Practical No. 6

AIM: Practical of Simple/Multiple Linear Regression

Theory:

In statistics, **linear regression** is a linear approach to modelling the relationship between a scalar response (or dependent variable) and one or more explanatory variables (or independent variables).

The case of one explanatory variable is called simple linear regression. For more than one explanatory variable, the process is called **multiple linear regression**. This term is distinct from multivariate linear regression, where multiple correlated dependent variables are predicted, rather than a single scalar variable.

In linear regression, the relationships are modelled using linear predictor functions whose unknown model parameters are estimated from the data. Such models are called linear models.

Most commonly, the conditional mean of the response given the values of the explanatory variables (or predictors) is assumed to be an affine function of those values; less commonly, the conditional median or some other quintile is used.

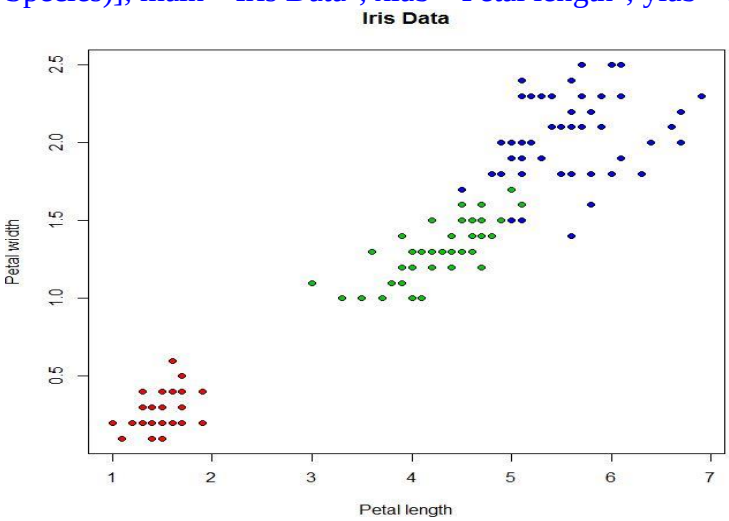
Like all forms of regression analysis, linear regression focuses on the conditional probability distribution of the response given the values of the predictors, rather than on the joint probability distribution of all of these variables, which is the domain of multivariate analysis.

To summarise, the iris dataset consists of four measurements (length and width of the petals and sepals) of one hundred and fifty Iris flowers from three species:

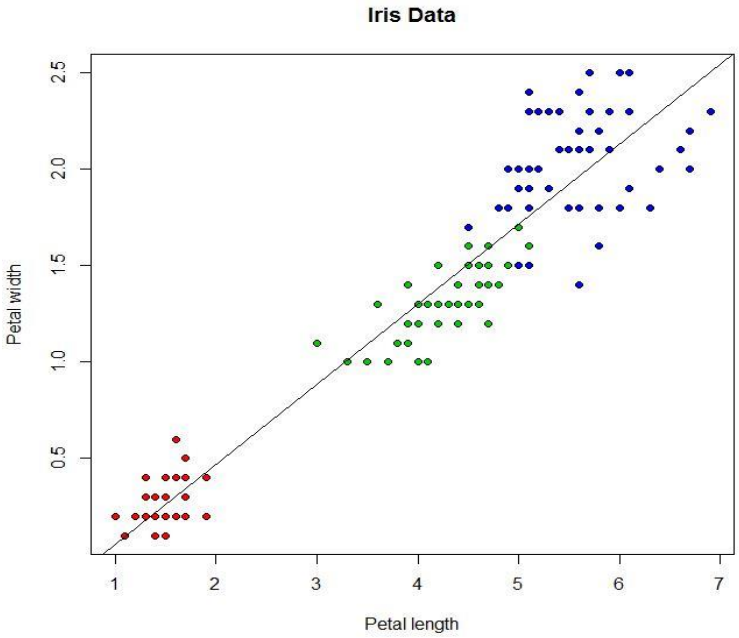
You will have noticed on the iris dataset, that petal length and petal width are highly correlated over all species. How about running a linear regression? First of all, using the "least squares fit" function lsfit gives this:

```
> lsfit(iris$Petal.Length, iris$Petal.Width)$coefficients
 Intercept          X
-0.3630755  0.4157554
```

```
> plot(iris$Petal.Length, iris$Petal.Width, pch=21, bg=c("red","green3","blue")[unclass(iris$Species)], main="Iris Data", xlab="Petal length", ylab="Petal width")
```



