercept)    1.320e-02  1.088e-02   1.213  0.23300      
## copper$exp_temp -1.534e-03  1.396e-03  -1.099  0.27916      
## I(copper$exp_temp^2) 5.407e-05  4.274e-05   1.265  0.21393      
## copper$Weight_g    1.128e-02  3.466e-03   3.254  0.00248 **  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0034 on 36 degrees of freedom  
## Multiple R-squared:  0.317, Adjusted R-squared:  0.2601  
## F-statistic:  5.57 on 3 and 36 DF,  p-value: 0.003032
```

```
drop1(full.med1.cp.mod1)
```

```
## Single term deletions  
##  
## Model:  
## copper$respirationrate ~ copper$exp_temp + I(copper$exp_temp^2) +  
##     copper$Weight_g  
##           Df Sum of Sq      RSS      AIC  
## <none>                 0.00041624 -450.93  
## copper$exp_temp        1 1.3959e-05 0.00043020 -451.61  
## I(copper$exp_temp^2)    1 1.8508e-05 0.00043475 -451.18  
## copper$Weight_g        1 1.2240e-04 0.00053864 -442.61
```

```
# drop Weight
```

```
temp.med1.cp.mod2 <- lm(copper$respirationrate~copper$exp_temp + I(copper$exp_temp^2))  
summary(temp.med1.cp.mod2)
```

```
##  
## Call:  
## lm(formula = copper$respirationrate ~ copper$exp_temp + I(copper$exp_temp^2))  
##  
## Residuals:  
##      Min       1Q   Median       3Q      Max   
##
```

```
## -0.0075599 -0.0025492 -0.0007555 0.0019726 0.0077142
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.456e-02  1.220e-02   1.193   0.241
## copper$exp_temp -1.367e-03  1.565e-03  -0.873   0.388
## I(copper$exp_temp^2) 5.143e-05  4.795e-05   1.073   0.290
##
## Residual standard error: 0.003815 on 37 degrees of freedom
## Multiple R-squared: 0.1162, Adjusted R-squared: 0.06839
## F-statistic: 2.432 on 2 and 37 DF, p-value: 0.1018
```

```
drop1(temp.med1.cp.mod2)
```

```
## Single term deletions
##
## Model:
## copper$respirationrate ~ copper$exp_temp + I(copper$exp_temp^2)
##              Df Sum of Sq      RSS      AIC
## <none>                0.00053864 -442.61
## copper$exp_temp        1 1.1104e-05 0.00054975 -443.80
## I(copper$exp_temp^2)    1 1.6747e-05 0.00055539 -443.39
```

```
# This is the best model
```

```
# Just to see others: drop squared
```

```
temp.med1.cp.mod3 <- lm(copper$respirationrate~copper$exp_temp)
summary(temp.med1.cp.mod3)
```

```
##
## Call:
## lm(formula = copper$respirationrate ~ copper$exp_temp)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.0071950 -0.0026951 -0.0008371  0.0024344  0.0085079
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.0018158  0.0028008   0.648   0.521
## copper$exp_temp 0.0003033  0.0001577   1.923   0.062 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.003823 on 38 degrees of freedom
## Multiple R-squared: 0.08869, Adjusted R-squared: 0.06471
## F-statistic: 3.698 on 1 and 38 DF, p-value: 0.06199
```

```
# leave squared and drop non squared term
```

```
temp.med1.cp.mod4 <- lm(copper$respirationrate~I(copper$exp_temp^2))
summary(temp.med1.cp.mod4)
```

```
##
## Call:
## lm(formula = copper$respirationrate ~ I(copper$exp_temp^2))
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-0.0073153	-0.0025981	-0.0009075	0.0022954	0.0082729

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	3.995e-03	1.631e-03	2.450	0.0190 *
I(copper\$exp_temp^2)	9.765e-06	4.807e-06	2.031	0.0493 *

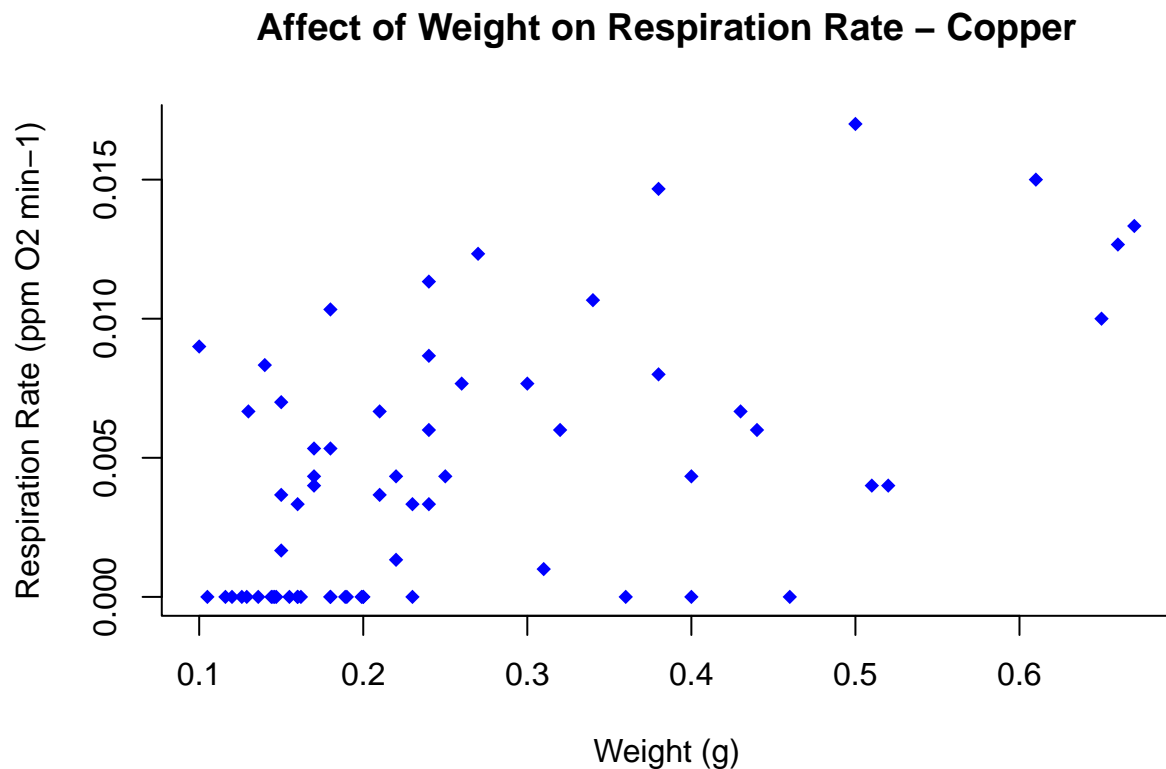
```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.003804 on 38 degrees of freedom
## Multiple R-squared:  0.09795,    Adjusted R-squared:  0.07421
## F-statistic: 4.126 on 1 and 38 DF,  p-value: 0.04926

### model 4 is significant
```

Method 2 - Same analysis, but with addition of zeros for those that died during the experiment

```
# Create dataframe with zero data
zeros.cp <- read.csv("zeros_cp.csv")
colnames(zeros.cp) <- c("Species", "Length_mm", "Weight_g", "Starting_DO_.ppm", "DO_30min_ppm", "Experiment")
copper.zeros <- rbind(copper, zeros.cp)

plot(copper.zeros$respirationrate~copper.zeros$Weight_g, bty = "n", pch = 18,
     col = "blue", main = "Affect of Weight on Respiration Rate - Copper",
     xlab = "Weight (g)", ylab = "Respiration Rate (ppm O2 min-1)" )
```

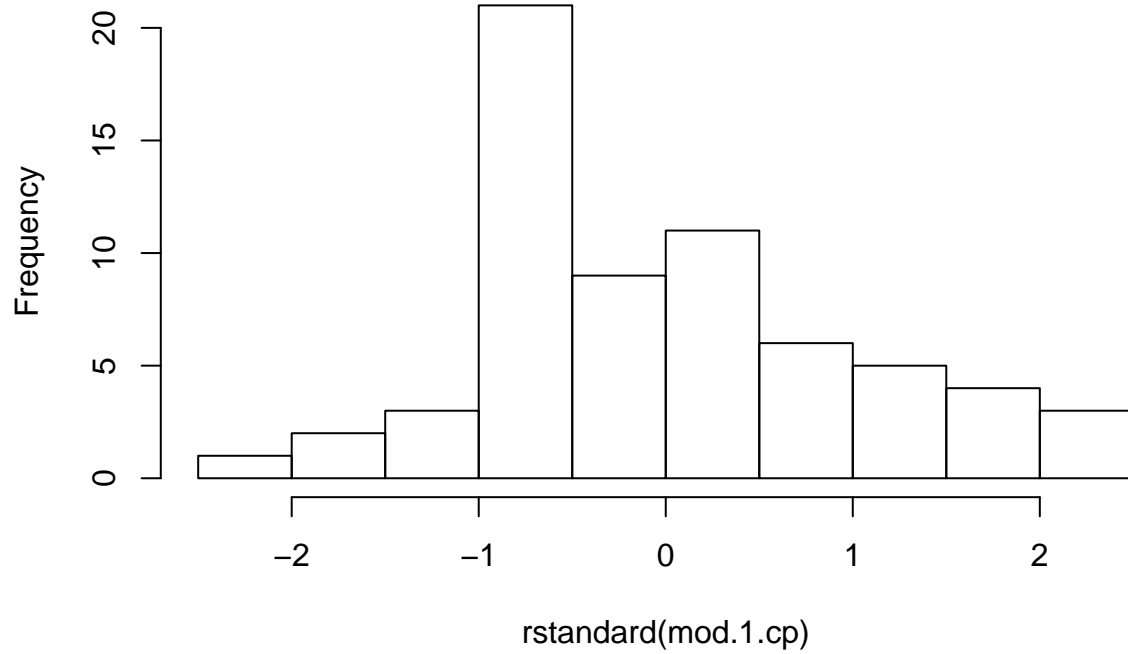


```
# cannot log transform the data because of zeros in data but may not be necessary due
# residuals being normally distributed

# created a linear model for non-transformed data
mod.1.cp <- lm(copper.zeros$respirationrate~copper.zeros$Weight_g)

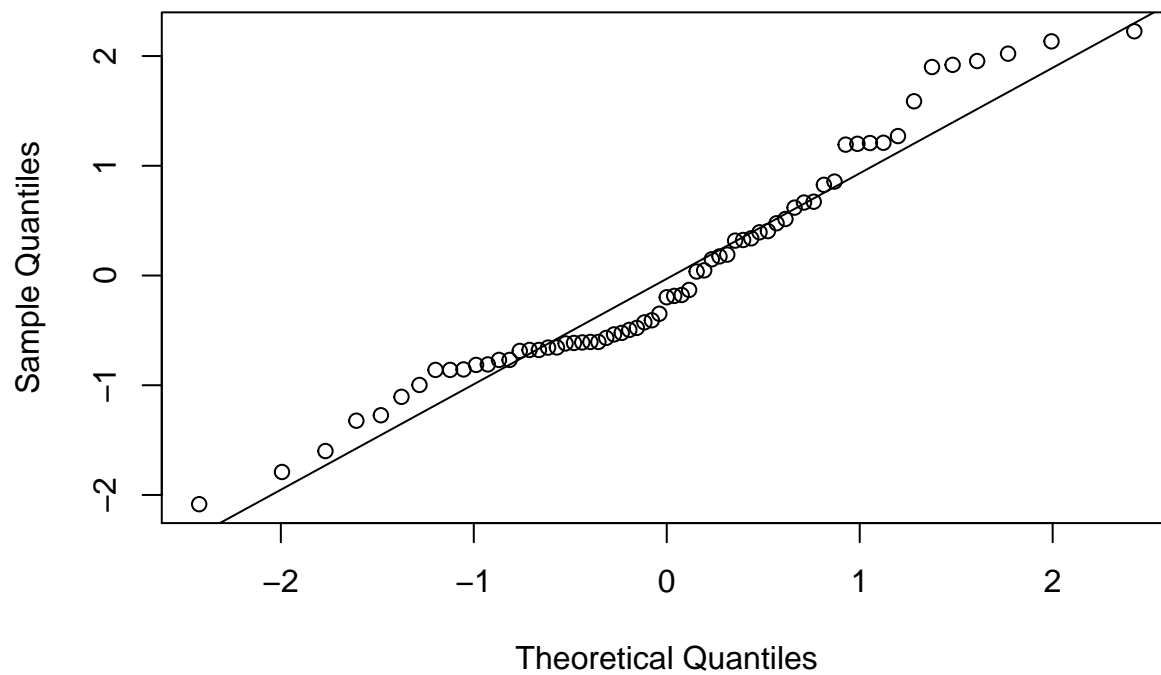
#Histogram of residuals
hist(rstandard(mod.1.cp))
```

### Histogram of rstandard(mod.1.cp)



```
#qqplot to test for normality in residuals  
qqnorm(rstandard(mod.1.cp))  
qqline(rstandard(mod.1.cp))
```

