

Pangasionodon hypophthalmus Validation Fw Opsu

Simon De Pooter

décembre 15, 2021,08:25

Contents

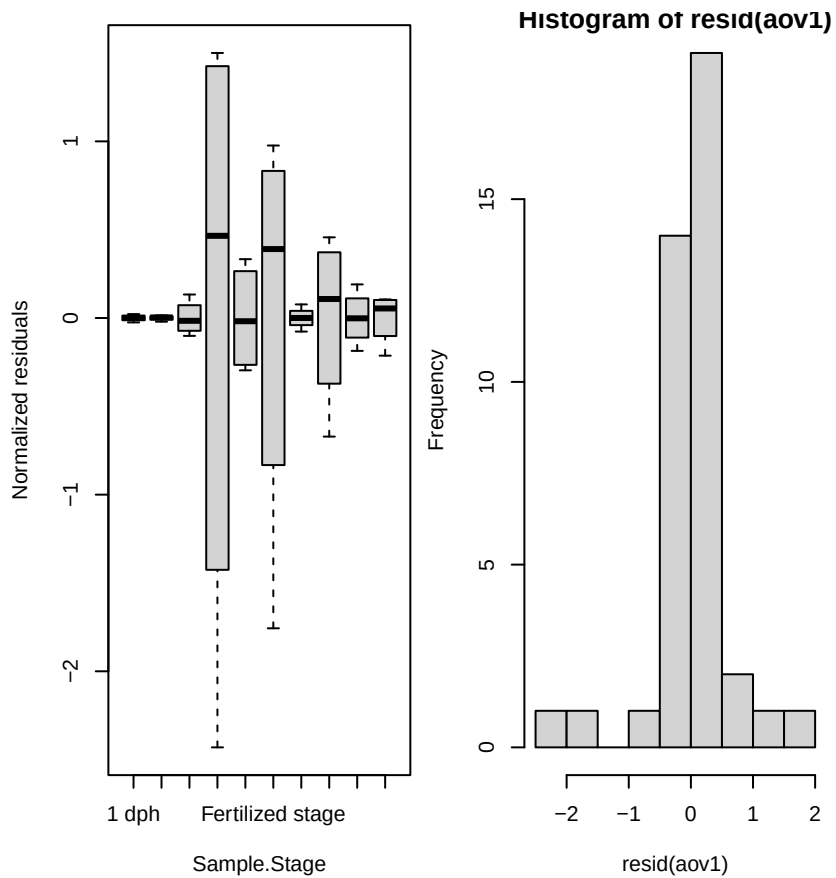
```
##
##  Shapiro-Wilk normality test
##
## data:  Gene$ExpNormal
## W = 0.66709, p-value = 2.924e-08

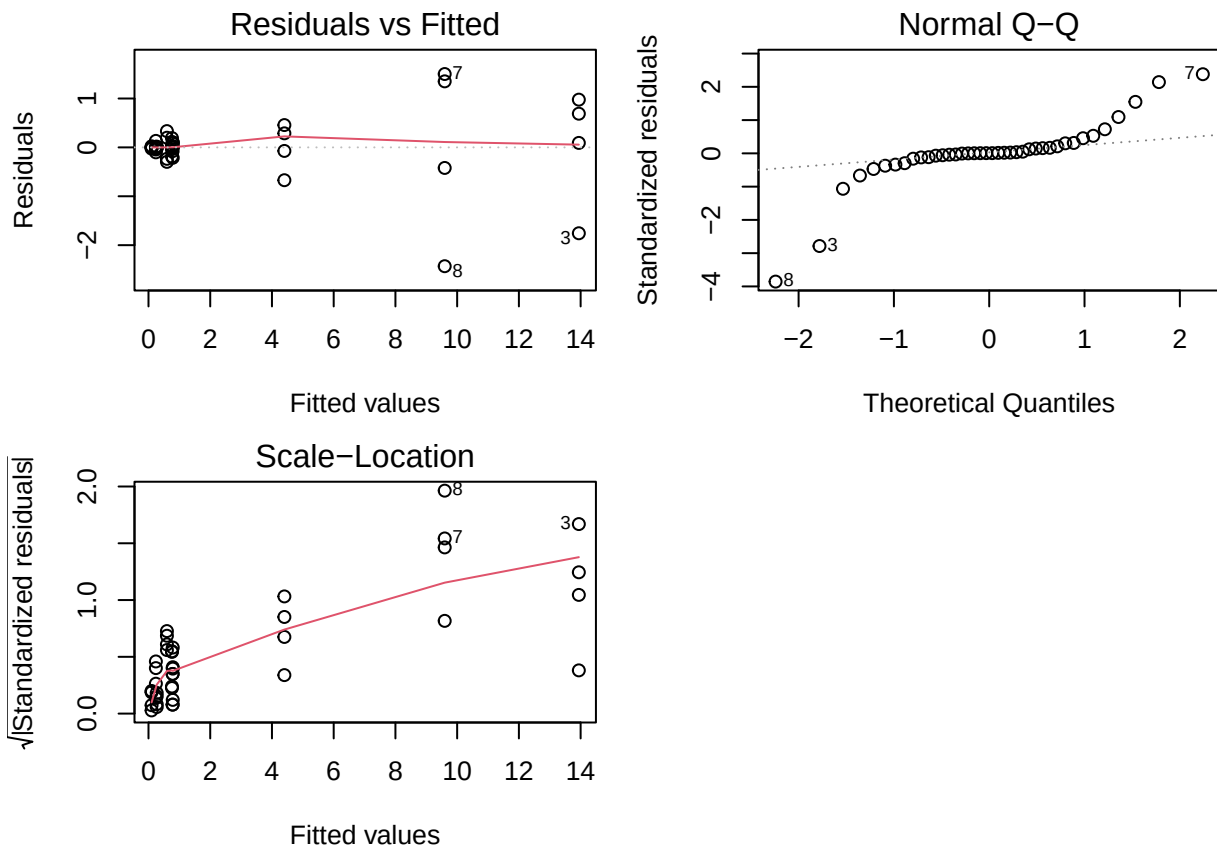
##
##  Bartlett test of homogeneity of variances
##
## data:  Gene$ExpNormal by Gene$Sample.Stage
## Bartlett's K-squared = 79.373, df = 9, p-value = 2.153e-13

## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value    Pr(>F)
## group  9   4.566 0.000755 ***
##      30
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

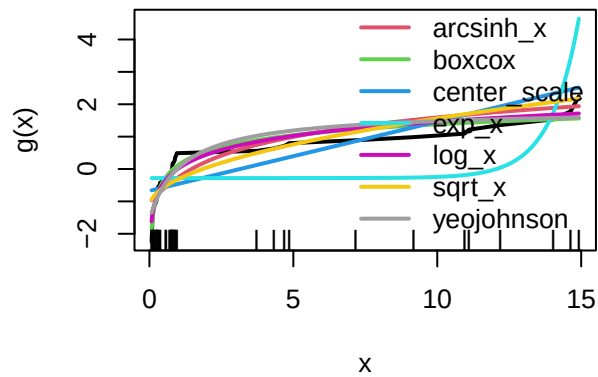
## $stats
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## [1,] -0.025042364 -0.020964833 -0.10123995 -2.430719 -0.29625947 -1.7566784
## [2,] -0.012767087 -0.009440309 -0.07245665 -1.425621 -0.26524067 -0.8326560
## [3,]  0.001467412  0.003193780 -0.01586660  0.465155 -0.01836922  0.3901568
## [4,]  0.012767087  0.009440309  0.07245665  1.425621  0.26524067  0.8326560
## [5,]  0.022107540  0.014577274  0.13297316  1.500409  0.33299791  0.9763648
##           [,7]      [,8]      [,9]      [,10]
## [1,] -0.0769691485 -0.6714448 -0.186239286 -0.21327621
## [2,] -0.0404321905 -0.3719507 -0.111048369 -0.10203973
## [3,]  0.0000425585  0.1074323 -0.001946847  0.05403842
## [4,]  0.0404321905  0.3719507  0.111048370  0.10203973
## [5,]  0.0768840315  0.4565803  0.190132979  0.10519936
##
## $n
## [1] 4 4 4 4 4 4 4 4 4 4
##
## $conf
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## [1,] -0.01870458 -0.01172191 -0.13034812 -1.787325 -0.4374495 -0.9254397
## [2,]  0.02163941  0.01810947  0.09861491  2.717635  0.4007110  1.7057533
##           [,7]      [,8]      [,9]      [,10]
```

```
## [1,] -0.06384030 -0.4802498 -0.1774033 -0.1071843
## [2,]  0.06392542  0.6951144  0.1735096  0.2152612
##
## $out
## numeric(0)
##
## $group
## numeric(0)
##
## $names
## [1] "1 dph"          "3 dph"          "6 dph"
## [4] "Early blastula" "Early Gastrula"  "Fertilized stage"
## [7] "Hatching"      "Late blastula"   "Late Gastrula"
## [10] "Somite development"
```





```
