

# Testosterone Analyses for O’Connell-Rodwell et al., 2022

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1/23/2022

## Age and Hormonally Driven Responses of Male African Elephants (*Loxodonta africana*) to Estrous Call Playbacks May Inform Conservation Management Tools

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*Due to an ongoing hormone study for this population, raw testosterone data has not yet been made publicly available. Therefore, we provide this output from an R Markdown file to show the results of the code used in the accompanying R script. Model names were kept the same as the R script for clarity. This document has been referenced in the paper as “R Markdown PDF”.*

### Model 1: Testosterone Analysis #1

Testing mean differences of testosterone levels between age classes in the non-musth 1Q-3Q male elephant group (n = 19).

*Testosterone was log transformed prior to these analyses.*

### Analysis and results

#### ANOVA

```
test1Q_3Q_anova <- aov(Log_T ~ AgeClass, testosterone1Q_3Q.log)
summary(test1Q_3Q_anova)
```

| ##           | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|--------------|----|--------|---------|---------|--------|
| ## AgeClass  | 2  | 0.869  | 0.4347  | 1.558   | 0.241  |
| ## Residuals | 16 | 4.464  | 0.2790  |         |        |

*Not significant,  $p = 0.241$ , suggesting that non-musth males yet to meet their reproductive prime (1Q-3Q age class) are hormonally similar.*

### Tukey post-hoc

```
TukeyHSD(test1Q_3Q_anova)
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = Log_T ~ AgeClass, data = testosterone1Q_3Q.log)
##
## $AgeClass
##      diff      lwr      upr      p adj
## 2Q-1Q -0.39720409 -1.4899791 0.6955709 0.6250262
## 3Q-1Q  0.05401542 -1.0017055 1.1097364 0.9904427
## 3Q-2Q  0.45121950 -0.2204397 1.1228787 0.2236100
```

*No significant between group comparisons detected*

### Check assumptions

#### Check for outliers

```
log.t.outliers.1Q.3Q <- testosterone1Q_3Q.log %>%
  group_by(AgeClass) %>%
  identify_outliers(Log_T)
```

*No outliers detected*

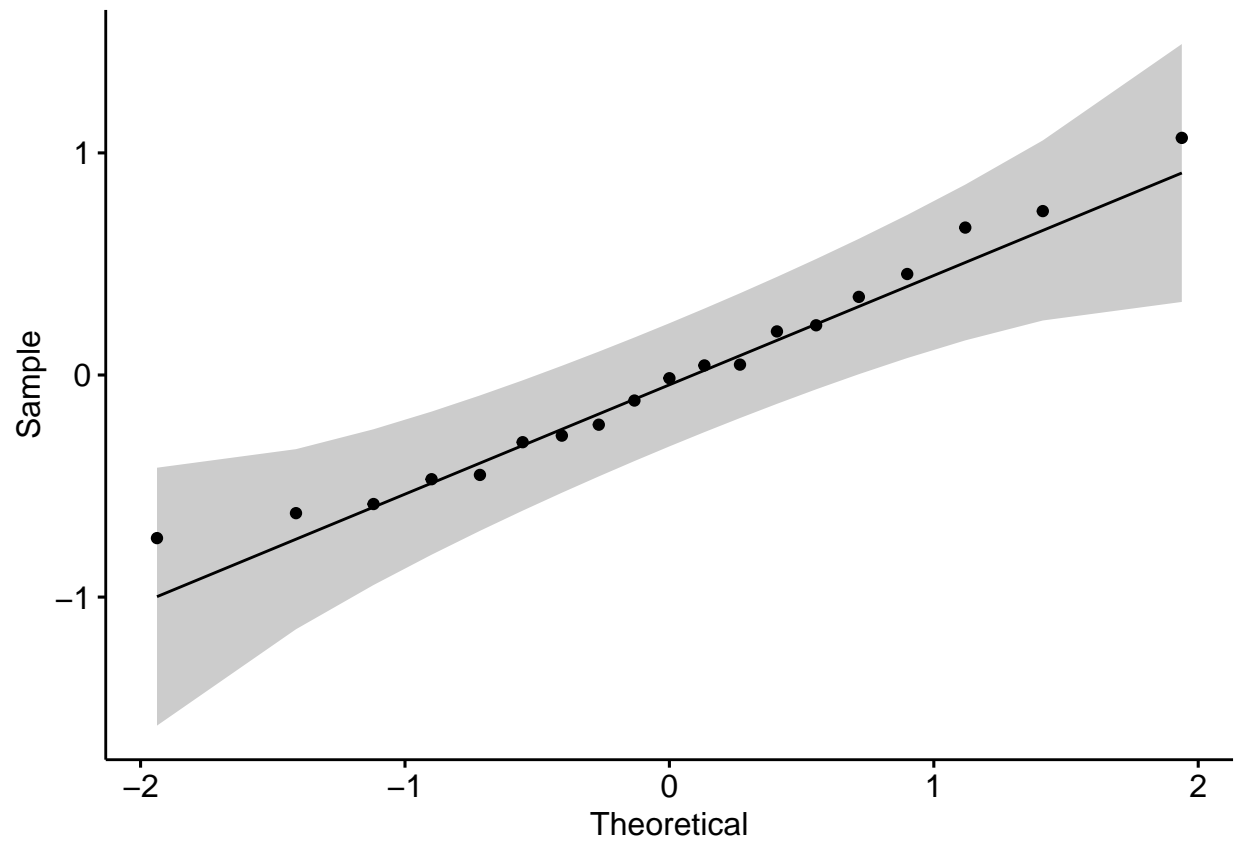
#### Check for normality

Build the model

```
model_logt_1Q_3Q <- lm(Log_T ~ AgeClass, data = testosterone1Q_3Q.log)
```

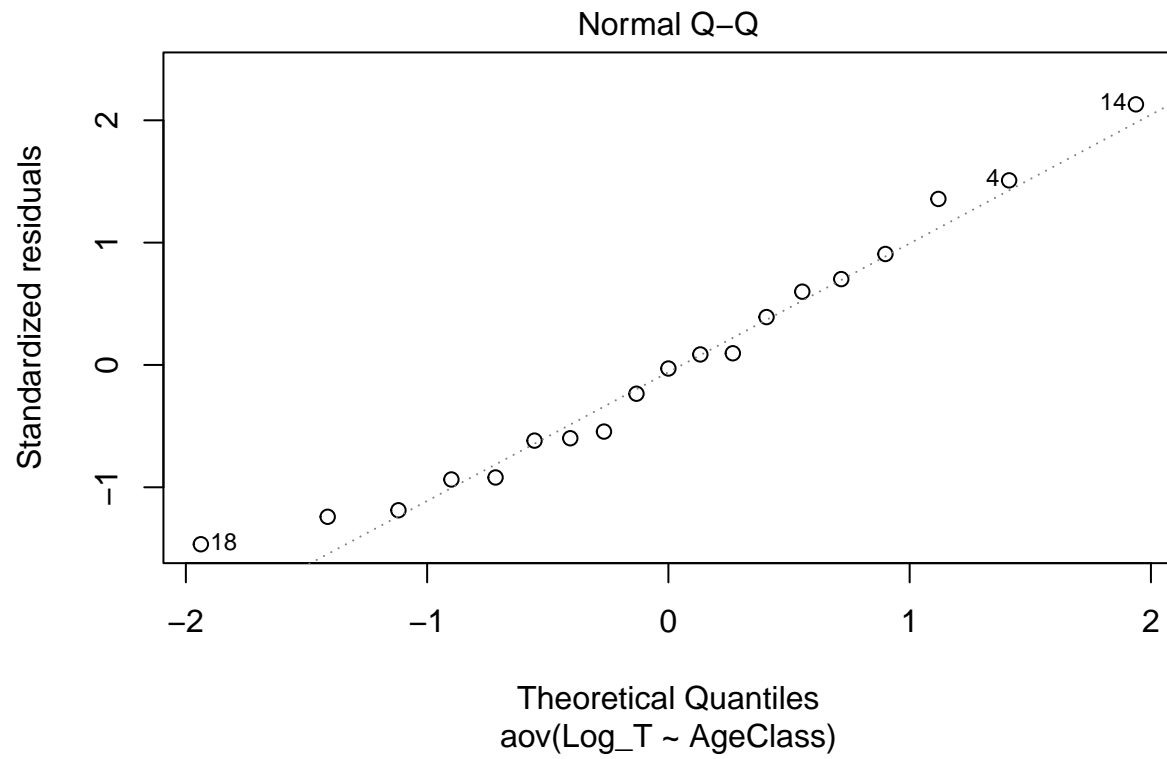
QQ plot

```
ggqqplot(residuals(model_logt_1Q_3Q))
```



