Part I: Exploratory Data Analysis, Linear Regression, ANOVA

Load Packages

First, we must load the packages that will be used in the first part of this workshop.

```
library(pastecs, quietly = TRUE)
library(lm.beta, quietly = TRUE)
library(lmtest, quietly = TRUE)
library(foreign, quietly = TRUE)
library(lattice, quietly = TRUE)
library(lme4, quietly = TRUE)
library(nlme, quietly = TRUE)
library(survival, quietly = TRUE)
library(dplyr, quietly = TRUE)
library(ggfortify, quietly = TRUE)
library(survminer, quietly = TRUE)
library(rms, quietly = TRUE)
```

Exploratory Data Analysis

Basic Statistical Analysis

Data set description

In this section, we will be using the iris data set. This data set contains measurement data of the flower of certain plant species. The data set has five variables:

- Sepal.Length measurements of Sepal length
- Sepal.Width measurements of Sepal width
- ► Petal.Length measurements of Petal length
- ▶ Petal.Width measurements of Petal width
- Species species of the plant

data = iris

Basic Statistical Analysis

Univariate descriptive statistics

The function, stat.desc, can be used to do a statistical analysis of data. It returns the mean, median, maximum, minimum, etc of a data set.

```
stat.desc(data$Sepal.Width)
```

```
##
        nbr val
                     nbr null
                                    nhr na
                                                     min
                                                                   max
## 150 00000000
                   0.00000000
                                0.00000000
                                              2.00000000
                                                            4 40000000
##
                                    median
                                                               SE.mean
          range
                                                    mean
     2 40000000 458 60000000
                                3.00000000
                                              3.05733333
                                                            0.03558833
## CT mean 0.95
                                    std dev
                                                coef var
     0.07032302
                  0.18997942
                                             0.14256420
                                0.43586628
```

Basic Statistical Analysis

Descriptive statistics by groups

Using tapply, we compute the same descriptive statistics above but grouped species with the same sepal width. tapply takes

- first argument: the input data to which we will apply the statistical function
- second argument: the grouping data which tells the statistical function how to group the input data
- third argument: the statistical function.

We will be considering the statistical functions: mean,sd and length.

Basic Statistical Analysis

Descriptive statistics by groups

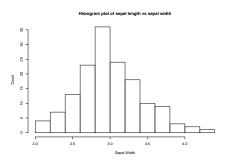
We will be considering the statistical functions: mean,sd and length.

```
mean <- tapply(data$Sepal.Length, data$Sepal.Width, mean)
standard_deviation <- tapply(data$Sepal.Length, data$Sepal.Width, sd)
number_of_observations <- tapply(data$Sepal.Length, data$Sepal.Width, length)
head(round(cbind(mean, standard_deviation, number_of_observations), digits = 6))</pre>
```

```
## mean standard_deviation number_of_observations
## 2 5.000000 NA 1
## 2.2 6.066667 0.115470 3
## 2.3 5.325000 0.767572 4
## 2.4 5.300000 0.346410 3
## 2.5 5.762500 0.625500 8
## 2.6 6.160000 0.887694 5
```

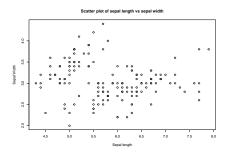
Histogram

It is important get an idea of the "structure" of your data. To do this, we can use histograms. We use the hist function to plot a distribution of sepal width.



Scatter Plot

We use the plot function to create a scatter plot of sepal length vs sepal width.



Stacking plots (without ggplot2)

We also differentiate the scatter plot above by species. We plot each species separately.

First, we call plot to create a canvas with an set of points associated with Setosa. If we were to call plot again, this would clear the previous plot.