## Best Normalizing transformation with 40 Observations
## Estimated Normality Statistics (Pearson P / df, lower => more normal):
## - arcsinh(x): 3.12
## - Box-Cox: 2.04
## - Center+scale: 3.8
## - Exp(x): 5.08
## - Log_b(x+a): 2.12
## - orderNorm (ORQ): 1.76
## - sqrt(x + a): 3.12
## - Yeo-Johnson: 2.48
## Estimation method: Out-of-sample via CV with 10 folds and 5 repeats
##
## Based off these, bestNormalize chose:
## orderNorm Transformation with 40 nonmissing obs and no ties
## - Original quantiles:
##   0%   25%   50%   75%  100%
## 0.075 0.279 0.789 4.420 14.919
## [1] TRUE
```



```
##
## Shapiro-Wilk normality test
##
## data: Gene$ExpNormal
## W = 0.85578, p-value = 0.0001246

##
## Bartlett test of homogeneity of variances
##
## data: Gene$ExpNormal by Gene$Sample.Stage
## Bartlett's K-squared = 47.765, df = 9, p-value = 2.825e-07

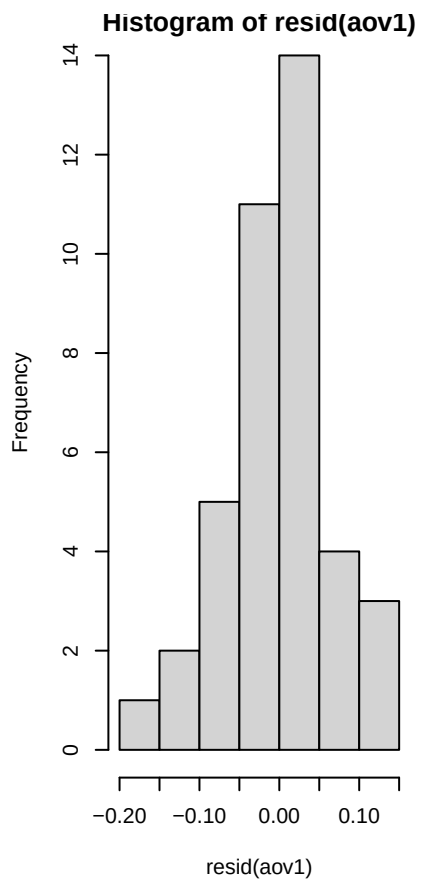
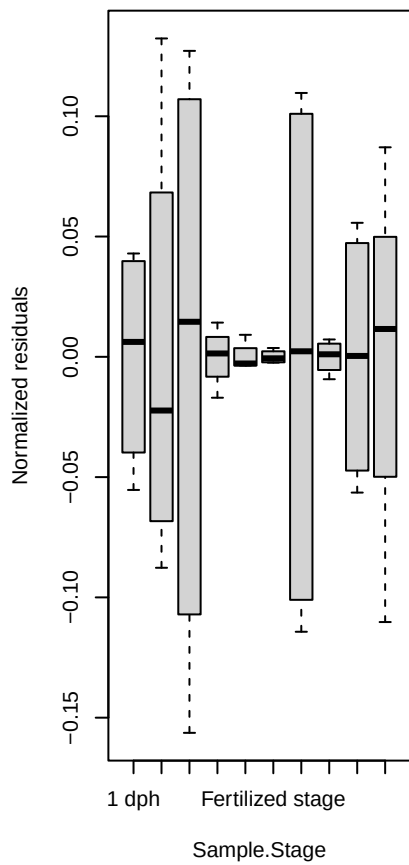
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value    Pr(>F)
## group  9  6.2484 6.082e-05 ***
##      30
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

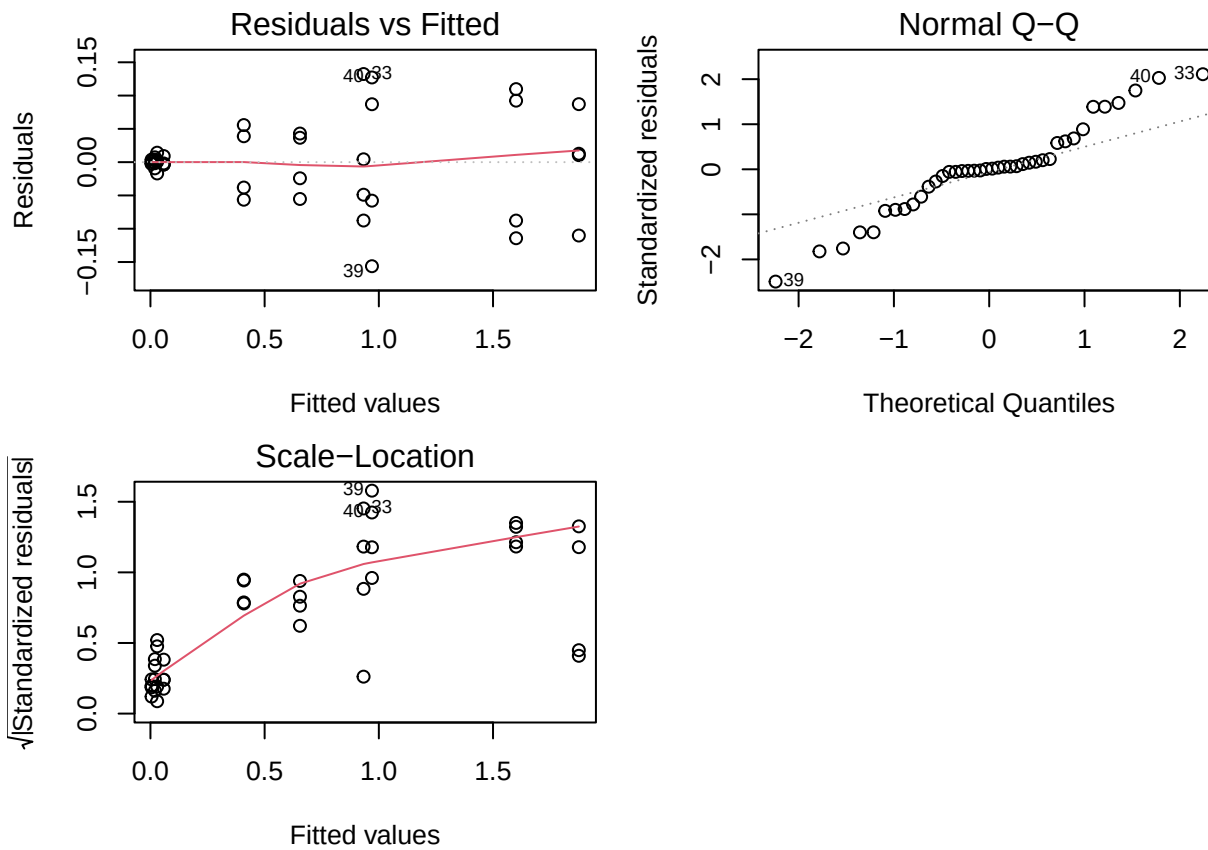
## $stats
##           [,1]      [,2]      [,3]      [,4]      [,5]
## [1,] -0.055332870 -0.08769460 -0.15630941 -0.017009821 -0.003605589
## [2,] -0.039781690 -0.06831688 -0.10708421 -0.008265499 -0.003600255
## [3,]  0.006190758 -0.02232616  0.01456494  0.001395318 -0.002770524
## [4,]  0.039781690  0.06831688  0.10708421  0.008265499  0.003600255
## [5,]  0.042951355  0.13234692  0.12717952  0.014219186  0.009146638
##           [,6]      [,7]      [,8]      [,9]     [,10]
## [1,] -0.0024198658 -0.11428558 -0.009314284 -0.0564333155 -0.11024876
```

```

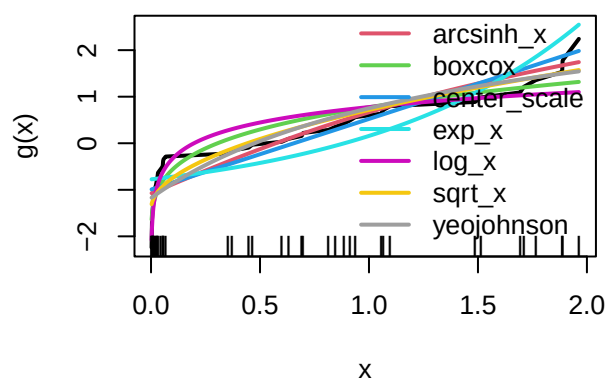
## [2,] -0.0022886268 -0.10102266 -0.005478144 -0.0472895580 -0.04987313
## [3,] -0.0006257432  0.00229783  0.001050561  0.0003647175  0.01157551
## [4,]  0.0022886268  0.10102266  0.005478144  0.0472895580  0.04987313
## [5,]  0.0036713522  0.10968992  0.007213161  0.0557038805  0.08709774
##
## $n
## [1] 4 4 4 4 4 4 4 4 4 4
##
## $conf
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## [1,] -0.05666431 -0.13026683 -0.1546281 -0.01166417 -0.008458927 -0.004241774
## [2,]  0.06904583  0.08561451  0.1837580  0.01445481  0.002917878  0.002990287
##           [,7]      [,8]      [,9]     [,10]
## [1,] -0.1573180 -0.007604906 -0.07435278 -0.06722403
## [2,]  0.1619136  0.009706029  0.07508222  0.09037505
##
## $out
## numeric(0)
##
## $group
## numeric(0)
##
## $names
## [1] "1 dph"          "3 dph"          "6 dph"
## [4] "Early blastula"  "Early Gastrula"  "Fertilized stage"
## [7] "Hatching"       "Late blastula"   "Late Gastrula"
## [10] "Somite development"