*Looks normal*

```
plot(test1Q_3Q_anova, 2)
```

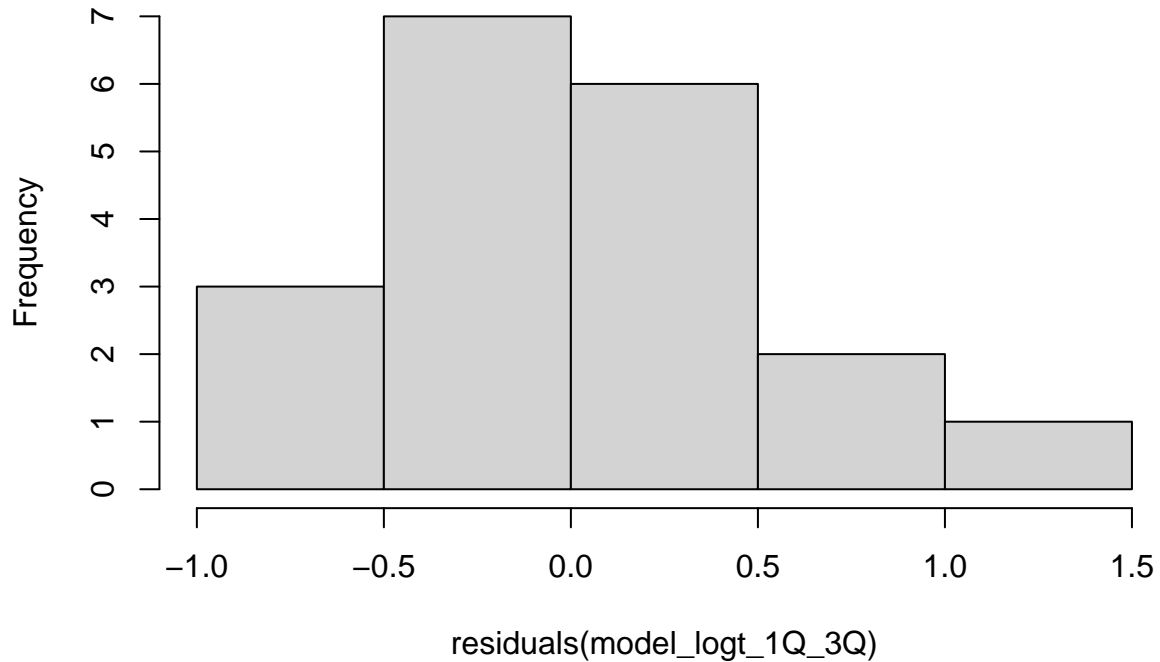


*Normal with a slightly heavier lower tail, but nothing too concerning*

Histogram

```
hist(residuals(model_logt_1Q_3Q))
```

## Histogram of residuals(model\_logt\_1Q\_3Q)



*Slightly right skewed but looks great overall*

Compute the Shapiro-Wilk test for normality

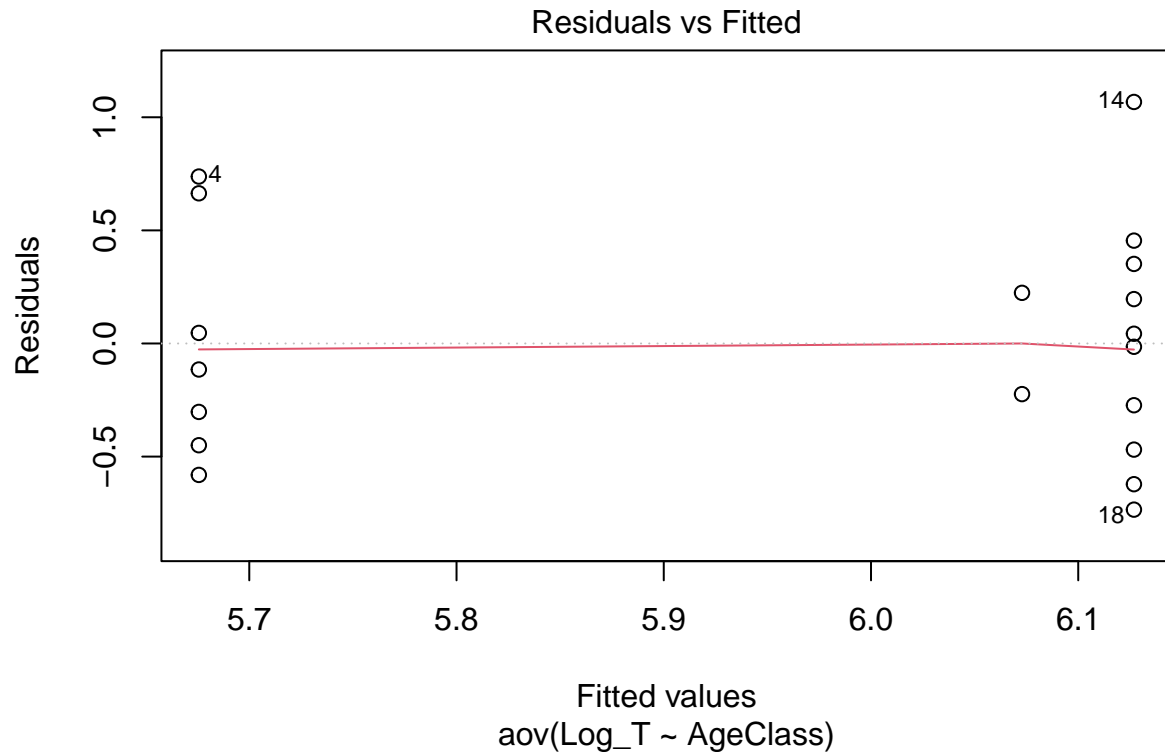
```
shapiro_test(residuals(model_logt_1Q_3Q))
```

```
## # A tibble: 1 x 3
##   variable                statistic p.value
##   <chr>                  <dbl>   <dbl>
## 1 residuals(model_logt_1Q_3Q)  0.968  0.727
```

*p-value = 0.72729, so we can assume normal distribution of the residuals.*

**Check for homogeneity of variance**

```
plot(test1Q_3Q_anova, 1)
```



*Homogeneous*

```
leveneTest(Log_T ~ AgeClass, data = testosterone1Q_3Q.log)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 2  0.3378 0.7183
##      16
```

*p-value = 0.7183, so can assume homogeneity!*

## Model 2: Testosterone Analysis #2

Testing mean differences of testosterone levels between three male elephant demographic groups ( $n = 37$ ).

*Testosterone was log transformed prior to these analyses.*

### Analysis and results

#### ANOVA

```
t.anova <- aov(Log_T ~ MaleType, data=testosterone.log)
summary(t.anova)
```

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## MaleType     2  7.875   3.937   14.16 3.37e-05 ***
## Residuals    34  9.456   0.278
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

*Significant difference between male types  $p = 3.37e-05$*

### Tukey post-hoc

```
TukeyHSD(t.anova)
```

```
##    Tukey multiple comparisons of means
##      95% family-wise confidence level
##
## Fit: aov(formula = Log_T ~ MaleType, data = testosterone.log)
##
## $MaleType
##              diff          lwr          upr      p adj
## musthadult-adult    1.3734649  0.7273120  2.0196178 0.0000269
## subadult-adult      0.6464536  0.1699363  1.1229710 0.0058896
## subadult-musthadult -0.7270113 -1.3321889 -0.1218336 0.0156206
```

*Significant difference between musth 4Q and non-musth 4Q ( $p=0.0000269$ ), musth 4Q and non-musth 1Q-3Q ( $p=0.0156206$ ), non-musth 4Q-non-musth 1Q-3Q group ( $p=0.0058896$ )*

## Check assumptions

### Check for outliers

```
t.log.outliers <- testosterone.log %>%
  group_by(MaleType) %>%
  identify_outliers(Log_T)
```

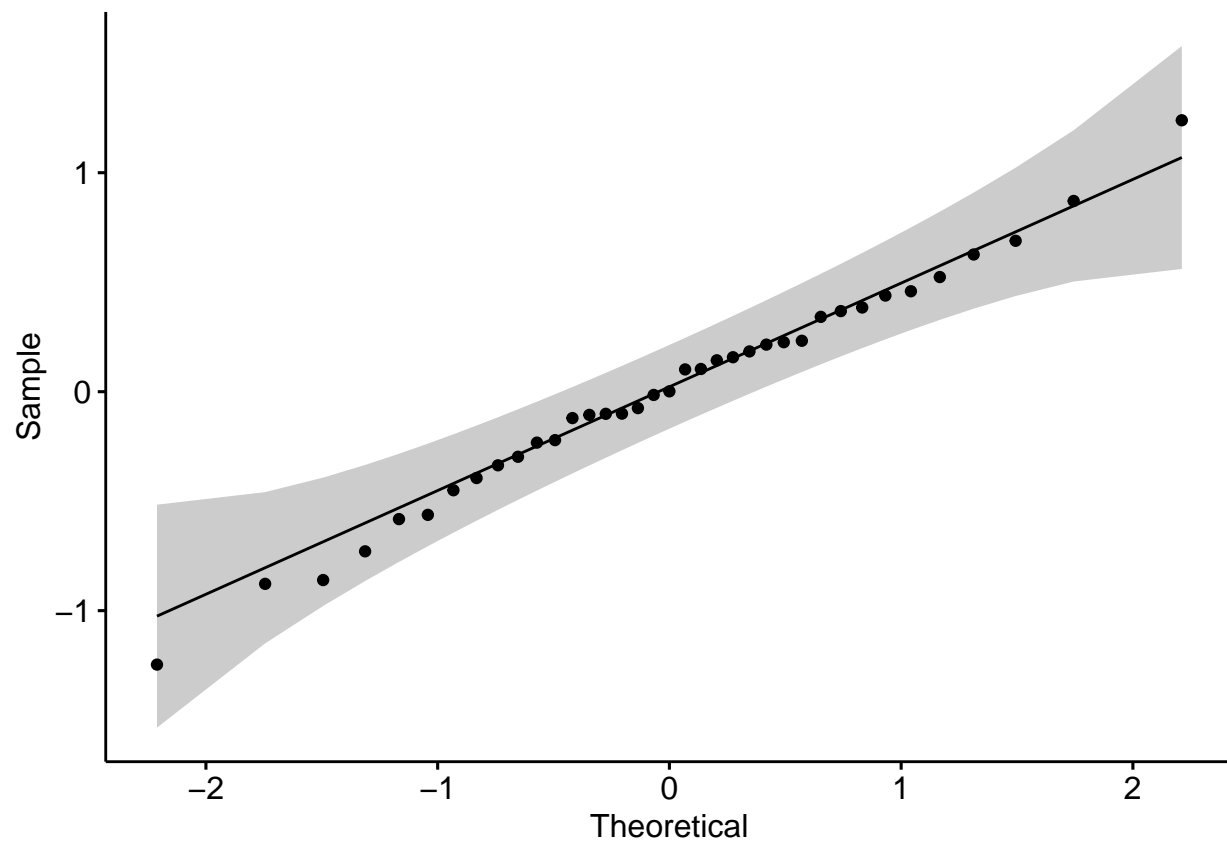
*Three outliers detected, but will keep if normality assumptions are not violated*

### Check for normality Build the model

```
model_t_log <- lm(Log_T ~ MaleType, data = testosterone.log)
```

Create a QQ plot of the residuals

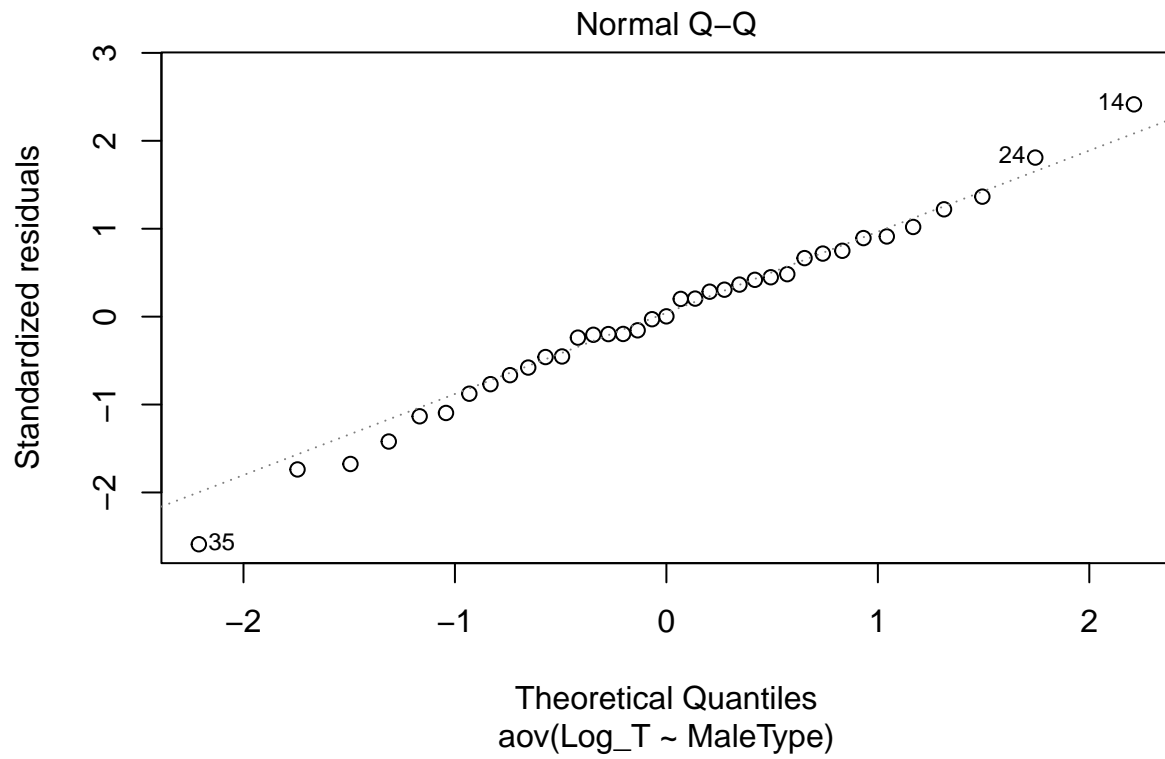
```
ggqqplot(residuals(model_t_log))
```