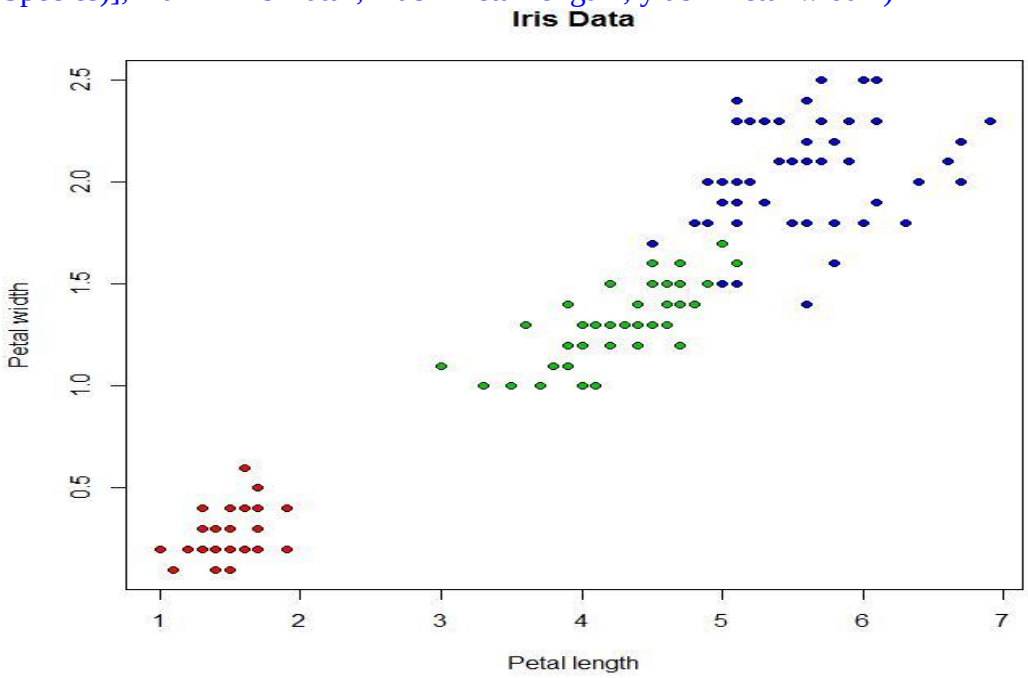

```
> abline(lsfit(iris$Petal.Length, iris$Petal.Width)$coefficients, col="black")
```