```





```
## Best Normalizing transformation with 40 Observations
## Estimated Normality Statistics (Pearson P / df, lower => more normal):
## - arcsinh(x): 2.32
## - Box-Cox: 2.12
## - Center+scale: 2.32
## - Exp(x): 3
## - Log_b(x+a): 2.2
## - orderNorm (ORQ): 1.4
## - sqrt(x + a): 2.24
## - Yeo-Johnson: 2.4
## Estimation method: Out-of-sample via CV with 10 folds and 5 repeats
##
## Based off these, bestNormalize chose:
## orderNorm Transformation with 40 nonmissing obs and no ties
## - Original quantiles:
##   0%   25%  50%  75% 100%
## 0.003 0.031 0.532 1.059 1.963
## [1] TRUE
```



```
##
## Shapiro-Wilk normality test
##
## data: Gene$ExpNormal
## W = 0.85004, p-value = 9.018e-05
##
## Bartlett test of homogeneity of variances
##
## data: Gene$ExpNormal by Gene$Sample.Stage
## Bartlett's K-squared = 74.008, df = 9, p-value = 2.48e-12
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 9  2.9688 0.01197 *
##      30
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

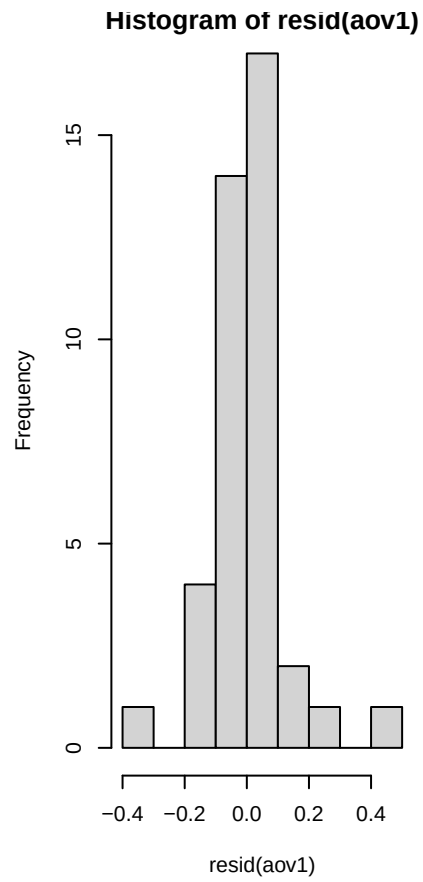
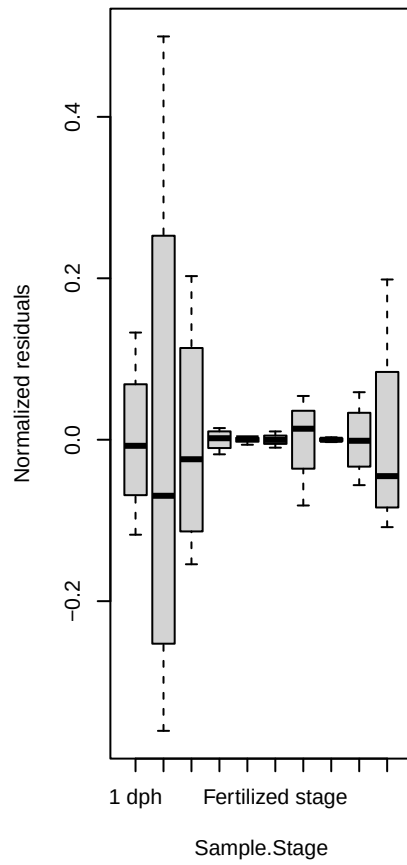
## $stats
##           [,1]      [,2]      [,3]      [,4]      [,5]
## [1,] -0.117694914 -0.36066256 -0.15429534 -0.018072230 -0.006220237
## [2,] -0.068703881 -0.25270931 -0.11362489 -0.010336529 -0.002458991
## [3,] -0.007539826 -0.06946881 -0.02419928  0.001823297  0.001746227
## [4,]  0.068703881  0.25270931  0.11362489  0.010336529  0.002458991
## [5,]  0.132774567  0.49960018  0.20269390  0.014425636  0.002727783
##           [,6]      [,7]      [,8]      [,9]     [,10]
## [1,] -0.009853258 -0.08147642 -2.912774e-03 -0.056269566 -0.10831164
```

