Lab 10: Multiple Regression

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In this lab, we are going to extend linear regression to cases where we have multiple independent variables. In multiple regression we have to deal with some familiar concepts, such as normally distributed errors, and a few new concepts, including multicollinearity and model comparison.

The learning goals of the lab are to:

- Gain an improved understanding of the assumptions of regression
- Learn to implement multiple regression in R
- Understand how to interpret the output from multiple linear regression
- Learn to make predictions from regression models.

At the end of the lab, there are a few problems to answer. *Submit your answers in R Markdown to the class Sakai site under the Assignments folder before 11:55 pm on either Mon., Nov. 5 (Section 03) or Wed., Nov., 7 (Sections 01 and 02).*

More functions in R

- `update()` - updates and refits an existing model so that you do not have to rewrite the entire model each time
- `stepAIC()` - performs stepwise model selection using AIC (Akaike Information Criterion), using either forward or backward selection procedures
- `curve()` - draws a curve corresponding to a function over a defined interval or using a variable, x
- `vif()` - function from the `HH` or `car` packages that calculates the variance inflation factor for each of the regression coefficients for the inputted model
- `I()` – changes the class of an object to indicate that it should be treated "as is"; most often used to allow terms in models to include mathematical symbols
- `na.omit()` - when applied to a dataframe, returns the dataframe excluding all missing value by removing any rows with NA's

Table 1: Table depicting syntax for defining models in R.

Syntax	Models	Comments
$Y \sim A$	$Y = \beta_0 + \beta_1$A	Straight line with an implicit y-intercept
$Y \sim -1 + A$	$Y = \beta_1 A$	Straight line with no y-intercept; that is a fit forced through (0,0)
$Y \sim A + I(A\hat{}2)$	$Y = \beta_0 + \beta_1 A + \beta_2 A^2$	Polynomial model; note that the identity function I() allows terms in the model to include normal mathematical symbols
$Y \sim A : B$	$Y = \beta_0 + \beta_1 AB$	A model containing only first-order interactions between A and B
$Y \sim A * B$	$Y = \beta_0 + \beta_1 A + \beta_2 B + \beta_3 AB$	A full first-order model with an interaction term; an equivalent code is $Y \sim A + B + A : B$
$Y \sim (A + B + C)\hat{}2$	$Y = \beta_0 + \beta_1 A + \beta_2 B + \beta_3 C + \beta_4 AB + \beta_5 AC + \beta_6 BC$	A model including all first-order effects and interactions up to the n^{th} order, where n is given by $()\hat{}n$. An equivalent code in this case is $Y \sim A * B * C - A : B : C$

Strategy for Data Analysis

Here is a general strategy for data analysis with multiple regression that extends to other types of multivariate models, such as generalized linear models.

1. *Define your research question.* Write down your question(s) of interest. Why are you analyzing the data? What hypotheses are you testing?
    - Explore the data. Summarize the data and use graphical tools such as histograms, boxplots, and pairwise plots to evaluate the distributions of the variables and the initial relationships between variables.
2. *Assess normality of variables.* Transform variables that are not normally distributed (square-root, log, or inverse transformations, or create dummy variables). It is most common to transform the dependent variable to be normally distributed. The goal in transforming independent variables is not to make them prettier and more symmetrical, but to make the relationship between the dependent and independent variable linear.
    - Assess the relationship of each independent variable with the dependent variable. Are the two variables linearly related? Do you need to consider other relationships between them?
    - Assess the relationship of the independent variables with each other. Are they too highly correlated? Are some variables redundant or better combined?
3. *Fit a tentative mode.* Fit a first model. Plot the residual plots, q-q plots, and leverage plots to check for outliers, non-constant variance, and problems with model fit.
4. *Refine the model.* Test whether extra terms in the full model can be dropped. Test and possibly drop interactions and quadratic terms or explore other types of non-linearity. Drop non-significant control variables.
    - Use stepwise methods to reduce model. Do not just let R choose the best model for you! It is preferable to use the `update()` function and to evaluate each model as you remove variables.
5. *Check the final model.* Run the diagnostics on your final model to check for issues that could influence the model: spread of residuals, multicollinearity, outliers and influential points, and missing data.
6. *Infer the answers to the questions of interest.* Calculate confident intervals, prediction intervals, test your hypotheses.
    - Evaluate the relative impact of variables using standardized coefficients.
    - Make conclusions as to the effect of each variable on the dependent variable.