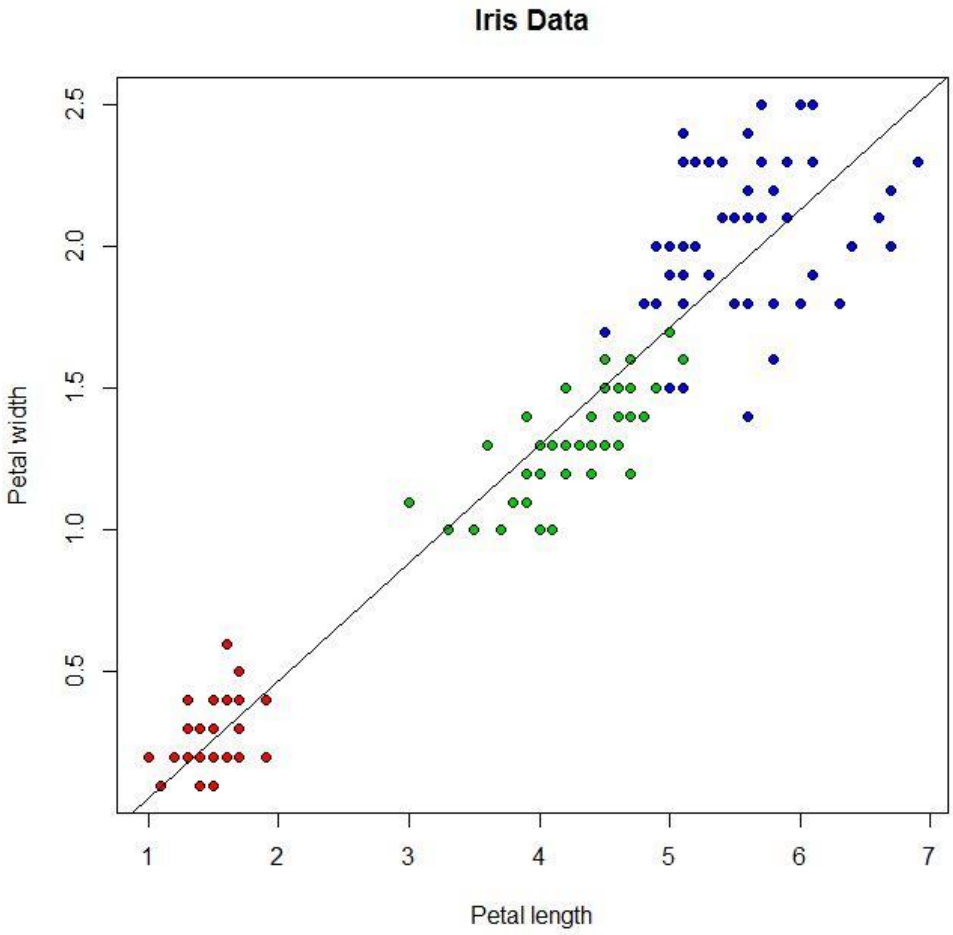
The function lsfit is a bit of a "one trick pony" and its a lot more flexible to use a linear model instead (function
lm). For this example you get exactly the same thing when we model petal width depending on petal length
(written as Petal.Width ~ Petal.Length in R's model syntax):

```
> lm(Petal.Width ~ Petal.Length, data=iris)$coefficients
 (Intercept) Petal.Length
  -0.3630755    0.4157554
```

```
> plot(iris$Petal.Length, iris$Petal.Width, pch=21, bg=c("red","green3","blue")[unclass(iris$
Species)], main="Iris Data", xlab="Petal length", ylab="Petal width")
```



```
> abline(lm(Petal.Width ~ Petal.Length, data=iris)$coefficients, col="black")
```



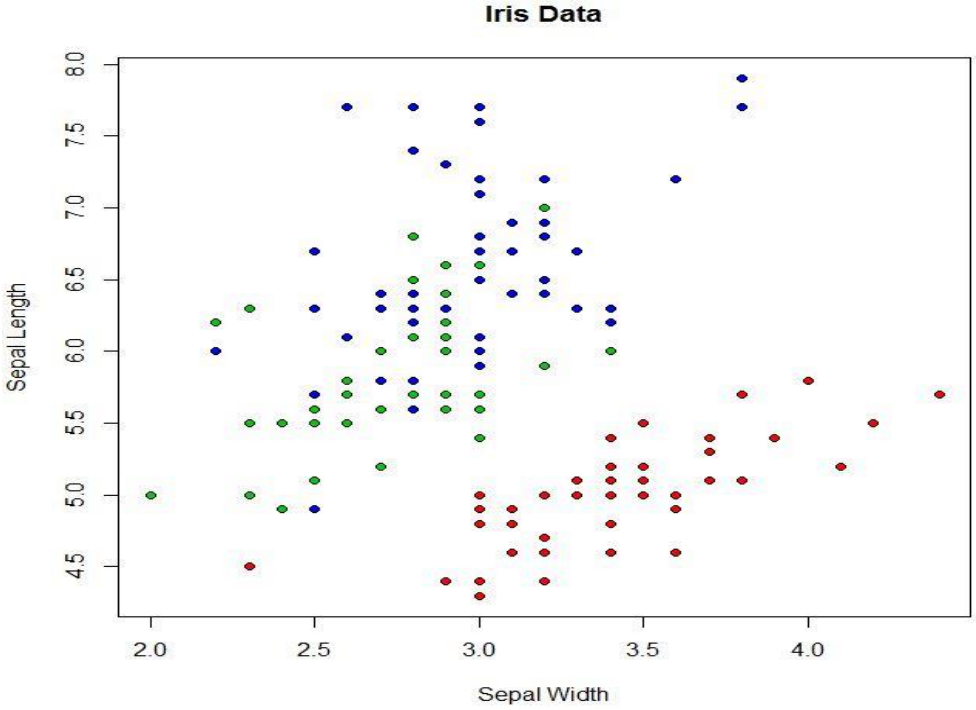
(same graph again)

