

Generalized-Linear-Model_GLM_.R

Shraddha Somani

```
# Use the Faraway gala data to first a Poisson regresssion model to Species using all the predictors.
```

```
# Compare the coefficients form this model to the Box-Cox Tranformed Normal Errors Linear Model that we used in the class notes.
```

```
require(faraway)
```

```
## Loading required package: faraway
```

```
require(arm)
```

```
## Loading required package: arm
```

```
## Loading required package: MASS
```

```
## Loading required package: Matrix
```

```
## Loading required package: lme4
```

```
##
```

```
## arm (Version 1.9-1, built: 2016-8-21)
```

```
## Working directory is C:/Users/Shraddha Somani/Desktop/GitHub
```

```
##
```

```
## Attaching package: 'arm'
```

```
## The following objects are masked from 'package:faraway':
```

```
##
```

```
##      fround, logit, pfround
```

```
require(car)
```

```
## Loading required package: car
```

```
##
```

```
## Attaching package: 'car'
```

```
## The following object is masked from 'package:arm':
```

```
##
```

```
##      logit
```

```
## The following objects are masked from 'package:faraway':
```

```
##
```

```
##      logit, vif
```

```
require(ggplot2)
```

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

```
head(gala)
```

```
##           Species Endemics  Area Elevation Nearest Scruz Adjacent
## Baltra          58       23 25.09       346      0.6   0.6    1.84
## Bartolome       31       21  1.24       109      0.6  26.3   572.33
## Caldwell        3        3  0.21       114      2.8  58.7    0.78
## Champion       25        9  0.10        46      1.9  47.4    0.18
## Coamano         2        1  0.05        77      1.9   1.9   903.82
## Daphne.Major    18       11  0.34       119      8.0   8.0    1.84
```

```
pois.mod = glm(Species ~ ., data = gala, family = poisson(link = "log"))
display(pois.mod)
```

```
## glm(formula = Species ~ ., family = poisson(link = "log"), data = gala)
```

```
##           coef.est coef.se
```

```
## (Intercept)  2.83    0.06
```

```
## Endemics    0.03    0.00
```

```
## Area        0.00    0.00
```

```
## Elevation   0.00    0.00
```

```
## Nearest     0.01    0.00
```

```
## Scruz       0.00    0.00
```

```
## Adjacent    0.00    0.00
```

```
## ---
```

```
##   n = 30, k = 7
```

```
##   residual deviance = 313.4, null deviance = 3510.7 (difference = 3197.4)
```

```
g = lm(Species ~ ., data = gala)
```

```
lambda = powerTransform(g)
```

```
lambda
```

```
## Estimated transformation parameters
```

```
##           Y1
```

```
## 0.5803311
```

