

Univariate Analysis

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Contents

Model 1: trait ~ mainland/island + year + (1 ID)	2
Mericarps	3
Flowers	17
Leaves	19
Model 1 LS means	25
Mericarp LS means plots	27
Petal Length	34
Leaves LS means plots	36
Model 2 trait ~ galapagos/other islands + year + (1 ID)	39
Flowers	39
Leaves	41
Model 2 LS means	47
Flowers	47
Leaves LS means plots	49
Model 3: trait ~ finch_beak + year + (1 ID)	52
Mericarps	53
Flowers	67
Leaves	69
Model 3 LS means	75
Mericarps:	75
Mericarp LS means plots	77
Flowers	84
Leaves	84
Leaves LS means plots	86

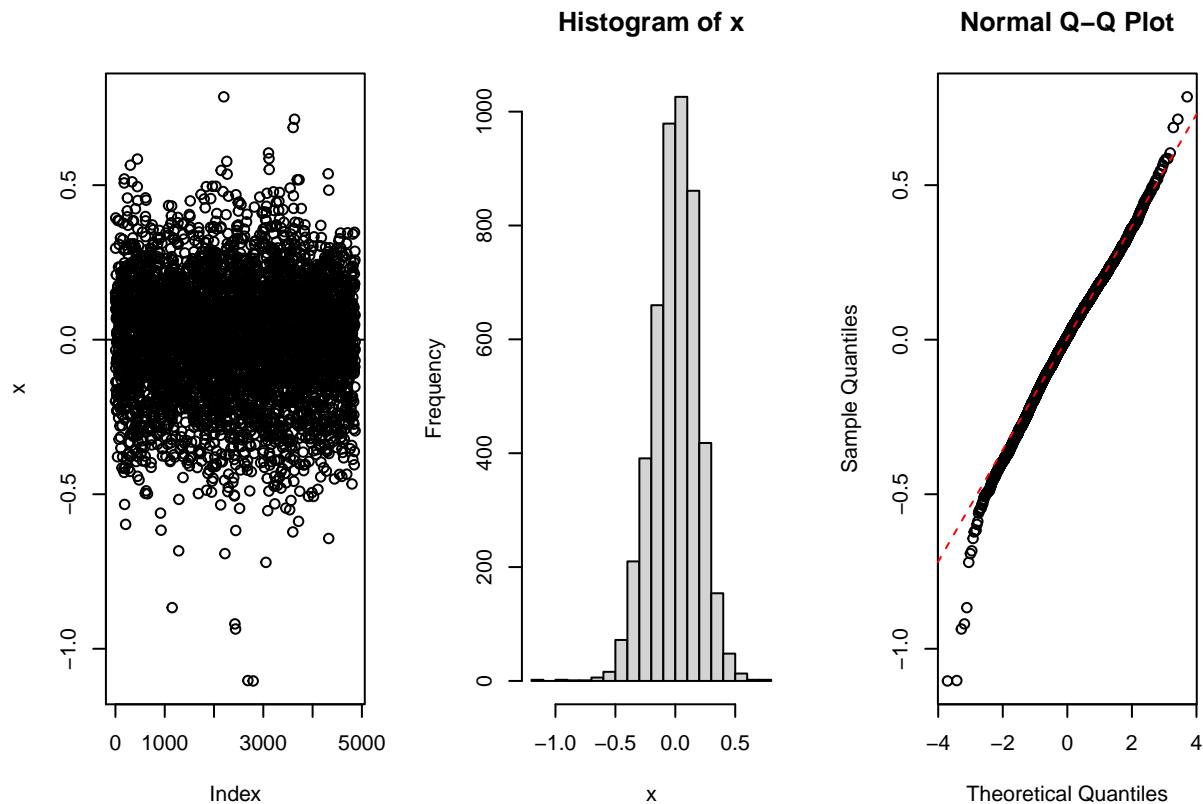
I ran different models per trait with un-transformed data, log-transformed and sqrt-transformed data. Then I used a custom *diagnostic* function and the package *DHARMa* to compare between models. Then I selected the model that better fit the assumptions. The model I will show here are the ones selected. Finally, I used the package *emmeans* to estimate the marginal means per model.

Model 1: $\text{trait} \sim \text{mainland/island} + \text{year} + (1|\text{ID})$

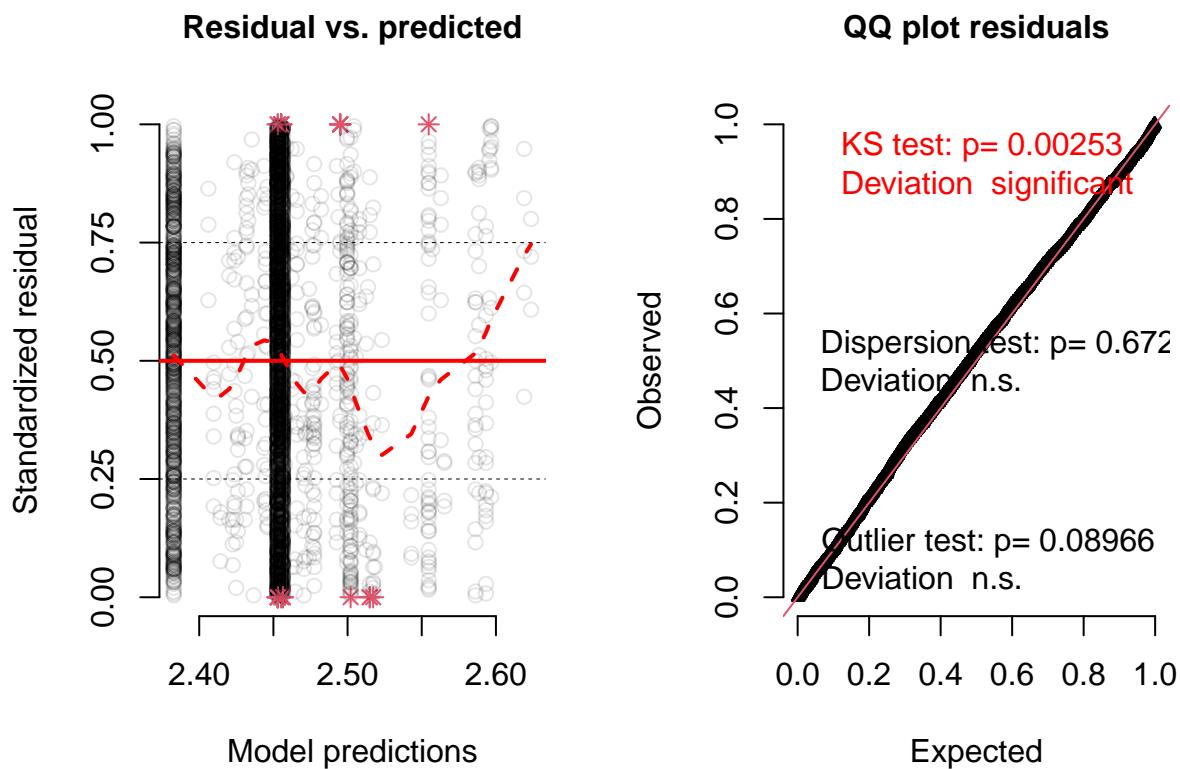
This is the first model that looks at the differences between *Tribulus* mericarps, flowers and leaves from mainland and island populations.

Mericarps

Length -> Sqrt-transformed



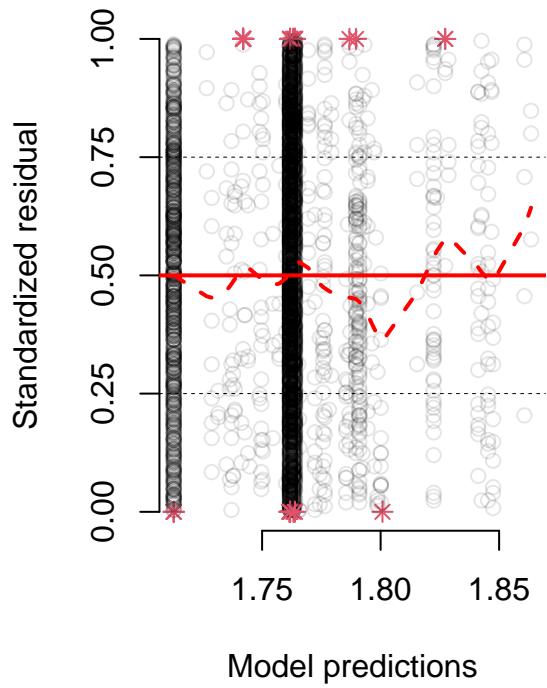
```
## [1] "Kurtosis=0.819189880248705"  
## [1] "Skew=-0.29428570229393"
```



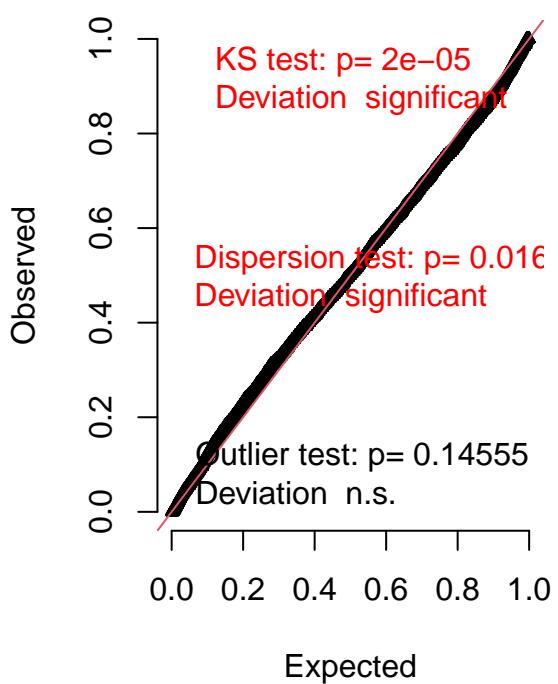
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sqrt(length)
##              Chisq Df Pr(>Chisq)
## mainland_island 9.3113  1   0.002277 **
## year_collected  9.9210  1   0.001634 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

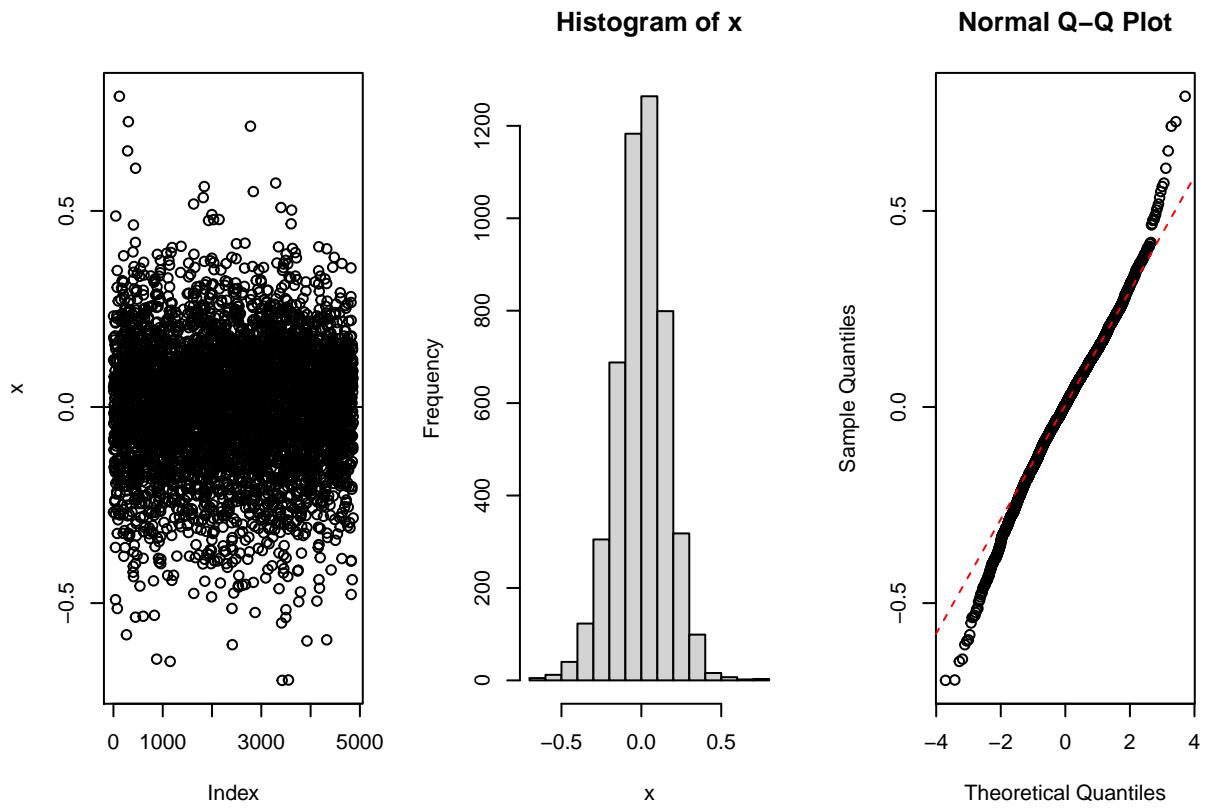
Width -> sqrt-transformed

Residual vs. predicted



QQ plot residuals





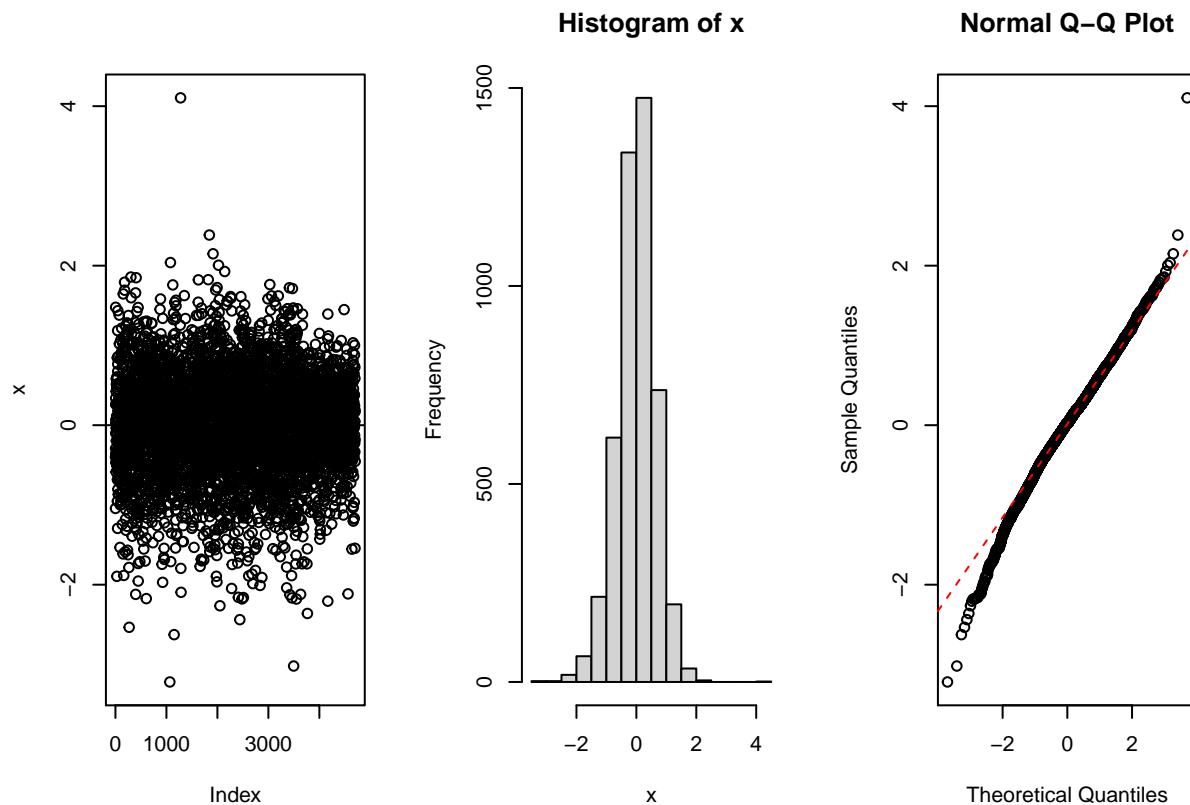
```

## [1] "Kurtosis=0.915288926843053"
## [1] "Skew=-0.184236416326029"

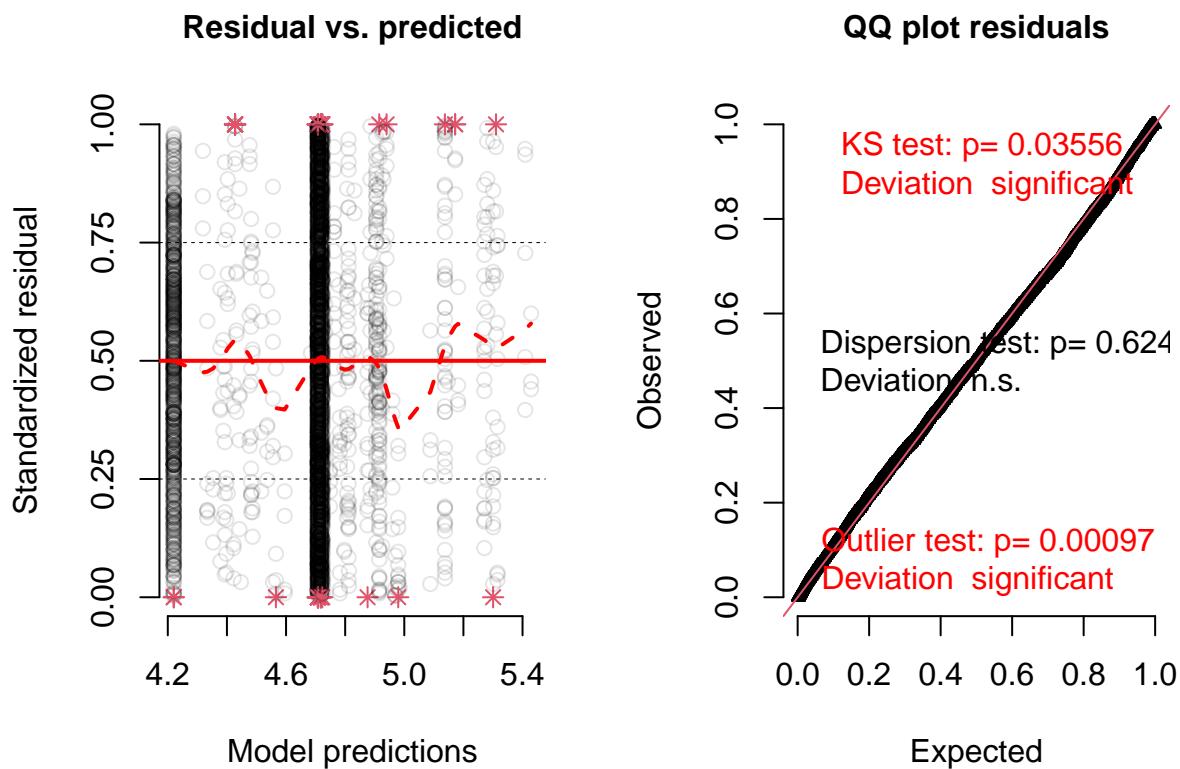
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sqrt(width)
##              Chisq Df Pr(>Chisq)
## mainland_island 10.36  1   0.001288 **
## year_collected   7.84  1   0.005110 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Depth -> Not transformed

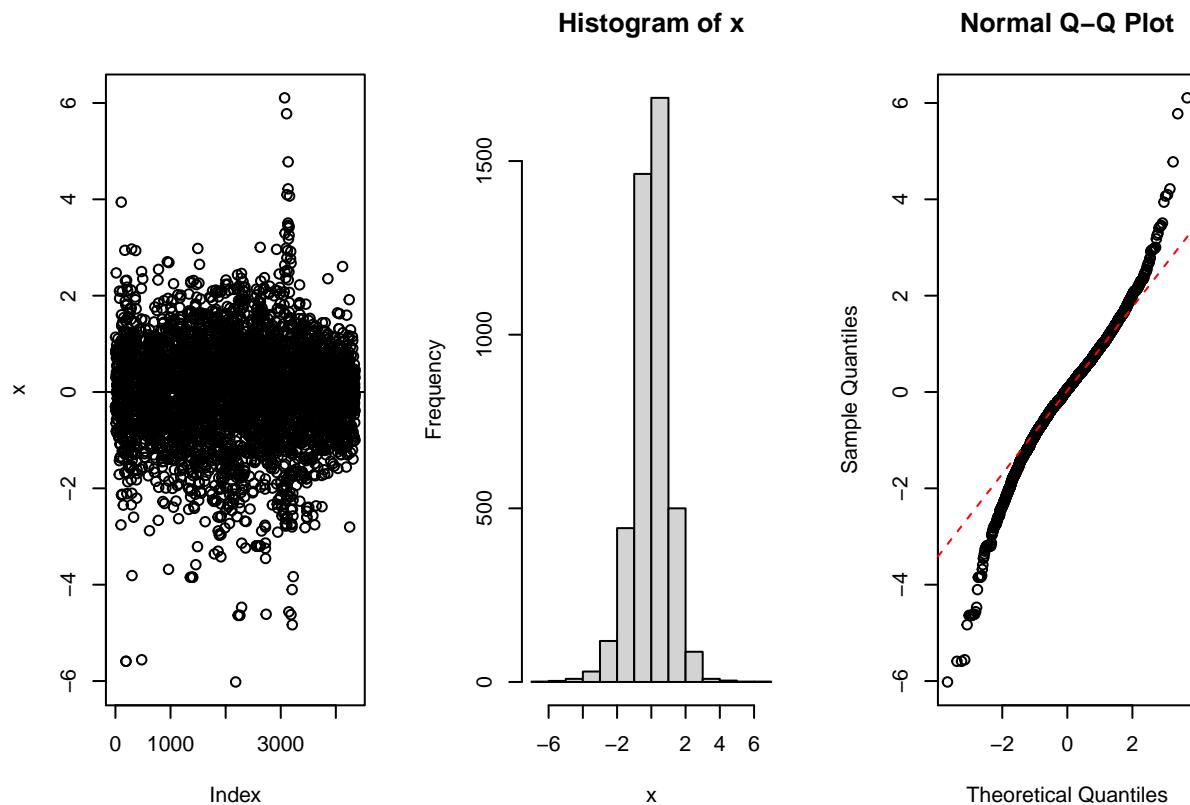


```
## [1] "Kurtosis=0.989267427953835"  
## [1] "Skew=-0.241253118215469"
```

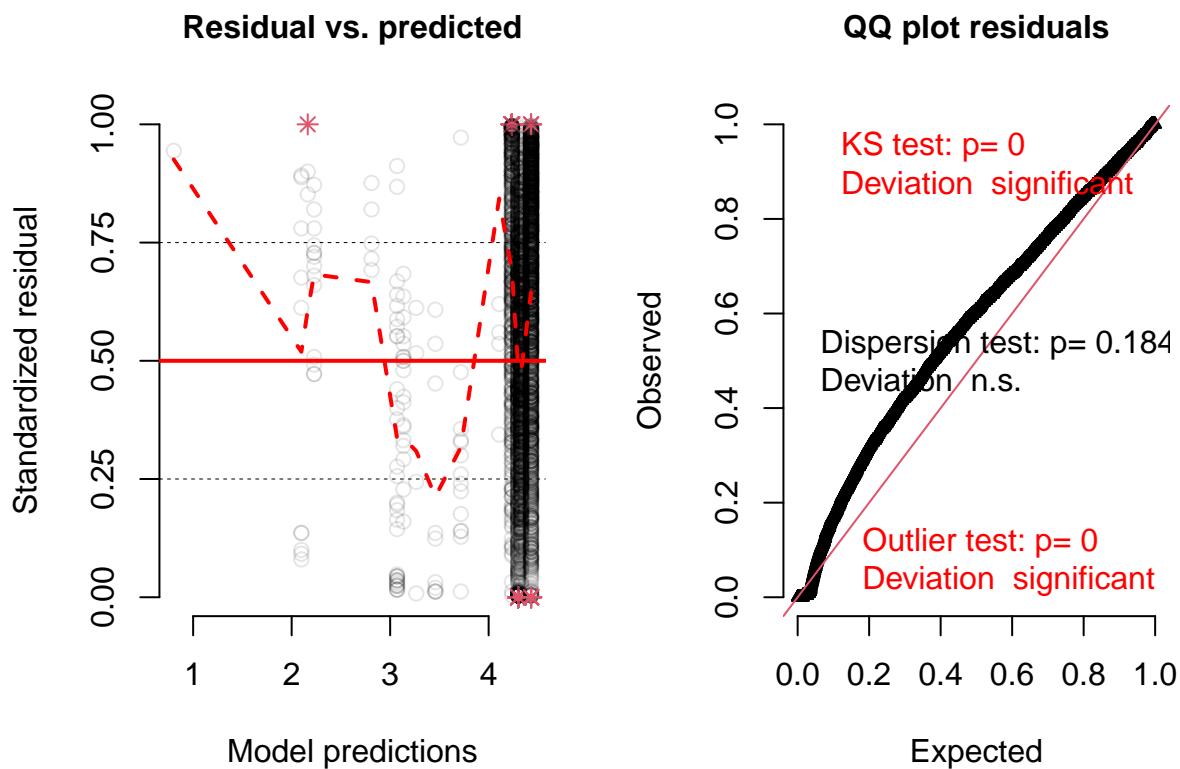


```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: depth
##              Chisq Df Pr(>Chisq)
## mainland_island 50.871  1 9.865e-13 ***
## year_collected   20.387  1 6.325e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Spine Length -> Not transformed

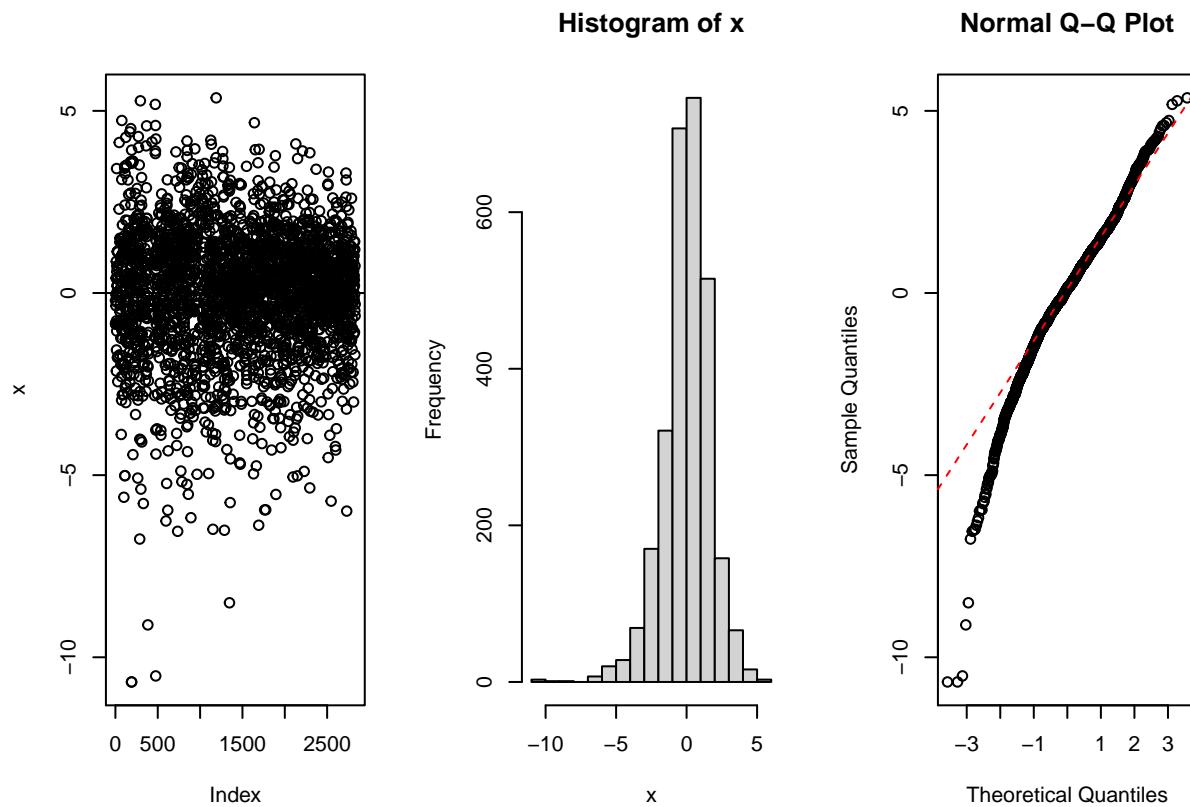


```
## [1] "Kurtosis=2.58419661904014"  
## [1] "Skew=-0.421423446072704"
```

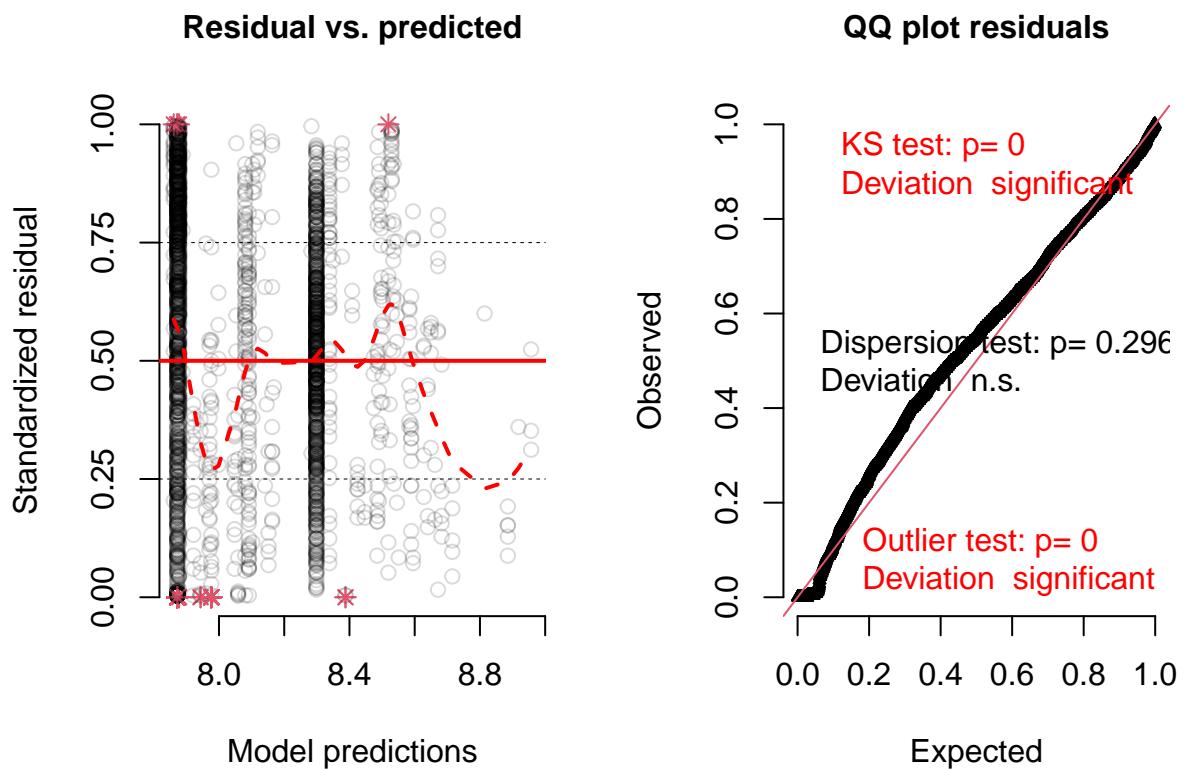


```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: spine_length
##              Chisq Df Pr(>Chisq)
## mainland_island  0.3219  1    0.5705
## year_collected   24.7144  1  6.649e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Spine Tip Distance -> Not transformed