You get more than just that with a linear model:

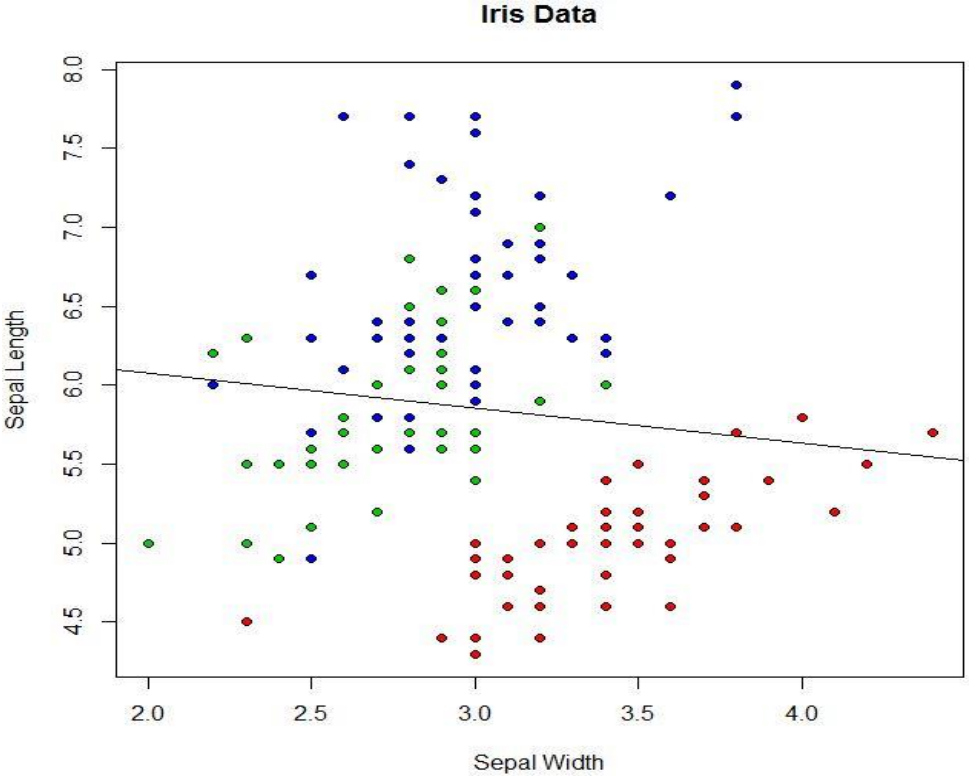
```
> summary(lm(Petal.Width ~ Petal.Length, data=iris))

Call:
lm(formula = Petal.Width ~ Petal.Length, data = iris)
Residuals:
     Min       1Q   Median       3Q      Max
-0.56515 -0.12358 -0.01898  0.13288  0.64272
Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  -0.363076   0.039762  -9.131  4.7e-16 ***
Petal.Length  0.415755   0.009582  43.387  < 2e-16 ***
---Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 0.2065 on 148 degrees of freedom
Multiple R-squared:  0.9271,            Adjusted R-squared:  0.9266
F-statistic:  1882 on 1 and 148 DF,  p-value: < 2.2e-16
```

The main point about using a linear model is we can consider more complicated examples. What about the sepal length as a function of the sepal width?

```
> plot(iris$Sepal.Width, iris$Sepal.Length, pch=21, bg=c("red","green3","blue")[unclass(iris
$Species)], main="Iris Data", xlab="Sepal Width", ylab="Sepal Length")
```




```
> abline(lm(Sepal.Length ~ Sepal.Width, data=iris)$coefficients, col="black")
```

