

• 5.3 [15 pts]

- First, define the following indicator variables,  
 $AI = 1$  if in “aerial insectivore” group,  $ai = 0$  otherwise  
 $G = 1$  if in “gleaner” group,  $g = 0$  otherwise  
then the ultimate full model is

$$\mu_{audnuc} = \alpha + \beta_1 bodywt + \delta_1 AI + \delta_2 G + \gamma_1 AI * bodywt + \gamma_2 G * bodywt$$

- The three submodels are then

Group	AI	G	Submodel ( $\mu_{audnuc} =$ )
phytophagous	0	0	$= \alpha + \beta_1 bodywt$
aerial insectivore	1	0	$= (\alpha + \delta_1) + (\beta_1 + \gamma_1) bodywt$
gleaner	0	1	$= (\alpha + \delta_2) + (\beta_1 + \gamma_2) bodywt$

- The data appear to be independent as each individual is a separate species and no species is simultaneously grouped into two diet categories. There is some evidence for a slight non-linearity with the groups (**Figure B.16**). The non-constant variance test ( $p=0.0001$ ) and the residual plot (**Figure B.16**) suggest a heteroscedasticity. The residuals do not appear to be normal (Anderson Darling  $p<0.00005$ ) and are right-skewed (**Figure B.17**). I did not test for outliers given the violations of the normality and homoscedasticity assumptions.

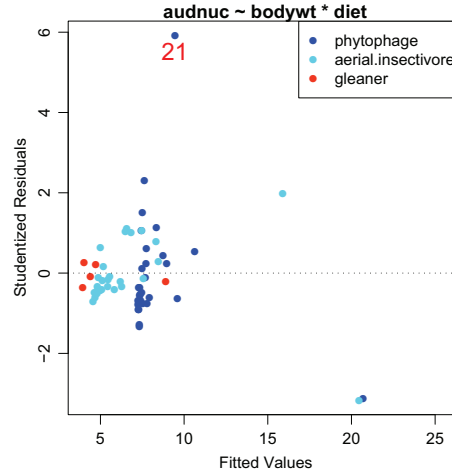


Figure B.16: Residual plot for the linear regression of auditory nuclei mass on bat body weight for three different diet groups.

Trial-and-error methods were used to determine that the auditory nuclei mass variable should be transformed with the natural logarithm. In addition, although the maximum to minimum ratio does not warrant it and none of the major regression assumptions are violated without it, the model appears to have no influential observations if the body weight variable was also transformed with natural logarithms. With both variables transformed to the natural log scale the models appeared linear within the groups (**Figure B.18**), the residuals were homoscedastic (non-constant variance

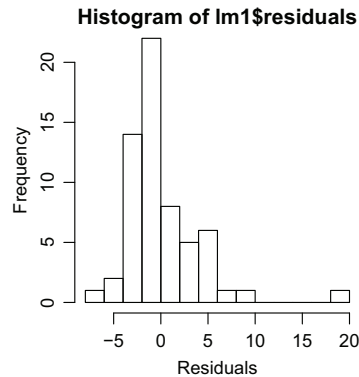


Figure B.17: Histogram of residuals from the linear regression of auditory nuclei mass on bat body weight for three different diet groups.

$p=0.1959$  ; **Figure B.18**) and normal (Anderson Darling  $p=0.0818$ ; **Figure B.19**), and there were not outlier individuals (outlier test  $p=0.7696$ ). Thus, the assumptions were adequately met on the log-log scale and all further analyses will be conducted on this scale.