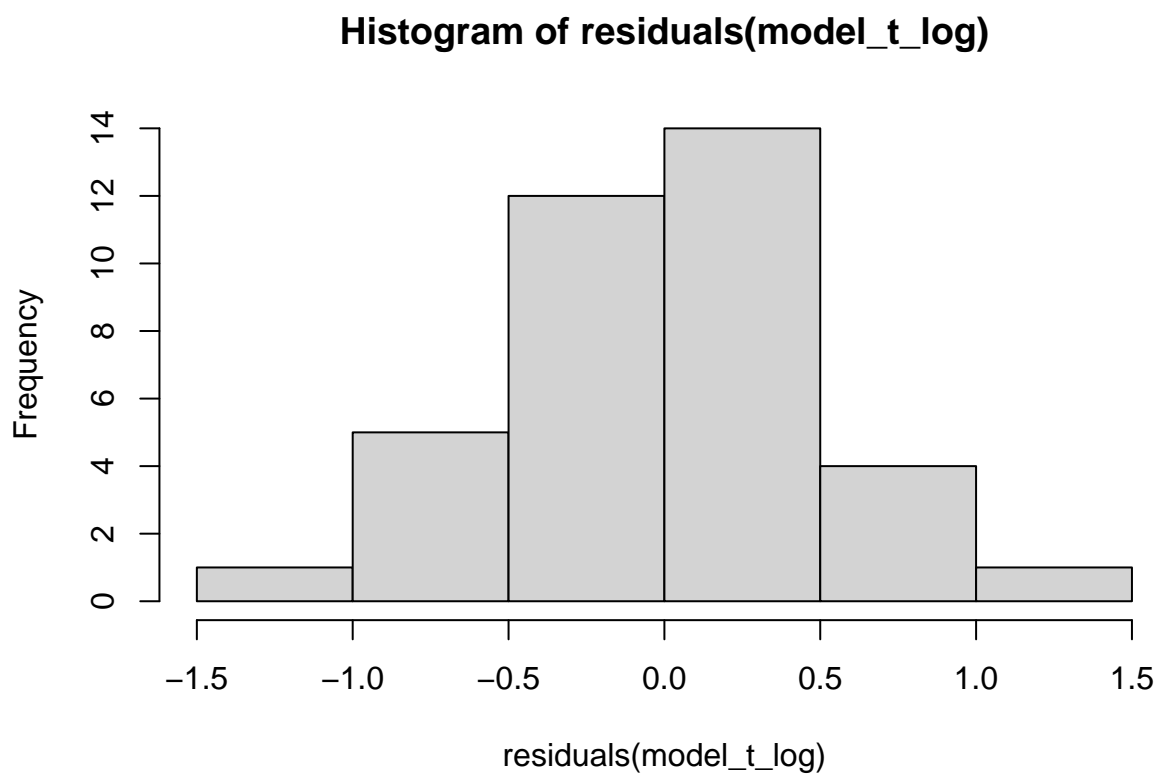


*QQ Plot looks normal!*

```
plot(t.anova, 2)
```







*Normal*

Compute the Shapiro-Wilk test of normality

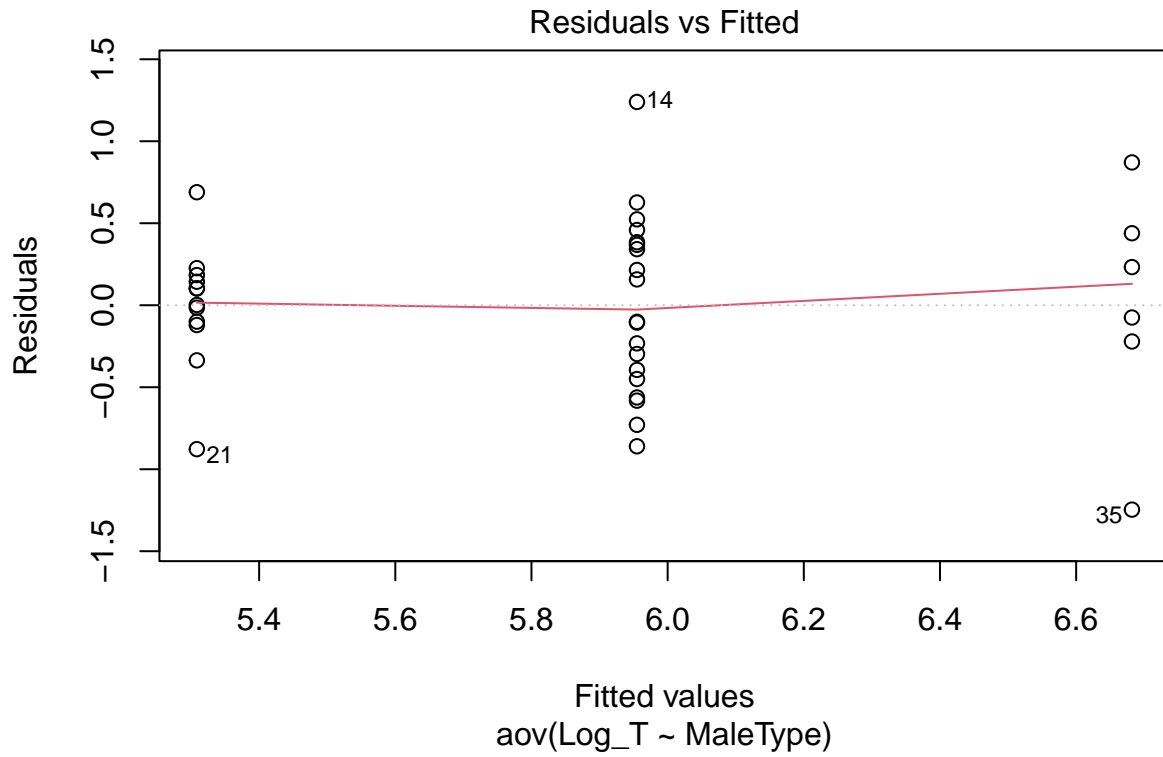
```
shapiro_test(residuals(model_t_log))
```

```
## # A tibble: 1 x 3
##   variable          statistic p.value
##   <chr>             <dbl>   <dbl>
## 1 residuals(model_t_log) 0.992 0.996
```

*p-value = 0.9956728, so we can assume normal distribution of the residuals*

**Check for homogeneity of variance**

```
plot(t.anova, 1)
```



*Looks good, and appears unbiased and homoscedastic*

```
leveneTest(Log_T ~ MaleType, data = testosterone.log)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group  2  1.9969 0.1514
##      34
```

*p-value = 0.1514, so can assume homogeneity*

## Model 4: Linear Regressions

Testing the predictive power of testosterone and male group on response score

### Model 4a. Simple Linear Regression (n = 19)

Analysis and results

```
simple_reg_model <- lm(ResponseScore ~ Testosterone, data = T.malegroup)
summary(simple_reg_model)
```

```
##
## Call:
## lm(formula = ResponseScore ~ Testosterone, data = T.malegroup)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.54814 -0.32363  0.06306  0.32076  0.37603
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.5958703  0.1234827   4.826 0.000158 ***
## Testosterone 0.0001225  0.0001814   0.675 0.508521
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3373 on 17 degrees of freedom
## Multiple R-squared:  0.02613,    Adjusted R-squared:  -0.03116
## F-statistic: 0.4561 on 1 and 17 DF,  p-value: 0.5085
```

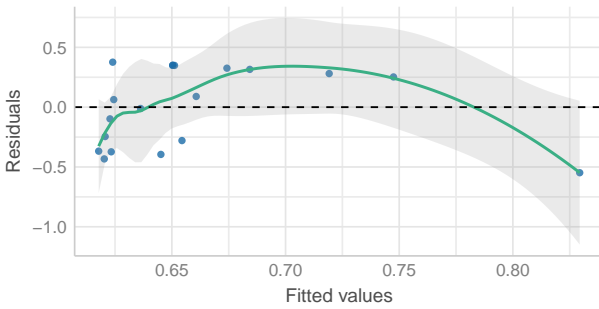
*Testosterone is not a significant predictor of response score ( $p = 0.509$ ).*

## Check assumptions

```
check_model(simple_reg_model, check=c("vif", "qq", "normality", "linearity",
                                       "homogeneity", "outliers"))
```

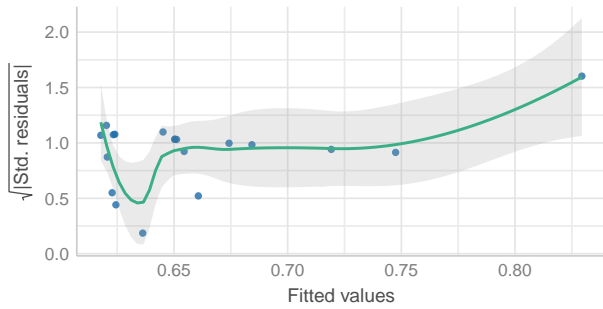
### Linearity

Reference line should be flat and horizontal



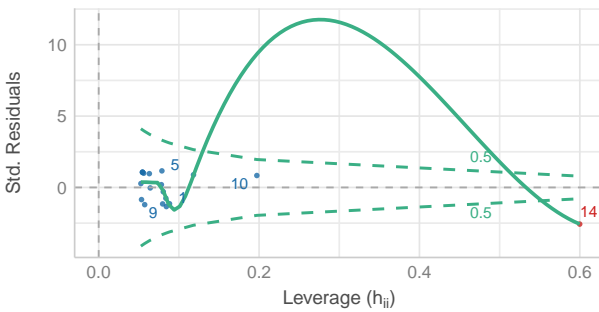
### Homogeneity of Variance

Reference line should be flat and horizontal



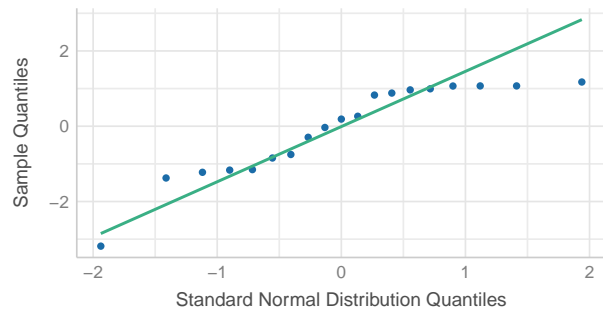
### Influential Observations

Points should be inside the contour lines



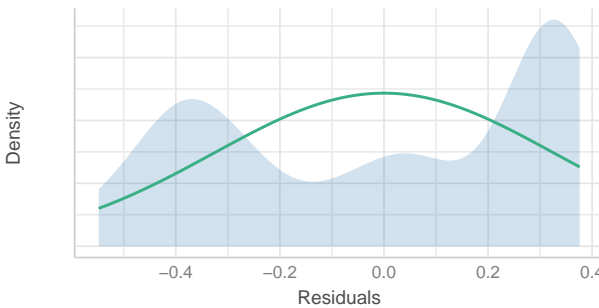
### Normality of Residuals

Dots should fall along the line



### Normality of Residuals

Distribution should be close to the normal curve



*Mild violations of linearity and homogeneity, as well as an extreme outlier.*

**Compute the Shapiro-Wilk test of normality**

```
shapiro_test(residuals(simple_reg_model))
```

```
## # A tibble: 1 x 3
##   variable      statistic p.value
##   <chr>          <dbl>   <dbl>
## 1 residuals(simple_reg_model) 0.873 0.0163
```

*p-value 0.016, so assume normality assumption is not met*

**Outlier evaluation**

```
simple_reg_model_diagnostics <- ls.diag(simple_reg_model)
```

## Leverage

```
simple_reg_model_diagnostics$hat
```

```
## [1] 0.08832879 0.06430430 0.05606815 0.08375517 0.07883458 0.05736951
## [7] 0.05444105 0.08054872 0.08438490 0.19721301 0.07818460 0.05342343
## [13] 0.11820877 0.59983369 0.07976961 0.05263205 0.05475283 0.05475283
## [19] 0.06319402
```

- Leverage should be considered moderately unusual when above  $2(k+1)/n$  and very unusual when above  $3(k+1)/n$ , where  $k$  is the number of predictors and  $n$  is the number of data points.
- In the case of our model, moderate:  $2(2+1)/19 = 0.3156$ ; very:  $3(2+1)/19 = 0.4737$
- We have one data point over this threshold with a leverage value of 0.5998 (very unusual).