```
## [1] "Kurtosis=2.81329973280421"  
## [1] "Skew=-0.769988792758626"
```

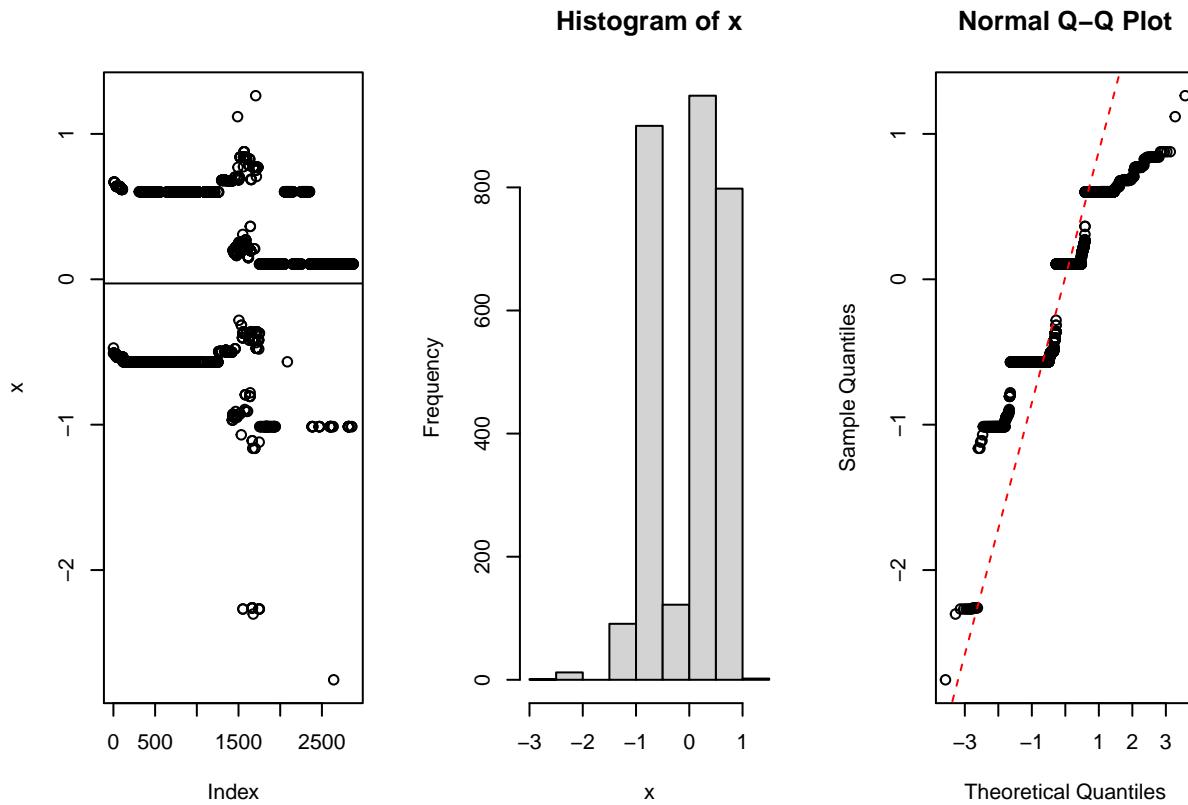


```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: tip_distance
##              Chisq Df Pr(>Chisq)
## mainland_island 2.0743  1      0.1498
## year_collected   1.5347  1      0.2154
```

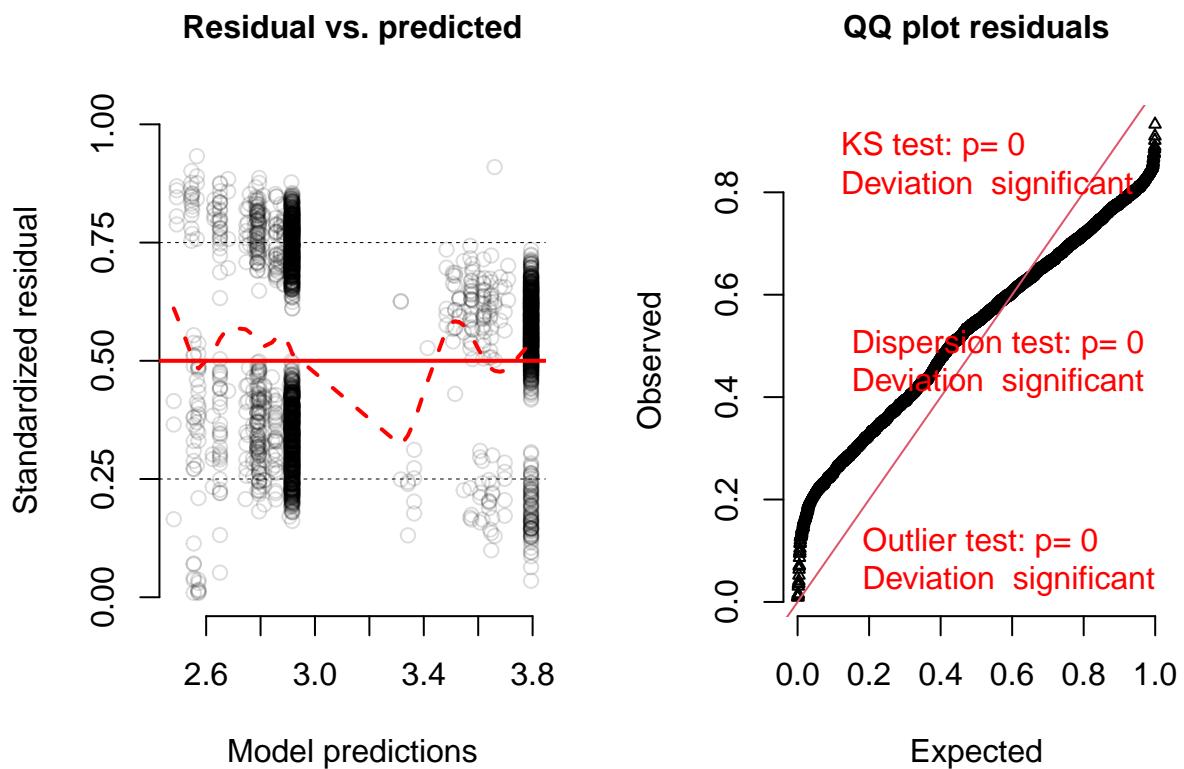
Spine Number -> Not transformed *For spine number, I think it is a count trait, so I used this model:*

`glm(spine_num ~ mainland_island + year_collected, data = meri_spine.number, family = poisson)`

But the diagnostic of this model looks different. How should I evaluate de assumptions of this model?

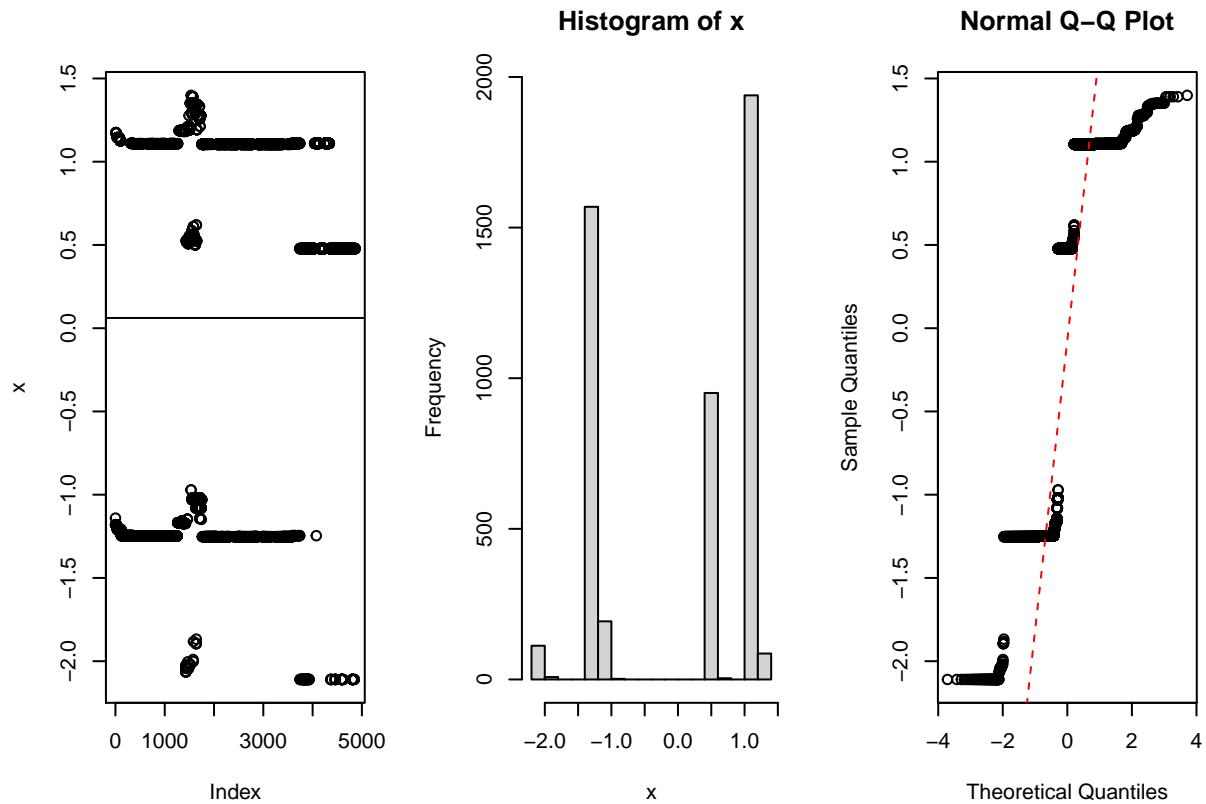


```
## [1] "Kurtosis=-0.0210478608607598"
## [1] "Skew=-0.395691016281737"
```

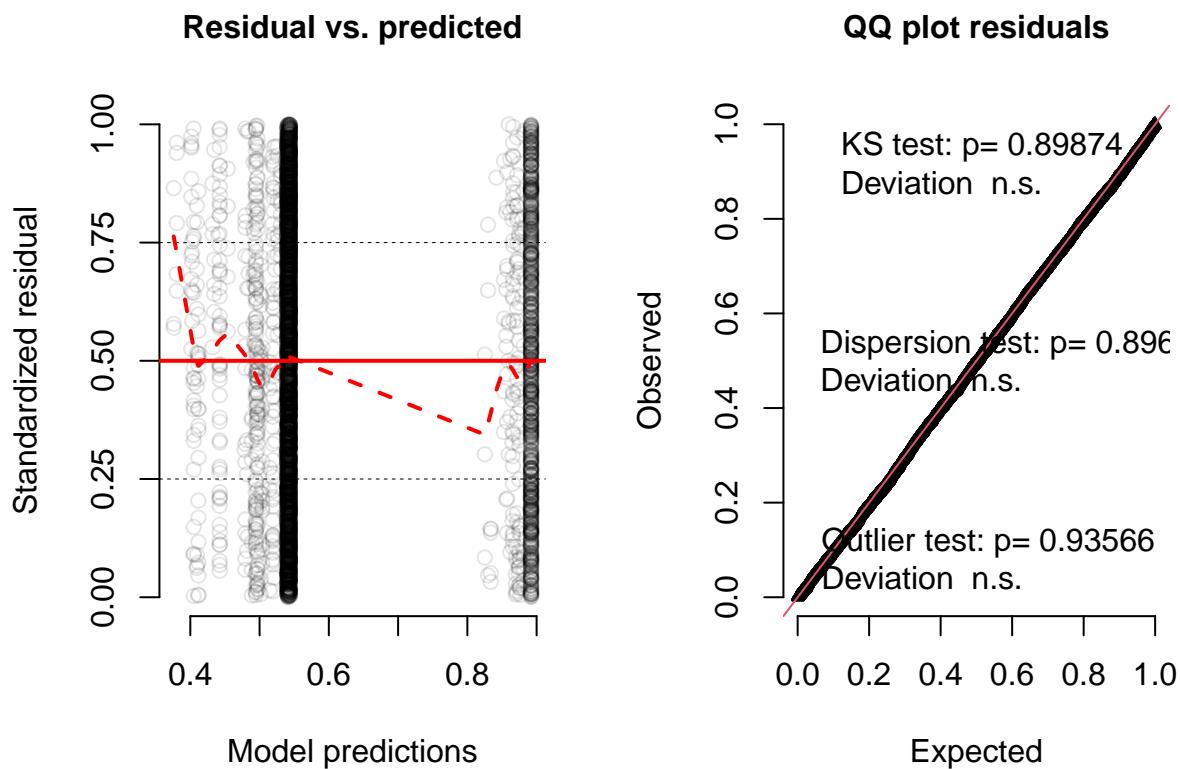


```
## Analysis of Deviance Table (Type II tests)
##
## Response: spine_num
##           LR Chisq Df Pr(>Chisq)
## mainland_island 154.622  1 < 2.2e-16 ***
## year_collected    7.279  1  0.006975 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Lower -> Not transformed *For lower spines, I think it is a count trait, so I used this model:*
`meri_lower.spines_m1 <- glm(lower_spines ~ mainland_island + year_collected, data = meri_lower.spines, family = "binomial")`



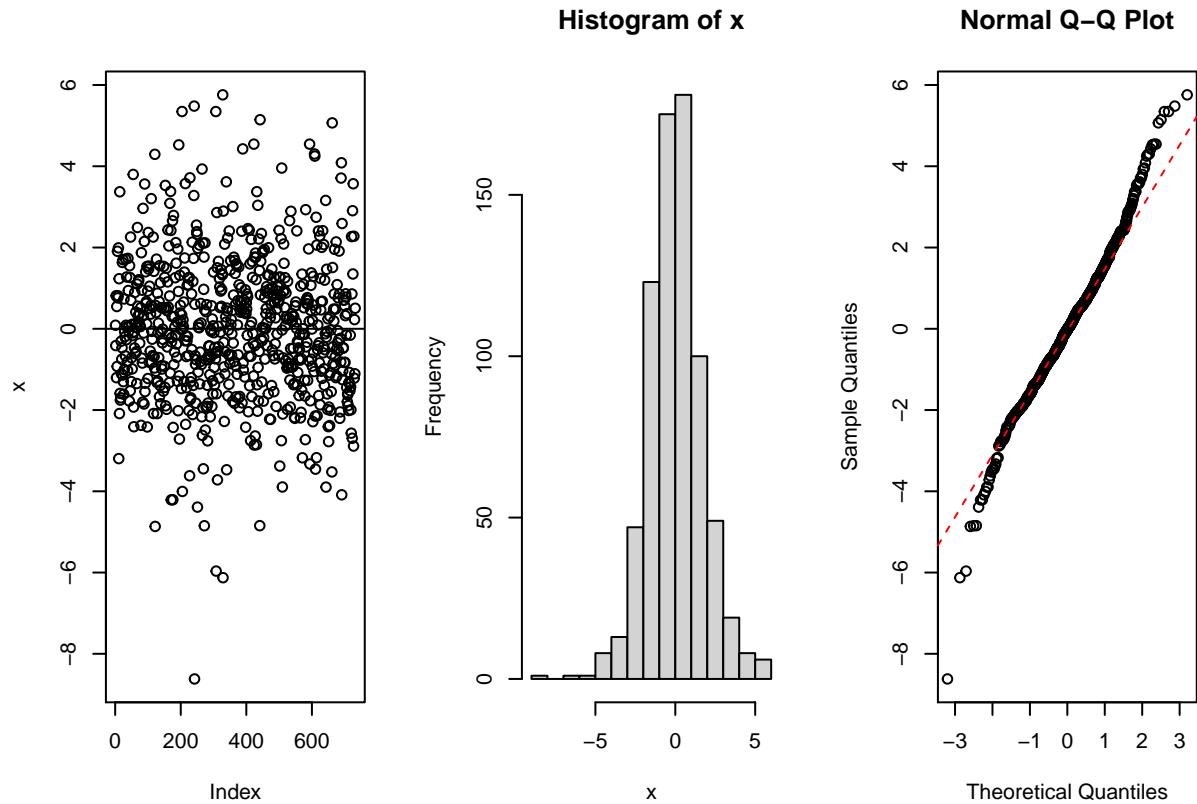
```
## [1] "Kurtosis=-1.61184279943993"
## [1] "Skew=-0.38863425255693"
```



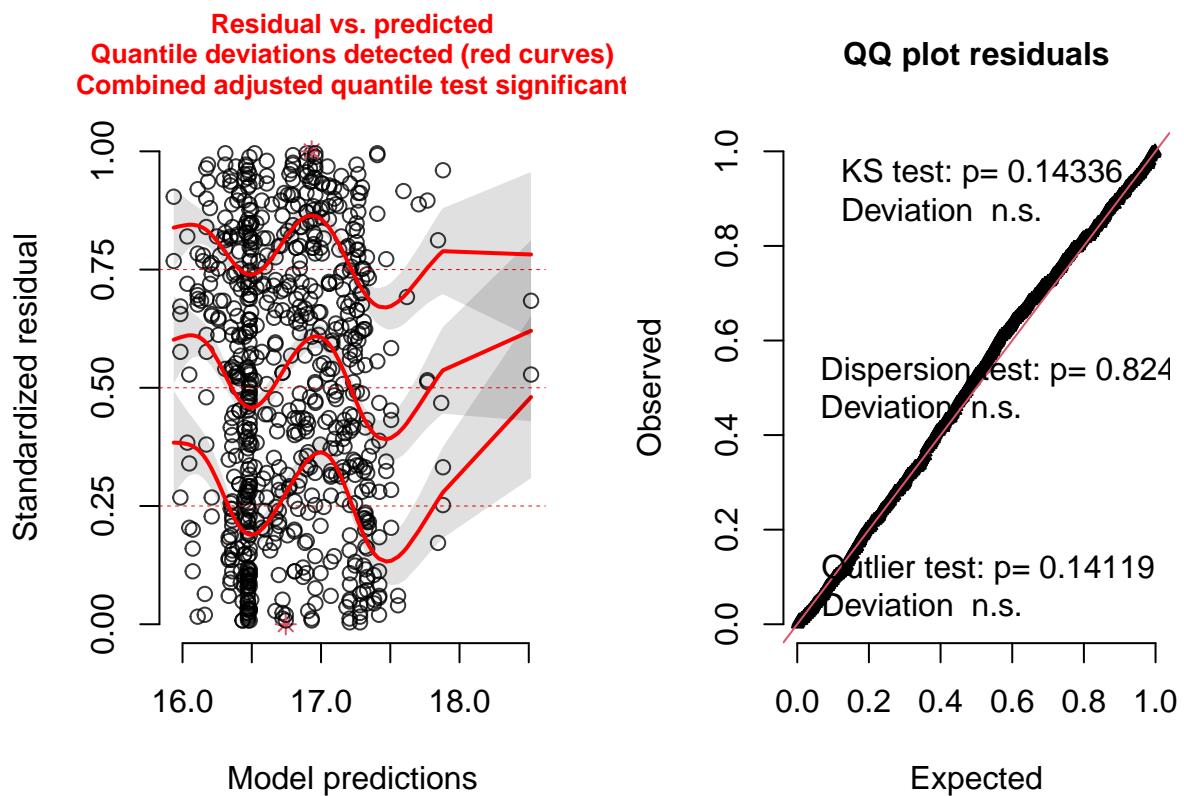
```
## Analysis of Deviance Table (Type II tests)
##
## Response: lower_spines
##           LR Chisq Df Pr(>Chisq)
## mainland_island 512.90  1 < 2.2e-16 ***
## year_collected   10.75  1  0.001042 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Flowers

Petal length -> Not transformed



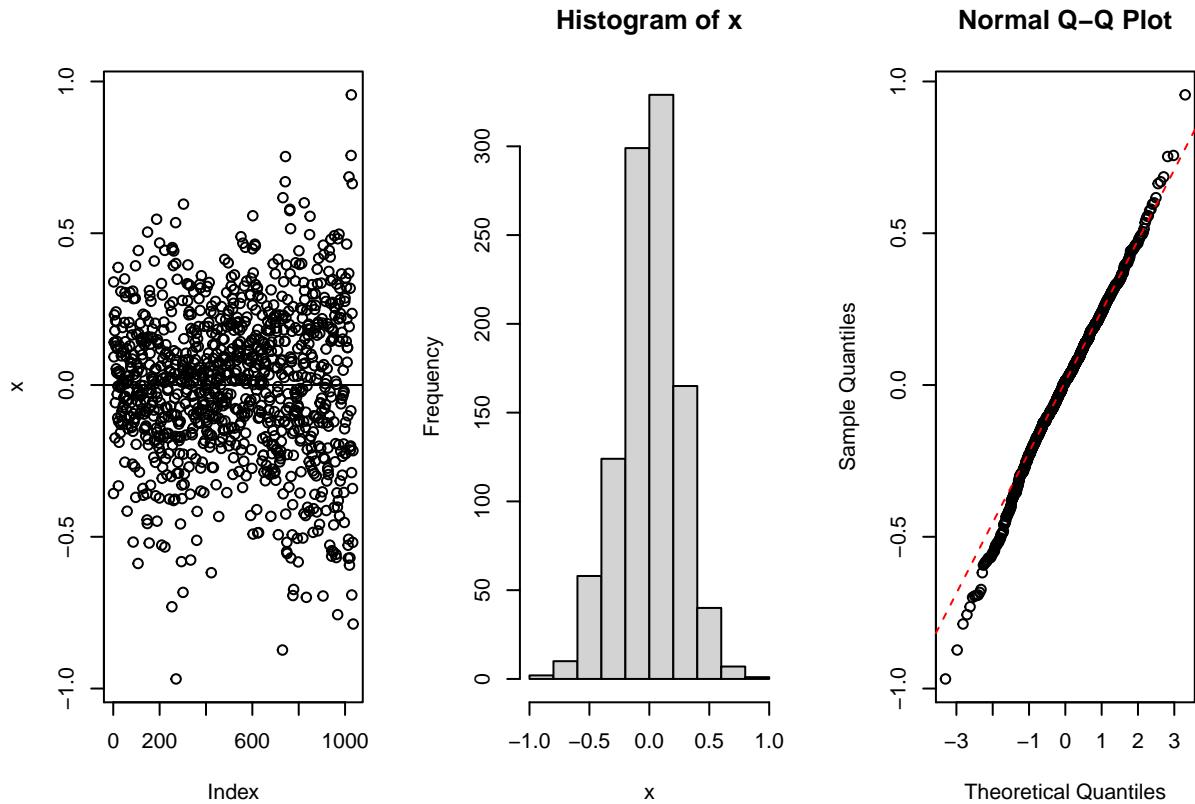
```
## [1] "Kurtosis=1.42347292893909"  
## [1] "Skew=0.00136618490346419"
```



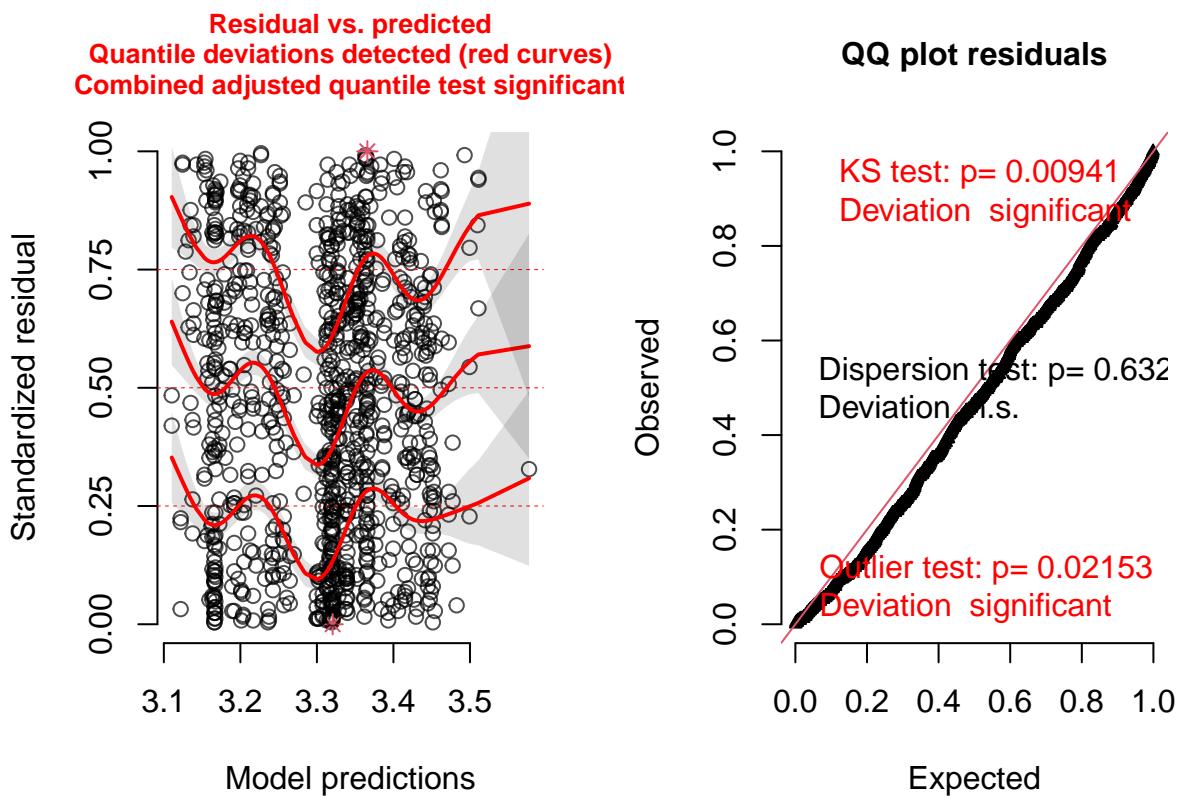
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: petal_length
##              Chisq Df Pr(>Chisq)
## mainland_island 0.0000  1    0.99656
## year_collected  3.7983  1    0.05131 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Leaves

Leaf Length -> Log Transformed

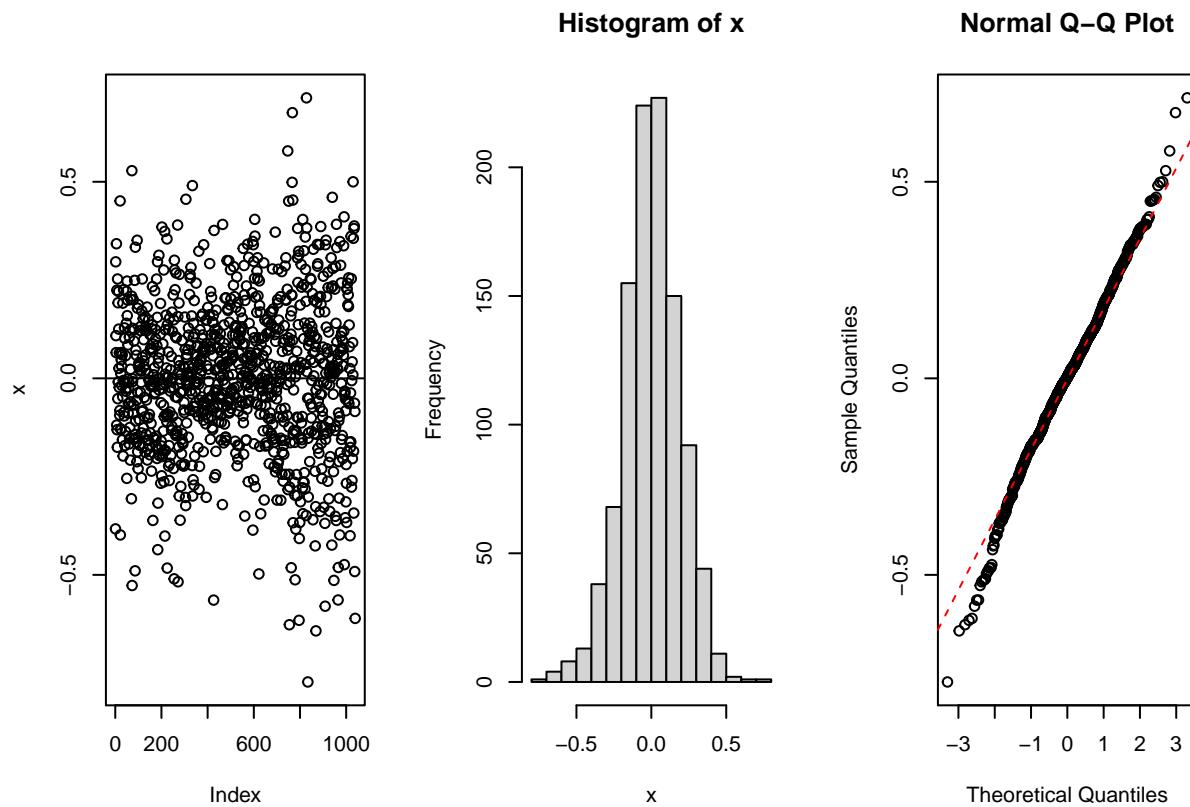


```
## [1] "Kurtosis=0.549228998714279"  
## [1] "Skew=-0.231629387219308"
```

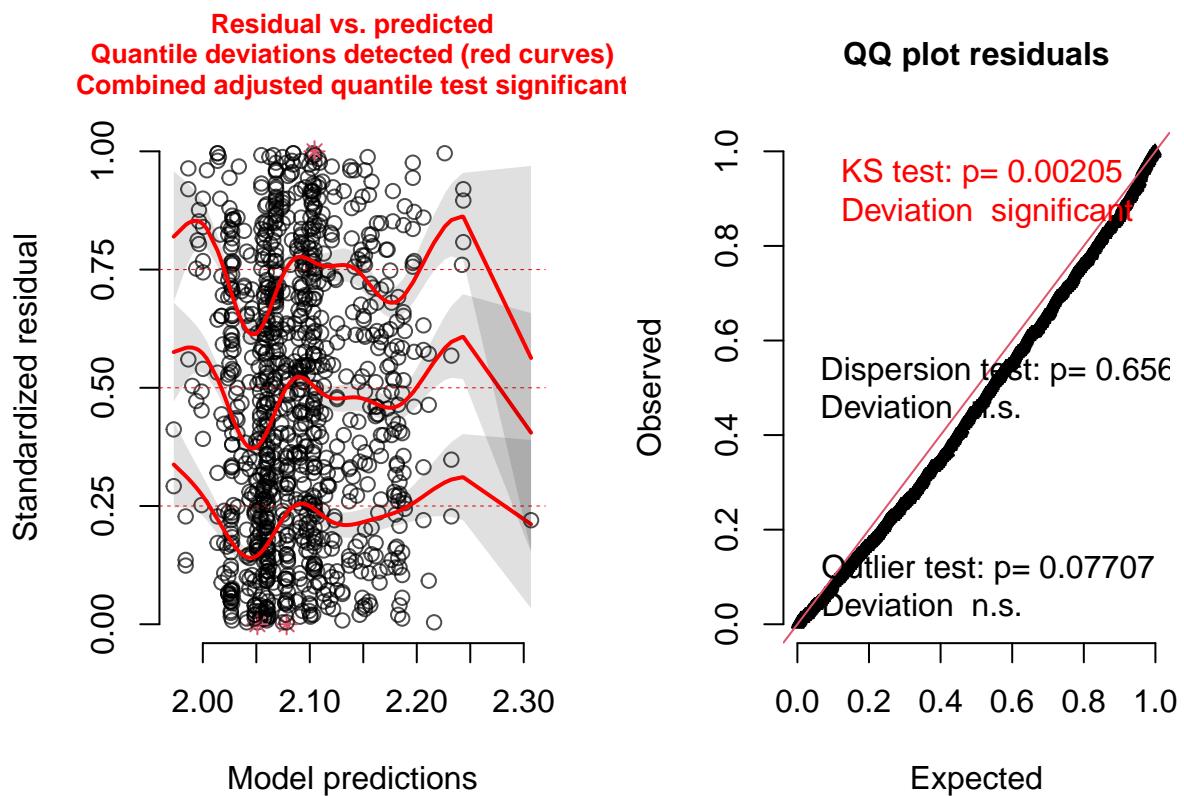


