Final Assignment_Group11

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We first read the "gala.txt" data via the following code and the output is shown in the same figure. We read the gala.txt to 'galadata' instead of 'gala' to avoid name overlapping.

Figure 1: read table and output

From Fig.1 we could know that the header of this table is Species, Area, Elevation, Nearest, Scruz, Adjacent.

Task 1

In this task, we use the step-down method to solve the problem for the response variable Species.

First code and output are shown in Fig.2.

```
> summary(lm(Species~Area+Elevation+Nearest+Scruz+Adjacent,data=galadata))
call:
lm(formula = Species ~ Area + Elevation + Nearest + Scruz + Adjacent,
    data = galadata)
Residuals:
             1Q Median 3Q
     Min
                                           Max
-111.679 -34.898 -7.862 33.460 182.584
Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 7.068221 19.154198 0.369 0.715351
         -0.023938 0.022422 -1.068 0.296318
Area
Elevation 0.319465 0.053663 5.953 3.82e-06 ***
Nearest 0.009144 1.054136 0.009 0.993151
Scruz -0.240524 0.215402 -1.117 0.275208
Adjacent -0.074805 0.017700 -4.226 0.000297 ***
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 60.98 on 24 degrees of freedom
Multiple R-squared: 0.7658, Adjusted R-squared: 0.7171
F-statistic: 15.7 on 5 and 24 DF, p-value: 6.838e-07
```

Figure 2: First step of step-down method

We could know that the p-value of "Nearest" is highest (0.993151) and is larger than 0.05, so we remove it. The next step code and output are shown in Fig.3.

```
call:
lm(formula = Species ~ Area + Elevation + Scruz + Adjacent, data = galadata)
Residuals:
                   Median
     Min
              1Q
                                 3Q
                                         Max
-111.637 -34.930
                   -7.864
                             33.432 182.524
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 7.07538 18.74982 0.377 0.709093
Area -0.02398 0.02151 -1.115 0.275554
Elevation 0.31957 0.05113 6.250 1.54e-06 ***
            -0.23936 0.16464 -1.454 0.158434
Scruz
Adjacent
                       0.01663 -4.501 0.000136 ***
            -0.07485
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '1
Residual standard error: 59.74 on 25 degrees of freedom
Multiple R-squared: 0.7658, Adjusted R-squared: 0.7284
F-statistic: 20.44 on 4 and 25 DF, p-value: 1.39e-07
                  Figure 3: Second step of step-down method
We could know that the p-value of "Area" is highest (0.275554) and is larger than
0.05, so we remove it. The next step code and output are shown in Fig.4.
> summary(lm(Species~Elevation+Scruz+Adjacent,data=galadata))
call:
lm(formula = Species ~ Elevation + Scruz + Adjacent, data = galadata)
Residuals:
   Min
            1Q Median
                           3Q
-88.70 -29.68 -11.12 24.25 192.67
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 14.25183 17.69201 0.806 0.427808
Elevation 0.27444
                         0.03137 8.749 3.17e-09 ***
                         0.16426 -1.326 0.196320
Scruz
            -0.21784
            -0.06744
                         0.01532 -4.404 0.000162 ***
Adjacent
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '1
Residual standard error: 60.02 on 26 degrees of freedom
Multiple R-squared: 0.7542,
                                 Adjusted R-squared:
F-statistic: 26.59 on 3 and 26 DF, p-value: 4.393e-08
```

> summary(lm(Species~Area+Elevation+Scruz+Adjacent,data=galadata))

Figure 4: Third step of step-down method

We could know that the p-value of "Scruz" is highest (0.196320) and is larger than 0.05, so we remove it. The next step code and output are shown in Fig.5.

```
> summary(lm(Species~Elevation+Adjacent,data=galadata))
call:
lm(formula = Species ~ Elevation + Adjacent, data = galadata)
Residuals:
            1Q Median
                            3Q
   Min
                                   Max
-103.41 -34.33 -11.43
                         22.57
                                203.65
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.43287
                    15.02469 0.095 0.924727
Elevation
           0.27657
                       0.03176
                                8.707 2.53e-09 ***
           -0.06889
                       0.01549 -4.447 0.000134 ***
Adjacent
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 60.86 on 27 degrees of freedom
Multiple R-squared: 0.7376,
                               Adjusted R-squared: 0.7181
F-statistic: 37.94 on 2 and 27 DF, p-value: 1.434e-08
```

Figure 5: Fourth step of step-down method

We could know that all the p-value is smaller than 0.05, So all explanatory variables in the model are significant.