## Standardized Residuals

```
simple_reg_model_diagnostics$std.res
```

```
## [1] -1.14189762 -0.03444435 0.99400759 -0.76077183 1.16137474 -1.20653659
## [7] 1.06341228 -0.30230381 -1.34063674 0.83542561 0.19471078 -0.85141476
## [13] 0.88641965 -2.56860367 -1.15361308 0.27196875 1.06603231 1.06603231
## [19] 0.96697277
```

- Standardized residuals should be considered moderately unusual when beyond  $\pm 2$ , and very unusual when beyond  $\pm 3$ .
- We have one data point at -2.5686 (moderately unusual).

## Cook's D

```
simple_reg_model_diagnostics$cooks
```

```
## [1] 6.316673e-02 4.076724e-05 2.934438e-02 2.645324e-02 5.771569e-02
## [6] 4.429867e-02 3.255451e-02 4.003015e-03 8.282168e-02 8.572763e-02
## [11] 1.607782e-03 2.045636e-02 5.266628e-02 4.944866e+00 5.768079e-02
## [16] 2.054658e-03 3.291334e-02 3.291334e-02 3.153732e-02
```

- Cook's D should be considered moderately unusual when beyond 0.5 and very unusual when beyond 1.
- We have one data point with a value of 4.9449 (very unusual).

Upon evaluation of which data points represented these values, it was revealed that all three were the same data point. Because of the extreme nature of this data point, we have removed it from proceeding linear regression models outlined in this section (section 4).

## Analysis and results: Without the outlier (n = 18)

```
simple_reg_nooutlier <- lm(ResponseScore ~ Testosterone,
                           data = T.malegroup.nooutlier)
summary(simple_reg_nooutlier)

##
## Call:
## lm(formula = ResponseScore ~ Testosterone, data = T.malegroup.nooutlier)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.39752 -0.23756  0.00866  0.18396  0.46795
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.3789507  0.1206237   3.142  0.00631 **
## Testosterone 0.0006673  0.0002250   2.965  0.00911 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.272 on 16 degrees of freedom
## Multiple R-squared:  0.3547, Adjusted R-squared:  0.3143
## F-statistic: 8.794 on 1 and 16 DF,  p-value: 0.009113
```

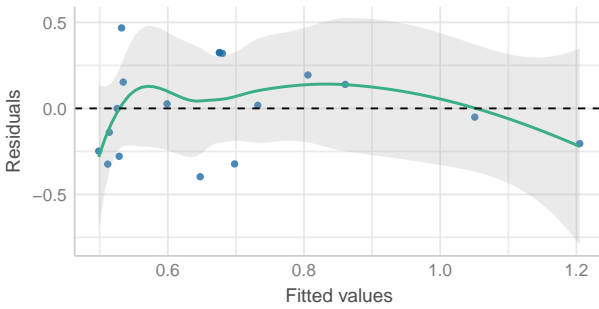
*Testosterone is a significant predictor of response score ( $p = 0.00911$ )*

## Check assumptions

```
check_model(simple_reg_nooutlier, check=c("vif", "qq", "normality", "linearity",
                                           "homogeneity", "outliers"))
```

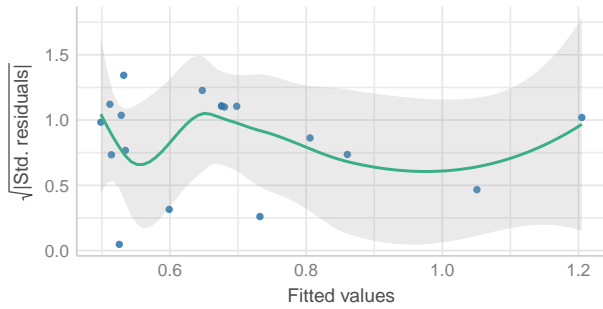
### Linearity

Reference line should be flat and horizontal



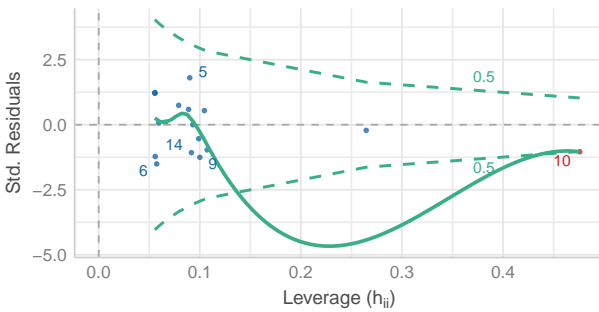
### Homogeneity of Variance

Reference line should be flat and horizontal



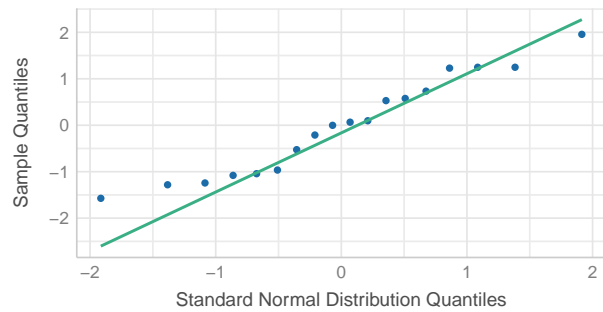
### Influential Observations

Points should be inside the contour lines



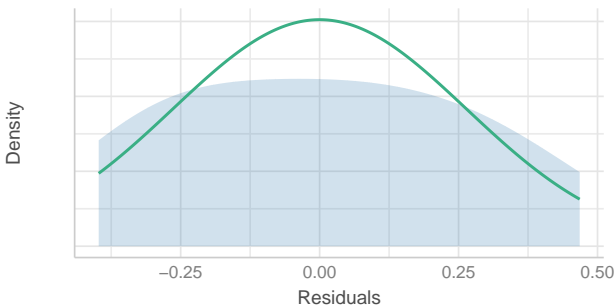
### Normality of Residuals

Dots should fall along the line



### Normality of Residuals

Distribution should be close to the normal curve



*Slight violations of linearity and homogeneity of variance. Another outlier but it was left in due to lack of severity and small sample size. See below.*

### Compute the Shapiro-Wilk test of normality

```
shapiro_test(residuals(simple_reg_nooutlier))
```

```
## # A tibble: 1 x 3
##   variable      statistic p.value
##   <chr>         <dbl>   <dbl>
## 1 residuals(simple_reg_nooutlier) 0.950 0.432
```

*p-value = 0.432, so we can assume normality.*

### Outlier evaluation



```
simple_reg_nooutlier_diagnostics <- ls.diag(simple_reg_nooutlier)
```

## Leverage

```
simple_reg_nooutlier_diagnostics$hat
```

```
## [1] 0.10730046 0.06616528 0.07909678 0.09890855 0.09008969 0.05737685
## [7] 0.05556048 0.09313386 0.10005386 0.47583011 0.08894401 0.05595297
## [13] 0.26463321 0.09174624 0.05942195 0.05561382 0.05561382 0.10455806
```

- Leverage should be considered moderately unusual when above  $2(k+1)/n$  and very unusual when above  $3(k+1)/n$ , where  $k$  is the number of predictors and  $n$  is the number of data points.
- In the case of our model, moderate:  $2(2+1)/18 = 0.33$ ; very:  $3(2+1)/18 = 0.5$
- We have one data point over this threshold with a leverage value of 0.4758 (moderately unusual).

## Standardized Residuals

```
simple_reg_nooutlier_diagnostics$std.res
```

```
## [1] -0.966763382 0.099448844 0.744342702 -0.538310744 1.803529184
## [6] -1.505256495 1.209963606 -0.002237635 -1.256741441 -1.040291671
## [11] 0.589094532 -1.222246822 -0.217670226 -1.074315638 0.067852176
## [16] 1.226521251 1.226521251 0.541960429
```

- Standardized residuals should be considered moderately unusual when beyond  $\pm 2$ , and very unusual when beyond  $\pm 3$ .
- None beyond either threshold.

## Cook's D

```
simple_reg_nooutlier_diagnostics$cooks
```

```
## [1] 5.617029e-02 3.503722e-04 2.379363e-02 1.590381e-02 1.610248e-01
## [6] 6.895879e-02 4.306321e-02 2.571063e-07 8.779690e-02 4.912020e-01
## [11] 1.693993e-02 4.427080e-02 8.525275e-03 5.829280e-02 1.454285e-04
## [16] 4.429485e-02 4.429485e-02 1.714846e-02
```

- Cook's D should be considered moderately unusual when beyond 0.5 and very unusual when beyond 1.
- None beyond either threshold.

**Outlier was not removed due to lack of severity.**

## Model 4b. Additive Linear Regression (n = 18)

*Same data used as simple linear regression: no outlier.*

### Analysis and results

```
additive_model <- lm(ResponseScore ~ Testosterone + MaleType,
                      data = T.malegroup.nooutlier)
summary(additive_model)

##
## Call:
## lm(formula = ResponseScore ~ Testosterone + MaleType, data = T.malegroup.nooutlier)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.41328 -0.10121 -0.04034  0.15191  0.35521
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.8819126   0.2110834     4.178 0.000929 ***
## Testosterone    0.0001517   0.0002364     0.642 0.531400
## MaleTypenonmusth1Q-3Q -0.1661757   0.1482690    -1.121 0.281243
## MaleTypenonmusth4Q   -0.5849980   0.1844563    -3.171 0.006795 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2069 on 14 degrees of freedom
## Multiple R-squared:  0.6734, Adjusted R-squared:  0.6035
## F-statistic: 9.623 on 3 and 14 DF,  p-value: 0.001052
```

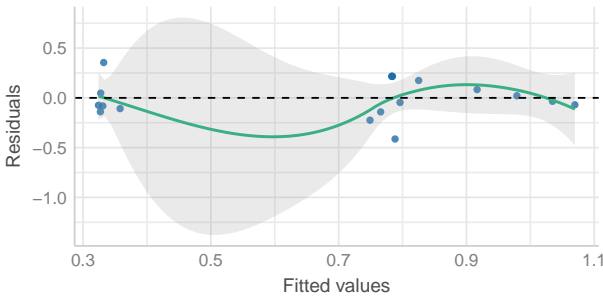
*MaleGroup:Non-musth4Q is significant ( $p = 0.0068$ )*

### Check assumptions

```
check_model(additive_model, check=c("vif", "qq", "normality", "linearity",
                                     "homogeneity", "outliers"))
```

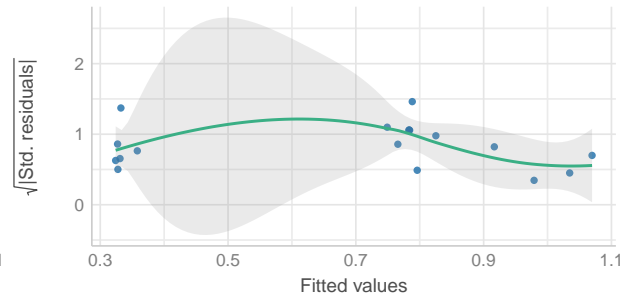
### Linearity

Reference line should be flat and horizontal



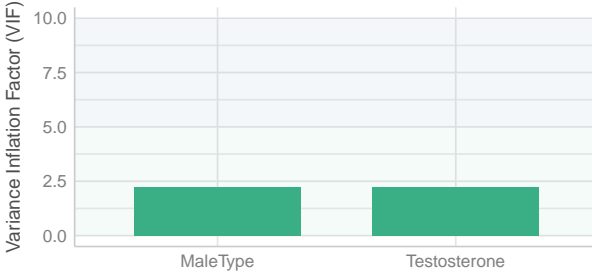
### Homogeneity of Variance

Reference line should be flat and horizontal



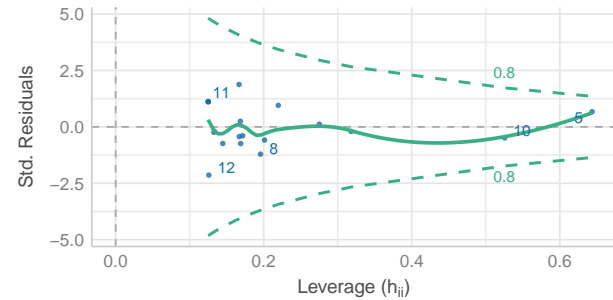
### Collinearity

Higher bars (>5) indicate potential collinearity issues



### Influential Observations

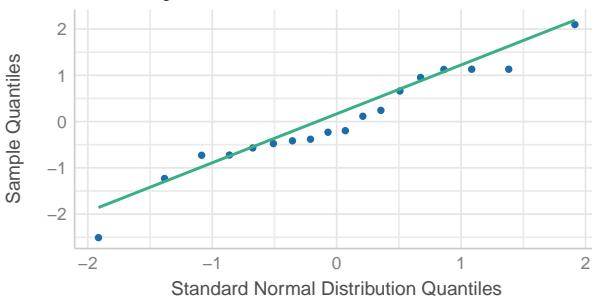
Points should be inside the contour lines



low (< 5) moderate (< 10) high (>= 10)