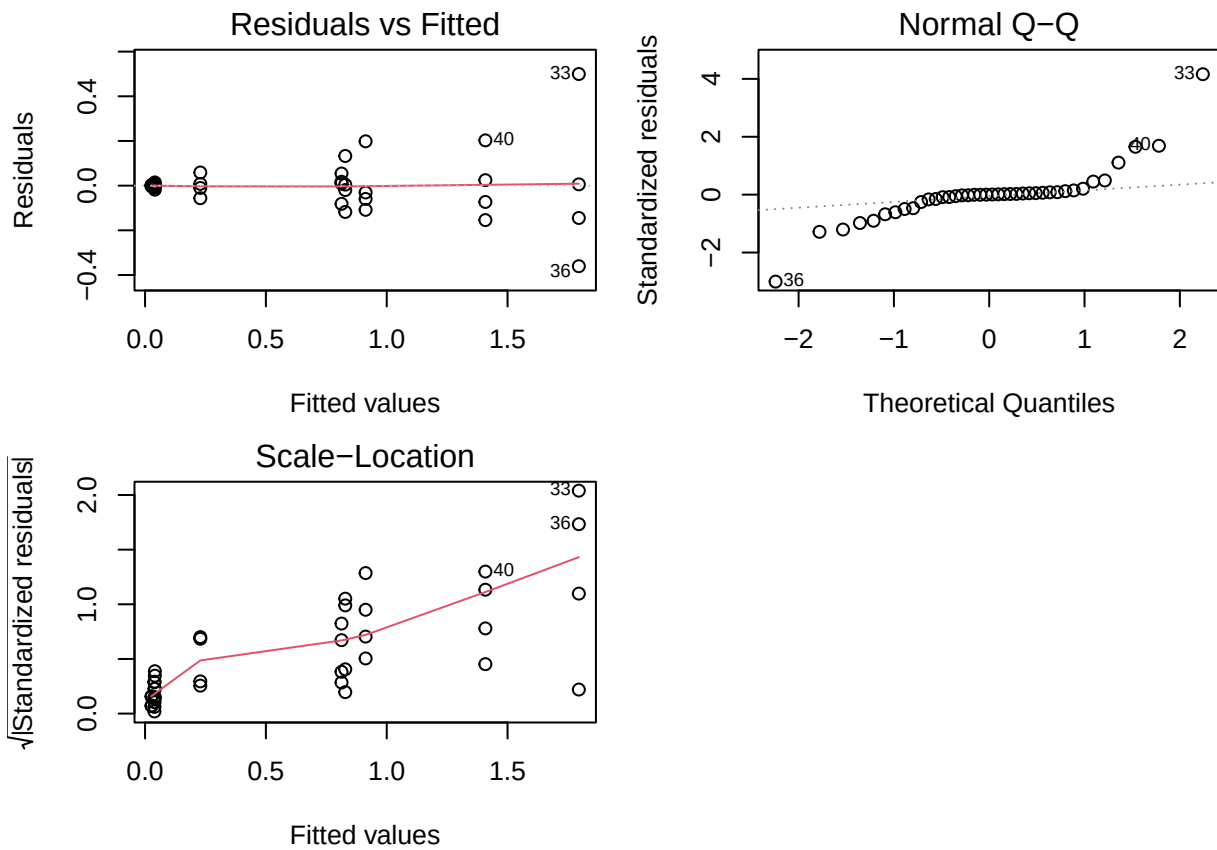


```

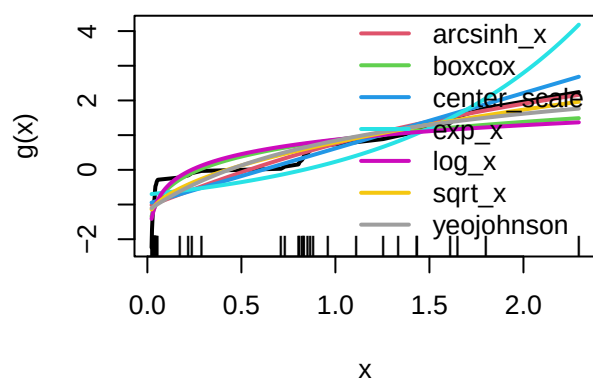
## [2,] -0.005151293 -0.03587602 -1.785550e-03 -0.033349088 -0.08396236
## [3,] -0.000201771  0.01363803 -4.294225e-05 -0.001285853 -0.04509413
## [4,]  0.005151293  0.03587602  1.785550e-03  0.033349088  0.08396236
## [5,]  0.010256799  0.05420036  2.998658e-03  0.058841272  0.19849991
##
## $n
## [1] 4 4 4 4 4 4 4 4 4 4
##
## $conf
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## [1,] -0.1160920 -0.4687495 -0.2037266 -0.01450842 -0.002138979 -0.008340813
## [2,]  0.1010123  0.3298119  0.1553281  0.01815501  0.005631433  0.007937271
##           [,7]      [,8]      [,9]     [,10]
## [1,] -0.04304609 -0.002864112 -0.05397741 -0.1777547
## [2,]  0.07032215  0.002778227  0.05140571  0.0875664
##
## $out
## numeric(0)
##
## $group
## numeric(0)
##
## $names
## [1] "1 dph"          "3 dph"          "6 dph"
## [4] "Early blastula"  "Early Gastrula"  "Fertilized stage"
## [7] "Hatching"       "Late blastula"   "Late Gastrula"
## [10] "Somite development"

```





```
## Best Normalizing transformation with 40 Observations
## Estimated Normality Statistics (Pearson P / df, lower => more normal):
## - arcsinh(x): 2.76
## - Box-Cox: 2.96
## - Center+scale: 2.6
## - Exp(x): 3.36
## - Log_b(x+a): 2.88
## - orderNorm (ORQ): 1.44
## - sqrt(x + a): 2.64
## - Yeo-Johnson: 3
## Estimation method: Out-of-sample via CV with 10 folds and 5 repeats
##
## Based off these, bestNormalize chose:
## orderNorm Transformation with 40 nonmissing obs and no ties
## - Original quantiles:
##   0%   25%   50%   75%  100%
## 0.022 0.040 0.499 0.902 2.295
## [1] TRUE
```



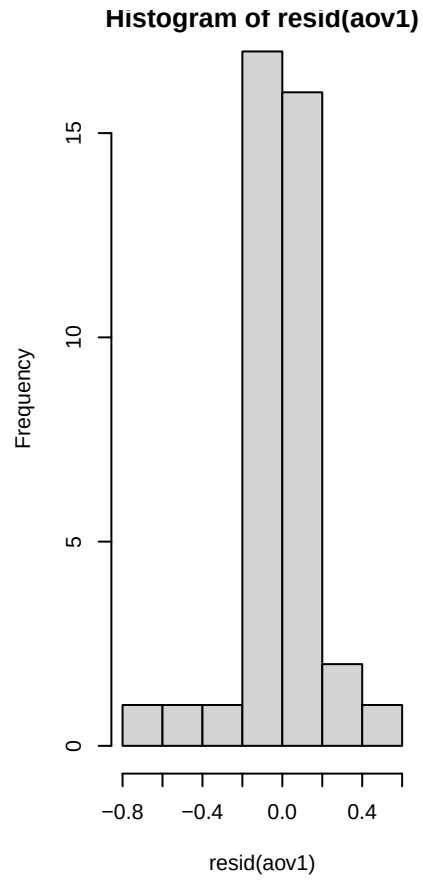
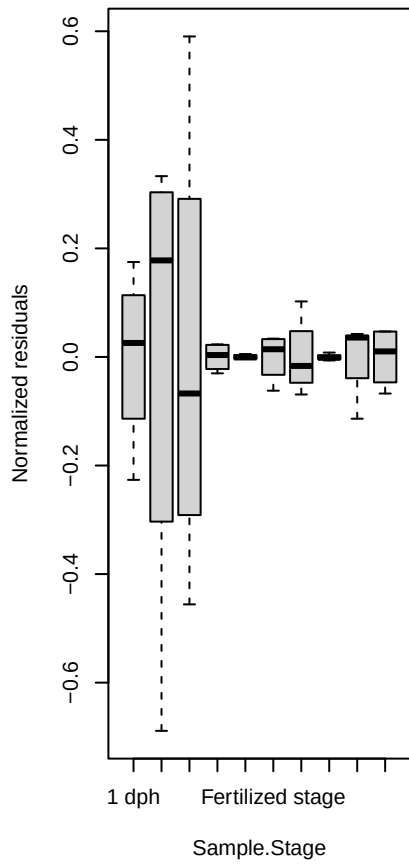
```
##
##  Shapiro-Wilk normality test
##
## data:  Gene$ExpNormal
## W = 0.85661, p-value = 0.0001565
##
##  Bartlett test of homogeneity of variances
##
## data:  Gene$ExpNormal by Gene$Sample.Stage
## Bartlett's K-squared = 64.657, df = 9, p-value = 1.682e-10
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value  Pr(>F)
## group  9  1.9767 0.07969 .
##      29
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

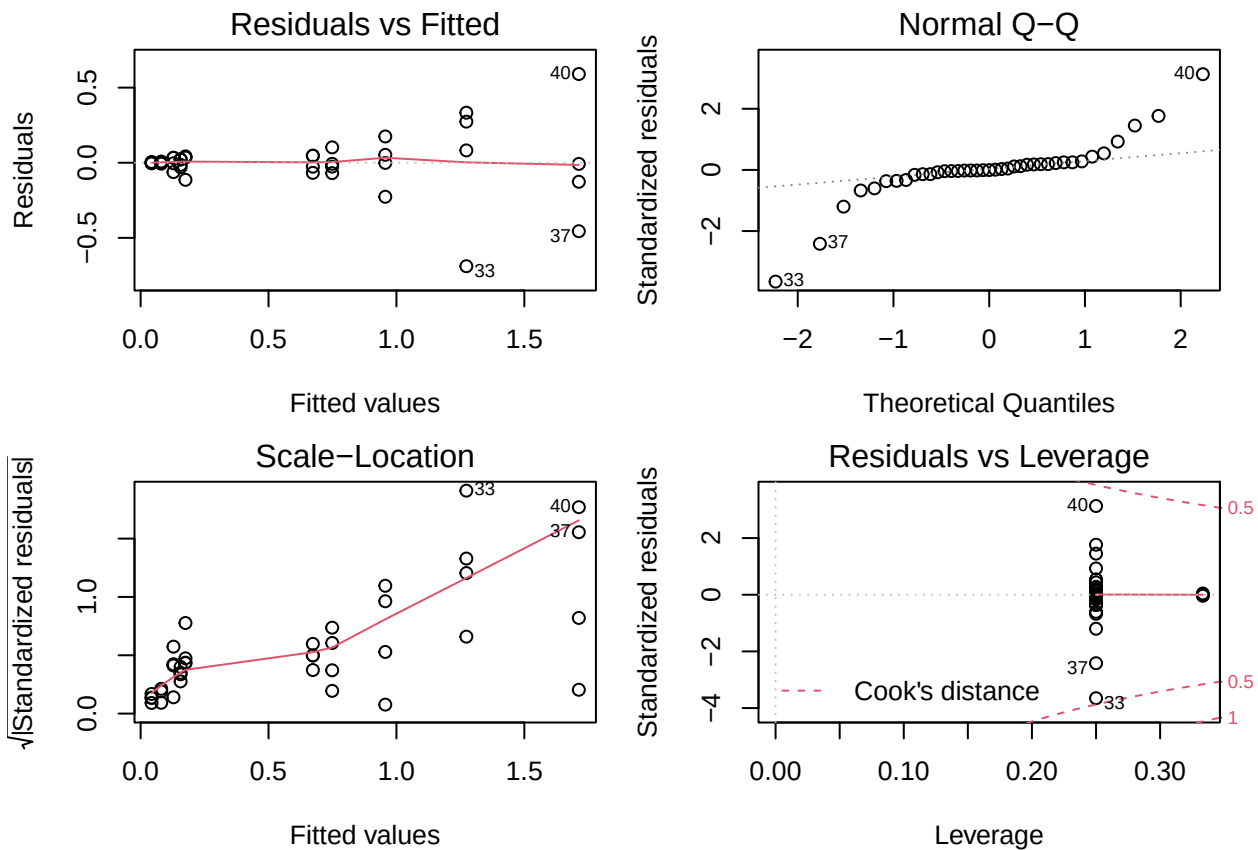
## $stats
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## [1,] -0.22644857 -0.6888054 -0.45578694 -0.030161965 -0.0034698385 -0.06213128
## [2,] -0.11378167 -0.3033711 -0.29128748 -0.022253020 -0.0034518685 -0.03290688
## [3,]  0.02578544  0.1778728 -0.06733384  0.003525275 -0.0009332105  0.01420130
## [4,]  0.11378167  0.3033711  0.29128748  0.022253020  0.0034518685  0.03290688
## [5,]  0.17487768  0.3330598  0.59045462  0.023111414  0.0053362595  0.03372869
##           [,7]      [,8]      [,9]     [,10]
## [1,] -0.06911270 -0.006494819 -0.11374436 -0.06738744
```

```

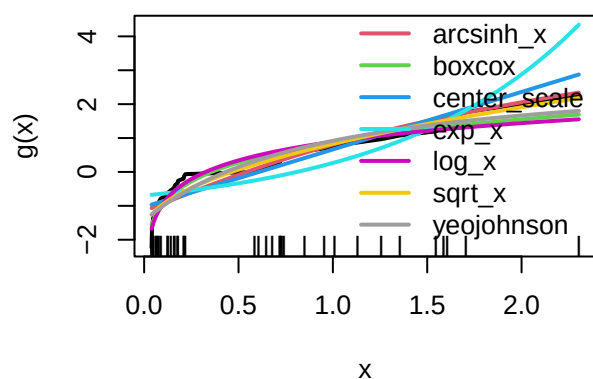
## [2,] -0.04755570 -0.004014063 -0.03914422 -0.04683114
## [3,] -0.01658206 -0.001533306 0.03570744 0.01023240
## [4,] 0.04755570 0.003247410 0.03914422 0.04683114
## [5,] 0.10227681 0.008028125 0.04232947 0.04692263
##
## $n
## [1] 4 4 4 4 4 4 4 3 4 4
##
## $conf
##          [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## [1,] -0.1539896 -0.3014535 -0.5275681 -0.03163450 -0.006387163 -0.03779158
## [2,] 0.2055605 0.6571991 0.3929004 0.03868505 0.004520742 0.06619417
##          [,7]      [,8]      [,9]      [,10]
## [1,] -0.09172006 -0.008157318 -0.02614043 -0.06376079
## [2,] 0.05855595 0.005090706 0.09755531 0.08422560
##
## $out
## numeric(0)
##
## $group
## numeric(0)
##
## $names
## [1] "1 dph"          "3 dph"          "6 dph"
## [4] "Early blastula"  "Early Gastrula"  "Fertilized stage"
## [7] "Hatching"       "Late blastula"   "Late Gastrula"
## [10] "Somite development"