The resulting of the step-up method is:

Species = 1.43287 + 0.27657*Elevation -0.06889*Adjacent + error

Task 2

For the transformed response variable sqrt(Species) we do the similar steps. First code and output are shown in Fig.6.

```
> summary(lm(sqrt(Species)~Area+Elevation+Nearest+Scruz+Adjacent,data=galadata))
call:
lm(formula = sqrt(Species) ~ Area + Elevation + Nearest + Scruz +
    Adjacent, data = galadata)
Residuals:
              1Q Median
-4.5572 -1.4969 -0.3031 1.3527 5.2110
Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept) 3.3919243 0.8712678 3.893 0.000690 ***
            -0.0019718 0.0010199 -1.933 0.065080
Area
             0.0164784 0.0024410 6.751 5.55e-07
0.0249326 0.0479495 0.520 0.607844
Elevation
                                      6.751 5.55e-07 ***
Nearest
Scruz
            -0.0134826 0.0097980 -1.376 0.181509
            -0.0033669 0.0008051 -4.182 0.000333 ***
Adjacent
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 2.774 on 24 degrees of freedom
Multiple R-squared: 0.7827, Adjusted R-squared: 0
F-statistic: 17.29 on 5 and 24 DF, p-value: 2.874e-07
                                 Adjusted R-squared: 0.7374
```

Figure 6: First step of step-down method

We could know that the p-value of "Nearest" is highest (0.607844) and is larger than 0.05, so we remove it. The next step code and output are shown in Fig.7.

```
> summary(lm(sqrt(Species)~Area+Elevation+Scruz+Adjacent,data=galadata))
call:
lm(formula = sqrt(Species) ~ Area + Elevation + Scruz + Adjacent,
    data = galadata
Residuals:
    Min
             1Q Median
                              3Q
                                     Max
-4.4407 -1.6642 -0.3444 1.2431 5.0482
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
                                   3.978 0.000525 ***
(Intercept) 3.4114369 0.8576631
            -0.0020798 0.0009839
                                   -2.114 0.044681 *
            0.0167745 0.0023387
                                   7.173 1.62e-07 ***
Elevation
            -0.0102950 0.0075309 -1.367 0.183784
Scruz
Adjacent
            Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '1
Residual standard error: 2.733 on 25 degrees of freedom
Multiple R-squared: 0.7802,
                                Adjusted R-squared: 0.7451
F-statistic: 22.19 on 4 and 25 DF, p-value: 6.392e-08
                 Figure 7: Second step of step-down method
We could know that the p-value of "Scruz" is highest (0.183784) and is larger than
0.05, so we remove it. The next step code and output are shown in Fig.8.
> summary(lm(sqrt(Species)~Area+Elevation+Adjacent,data=galadata))
call:
lm(formula = sqrt(Species) ~ Area + Elevation + Adjacent, data = galadata)
Residuals:
             1Q Median
    Min
                             30
                                   Max
-4.9752 -1.7377 -0.4927 1.4342 5.6267
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
                                  3.716 0.000975 ***
(Intercept) 2.8611345 0.7698707
           -0.0019221 0.0009933 -1.935 0.063931 .
Area
Elevation
            0.0165770 0.0023729
                                   6.986 2.04e-07 ***
            -0.0035043 0.0007731 -4.533 0.000115 ***
Adjacent
Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' ' 1
Residual standard error: 2.778 on 26 degrees of freedom
Multiple R-squared: 0.7638, Adjusted R-squared: (F-statistic: 28.03 on 3 and 26 DF, p-value: 2.63e-08
                               Adjusted R-squared: 0.7366
```