Multiple Linear Regression

For this lab, we are going to examine a couple of datasets from the *Statistical Sleuth*. They are conveniently located in an R package, `Sleuth3`. Download this package and install it in your workspace. We will also need to download either the `HH` or `car` package to use the `vif()` function and install the `pair.fun` function or `ggpairs` for plotting pairwise plots of variables.

Load the first dataset from `Sleuth3`:

```
dat1 <- case0901
```

The data are from a study on variables that influence flower production in seedlings. The design consists of 12 treatment groups: 6 light intensities at two timing levels (0 days and 24 days) prior to photoperiodic flower induction (PFI). PFI is the production of a flowering stimulus in the leaves and its translocation to the

stem apex under certain day lengths. Ten seedlings were randomly assigned to each treatment group. The number of flowers per plant is the primary measure of production, averaging the number of flowers produced by 10 seedlings in each group.

Our questions of interest are:

1. What is the effect of light intensity on flower production?
2. What is the effect of timing on flower production?
3. Does the effect of intensity depend on timing?

Let's look at the data and run an initial model including all the variables and interactions. Note that we are including *Time* as a factor (categorical variable).

To Do

Use histograms and q-q plots to evaluate whether or not the dependent variable should be log-transformed.

Through histograms and q-q plots, it is apparent that the dependent variable, *Flowers*, is not normally distributed. As a start, we log-transform the variable, which makes it look a little better (the q-q plot looks better than the histogram). The variable `Intensity` is also not normally distributed, but we don't expect it to be since each experiment was conducted the same number of times at a few light intensities. Let's build our initial model with the log-transformed dependent variable and decide if we need to do more transformation or use different probability models if the model fit looks bad.

```
lm.flw <- with(dat1, lm(log(Flowers) ~ Intensity + factor(Time) +
                          Intensity:factor(Time)))
```

In the initial model, only light intensity is statistically significant. Because the interaction is not significant, we can drop it and evaluate each of the main effects. We are going to use the `update()` function to run our model, taking out variables one at a time. Look at the `summary()` of each of the models.

```
lm.flw1 <- update(lm.flw,~.-Intensity:factor(Time))
 lm.flw1.sum <- summary(lm.flw1)

lm.flw2 <- update(lm.flw1,~.-factor(Time))
 lm.flw2.sum <- summary(lm.flw2)

lm.flw3 <- update(lm.flw2,~.-Intensity)
 lm.flw3.sum <- summary(lm.flw3)
```

So, what have we learned?

First, the adjusted R^2 did not change much with the removal of the interaction terms (comparison of `lm.flw` and `lm.flw1`). We can safely remove the interaction as it did not contribute much to the model. In `lm.flw1`, both *Time* and *Intensity* are statistically significant main factors. When we remove *Time* in model `lm.flw2`, our adjusted R^2 falls from 0.7668842 to 0.5533525, and the residual standard error increases from 0.1220637 to 0.1689597. There is very good evidence that both *Time* and *Intensity* should be left in the model as main effects. Incidentally, if *Intensity* is also removed from the model (`lm.flw3`) the residual error goes up to 0.2528137; there is no R^2 because there are no variables left in the model to explain variation in flower production.

Let's use the partial F-test to more formally evaluate the best model. This is done with the `anova` function. In this table, the first model is the full model with the interaction. In each of the subsequent models, a single