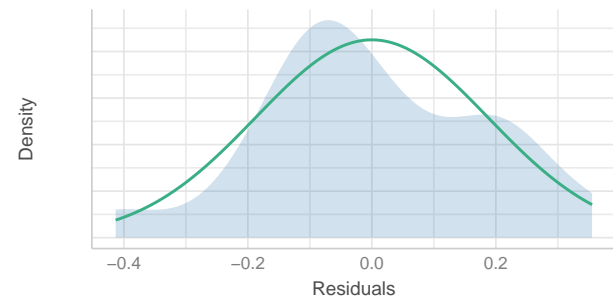
### Normality of Residuals

Dots should fall along the line



### Normality of Residuals

Distribution should be close to the normal curve



Moderate violations of linearity and homogeneity of variance. See section “Model 4b assumptions violations tests” below for attempts to correct for these violations.

### Compute the Shapiro-Wilk test of normality

```
shapiro_test(residuals(additive_model))
```

```
## # A tibble: 1 x 3
##   variable      statistic p.value
##   <chr>         <dbl>   <dbl>
## 1 residuals(additive_model)  0.968  0.760
```

*p-value 0.760 so we can assume normality.*

### Model Comparisons: Simple linear regression and additive linear regression

```
anova(simple_reg_nooutlier, additive_model)
```

```
## Analysis of Variance Table
##
## Model 1: ResponseScore ~ Testosterone
## Model 2: ResponseScore ~ Testosterone + MaleType
##   Res.Df    RSS Df Sum of Sq    F    Pr(>F)
## 1      16 1.18380
## 2      14 0.59907  2    0.58473 6.8325 0.008499 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The additive model significantly better at explaining variation in response score ( $p = 0.0085$ ).

## Model 4b assumptions violations tests

Several methods were used to address the linearity and homogeneity of variance assumption violations including, (1) log transformation of the predictor variable testosterone, (2) log transformation of the response variable, (3) log transformation of both testosterone and the response variable in the same model, (4) quadratic transformation of testosterone, (5) taking the recipricol of testosterone, and (6) generalized additive models (GAM) of the simple linear regression (Model 4a) and the additive linear regression (Model 4b), all of which are detailed below. None of these were successful, therefore the linear models were used in the analysis.

*n = 18 for all proceeding models*

### 1. Log tranformation of the predictor variable, testosterone

#### Analysis and results

```
log_T_model <- lm(ResponseScore ~ logT + MaleType, data = T.malegroup.nooutlier)
summary(log_T_model)
```

```
##
## Call:
## lm(formula = ResponseScore ~ logT + MaleType, data = T.malegroup.nooutlier)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.42001 -0.11814 -0.04955  0.14899  0.35319
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.3422    0.7788   0.439  0.66709
## logT              0.1015    0.1191   0.852  0.40850
## MaleTypenonmusth1Q-3Q -0.1732    0.1348  -1.285  0.21974
## MaleTypenonmusth4Q   -0.5611    0.1811  -3.098  0.00787 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

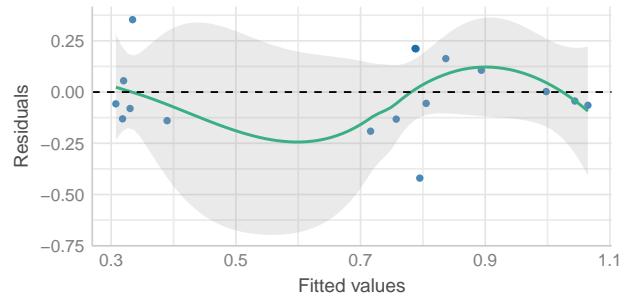
```
## Residual standard error: 0.2046 on 14 degrees of freedom
## Multiple R-squared:  0.6804, Adjusted R-squared:  0.6119
## F-statistic: 9.935 on 3 and 14 DF,  p-value: 0.000908
```

## Check assumptions

```
check_model(log_T_model, check=c("vif", "qq", "normality", "linearity",
                                "homogeneity", "outliers"))
```

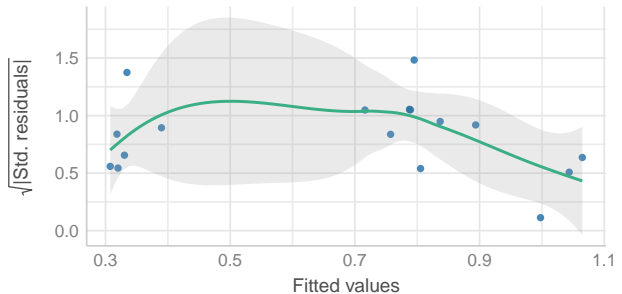
### Linearity

Reference line should be flat and horizontal



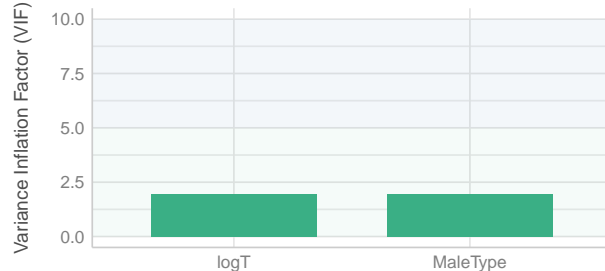
### Homogeneity of Variance

Reference line should be flat and horizontal



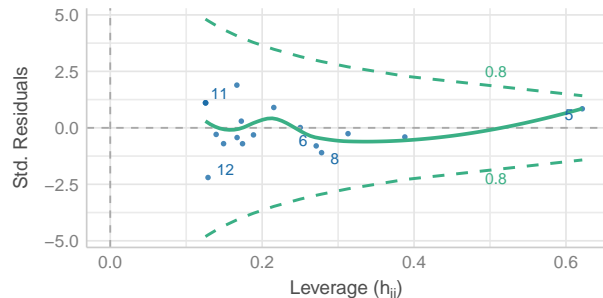
### Collinearity

Higher bars (>5) indicate potential collinearity issues



### Influential Observations

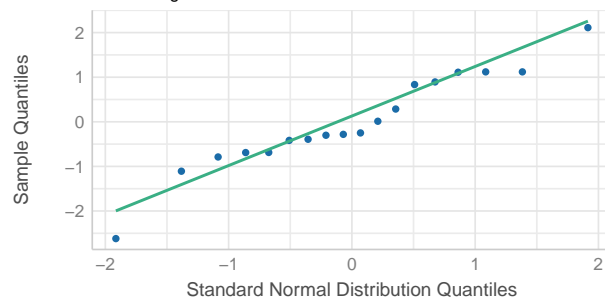
Points should be inside the contour lines



low (< 5) moderate (< 10) high (>= 10)

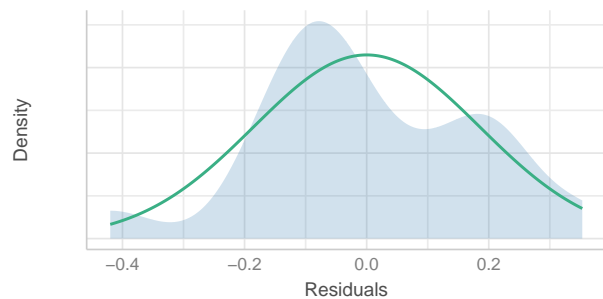
### Normality of Residuals

Dots should fall along the line



### Normality of Residuals

Distribution should be close to the normal curve



*Very similar to non-transformed additive model, if not violating the assumption of homogeneity of variance a bit more.*

## 2. Log transformation of the response variable

### Analysis and results

```
log_resp_model <- lm(logResp ~ Testosterone + MaleType,
                     data = T.malegroup.nooutlier)
summary(log_resp_model)

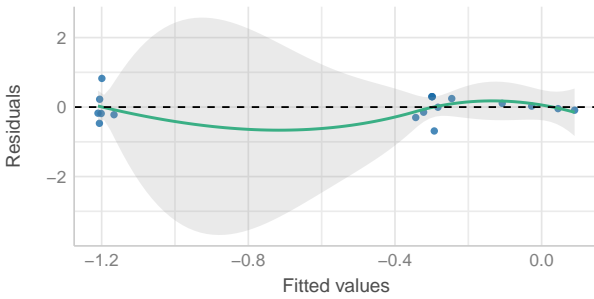
##
## Call:
## lm(formula = logResp ~ Testosterone + MaleType, data = T.malegroup.nooutlier)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.68801 -0.18291 -0.02479  0.24001  0.82471
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -0.1523937   0.3856532   -0.395   0.6987
## Testosterone    0.0001958   0.0004319    0.453   0.6573
## MaleTypenonmusth1Q-3Q -0.2340439   0.2708901   -0.864   0.4022
## MaleTypenonmusth4Q   -1.0926689   0.3370050   -3.242   0.0059 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3779 on 14 degrees of freedom
## Multiple R-squared:  0.6806, Adjusted R-squared:  0.6122
## F-statistic: 9.946 on 3 and 14 DF,  p-value: 0.0009034
```

### Check assumptions

```
check_model(log_resp_model, check=c("vif", "qq", "normality", "linearity",
                                   "homogeneity", "outliers"))
```

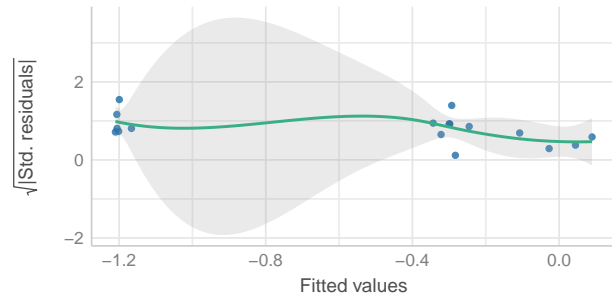
#### Linearity

Reference line should be flat and horizontal



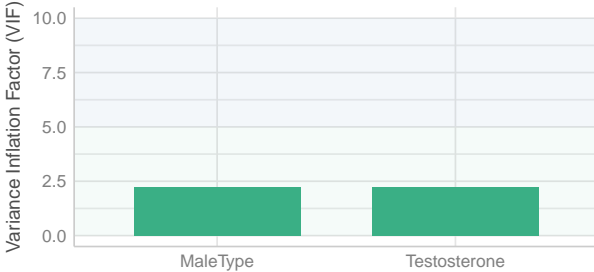
#### Homogeneity of Variance

Reference line should be flat and horizontal



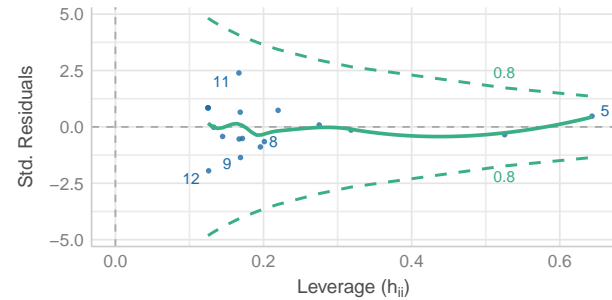
#### Collinearity

Higher bars (>5) indicate potential collinearity issues



#### Influential Observations

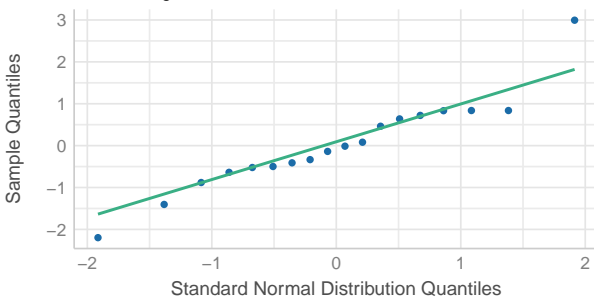
Points should be inside the contour lines



low (< 5) moderate (< 10) high ( $\geq 10$ )