Figure 8: Third step of step-down method

We could know that the p-value of "Area" is highest (0.063931) and is larger than 0.05, so we remove it. The next step code and output are shown in Fig.9.

```
> summary(lm(sqrt(Species)~Elevation+Adjacent,data=galadata))
call:
lm(formula = sqrt(Species) ~ Elevation + Adjacent, data = galadata)
Residuals:
   Min
            1Q Median
                             3Q
                                    Max
-5.1626 -2.1405 -0.1246 1.6201
                                 6.3530
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
                       0.7198603
                                    4.915 3.83e-05 ***
(Intercept)
            3.5378950
                        0.0015218
Elevation
            0.0129421
                                    8.504 4.06e-09 ***
Adjacent
            -0.0028992
                       0.0007421
                                  -3.907 0.000566 ***
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '1
Residual standard error: 2.916 on 27 degrees of freedom
Multiple R-squared: 0.7298,
                                Adjusted R-squared: 0.7098
F-statistic: 36.46 on 2 and 27 DF, p-value: 2.126e-08
```

Figure 9: Third step of step-down method

We could know that all the p-value is smaller than 0.05, So all explanatory variables in the model are significant.

The resulting of the step-up method is:

sqrt(Species) = 3.5378950 + 0.0129421*Elevation - 0.0028992*Adjacent + error

Task 3

The codes making plots are shown below:

- > gala_lm = lm(Species~Elevation+Adjacent,data=galadata)
- > gala_lm2 = lm(sqrt(Species)~Elevation+Adjacent,data=galadata)
- > plot(fitted(gala_lm),residuals(gala_lm))
- > plot(fitted(gala_lm2),residuals(gala_lm2))
- > qqnorm(residuals(gala_lm))
- > gqnorm(residuals(gala_lm2))

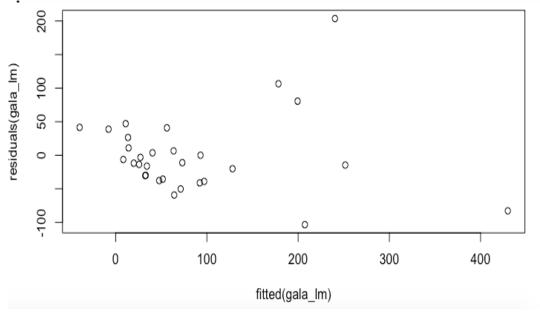


Figure 10: fitted(gala_lm)

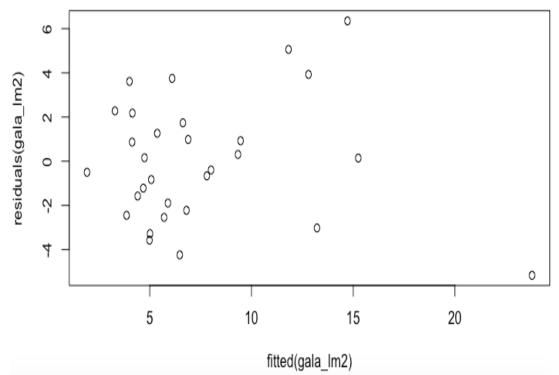


Figure 11: fitted(gala_lm2)

Normal Q-Q Plot

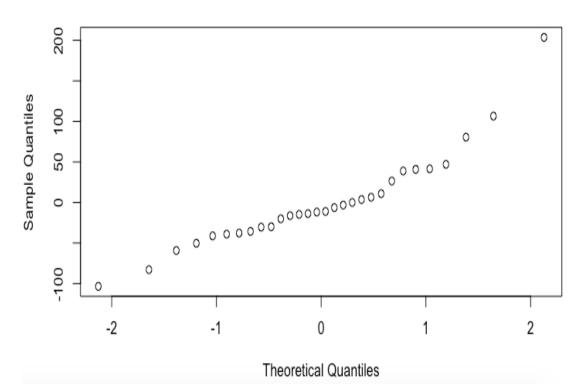


Figure 12: qqnorm(gala_lm)