### Normal Q-Q Plot



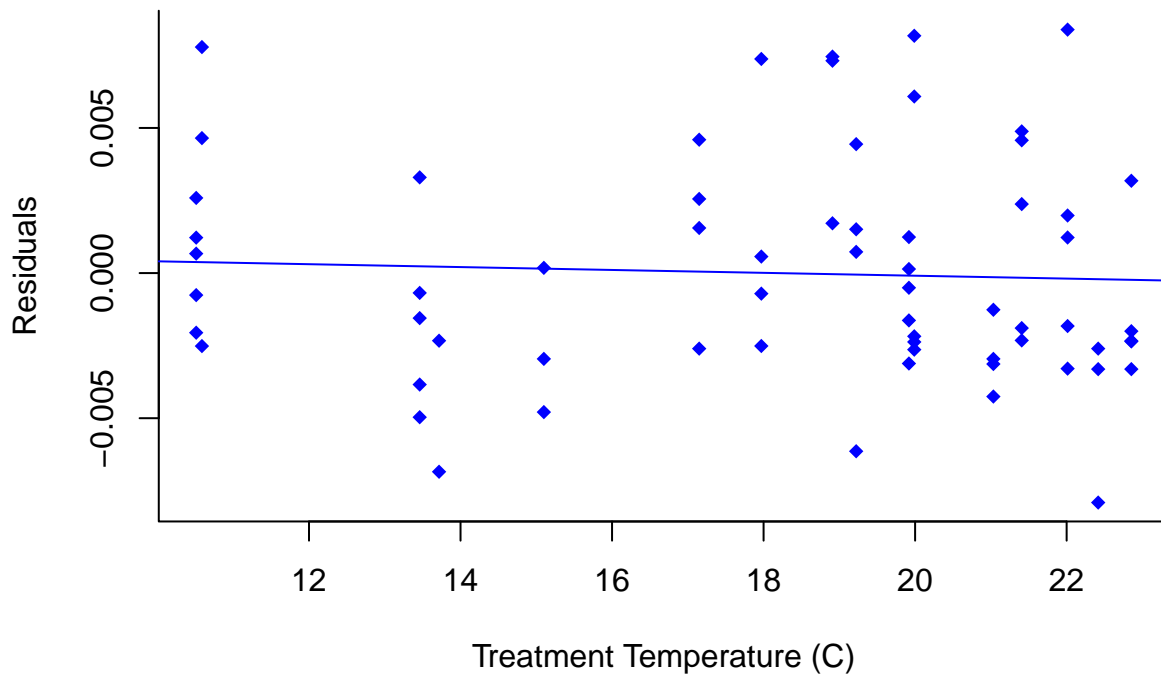


```
#Residuals of the model are normally distributed

# Plot the residuals
copper.zeros$residuals <- resid(mod.1.cp)
plot(copper.zeros$residuals~copper.zeros$exp_temp, bty = "l", pch = 18,
     col = "blue", main = "Affect of Temperature on Respiration Rate - Copper Rockfish",
     ylab = "Residuals", xlab = "Treatment Temperature (C)" )

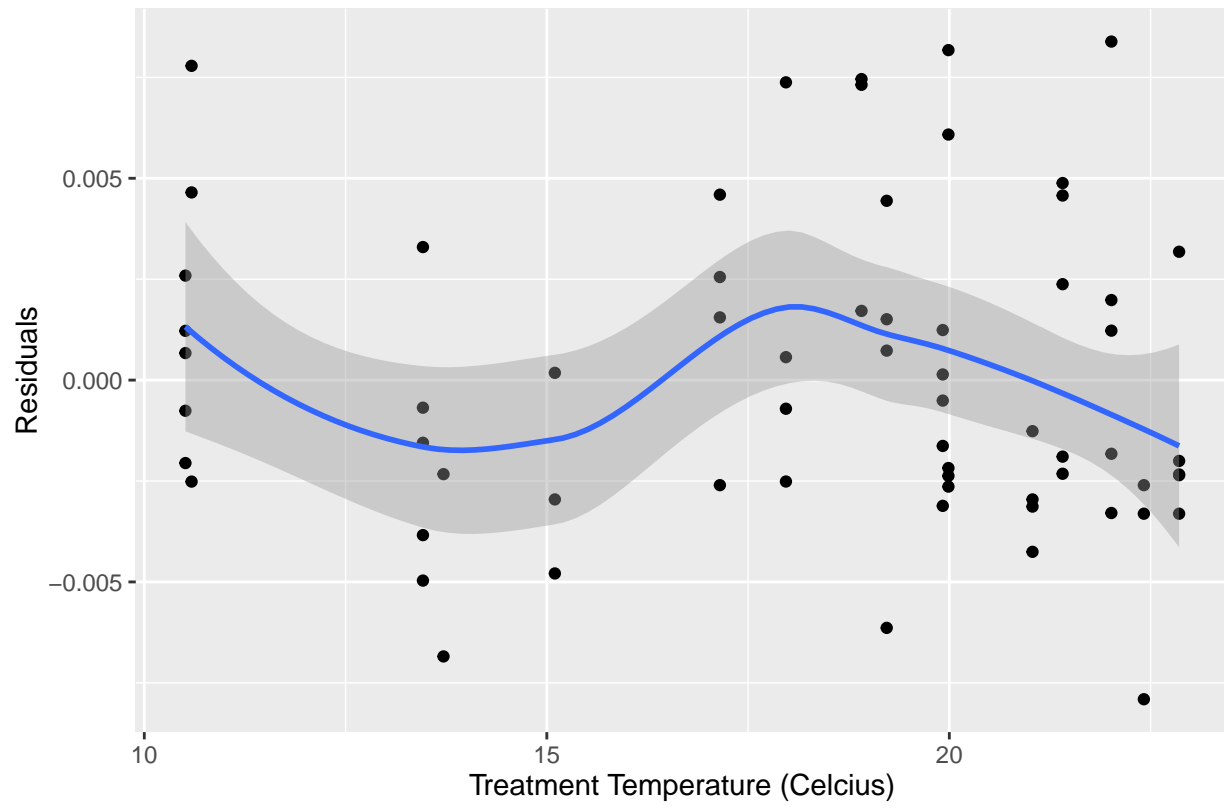
abline(lm(copper.zeros$residuals~copper.zeros$exp_temp), col = "blue")
```

## Affect of Temperature on Respiration Rate – Copper Rockfish



```
ggplot(copper.zeros, aes(x=exp_temp, y=residuals)) + labs(x = "Treatment Temperature (Celcius)", y = "R
```

Affect of Temperature on Respiration Rate – Copper Rockfish



## Models - AIC model selection

```
# model data
```

```
full.meth2.cp.mod1 <- lm(copper.zeros$respirationrate~copper.zeros$exp_temp + I(copper.zeros$exp_temp^2)
summary(full.meth2.cp.mod1)
```

```
##
## Call:
## lm(formula = copper.zeros$respirationrate ~ copper.zeros$exp_temp +
##     I(copper.zeros$exp_temp^2) + copper.zeros$Weight_g)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.0073746 -0.0027169 -0.0009926  0.0023547  0.0088314
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -3.818e-03  9.857e-03  -0.387    0.700
## copper.zeros$exp_temp    5.347e-04  1.246e-03   0.429    0.669
## I(copper.zeros$exp_temp^2) -1.750e-05  3.716e-05  -0.471    0.639
## copper.zeros$Weight_g    1.740e-02  3.399e-03   5.118 3.32e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.003932 on 61 degrees of freedom
## Multiple R-squared:  0.3163, Adjusted R-squared:  0.2827
## F-statistic: 9.406 on 3 and 61 DF,  p-value: 3.371e-05
```

```
drop1(full.meth2.cp.mod1)
```

```
## Single term deletions
##
## Model:
## copper.zeros$respirationrate ~ copper.zeros$exp_temp + I(copper.zeros$exp_temp^2) +
##     copper.zeros$Weight_g
##              Df Sum of Sq      RSS      AIC
## <none>                 0.00094320 -716.14
## copper.zeros$exp_temp    1 0.00000284 0.00094604 -717.94
## I(copper.zeros$exp_temp^2) 1 0.00000343 0.00094663 -717.90
## copper.zeros$Weight_g    1 0.00040508 0.00134828 -694.92
```

```
# drop Weight
```

```
temp.med2.cp.mod2 <- lm(copper.zeros$respirationrate~copper.zeros$exp_temp + I(copper.zeros$exp_temp^2)
summary(temp.med2.cp.mod2)
```

```
##
## Call:
## lm(formula = copper.zeros$respirationrate ~ copper.zeros$exp_temp +
##     I(copper.zeros$exp_temp^2))
##
## Residuals:
```

```
##           Min           1Q       Median           3Q           Max
## -0.005275 -0.003702 -0.001272  0.003048  0.013382
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -7.566e-03  1.166e-02  -0.649    0.519
## copper.zeros$exp_temp      1.598e-03  1.458e-03   1.096    0.277
## I(copper.zeros$exp_temp^2) -4.949e-05  4.344e-05  -1.139    0.259
##
## Residual standard error: 0.004663 on 62 degrees of freedom
## Multiple R-squared:  0.02265,    Adjusted R-squared:  -0.008874
## F-statistic: 0.7185 on 2 and 62 DF,  p-value: 0.4915
```

```
drop1(temp.med2.cp.mod2)
```

```
## Single term deletions
##
## Model:
## copper.zeros$respirationrate ~ copper.zeros$exp_temp + I(copper.zeros$exp_temp^2)
##               Df Sum of Sq      RSS      AIC
## <none>                        0.0013483 -694.92
## copper.zeros$exp_temp      1 2.6127e-05 0.0013744 -695.67
## I(copper.zeros$exp_temp^2)  1 2.8232e-05 0.0013765 -695.57
```

```
# This is the best model
```

```
# Just to see others: drop squared
```

```
temp.med2.cp.mod3 <- lm(copper.zeros$respirationrate~copper.zeros$exp_temp)
summary(temp.med2.cp.mod3)
```

```
##
## Call:
## lm(formula = copper.zeros$respirationrate ~ copper.zeros$exp_temp)
##
## Residuals:
##           Min           1Q       Median           3Q           Max
## -0.0047724 -0.0041435 -0.0007724  0.0028234  0.0128565
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      5.347e-03  2.734e-03   1.956    0.055 .
## copper.zeros$exp_temp -5.468e-05  1.471e-04  -0.372    0.711
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.004674 on 63 degrees of freedom
## Multiple R-squared:  0.002188,    Adjusted R-squared:  -0.01365
## F-statistic: 0.1382 on 1 and 63 DF,  p-value: 0.7114
```

```
# leave squared and drop non squared term
```

```
temp.med2.cp.mod4 <- lm(copper.zeros$respirationrate~I(copper.zeros$exp_temp^2))
summary(temp.med2.cp.mod4)
```

```
##
## Call:
## lm(formula = copper.zeros$respirationrate ~ I(copper.zeros$exp_temp^2))
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-0.0048528	-0.0040586	-0.0008528	0.0028138	0.0129414

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	5.087e-03	1.621e-03	3.139	0.00258 **
I(copper.zeros\$exp_temp^2)	-2.123e-06	4.381e-06	-0.485	0.62961

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.004671 on 63 degrees of freedom
## Multiple R-squared:  0.003714,    Adjusted R-squared:  -0.0121
## F-statistic: 0.2349 on 1 and 63 DF,  p-value: 0.6296

### nothing is significant
```

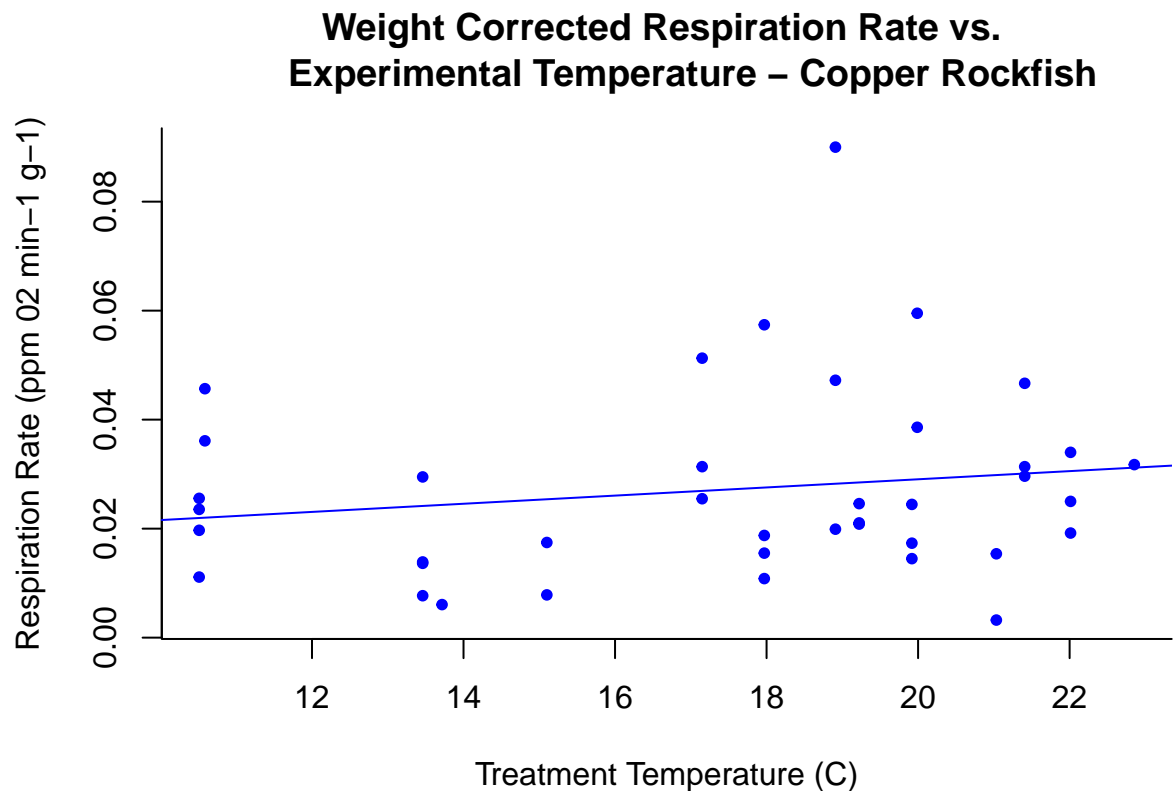
### Method 3 - Weight Correct Respiration Rate first without zeros

```
# Correct respiration rate with individual weight
copper$corr.resp.rate <- copper$respirationrate/copper$Weight_g

# Plot corrected respiration rate against treatment temperature
plot(copper$corr.resp.rate~copper$exp_temp, bty = "l", pch = 20,
     col = "blue", main = "Weight Corrected Respiration Rate vs.
     Experimental Temperature - Copper Rockfish",
     xlab = "Treatment Temperature (C)",
     ylab = "Respiration Rate (ppm O2 min-1 g-1)")

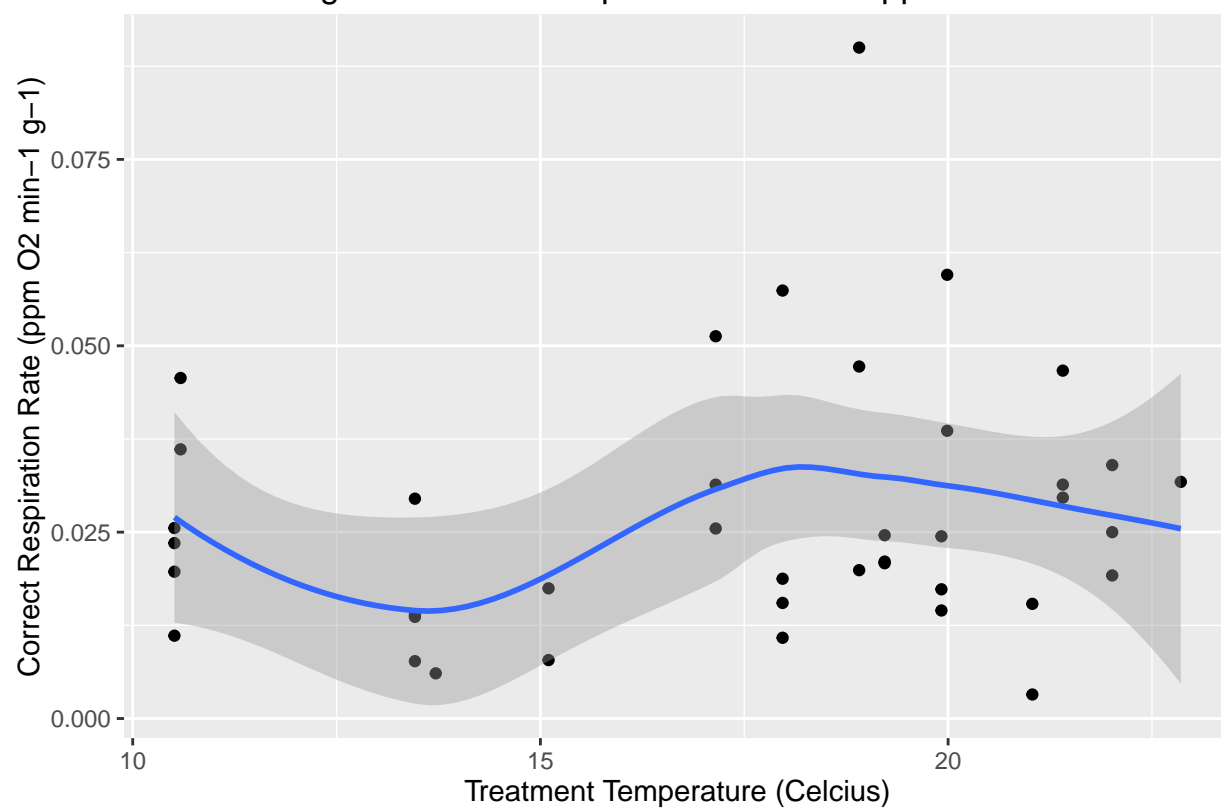
# Fit linear model to data
mod.3.cp <- lm(copper$corr.resp.rate~copper$exp_temp)

# Plot linear model on graph
abline(mod.3.cp, col = "blue")
```



```
# Use General Additive Model
ggplot(copper, aes(x=exp_temp, y=corr.resp.rate)) + labs(x = "Treatment Temperature (Celcius)", y = "Co
```