```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: log(leaf_length)
##              Chisq Df Pr(>Chisq)
## mainland_island 24.6162  1  6.996e-07 ***
## year_collected   5.3636  1    0.02056 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Leaflet Length -> Log Transformed



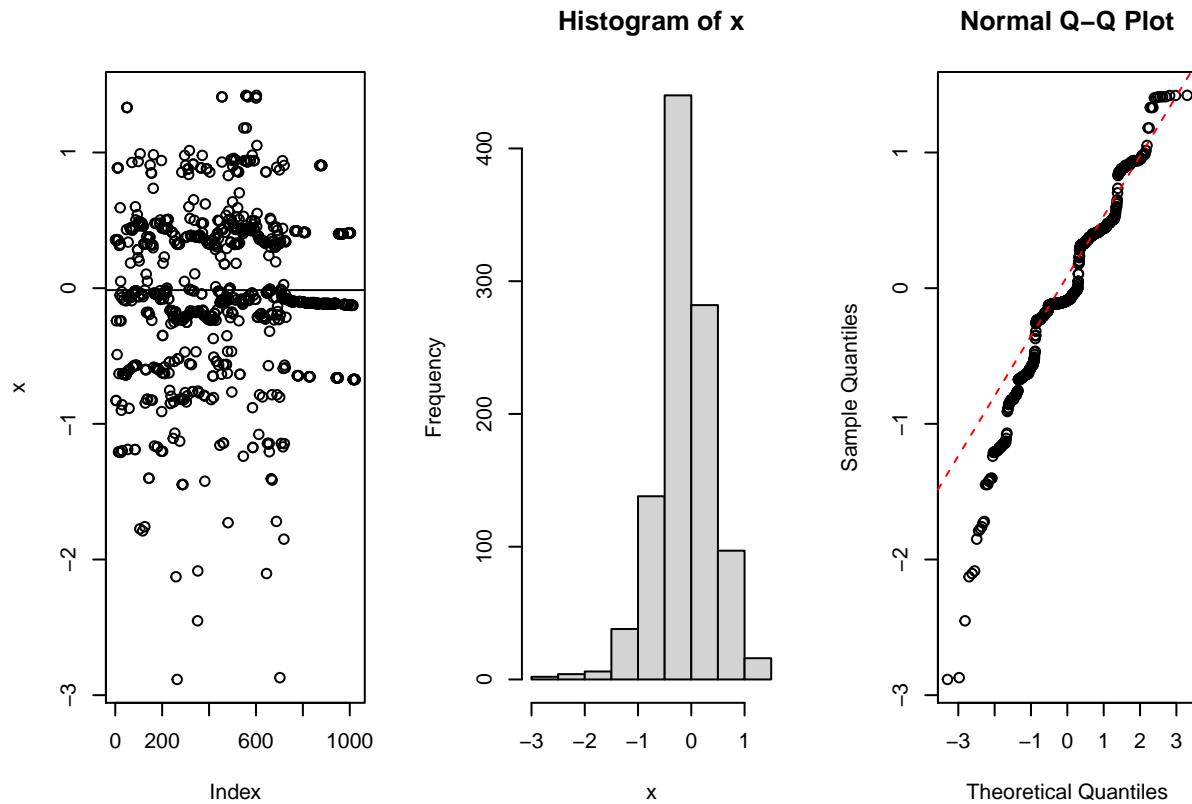
```
## [1] "Kurtosis=0.704811597680861"  
## [1] "Skew=-0.168061416832369"
```



```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: log(leaflet_length)
##              Chisq Df Pr(>Chisq)
## mainland_island 5.4526  1   0.019539 *
## year_collected  7.2378  1   0.007138 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

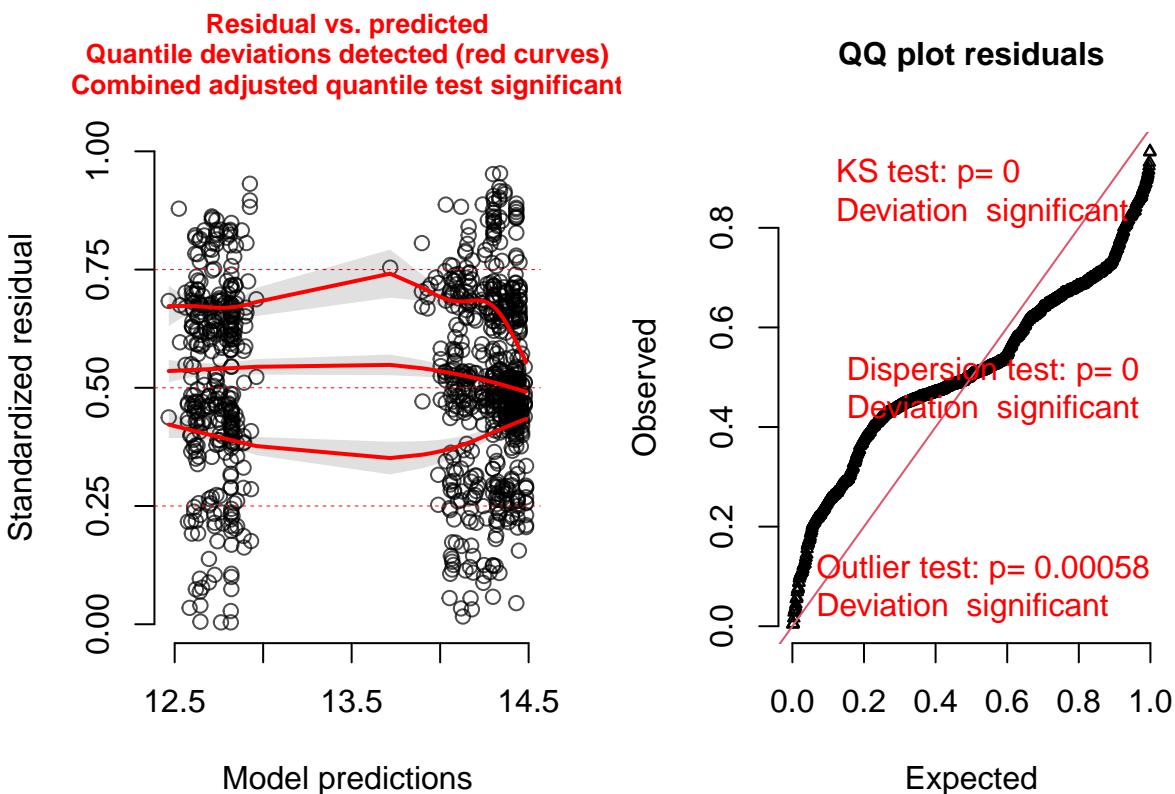
Leaflet number -> Not transformed *For leaflet number, I think it is a count trait, so I used this model:*

`glm(number_of_leaflets ~ mainland_island + year_collected, family = poisson, data=leaf_length)`



```
## [1] "Kurtosis=2.12466116567275"
## [1] "Skew=-0.651977029226767"
```

```
## DHARMA:plot used testOutliers with type = binomial for computational reasons (nObs > 500). Note that
```



```
## Analysis of Deviance Table (Type II tests)
##
## Response: number_of_leaflets
##           LR Chisq Df Pr(>Chisq)
## mainland_island 33.467  1  7.25e-09 ***
## year_collected   1.189  1    0.2755
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model 1 LS means

Mericarps:

Length

```
## mainland_island response      SE  df asymp.LCL asymp.UCL
##   island            6.06 0.0788 Inf     5.91     6.22
##   mainland          5.71 0.0897 Inf     5.53     5.88
##
## Degrees-of-freedom method: asymptotic
## Confidence level used: 0.95
## Intervals are back-transformed from the sqrt scale
```

Width

```
## mainland_island response      SE  df asymp.LCL asymp.UCL
##   island            3.12 0.0369 Inf     3.05     3.20
##   mainland          2.95 0.0426 Inf     2.86     3.03
##
## Degrees-of-freedom method: asymptotic
## Confidence level used: 0.95
## Intervals are back-transformed from the sqrt scale
```

Depth

```
## mainland_island emmean      SE  df asymp.LCL asymp.UCL
##   island            4.75 0.0466 Inf     4.66     4.84
##   mainland          4.25 0.0547 Inf     4.14     4.35
##
## Degrees-of-freedom method: asymptotic
## Confidence level used: 0.95
```

Spine Length

```
## mainland_island emmean      SE  df asymp.LCL asymp.UCL
##   island            4.30 0.106 Inf     4.09     4.51
##   mainland          4.39 0.129 Inf     4.14     4.64
##
## Degrees-of-freedom method: asymptotic
## Confidence level used: 0.95
```

Spine Tip Distance

```
## mainland_island emmean      SE  df lower.CL upper.CL
##   island            7.93 0.202 277     7.53     8.33
##   mainland          8.35 0.218 284     7.92     8.78
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
```

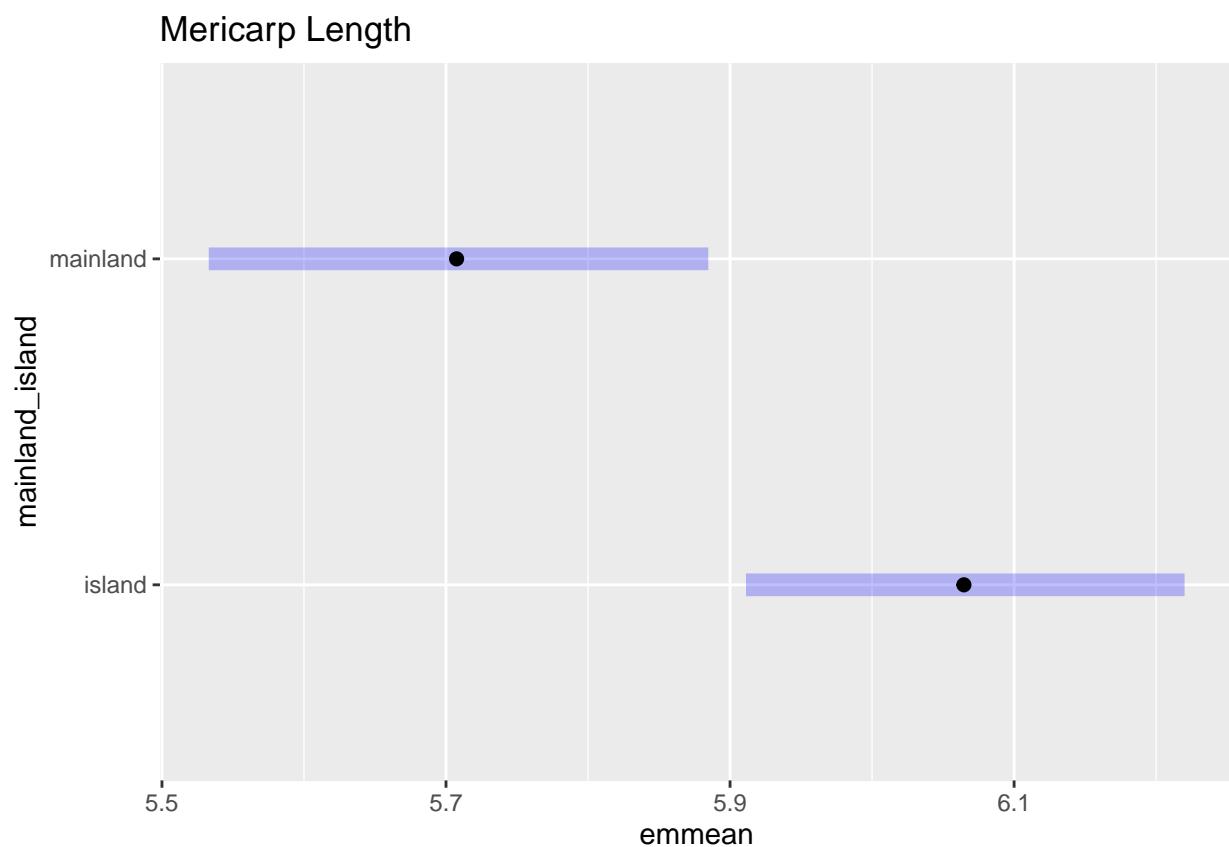
Spine Number

```
##  mainland_island rate      SE  df asymp.LCL asymp.UCL
##  island            2.88 0.0401 Inf     2.80     2.96
##  mainland          3.75 0.0593 Inf     3.63     3.87
##
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
```

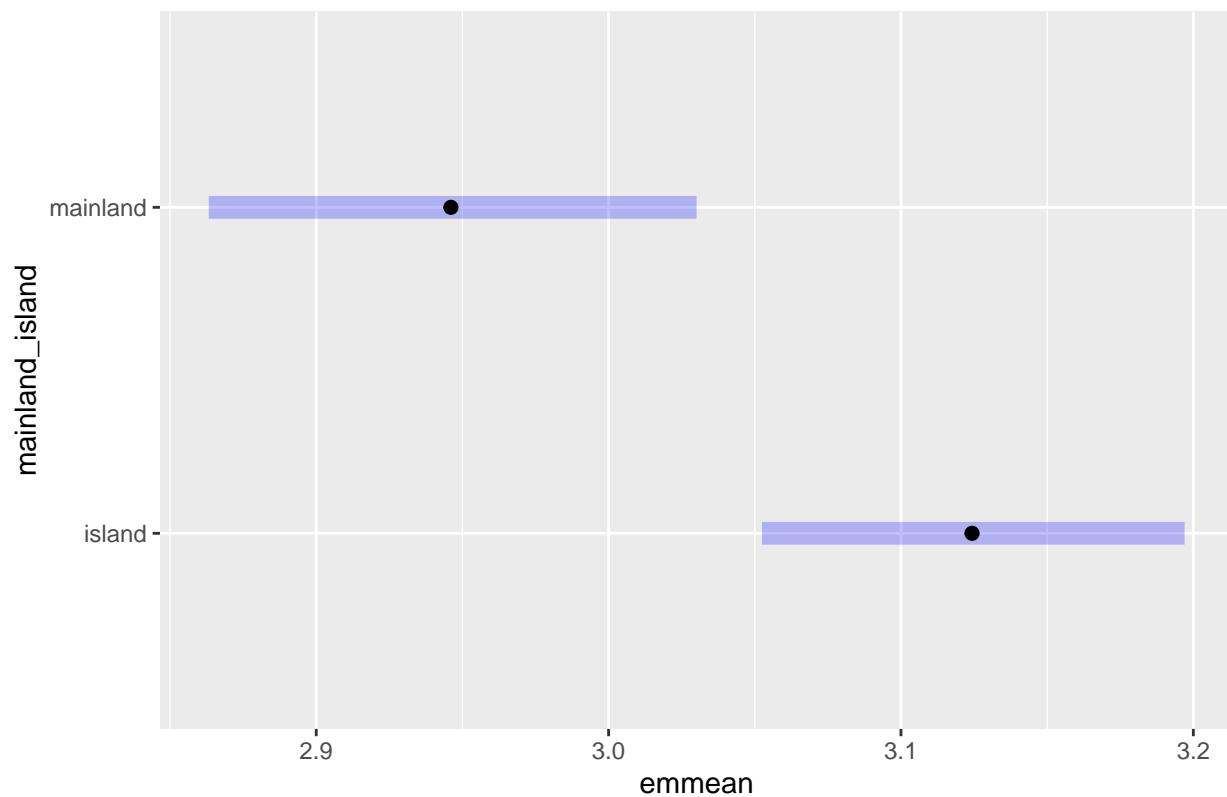
Lower Spines

```
##  mainland_island emmean      SE  df asymp.LCL asymp.UCL
##  island            0.136 0.0326 Inf    0.0716    0.199
##  mainland          2.086 0.0970 Inf   1.8962    2.277
##
## Results are given on the logit (not the response) scale.
## Confidence level used: 0.95
```

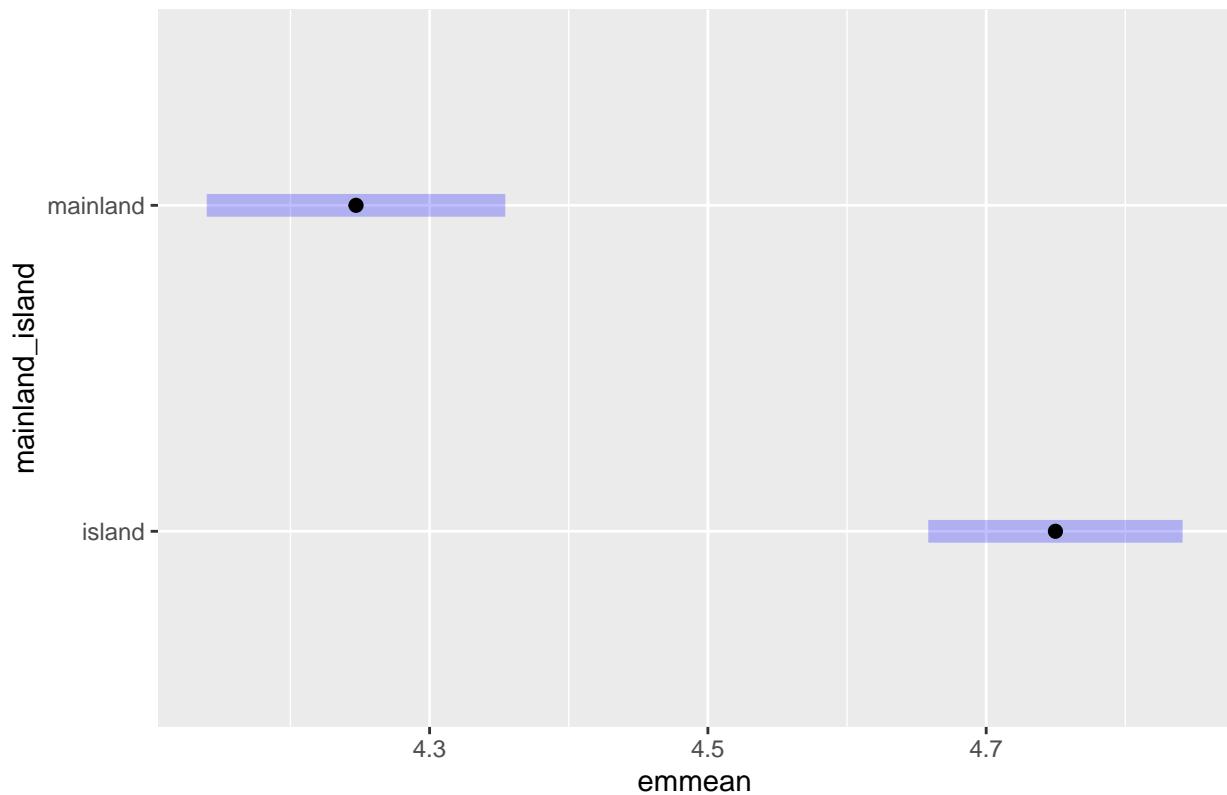
Mericarp LS means plots



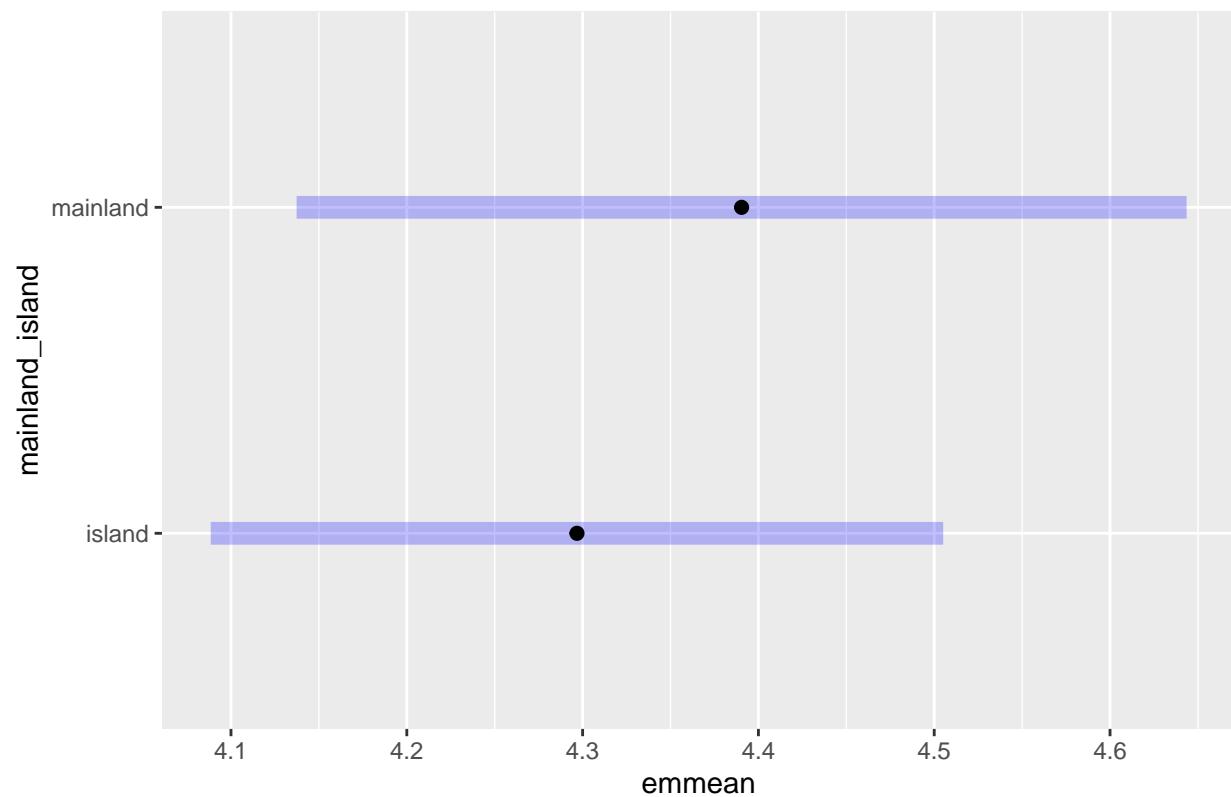
Mericarp Width



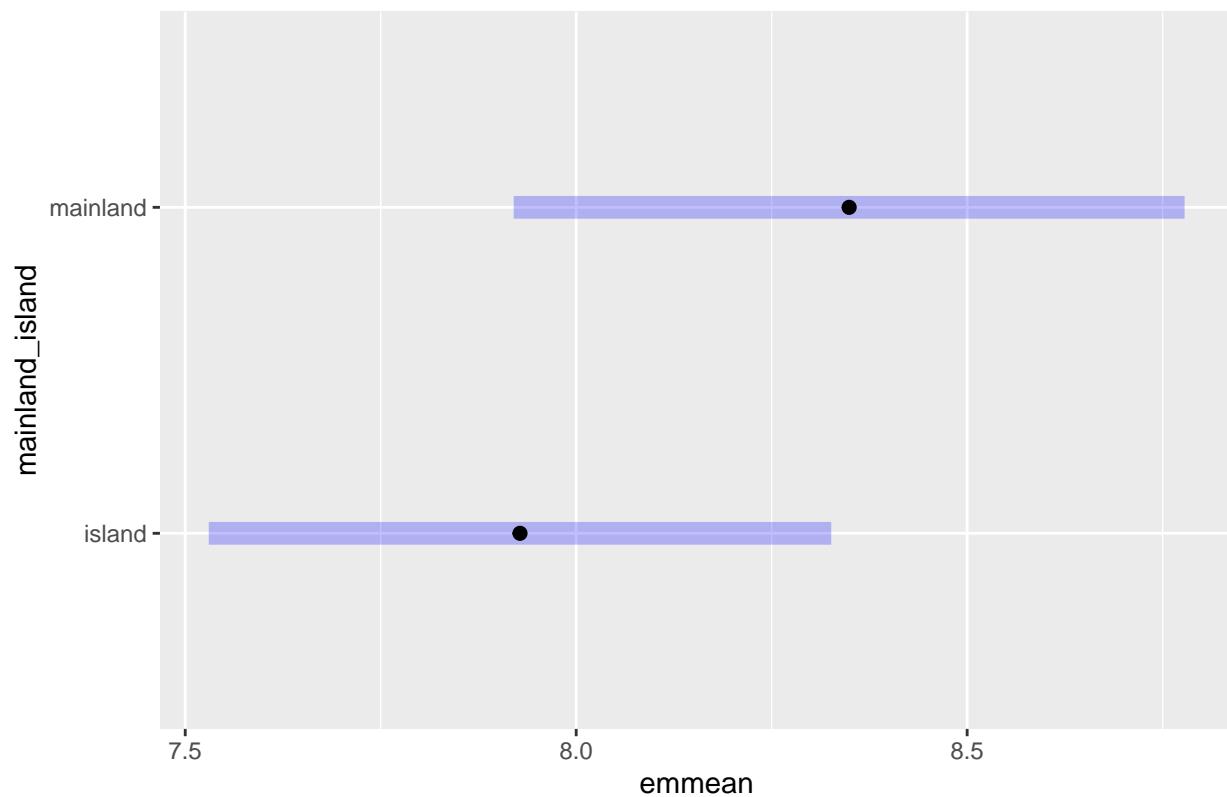
Mericarp Depth



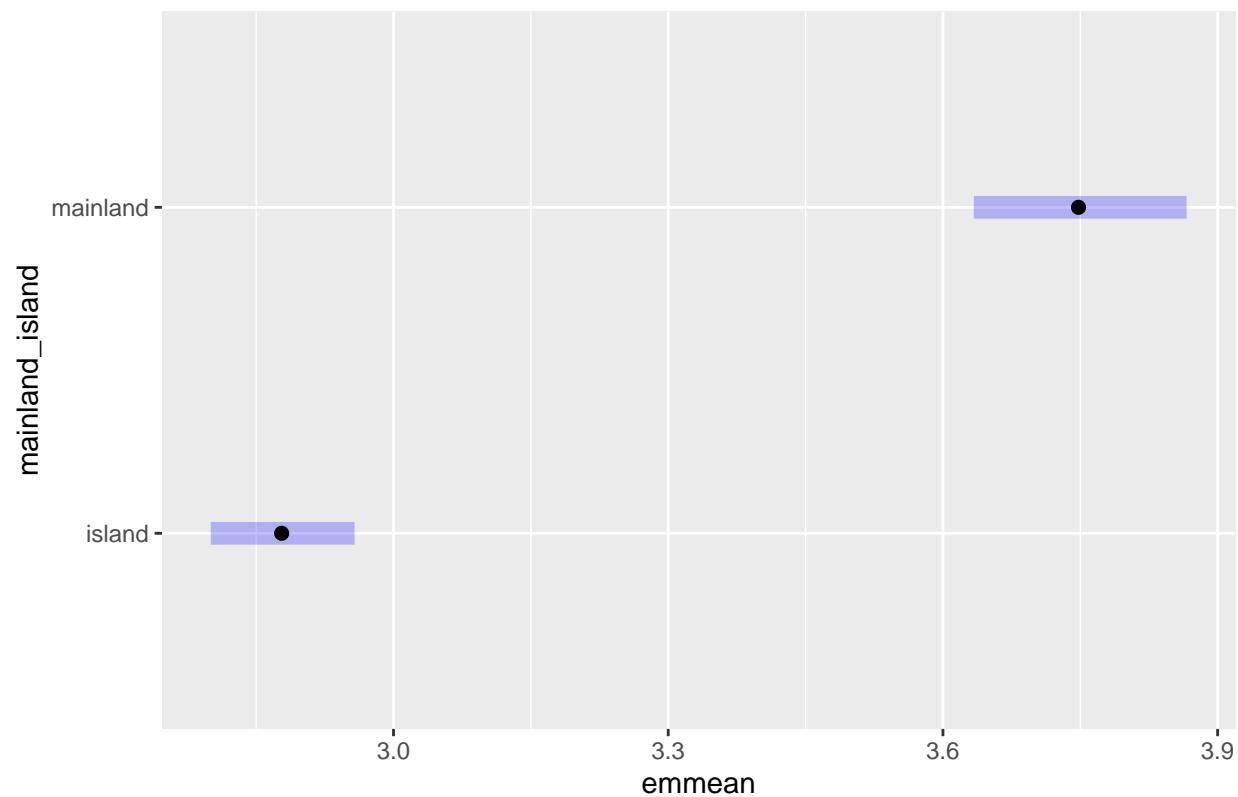
Mericarp Spine Length



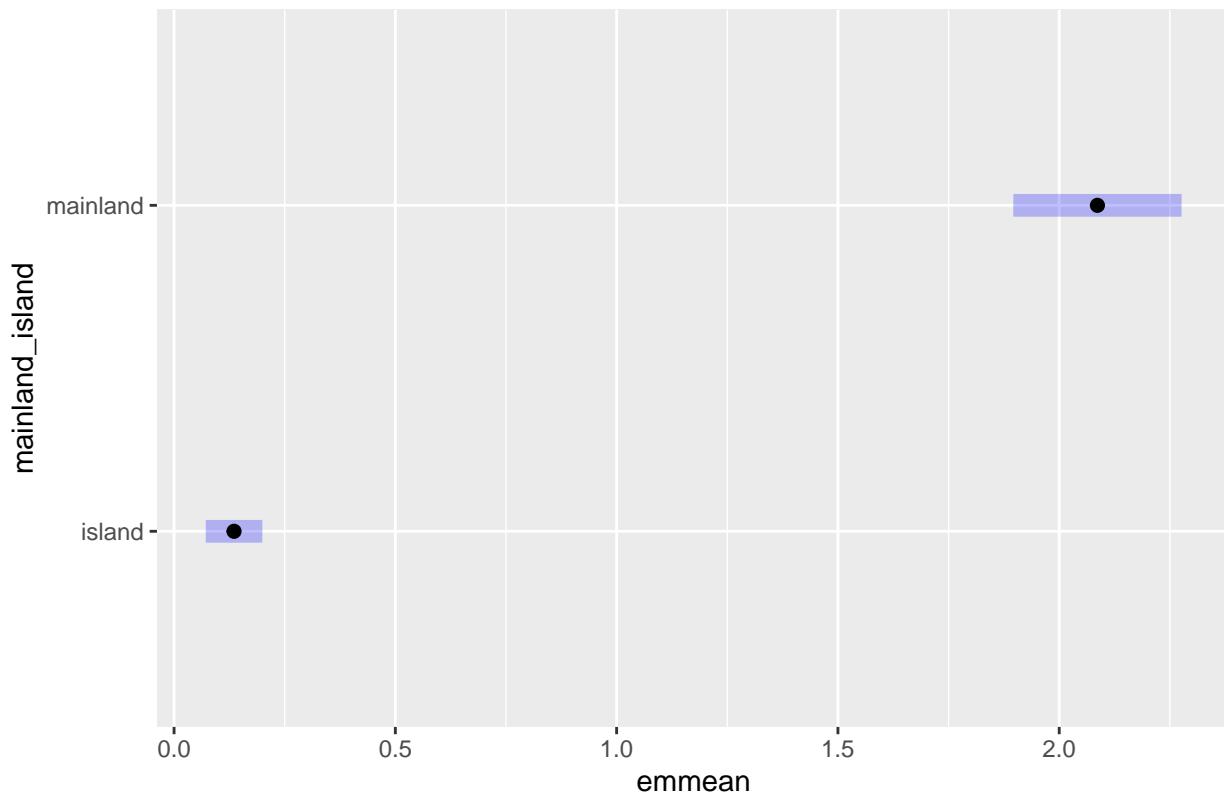
Mericarp Spine Tip Distance



Mericarp Spine number



Mericarp Lower Spines

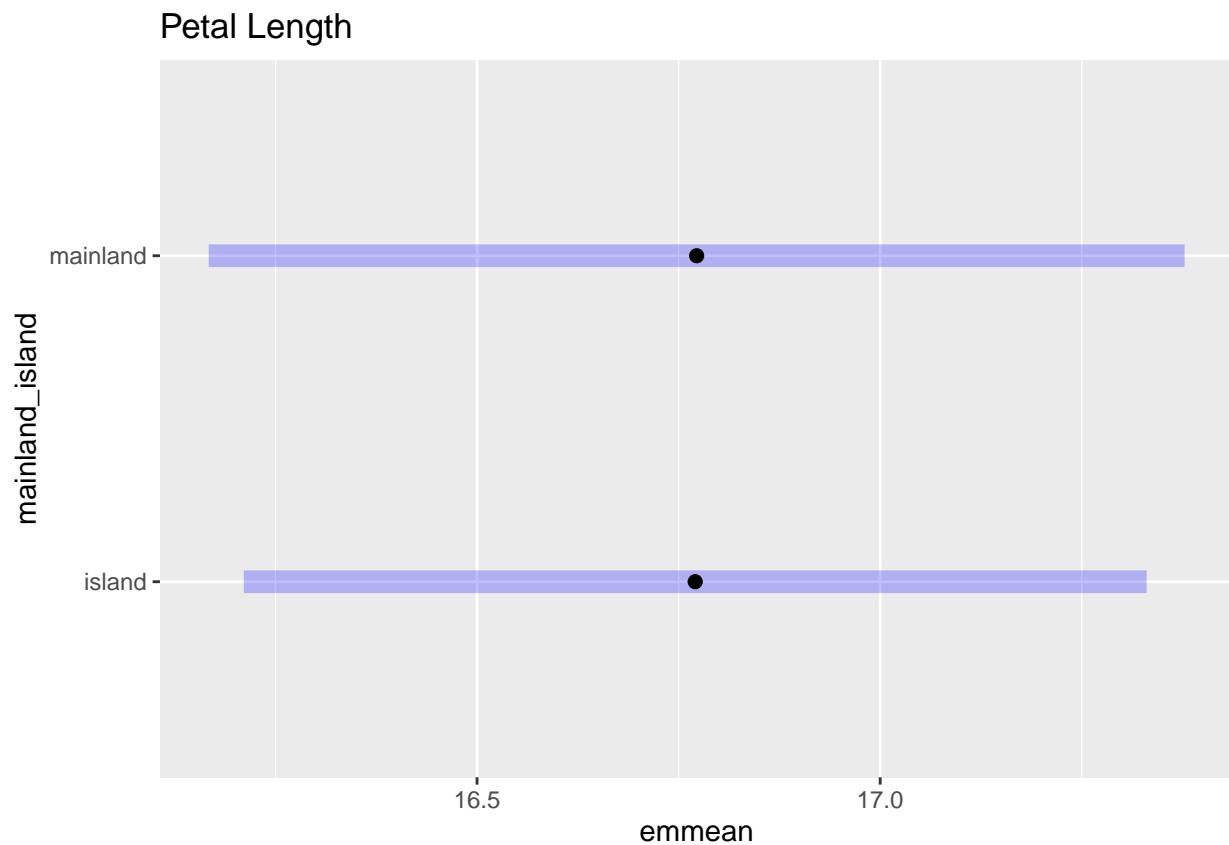


In general mericarps from mainland populations are smaller than island mericarps. However, spine size seems to differ with mainland populations having longer tip distances and higher spine numbers than island populations.