Normal Q-Q Plot

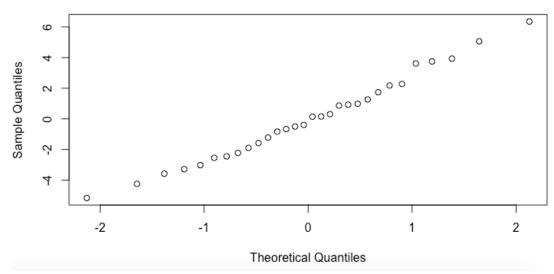


Figure 13: qqnorm(gala_lm2)

```
> shapiro.test(residuals(gala_lm))
```

Shapiro-Wilk normality test

data: residuals(gala_lm)
W = 0.89306, p-value = 0.005706

> shapiro.test(residuals(gala_lm2))

Shapiro-Wilk normality test

data: residuals(gala_lm2) W = 0.98489, p-value = 0.9353

Figure 14: Shapiro-test

The QQ-plot of residuals and fitted plot are shown as Figure 10 to 13.

From the QQ-plot of "gala_lm" we can see it have some curves and the second QQ-plot for sqrt model is approximating a straight line.

From the Shapiro.test we can see the p-value of residuals(gala_lm) is smaller than 0.05 and p-value of residuals(gala_lm2) is greater than 0.05. So the first sample is not normal while the second sqrt sample can be considered as normal. So we believe the second resulting model using sqrt is better.

Task 4

We have two explanatory variables in our formula, which is "Elevation" and "Adjacent". So we perform the Cook's distance respectively.

The code for the "Elevation" and output is shown in Fig.15 and Fig.16.

sqrtlm=lm(sqrt(Species)~Elevation+Adjacent,data=galadata)
round(cooks.distance(sqrtlm),2) Baltra Bartolome caldwell Champion Coamano Daphne.Major 0.00 Espanola 0.00 0.02 0.02 Eden 0.00 Enderby 0.00 Fernandina Daphne.Minor Darwin 0.00 0.01 0.03 0.02 Gardner1 Gardner 2 Genovesa Isabela Marchena onslow 0.03 0.03 0.01 0.00 0.02 1.64 Pinta Pinzon Plazas Rabida SanCristobal sansalvador 0.04 0.00 0.00 0.01 0.06 0.00 Wolf SantaCruz SantaFe SantaMaria Seymour Tortuga 0.25 0.00 0.00 0.01 0.01 0.08 > plot(1:30,cooks.distance(sqrtlm))

Figure 15: Code and output for Cook's distance

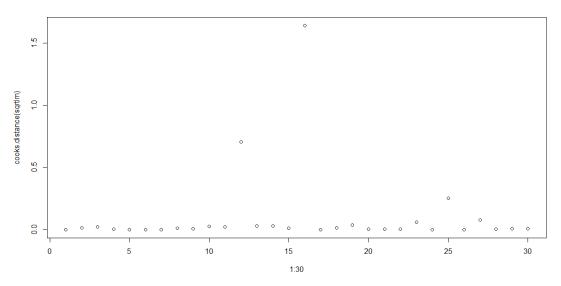


Figure 16: Output for Cook's distance

From the output we could know that the value of "Isabela" is 1.64 larger than 1, so it is the influence point in this model.

We then remove the "Isabela", from the data we could it is the 16th point. The code and output are shown in Fig.17 and Fig.18.

> newgala=galadata[-16,] > newsqrtlm=lm(sqrt(Species)~Elevation+Adjacent,data=newgala) round(cooks.distance(newsqrtlm),2) Baltra caldwell Bartolome Champion Coamano Daphne.Major 0.00 0.04 0.02 0.01 0.00 0.00 Eden Enderby Fernandina Daphne.Minor Darwin Espanola. 0.00 0.00 0.03 0.03 0.01 7.25 Gardner1 Gardner2 Genovesa Marchena ons low Pinta 0.06 0.04 0.00 0.01 0.02 0.22 Pinzon Las.Plazas Rabida SanCristobal SanSalvador SantaCruz 0.00 0.00 0.01 0.05 0.08 0.30 SantaFe SantaMaria Seymour Tortuga Wo1f 0.00 0.09 0.01 plot(1:29,cooks.distance(newsqrtlm))