Weight Corrected Respiration Rate – Copper Rockfish



## Models - AIC model selection

```
# Create full model
full.med3.cp.mod1 <- lm(copper$corr.resp.rate~copper$exp_temp + I(copper$exp_temp^2))
summary(full.med3.cp.mod1)
```

```
##
## Call:
## lm(formula = copper$corr.resp.rate ~ copper$exp_temp + I(copper$exp_temp^2))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.026759 -0.011313 -0.004114  0.004963  0.061954
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.954e-02  5.577e-02   0.350   0.728
## copper$exp_temp    3.354e-05  7.152e-03   0.005   0.996
## I(copper$exp_temp^2) 2.201e-05  2.191e-04   0.100   0.921
##
## Residual standard error: 0.01744 on 37 degrees of freedom
## Multiple R-squared:  0.02869,    Adjusted R-squared:  -0.02382
## F-statistic: 0.5464 on 2 and 37 DF,  p-value: 0.5837
```

```
drop1(full.med3.cp.mod1)
```

```
## Single term deletions
##
## Model:
## copper$corr.resp.rate ~ copper$exp_temp + I(copper$exp_temp^2)
##              Df Sum of Sq    RSS    AIC
## <none>                 0.011248 -321.06
## copper$exp_temp        1 6.6900e-09 0.011248 -323.06
## I(copper$exp_temp^2)    1 3.0683e-06 0.011251 -323.05
```

```
# This is the best model
```

```
# Just to see others: drop squared
temp.med3.cp.mod2 <- lm(copper$corr.resp.rate~copper$exp_temp)
summary(temp.med3.cp.mod2)
```

```
##
## Call:
## lm(formula = copper$corr.resp.rate ~ copper$exp_temp)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.026603 -0.010974 -0.004216  0.004669  0.061761
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```



```
## (Intercept)      0.0140871  0.0126062   1.117    0.271
## copper$exp_temp  0.0007484  0.0007098   1.054    0.298
##
## Residual standard error: 0.01721 on 38 degrees of freedom
## Multiple R-squared:  0.02842,    Adjusted R-squared:  0.002853
## F-statistic: 1.112 on 1 and 38 DF,  p-value: 0.2984

# leave squared and drop non squared term
temp.med3.cp.mod3 <- lm(copper$corr.resp.rate~I(copper$exp_temp^2))
summary(temp.med3.cp.mod3)

##
## Call:
## lm(formula = copper$corr.resp.rate ~ I(copper$exp_temp^2))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.026765 -0.011327 -0.004108  0.004976  0.061963
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.980e-02  7.378e-03   2.684   0.0107 *
## I(copper$exp_temp^2) 2.304e-05  2.174e-05   1.059   0.2961
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0172 on 38 degrees of freedom
## Multiple R-squared:  0.02869,    Adjusted R-squared:  0.003125
## F-statistic: 1.122 on 1 and 38 DF,  p-value: 0.2961
```

## Method 4 - Weight Correct Respiration Rate first with zeros

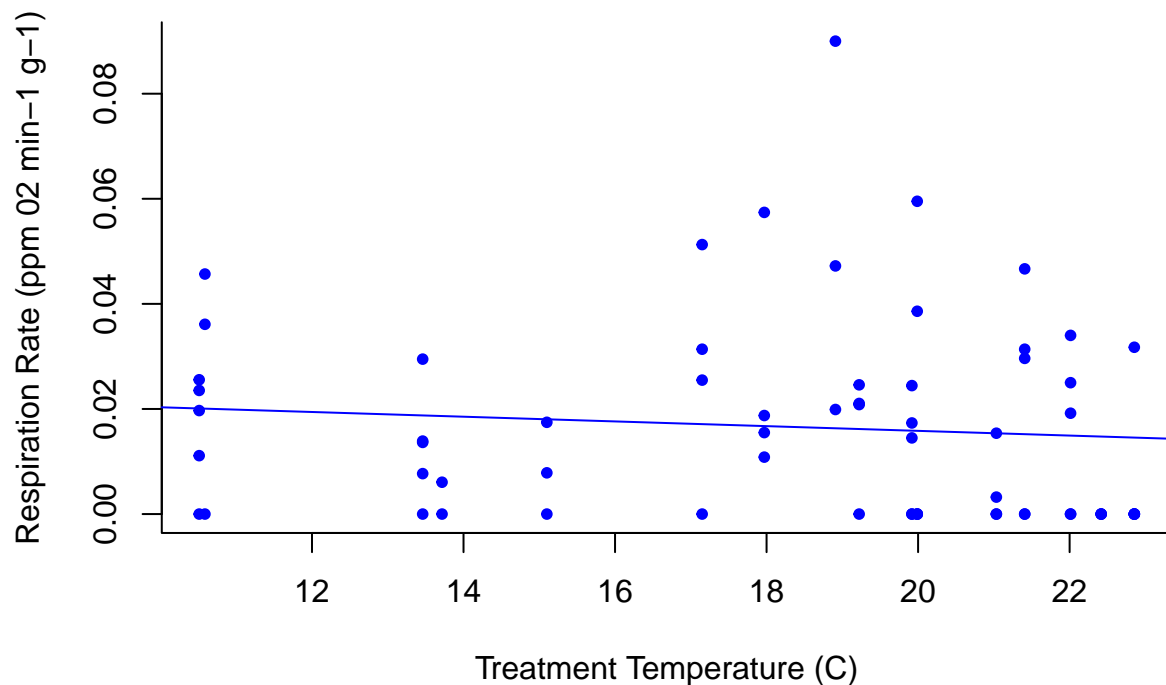
```
# Correct respiration rate with individual weight
copper.zeros$corr.resp.rate <- copper.zeros$respirationrate/copper.zeros$Weight_g

# Plot corrected respiration rate against treatment temperature
plot(copper.zeros$corr.resp.rate~copper.zeros$exp_temp, bty = "l", pch = 20,
     col = "blue", main = "Weight Corrected Respiration Rate vs.
     Experimental Temperature - Copper Rockfish",
     xlab = "Treatment Temperature (C)",
     ylab = "Respiration Rate (ppm O2 min-1 g-1)")

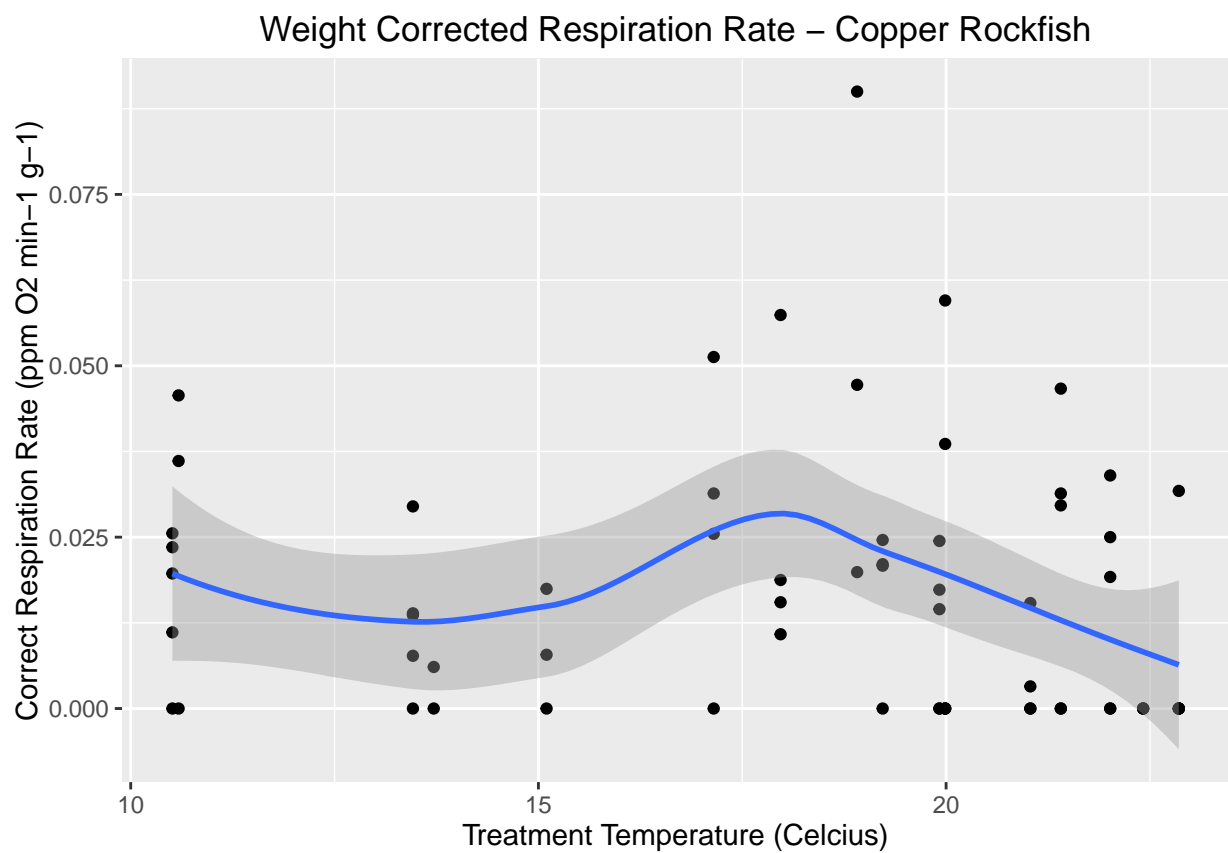
# Fit linear model to data
mod.4.cp <- lm(copper.zeros$corr.resp.rate~copper.zeros$exp_temp)

# Plot linear model on graph
abline(mod.4.cp, col = "blue")
```

### Weight Corrected Respiration Rate vs. Experimental Temperature – Copper Rockfish



```
# Use General Additive Model
ggplot(copper.zeros, aes(x=exp_temp, y=corr.resp.rate)) + labs(x = "Treatment Temperature (Celcius)", y =
```



## Models - AIC model selection

```
# Create full model
```

```
full.med4.cp.mod1 <- lm(copper.zeros$corr.resp.rate~copper.zeros$exp_temp + I(copper.zeros$exp_temp^2))  
summary(full.med4.cp.mod1)
```

```
##  
## Call:  
## lm(formula = copper.zeros$corr.resp.rate ~ copper.zeros$exp_temp +  
##     I(copper.zeros$exp_temp^2))  
##  
## Residuals:  
##      Min       1Q   Median       3Q      Max   
## -0.022071 -0.013993 -0.005518  0.008894  0.070274   
##  
## Coefficients:  
##              Estimate Std. Error t value Pr(>|t|)      
## (Intercept)    -0.0446598   0.0469042  -0.952    0.345      
## copper.zeros$exp_temp      0.0084399   0.0058647   1.439    0.155      
## I(copper.zeros$exp_temp^2) -0.0002663   0.0001748  -1.523    0.133      
##  
## Residual standard error: 0.01876 on 62 degrees of freedom  
## Multiple R-squared:  0.04466,    Adjusted R-squared:  0.01384   
## F-statistic: 1.449 on 2 and 62 DF,  p-value: 0.2426
```

```
drop1(full.med4.cp.mod1)
```

```
## Single term deletions  
##  
## Model:  
## copper.zeros$corr.resp.rate ~ copper.zeros$exp_temp + I(copper.zeros$exp_temp^2)  
##              Df Sum of Sq    RSS    AIC  
## <none>                 0.021829 -513.93  
## copper.zeros$exp_temp    1 0.00072917 0.022559 -513.79  
## I(copper.zeros$exp_temp^2) 1 0.00081707 0.022646 -513.54
```