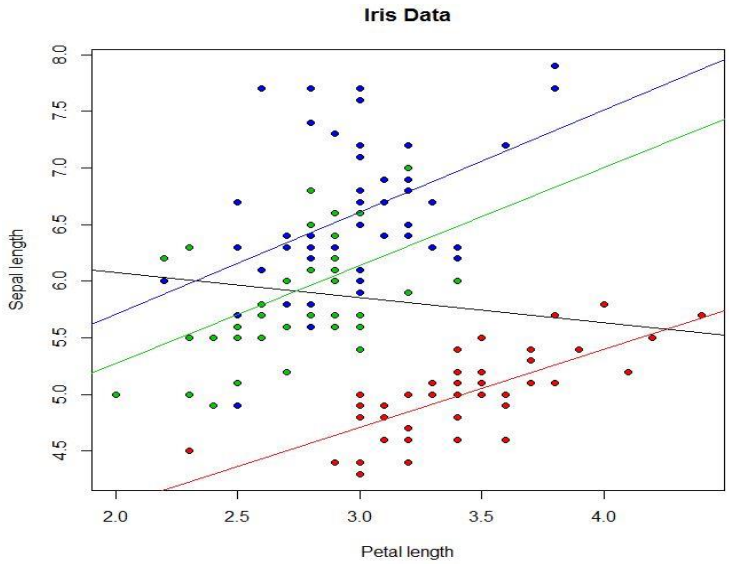


It very clear that the linear model Sepal.Length ~ Sepal.Width (black line) is not doing a very good job, even without looking at the statistics:

```
> summary(lm(Sepal.Length ~ Sepal.Width, data=iris))

Call:
lm(formula = Sepal.Length ~ Sepal.Width, data = iris)

Residuals:
    Min      1Q  Median      3Q     Max
-1.5561 -0.6333 -0.1120  0.5579  2.2226

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)   6.5262     0.4789   13.63   <2e-16 ***
Sepal.Width  -0.2234     0.1551   -1.44    0.152
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.8251 on 148 degrees of freedom
Multiple R-squared:  0.01382,           Adjusted R-squared:  0.007159
F-statistic: 2.074 on 1 and 148 DF,  p-value: 0.1519
```

What happens if we divide the data up by species, and run three separate linear regressions?

```
> plot(iris$Sepal.Width, iris$Sepal.Length, pch=21, bg=c("red","green3","blue")[unclass(iris$Species)], main="Iris Data", xlab="Petal length", ylab="Sepal length")
> abline(lm(Sepal.Length ~ Sepal.Width, data=iris)$coefficients, col="black")
> abline(lm(Sepal.Length ~ Sepal.Width, data=iris[which(iris$Species=="setosa"),])$coefficients, col="red")
> abline(lm(Sepal.Length ~ Sepal.Width, data=iris[which(iris$Species=="versicolor"),])$coefficients, col="green3")
> abline(lm(Sepal.Length ~ Sepal.Width, data=iris[which(iris$Species=="virginica"),])$coefficients, col="blue")
```



The coefficients doing separate per species regressions of Sepal.Length ~ Sepal.Width are:

```
> lm(Sepal.Length ~ Sepal.Width, data=iris[which(iris$Species=="setosa"),])$coefficients
(Intercept) Sepal.Width
  2.6390012   0.6904897
> lm(Sepal.Length ~ Sepal.Width, data=iris[which(iris$Species=="versicolor"),])$coefficients
(Intercept) Sepal.Width
  3.5397347   0.8650777
> lm(Sepal.Length ~ Sepal.Width, data=iris[which(iris$Species=="virginica"),])$coefficients
(Intercept) Sepal.Width
  3.9068365   0.9015345
```