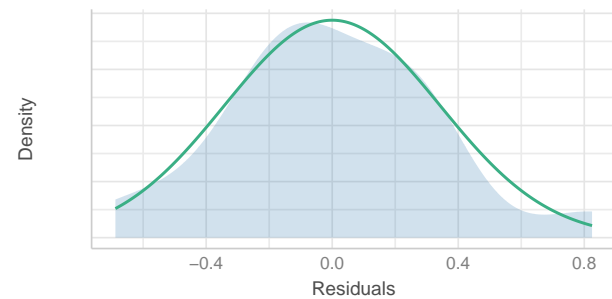
#### Normality of Residuals

Dots should fall along the line



#### Normality of Residuals

Distribution should be close to the normal curve



*Extremely similar to non-transformed additive model, normality assumption slightly better*

### 3. Log transformation of both testosterone and the response variable in the same model

#### Analysis and results

```
two_logs_model <- lm(logResp ~ logT + MaleType, data = T.malegroup.nooutlier)
summary(two_logs_model)
```

```
##
## Call:
## lm(formula = logResp ~ logT + MaleType, data = T.malegroup.nooutlier)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.69702 -0.17668 -0.03766  0.23336  0.82208
```

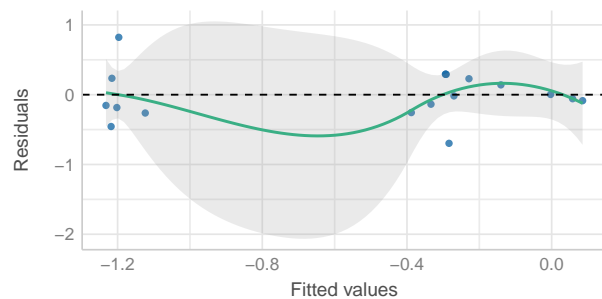
```
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -0.8689     1.4297  -0.608  0.55306
## logT           0.1340     0.2186   0.613  0.54964
## MaleTypenonmusth1Q-3Q -0.2419     0.2475  -0.977  0.34513
## MaleTypenonmusth4Q   -1.0586     0.3325  -3.183  0.00664 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3757 on 14 degrees of freedom
## Multiple R-squared:  0.6844, Adjusted R-squared:  0.6168
## F-statistic: 10.12 on 3 and 14 DF,  p-value: 0.000833
```

## Check assumptions

```
check_model(two_logs_model, check=c("vif", "qq", "normality", "linearity",
                                     "homogeneity", "outliers"))
```

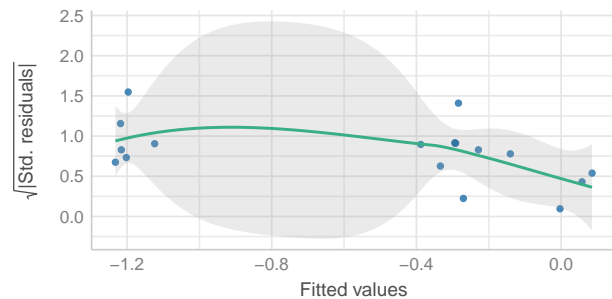
### Linearity

Reference line should be flat and horizontal



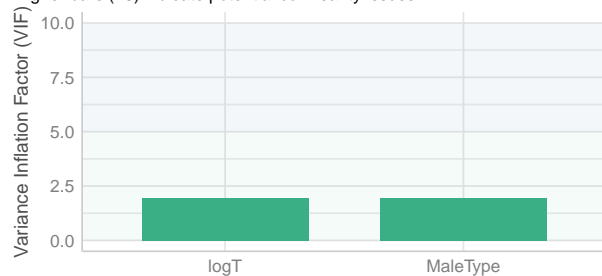
### Homogeneity of Variance

Reference line should be flat and horizontal



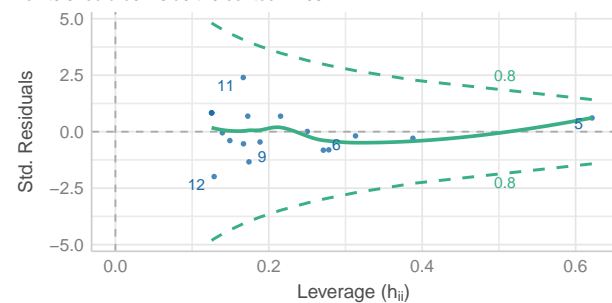
### Collinearity

Higher bars (>5) indicate potential collinearity issues



### Influential Observations

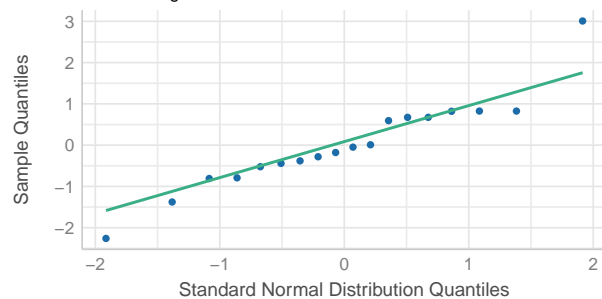
Points should be inside the contour lines



low (< 5) moderate (< 10) high (>= 10)

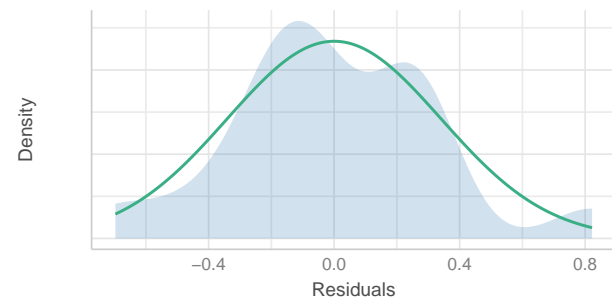
### Normality of Residuals

Dots should fall along the line



### Normality of Residuals

Distribution should be close to the normal curve





*Similar to non-transformed additive model, normality assumption slightly worse.*

## 4. Quadratic transformation of testosterone

### Analysis and results

```
quad_T_model <- lm(ResponseScore ~ Testosterone + quadT + MaleType,
                    data = T.malegroup.nooutlier)
summary(quad_T_model)
```

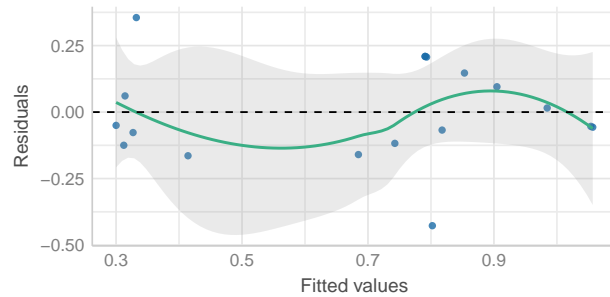
```
##
## Call:
## lm(formula = ResponseScore ~ Testosterone + quadT + MaleType,
##     data = T.malegroup.nooutlier)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.42719 -0.10748 -0.05195  0.13390  0.35531
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    7.481e-01  2.804e-01   2.668  0.01933 *
## Testosterone    7.947e-04  9.001e-04   0.883  0.39335
## quadT          -4.877e-07  6.580e-07  -0.741  0.47175
## MaleTypenonmusth1Q-3Q -2.144e-01  1.642e-01  -1.306  0.21417
## MaleTypenonmusth4Q    -5.747e-01  1.880e-01  -3.057  0.00918 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2103 on 13 degrees of freedom
## Multiple R-squared:  0.6867, Adjusted R-squared:  0.5903
## F-statistic: 7.123 on 4 and 13 DF,  p-value: 0.002894
```

### Check assumptions

```
check_model(quad_T_model, check=c("vif", "qq", "normality", "linearity",
                                   "homogeneity", "outliers"))
```

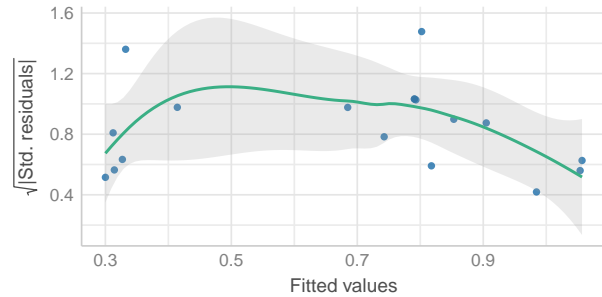
### Linearity

Reference line should be flat and horizontal



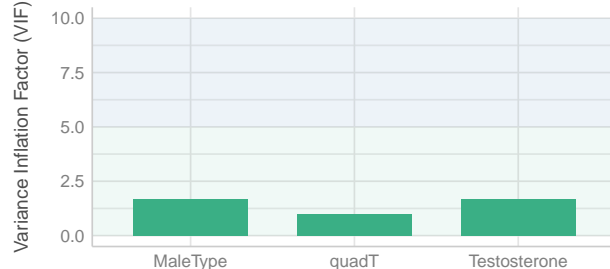
### Homogeneity of Variance

Reference line should be flat and horizontal



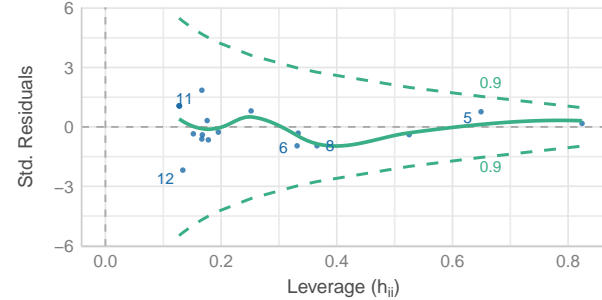
### Collinearity

Higher bars (>5) indicate potential collinearity issues



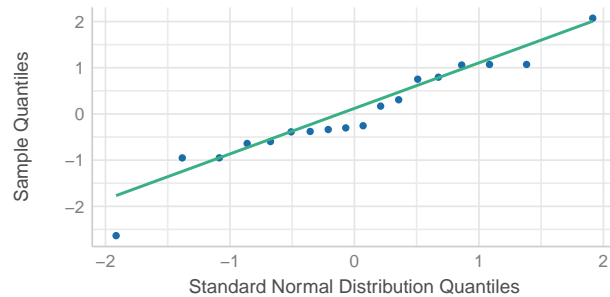
### Influential Observations

Points should be inside the contour lines



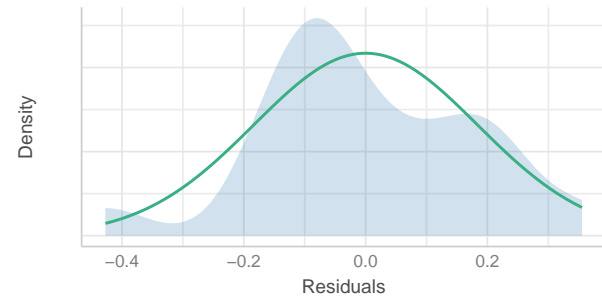
### Normality of Residuals

Dots should fall along the line



### Normality of Residuals

Distribution should be close to the normal curve



*Similar to non-transformed additive model, normality assumption slightly worse*

## 5. Reciprical transformation of testosterone

### Analysis and results

```
recip_T_model <- lm(ResponseScore ~ recipT + MaleType,
                     data = T.malegroup.nooutlier)
summary(recip_T_model)
```

```
##
## Call:
## lm(formula = ResponseScore ~ recipT + MaleType, data = T.malegroup.nooutlier)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.42541 -0.11188 -0.03768  0.15309  0.34649
```