```
# This is the best model
```

```
# Just to see others: drop squared
```

```
temp.med4.cp.mod2 <- lm(copper.zeros$corr.resp.rate~copper.zeros$exp_temp)  
summary(temp.med4.cp.mod2)
```

```
##  
## Call:  
## lm(formula = copper.zeros$corr.resp.rate ~ copper.zeros$exp_temp)  
##  
## Residuals:  
##      Min       1Q   Median       3Q      Max   
## -0.020091 -0.014928 -0.004878  0.008576  0.073679   
##  
## Coefficients:
```

```
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.0248085  0.0110910   2.237  0.0288 *
## copper.zeros$exp_temp -0.0004488  0.0005967  -0.752  0.4547
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01896 on 63 degrees of freedom
## Multiple R-squared:  0.008901,    Adjusted R-squared:  -0.00683
## F-statistic: 0.5658 on 1 and 63 DF,  p-value: 0.4547

# leave squared and drop non squared term
temp.med4.cp.mod3 <- lm(copper.zeros$corr.resp.rate~I(copper.zeros$exp_temp^2))
summary(temp.med4.cp.mod3)

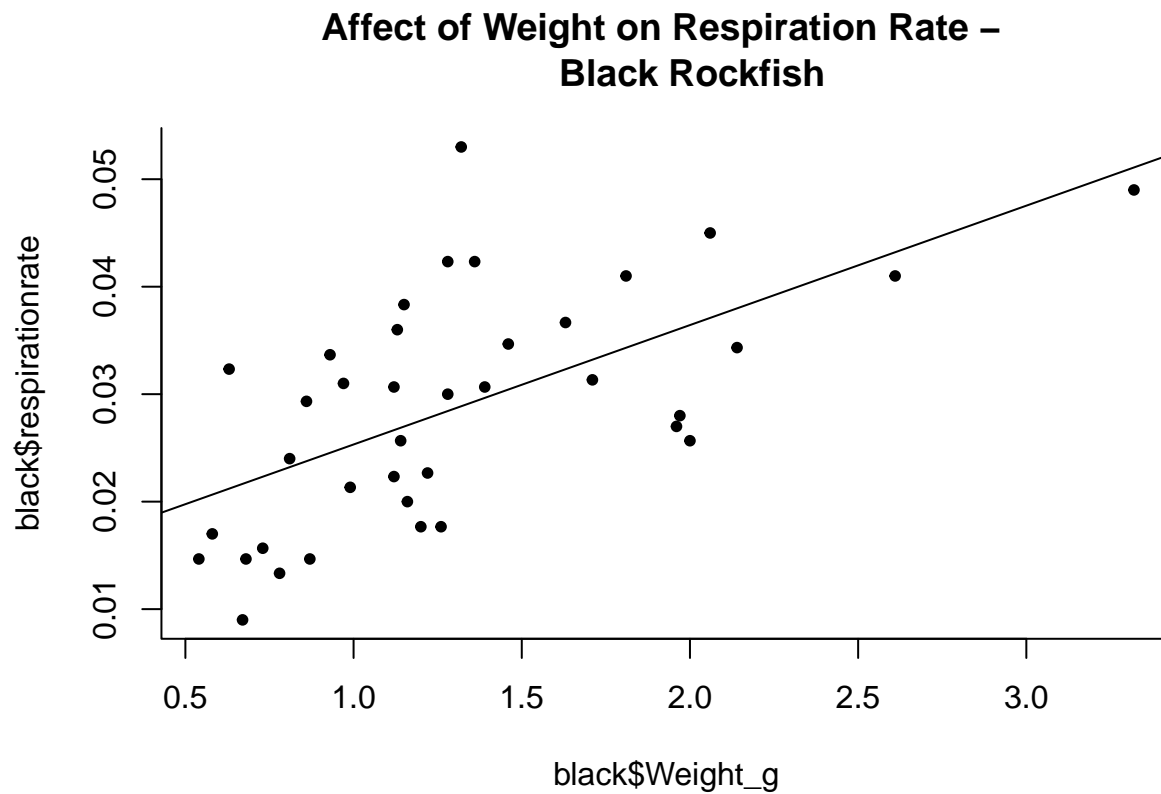
##
## Call:
## lm(formula = copper.zeros$corr.resp.rate ~ I(copper.zeros$exp_temp^2))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.020418 -0.014429 -0.005397  0.008609  0.073537
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.219e-02  6.566e-03   3.379  0.00125 **
## I(copper.zeros$exp_temp^2) -1.601e-05  1.775e-05  -0.902  0.37052
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01892 on 63 degrees of freedom
## Multiple R-squared:  0.01275,    Adjusted R-squared:  -0.002922
## F-statistic: 0.8135 on 1 and 63 DF,  p-value: 0.3705

### Nothing is significant
```

## Black Rockfish

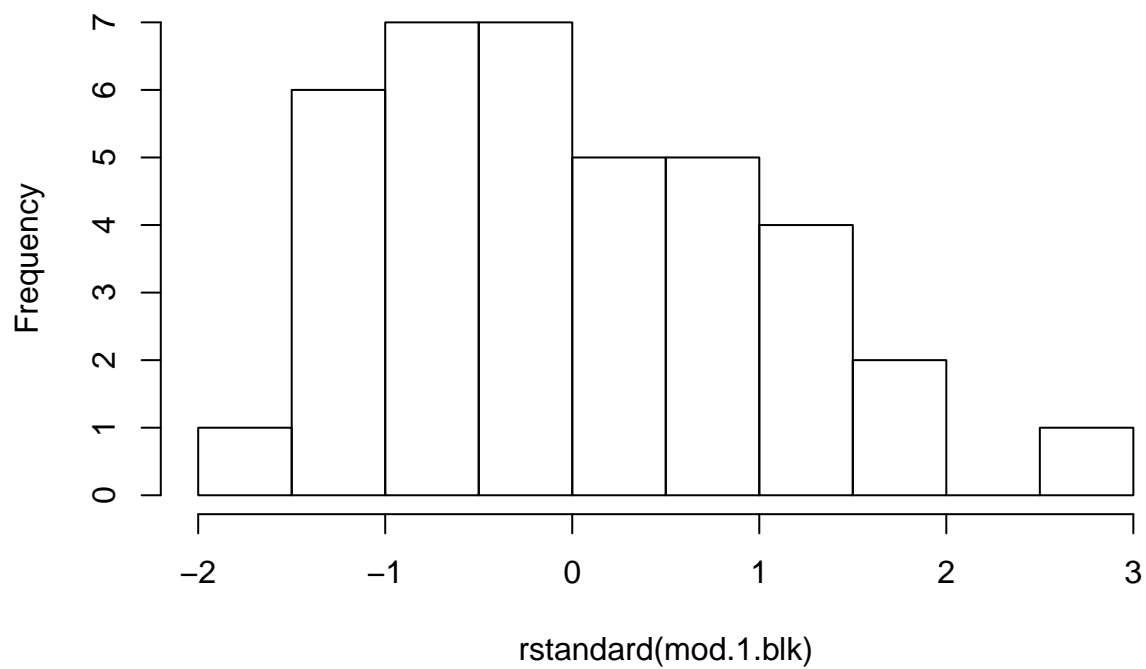
### Method 1 - Calculating the residuals

```
# Plot respiration rate vs. weight
plot(black$respirationrate~black$Weight_g, bty = "l", pch = 20,
     col = "black", main = "Affect of Weight on Respiration Rate -
     Black Rockfish")
mod.1.blk <- lm(black$respirationrate~black$Weight_g)
abline(mod.1.blk)
```



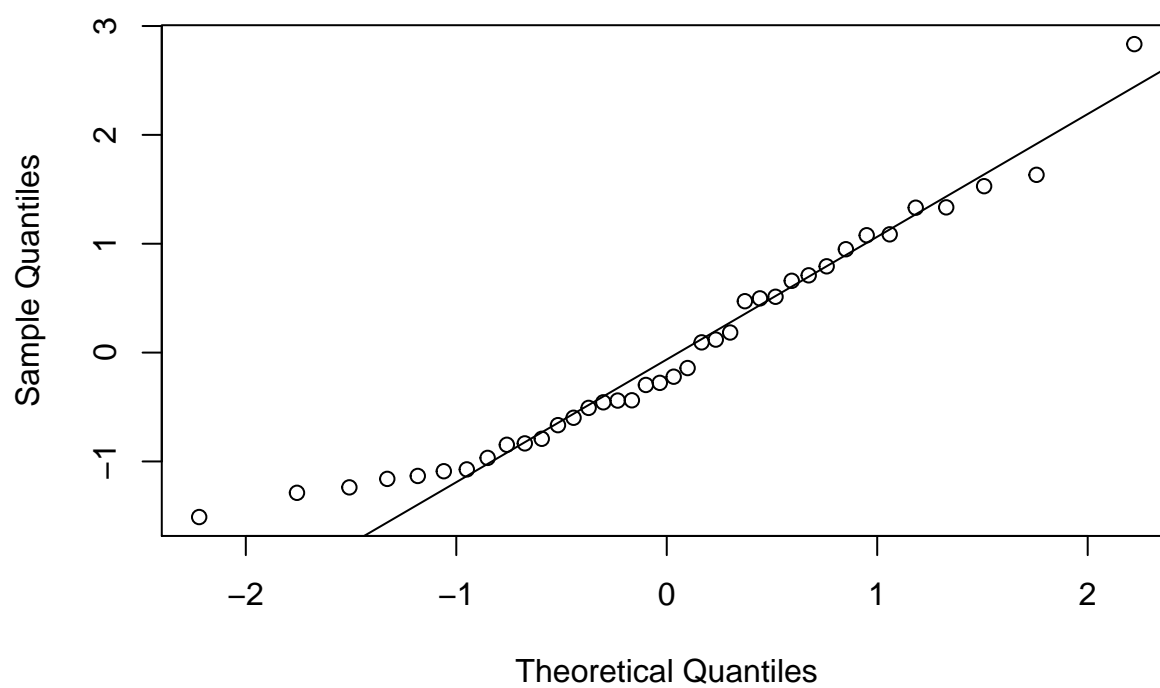
```
#Histogram of residuals
hist(rstandard(mod.1.blk))
```

### Histogram of rstandard(mod.1.blk)



```
#qqplot to test for normality in residuals  
qqnorm(rstandard(mod.1.blk))  
qqline(rstandard(mod.1.blk))
```

### Normal Q-Q Plot

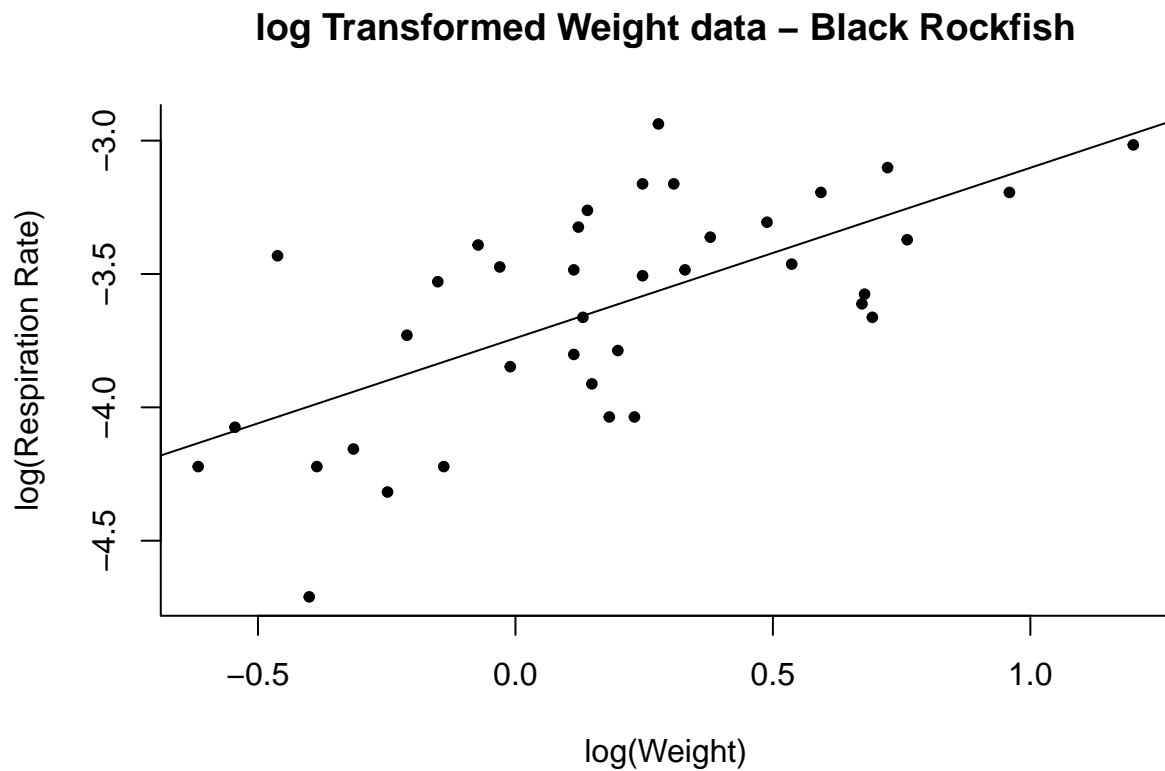


```
#Residuals of the model are normally distributed
```

```
# log transform data and plot it
```

```
plot(log(black$respirationrate)~log(black$Weight_g), bty = "l", pch = 20,  
      col = "black", main = "log Transformed Weight data - Black Rockfish",  
      xlab = "log(Weight)", ylab = "log(Respiration Rate)")
```