```





```
## Best Normalizing transformation with 39 Observations
## Estimated Normality Statistics (Pearson P / df, lower => more normal):
## - arcsinh(x): 2.66
## - Box-Cox: 2.2333
## - Center+scale: 2.78
## - Exp(x): 3.34
## - Log_b(x+a): 2.0333
## - orderNorm (ORQ): 1.78
## - sqrt(x + a): 2.34
## - Yeo-Johnson: 2.3933
## Estimation method: Out-of-sample via CV with 10 folds and 5 repeats
##
## Based off these, bestNormalize chose:
## orderNorm Transformation with 39 nonmissing obs and no ties
## - Original quantiles:
##   0%   25%  50%  75% 100%
## 0.039 0.125 0.585 0.903 2.304
## [1] TRUE
```



```
##
## Shapiro-Wilk normality test
##
## data: Gene$ExpNormal
## W = 0.87259, p-value = 0.0007844
##
## Bartlett test of homogeneity of variances
##
## data: Gene$ExpNormal by Gene$Sample.Stage
## Bartlett's K-squared = 50.046, df = 9, p-value = 1.056e-07
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 9  2.2664 0.05142 .
##      25
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

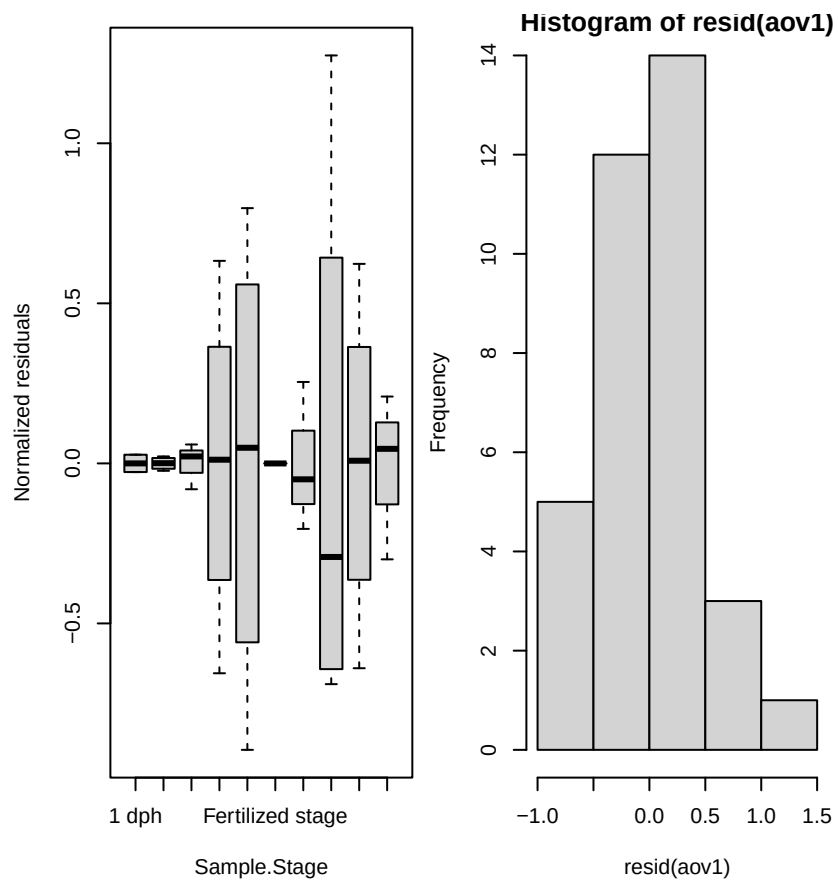
## $stats
##           [,1]      [,2]      [,3]      [,4]      [,5]
## [1,] -2.711253e-02 -0.0231466427 -0.08078973 -0.65563305 -0.89491705
## [2,] -2.711253e-02 -0.0167698462 -0.02952585 -0.36428307 -0.55902617
## [3,]  1.110223e-16  0.0006753487  0.02173804  0.01144065  0.04876567
## [4,]  2.711253e-02  0.0167698463  0.04039487  0.36428307  0.55902617
## [5,]  2.711253e-02  0.0217959452  0.05905170  0.63275176  0.79738571
##           [,6]      [,7]      [,8]      [,9]     [,10]
## [1,] -0.0006697737 -0.20462283 -0.6896759 -0.639933100 -0.2997623
```