The equivalent linear model would be something like Sepal.Length ~ Petal.Length:Species + Species- 1, which gives identical coef□cients (see later for why I did this):

```
> lm(Sepal.Length ~ Sepal.Width:Species + Species - 1, data=iris)$coefficients
             Speciessetosa         Speciesversicolor          Speciesvirginica
                 2.6390012                 3.5397347                 3.9068365
Sepal.Width:Speciessetosa Sepal.Width:Speciesversicolor  Sepal.Width:Speciesvirginica
                 0.6904897                 0.8650777                 0.9015345
```

What are these new terms? Because Species is a categorical input variable (a factor in R's terminology) it can't be used directly in a linear model as they need actual numbers (a linear model is basically a matrix equation). So,the following "dummy variables" have been invented for each data point (which *are* just numbers)

Speciessetosa = 1 if Species is "setosa", 0 otherwise
Speciesversicolor = 1 if Species is "versicolor", 0 otherwise
Speciesvirginica = 1 if Species is "virginica", 0 otherwise
Sepal.Width:Speciessetosa = Sepal.Width if Species is "setosa", 0 otherwise
Sepal.Width:Speciesversicolor = Sepal.Width if Species is "versicolor", 0 otherwise
Sepal.Width:Speciesvirginica = Sepal.Width if Species is "virginica", 0 otherwise

Using the summary command on the linear model object gives:

```
> summary(lm(Sepal.Length ~ Sepal.Width:Species + Species - 1, data=iris))

Call:
lm(formula = Sepal.Length ~ Sepal.Width:Species + Species - 1,
    data = iris)

Residuals:
     Min       1Q   Median       3Q      Max
-1.26067 -0.25861 -0.03305  0.18929  1.44917

Coefficients:
                                Estimate Std. Error t value Pr(>|t|)
Speciessetosa                    2.6390     0.5715   4.618 8.53e-06 ***
Speciesversicolor                3.5397     0.5580   6.343 2.74e-09 ***
Speciesvirginica                 3.9068     0.5827   6.705 4.25e-10 ***
Sepal.Width:Speciessetosa        0.6905     0.1657   4.166 5.31e-05 ***
Sepal.Width:Speciesversicolor    0.8651     0.2002   4.321 2.88e-05 ***
Sepal.Width:Speciesvirginica     0.9015     0.1948   4.628 8.16e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4397 on 144 degrees of freedom
Multiple R-squared:  0.9947,            Adjusted R-squared:  0.9944
F-statistic:  4478 on 6 and 144 DF,  p-value: < 2.2e-16
```

Just look at those p-values! Every single term has an excellent p-value, as does the model as a whole. And the residual standard error has also been halved.
In this case, the Sepal.Length ~ Sepal.Width:Species + Species - 1 model is clearly much better than just Sepal.Length ~ Sepal.Width.

Simplify with AIC
On the other hand, what about this choice instead: Sepal.Length ~ Sepal.Width + Species. In fact, this is what the AIC (Akaike Information Criterion) step function gives you if you start with all possible interactions between sepal width and species, which is written Sepal.Length ~ Sepal.Width * Species (using a asterix instead of a plus or colon) in R:

```
> summary(step(lm(Sepal.Length ~ Sepal.Width * Species, data=iris)))
Start:  AIC=-240.59
Sepal.Length ~ Sepal.Width * Species

                    Df Sum of Sq    RSS     AIC
- Sepal.Width:Species  2   0.15719 28.004 -243.75
<none>                           27.846 -240.59

Step:  AIC=-243.74
Sepal.Length ~ Sepal.Width + Species
```

```
             Df Sum of Sq     RSS     AIC
<none>                     28.004 -243.75
- Sepal.Width  1    10.953  38.956 -196.23
- Species      2    72.752 100.756  -55.69

Call:
lm(formula = Sepal.Length ~ Sepal.Width + Species, data = iris)

Residuals:
     Min       1Q   Median       3Q      Max
-1.30711 -0.25713 -0.05325  0.19542  1.41253

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)         2.2514     0.3698   6.089 9.57e-09 ***
Sepal.Width         0.8036     0.1063   7.557 4.19e-12 ***
Speciesversicolor   1.4587     0.1121  13.012  < 2e-16 ***
Speciesvirginica    1.9468     0.1000  19.465  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.438 on 146 degrees of freedom
Multiple R-squared:  0.7259,            Adjusted R-squared:  0.7203
F-statistic: 128.9 on 3 and 146 DF,  p-value: < 2.2e-16
```