Figure 17: Code and output for Cook's distance 2

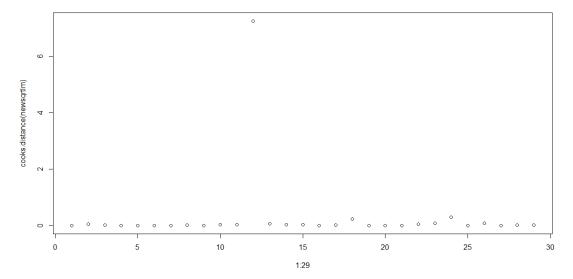


Figure 18: Output for Cook's distance 2

From the output we could know that the value of "Fernandina" is 7.25 larger than 1, so it is still influence point.

We then remove the "Fernandina", from the data we could it is the 12^{th} point. The code and output are shown in Fig.19 and Fig.20.

- > newgala2=galadata[-c(12,16),]
 > newsqrtlm2=lm(sqrt(Species)~Elevation+Adjacent,data=newgala2)
 > round(cooks.distance(newsqrtlm2),2)

> Tourid(cooks, discarice(newsqr clinz), 2)						
Baltra	Bartolome	Caldwell	Champion	Coamano	Daphne.Major	
0.00	0.07	0.02	0.01	0.22	0.00	
Daphne.Minor	Darwin	Eden	Enderby	Espanola	Gardner1	
0.00	0.01	0.00	0.03	0.04	0.07	
Gardner2	Genovesa	Marchena	onslow	Pinta	Pinzon	
0.04	0.02	0.00	0.01	0.34	0.00	
Las.Plazas	Rabida	SanCristobal	SanSalvador	SantaCruz	SantaFe	
0.00	0.00	0.04	0.11	0.28	0.00	
SantaMaria	Seymour	Tortuga	Wolf			
0.09	0.01	0.01	0.01			
<pre>> plot(1:28,cooks.distance(newsqrtlm2))</pre>						

Figure 19: Code and output for Cook's distance 3

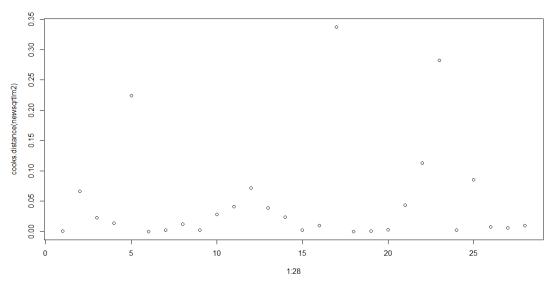


Figure 20: Output for Cook's distance 3

From the output we could know that all the output is smaller than 1 so there is no influence points now.

For the model, the code and output are shown in Fig21.

> summary(newsqrt1m2) call: lm(formula = sqrt(Species) ~ Elevation + Adjacent, data = newgala2) Residuals: Min 1Q Median 3Q Max -5.2124 -1.7094 -0.3825 1.8110 Coefficients: Estimate Std. Error t value Pr(>|t|) (Intercept) 2.455151 0.784143 3.131 0.0044 ** Elevation 0.016866 0.001933 8.724 4.68e-09 *** Adjacent -0.001157 0.002336 -0.495 0.6247 Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1 Residual standard error: 2.624 on 25 degrees of freedom Multiple R-squared: 0.7597, Adjusted R-squared: 0.7405 F-statistic: 39.52 on 2 and 25 DF, p-value: 1.817e-08

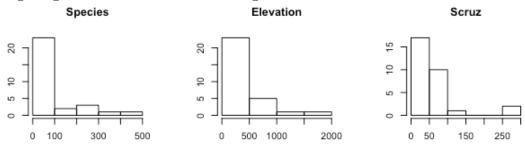
Figure 21: New model output

We could know that the new model is:

sqrt(Species) = 2.455151 + 0.016866*Elevation - 0.001157*Adjacent + error Which changed to some extent after removing the influence points.