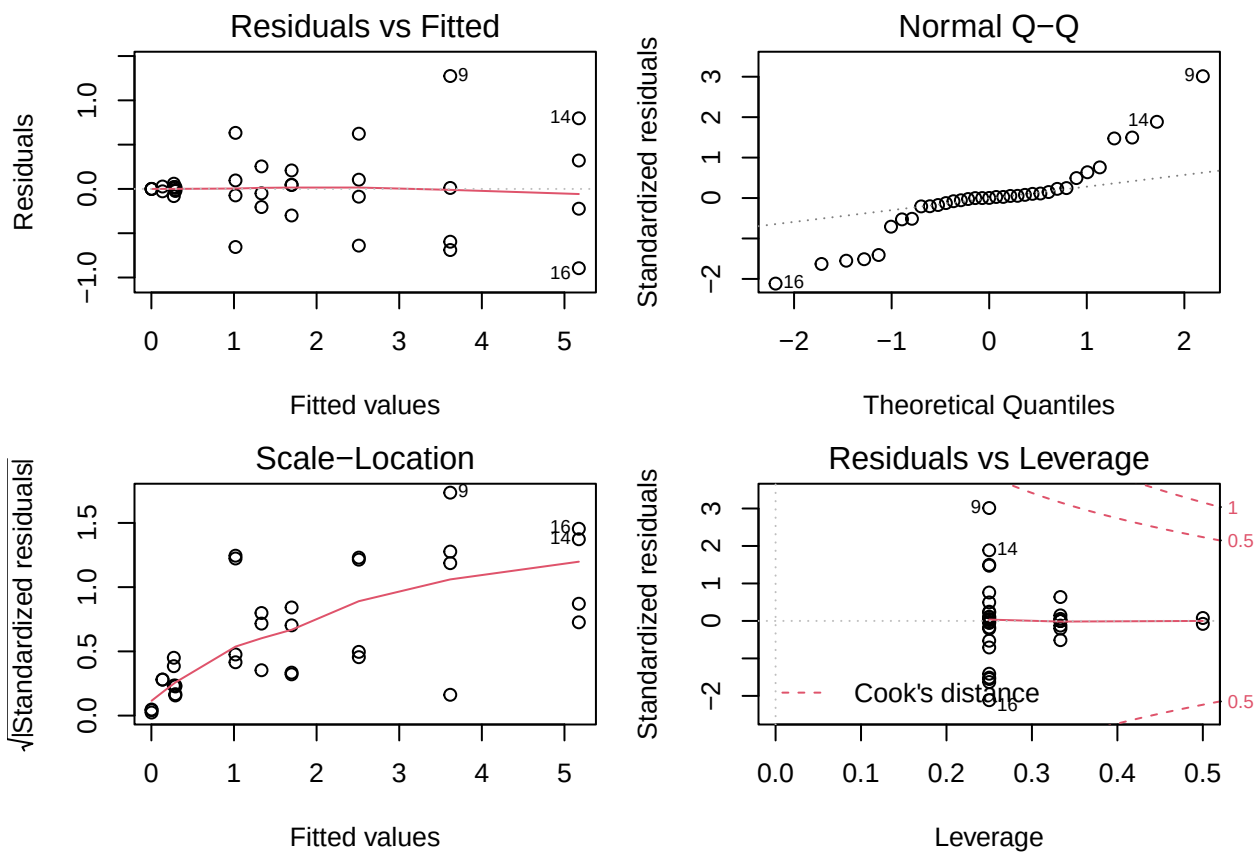


```

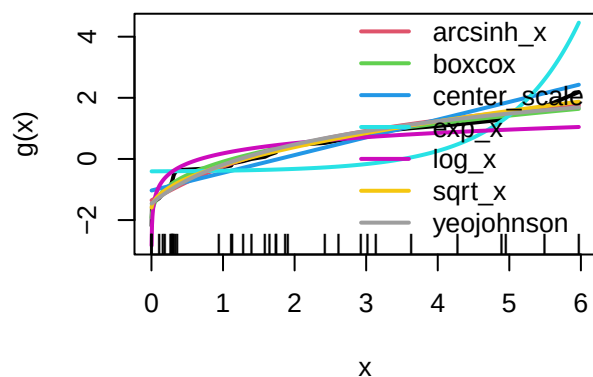
## [2,] -0.0004463167 -0.12718194 -0.6427734 -0.363705066 -0.1280625
## [3,] -0.0002228597 -0.04974105 -0.2923933 0.008316553 0.0454657
## [4,] 0.0003348868 0.10231142 0.6427734 0.363705066 0.1280625
## [5,] 0.0008926333 0.25436389 1.2744624 0.623299994 0.2088309
##
## $n
## [1] 2 4 3 4 4 3 3 4 4 4
##
## $conf
##          [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## [1,] -0.0605818 -0.02582101 -0.04204458 -0.5641266 -0.8344957 -0.0009354840
## [2,] 0.0605818 0.02717171 0.08552065 0.5870079 0.9320270 0.0004897647
##          [,7]      [,8]      [,9]      [,10]
## [1,] -0.2590880 -1.3079753 -0.5663375 -0.1568731
## [2,] 0.1596059 0.7231888 0.5829706 0.2478045
##
## $out
## numeric(0)
##
## $group
## numeric(0)
##
## $names
## [1] "1 dph"          "3 dph"          "6 dph"
## [4] "Early blastula" "Early Gastrula" "Fertilized stage"
## [7] "Hatching"      "Late blastula"  "Late Gastrula"
## [10] "Somite development"