I just introduced a model of the form Sepal.Length ~ Sepal.Width:Species + Species - 1, which gave identical coef□cients to those found doing species speci□c regressions:

```
> lm(Sepal.Length ~ Sepal.Width:Species + Species - 1, data=iris)$coefficients
            Speciessetosa        Speciesversicolor         Speciesvirginica
                2.6390012                3.5397347                3.9068365
Sepal.Width:Speciessetosa Sepal.Width:Speciesversicolor  Sepal.Width:Speciesvirginica
                0.6904897                0.8650777                0.9015345
```

The use of the "- 1" in the model above told R not to automatically include a default intercept term. The alternative is the following:

```
> lm(Sepal.Length ~ Sepal.Width:Species + Species, data=iris)$coefficients
            (Intercept)        Speciesversicolor         Speciesvirginica
                2.6390012                0.9007335                1.2678352
Sepal.Width:Speciessetosa Sepal.Width:Speciesversicolor  Sepal.Width:Speciesvirginica
                0.6904897                0.8650777                0.9015345
```

All Command:

```
lsfit(iris$Petal.Length, iris$Petal.Width)$coefficients

plot(iris$Petal.Length, iris$Petal.Width, pch=21,
bg=c("red","green3","blue")[unclass(iris$Species)], main="Iris Data", xlab="Petal length",
ylab="Petal width")

abline(lsfit(iris$Petal.Length, iris$Petal.Width)$coefficients, col="black")

lm(Petal.Width ~ Petal.Length, data=iris)$coefficients

plot(iris$Petal.Length, iris$Petal.Width, pch=21,
bg=c("red","green3","blue")[unclass(iris$Species)], main="Iris Data", xlab="Petal length",
ylab="Petal width")

abline(lm(Petal.Width ~ Petal.Length, data=iris)$coefficients, col="black")

summary(lm(Petal.Width ~ Petal.Length, data=iris))

plot(iris$Sepal.Width, iris$Sepal.Length, pch=21,
bg=c("red","green3","blue")[unclass(iris$Species)], main="Iris Data", xlab="Sepal Width",
ylab="Sepal Length")

abline(lm(Sepal.Length ~ Sepal.Width, data=iris)$coefficients, col="black")

summary(lm(Sepal.Length ~ Sepal.Width, data=iris))

plot(iris$Sepal.Width, iris$Sepal.Length, pch=21,
bg=c("red","green3","blue")[unclass(iris$Species)], main="Iris Data", xlab="Petal length",
ylab="Sepal length")

abline(lm(Sepal.Length ~ Sepal.Width, data=iris)$coefficients, col="black")

abline(lm(Sepal.Length ~ Sepal.Width,
data=iris[which(iris$Species=="setosa"),])$coefficients, col="red")

abline(lm(Sepal.Length ~ Sepal.Width,
data=iris[which(iris$Species=="versicolor"),])$coefficients, col="green3")

abline(lm(Sepal.Length ~ Sepal.Width,
data=iris[which(iris$Species=="virginica"),])$coefficients, col="blue")

lm(Sepal.Length ~ Sepal.Width, data=iris[which(iris$Species=="setosa"),])$coefficients

lm(Sepal.Length ~ Sepal.Width, data=iris[which(iris$Species=="versicolor"),])$coefficients

lm(Sepal.Length ~ Sepal.Width, data=iris[which(iris$Species=="virginica"),])$coefficients

lm(Sepal.Length ~ Sepal.Width:Species + Species - 1, data=iris)$coefficients
```

```
summary(lm(Sepal.Length ~ Sepal.Width:Species + Species - 1, data=iris))

summary(step(lm(Sepal.Length ~ Sepal.Width * Species, data=iris)))

lm(Sepal.Length ~ Sepal.Width:Species + Species - 1, data=iris)$coefficients

lm(Sepal.Length ~ Sepal.Width:Species + Species, data=iris)$coefficients
```