```
mod.2.blk <- lm(log(black$respirationrate)~log(black$Weight_g))  
abline(mod.2.blk)
```

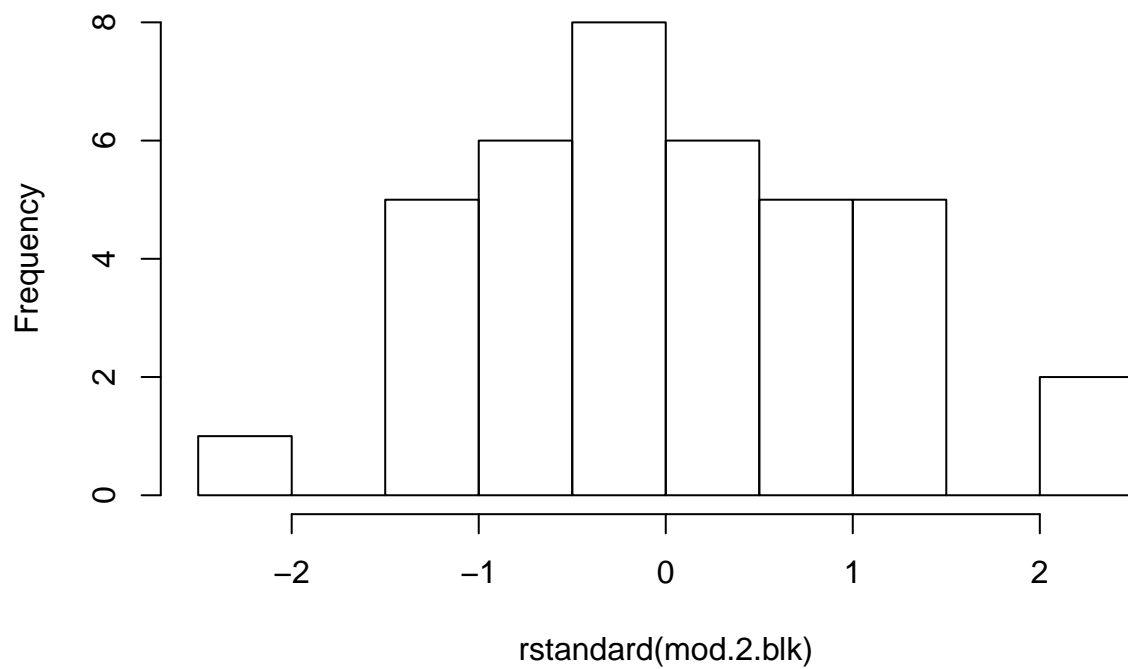


```
#Histogram of residuals
```

```
hist(rstandard(mod.2.blk))
```

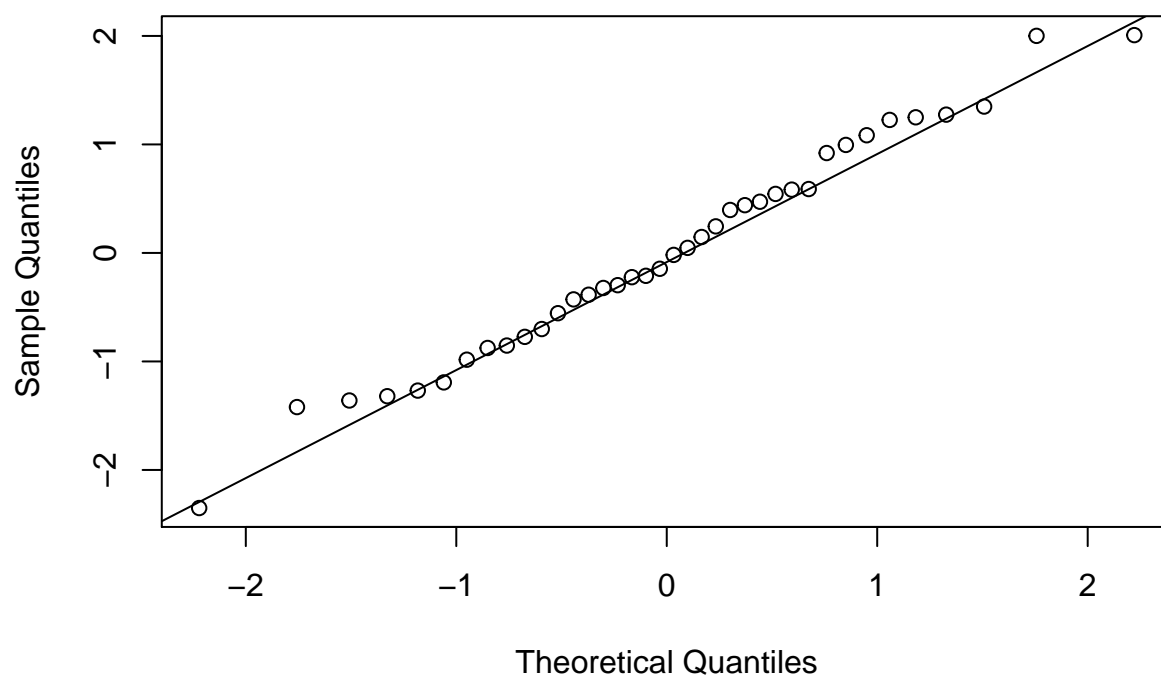


### Histogram of rstandard(mod.2.blk)



```
#qqplot to test for normality in residuals  
qqnorm(rstandard(mod.2.blk))  
qqline(rstandard(mod.2.blk))
```

### Normal Q-Q Plot



```

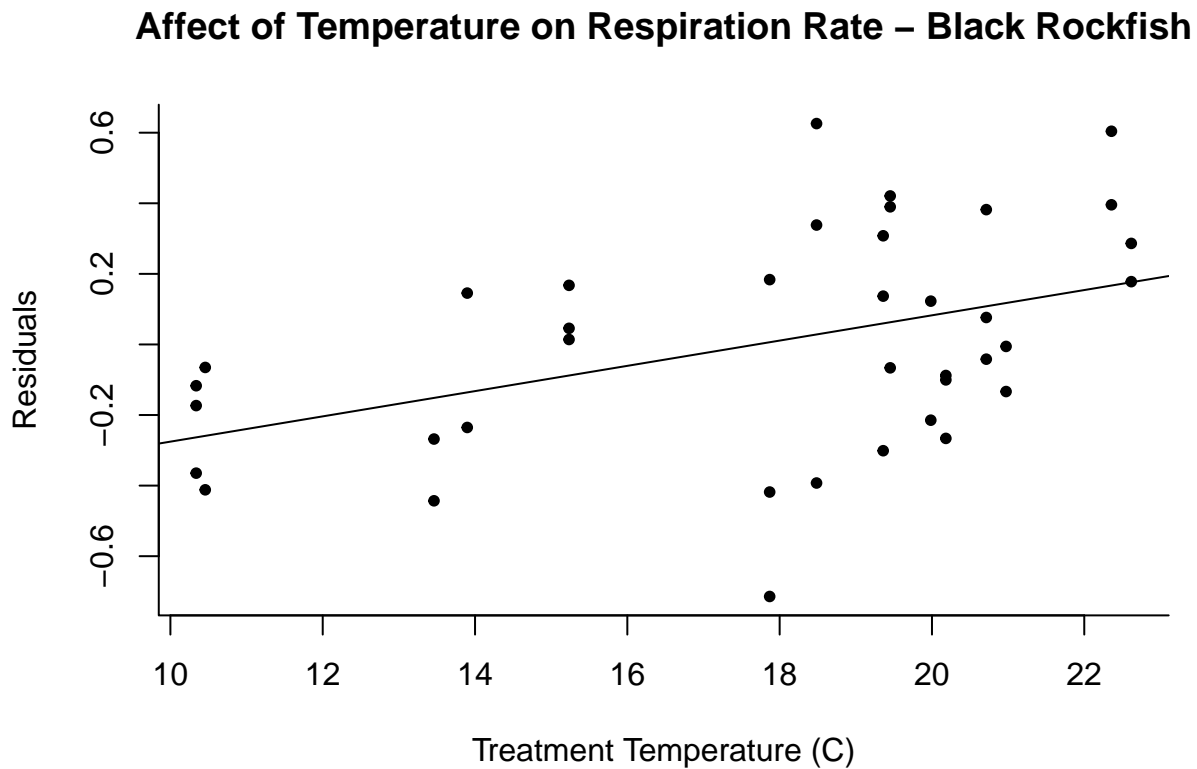
#Residuals of the model are normally distributed

# Calculate the residuals
black$residuals <- resid(mod.2.blk)

# Plot the residuals vs treatment temperature
plot(black$residuals~black$exp_temp, bty = "l", pch = 20,
     col = "black", main = "Affect of Temperature on Respiration Rate - Black Rockfish",
     ylab = "Residuals", xlab = "Treatment Temperature (C)")

mod.3.blk <- lm(black$residuals~black$exp_temp)
abline(mod.3.blk)

```

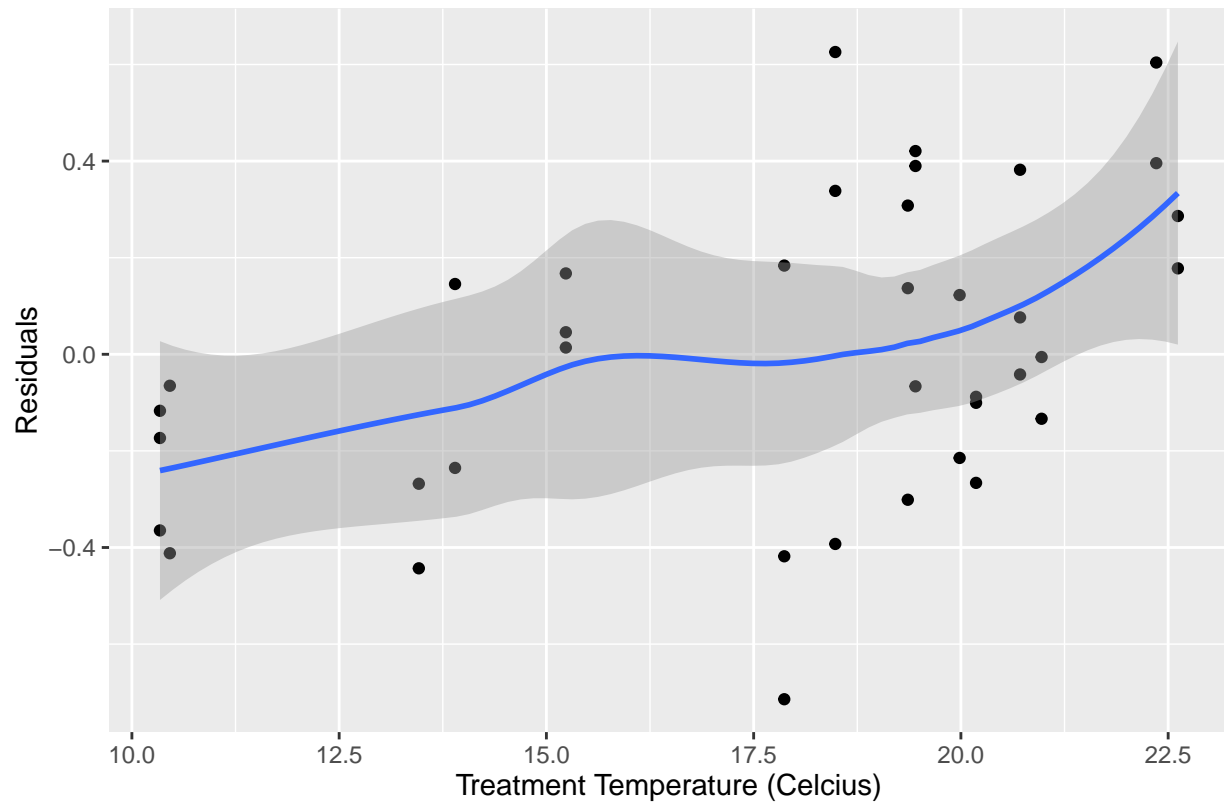


```

ggplot(black, aes(x=exp_temp, y=residuals)) + labs(x = "Treatment Temperature (Celcius)", y = "Residuals")

```

Affect of Temperature on Respiration Rate – Black Rockfish



## Models - AIC model selection

```
# Create full model
```

```
full.med1.blk.mod1 <- lm(black$respirationrate~black$exp_temp + I(black$exp_temp^2) + black$Weight_g)
summary(full.med1.blk.mod1)
```

```
##
## Call:
## lm(formula = black$respirationrate ~ black$exp_temp + I(black$exp_temp^2) +
##     black$Weight_g)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.0119757 -0.0061166  0.0001893  0.0043842  0.0237147
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    4.120e-03  2.750e-02   0.150   0.882
## black$exp_temp -6.590e-05  3.416e-03  -0.019   0.985
## I(black$exp_temp^2) 3.182e-05  1.043e-04   0.305   0.762
## black$Weight_g   1.175e-02  2.267e-03   5.184 9.91e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.007997 on 34 degrees of freedom
## Multiple R-squared:  0.4938, Adjusted R-squared:  0.4492
## F-statistic: 11.06 on 3 and 34 DF,  p-value: 3.227e-05
```

```
drop1(full.med1.blk.mod1)
```

```
## Single term deletions
##
## Model:
## black$respirationrate ~ black$exp_temp + I(black$exp_temp^2) +
##     black$Weight_g
##              Df Sum of Sq      RSS      AIC
## <none>                 0.0021741 -363.21
## black$exp_temp         1 0.00000002 0.0021741 -365.21
## I(black$exp_temp^2)     1 0.00000595 0.0021800 -365.11
## black$Weight_g         1 0.00171846 0.0038926 -343.08
```

```
# drop Weight
```

```
temp.med1.blk.mod2 <- lm(black$respirationrate~black$exp_temp + I(black$exp_temp^2))
summary(temp.med1.blk.mod2)
```

```
##
## Call:
## lm(formula = black$respirationrate ~ black$exp_temp + I(black$exp_temp^2))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -0.0181079 -0.0079994 -0.0009461 0.0077149 0.0251221
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.0483400  0.0344805   1.402   0.170
## black$exp_temp -0.0035464  0.0044170  -0.803   0.427
## I(black$exp_temp^2) 0.0001320  0.0001352   0.976   0.336
##
## Residual standard error: 0.01055 on 35 degrees of freedom
## Multiple R-squared: 0.09374, Adjusted R-squared: 0.04195
## F-statistic: 1.81 on 2 and 35 DF, p-value: 0.1786
```

```
drop1(temp.med1.blk.mod2)
```

```
## Single term deletions
##
## Model:
## black$respirationrate ~ black$exp_temp + I(black$exp_temp^2)
##              Df Sum of Sq      RSS      AIC
## <none>                0.0038926 -343.08
## black$exp_temp         1 7.1696e-05 0.0039643 -344.38
## I(black$exp_temp^2)     1 1.0594e-04 0.0039985 -344.06
```

```
# This is the best model
```

```
# Just to see others: drop squared
```

```
temp.med1.blk.mod3 <- lm(black$respirationrate~black$exp_temp)
summary(temp.med1.blk.mod3)
```

```
##
## Call:
## lm(formula = black$respirationrate ~ black$exp_temp)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.0199101 -0.0086527 -0.0002815  0.0075987  0.0236335
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.0156564  0.0082102   1.907   0.0645 .
## black$exp_temp 0.0007417  0.0004538   1.634   0.1109
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01054 on 36 degrees of freedom
## Multiple R-squared: 0.06907, Adjusted R-squared: 0.04321
## F-statistic: 2.671 on 1 and 36 DF, p-value: 0.1109
```

```
# leave squared and drop non squared term
```

```
temp.med1.blk.mod4 <- lm(black$respirationrate~I(black$exp_temp^2))
summary(temp.med1.blk.mod4)
```

```
##
## Call:
## lm(formula = black$respirationrate ~ I(black$exp_temp^2))
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-0.0195892	-0.0087628	-0.0005856	0.0075527	0.0238744

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	2.093e-02	4.837e-03	4.327	0.000115 ***
I(black\$exp_temp^2)	2.398e-05	1.383e-05	1.734	0.091558 .