Task 5

Using the given codes we can make 4 diagrams shown as below:



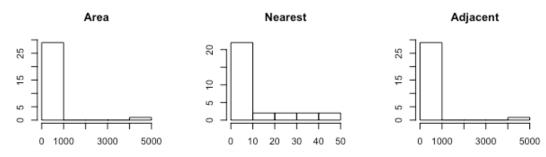


Figure 22 histogram for each variables

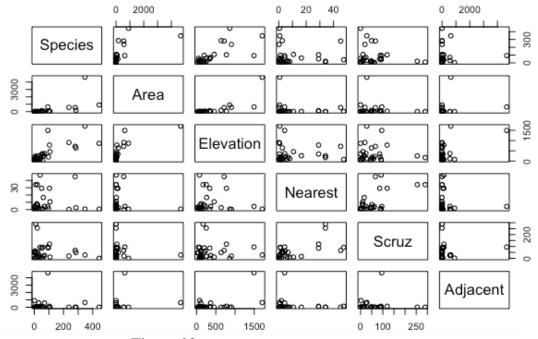


Figure 23: Scatter plot for each variables

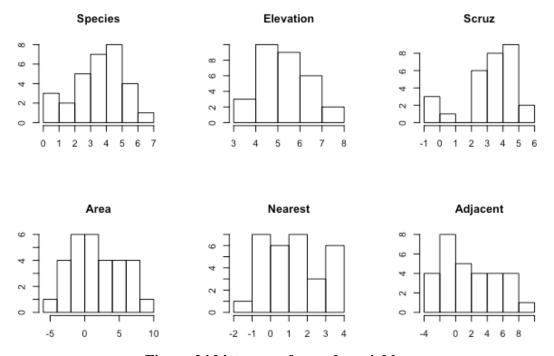


Figure 24 histogram for each variables

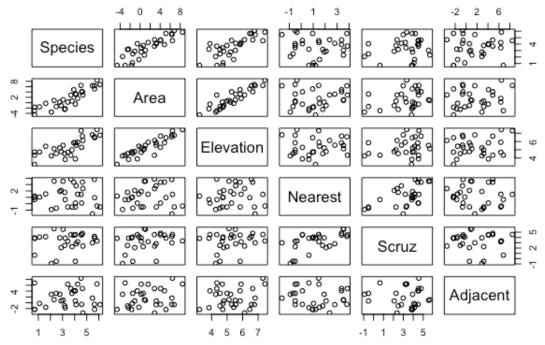


Figure 25: Scatter plot for each variables

For the histograms, we can see the former ones without log show a Poisson distribution. After applying logarithm the distribution shown by the histograms is close to the normal distribution.

And for the pairs, in the first diagram most of the data stack together, which make it difficult to observe and give a conclusion. But in the second diagram, we can find that the data get much scattered. And we can also find that there are some correlation between Species~Area, Species~Elevation, Area~Elevation.

In general we can get a normal distribution, have a clearer view to the data and can find some relationship between the data.

Task 6

According to the instruction, the code and output are shown in Fig.26 and Fig.27.

```
> modlog=lm(log(species)~log(Area)+log(Elevation)+log(Nearest)+log(Scruz+1)+log(Adjacent),data=galadata)
 modlog1=step(modlog)
Start: AIC=-9.33
log(Species) ~ log(Area) + log(Elevation) + log(Nearest) + log(Scruz +
    1) + log(Adjacent)
                  Df Sum of Sq RSS AIC
1 0.1360 14.872 -11.0521
- log(Nearest)
 log(Adjacent)
                         0.1913 14.927 -10.9407
- log(Scruz + 1) 1
- log(Elevation) 1
                         0.6238 15.360 -10.0839
                         0.8992 15.635
                                         -9.5506
                       16.0642 30.800 10.7895
- log(Area)
Step: AIC=-11.05
log(Species) ~ log(Area) + log(Elevation) + log(Scruz + 1) + log(Adjacent)
                  Df Sum of Sq RSS AIC
1 0.1547 15.026 -12.7416
- log(Adjacent)
- log(Elevation) 1
                         0.9713 15.843 -11.1541
<none>
                                 14.872 -11.0521
- log(Scruz + 1)
                         1.5889 16.461 -10.0069
- log(Area)
                        16.3631 31.235
Step: AIC=-12.74
log(Species) ~ log(Area) + log(Elevation) + log(Scruz + 1)
                  Df Sum of Sq
- log(Elevation) 1
                         0.9848 16.011 -12.8373
                                 15.026 -12.7416
<none>
                        1.5722 16.599 -11.7563
16.2288 31.255 7.2297
 log(Scruz + 1) 1
- log(Area)
```