```





```
## Best Normalizing transformation with 35 Observations
## Estimated Normality Statistics (Pearson P / df, lower => more normal):
## - arcsinh(x): 1.8867
## - Box-Cox: 1.7133
## - Center+scale: 2.0467
## - Exp(x): 3.4467
## - Log_b(x+a): 2.1267
## - orderNorm (ORQ): 1.5133
## - sqrt(x + a): 1.7533
## - Yeo-Johnson: 1.7933
## Estimation method: Out-of-sample via CV with 10 folds and 5 repeats
##
## Based off these, bestNormalize chose:
## orderNorm Transformation with 35 nonmissing obs and no ties
## - Original quantiles:
##   0%   25%  50%  75% 100%
## 0.002 0.298 1.398 2.772 5.971
## [1] TRUE
```



```
##
## Shapiro-Wilk normality test
##
## data: Gene$ExpNormal
## W = 0.57877, p-value = 1.624e-09

##
## Bartlett test of homogeneity of variances
##
## data: Gene$ExpNormal by Gene$Sample.Stage
## Bartlett's K-squared = 59.219, df = 9, p-value = 1.895e-09

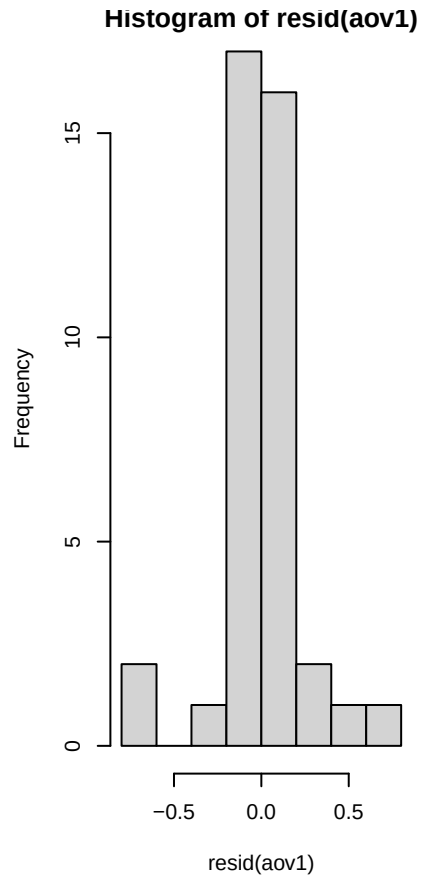
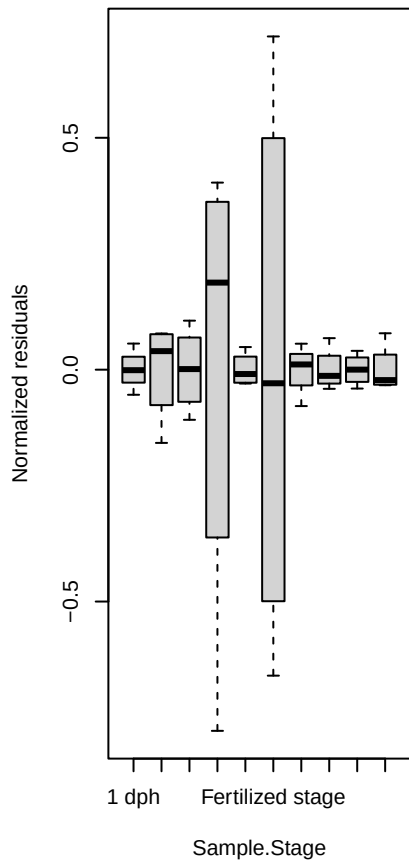
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value    Pr(>F)
## group 9   4.947 0.0004128 ***
##      30
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

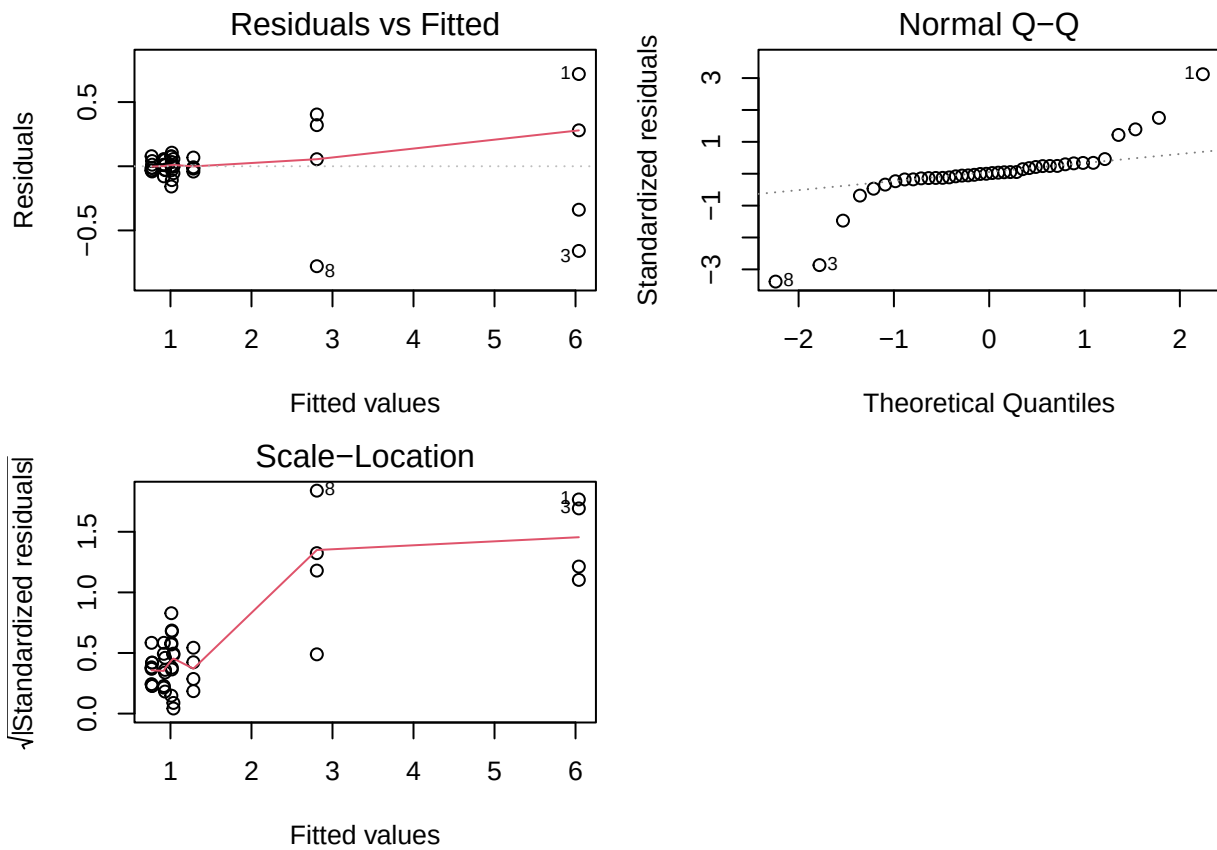
## $stats
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## [1,] -0.054109512 -0.15792409 -0.108131614 -0.7787750 -0.029918079 -0.65978811
## [2,] -0.027945496 -0.07644663 -0.069330525 -0.3618733 -0.028161322 -0.49927263
## [3,] -0.001094341  0.03995827  0.001223065  0.1877188 -0.009400559 -0.02935959
## [4,]  0.027945496  0.07644663  0.069330525  0.3618733  0.028161322  0.49927263
## [5,]  0.056298195  0.07800756  0.105685485  0.4033373  0.048719198  0.71850728
##           [,7]      [,8]      [,9]     [,10]
## [1,] -0.07849520 -0.04130404 -4.073394e-02 -0.03351852
```

```

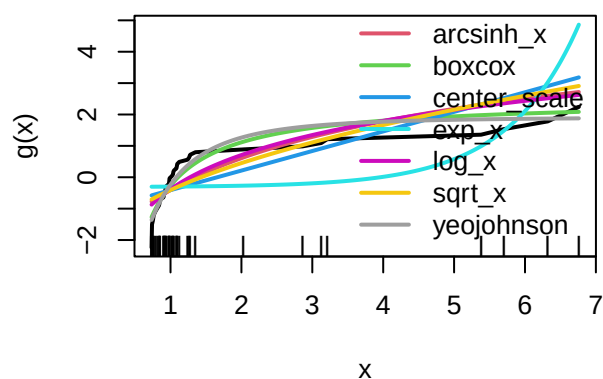
## [2,] -0.03395544 -0.03004556 -2.633244e-02 -0.03244546
## [3,]  0.01126308 -0.01333071  8.004725e-05 -0.02248784
## [4,]  0.03395544  0.03004556  2.633244e-02  0.03244546
## [5,]  0.05596903  0.06796545  4.057384e-02  0.07849420
##
## $n
## [1] 4 4 4 4 4 4 4 4 4 4
##
## $conf
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## [1,] -0.04524822 -0.0808274 -0.1083192 -0.3840410 -0.05389545 -0.8182103
## [2,]  0.04305954  0.1607439  0.1107653  0.7594787  0.03509433  0.7594912
##           [,7]      [,8]      [,9]     [,10]
## [1,] -0.04238651 -0.06080269 -0.04152521 -0.07375166
## [2,]  0.06491267  0.03414127  0.04168531  0.02877599
##
## $out
## numeric(0)
##
## $group
## numeric(0)
##
## $names
## [1] "1 dph"          "3 dph"          "6 dph"
## [4] "Early blastula"  "Early Gastrula"  "Fertilized stage"
## [7] "Hatching"       "Late blastula"   "Late Gastrula"
## [10] "Somite development"