Flowers

Petal Length

```
##  mainland_island emmean    SE  df lower.CL upper.CL
##  island          16.8 0.285 396     16.2     17.3
##  mainland        16.8 0.308 377     16.2     17.4
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
```



Leaves

Leaf Length

```
## mainland_island response      SE  df lower.CL upper.CL
## island                  29.3 0.765 384     27.8    30.8
## mainland                24.0 0.760 417     22.5    25.5
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
```

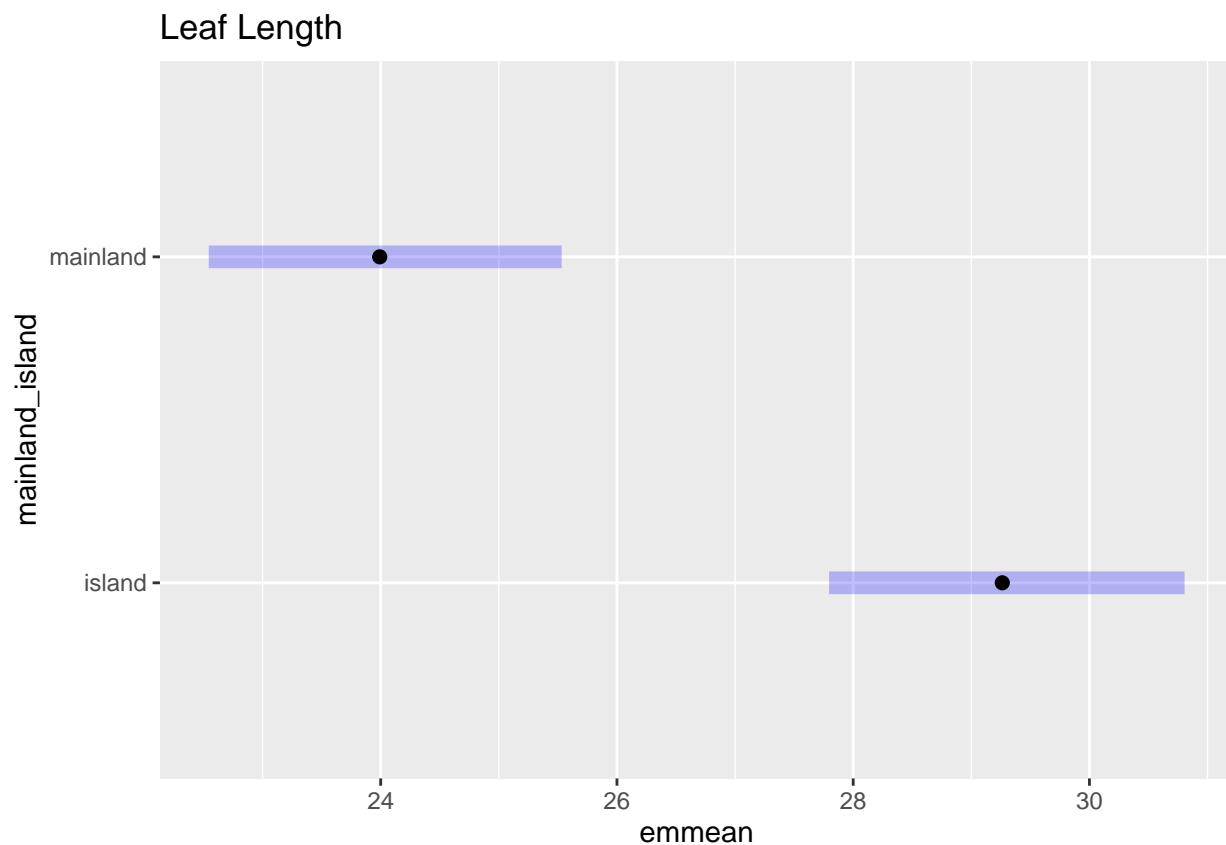
Leaflet Length

```
## mainland_island response      SE  df lower.CL upper.CL
## island                  8.29 0.179 391     7.94    8.64
## mainland                7.67 0.200 417     7.29    8.07
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
```

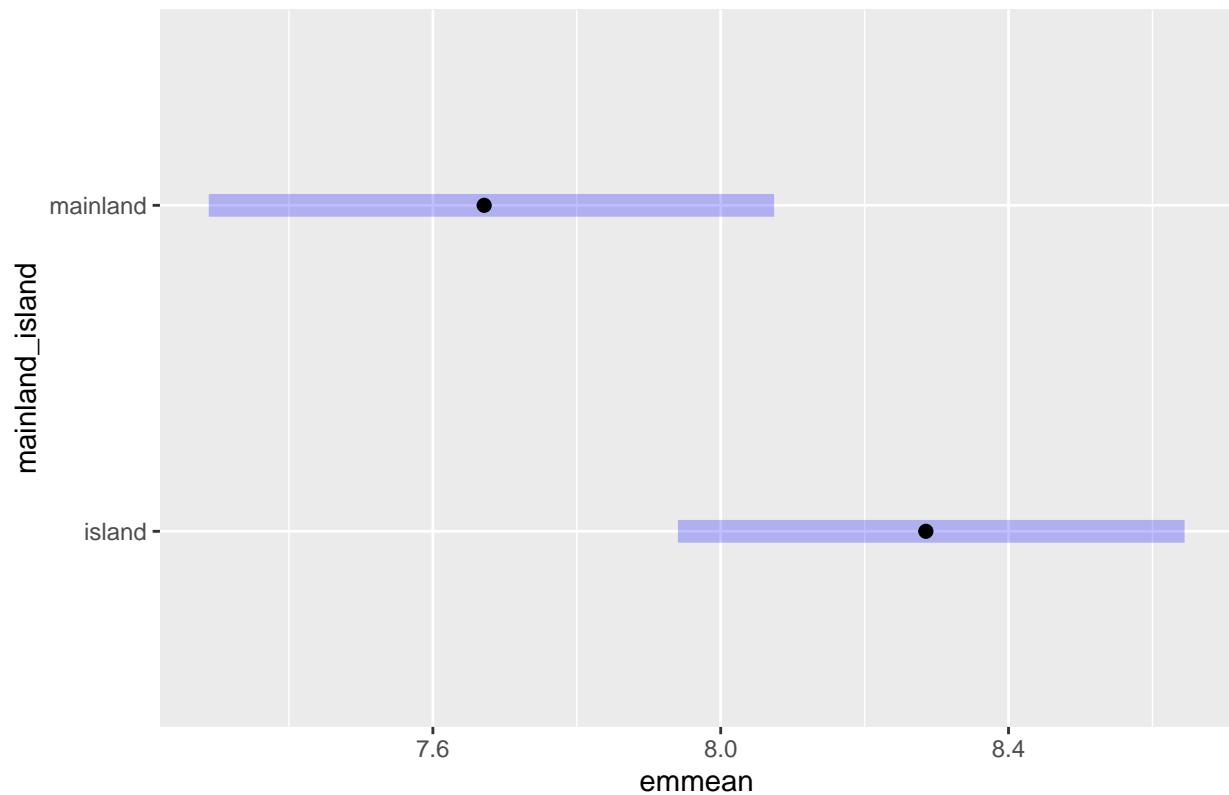
Leaflet Number

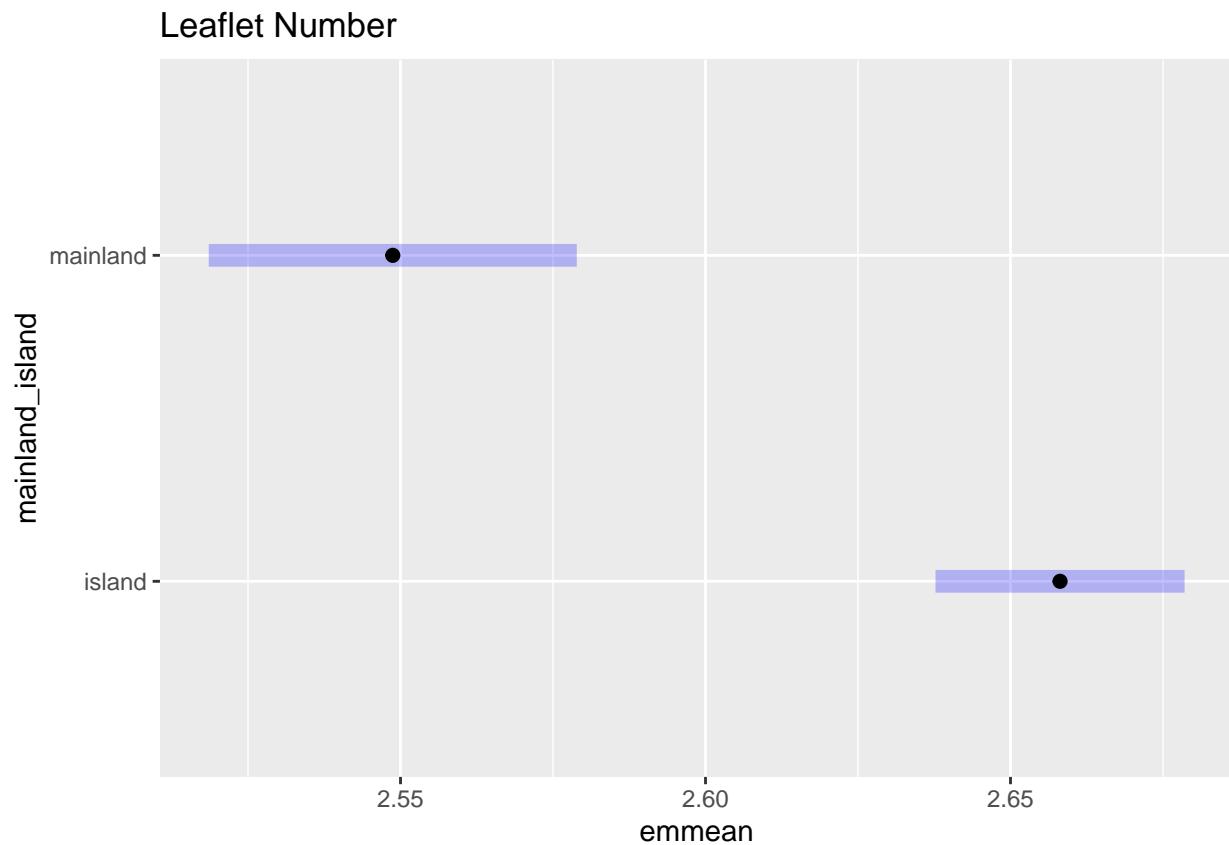
```
## mainland_island emmean      SE  df asympt.LCL asympt.UCL
## island                  2.66 0.0104 Inf     2.64    2.68
## mainland                2.55 0.0154 Inf     2.52    2.58
##
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
```

Leaves LS means plots



Leaflet Length





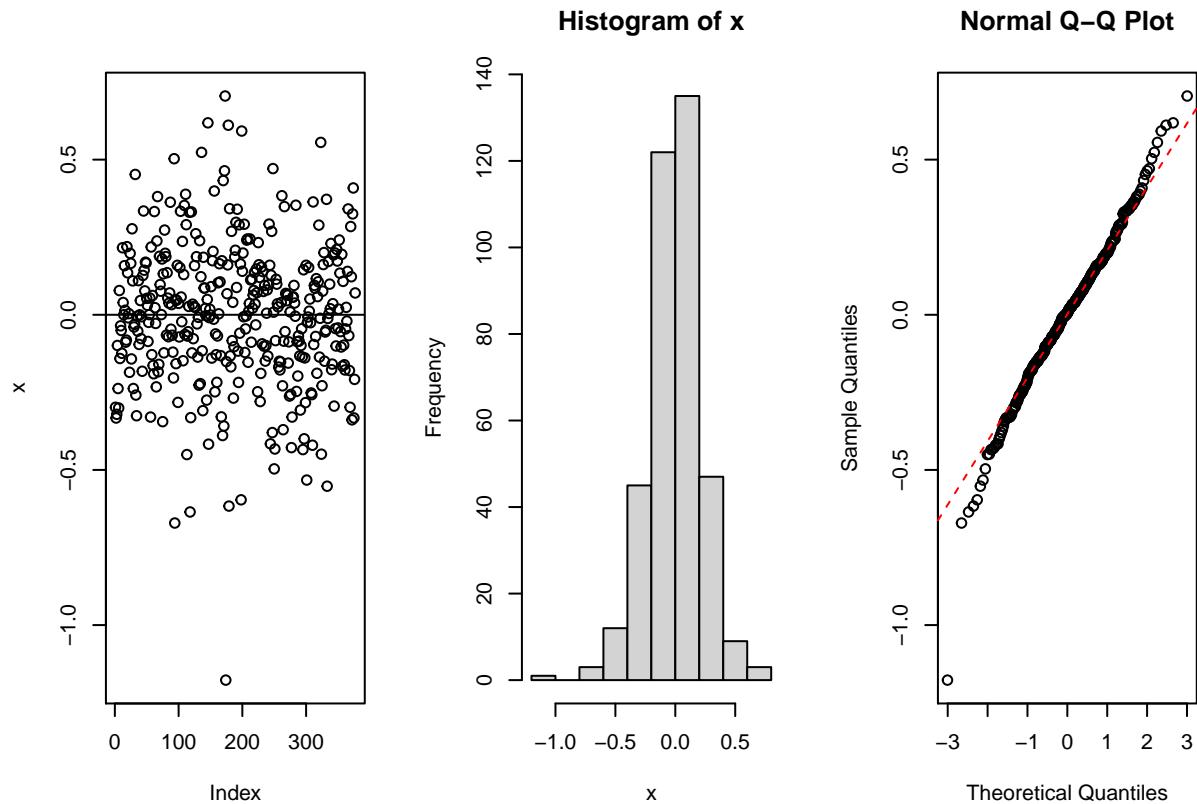
Mainland populations seems to have smaller leaves and less leaflets than island populations.

Model 2 trait ~ galapagos/other islands + year + (1|ID)

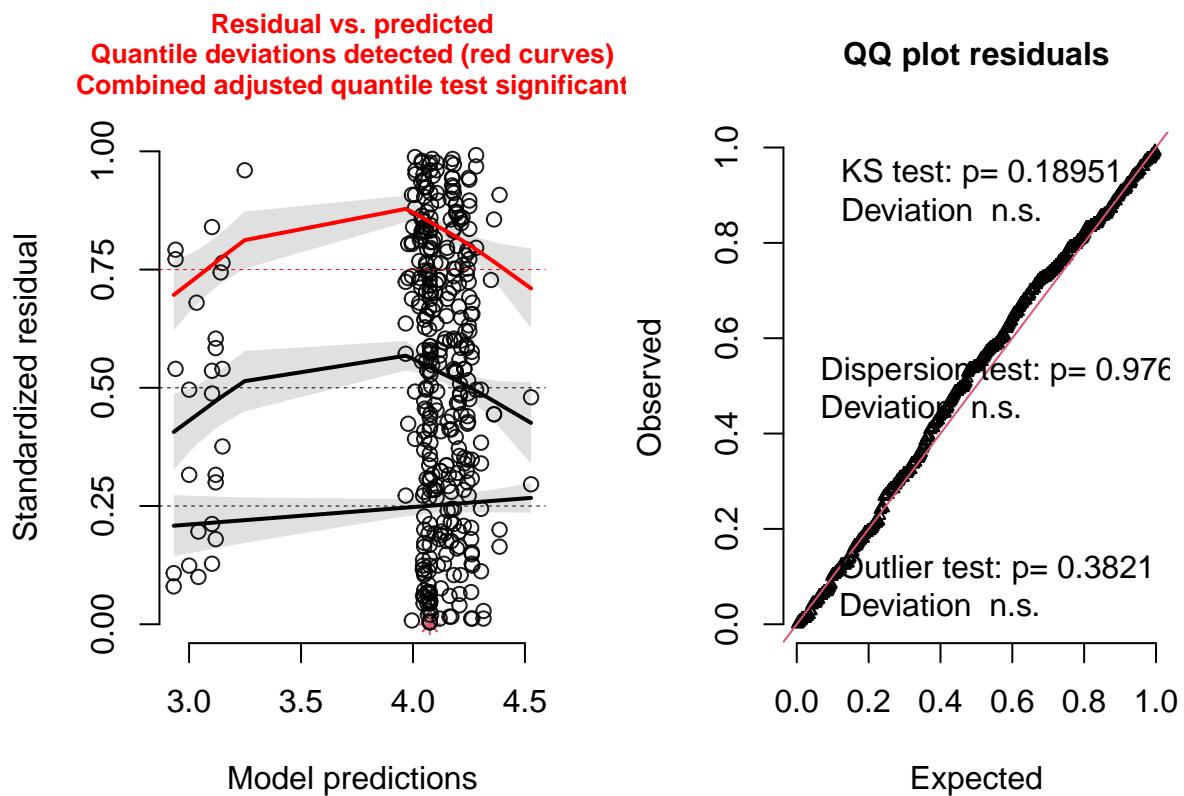
This is the second model, that shows the differences of *Tribulus* traits from Galapagos populations and other Islands.

Flowers

Petal length -> Root squared transformed data



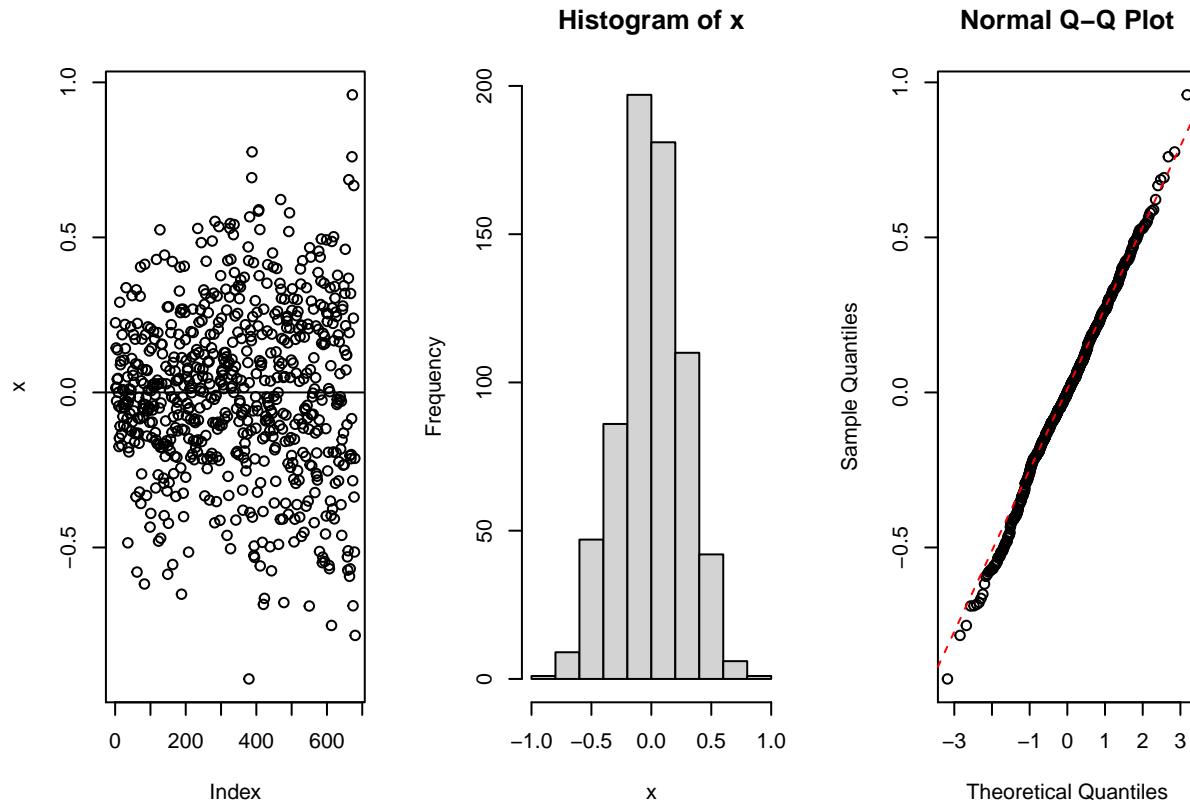
```
## [1] "Kurtosis=1.82233135992289"  
## [1] "Skew=-0.357589730850339"
```



```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sqrt(petal_length)
##          Chisq Df Pr(>Chisq)
## galapagos_other 87.9227  1 < 2.2e-16 ***
## year_collected   8.8887  1  0.002869 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Leaves

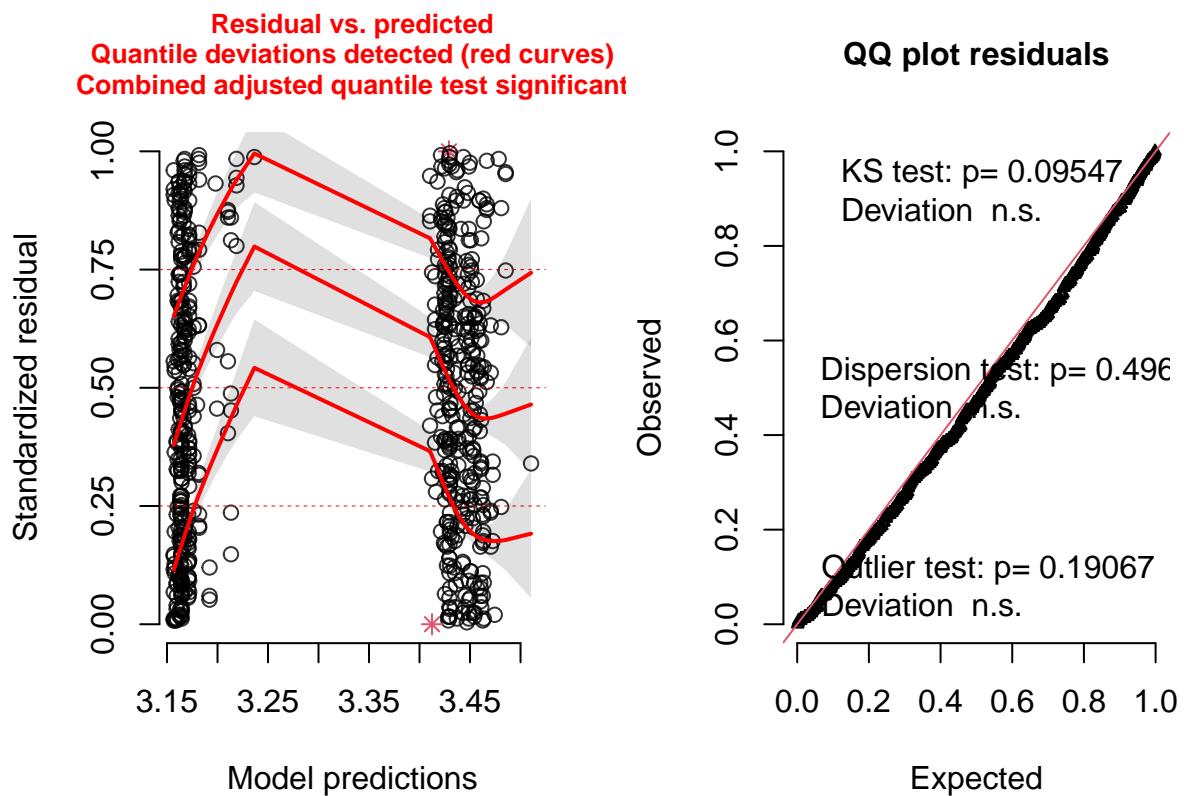
Leaf Length -> Log Transformed



```
## [1] "Kurtosis=0.174591449444752"
## [1] "Skew=-0.094965010791886"

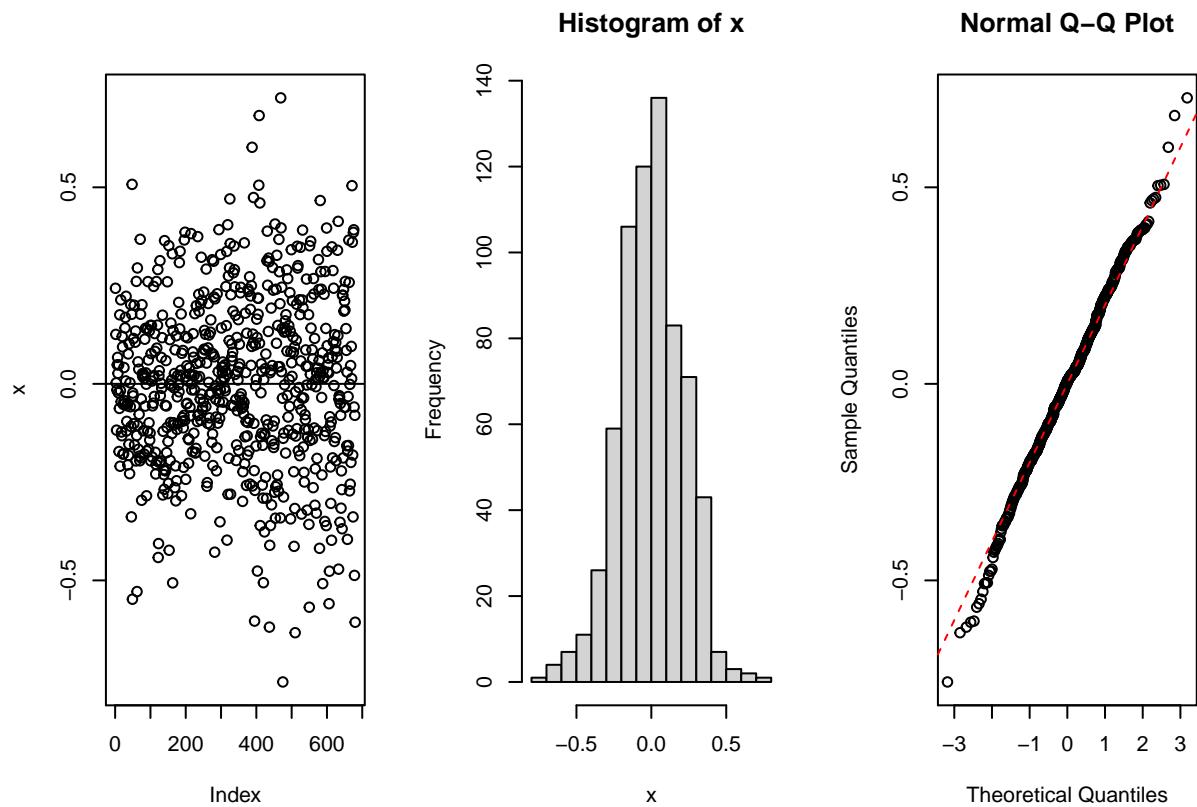
## qu = 0.75, log(sigma) = -2.141644 : outer Newton did not converge fully.