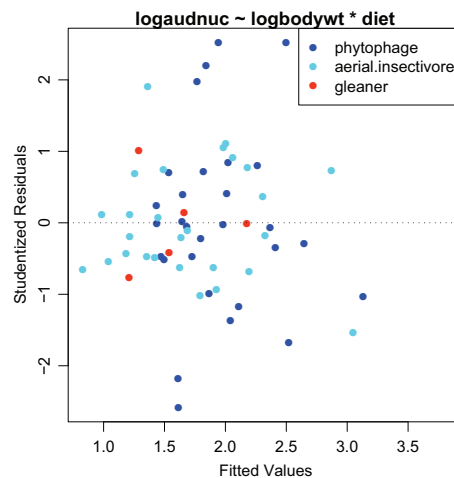


Figure B.18: Residual plot for the linear regression of log-transformed auditory nuclei mass on log-transformed bat body weight for three different diet groups.

4. The slopes between log auditory nuclei mass and log body weight are statistical similar among the three diet groups ( $p=0.1308$  ; **Table B.24**); thus, the lines describing the relationship between these two variables are parallel.
5. The intercepts (assuming parallel lines) for the lines describing the relationship between log auditory nuclei mass and log body weight are statistical similar among the three diet groups ( $p=0.1586$  ; **Table B.24**); thus, the lines all have the same intercept.
6. The results of the previous analysis show that the relationship between log auditory nuclei mass and log body weight can be modeled by the same line for each of the three different diet groups (**Figure B.20**). In other words, there is no difference in the relationship between log auditory nuclei mass and log body weight among the three diet groups. In addition, at any given log body weight there is no difference in log auditory nuclei mass among the three groups.

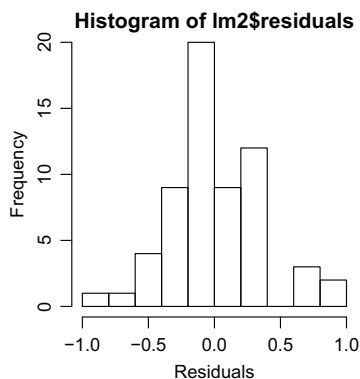


Figure B.19: Histogram of residuals from the linear regression of log-transformed auditory nuclei mass on log-transformed bat body weight for three different diet groups.

Table B.24: ANOVA table for linear regression results of log-transformed auditory nuclei mass on log-transformed bat's body weight for three different diet groups.

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
logbodywt	1	13.2492	13.2492	102.4449	3.614e-14
diet	2	0.4927	0.2463	1.9047	0.1586
logbodywt:diet	2	0.5462	0.2731	2.1116	0.1308
Residuals	55	7.1131	0.1293		
Total	60	21.4012			

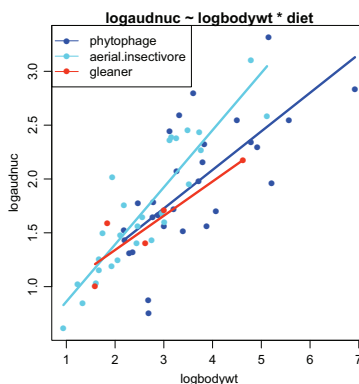


Figure B.20: Fitted line plot from the linear regression of log-transformed auditory nuclei mass on log-transformed bat body weight for three different diet groups. Note that there is no statistical difference in the lines among the three groups.

#### R Command

```
> b <- read.table("batmorph2.txt", head = TRUE)
> b <- Subset(b, diet != "vampire")
> b$diet <- relevel(b$diet, "phytophage")
> attach(b)
> lm1 <- lm(audnuc ~ bodywt * diet)
> ncv.test(lm1)
> ad.test(lm1$residuals)
```

```
> residual.plot(lm1)
> hist(lm1$residuals, xlab = "Residuals", breaks = 10)
> trans.chooser(lm1)
> detach(b)
> b$logaudnuc <- log(b$audnuc)
> b$logbodywt <- log(b$bodywt)
> attach(b)
> lm2 <- lm(logaudnuc ~ logbodywt * diet)
> ncv.test(lm2)
> ad.test(lm2$residuals)
> outlier.test(lm2)
> residual.plot(lm2)
> hist(lm2$residuals, xlab = "Residuals", breaks = 10)
> anova(lm2)
> comp.slopes(lm2)
> fit.plot(lm2)
> detach(b)
```