1) Use a Linear model to predict the log of the abundance.

Model coefficients

```python
lm(formula = log(Abundance) ~ Start.Year + Net + Visual + Pan +
    Species + Genus + Morphospecies + Family + No..of.Years +
    No..of.Sites..Avg. + Sample.Trips.Year..Avg. + Sampling.Time.min,
    data = LI.corpus)
```

```
Coefficients: (1 not defined because of singularities)
                          Estimate Std. Error t value Pr(>|t|)
(Intercept)              4.627e+01  8.850e+01   0.523  0.60257
Start.Year              -1.956e-02  4.387e-02  -0.446  0.65696
Net                     -3.970e-01  4.254e-01  -0.933  0.35350
Visual                   2.933e-01  4.559e-01   0.643  0.52188
Pan                      3.656e-01  5.026e-01   0.728  0.46906
Species                 -2.013e-01  9.193e-01  -0.219  0.82728
Genus                   -5.707e-01  9.176e-01  -0.622  0.53582
Morphospecies           -9.420e-02  9.324e-01  -0.101  0.91978
Family                         NA         NA      NA       NA
No..of.Years             2.831e-01  9.761e-02   2.900  0.00484 **
No..of.Sites..Avg.       1.683e-03  8.684e-04   1.938  0.05619 .
Sample.Trips.Year..Avg.  5.634e-02  5.980e-02   0.942  0.34906
Sampling.Time.min        1.500e-05  4.001e-05   0.375  0.70877
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
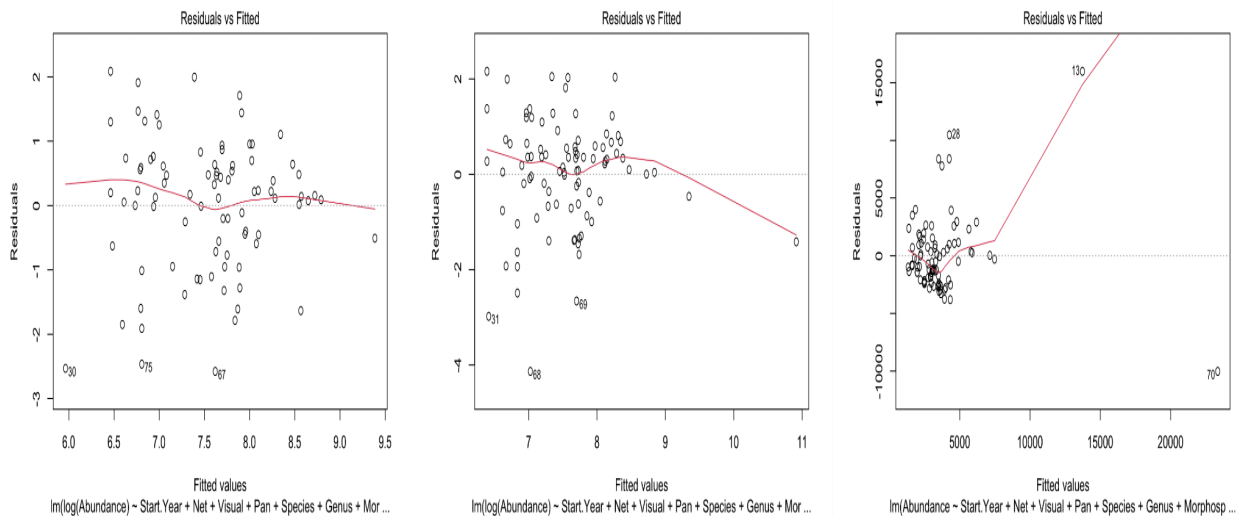
Model provided earlier had 4 significant variables

	lm(Abundance ~ IV)	lm(log(Abundance) ~ IV)	lm(log(Abundance) ~IV) without outliers
Multiple R-squared	0.3907	0.2611	0.2902
Adjusted R-squared	0.3048	0.1569	0.1861
p-value	2.654e-05	0.009383	0.004302

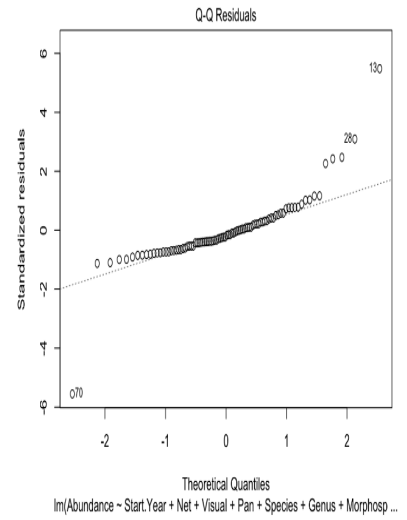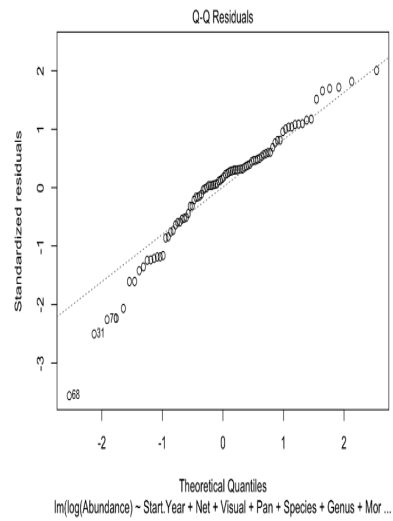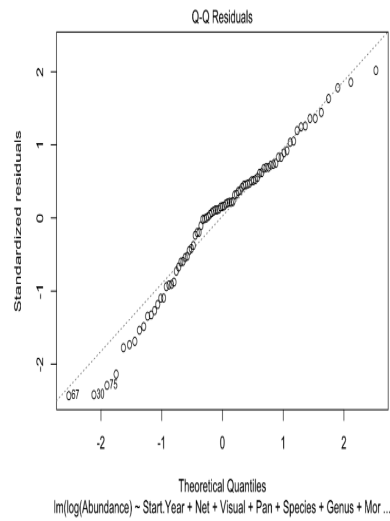IV = Independent Variables