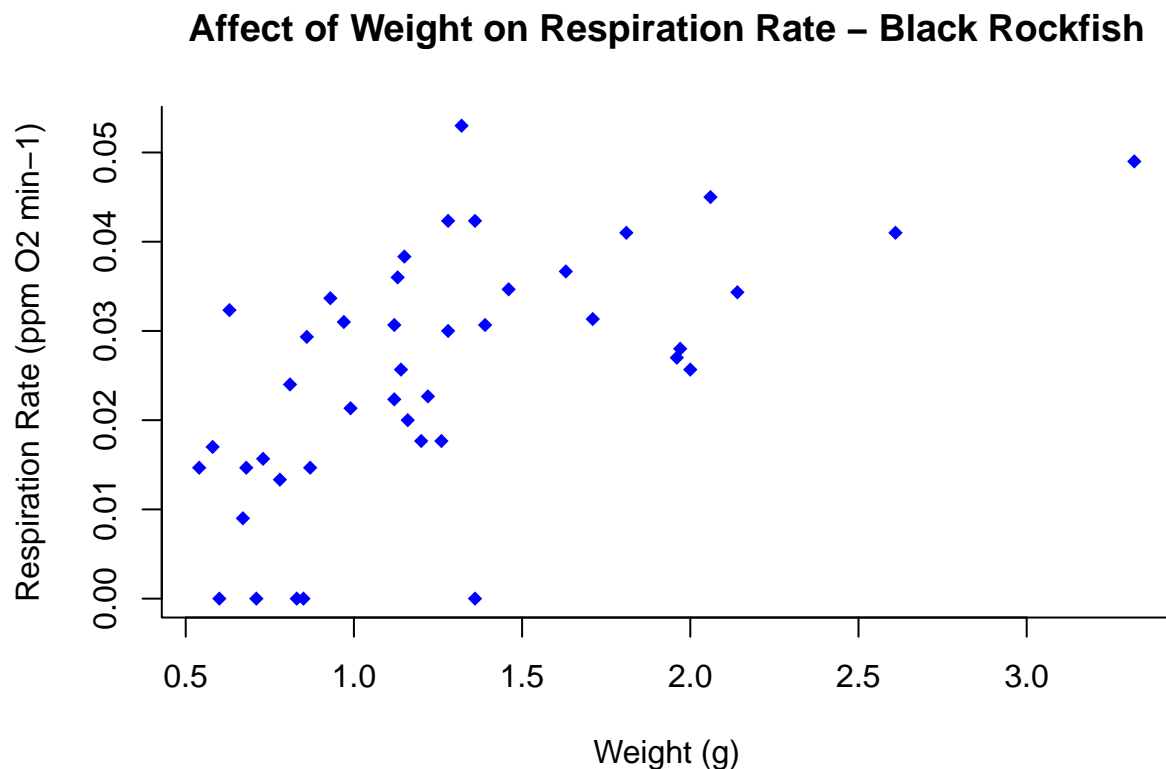
```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01049 on 36 degrees of freedom
## Multiple R-squared:  0.07705,    Adjusted R-squared:  0.05141
## F-statistic: 3.005 on 1 and 36 DF,  p-value: 0.09156

### Nothing is significant
```

Method 2 - Same analysis but adding in zeros for those that died during the experiment

```
zeros.blk <- read.csv("zeros_blk.csv", header= FALSE)
colnames(zeros.blk) <- c("Species", "Length_mm", "Weight_g", "Starting_DO_.ppm", "DO_30min_ppm", "Experiment")
black.zeros <- rbind(black, zeros.blk)

# Plot initial data
plot(black.zeros$respirationrate~black.zeros$Weight_g, bty = "l", pch = 18,
     col = "blue", main = "Affect of Weight on Respiration Rate - Black Rockfish",
     xlab = "Weight (g)", ylab = "Respiration Rate (ppm O2 min-1)" )
```

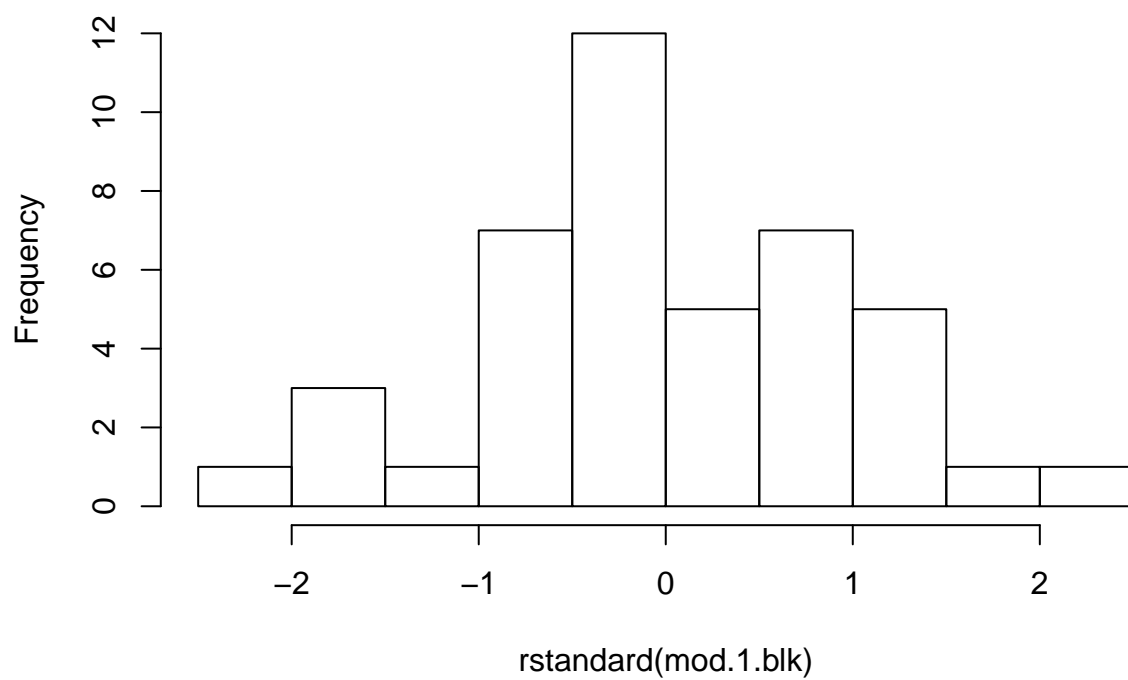


```
# cannot log transform the data because of zeros in data but may not be necessary due
# residuals being normally distributed

# created a linear model for non-transformed data
mod.1.blk <- lm(black.zeros$respirationrate~black.zeros$Weight_g)

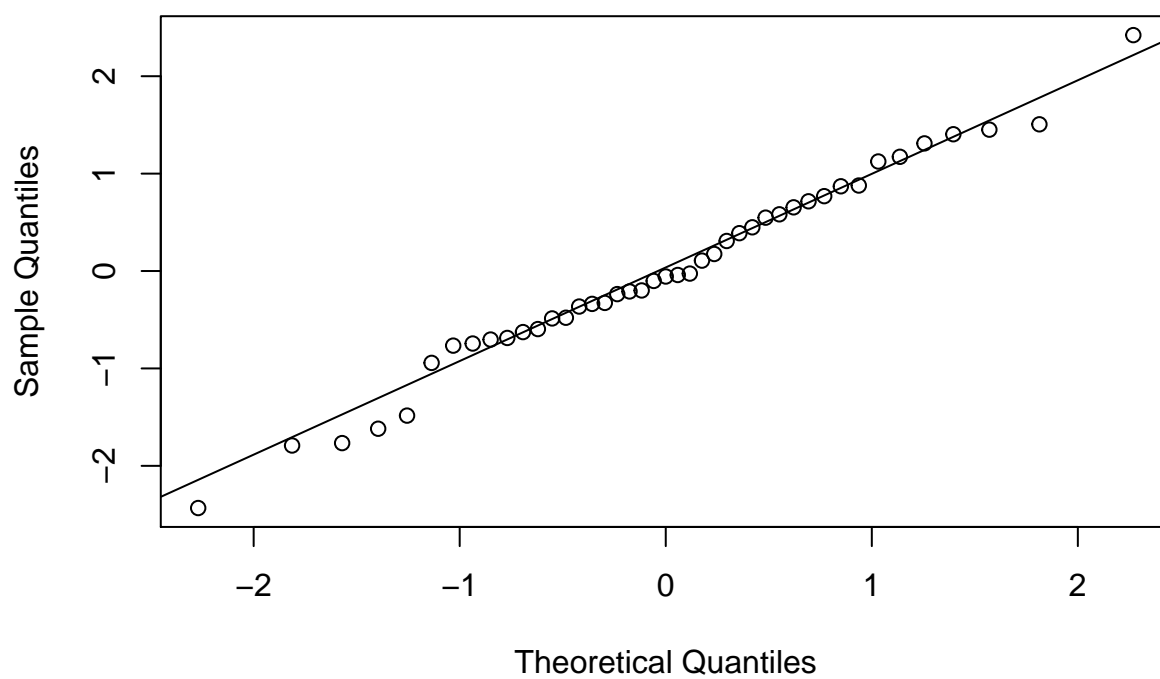
#Histogram of residuals
hist(rstandard(mod.1.blk))
```

### Histogram of rstandard(mod.1.blk)



```
#qqplot to test for normality in residuals  
qqnorm(rstandard(mod.1.blk))  
qqline(rstandard(mod.1.blk))
```

### Normal Q-Q Plot



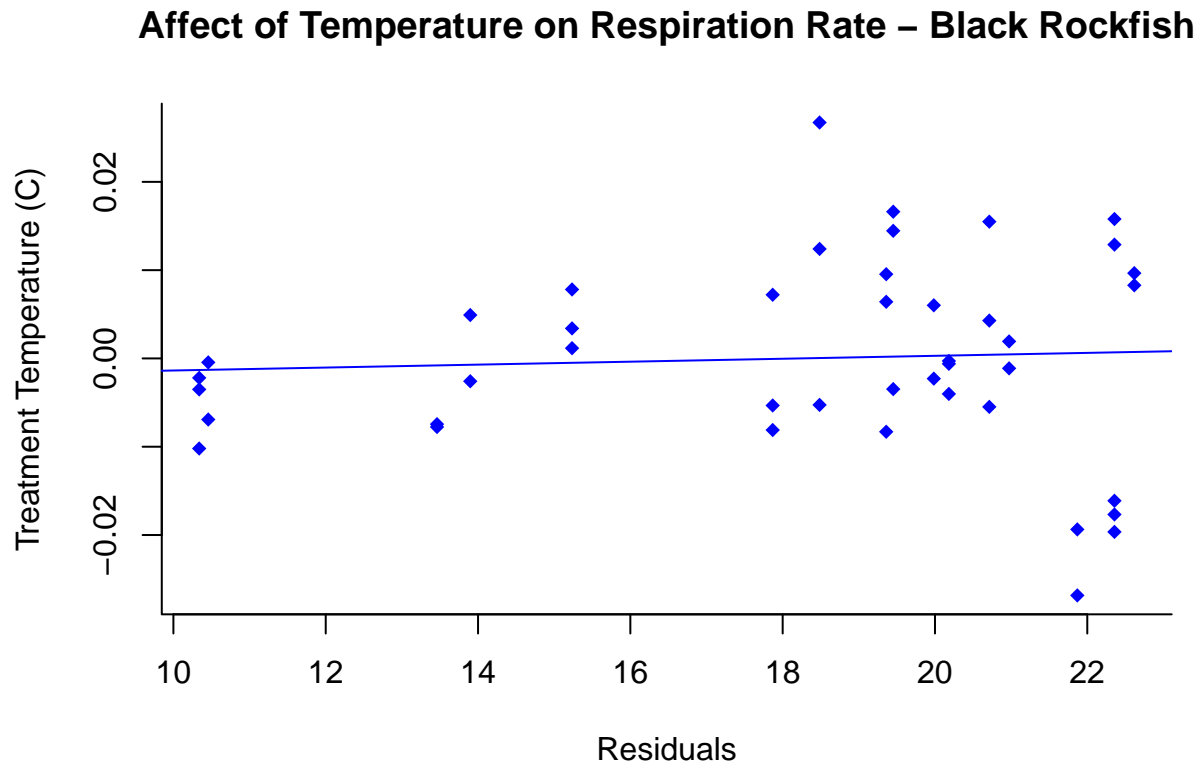


```
#Residuals of the model are normally distributed

# Plot the residuals
black.zeros$residuals <- resid(mod.1.blk)

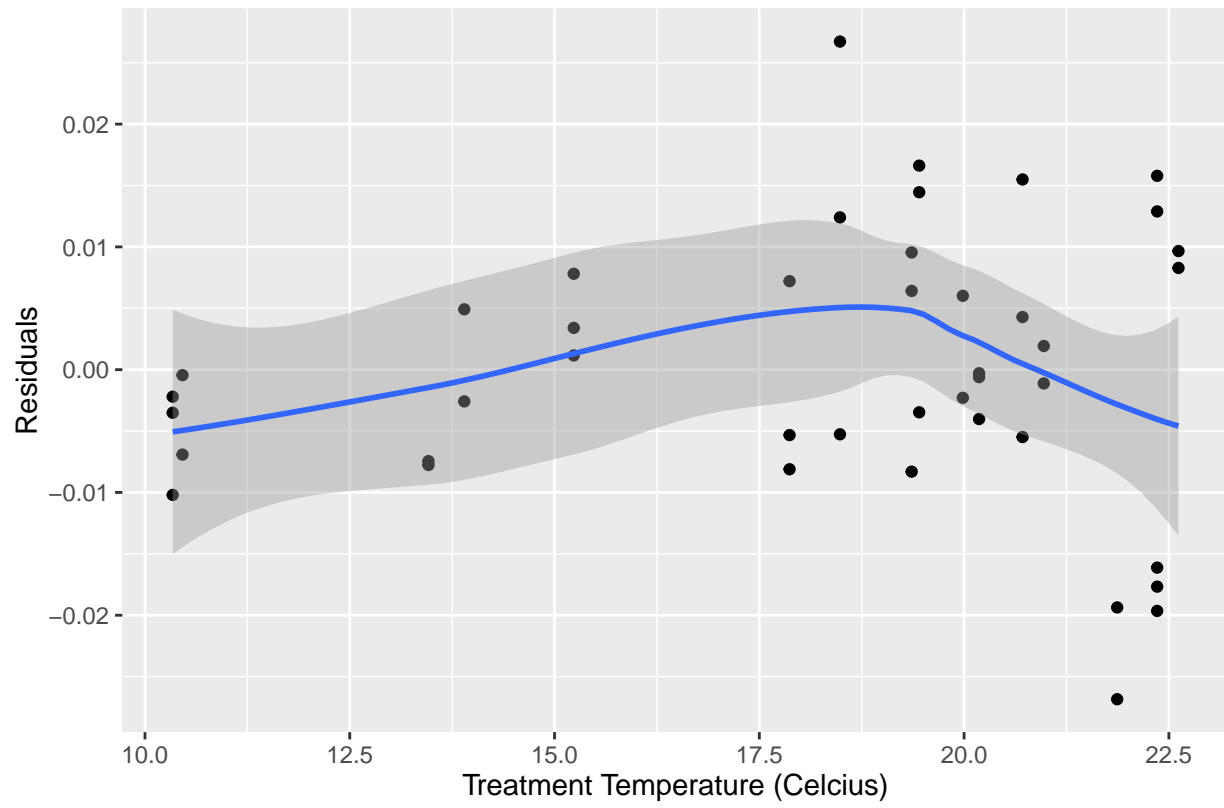
plot(black.zeros$residuals~black.zeros$exp_temp, bty = "l", pch = 18,
     col = "blue", main = "Affect of Temperature on Respiration Rate - Black Rockfish",
     xlab = "Residuals", ylab = "Treatment Temperature (C)" )

abline(lm(black.zeros$residuals~black.zeros$exp_temp), col = "blue")
```



```
ggplot(black.zeros, aes(x=exp_temp, y=residuals)) + labs(x = "Treatment Temperature (Celcius)", y = "Re
```