## qu = 0.75, log(sigma) = -2.176578 : outer Newton did not converge fully.
```

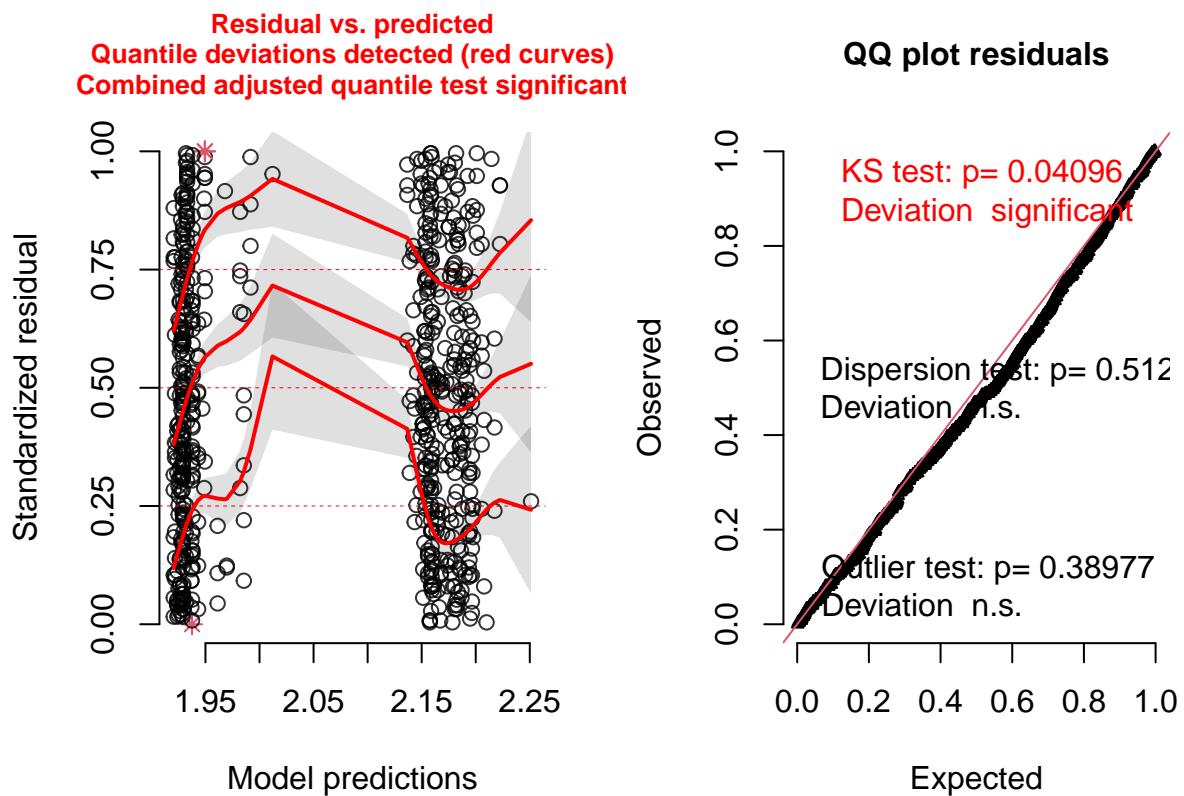


```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: log(leaf_length)
##              Chisq Df Pr(>Chisq)
## galapagos_other 18.0889  1  2.108e-05 ***
## year_collected   0.5641  1      0.4526
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Leaflet Length -> Log Transformed



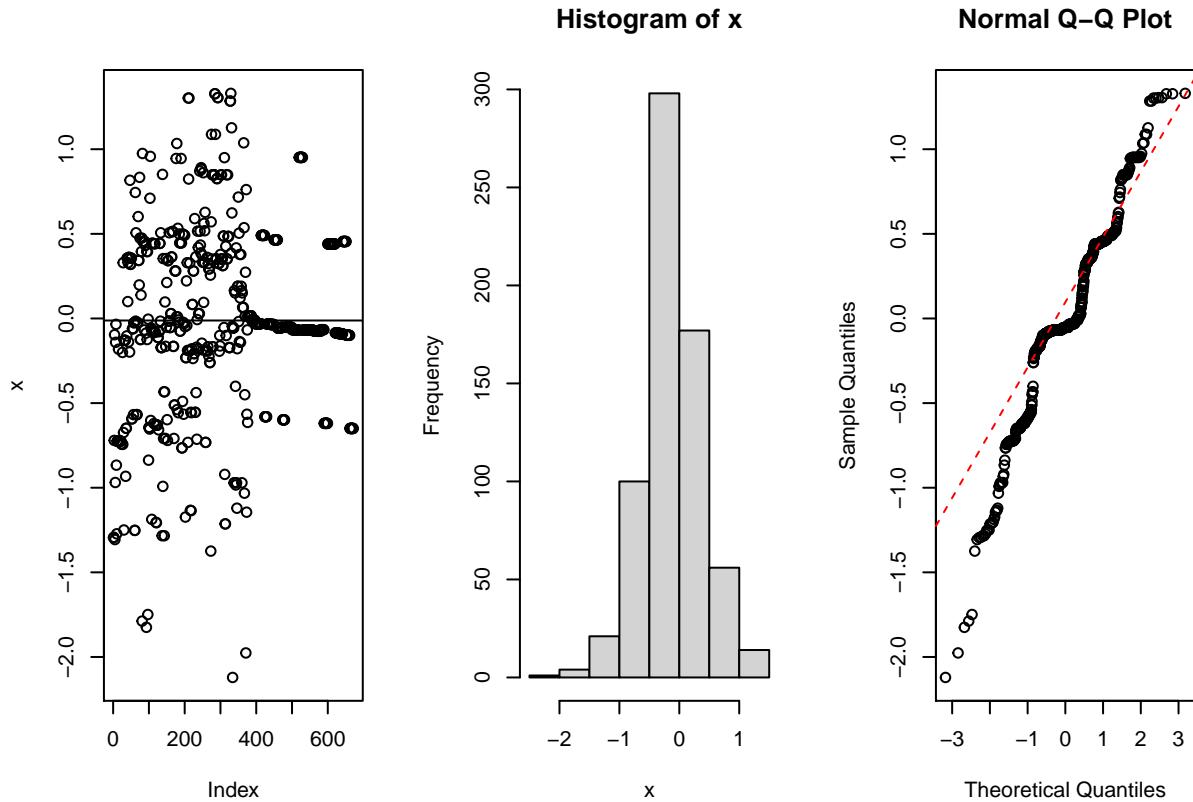
```
## [1] "Kurtosis=0.295097534906618"  
## [1] "Skew=-0.0991019439431268"
```



```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: log(leaflet_length)
##             Chisq Df Pr(>Chisq)
## galapagos_other 17.3782  1  3.063e-05 ***
## year_collected   1.0138  1      0.314
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

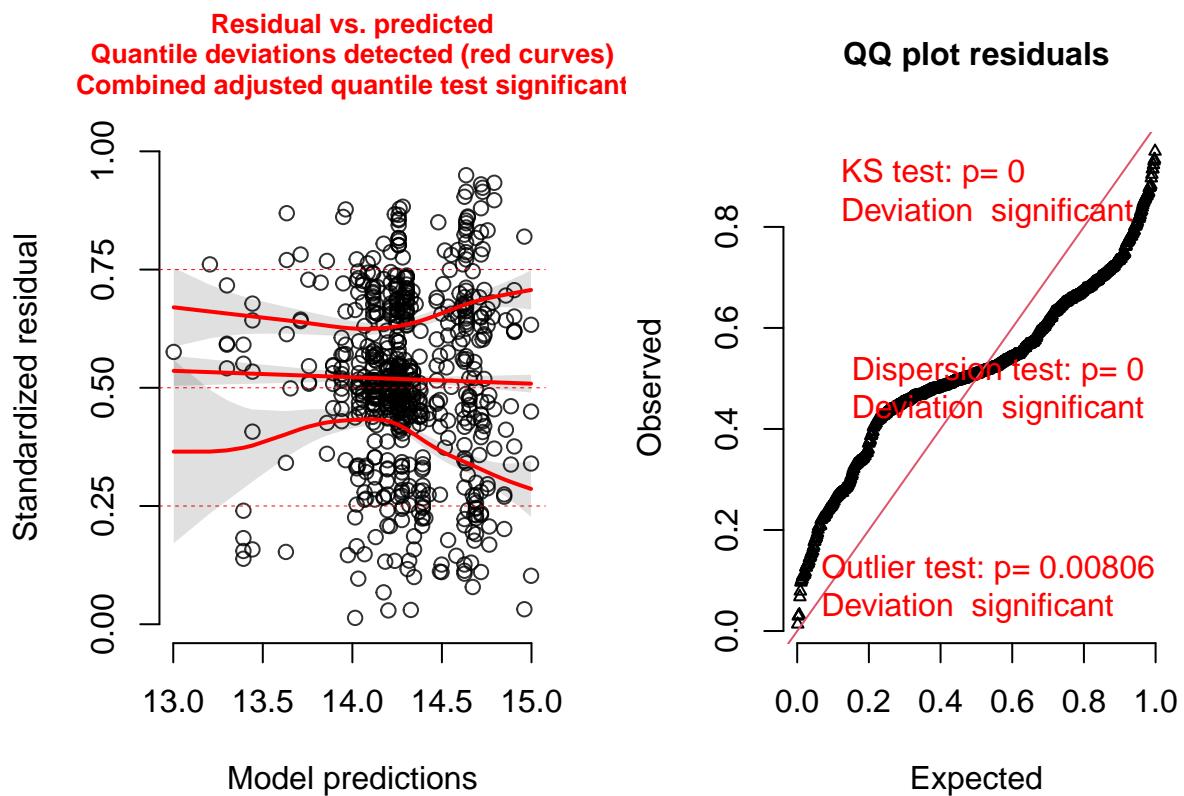
Leaflet number -> Not transformed *For leaflet number, I think it is a count trait, so I used this model:*

`glm(number_of_leaflets ~ mainland_island + year_collected, family = poisson, data=leaf_length)`



```
## [1] "Kurtosis=1.11565272013564"
## [1] "Skew=-0.378042815760105"
```

```
## DHARMA:plot used testOutliers with type = binomial for computational reasons (nObs > 500). Note that
```



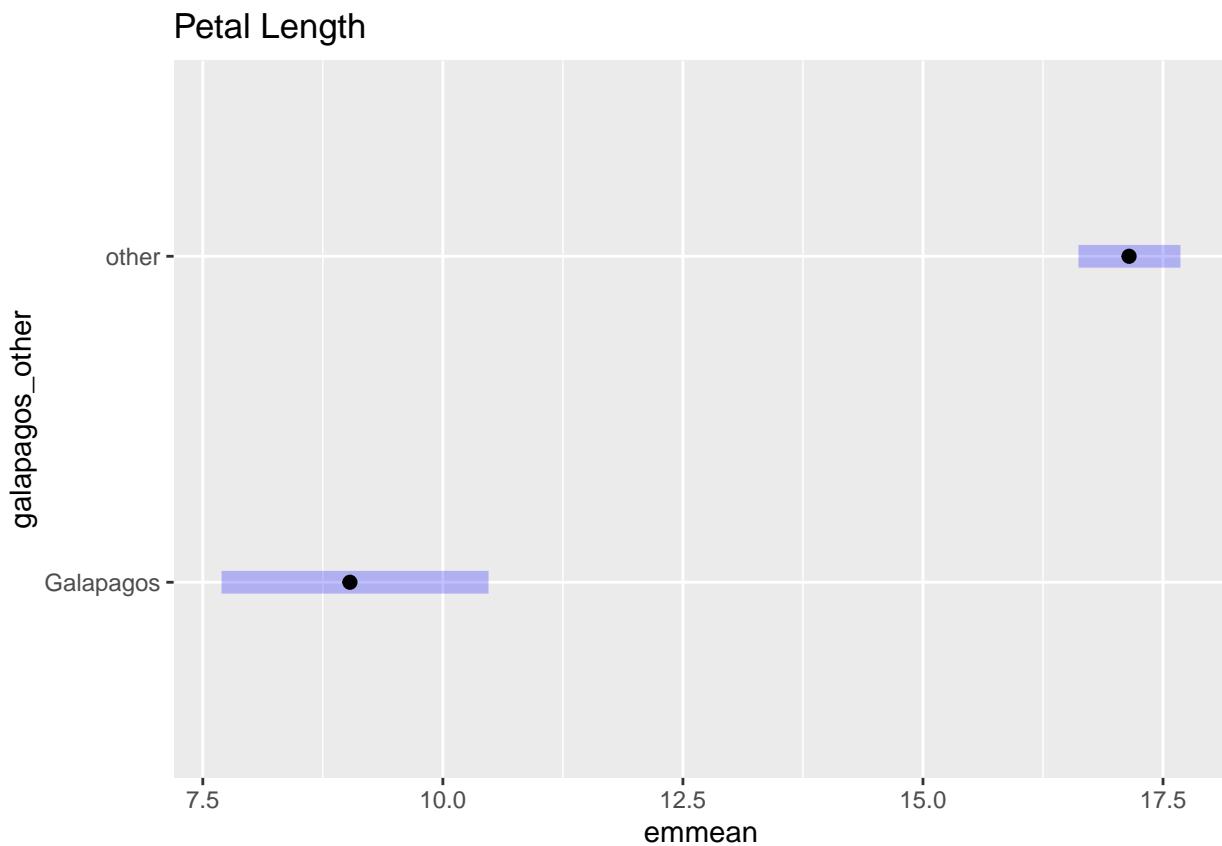
```
## Analysis of Deviance Table (Type II tests)
##
## Response: number_of_leaflets
##           LR Chisq Df Pr(>Chisq)
## galapagos_other   3.3502  1    0.06720 .
## year_collected    3.3740  1    0.06623 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model 2 LS means

Flowers

Petal Length

```
##  galapagos_other response      SE  df lower.CL upper.CL
##  Galapagos              9.03 0.705 219     7.7    10.5
##  other                  17.15 0.269 211    16.6    17.7
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Intervals are back-transformed from the sqrt scale
```



Petal length from Galapagos seems to be smaller than other island systems.

Leaves

Leaf Length

```
##  galapagos_other response      SE  df lower.CL upper.CL
##  Galapagos            24.1 1.155 158    21.9    26.5
##  other                30.9 0.945 265    29.1    32.8
##
```

```
## Degrees-of-freedom method: kenward-roger  
## Confidence level used: 0.95  
## Intervals are back-transformed from the log scale
```

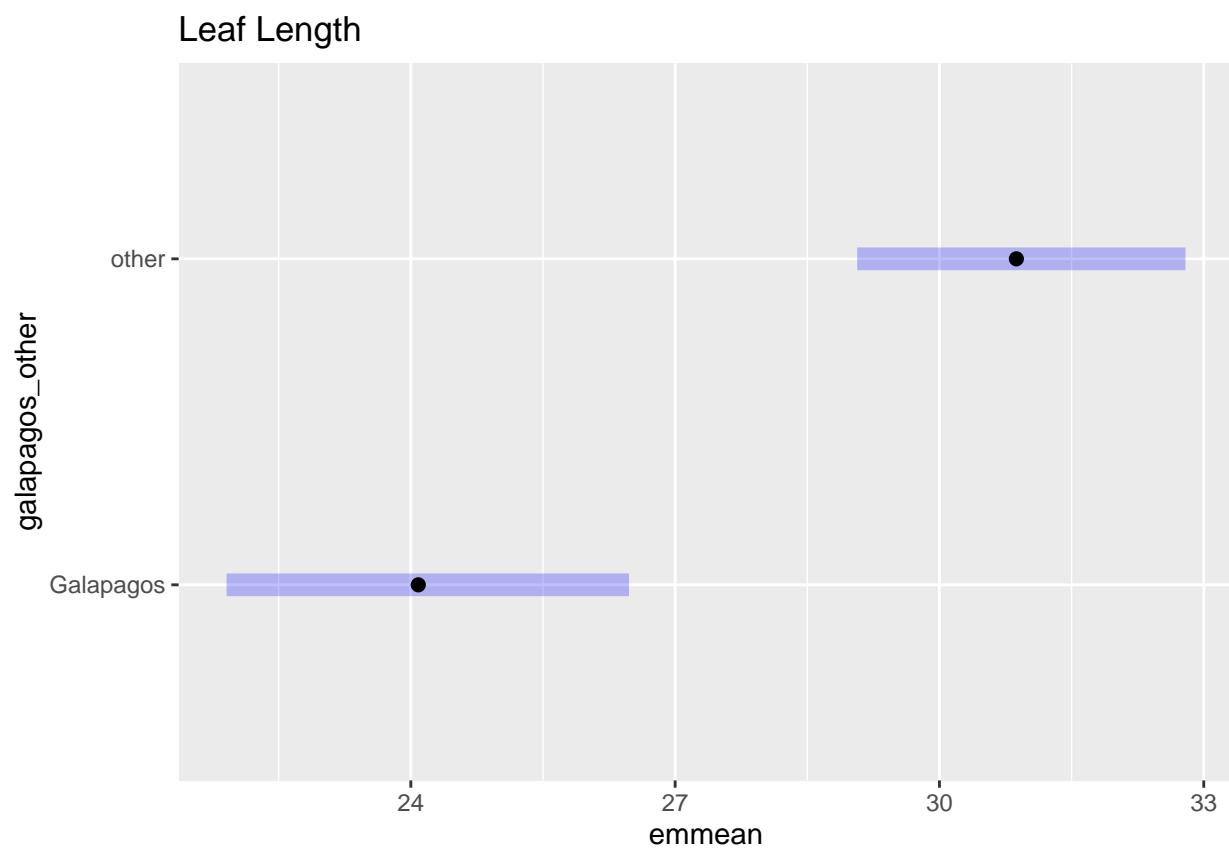
Leaflet Length

```
## galapagos_other response      SE  df lower.CL upper.CL  
## Galapagos                 7.02 0.293 169     6.47    7.63  
## other                      8.66 0.226 260     8.23    9.12  
##  
## Degrees-of-freedom method: kenward-roger  
## Confidence level used: 0.95  
## Intervals are back-transformed from the log scale
```

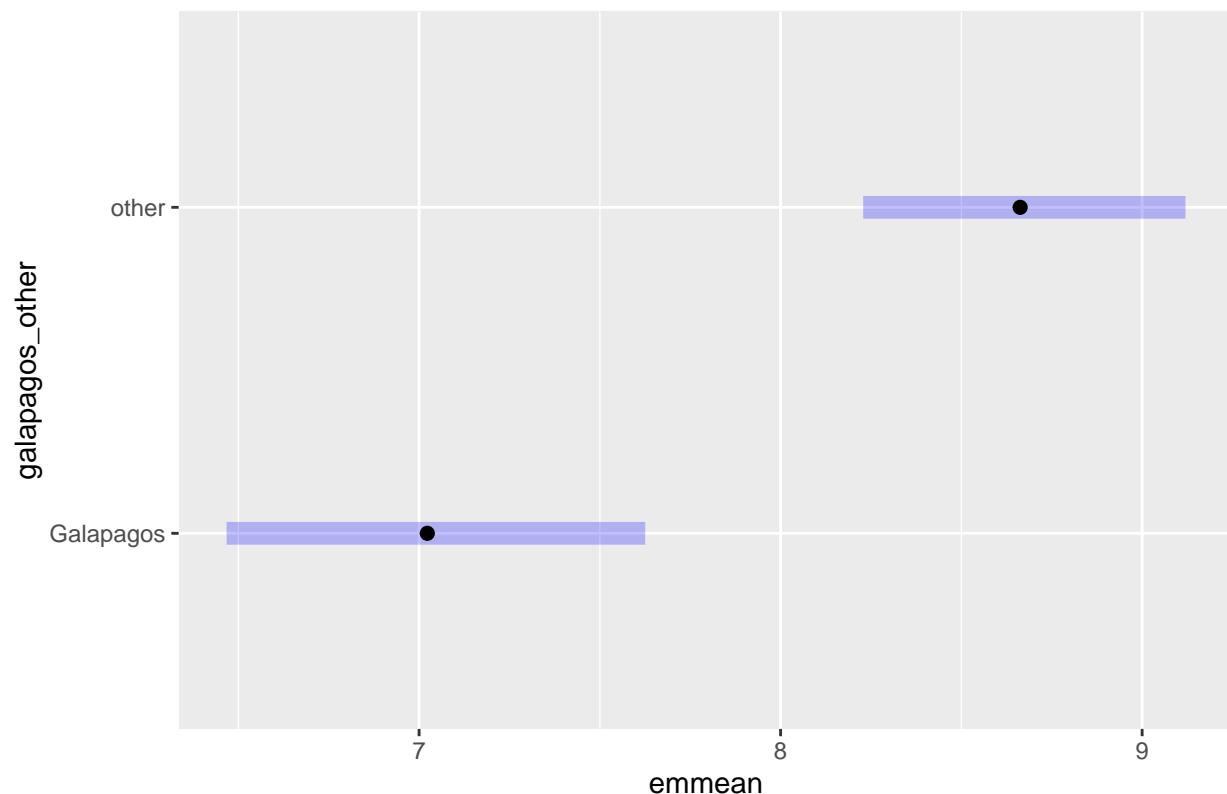
Leaflet Number

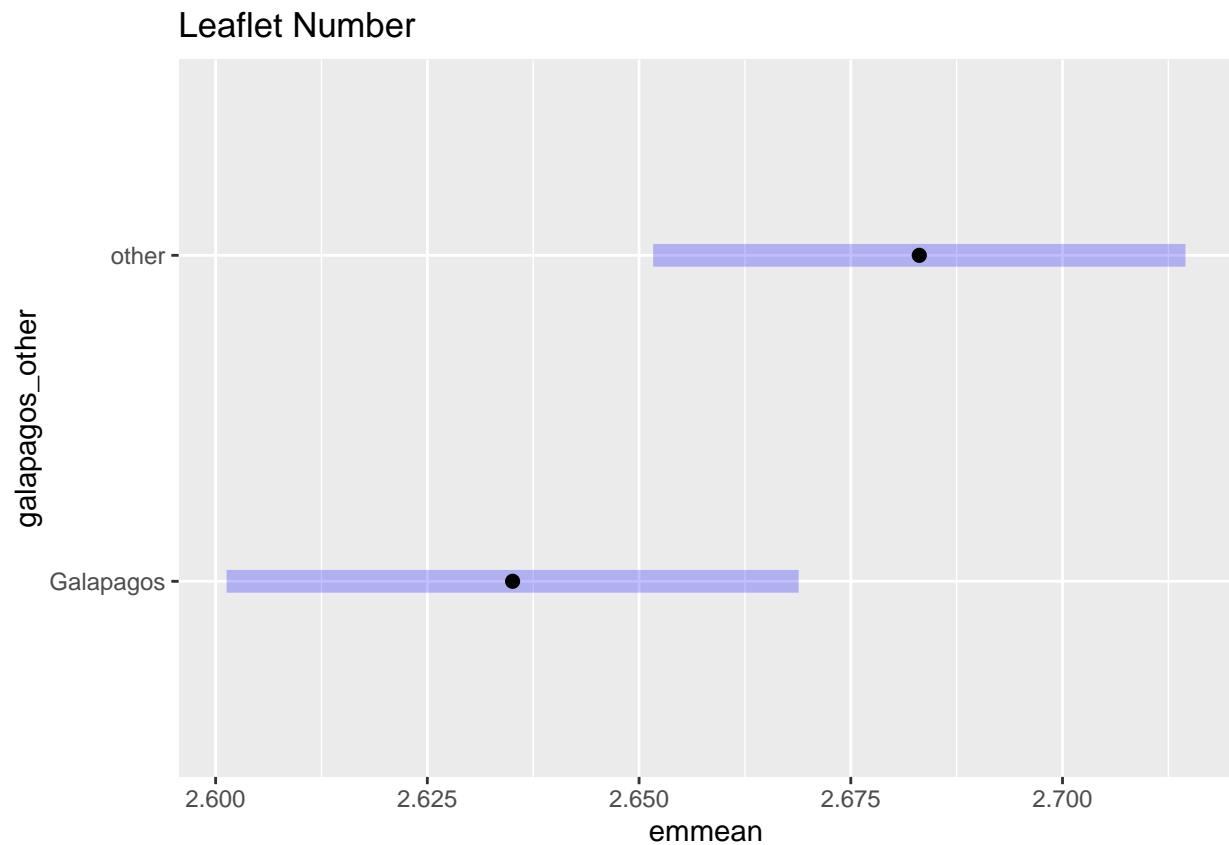
```
## galapagos_other emmean      SE  df asymp.LCL asymp.UCL  
## Galapagos                  2.64 0.0172 Inf     2.60    2.67  
## other                      2.68 0.0160 Inf     2.65    2.71  
##  
## Results are given on the log (not the response) scale.  
## Confidence level used: 0.95
```

Leaves LS means plots



Leaflet Length





Leaf, leaflet are smaller in the Galapagos compared to other islands. Leaflet number are also fewer in Galapagos.

Model 3: trait ~ finch_beak + year + (1|ID)

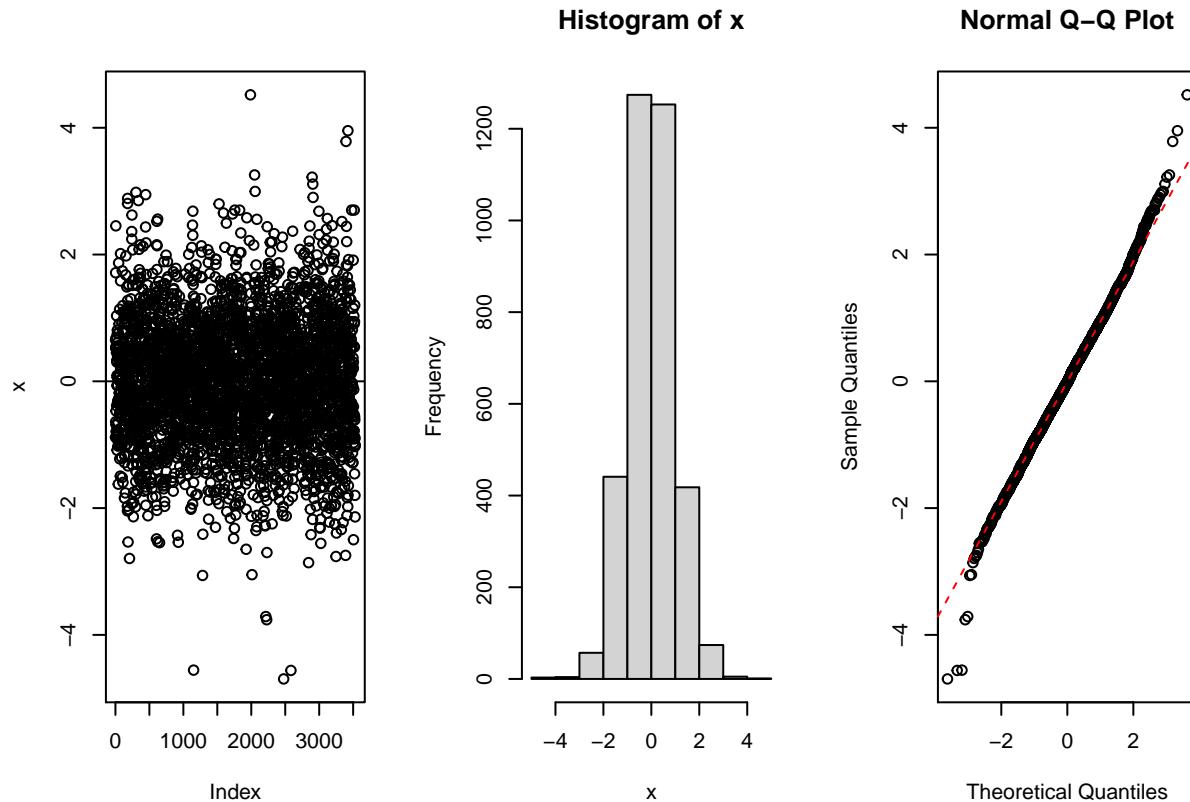
For this third model I filter the samples from Galapagos only. Then I defined the Islands that have different finch communities based on the presence or absence of large ground finches: *G. magnirostris*, *G. cornirostris*.

Floreana, San Cristobal, Santa Fe, Champion, Baltra, Enderby, Gardner and Daphne Major, previous 1983 are considered **without** magnis or cornirostris.

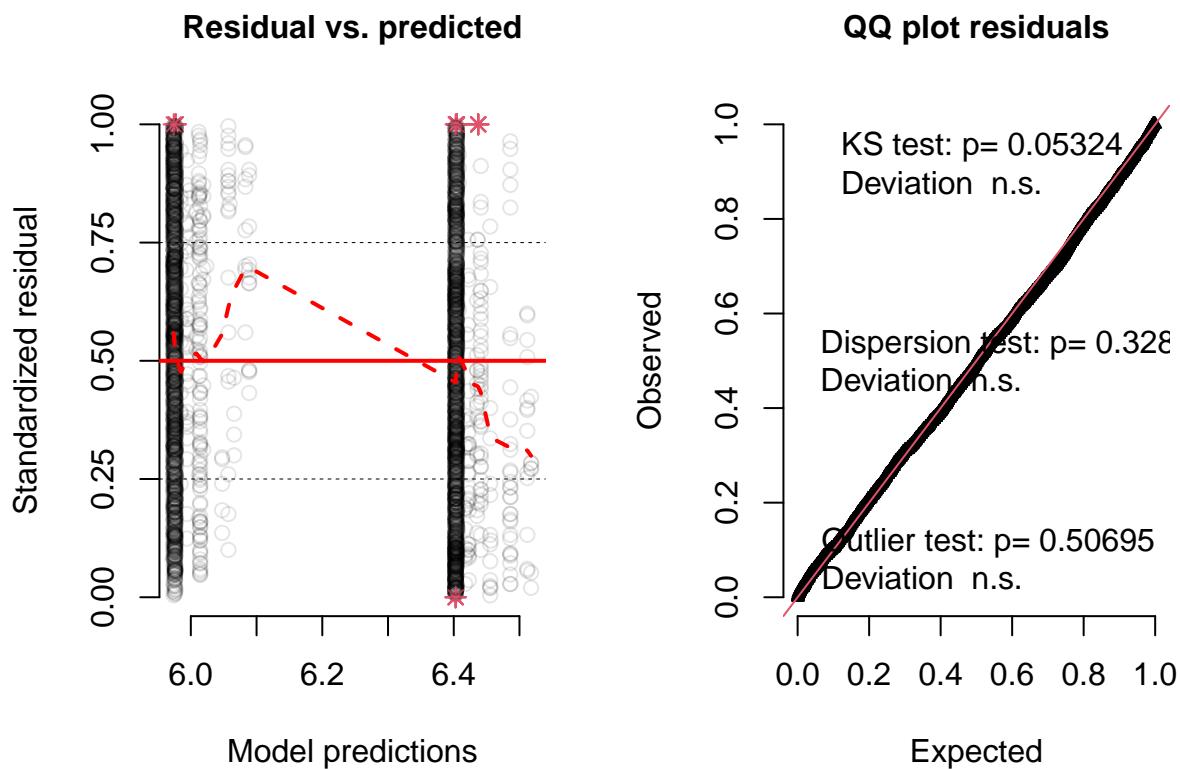
The rest of the Islands are considered **with** large ground finches.

