Assignment 1

An Intense Course in Data Analysis Using MultiLevel Regression Models Peking University Summer School, 2010

Read the sleep data into a dataframe called sleep, and do the following to get a sense of the data.

- 1. Print out the first 10 rows of the data, using either the function head or subscripting the data frame, and then print out every fifth row, using the seq function. (Looking at some of the data can help identify errors in reading in the data or the original data file.)
- 2. Count the number of NAs (missing values) in each variable.
 - (a) Look at the help for the command is .na by typing ?is.na.
 - (b) A dataframe is both a list and a matrix. To compute a function on each column of the dataframe, use the function sapply.
- 3. We've worked with the predictors sleep, body and danger in class. Describe the other possible predictors (brain, life, gestation and predation) using plots and words less than a page of words.
- 4. Fit a linear regression model for sleep with one of the above as a predictor, and describe the fit of the model compared to the one based on log body weight. Explain why you chose that predictor.
- 5. Fit a linear regression to that predictor, log(body) and danger.
 - (a) What do you think about that model?
 - (b) Now read the data file into R again, but this time keep all the rows, even those for which the outcome is NA. Using your linear regression model, get the fitted value for each species with NA as its outcome.
 - (c) Plot the fitted values against each of the predictors for your model. Using panel.points, add the fitted values for the species with NA for their outcomes to the plot using a different color. Would you be happy using those predictions?
 - (d) Repeat the previous plot, but use observed values for the species in the data instead of the fitted values (and still use the fitted values for the species with missing outcomes). How do the predictions for the species with missing values compare to the observed outcomes for the other species?