Affet of Temperature on Respiration Rate – Black Rockfish



## Models - AIC model selection

```
# model data
full.med2.blk.mod1 <- lm(black.zeros$respirationrate~black.zeros$exp_temp + I(black.zeros$exp_temp^2) +
summary(full.med2.blk.mod1)
```

```
##
## Call:
## lm(formula = black.zeros$respirationrate ~ black.zeros$exp_temp +
##      I(black.zeros$exp_temp^2) + black.zeros$Weight_g)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.0248854 -0.0078746 -0.0005769  0.0050331  0.0232706
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -0.0598453   0.0342990   -1.745   0.0889 .
## black.zeros$exp_temp    0.0083525   0.0042239    1.977   0.0551 .
## I(black.zeros$exp_temp^2) -0.0002468   0.0001267   -1.947   0.0587 .
## black.zeros$Weight_g    0.0147749   0.0029570    4.996 1.27e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01091 on 39 degrees of freedom
## Multiple R-squared:  0.4163, Adjusted R-squared:  0.3714
## F-statistic: 9.273 on 3 and 39 DF,  p-value: 9.326e-05
```

```
drop1(full.med2.blk.mod1)
```

```
## Single term deletions
##
## Model:
## black.zeros$respirationrate ~ black.zeros$exp_temp + I(black.zeros$exp_temp^2) +
##      black.zeros$Weight_g
##              Df Sum of Sq      RSS      AIC
## <none>                 0.0046432 -384.74
## black.zeros$exp_temp    1 0.00046553 0.0051087 -382.63
## I(black.zeros$exp_temp^2) 1 0.00045139 0.0050945 -382.75
## black.zeros$Weight_g    1 0.00297221 0.0076154 -365.47
```

```
# drop Weight
temp.med2.blk.mod2 <- lm(black.zeros$respirationrate~black.zeros$exp_temp + I(black.zeros$exp_temp^2))
summary(temp.med2.blk.mod2)
```

```
##
## Call:
## lm(formula = black.zeros$respirationrate ~ black.zeros$exp_temp +
##      I(black.zeros$exp_temp^2))
##
## Residuals:
```

```
##           Min           1Q       Median           3Q           Max
## -0.022275 -0.010837  0.001318  0.010807  0.024929
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -0.0206680   0.0422247  -0.489   0.627
## black.zeros$exp_temp    0.0063132   0.0053164   1.187   0.242
## I(black.zeros$exp_temp^2) -0.0001989   0.0001598  -1.245   0.221
##
## Residual standard error: 0.0138 on 40 degrees of freedom
## Multiple R-squared:  0.04272,    Adjusted R-squared:  -0.005141
## F-statistic: 0.8926 on 2 and 40 DF,  p-value: 0.4176
```

```
drop1(temp.med2.blk.mod2)
```

```
## Single term deletions
##
## Model:
## black.zeros$respirationrate ~ black.zeros$exp_temp + I(black.zeros$exp_temp^2)
##               Df Sum of Sq      RSS      AIC
## <none>                        0.0076154 -365.47
## black.zeros$exp_temp          1 0.00026846 0.0078838 -365.98
## I(black.zeros$exp_temp^2)      1 0.00029488 0.0079102 -365.83
```

```
# This is the best model
```

```
# Just to see others: drop squared
```

```
temp.med2.blk.mod3 <- lm(black.zeros$respirationrate~black.zeros$exp_temp)
summary(temp.med2.blk.mod3)
```

```
##
## Call:
## lm(formula = black.zeros$respirationrate ~ black.zeros$exp_temp)
##
## Residuals:
##           Min           1Q       Median           3Q           Max
## -0.024456 -0.009569  0.001293  0.009440  0.027638
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.0303103   0.0103175   2.938   0.0054 **
## black.zeros$exp_temp -0.0002677   0.0005544  -0.483   0.6317
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01389 on 41 degrees of freedom
## Multiple R-squared:  0.005655,    Adjusted R-squared:  -0.0186
## F-statistic: 0.2332 on 1 and 41 DF,  p-value: 0.6317
```

```
# leave squared and drop non squared term
```

```
temp.med2.blk.mod4 <- lm(black.zeros$respirationrate~I(black.zeros$exp_temp^2))
summary(temp.med2.blk.mod4)
```

```
##
## Call:
## lm(formula = black.zeros$respirationrate ~ I(black.zeros$exp_temp^2))
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-0.024097	-0.009871	0.001181	0.009655	0.027519

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	2.895e-02	6.138e-03	4.716	2.78e-05 ***
I(black.zeros\$exp_temp^2)	-1.014e-05	1.664e-05	-0.609	0.546

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01387 on 41 degrees of freedom
## Multiple R-squared:  0.008976,    Adjusted R-squared:  -0.0152
## F-statistic: 0.3713 on 1 and 41 DF,  p-value: 0.5456

### nothing is significant
```

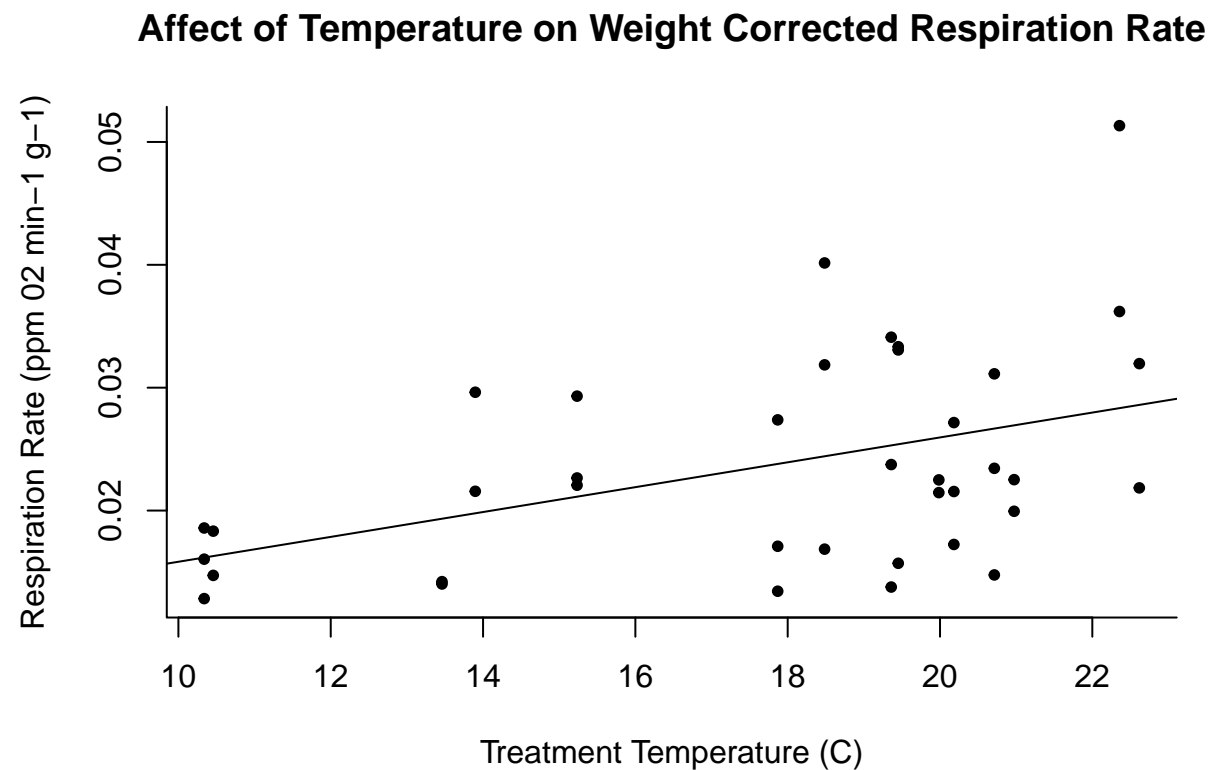
### Method 3 - Correcting for weight first

```
# Correct respiration rate with individual weight
black$corr.resp.rate <- black$respirationrate/black$Weight_g

# Plot corrected respiration rate against treatment temperature
plot(black$corr.resp.rate~black$exp_temp, bty = "l", pch = 20,
     col = "black", main = "Affect of Temperature on Weight Corrected Respiration Rate",
     xlab = "Treatment Temperature (C)", ylab = "Respiration Rate (ppm O2 min-1 g-1)")

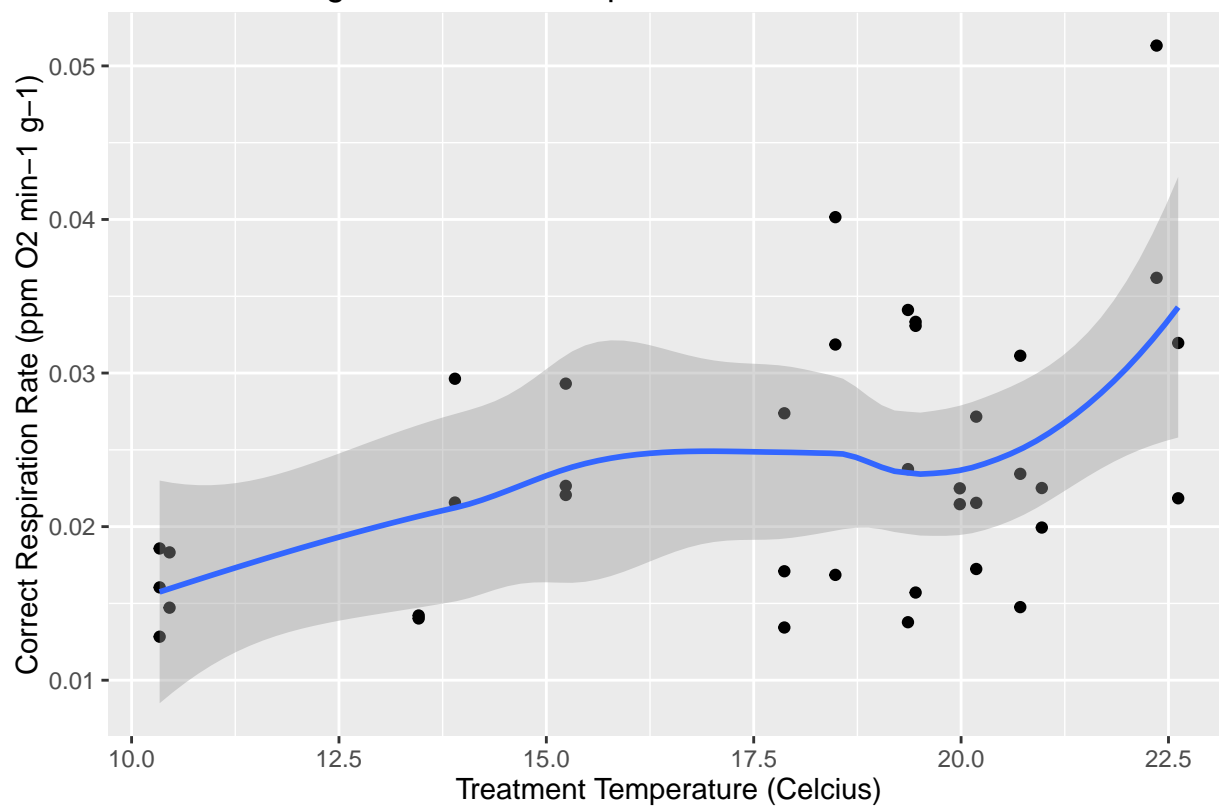
# Fit linear model to data
mod.4.blk <- lm(black$corr.resp.rate~black$exp_temp)

# Plot linear model on graph
abline(mod.4.blk)
```



```
# Use General Additive Model
ggplot(black, aes(x=exp_temp, y=corr.resp.rate)) + labs(x = "Treatment Temperature (Celcius)", y = "Corr
```