Figure 26: Code and output 1

Figure 27: Code and output 2 (continue)

From the AIC-criterion method, we know that there are finally 2 explanatory values, namely log(Scruz+1) and log(Area). We then summary the new modlog1, the code and output are shown in Fig.28.

```
> summary(modlog1)
lm(formula = log(Species) ~ log(Area) + log(Scruz + 1), data = galadata)
Residuals:
    Min
                   Median
              10
                                30
                                        Max
-1.42781 -0.46073 0.03252 0.43723 1.56320
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
              3.32961 0.33602
                                    9.909 1.73e-10 ***
(Intercept)
                                    9.620 3.24e-10 ***
log(Area)
               0.39721
                          0.04129
                          0.09394 -1.427
log(Scruz + 1) -0.13403
                                             0.165
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '1
Residual standard error: 0.7701 on 27 degrees of freedom
Multiple R-squared: 0.7741,
                              Adjusted R-squared: 0.7574
```

Figure 28: Summary for the model based on AIC-criterion

F-statistic: 46.27 on 2 and 27 DF, p-value: 1.893e-09

From the output we could know that the p-value of log(Scruz+1) is 0.165 larger than 0.05 and log(Area) is much smaller than 0.05. Hence, we know that only the log(Area) is significant.

Task 7

In task 5 we found the log(galadata) is from a normal distribution and some collinearities between log(Species) and log(Area). But we cannot find any collinearities between the variables without logarithm. Also we know the variable Species is follow a Poisson distribution, so it's reasonable to use logarithm to model a linear function between log(Species) and log(Area).

Task 8

From Task 6 we could get the result of modlog1. We first plot Cook's distance. The code and result are shown in Fig.29 and Fig.30.

```
> round(cooks.distance(modlog1), 2)
     Baltra
                            Caldwell
              Bartolome
                                         Champion
                                                      Coamano Daphne.Major
       0.03
                    0.01
                                0.06
                                             0.10
                                                         0.19
                                                                      0.00
                                          Enderby
                                                     Espanola
Daphne.Minor
                  Darwin
                                Eden
                                                                Fernandina
       0.08
                    0.03
                                0.01
                                             0.10
                                                         0.00
                                                                      0.05
   Gardner1
                Gardner2
                           Genovesa
                                          Isabela
                                                     Marchena
                                                                    ons low
       0.12
                    0.04
                                0.00
                                            0.02
                                                         0.03
                                                                      0.01
                  Pinzon Las.Plazas
                                          Rabida SanCristobal SanSalvador
      Pinta
                                            0.01
                   0.01
                                0.01
       0.01
                                                         0.01
                                                                      0.00
                 SantaFe
                          SantaMaria
                                                                      Wo1f
                                          Seymour
  SantaCruz
                                                      Tortuga
       0.00
                   0.00
                                0.03
                                             0.01
                                                         0.00
                                                                      0.00
> plot(cooks.distance(modlog1))
```

Figure 29: Code and output for Cook's distance of modlog1

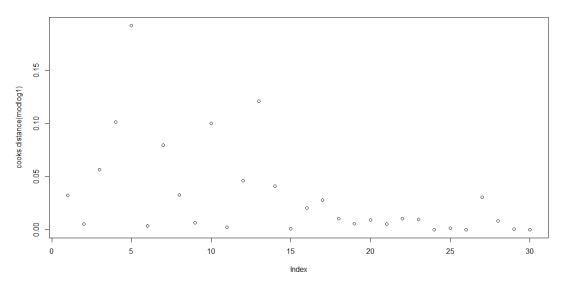


Figure 30: Output for Cook's distance

From the output we could know that all values of cook distance are smaller than 1, there is no influence point in this model.