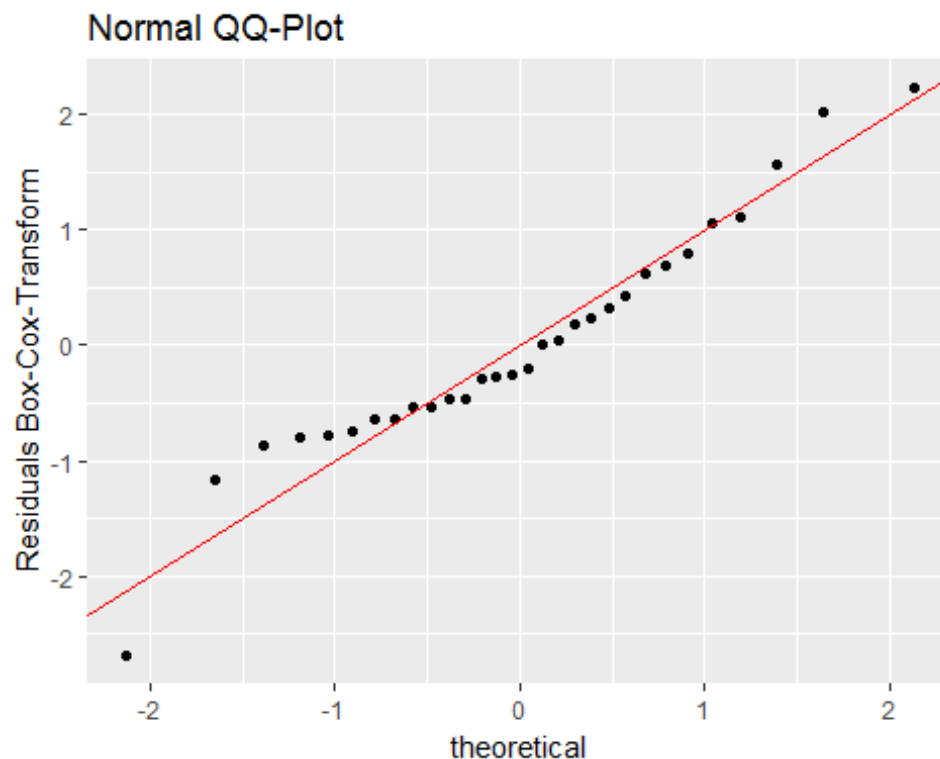
```
lam = lambda$lambda
```

```
glam = lm(Species^lam ~ ., gala)
```

```
modlam = fortify(glam)
```

```
p1 = qplot(sample = scale(.resid), data = modlam) + geom_abline(intercept =
0, slope = 1, color = "red") + labs(title = "Normal QQ-Plot", y = "Residuals
Box-Cox-Transform")
```

```
p1
```



```
summary(glam)
```

```
##
## Call:
## lm(formula = Species^lam ~ ., data = gala)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.6863 -1.0684 -0.3981  1.0026  3.8970
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.3931431  0.6368955   3.758  0.00103 **
## Endemics     0.3350357  0.0325224  10.302 4.35e-10 ***
## Area        -0.0002086  0.0007707  -0.271  0.78907
## Elevation    -0.0008701  0.0032168  -0.270  0.78920
## Nearest       0.0248540  0.0338516   0.734  0.47024
## Scruz        -0.0028778  0.0071562  -0.402  0.69130
## Adjacent      0.0001690  0.0008028   0.210  0.83516
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.958 on 23 degrees of freedom
## Multiple R-squared:  0.9623, Adjusted R-squared:  0.9525
## F-statistic: 97.87 on 6 and 23 DF, p-value: 3.33e-15
```

```
compareCoefs(pois.mod, glam)
```

```
##
## Call:
## 1: glm(formula = Species ~ ., family = poisson(link = "log"), data =
##   gala)
## 2: lm(formula = Species^lam ~ ., data = gala)
##           Est. 1      SE 1      Est. 2      SE 2
## (Intercept) 2.83e+00 5.96e-02 2.39e+00 6.37e-01
## Endemics    3.39e-02 1.74e-03 3.35e-01 3.25e-02
## Area        -1.07e-04 3.74e-05 -2.09e-04 7.71e-04
## Elevation    2.64e-04 1.93e-04 -8.70e-04 3.22e-03
## Nearest      1.05e-02 1.61e-03 2.49e-02 3.39e-02
## Scrutz       -6.83e-04 5.80e-04 -2.88e-03 7.16e-03
## Adjacent     4.54e-05 4.80e-05 1.69e-04 8.03e-04

# Fit the fpe data using a GLM-Poisson model.
# Compare coefficients from this model to the Weighted Least Squares Normal
# Errors Linear Model that we used in the class notes.
head(fpe)

##           EI      A      B      C      D      E      F      G      H      J      K      A2      B2      N
## Ain          260    51    64    36    23    9    5    4    4    3    3   105   114   17
## Alpes         75    14    17     9     9    3    1    2    1    1    1    32    31    5
## Ariege        107    27    18    13    17    2    2    2    1    1    1    57    33    6
## Bouches.du.Rhone 1036 191 204 119 205 29 13 13 10 10 6 466 364 30
## Charente.Maritime 367  71  76  47  37  8 34  5  4  4  2 163 142 17
## Cotes.du.Nord    396  93  90  57  54 13  5  9  4  3  5 193 155 15

pois.mod = glm(EI ~ ., data = fpe, family = poisson(link = "log"))
display(pois.mod)

## glm(formula = EI ~ ., family = poisson(link = "log"), data = fpe)
##           coef.est coef.se
## (Intercept)  4.55      0.05
## A            -0.04      0.01
## B             0.00      0.01
## C             0.01      0.01
## D            -0.04      0.01
## E             0.01      0.02
## F            -0.02      0.01
## G             0.00      0.02
## H            -0.07      0.03
## J             0.02      0.04
## K            -0.13      0.02
## A2            0.04      0.01
## B2            0.00      0.01
## ---
##      n = 24, k = 13
##      residual deviance = 113.2, null deviance = 3389.1 (difference = 3275.9)
```