```





```
## Best Normalizing transformation with 40 Observations
## Estimated Normality Statistics (Pearson P / df, lower => more normal):
## - arcsinh(x): 3
## - Box-Cox: 1.76
## - Center+scale: 3.6
## - Exp(x): 4.08
## - Log_b(x+a): 2.64
## - orderNorm (ORQ): 1.2
## - sqrt(x + a): 3.12
## - Yeo-Johnson: 1.64
## Estimation method: Out-of-sample via CV with 10 folds and 5 repeats
##
## Based off these, bestNormalize chose:
## orderNorm Transformation with 40 nonmissing obs and no ties
## - Original quantiles:
##   0%   25%   50%   75%  100%
## 0.733 0.890 1.001 1.267 6.760
## [1] TRUE
```



```
##
##  Shapiro-Wilk normality test
##
## data:  Gene$ExpNormal
## W = 0.91132, p-value = 0.004735

##
##  Bartlett test of homogeneity of variances
##
## data:  Gene$ExpNormal by Gene$Sample.Stage
## Bartlett's K-squared = 60.328, df = 9, p-value = 1.159e-09

## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value  Pr(>F)
## group  9  2.3468 0.03958 *
##      29
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

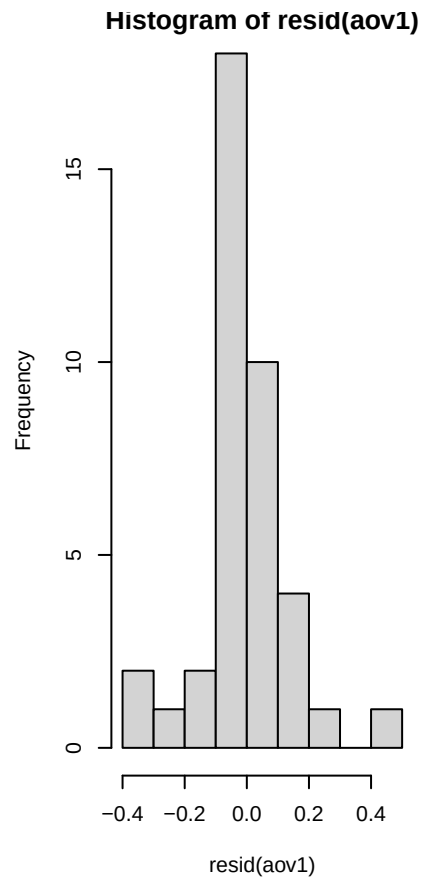
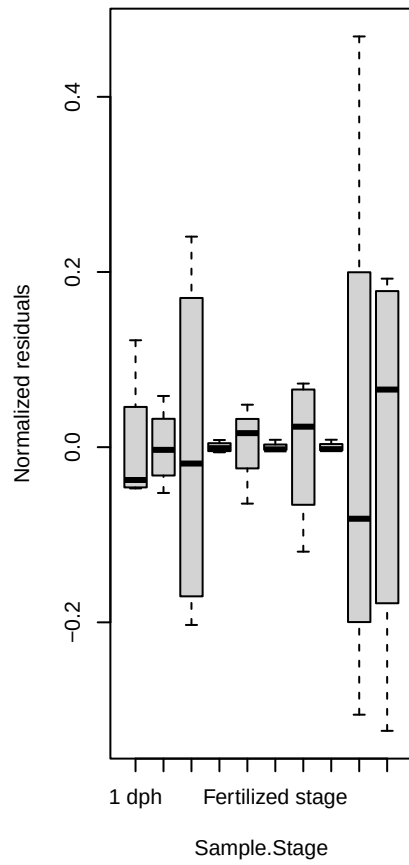
## $stats
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## [1,] -0.04710503 -0.052287217 -0.20298618 -0.005853590 -0.06446334 -0.003429655
## [2,] -0.04594887 -0.032374434 -0.17032457 -0.004528526 -0.02423370 -0.003028408
## [3,] -0.03747668 -0.003076497 -0.01869517 -0.001144647  0.01599594 -0.002489254
## [4,]  0.04594887  0.032374434  0.17032457  0.004528526  0.03223167  0.003028408
## [5,]  0.12205839  0.058440212  0.24037652  0.008142884  0.04846740  0.008408162
##           [,7]      [,8]      [,9]      [,10]
## [1,] -0.11932741 -0.003952907 -0.30545002 -0.32388502
```

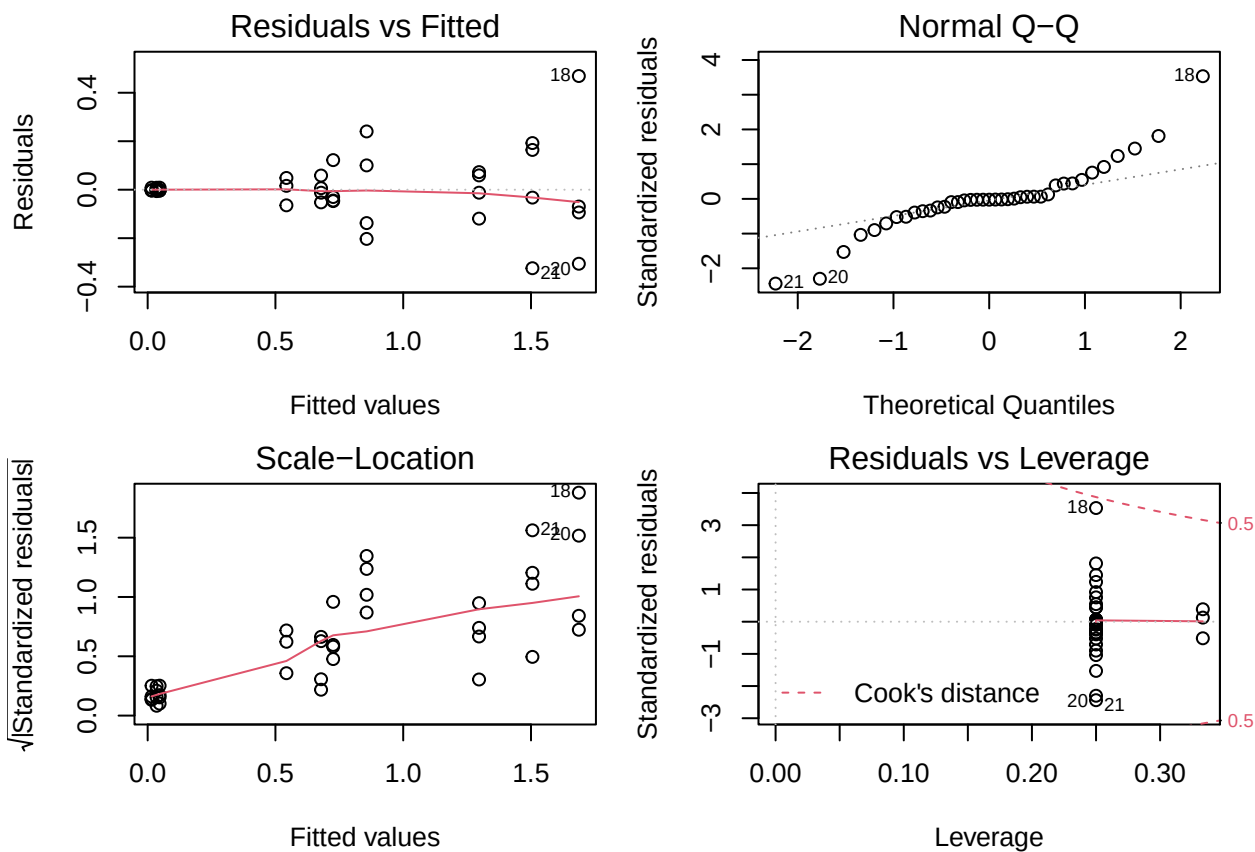


```

## [2,] -0.06581142 -0.003545100 -0.19970006 -0.17820578
## [3,]  0.02336628 -0.002247347 -0.08173811  0.06574744
## [4,]  0.06581142  0.003545100  0.19970006  0.17820578
## [5,]  0.07259484  0.008447600  0.46892624  0.19239014
##
## $n
## [1] 4 4 4 4 3 4 4 4 4 4
##
## $conf
##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## [1,] -0.11007589 -0.05422810 -0.2878080 -0.008299719 -0.03551253 -0.007274138
## [2,]  0.03512253  0.04807511  0.2504176  0.006010424  0.06750440  0.002295630
##           [,7]      [,8]      [,9]     [,10]
## [1,] -0.08061576 -0.007848605 -0.3972642 -0.2158177
## [2,]  0.12734833  0.003353912  0.2337880  0.3473126
##
## $out
## numeric(0)
##
## $group
## numeric(0)
##
## $names
## [1] "1 dph"          "3 dph"          "6 dph"
## [4] "Early blastula"  "Early Gastrula" "Fertilized stage"
## [7] "Hatching"       "Late blastula"  "Late Gastrula"
## [10] "Somite development"

```





```
## Best Normalizing transformation with 39 Observations
## Estimated Normality Statistics (Pearson P / df, lower => more normal):
## - arcsinh(x): 1.82
## - Box-Cox: 2.3
## - Center+scale: 1.62
## - Exp(x): 2.22
## - Log_b(x+a): 3.1267
## - orderNorm (ORQ): 1.18
## - sqrt(x + a): 2.1
## - Yeo-Johnson: 1.9
## Estimation method: Out-of-sample via CV with 10 folds and 5 repeats
##
## Based off these, bestNormalize chose:
## orderNorm Transformation with 39 nonmissing obs and no ties
## - Original quantiles:
##   0%   25%   50%   75%  100%
## 0.012 0.045 0.681 1.233 2.156
## [1] TRUE
```

