

Tiger Prey Equation

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The `lmtest` and `sandwich` package is used for testing heteroskedasticity in the equation and transform variables to remove heteroskedasticity

```
library(lmtest)
library(sandwich)
library(dplyr)
```

Load the data and check

```
density_dat <-read.csv("D:/Papers/tiger density India/Submission/Tiger_preay_density_data.csv",header=TR
```

`log_chital_biomass..chital_biomass_prop`, `log_sambar_biomass..sambar_biomass_prop` these stands for individual species density*proportion of species biomass where,

$$sp_1biomassproportion = sp_1density.sp_1wt/sp_1density.sp_1wt + sp_2density.sp_2wt + \dots + sp_ndensity.sp_nwt$$

Data preparation

We calculated individual *species biomass* columns using the log-transformation. We substituted the NA values with 0 as $\log(0)$ would give the output of NA.

Later, we multiplied the *log_species_biomass* column with the *species_biomass_prop* to derive the final columns to be used in the regression equation.

```
density_dat <-density_dat |>
  mutate(log_chital_bio = ifelse(!is.finite(log10(chital_biomass)),0, log10(chital_biomass)),
         log_sambar_bio = ifelse(!is.finite(log10(sambar_biomass)),0, log10(sambar_biomass)),
         log_langur_bio = ifelse(!is.finite(log10(langur_biomass)),0, log10(langur_biomass)),
         log_barkingdeer_bio = ifelse(!is.finite(log10(barking_deer_biomass)),0, log10(barking_deer_biomass)),
         log_wildpig_bio = ifelse(!is.finite(log10(wild_pig_biomass)),0, log10(wild_pig_biomass)),
         log_nilgai_bio = ifelse(!is.finite(log10(nilgai_biomass)),0, log10(nilgai_biomass)),
         log_gaur_bio = ifelse(!is.finite(log10(gaur_biomass)),0, log10(gaur_biomass)))|>
  mutate(chital_bio_prop = log_chital_bio*chital_biomass_prop,
         sambar_bio_prop = log_sambar_bio*sambar_biomass_prop,
         langur_bio_prop = log_langur_bio*langur_biomass_prop,
         gaur_bio_prop = log_gaur_bio*gaur_biomass_prop,
         nilgai_bio_prop = log_nilgai_bio*nilgai_biomass_prop,
         wildpig_bio_prop = log_wildpig_bio*wild_pig_biomass_prop,
         barkingdeer_bio_prop = log_barkingdeer_bio*barking_deer_biomass_prop)

head(density_dat)
```