Mericarps

Length -> Not transformed data

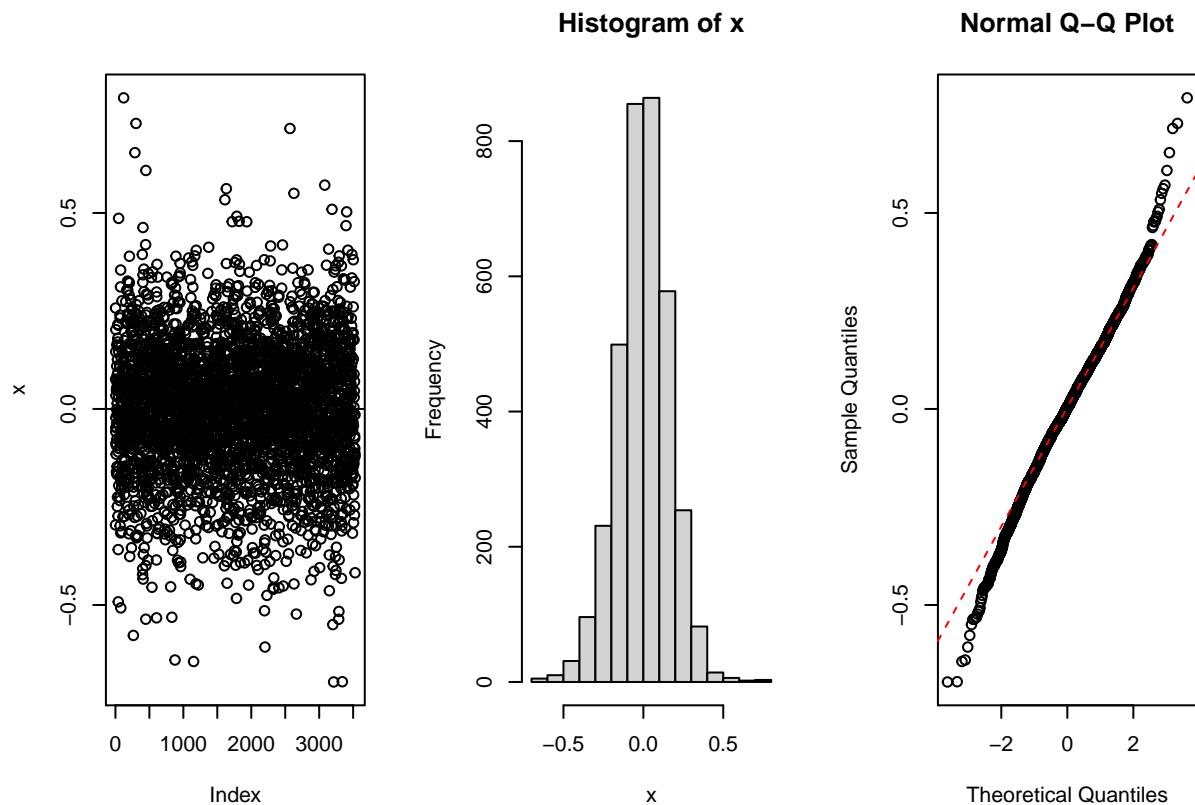


```
## [1] "Kurtosis=0.640272917671844"  
## [1] "Skew=0.0069518899108278"
```

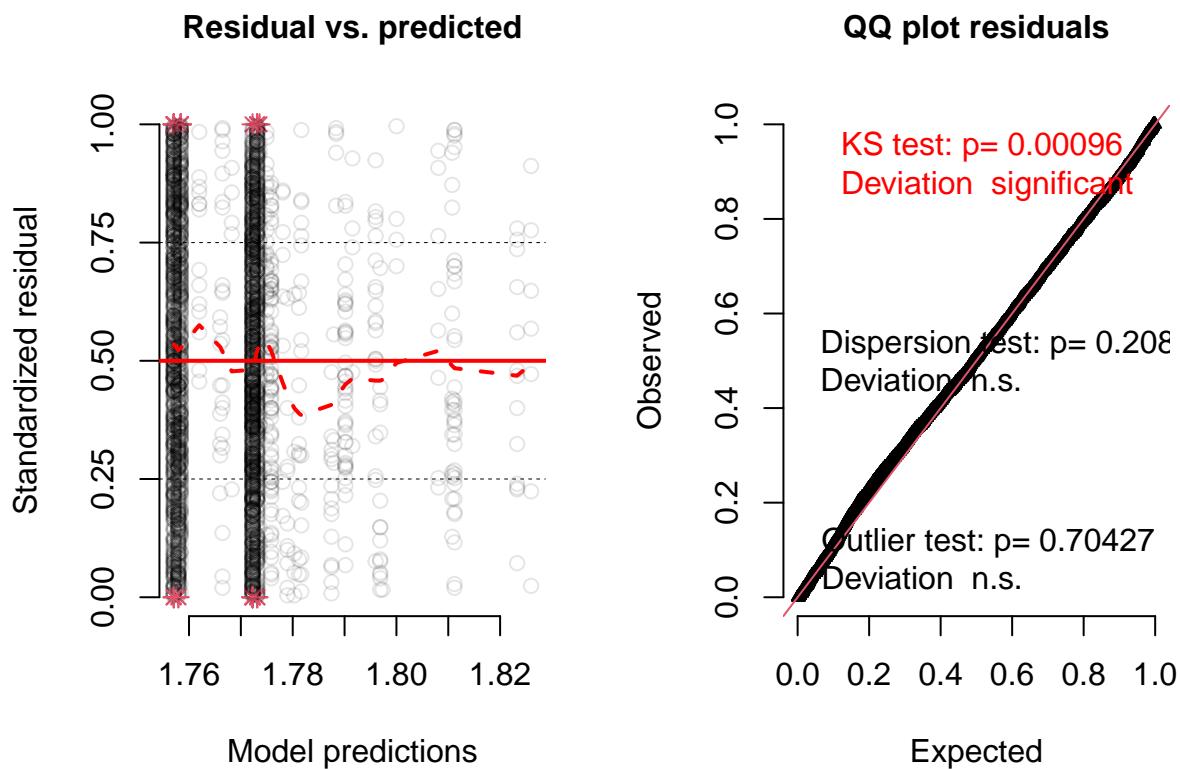


```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: length
##              Chisq Df Pr(>Chisq)
## finch_beak    5.0459  1   0.02468 *
## year_collected 0.0972  1   0.75522
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Width -> sqrt-transformed

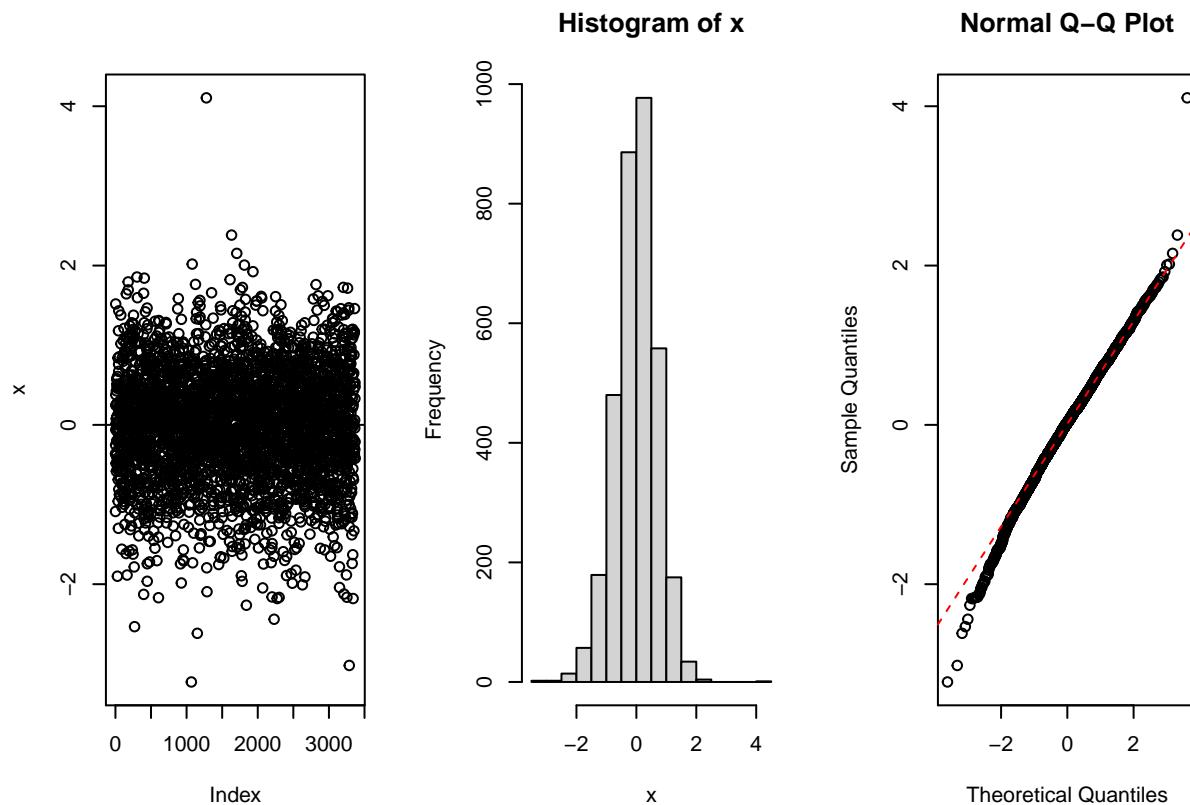


```
## [1] "Kurtosis=0.866086533593143"  
## [1] "Skew=-0.13190943721093"
```

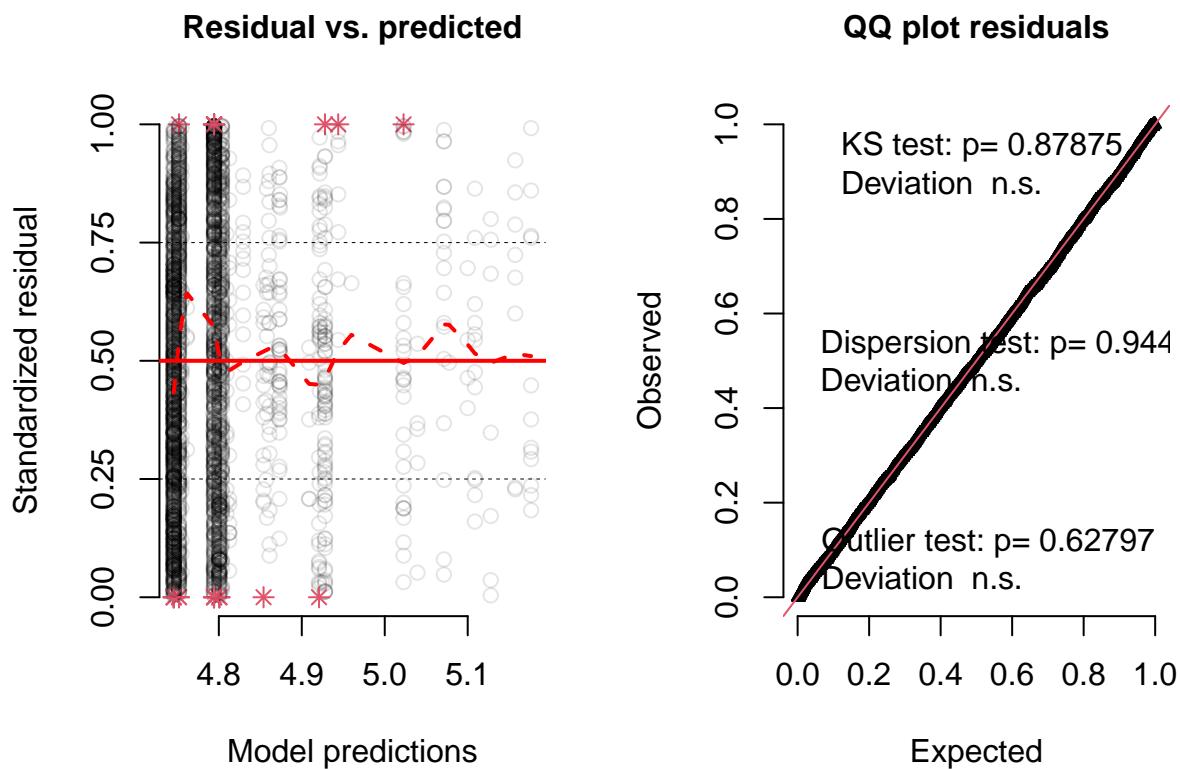


```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sqrt(width)
##             Chisq Df Pr(>Chisq)
## finch_beak    0.5813  1    0.4458
## year_collected 1.7970  1    0.1801
```

Depth -> Not transformed

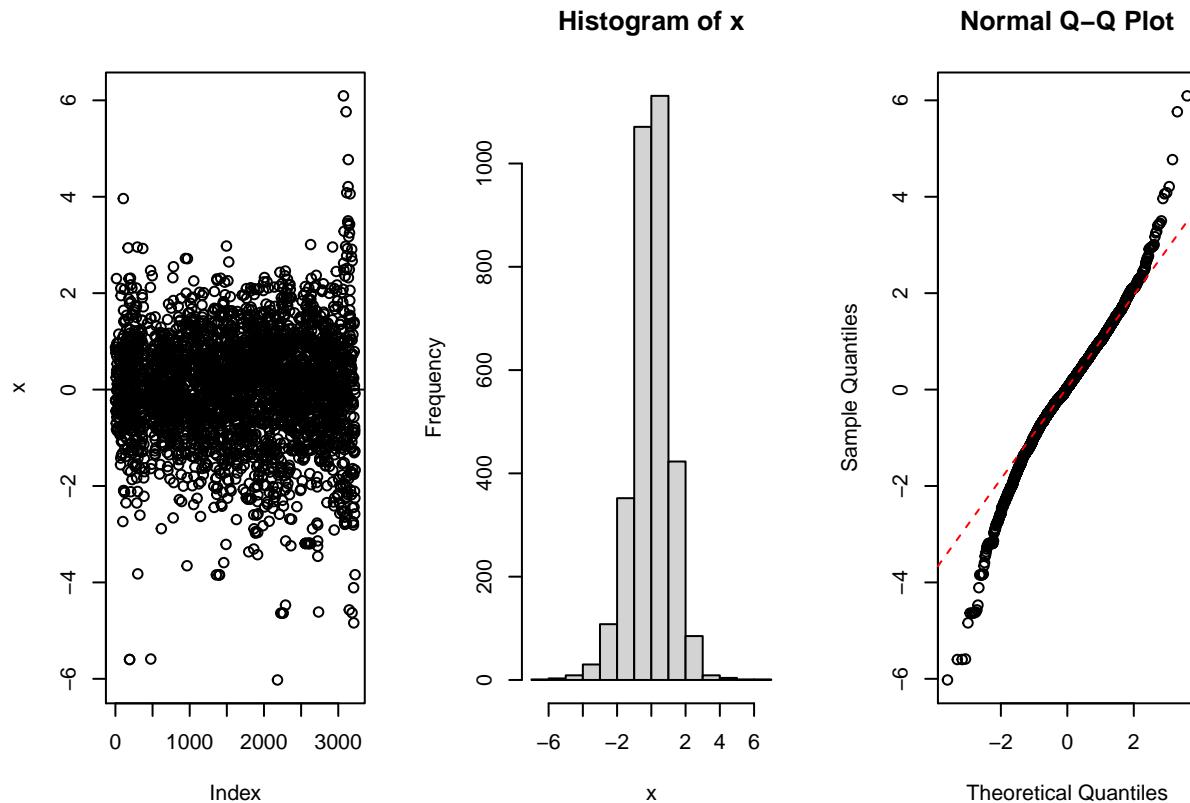


```
## [1] "Kurtosis=0.741297164859156"  
## [1] "Skew=-0.20439673252663"
```

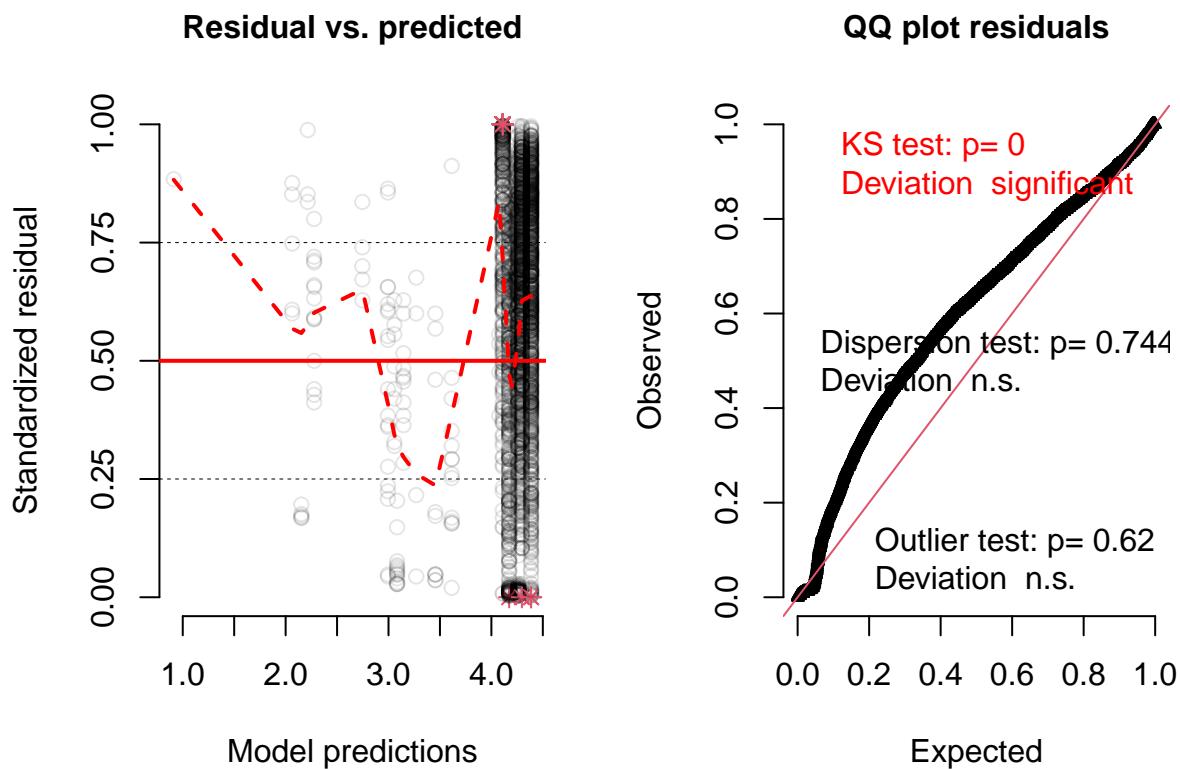


```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: depth
##              Chisq Df Pr(>Chisq)
## finch_beak    0.2483  1    0.61824
## year_collected 3.9913  1    0.04574 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Spine Length -> Not transformed

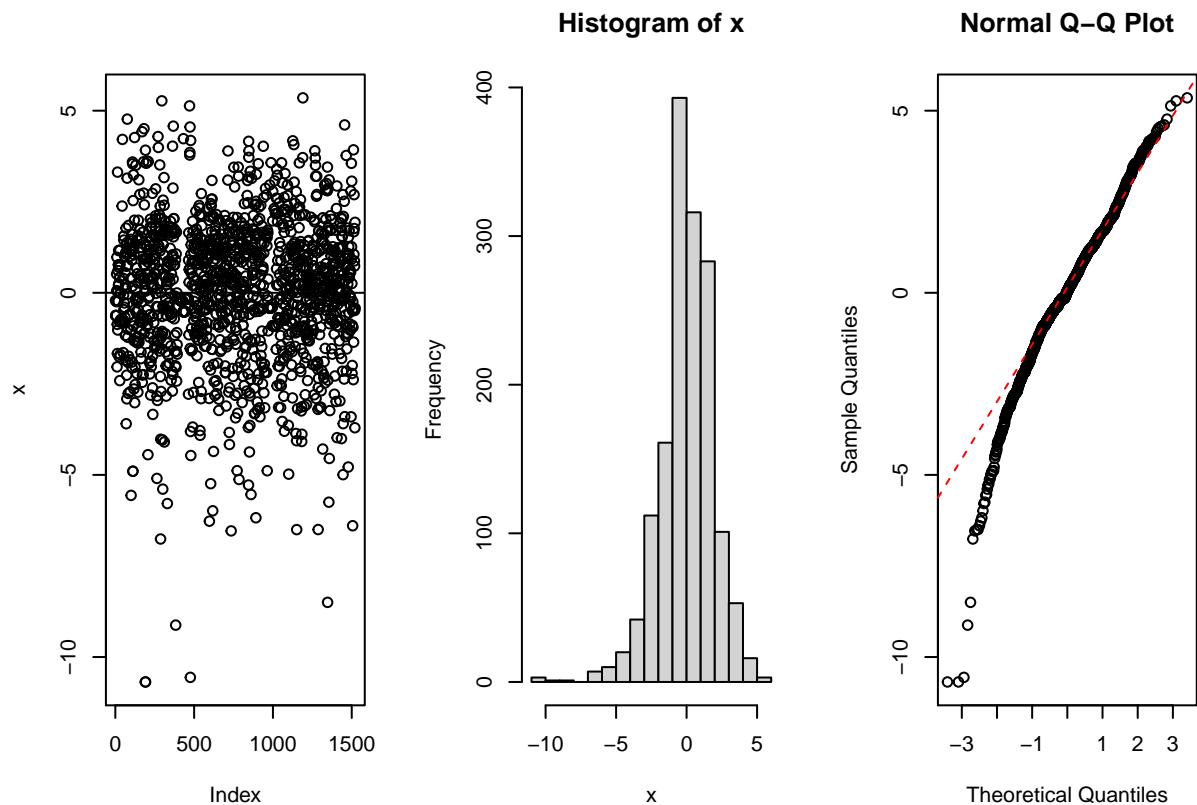


```
## [1] "Kurtosis=2.22346563111609"  
## [1] "Skew=-0.405909926348517"
```

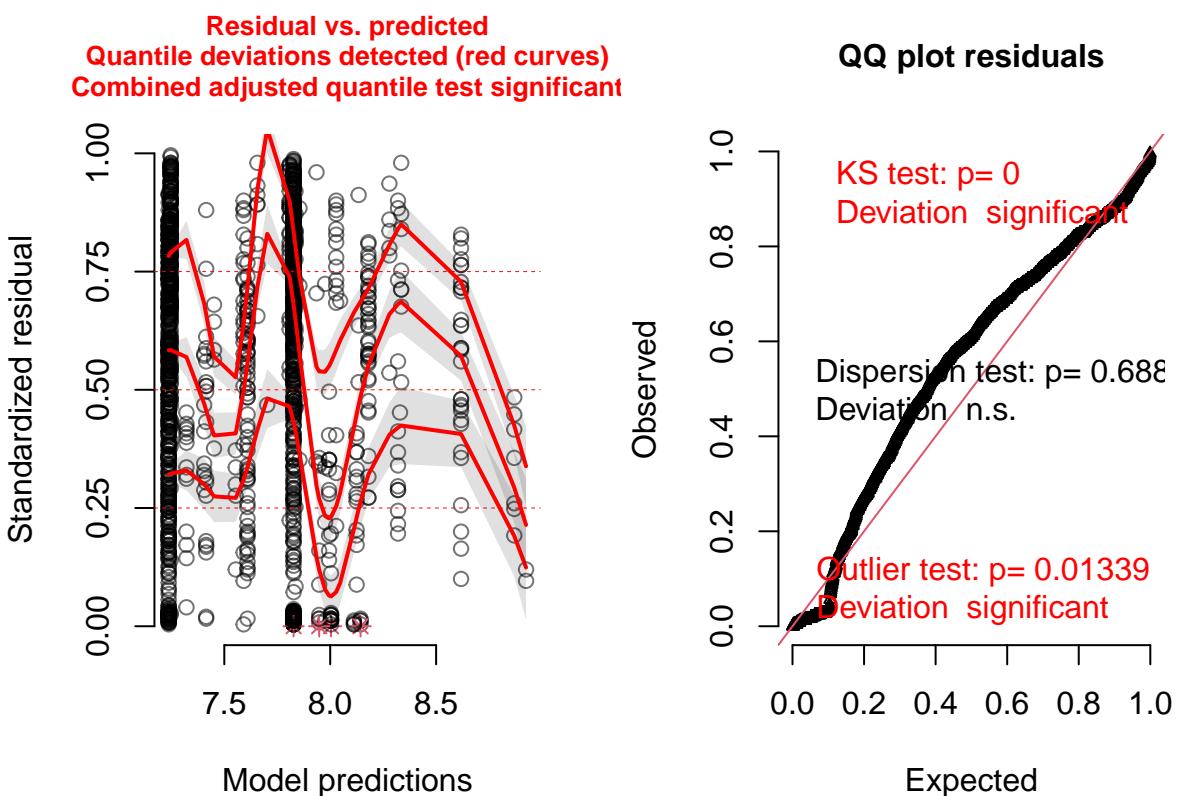


```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: spine_length
##              Chisq Df Pr(>Chisq)
## finch_beak      0.0991  1   0.7529296
## year_collected 14.3737  1   0.0001499 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Spine Tip Distance -> Not transformed



```
## [1] "Kurtosis=2.76047469083229"  
## [1] "Skew=-0.776310384626465"
```

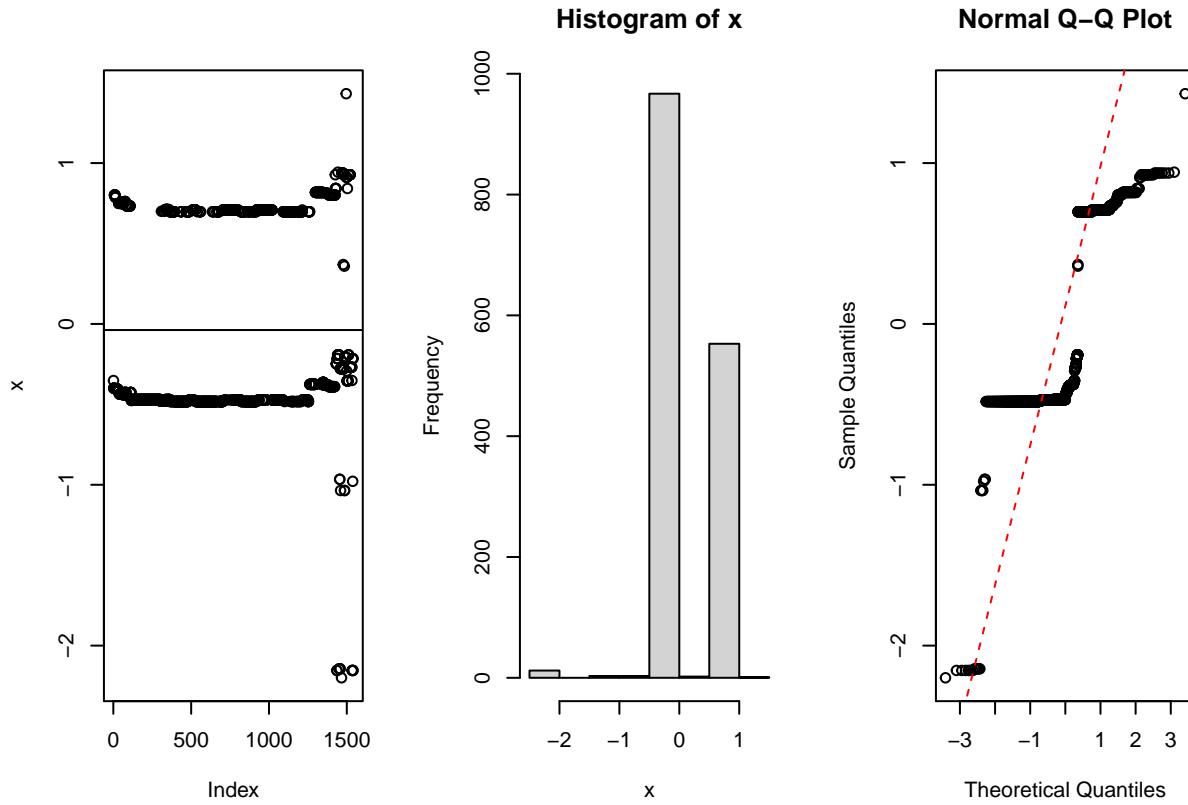


```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: tip_distance
##              Chisq Df Pr(>Chisq)
## mainland_island 2.0743  1    0.1498
## year_collected   1.5347  1    0.2154
```

Spine Number -> Not transformed *For spine number, I think it is a count trait, so I used this model:*

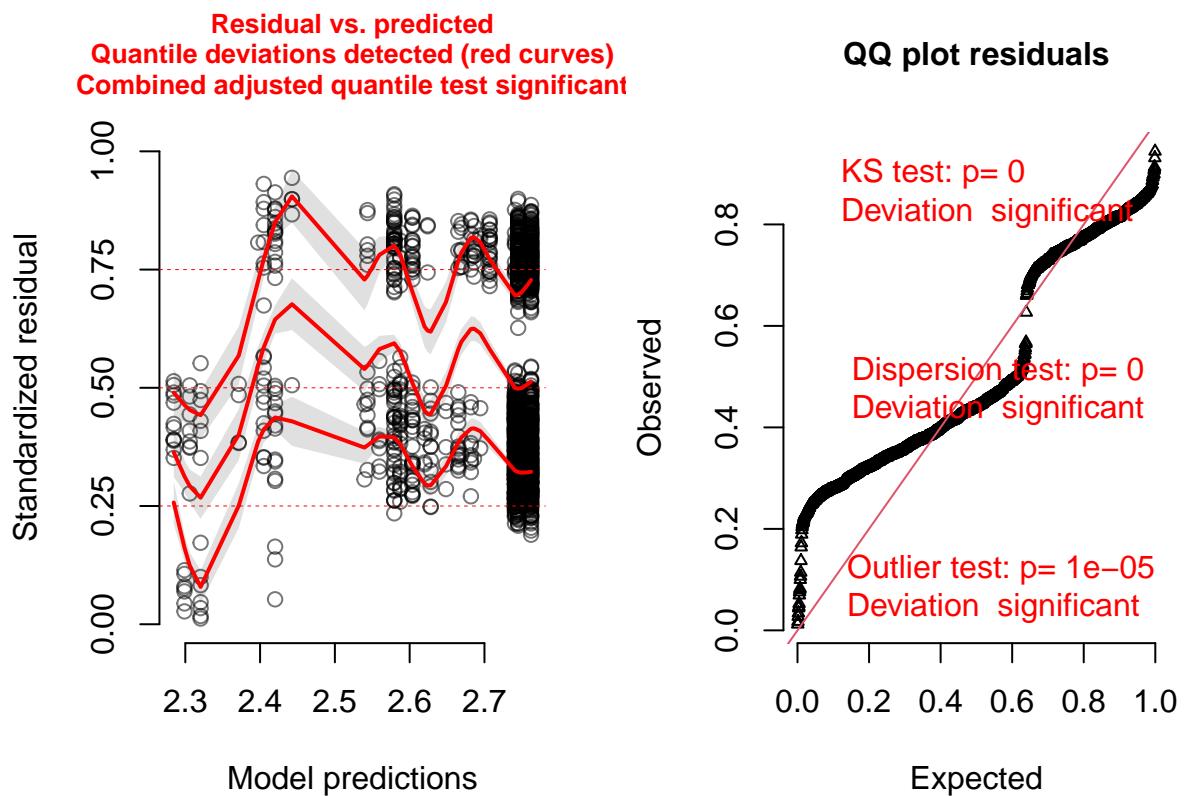
```
glm(spine_num ~ mainland_island + year_collected, data = meri_spine.number, family = poisson)
```

But the diagnostic of this model looks different. How should I evaluate de assumptions of this model?



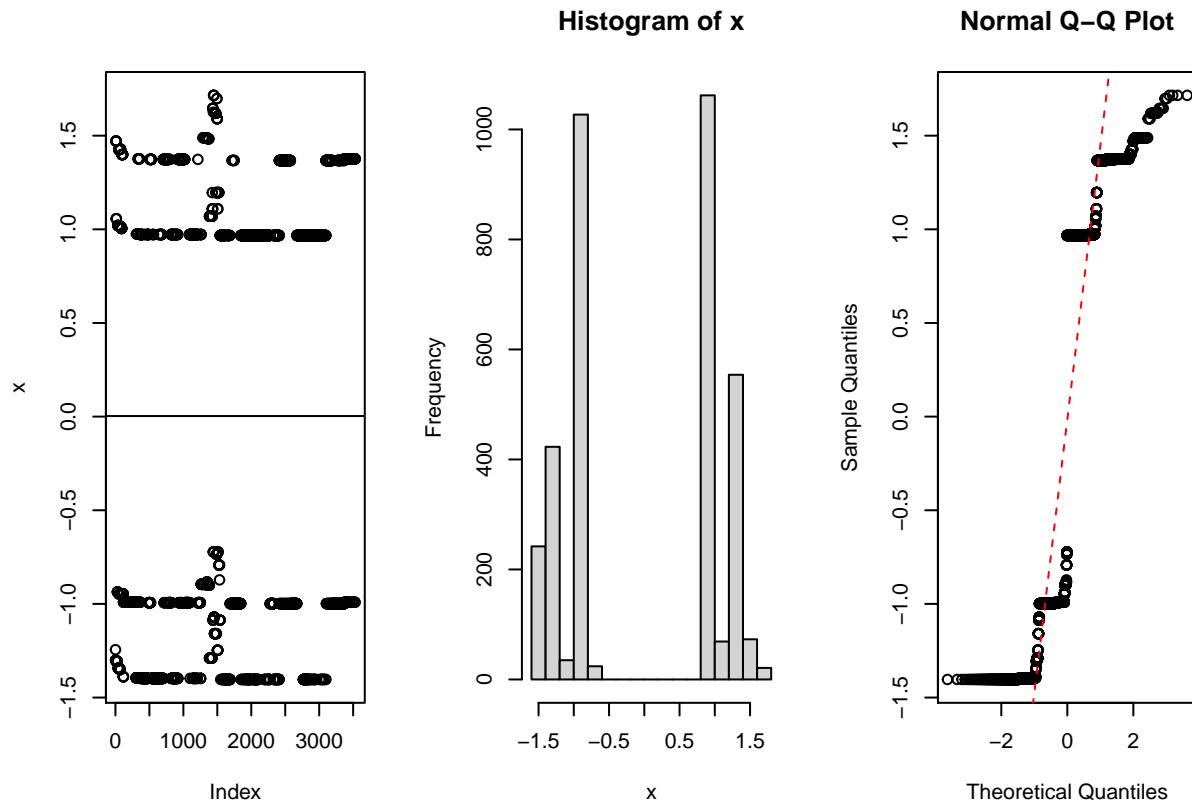
```
## [1] "Kurtosis=-0.622289864714663"
## [1] "Skew=0.211561144749239"
```