variable is omitted. Recall that we are testing the H_0 that the reduced model is adequate. Therefore, a significant p-value means that we reject the reduced model (the one in which a variable was removed.) For example, the table shows that omitting the 2-way interaction had no strong effect ($F_{1,21} = 0.6486, p = 0.430$). However, removing *Time* did have a significant effect ($F_{1,22} = 20.798, p = 0.00019$), and we reject the null that the reduced model is better. We need to keep *Time* in the model. The same goes for the subsequent variables.

```
anova(lm.flw, lm.flw1, lm.flw2, lm.flw3)
```

```
## Analysis of Variance Table
##
## Model 1: log(Flowers) ~ Intensity + factor(Time) + Intensity:factor(Time)
## Model 2: log(Flowers) ~ Intensity + factor(Time)
## Model 3: log(Flowers) ~ Intensity
## Model 4: log(Flowers) ~ 1
##   Res.Df     RSS Df Sum of Sq       F    Pr(>F)
## 1     20 0.30306
## 2     21 0.31289 -1  -0.00983  0.6486   0.43009
## 3     22 0.62804 -1  -0.31515 20.7978   0.00019 ***
## 4     23 1.47004 -1  -0.84200 55.5660 3.411e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

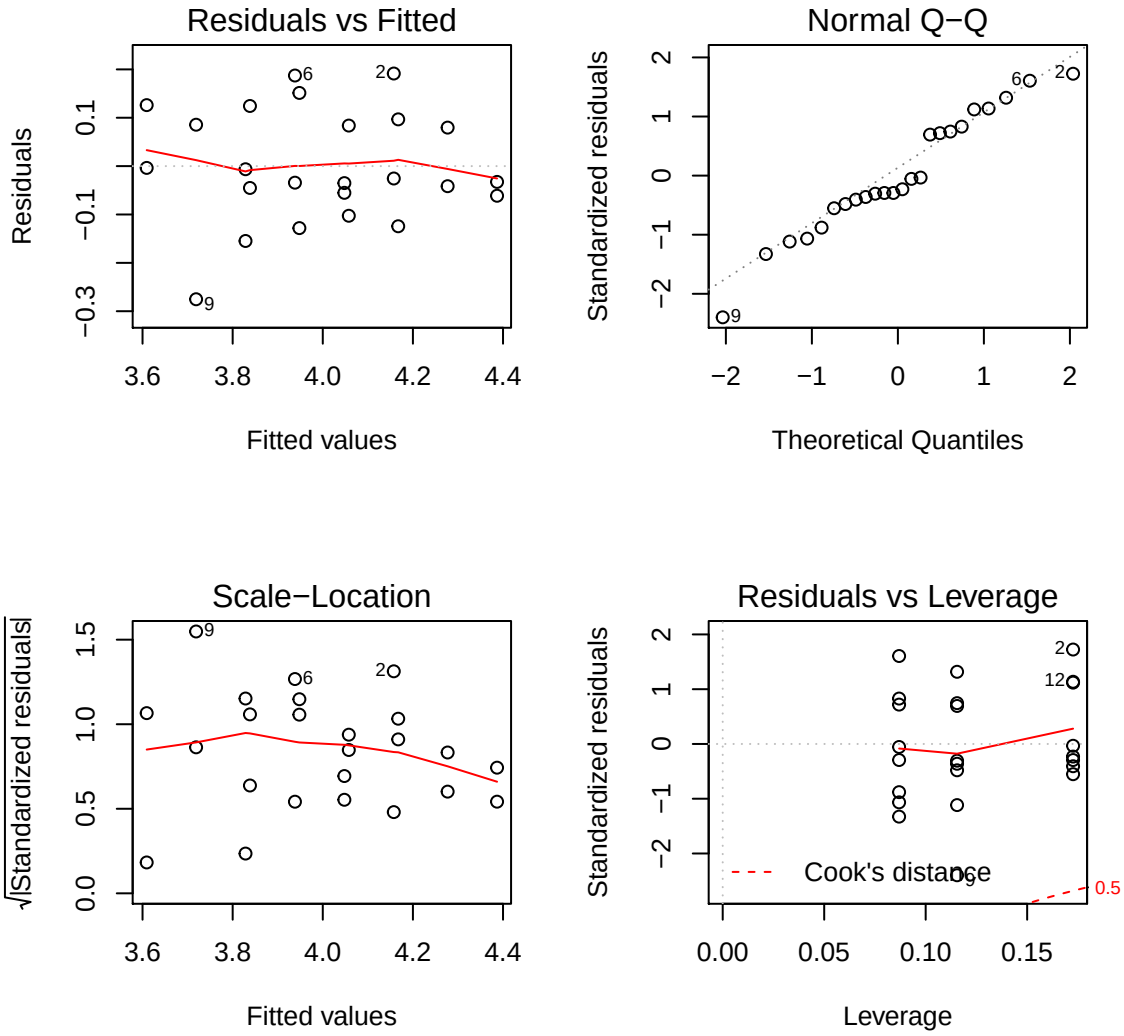
Conversely, we could use the Akaike Information Criterion (AIC) to compare models. With AIC, we choose the model with the lowest AIC. Here model `lm.flw1` has the lowest AIC (-28.05). We will talk more about rules of thumb for AIC in lecture and future labs.