Weight Corrected Respiration Rate – Black Rockfish



## Models - AIC model selection

```
require(AICcmodavg)
```

```
## Loading required package: AICcmodavg
```

```
# Create full model
```

```
full.med3.blk.mod1 <- lm(black$corr.resp.rate~black$exp_temp + I(black$exp_temp^2))  
summary(full.med3.blk.mod1)
```

```
##  
## Call:  
## lm(formula = black$corr.resp.rate ~ black$exp_temp + I(black$exp_temp^2))  
##  
## Residuals:  
##      Min       1Q   Median       3Q      Max   
## -0.012080 -0.004878 -0.001118  0.004268  0.022031   
##  
## Coefficients:  
##              Estimate Std. Error t value Pr(>|t|)      
## (Intercept)    1.697e-02  2.598e-02   0.653   0.518      
## black$exp_temp -4.648e-04  3.329e-03  -0.140   0.890      
## I(black$exp_temp^2) 4.544e-05  1.019e-04   0.446   0.658      
##  
## Residual standard error: 0.007947 on 35 degrees of freedom  
## Multiple R-squared:  0.2034, Adjusted R-squared:  0.1579   
## F-statistic: 4.469 on 2 and 35 DF,  p-value: 0.01868
```

```
drop1(full.med3.blk.mod1)
```

```
## Single term deletions  
##  
## Model:  
## black$corr.resp.rate ~ black$exp_temp + I(black$exp_temp^2)  
##              Df Sum of Sq      RSS      AIC  
## <none>                 0.0022107 -364.58  
## black$exp_temp         1 1.2318e-06 0.0022119 -366.56  
## I(black$exp_temp^2)     1 1.2561e-05 0.0022232 -366.36
```

```
# this is the best model
```

```
# Just to see others: drop squared
```

```
temp.med3.blk.mod2 <- lm(black$corr.resp.rate~black$exp_temp)  
summary(temp.med3.blk.mod2)
```

```
##  
## Call:  
## lm(formula = black$corr.resp.rate ~ black$exp_temp)  
##  
## Residuals:
```



```
##           Min           1Q           Median           3Q           Max
## -0.0119132 -0.0052657 -0.0008451  0.0042379  0.0229878
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.0057159  0.0061221   0.934  0.35670
## black$exp_temp 0.0010117  0.0003384   2.990  0.00501 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.007858 on 36 degrees of freedom
## Multiple R-squared:  0.1989, Adjusted R-squared:  0.1767
## F-statistic: 8.939 on 1 and 36 DF,  p-value: 0.00501
```

```
## Significant
```

```
# leave squared and drop non squared term
temp.med3.blk.mod3 <- lm(black$corr.resp.rate~I(black$exp_temp^2))
summary(temp.med3.blk.mod3)
```

```
##
## Call:
## lm(formula = black$corr.resp.rate ~ I(black$exp_temp^2))
##
## Residuals:
##           Min           1Q           Median           3Q           Max
## -0.012043 -0.004978 -0.001019  0.004247  0.022306
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.338e-02  3.613e-03   3.703 0.000711 ***
## I(black$exp_temp^2) 3.129e-05  1.033e-05   3.028 0.004532 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.007838 on 36 degrees of freedom
## Multiple R-squared:  0.203, Adjusted R-squared:  0.1809
## F-statistic: 9.169 on 1 and 36 DF,  p-value: 0.004532
```

```
## Significant
```

```
AICc(temp.med3.blk.mod2)
```

```
## [1] -255.8176
```

```
# model 2 is the best model
```

```
AICc(temp.med3.blk.mod3)
```

```
## [1] -256.0118
```

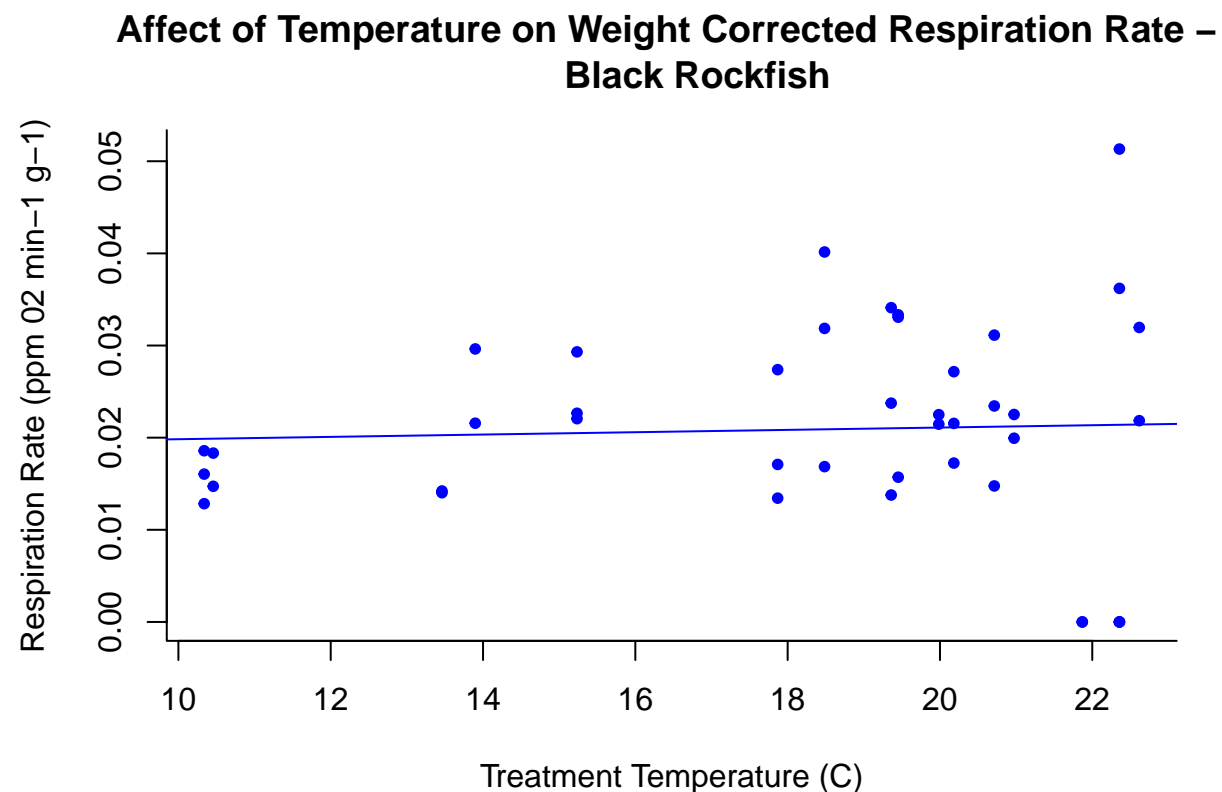
## Method 4 - Correcting for weights with zero data

```
# Correct respiration rate with individual weight
black.zeros$corr.resp.rate <- black.zeros$respirationrate/black.zeros$Weight_g

# Plot corrected respiration rate against treatment temperature
plot(black.zeros$corr.resp.rate~black.zeros$exp_temp, bty = "l", pch = 20,
     col = "blue", main = "Affect of Temperature on Weight Corrected Respiration Rate -
     Black Rockfish", xlab = "Treatment Temperature (C)",
     ylab = "Respiration Rate (ppm O2 min-1 g-1)")

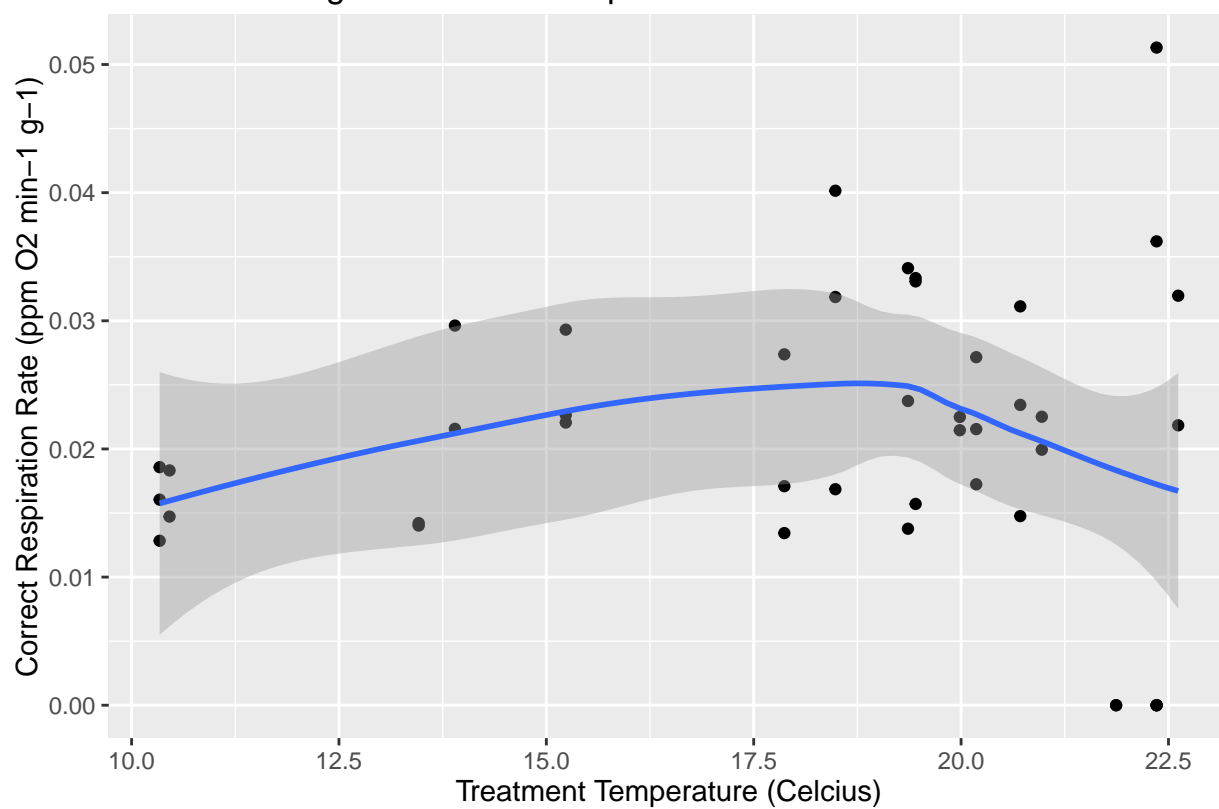
# Fit linear model to data
mod.4.blk <- lm(black.zeros$corr.resp.rate~black.zeros$exp_temp)

# Plot linear model on graph
abline(mod.4.blk, col = "blue")
```



```
# Use General Additive Model
ggplot(black.zeros, aes(x=exp_temp, y=corr.resp.rate)) + labs(x = "Treatment Temperature (Celcius)", y = "Respiration Rate (ppm O2 min-1 g-1)")
```

Weight Corrected Respiration Rate – Black Rockfish



## Models - AIC model selection

```
# Create full model
full.med4.blk.mod1 <- lm(black.zeros$corr.resp.rate~black.zeros$exp_temp + I(black.zeros$exp_temp^2))
summary(full.med4.blk.mod1)
```

```
##
## Call:
## lm(formula = black.zeros$corr.resp.rate ~ black.zeros$exp_temp +
##      I(black.zeros$exp_temp^2))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.018792 -0.007282 -0.000534  0.005130  0.033729
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -0.0408621  0.0336247  -1.215   0.2314
## black.zeros$exp_temp    0.0077983  0.0042336   1.842   0.0729 .
## I(black.zeros$exp_temp^2) -0.0002319  0.0001273  -1.822   0.0760 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01099 on 40 degrees of freedom
## Multiple R-squared:  0.0784, Adjusted R-squared:  0.03232
## F-statistic: 1.701 on 2 and 40 DF,  p-value: 0.1954
```

```
drop1(full.med4.blk.mod1)
```

```
## Single term deletions
##
## Model:
## black.zeros$corr.resp.rate ~ black.zeros$exp_temp + I(black.zeros$exp_temp^2)
##              Df Sum of Sq      RSS      AIC
## <none>                 0.0048292 -385.05
## black.zeros$exp_temp    1 0.00040963 0.0052388 -383.55
## I(black.zeros$exp_temp^2) 1 0.00040074 0.0052299 -383.63
```

```
# drop squared
temp.med4.blk.mod2 <- lm(black.zeros$corr.resp.rate~black.zeros$exp_temp)
summary(temp.med4.blk.mod2)
```

```
##
## Call:
## lm(formula = black.zeros$corr.resp.rate ~ black.zeros$exp_temp)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.0213963 -0.0056884  0.0004154  0.0076842  0.0299265
##
## Coefficients:
```

```
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.0185663  0.0083893   2.213   0.0325 *
## black.zeros$exp_temp 0.0001266  0.0004508   0.281   0.7803
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01129 on 41 degrees of freedom
## Multiple R-squared:  0.00192,    Adjusted R-squared:  -0.02242
## F-statistic: 0.07885 on 1 and 41 DF,  p-value: 0.7803
```

```
# leave squared and drop non squared term
temp.med4.blk.mod3 <- lm(black.zeros$corr.resp.rate~I(black.zeros$exp_temp^2))
summary(temp.med4.blk.mod3)
```

```
##
## Call:
## lm(formula = black.zeros$corr.resp.rate ~ I(black.zeros$exp_temp^2))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.0210709 -0.0060312  0.0005979  0.0075654  0.0302519
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.042e-02  5.004e-03   4.082 0.000202 ***
## I(black.zeros$exp_temp^2) 1.297e-06  1.356e-05   0.096 0.924295
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0113 on 41 degrees of freedom
## Multiple R-squared:  0.0002229,    Adjusted R-squared:  -0.02416
## F-statistic: 0.009141 on 1 and 41 DF,  p-value: 0.9243
```

```
### Nothing is significant
```