```
## DHARMa:plot used testOutliers with type = binomial for computational reasons (nObs > 500). Note that
```

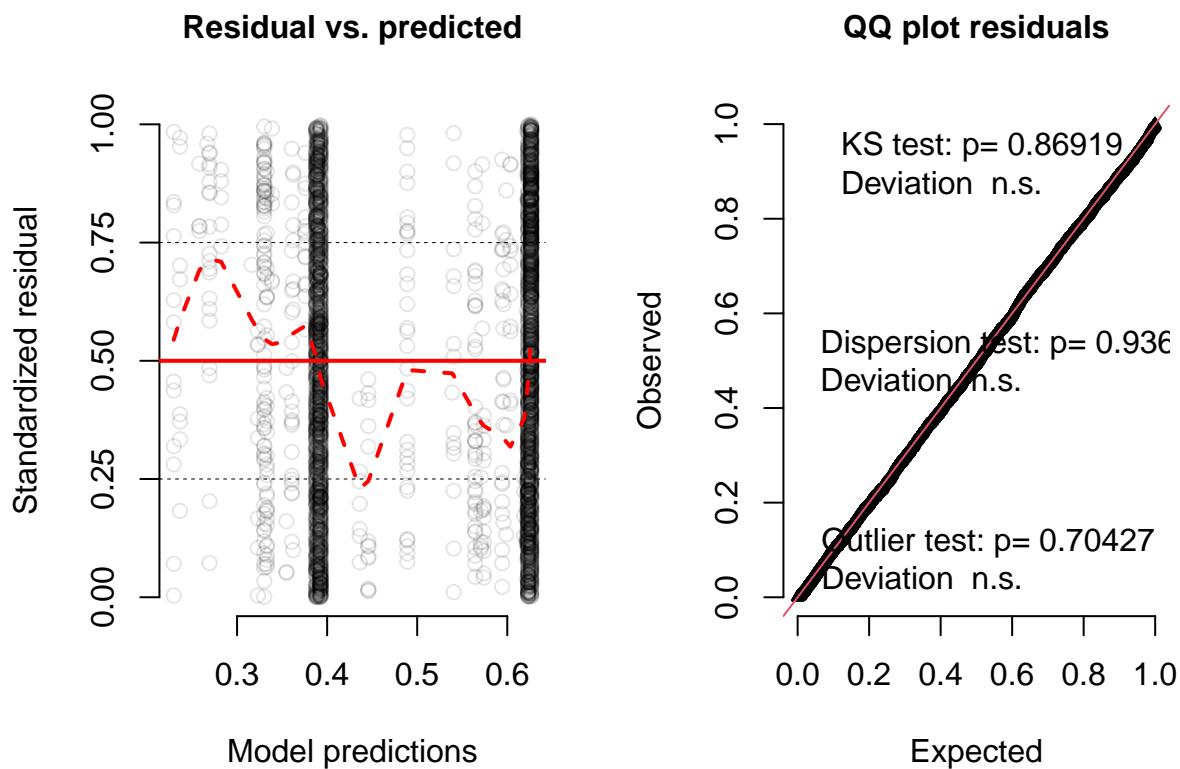


```
## Analysis of Deviance Table (Type II tests)
##
## Response: spine_num
##           LR Chisq Df Pr(>Chisq)
## finch_beak    0.0408  1   0.83990
## year_collected 6.5550  1   0.01046 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Lower -> Not transformed *For lower spines, I think it is a count trait, so I used this model:*
`meri_lower.spines_m1 <- glm(lower_spines ~ mainland_island + year_collected, data = meri_lower.spines, family = "binomial")`



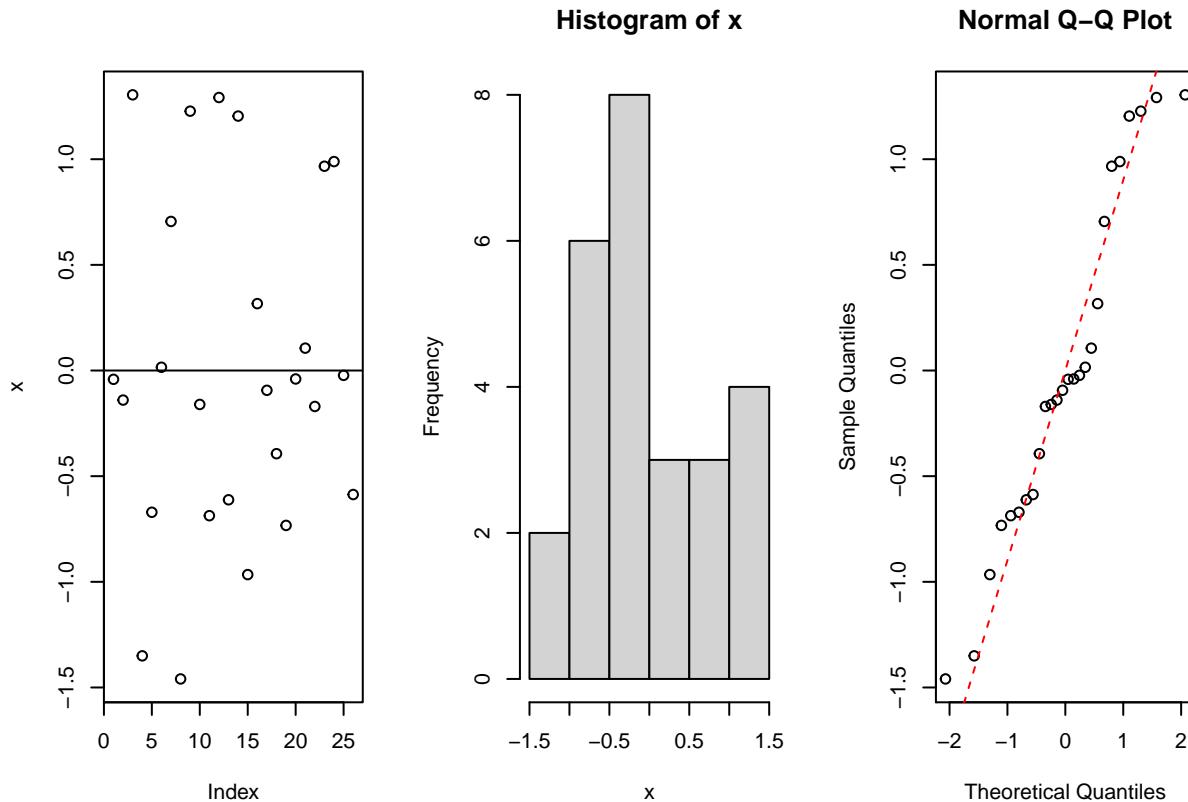
```
## [1] "Kurtosis=-1.86746698858495"
## [1] "Skew=-0.0114759981319253"
```



```
## Analysis of Deviance Table (Type II tests)
##
## Response: lower_spines
##           LR Chisq Df Pr(>Chisq)
## finch_beak    193.586  1 < 2.2e-16 ***
## year_collected 11.904  1 0.0005601 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

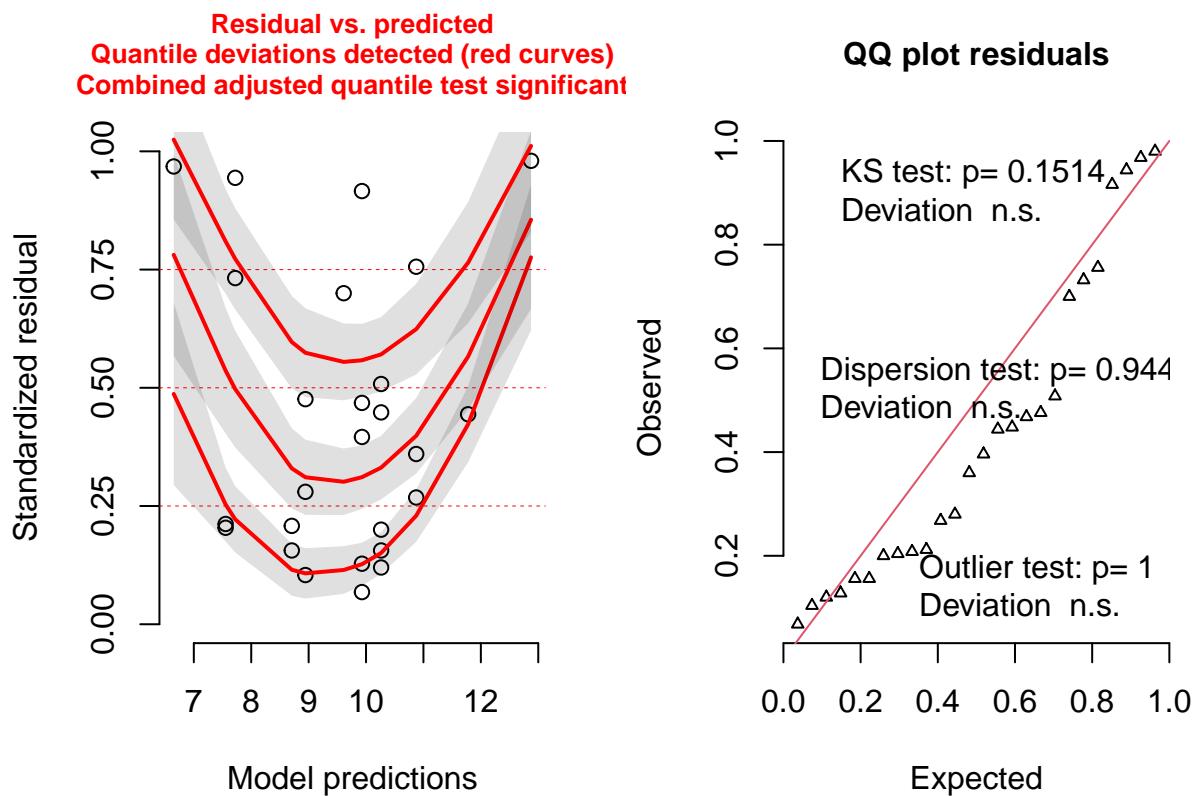
Flowers

Petal length -> Not transformed



```
## [1] "Kurtosis=-0.98535796283949"  
## [1] "Skew=0.165132634915697"
```

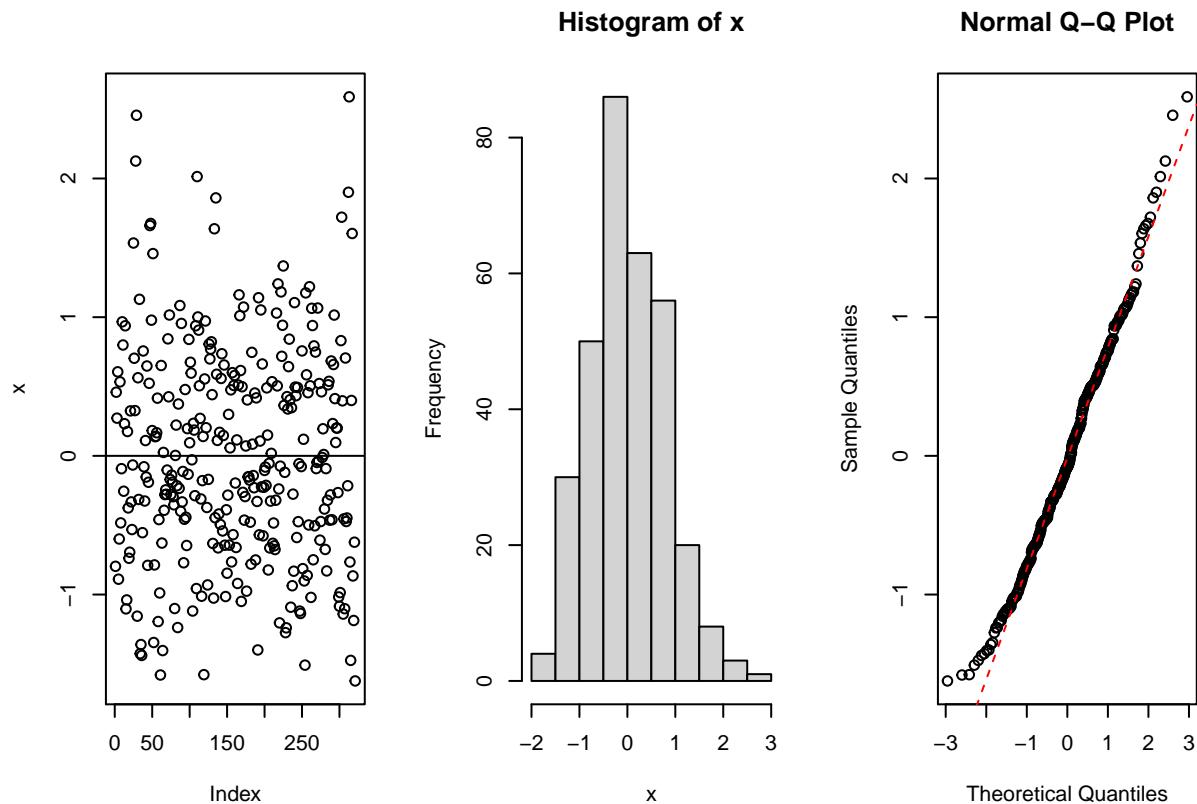
```
## qu = 0.25, log(sigma) = -3.886972 : outer Newton did not converge fully.
```



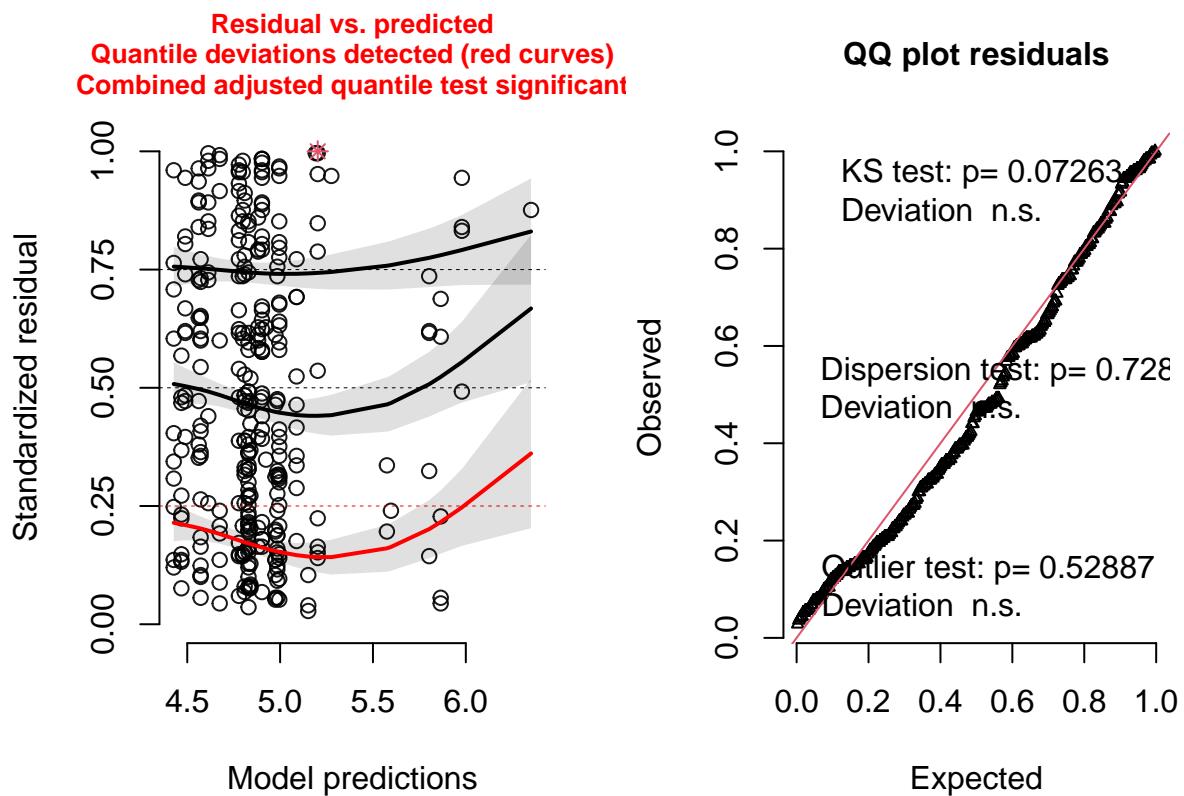
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: petal_length
##              Chisq Df Pr(>Chisq)
## finch_beak    0.5165  1    0.4724
## year_collected 6.2386  1    0.0125 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Leaves

Leaf Length -> Squared Root Transformed

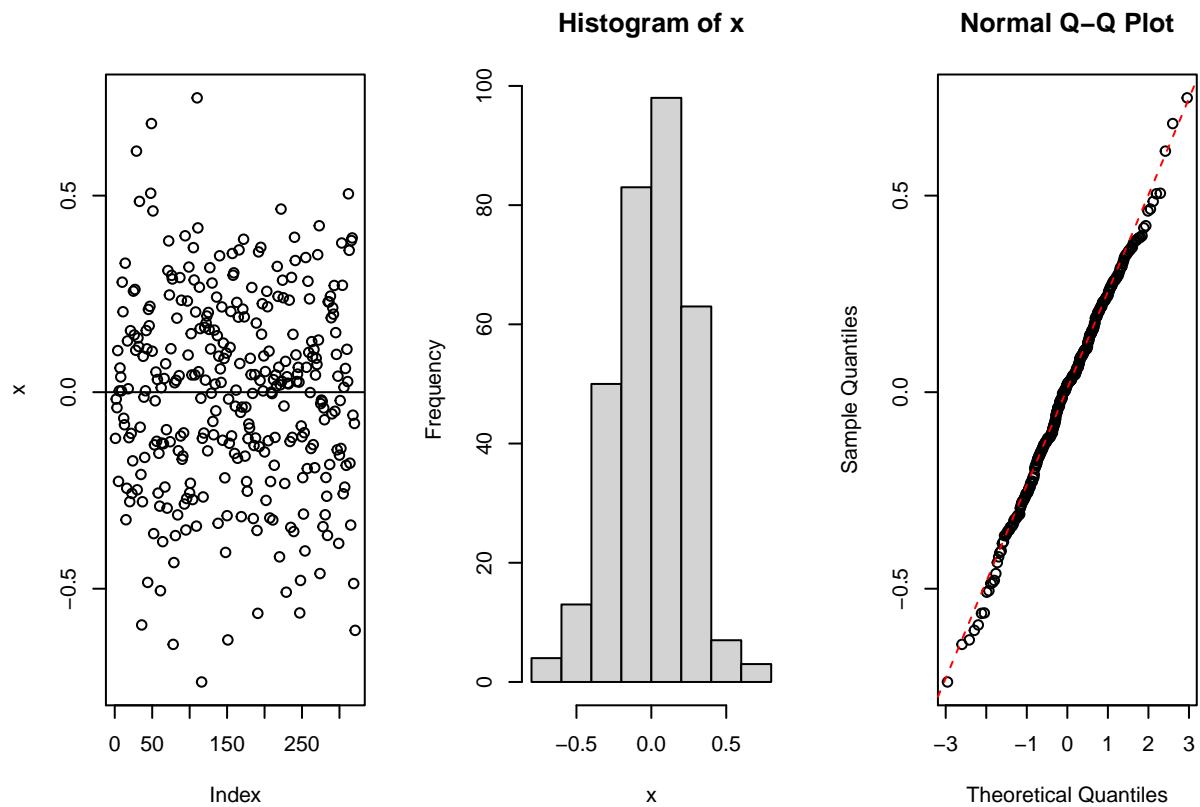


```
## [1] "Kurtosis=-0.0288924193805786"
## [1] "Skew=0.340587284158791"
```

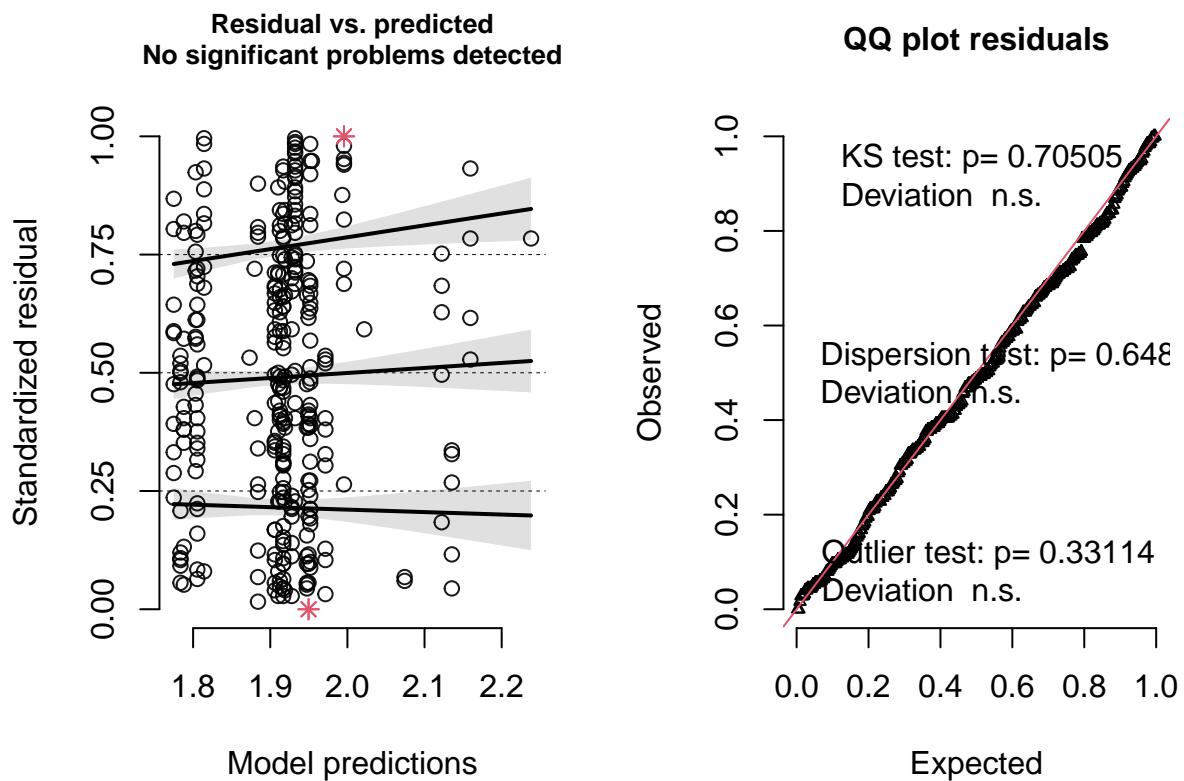


```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: sqrt(leaf_length)
##              Chisq Df Pr(>Chisq)
## finch_beak     1.2475  1  0.2640318
## year_collected 13.6747  1  0.0002174 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Leaflet Length -> Log Transformed



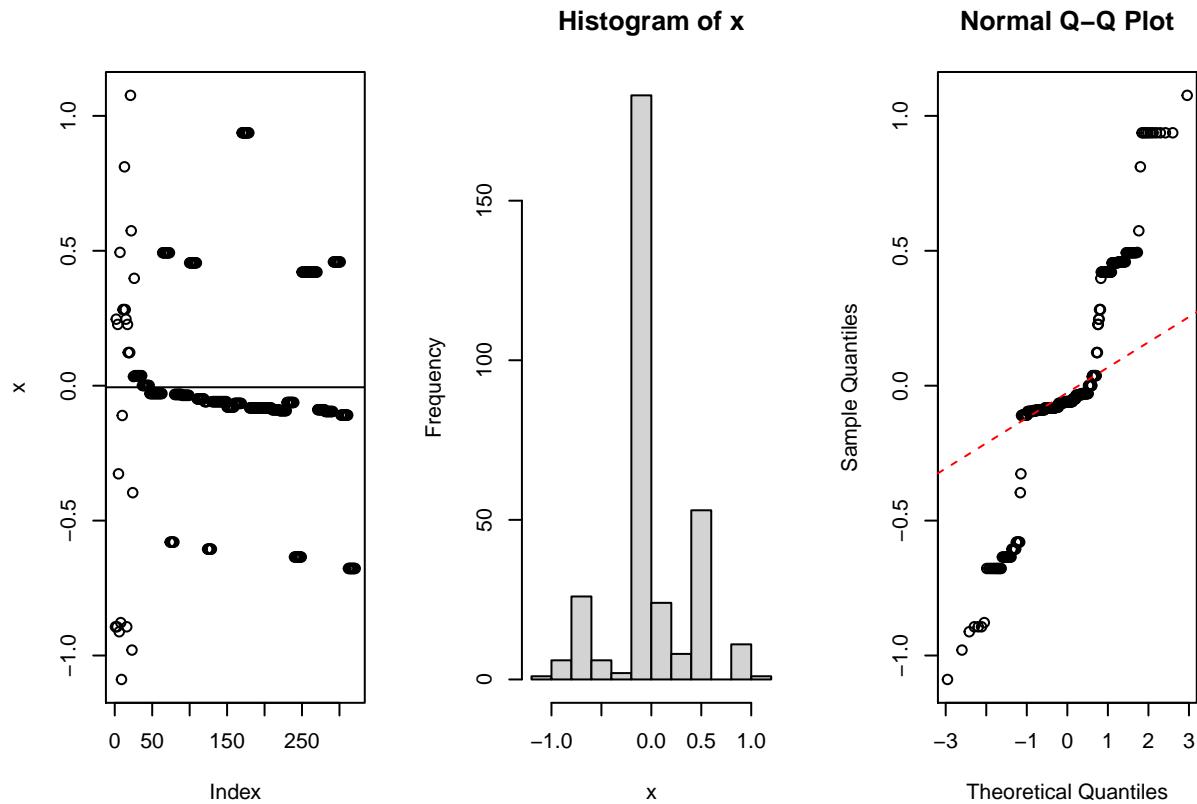
```
## [1] "Kurtosis=-0.0292060182499396"  
## [1] "Skew=-0.135277570705385"
```



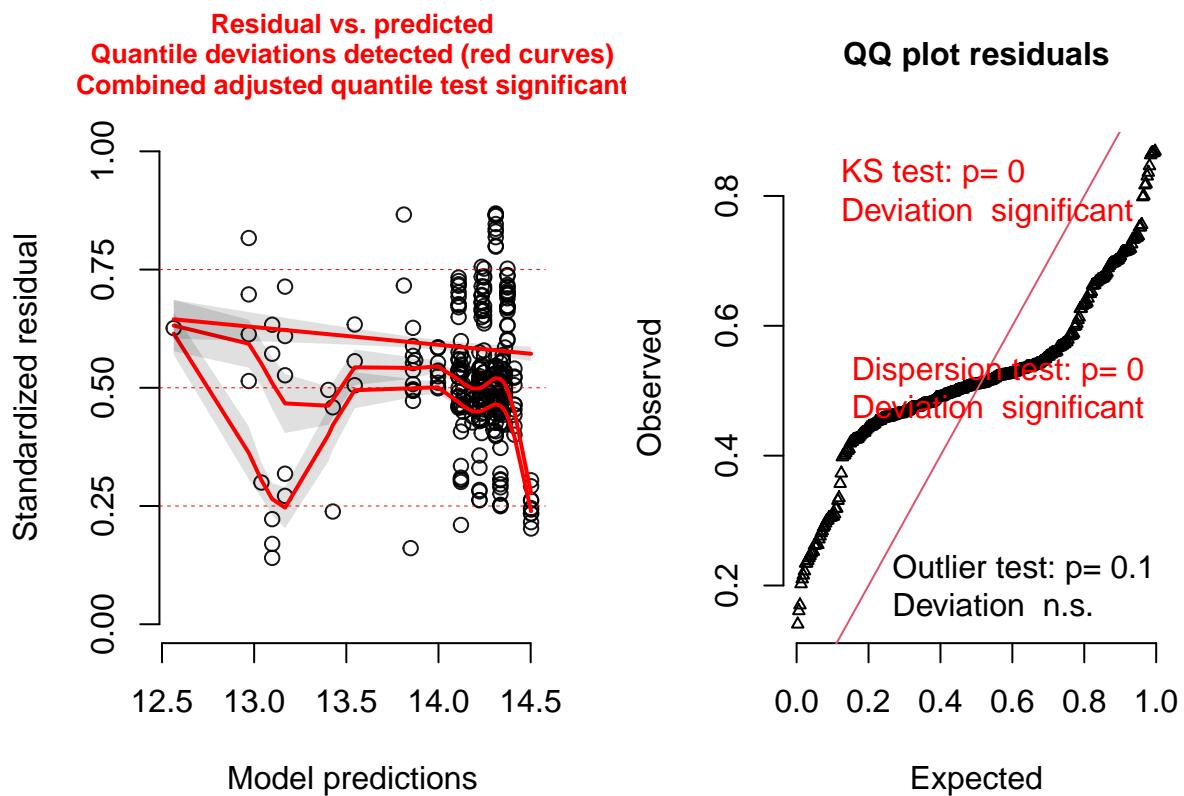
```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: log(leaflet_length)
##              Chisq Df Pr(>Chisq)
## finch_beak    1.6469  1   0.19938
## year_collected 4.8053  1   0.02837 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Leaflet number -> Not transformed *For leaflet number, I think it is a count trait, so I used this model:*

`glm(number_of_leaflets ~ mainland_island + year_collected, family = poisson, data=leaf_length)`



```
## [1] "Kurtosis=1.0223498497344"
## [1] "Skew=0.114640438164658"
```



```
## Analysis of Deviance Table (Type II tests)
##
## Response: number_of_leaflets
##           LR Chisq Df Pr(>Chisq)
## finch_beak    0.01639  1    0.8981
## year_collected 2.17625  1    0.1402
```

Model 3 LS means

Mericarps:

Length

```
## finch_beak emmean     SE  df asymp.LCL asymp.UCL
## 0          5.98 0.146 Inf      5.69      6.27
## 1          6.41 0.131 Inf      6.15      6.67
##
## Degrees-of-freedom method: asymptotic
## Confidence level used: 0.95
```

Width