##	Site	tiger_density	log.tiger_density.	chital_biomass	sambar_biomass
## 1	Rajaji	2.90	0.4623980	480.6	2412
## 2	Corbett	11.00	1.0413927	1931.4	1818
## 3	Ramnagar	9.71	0.9872192	1152.9	956
## 4	Pilibhit	2.60	0.4149733	1173.9	0
## 5	Valmiki	1.49	0.1731863	119.4	310
## 6		1.65	0.2174839	567.6	2772
##	langur_biomass	barking_deer_biomass	wild_pig_biomass	nilgai_biomass	
## 1	33.85	0.00	0.0	0.00	
## 2	115.90	42.84	522.0	613.47	
## 3	39.50	30.52	0.0	0.00	
## 4	0.00	0.00	0.0	1921.53	
## 5	0.00	15.96	168.0	748.67	
## 6	0.00	0.00	476.4	2619.50	
##	gaur_biomass	chital_biomass_prop	sambar_biomass_prop	langur_biomass_prop	
## 1	0	0.16422628	0.8242068	0.01156692	
## 2	0	0.38294000	0.3604561	0.02297957	
## 3	0	0.52911534	0.4387495	0.01812825	
## 4	0	0.37923649	0.0000000	0.00000000	
## 5	0	0.08766327	0.2276014	0.00000000	
## 6	0	0.08819828	0.4307358	0.00000000	
##	barking_deer_biomass_prop	wild_pig_biomass_prop	nilgai_biomass_prop		
## 1	0.00000000	0.00000000	0.0000000		
## 2	0.008493916	0.10349730	0.1216331		
## 3	0.014006939	0.00000000	0.0000000		
## 4	0.000000000	0.00000000	0.6207635		
## 5	0.011717804	0.12334530	0.5496722		
## 6	0.000000000	0.07402688	0.4070391		
##	gaur_biomass_prop	log_chital_bio	log_sambar_bio	log_langur_bio	
## 1	0	2.681784	3.382377	1.529559	
## 2	0	3.285872	3.259594	2.064083	
## 3	0	3.061792	2.980458	1.596597	
## 4	0	3.069631	0.000000	0.000000	
## 5	0	2.077004	2.491362	0.000000	
## 6	0	2.754042	3.442793	0.000000	
##	log_barkingdeer_bio	log_wildpig_bio	log_nilgai_bio	log_gaur_bio	
## 1	0.000000	0.000000	0.000000	0	
## 2	1.631849	2.717671	2.787793	0	
## 3	1.484585	0.000000	0.000000	0	
## 4	0.000000	0.000000	3.283647	0	
## 5	1.203033	2.225309	2.874290	0	
## 6	0.000000	2.677972	3.418218	0	
##	chital_bio_prop	sambar_bio_prop	langur_bio_prop	gaur_bio_prop	nilgai_bio_prop
## 1	0.4404194	2.7877784	0.01769228	0	0.000000
## 2	1.2582919	1.1749405	0.04743175	0	0.339088
## 3	1.6200409	1.3076743	0.02894351	0	0.000000
## 4	1.1641161	0.0000000	0.00000000	0	2.038368
## 5	0.1820770	0.5670375	0.00000000	0	1.579917
## 6	0.2429018	1.4829342	0.00000000	0	1.391348
##	wildpig_bio_prop	barkingdeer_bio_prop			
## 1	0.0000000	0.00000000			
## 2	0.2812716	0.01386079			
## 3	0.0000000	0.02079448			
## 4	0.0000000	0.00000000			

```
## 5      0.2744814      0.01409690
## 6      0.1982419      0.00000000
```

Regression

Ordinary linear regression equation for species-wise prey-predator equation

```
aleqt1 <-lm(log.tiger_density. ~ chital_bio_prop + sambar_bio_prop +
            langur_bio_prop + gaur_bio_prop + nilgai_bio_prop +
            wildpig_bio_prop + barkingdeer_bio_prop, data = density_dat)
```