Residual Diagnostics

First image, removing outliers from lm(log(Abundance)), second is lm(log(Abundance)) and the last is lm(Abundance).

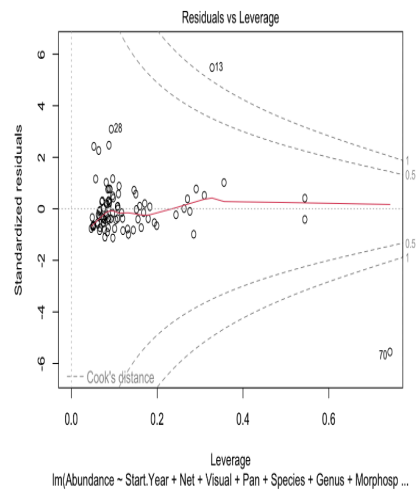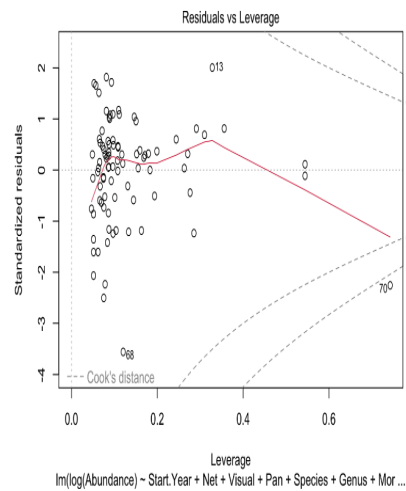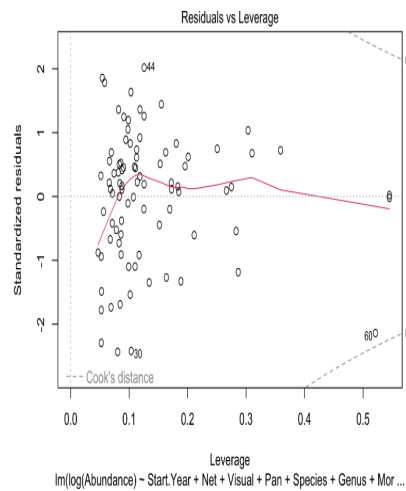1. Residual vs Fitted Plot

2. Q-Q plot

Q-Q Residuals (three panels)

lm(log(Abundance) ~ Start.Year + Net + Visual + Pan + Species + Genus + Mor ...
lm(log(Abundance) ~ Start.Year + Net + Visual + Pan + Species + Genus + Mor ...
lm(Abundance ~ Start.Year + Net + Visual + Pan + Species + Genus + Morphosp ...

3.   Residuals vs Leverage - helps to identify influential points

Residuals vs Leverage (three panels)

lm(log(Abundance) ~ Start.Year + Net + Visual + Pan + Species + Genus + Mor ...
lm(log(Abundance) ~ Start.Year + Net + Visual + Pan + Species + Genus + Mor ...
lm(Abundance ~ Start.Year + Net + Visual + Pan + Species + Genus + Morphosp ...

2) Use an exponential model to predict Richness from abundance

```python
exp.Rch<-nls(Richness~mx*(1-(exp(-rc*Abundance))),data=LI.corpus,start=list(mx=
75,rc=0.0002))
```

3) Adjust Richness up and down off the Abundance Richness curve based on the linear model coefficients on the residuals.

```python
resid.Rch<-lm(r.Rch~Net+Visual+Pan+Species+Genus+Morphospecies+No..of.Years+No.
.of.Sites..Avg.+Sample.Trips.Year..Avg.+Sampling.Time.min,data=LI.corpus)
```

Adjusted_richness = predicted_richness (from Step 2) +- predicted_residuals (from Step 3)

We can give them a range, where predicted_richness will be the mean value and residual_sd <- sqrt(mean(resid(resid.Rch)^2))

richness_lower <- predicted_richness_base + predicted_residuals - 1.96 * residual_sd
richness_upper <- predicted_richness_base + predicted_residuals + 1.96 * residual_sd