We then draw the Q-Q plot of residuals and a plot of residuals versus fitted values via the following code as shown in Fig.31.

```
qqnorm(residuals(modlog1))
plot(residuals(modlog1), fitted(modlog1))
```

Figure 31: Code for the rest of task 8

The outputs are shown in Fig.32 and Fig.33 respectively.

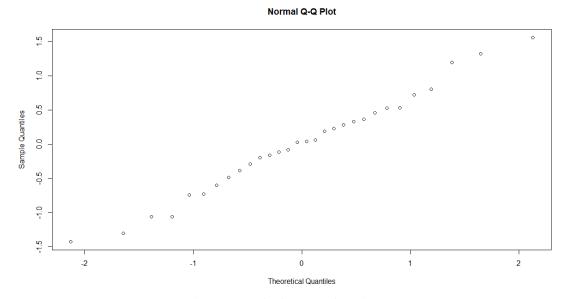


Figure 32: Q-Q plot of residuals

As the Q-Q plot shown, the distribution of residuals is normal distribution.

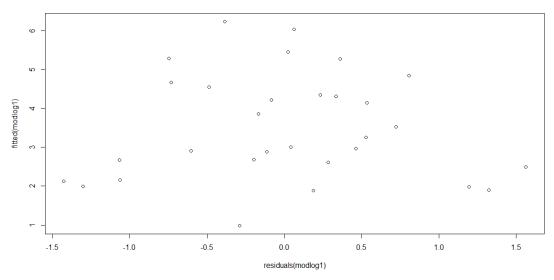


Figure 33: Q-Q plot of fitted values

From the plot of residuals versus fitted values, we can see there is scattered and no obvious structure, so there is no significant relation between the residuals and fitted values.

Task 9

After using the given codes to add columns to the gala_data, we use pairs to make a plot as figure 34.

> pairs(gala_data)

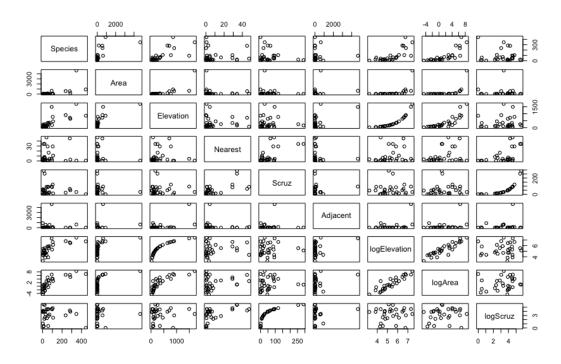


Figure 34 Scatter plot for each variables

From the diagram we can see that there might have possible collinearities between "logElevation" and "logArea".

To check whether it is useful to include interactions between "logArea" and "logElevation", we check the linear correlations between these two variables, the result is shown as figure 35

<pre>> round(cor(galadata[,7:8]),2)</pre>					
	logElevation	logArea			
logElevation	1.0	0.9			
logArea	0.9	1.0			

Figure 35 round for galadata

We can find that both of variables have a 0.9 correlations coefficients to the other in this pair. So it's not useful to include interactions between "logElevation" and "logArea".

Task 10

In task 3 we have compared two models and the model using sqrt(Species) is better than the model using Species.

For modlog1, there is scattered and no obvious structure, which means there's no significant relation between residuals and fitted values. Therefore, we also discard this model.

And for modlog2, it contains two variables "logElevation" and "logArea" which have collinearities. Since it's not useful to fit them in the same model, modlog2 is not the best choice.

To conclude, we prefer the model using sqrt(Species). Because it contains less variables and most of the variables in the model are relevant and easy to observe.