Checking for heteroskedasticity

Conducting Breusch-Pagan test for heteroskedasticity and estimating the heteroskedasticity-consistent covariance matrix. Comparing the standard error of the equation with the robust standard errors reflect which variable has the major issue with variance. There are multiple options for the covariance matrix, this HC4m was recommended by Cribari-Neto & Da Silva 2011.

```
summary(aleqt1)
```

```
##
## Call:
## lm(formula = log.tiger_density. ~ chital_bio_prop + sambar_bio_prop +
##     langur_bio_prop + gaur_bio_prop + nilgai_bio_prop + wildpig_bio_prop +
##     barkingdeer_bio_prop, data = density_dat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.74458 -0.13151  0.01724  0.20239  0.41611
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -1.6133     0.6925  -2.330  0.03419 *
## chital_bio_prop  1.2102     0.3169   3.819  0.00168 **
## sambar_bio_prop  0.6727     0.2320   2.899  0.01102 *
## langur_bio_prop -2.6442     2.3953  -1.104  0.28703
## gaur_bio_prop   0.7411     0.2240   3.309  0.00477 **
## nilgai_bio_prop  0.4068     0.2296   1.772  0.09678 .
## wildpig_bio_prop 1.0853     0.5538   1.960  0.06889 .
## barkingdeer_bio_prop -9.5009     5.3835  -1.765  0.09794 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.343 on 15 degrees of freedom
## Multiple R-squared:  0.6291, Adjusted R-squared:  0.456
## F-statistic: 3.635 on 7 and 15 DF,  p-value: 0.01709
```

```
coeftest(aleqt1, vcov = vcovHC(aleqt1, "HC4m"))
```

```
##
## t test of coefficients:
```

```
##
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -1.61334    1.07820  -1.4963  0.15531
## chital_bio_prop    1.21019    0.49851   2.4276  0.02825 *
## sambar_bio_prop    0.67268    0.35920   1.8727  0.08073 .
## langur_bio_prop   -2.64421    2.42735  -1.0893  0.29320
## gaur_bio_prop     0.74107    0.31313   2.3667  0.03183 *
## nilgai_bio_prop    0.40682    0.35019   1.1617  0.26351
## wildpig_bio_prop   1.08526    0.51221   2.1188  0.05121 .
## barkingdeer_bio_prop -9.50086    6.63240  -1.4325  0.17251
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

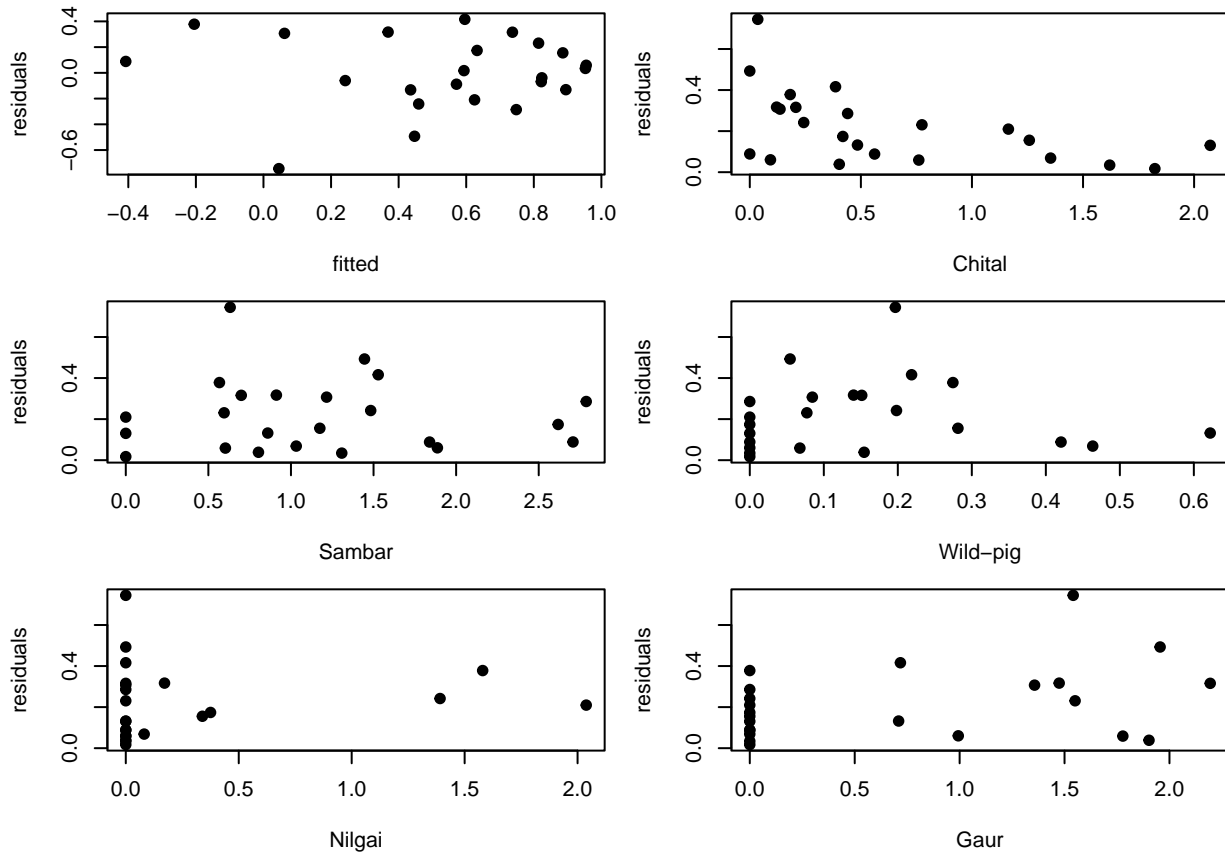
```
bptest(aleqt1)
```