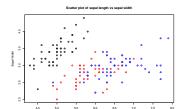
Stacking plots (without ggplot2)

Rather, we call points to add scatter plots to existing plot. points does not clear the previous plot.

```
plot(data[data$Species == "setosa", ]$Sepal.Length,
    data[data$Species == "setosa", ]$Sepal.Width,
    xlab = 'Sepal Length', ylab= 'Sepal Width',
    xlim = range(as.matrix(data$Sepal.Length)),
    ylim = range(as.matrix(data$Sepal.Width)),
    main= 'Scatter plot of sepal length vs sepal width')

points(data[data$Species == "versicolor", ]$Sepal.Length,
    data[data$Species == "versicolor", ]$Sepal.Width,
    col = 'red')

points(data[data$Species == "virginica", ]$Sepal.Length,
    data[data$Species == "virginica", ]$Sepal.Length,
    data[data$Species == "virginica", ]$Sepal.Length,
    data[data$Species == "virginica", ]$Sepal.Width, col = 'blue')
```



Scatter plot matrix

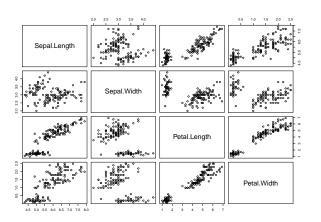
It is quite cumbersome to call to plot multiple times to create scatter plots for various pairs of explanatory variables.

There exists a convience function, pairs, that will create a matrix of scatter plots for all possible explanatory variable combination.

We give the pairs the first four columns of data. It will create a scatter plot matrix for sepal length, sepal width, petal length and petal width.

Scatter plot matrix

pairs(data[,c(1:4)])



Correlation matrix

From the scatter plot matrix above, we can see the qualitative correlation patterns between explanatory variables. We can also calculate these correlations explicitly and as a matrix using the corfunction.

```
cor(data[,c(1:4)])
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width
## Sepal.Length 1.0000000 -0.1175698 0.8717538 0.8179411
## Sepal.Width -0.1175698 1.0000000 -0.4284401 -0.3661219
## Petal.Length 0.8717538 -0.4284401 1.0000000 0.9628654
## Petal.Width 0.8179411 -0.3661259 0.9628654 1.0000000
```

Linear regression

Given a response variable, y, explanatory variables, X_i , and assuming that

$$y_i = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \dots + \beta_n X_{ni} + \varepsilon$$

where ε is a noise term, linear regression attempts the find the coefficients β_i that makes ε as small as possible.

The formula above assumes that response variable is a linear function explanatory variables. The noise term is added to account for the fact that most data is noisy and will not perfectly fit its 'true' function.

Linear regression also assumes that the noise is normally distributed with zero mean.

Linear regression

If these two assumptions are violated then

$$r_i = y_i - \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \dots + \beta_n X_{ni}$$

and $\sum_{i=1}^{m} r_i^2$ is generally a large number. $\sum_{i=1}^{m} r_i^2$ is called the residual standard error.

To regress the response variable, Sepal.Width, with explanatory variables, Sepal.Length, Species, Petal.Length and Petal.Width, we use the 1m function.

The first argument is 1m is the formula. The name of the column of the response variable is written first. It is followed by a tilde, \sim . After the tilde, we write names of the explanatory variable each separated by a +. 1 can also be added to the formula to represent a constant term.

General Syntax: Constant Term

First, I use the formula Sepal.Width $\,\sim\,$ 1. This formula is equivalent to

Sepal.Width =
$$\beta_0 + \varepsilon$$
.

Note that constant term is simply the mean response variable.

General Syntax: Constant Term

```
ols <- lm(Sepal.Width ~ 1, data = data)
summary(ols)
##
## Call:
## lm(formula = Sepal.Width ~ 1, data = data)
##
## Residuals:
       Min
              10 Median
## -1.05733 -0.25733 -0.05733 0.24267 1.34267
##
## Coefficients:
              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.05733 0.03559 85.91 <2e-16 ***
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 0.4359 on 149 degrees of freedom
print(mean(data$Sepal.Width))
```

```
## [1] 3.057333
```

General Syntax: Constant Term

Note that constant term is simply the mean response variable.

```
coef(ols)

## (Intercept)
## 3.057333

print(mean(data$Sepal.Width))

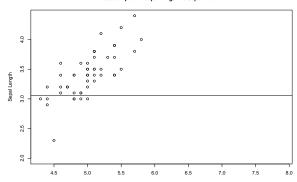
## [1] 3.057333
```

General Syntax: Constant Term

```
plot(data[data$Species == "setosa", ]$Sepal.Length,
    data[data$Species == "setosa", ]$Sepal.Width,
    xlab = 'Sepal Width', ylab= 'Sepal Length',
    xlim = range(as.matrix(data$Sepal.Length)),
    ylim = range(as.matrix(data$Sepal.Width)),
    main= 'Scatter plot of sepal length vs sepal width')

coefs = coef(ols)
abline(coefs[1],0)
```