```
## finch_beak response     SE  df asymp.LCL asymp.UCL
## 0          3.10 0.0529 Inf      2.99      3.20
## 1          3.15 0.0487 Inf      3.06      3.25
##
## Degrees-of-freedom method: asymptotic
## Confidence level used: 0.95
## Intervals are back-transformed from the sqrt scale
```

Depth

```
## finch_beak emmean     SE  df asymp.LCL asymp.UCL
## 0          4.82 0.0744 Inf      4.67      4.96
## 1          4.77 0.0663 Inf      4.64      4.90
##
## Degrees-of-freedom method: asymptotic
## Confidence level used: 0.95
```

Spine Length

```
## finch_beak emmean     SE  df asymp.LCL asymp.UCL
## 0          4.19 0.216 Inf      3.76      4.61
## 1          4.28 0.194 Inf      3.90      4.66
##
## Degrees-of-freedom method: asymptotic
## Confidence level used: 0.95
```

Spine Tip Distance

```
## finch_beak emmean     SE  df lower.CL upper.CL
## 0          7.34 0.439 122      6.47      8.2
## 1          7.93 0.391 126      7.15      8.7
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
```

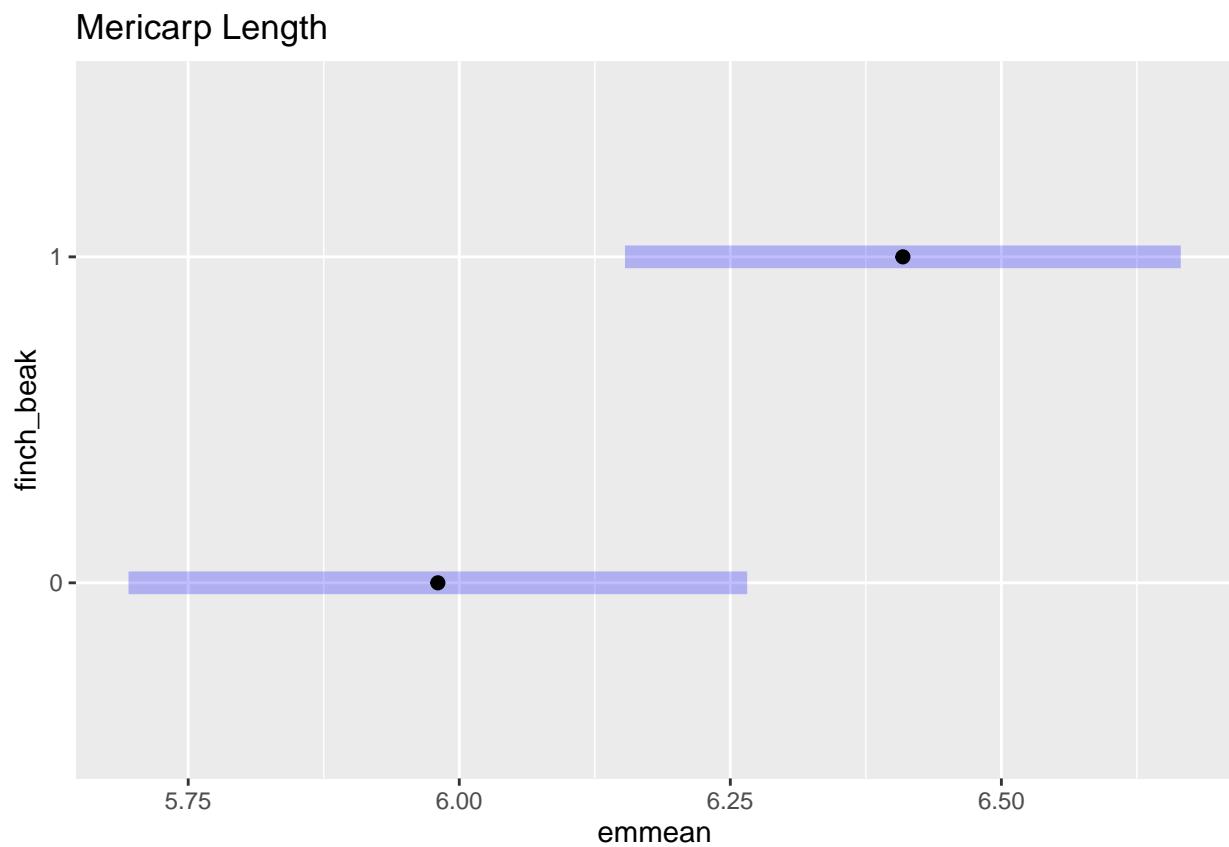
Spine Number

```
## finch_beak emmean     SE  df asymp.LCL asymp.UCL
## 0          0.990 0.0215 Inf    0.948      1.03
## 1          0.996 0.0224 Inf    0.952      1.04
##
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
```

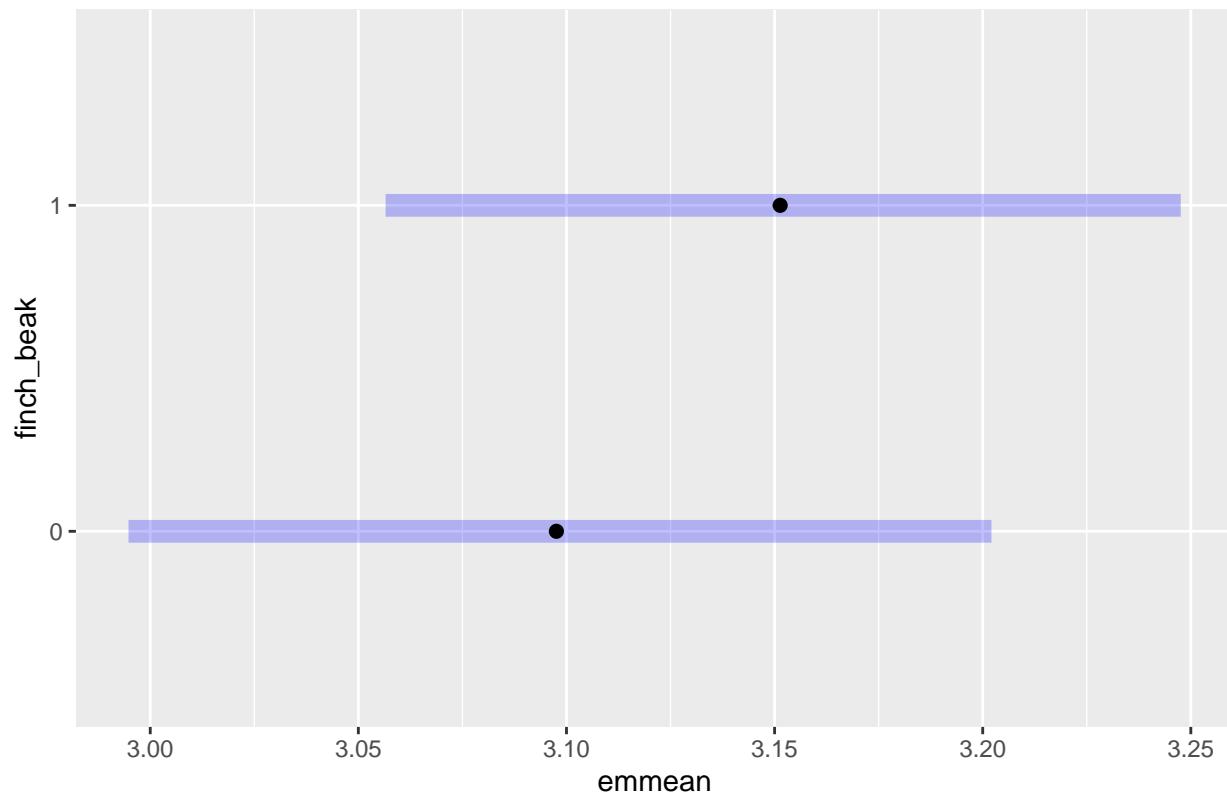
Lower Spines

```
## finch_beak prob     SE  df asymp.LCL asymp.UCL
## 0          0.382 0.0118 Inf    0.360      0.406
## 1          0.616 0.0114 Inf    0.594      0.639
##
## Confidence level used: 0.95
## Intervals are back-transformed from the logit scale
```

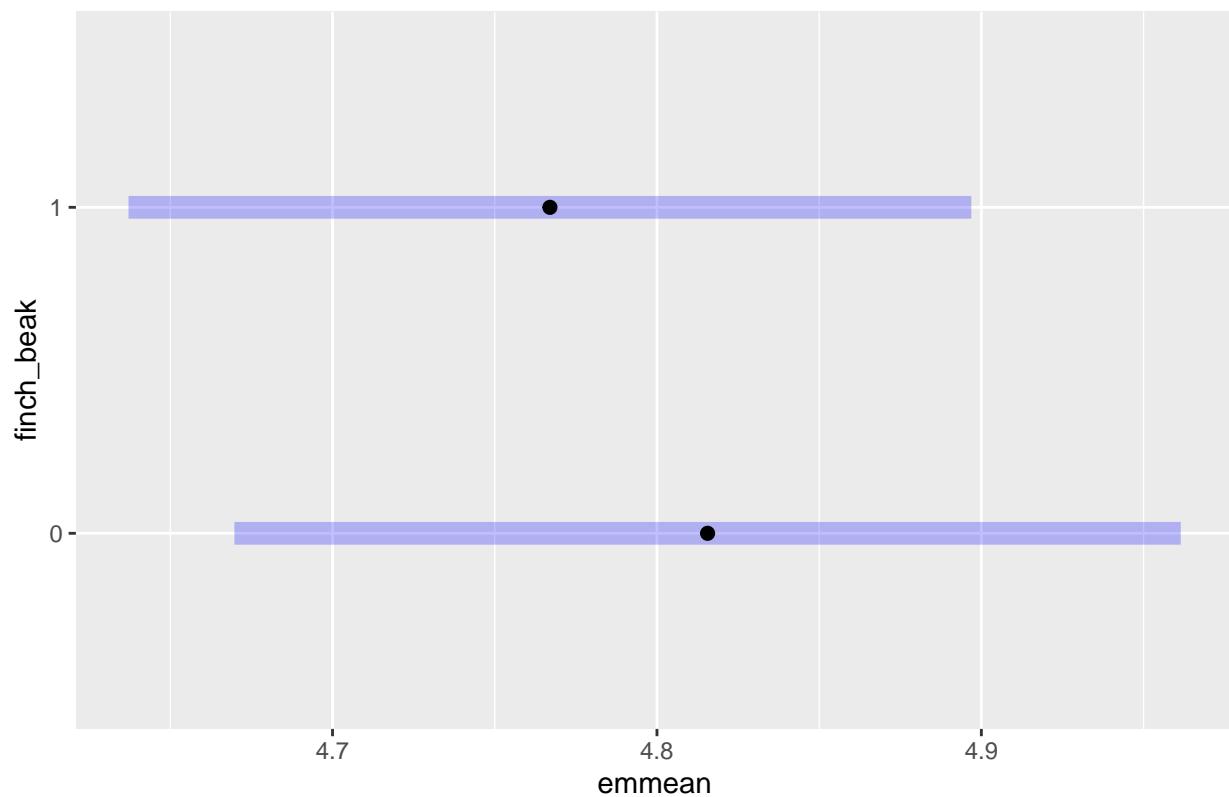
Mericarp LS means plots



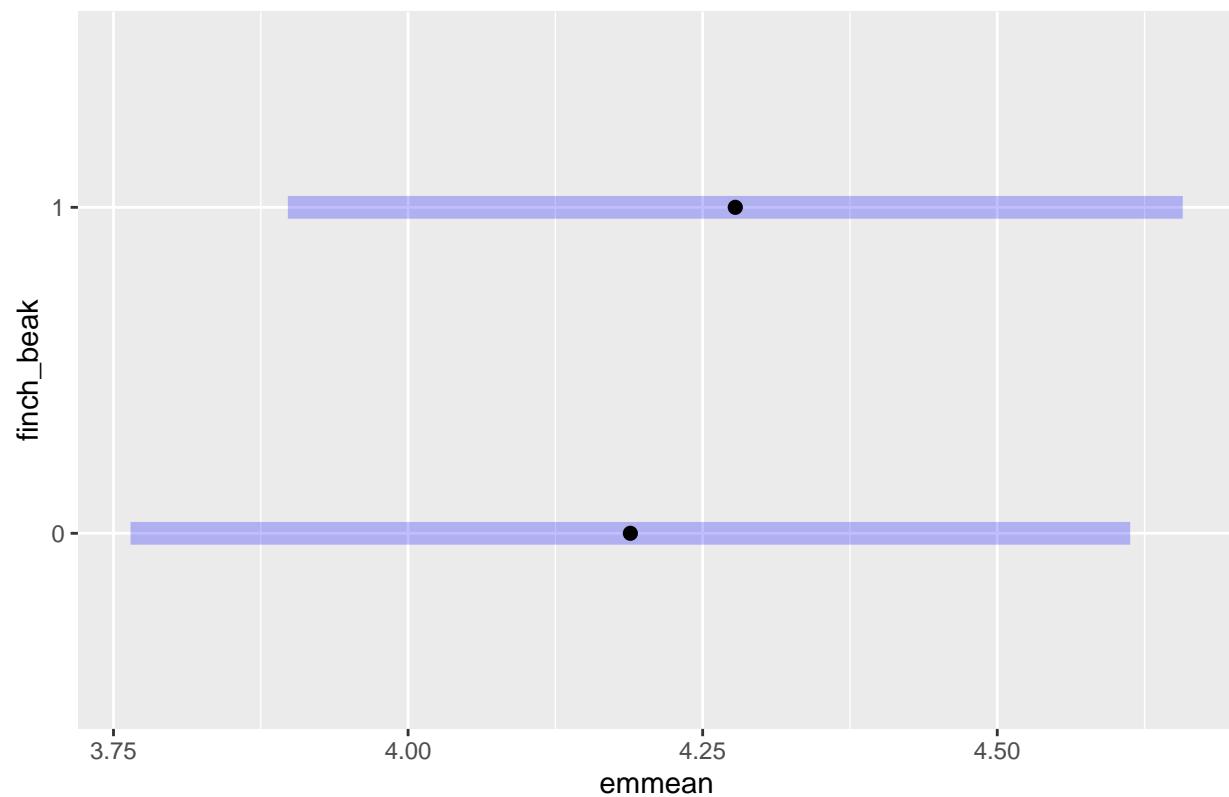
Mericarp Width



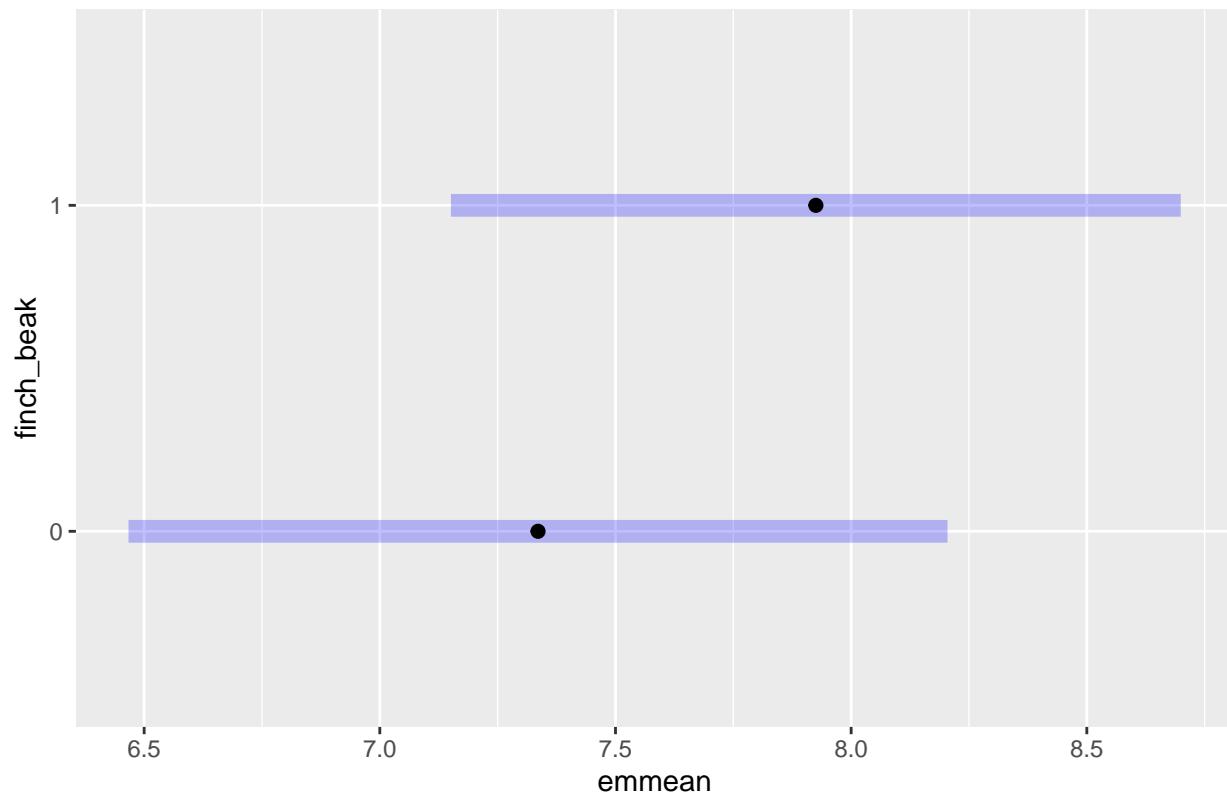
Mericarp Depth



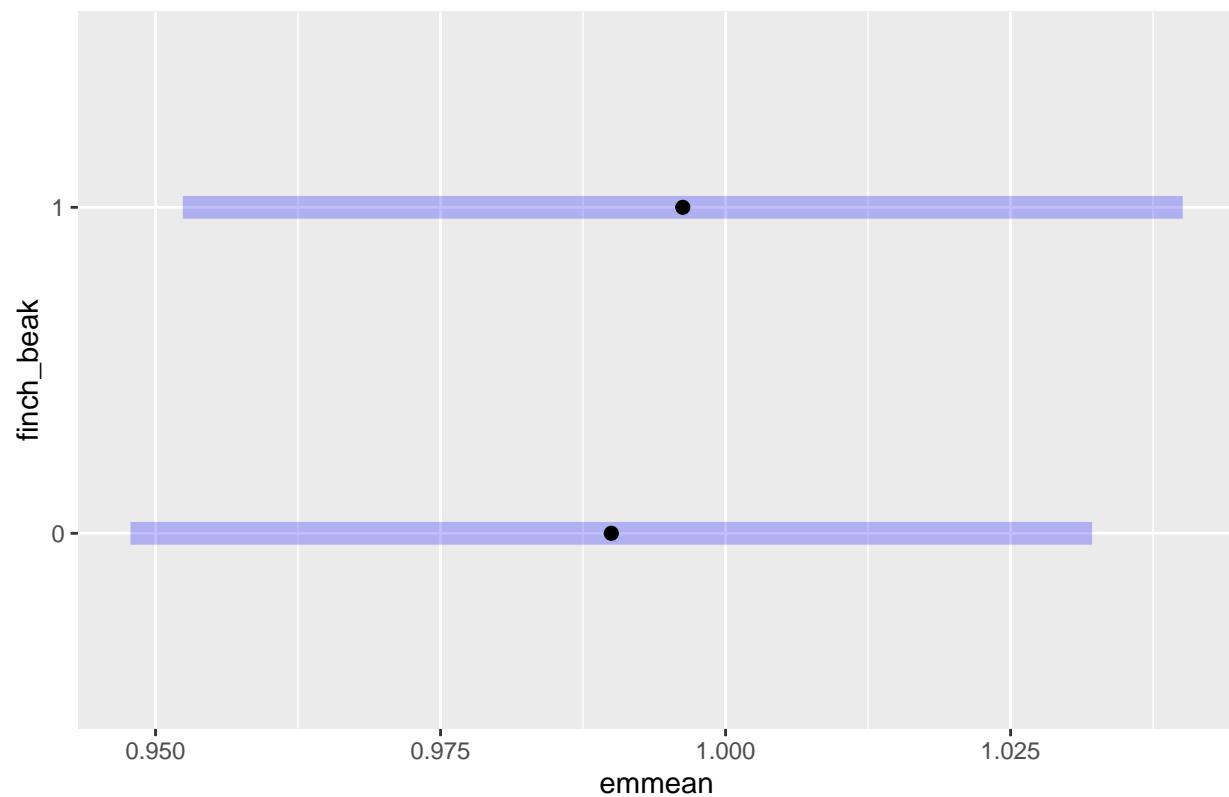
Mericarp Spine Length



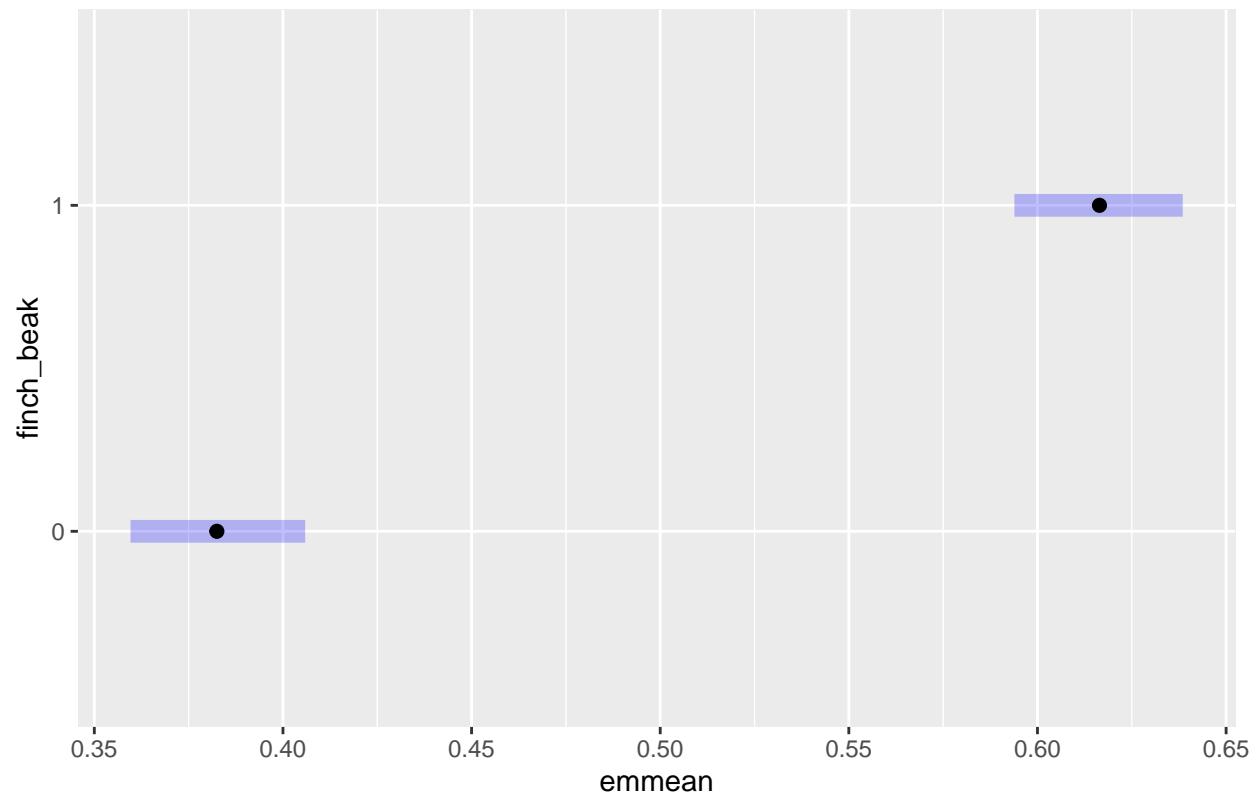
Mericarp Spine Tip Distance



Mericarp Spine number



Mericarp Lower Spines



Within the Galapagos Islands *Tribulus* mericarps have differences associated to finch communities. Mericarps that are **larger** in length (more seeds) and have **lower spines** are associated with large finch communities.

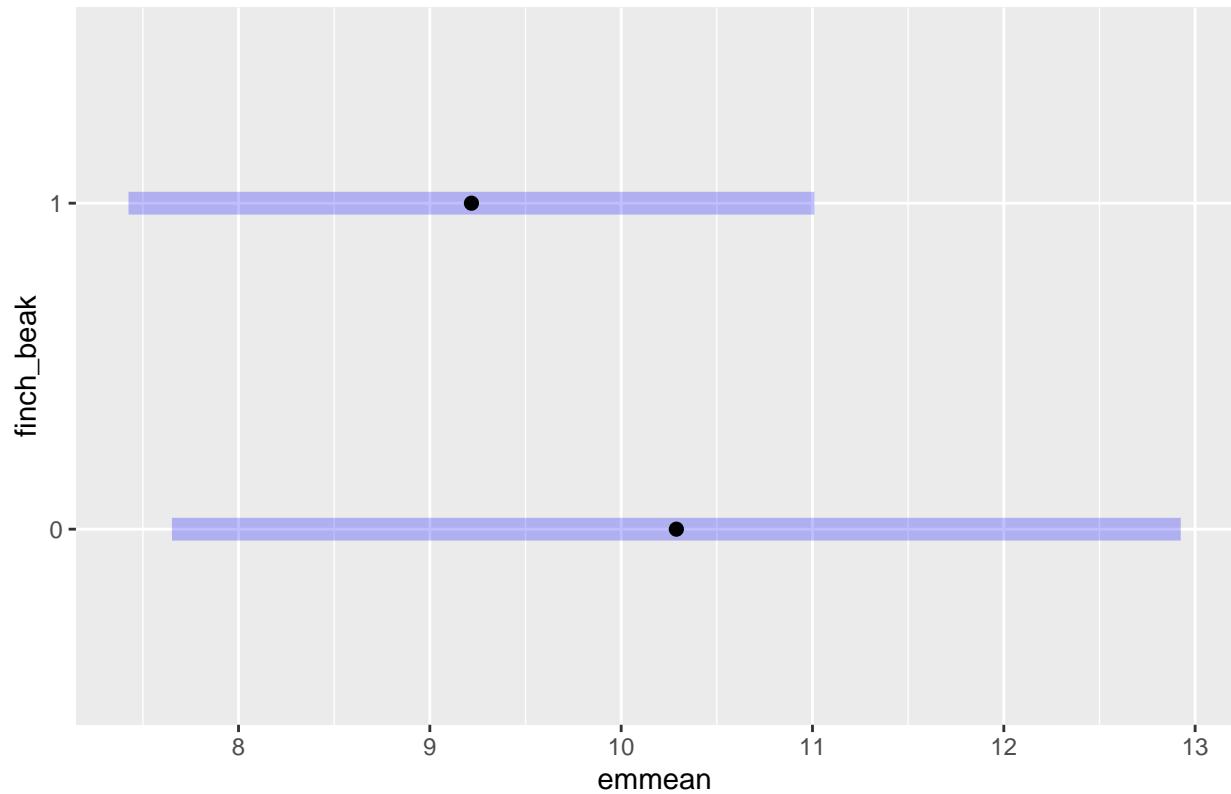
Width, Depth, Spine Length, Tip Distance and Spine Number do not show a large difference between communities.

Flowers

Petal Length

```
##  finch_beak emmean   SE   df lower.CL upper.CL
##  0          10.29 1.27 20.4     7.65    12.9
##  1          9.22 0.86 20.3     7.43    11.0
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
```

Petal Length



Leaves

Leaf Length

```
##  finch_beak response   SE   df lower.CL upper.CL
##  0          21.8 2.00 47.4     18.0    26.0
##  1          24.4 1.29 40.5     21.8    27.1
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Intervals are back-transformed from the sqrt scale
```

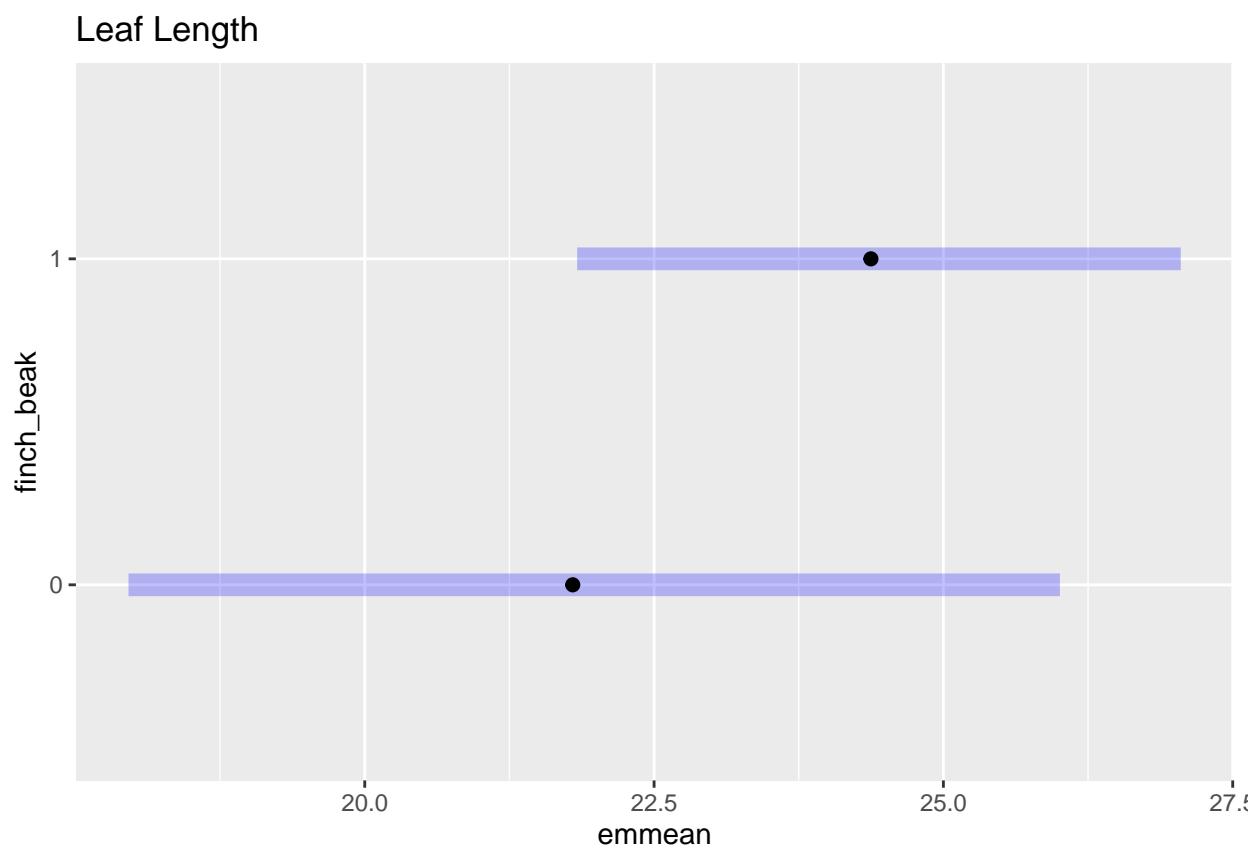
Leaflet Length

```
## finch_beak response      SE   df lower.CL upper.CL
## 0                  6.21 0.489 48.0      5.3     7.27
## 1                  6.96 0.339 41.4      6.3     7.67
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
```

Leaflet Number

```
## finch_beak emmean      SE   df asymp.LCL asymp.UCL
## 0             2.65 0.0302 Inf    2.59     2.71
## 1             2.65 0.0171 Inf    2.62     2.69
##
## Results are given on the log (not the response) scale.
## Confidence level used: 0.95
```

Leaves LS means plots



Leaflet Length