```
AIC(lm.flw, lm.flw1, lm.flw2, lm.flw3)
```

```
##         df        AIC
## lm.flw   5 -26.815844
## lm.flw1  4 -28.049898
## lm.flw2  3 -13.327798
## lm.flw3  2   5.082701
```

We choose `lm.flw1`, which includes both *Intensity* and *Time*, as our best model. Let's take a look at the diagnostic plots to see if there are any problems. Also calculate the variance inflation factor to check for strong correlation between *Time* and *Intensity*.

```
par(mfrow = c(2,2))
 plot(lm.flw1)
```




```
mean(residuals(lm.flw1))
```

```
## [1] -4.336809e-19
```

The mean error (mean of the residuals) is very small or close to 0 as expected.

```
vif(lm.flw1)
```

```
##    Intensity factor(Time)
##            1            1
```

The variance inflation factor (VIF) is an index of how much the variance of an estimated regression coefficient increases because of collinearity. A common rule of thumb is that if $\text{VIF}(\hat{\beta}) > 5$, then multicollinearity is high; others have proposed a cut-off of 10. If the VIF of a predictor variable were 4.3, this can be interpreted as meaning that the variance for the coefficient of that variable is 4.3 times as large as it would be if that predictor were uncorrelated with the other predictor variables.

The residual plots show a nice scattered cloud of points. The q-q plot doesn't look too bad. However, in all the plots, including the q-q plot, observation #9 sticks out as a potential outlier with lower flower production than the rest of the data. Let's redo the analysis, taking that observation out and see if it changes our results.

```
lm.flw4 <- with(dat1[-9,], lm(log(Flowers) ~ Intensity +
                factor(Time)))
lm.flw4.sum <- summary(lm.flw4)
```

Taking out the 9th observation improves the model fit and reduces the error leftover in the model. Even so, it doesn't change our conclusions about the importance of *Time* and *Intensity*. We don't have any reason to think it is an outlier (rather than just an extreme data point); therefore, we will continue using `lm.flw1` with all the data.

Now let's plot the data for each level of *Time*. Below, back-transform the data in the calls to `curve()` to look at the number of flowers produced over different levels of light intensity at the two different PFI times.

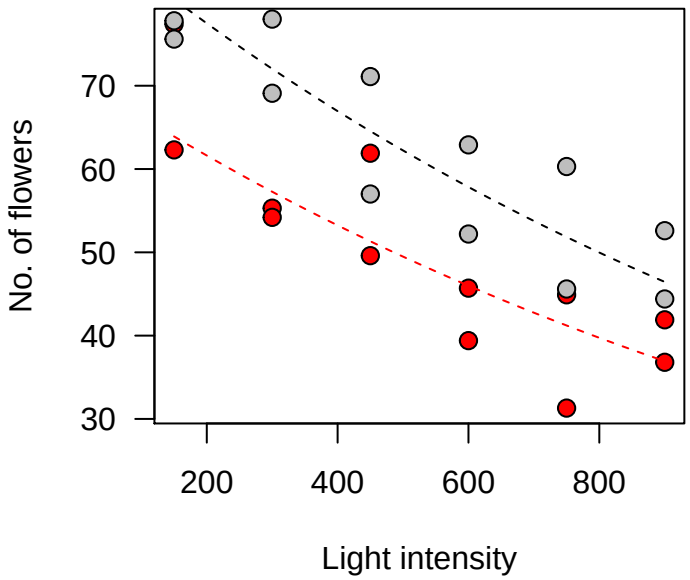
```
with(dat1, plot(Intensity[Time == 1], Flowers[Time==1],
         pch=21, bg="red", ylab="No. of flowers",
         xlab = "Light intensity", las=1, cex=1.2))

with(dat1, points(Intensity[Time == 2], Flowers[Time==2],
         pch=21, bg="grey", cex=1.2))

x <- with(dat1, seq(min(Intensity), max(Intensity), length=30))

coefs <- coefficients(lm.flw1)

curve(exp(coefs[1]+coefs[2]*x+coefs[3]), add=T, lty=2, col = 1)
curve(exp(coefs[1]+coefs[2]*x), add=T, lty=2, col = 2)
```



Because we log-transformed the data, our results are on the geometric scale. The relationship follows the equation:

$$log(Y_i) = \beta_0 + \beta_1 \text{Intensity}_i + \beta_2 \text{Time}_i + \varepsilon_i$$

To make the coefficients easier to manipulate, let's first save the regression coefficients to a variable.