```
##
## studentized Breusch-Pagan test
##
## data:  aleqt1
## BP = 8.5713, df = 7, p-value = 0.2849
```

Plotting

Plotting the residuals vs Fitted and the modulus of the residuals for each of the explanatory variable. We detected a decrease in the residuals of the chital variable as the value increases. This was supposed to be a source of heteroskedascity and we did transformation to remove that

```
attach(density_dat)
par(mfrow=c(3,2))
par(mar=c(4,4,1,1))
plot(aleqt1$fitted.values, aleqt1$residuals, xlab="fitted", ylab="residuals", pch=19)
plot(chital_bio_prop, abs(aleqt1$residuals), xlab="Chital", ylab="residuals", pch=19)
plot(sambar_bio_prop, abs(aleqt1$residuals), xlab="Sambar", ylab="residuals", pch=19)
plot(wildpig_bio_prop, abs(aleqt1$residuals), xlab="Wild-pig", ylab="residuals", pch=19)
plot(nilgai_bio_prop, abs(aleqt1$residuals), xlab="Nilgai", ylab="residuals", pch=19)
plot(gaur_bio_prop, abs(aleqt1$residuals), xlab="Gaur", ylab="residuals", pch=19)
```



Transformation

We did one transformation for converting the heteroskedastic model into a homoskedastic one

$$\sigma_i^2 = \sigma^2 / ((x_i + 1))$$

We multiplied the previous equation with

$$\sqrt{(x_i + 1)}$$

for the transformation

First transformation

We used a square-root transformation first to remove the heteroskedasticity from the variables.

```
x1 <-sqrt(chital_bio_prop+1)
y1 <-log.tiger_density.*x1
x2 <- chital_bio_prop*x1
x3 <- sambar_bio_prop*x1
x4 <- wildpig_bio_prop*x1
x5 <- nilgai_bio_prop*x1
x6 <- gaur_bio_prop*x1
x7 <- langur_bio_prop*x1
x8 <- barkingdeer_bio_prop*x1
```

New linear regression equation with the transformed variable

```
new_eqn <-lm (y11 ~x1 +x2+x3+x4+x5+x6-1)
summary(new_eqn)

##
## Call:
## lm(formula = y11 ~ x1 + x2 + x3 + x4 + x5 + x6 - 1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.78452 -0.16000 -0.02785  0.25200  0.69635
##
## Coefficients:
##      Estimate Std. Error t value Pr(>|t|)
## x1  -1.5491     0.5809  -2.667 0.016267 *
## x2   1.1419     0.2686   4.251 0.000539 ***
## x3   0.5664     0.1825   3.104 0.006449 **
## x4   0.7413     0.4255   1.742 0.099509 .
## x5   0.4035     0.1900   2.124 0.048637 *
## x6   0.6981     0.1992   3.504 0.002721 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3954 on 17 degrees of freedom
## Multiple R-squared:  0.8677, Adjusted R-squared:  0.821
## F-statistic: 18.58 on 6 and 17 DF,  p-value: 1.325e-06
```

```
bptest(new_eqn)
```

```
##
## studentized Breusch-Pagan test
##
## data:  new_eqn
## BP = 4.5292, df = 5, p-value = 0.476
```

Plotting

The residual vs fitted plot and the species wise residuals looks like the following. Here the residuals have significantly less heteroskedasticity compared to the the earlier equation.

```
par(mfrow=c(3,2))
par(mar=c(4,4,1,1))
plot(new_eqn$fitted.values, new_eqn$residuals, xlab="fitted", ylab="residuals", pch=19)
plot(x2, abs(new_eqn$residuals), xlab="Chital", ylab="residuals", pch=19)
plot(x3, abs(new_eqn$residuals), xlab="Sambar", ylab="residuals", pch=19)
plot(x4, abs(new_eqn$residuals), xlab="Wild-pig", ylab="residuals", pch=19)
plot(x5, abs(new_eqn$residuals), xlab="Nilgai", ylab="residuals", pch=19)
plot(x6, abs(new_eqn$residuals), xlab="Gaur", ylab="residuals", pch=19)
```

