Intro to R for Epidemiologists

Lab 13 (4/16/15)

Part 0. Course evaluations

Please complete the evaluations for this course before preceding to the next section. Evaluations can be found at http://www.sph.emory.edu/rollins-life/evaluation/index.html

Part 1. Function to compute skewness

Skewness is a measure of asymmetry of a probability distribution. We have written the function below to compute skewness, which is defined by the following mathematical equation:

$$\frac{\frac{1}{n}(\sum_{i=1}^{n}(x_i - \bar{x})^3)}{sd(x)^3}$$

```
skewness <- function(x) {
    n <- length(x)
    sd1 <- sd(x)
    m <- mean(x)
    third.moment <- (1/n) * sum((x - m)^3)
    skew <- third.moment/(sd1^3)

    return(skew)
}
```

Modify the above function so that if the skewness is greater than 1 or less than -1, it prints a warning message that says, "Caution: Skewed data!" Use your new function to obtain the skewness of Petal length and Petal width by species in the Iris dataset as below.

```
## Source: local data frame [3 x 3]
##
##      Species Petal.Length Petal.Width
## 1     setosa       0.1001     1.17963
## 2 versicolor      -0.5706    -0.02933
## 3  virginica       0.5169    -0.12181
```

Part 2. Debugging

The function posted on the website in `debugging.R` contains some errors. Copy the function into your R script and use debugging commands (e.g. `traceback()`, `debug(myfun)`, `browser()`) to find and fix the errors.

Part 3. Plotting

Use the error-free function `glmOR` from the Debugging section above and the `gfun` from class to create new nested function that takes only the arguments of the full dataset (e.g. `diabetes`), variables (e.g. `c("hdl", "chol")`), and outcome (e.g. `diab1`) and plots the corresponding univariate and multivariate odds ratios

as shown below. Hint: you do not need to rewrite the `glmOR` function above, but only need to call it from within your new plotting function.