```
coefs <- coefficients(lm.flw1)
```

The intercept, e^{β_0} or `exp(coefs[1])`, is the mean number of flowers at *Time* 0 when *Intensity* is equal to 0. e^{β_1}, `exp(coefs[2])`, is the percent change in number of flowers with a 1-unit change in *Intensity*. Because of the natural range of light intensity, it is more intuitive to think about a 100 unit change in light intensity: `exp(coefs[2]*100) = 0.929`. Therefore, we conclude that a 100-unit increase in light intensity results in 0.929 of the flower production, or a 7.1% decrease in flower production (t = -7.57, df =21, $p < 0.001$). (Note the way the previous sentence was written – this is how you should report statistics, in this class and outside of it.)

We can check the above results by inserting two levels of light intensity, 800 and 700 μ mol/m^2/ sec, and see the outcome:

```
(exp(coefs[1]+coefs[2]*800)-exp(coefs[1]+coefs[2]*700))/
  (exp(coefs[1]+coefs[2]*700))
```

```
## (Intercept)
## -0.07050742
```

The effect of the categorical variable `Time8` is estimated by taking the ratio between the level 24 days and the reference level 0 days: 1.258. There is a $\sim$ 26% increase in flower production by beginning the light treatment 24 days prior to PFI, after taking into account light intensity ($t = 4.599$, df = 21, $p < 0.001$). At the average light intensity, beginning the light treatment 24 days prior to PFI results in 12.5 more flowers per plant compared to beginning at PFI.

```
x1<-mean(dat1$Intensity)
 flwrs24 <- exp(coefs[1]+coefs[2]*x1+coefs[3])
  flwrs0 <- exp(coefs[1]+coefs[2]*x1+coefs[3]*0)
   flwrs24 - flwrs0
```

```
## (Intercept)
##    12.51507
```

Problems

Your assignment is to conduct two different analyses (see descriptions below).

For each regression, write a 1-page description (not including figures and code) of your analysis, results, and inference.

Problem 1

In this problem, analyze the `TreePlots` data on Sakai. The database contains information on approximately 70 tree plots, including: (1) plot biomass (`AGBH.Mg.ha`), (2) mean tree diameter (`mDBH.cm`), (3) mean height (`mH.m`), (4) mean wood density (`mWD.g.m3`), mean basal area (`mBA.cm2`), and (5) presence of tree falls in the plot (`Tree.Fall`). Note that `Tree.Fall` is a factor with three levels: majeur (major tree fall), mineur (minor tree fall), and rien (no tree fall).

The goal of the analysis is to determine the variables that influence the plot biomass, `AGBH.Mg.ha`, and the direction and magnitude of their effect on biomass.

There are NA's in the dataset. You can either use `na.omit` to remove the missing values from the dataframe before the analysis, or the `lm()` function will do it for you. Also, just evaluate the main effects of IV's, do not include interactions.

Your write-up should include the following information:

- A statement of the research questions and your null and alternative hypotheses
- A description of Methods, including explanations of:
  - How you determine the variables to be in your full model
  - Process of model reduction or how you determine the minimum adequate model
- Results of your statistical test, including interpreting your test in 2-3 sentences that include the appropriate reporting of the statistics
- A description of how you checked the assumptions of your statistical test, including an interpretation of diagnostic figures
- Create plots (or a combined plot) that demonstrate the effects of the IV's on the DV
  - In other words, plot the regression equations to illustrate the results

Problem 2

The dataset `ozone.data.csv` consists of data on air quality (in terms of ozone concentration) and several weather variables, including temperature, solar radiation, and wind speed. Model the relationship of the weather variables to ozone concentration, making sure to consider interactions between the independent variables. (Do not worry about units in this example.) Once you have determined the best model to predict ozone concentration, write a one-page report that includes the following:

- Null and alternative hypotheses of your model
- Results of your statistical test, interpreting the fit of the model in 2-3 sentences that include the appropriate reporting of the statistics
- An interpretation of the regression model coefficients (i.e., what do each of the main effect(s) and interaction effect(s) mean
- A description of how you checked the assumptions of your statistical test
- Graphs that depict (i) the relationship between the independent variable and dependent variable when a variable is only included as a main effect, (ii) the relationship between the interacting independent variables with the dependent variable (i.e., plug in 2-3 interesting values for one of the independent variables and plot the other independent variable against the dependent variable).