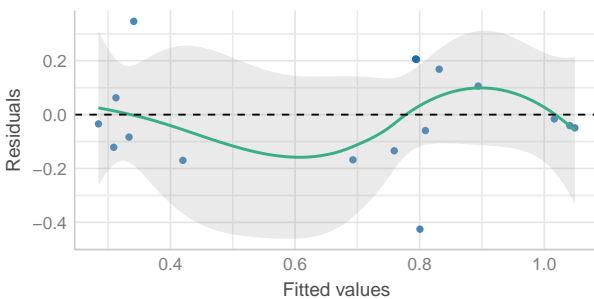
```
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.0844    0.1337   8.113 1.16e-06 ***
## recipT           -43.7318   44.9987  -0.972  0.34762
## MaleTypenonmusth1Q-3Q -0.1926    0.1266  -1.521  0.15060
## MaleTypenonmusth4Q   -0.5559    0.1737  -3.200  0.00643 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2031 on 14 degrees of freedom
## Multiple R-squared:  0.6851, Adjusted R-squared:  0.6176
## F-statistic: 10.15 on 3 and 14 DF,  p-value: 0.0008214
```

## Check assumptions

```
check_model(recip_T_model, check=c("vif", "qq", "normality", "linearity",
                                   "homogeneity", "outliers"))
```

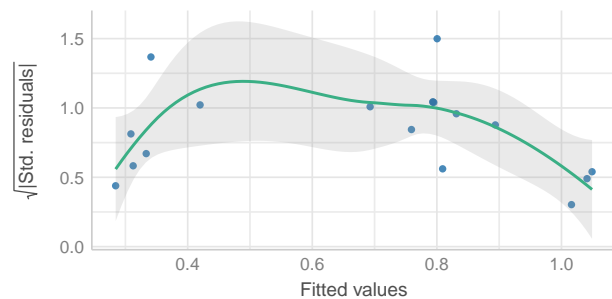
### Linearity

Reference line should be flat and horizontal



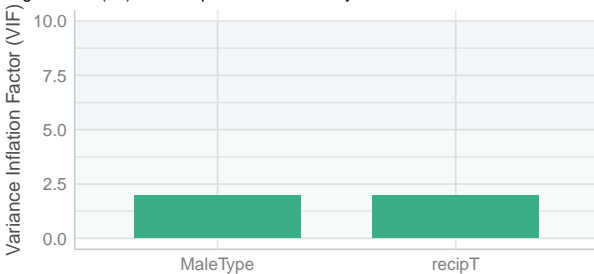
### Homogeneity of Variance

Reference line should be flat and horizontal



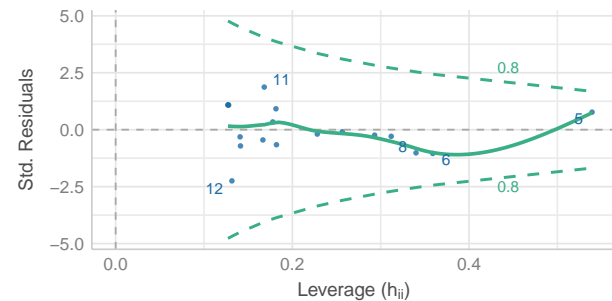
### Collinearity

Higher bars (>5) indicate potential collinearity issues



### Influential Observations

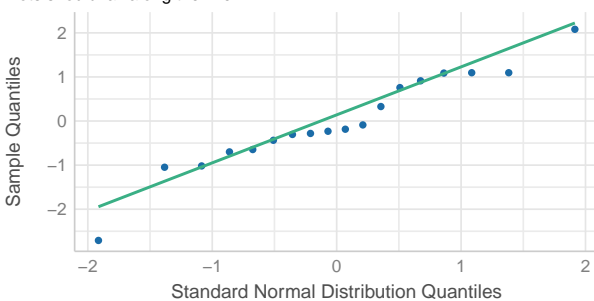
Points should be inside the contour lines



low (< 5) moderate (< 10) high (>= 10)

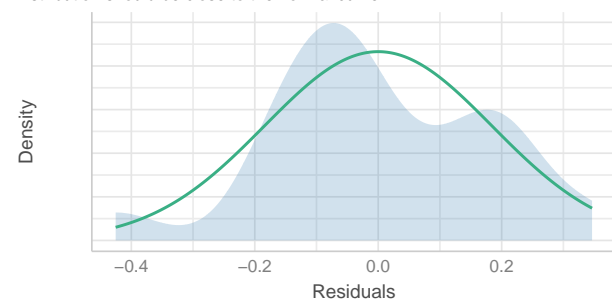
### Normality of Residuals

Dots should fall along the line



### Normality of Residuals

Distribution should be close to the normal curve



*Similar to non-transformed additive model, homogeneity of variance and normality assumptions slightly worse*

## 6. GAM simple regression (testosterone predictor only) and GAM additive regression (testosterone and male group predictors)

Both GAM models will have their linear counterparts ran using the `gam()` function for easy comparison. GAM models were run using a smoothing factor of 0.5 on the predictor variable, testosterone. This allows for a curvature in the line to fit the data at its upper limit.

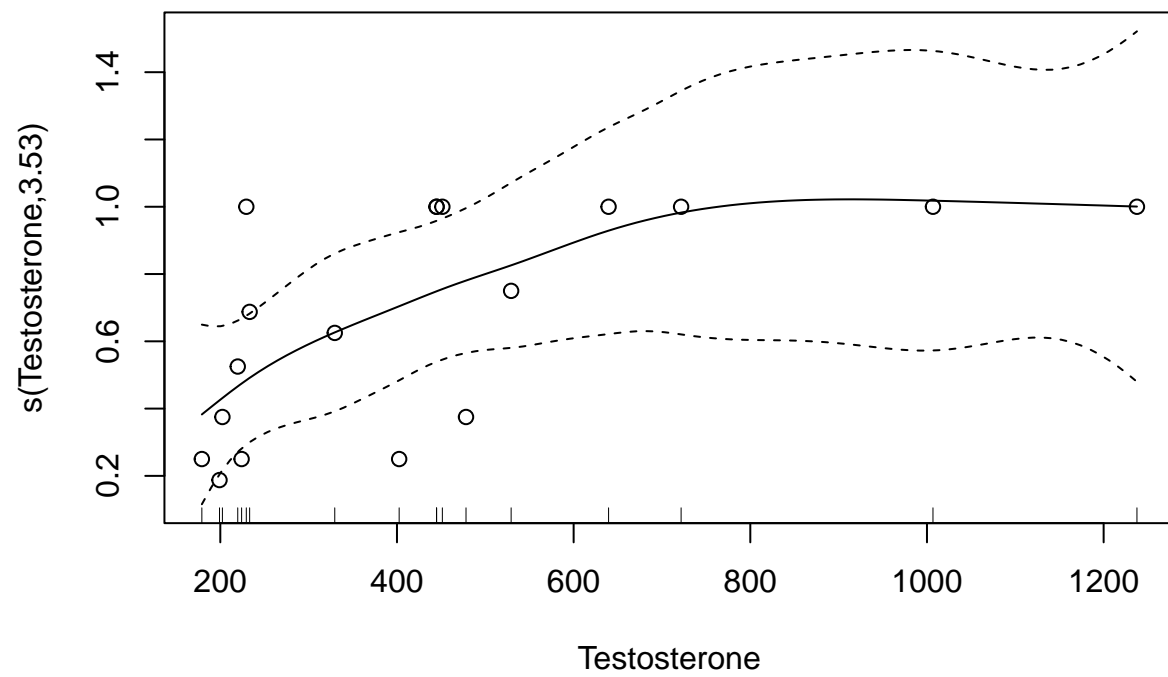
### GAM simple regression

#### Smoothed model

```
gam_smoothed_T <- gam(ResponseScore ~ s(Testosterone, sp=0.5), data = T.malegroup.nooutlier)
summary(gam_smoothed_T)
```

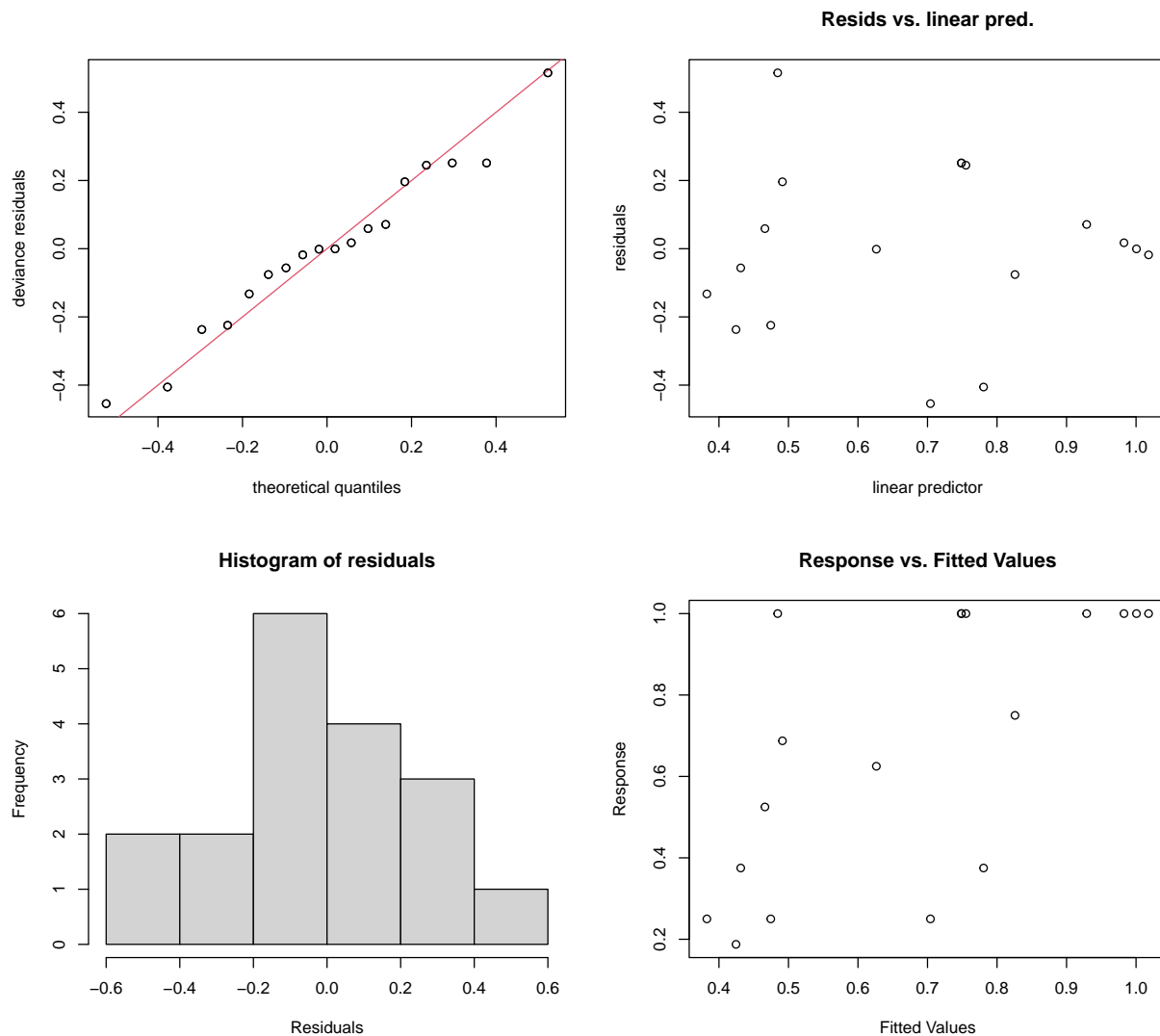
```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## ResponseScore ~ s(Testosterone, sp = 0.5)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.68194    0.06434    10.6 6.55e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##             edf Ref.df    F p-value
## s(Testosterone) 3.533  4.269 2.522  0.089 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.309   Deviance explained = 45.3%
## GCV = 0.099597   Scale est. = 0.074516   n = 18
```

```
plot(gam_smoothed_T, residuals=TRUE, pch=1, seWithMean = T,
     shift = coef(gam_smoothed_T)[1])
```



Assumptions

```
gam.check(gam_smoothed_T, pch=1)
```



```
##
## Method: GCV   Optimizer: magic
## Model required no smoothing parameter selectionModel rank = 10 / 10
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##               k'   edf k-index p-value
## s(Testosterone) 9.00 3.53    1.1    0.61
```

*Similar to simple linear regression model.*

### Linear model

```
gam_linear_T <- gam(ResponseScore ~ Testosterone, data = T.malegroup.nooutlier)
summary(gam_linear_T)
```

```
##
```

```
## Family: gaussian
## Link function: identity
##
## Formula:
## ResponseScore ~ Testosterone
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.3789507  0.1206237   3.142  0.00631 **
## Testosterone 0.0006673  0.0002250   2.965  0.00911 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
## R-sq.(adj) =  0.314   Deviance explained = 35.5%
## GCV = 0.083236   Scale est. = 0.073988   n = 18
```

**AIC model comparison of GAM smoothed and GAM linear for the simple regression model**

```
AIC(gam_linear_T, gam_smoothed_T)
```

```
##             df      AIC
## gam_linear_T  3.000000  8.092292
## gam_smoothed_T 5.532829 10.184040
```

*GAM linear has a lower AIC and can therefore be considered a better fitting model.*

## GAM additive regression

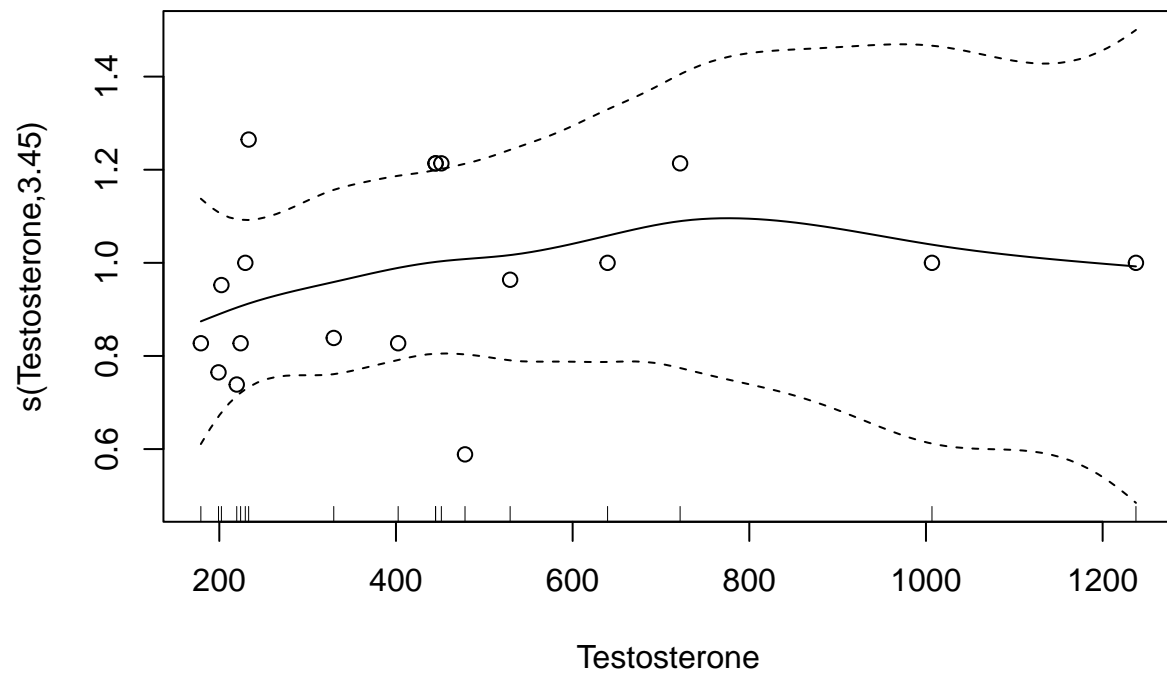
### Smoothed model

```
gam_additive_smoothed_T <- gam(ResponseScore ~ s(Testosterone, sp=0.5) +
                               MaleType, data = T.malegroup.nooutlier)
summary(gam_additive_smoothed_T)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## ResponseScore ~ s(Testosterone, sp = 0.5) + MaleType
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.9693     0.1446   6.704 2.64e-05 ***
## MaleTypenonmusth1Q-3Q -0.2137     0.1835  -1.164    0.268
## MaleTypenonmusth4Q   -0.5773     0.1997  -2.891    0.014 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
```

```
##              edf Ref.df      F p-value
## s(Testosterone) 3.454  4.189 0.207  0.939
##
## R-sq.(adj) =  0.55   Deviance explained = 69.4%
## GCV = 0.0757   Scale est. = 0.048559   n = 18
```

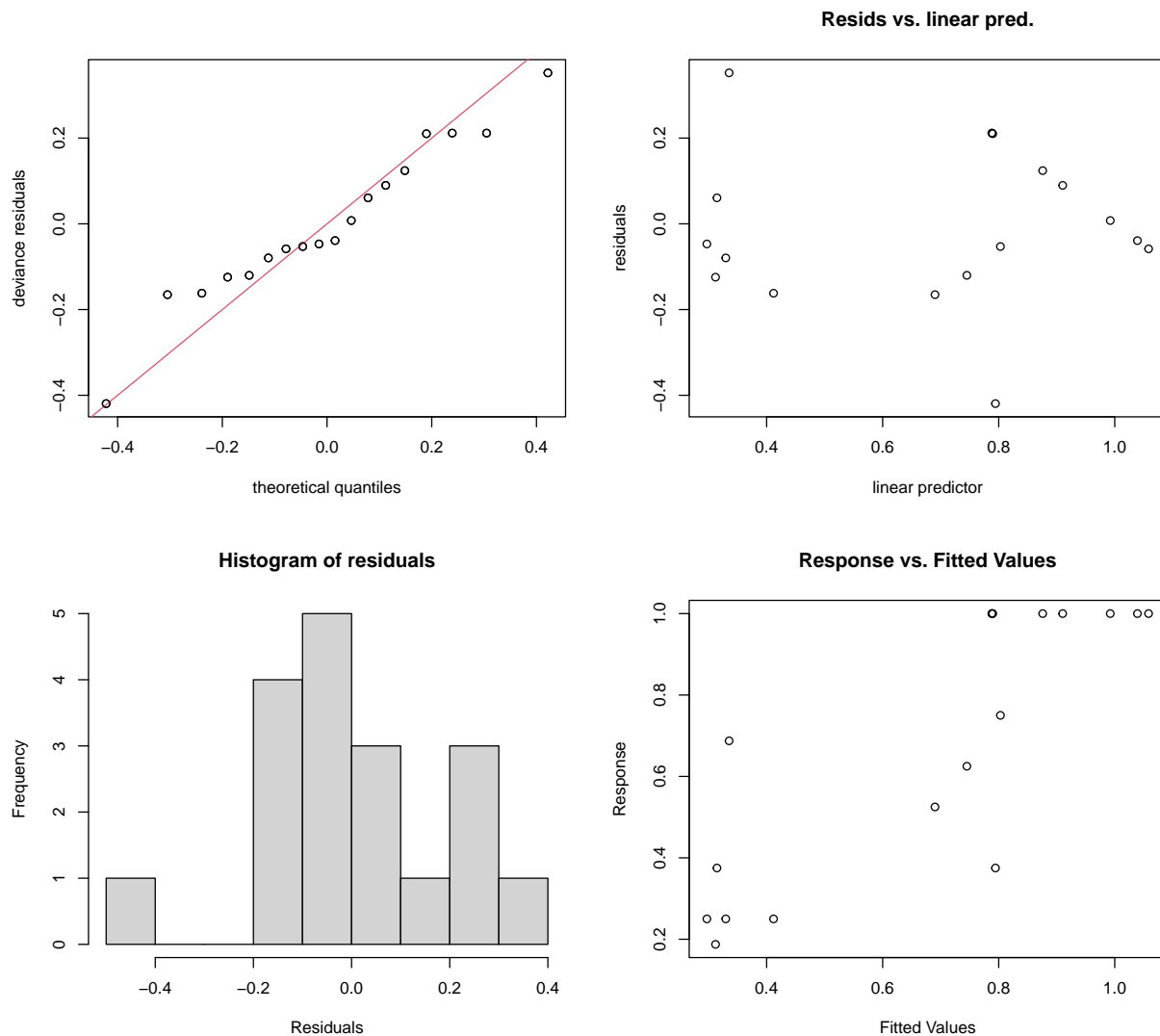
```
plot(gam_additive_smoothed_T, residuals=TRUE, pch=1, seWithMean = T,
     shift = coef(gam_additive_smoothed_T)[1])
```



Assumptions

```
gam.check(gam_additive_smoothed_T, pch=1)
```





```
##
## Method: GCV   Optimizer: magic
## Model required no smoothing parameter selectionModel rank = 12 / 12
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##           k'   edf k-index p-value
## s(Testosterone) 9.00 3.45   1.09   0.53
```

*Similar to additive linear regression model, normality appears worse.*

## Linear model

```
gam_linear_additive <- gam(ResponseScore ~ Testosterone + MaleType,
                           data = T.malegroup.nooutlier)
summary(gam_linear_additive)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## ResponseScore ~ Testosterone + MaleType
##
## Parametric coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.8819126  0.2110834   4.178 0.000929 ***
## Testosterone    0.0001517  0.0002364   0.642 0.531400
## MaleTypenonmusth1Q-3Q -0.1661757  0.1482690  -1.121 0.281243
## MaleTypenonmusth4Q   -0.5849980  0.1844563  -3.171 0.006795 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
## R-sq.(adj) =  0.603   Deviance explained = 67.3%
## GCV = 0.055017   Scale est. = 0.042791   n = 18
```

**AIC model comparison of GAM smoothed and GAM linear for the additive regression model**

```
AIC(gam_linear_additive, gam_additive_smoothed_T)
```

```
##              df          AIC
## gam_linear_additive    5.00000 -0.1677059
## gam_additive_smoothed_T 7.45367  3.5473358
```

*GAM linear has a lower AIC and can therefore be considered a better fitting model.*

**AIC model comparison of GAM simple regression and GAM additive regression**

```
AIC(gam_smoothed_T, gam_additive_smoothed_T)
```

```
##              df          AIC
## gam_smoothed_T        5.532829 10.184040
## gam_additive_smoothed_T 7.453670  3.547336
```

*GAM additive a better fit, same as for the linear versions of these models.*