Scatter plot of sepal length vs sepal width



General Syntax: Explanatory Variable and Constant Term

l use then formula Sepal.Width ~ 1 + Sepal.Length. This
formula is equivalent to

Sepal.Width = $\beta_0 + \beta_1$ Sepal.Length + ε

General Syntax: Explanatory Variable and Constant Term

```
ols <- lm(Sepal.Width - 1 + Sepal.Length, data = data)
summary(ols)</pre>
```

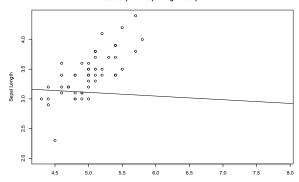
```
##
## Call:
## lm(formula = Sepal.Width ~ 1 + Sepal.Length, data = data)
##
## Residuals:
      Min
          10 Median
                                    Max
## -1.1095 -0.2454 -0.0167 0.2763 1.3338
##
## Coefficients:
              Estimate Std. Error t value Pr(>|t|)
##
## (Intercept) 3.41895 0.25356 13.48 <2e-16 ***
## Sepal.Length -0.06188 0.04297 -1.44 0.152
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4343 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
```

General Syntax: Explanatory Variable and Constant Term

```
plot(data[data$Species == "setosa", ]$Sepal.Length,
    data[data$Species == "setosa", ]$Sepal.Width,
    xlab = 'Sepal Width', ylab= 'Sepal Length',
    xlim = range(as.matrix(data$Sepal.Length)),
    ylim = range(as.matrix(data$Sepal.Width)),
    main= 'Scatter plot of sepal length vs sepal width')

coefs = coef(ols)
abline(coefs[1],coefs[2])
```

Scatter plot of sepal length vs sepal width



General Syntax: Factors

I use then formula Sepal.Width ~ 1 + Sepal.Length +
as.factor(Species). This formula is equivalent to

Sepal.Width
$$= eta_0 + eta_1$$
Sepal.Length $+ eta_2 I$ (Species $=$ Veriscolor) $+ eta_3 I$ (Species $=$ Virginica) $+ arepsilon$

General Syntax: Factors

```
ols <- lm(Sepal.Width - 1 + Sepal.Length + as.factor(Species), data = data)
summary(ols)</pre>
```

```
##
## Call:
## lm(formula = Sepal.Width ~ 1 + Sepal.Length + as.factor(Species),
      data = data)
##
##
## Residuals:
##
       Min
                 1Q Median
                                          Max
## -0.95096 -0.16522 0.00171 0.18416 0.72918
##
## Coefficients:
                              Estimate Std. Error t value Pr(>|t|)
##
## (Intercept)
                              1.67650 0.23536 7.123 4.46e-11 ***
## Sepal.Length
                               0.34988 0.04630 7.557 4.19e-12 ***
## as.factor(Species)versicolor -0.98339 0.07207 -13.644 < 2e-16 ***
## as.factor(Species)virginica -1.00751 0.09331 -10.798 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.289 on 146 degrees of freedom
## Multiple R-squared: 0.5693, Adjusted R-squared: 0.5604
## F-statistic: 64.32 on 3 and 146 DF, p-value: < 2.2e-16
```

General Syntax: Factors

```
plot(data[data$Species == "setosa", ]$Sepal.Length,
    data[data$Species == "setosa", ]$Sepal.Width,
    xlab = 'Sepal Width', ylab= 'Sepal Length',
    xlim = range(as.matrix(data$Sepal.Length)),
    ylim = range(as.matrix(data$Sepal.Width)),
    main= 'Scatter plot of sepal length vs sepal width')

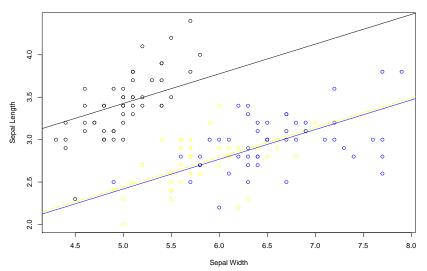
points(data[data$Species == "versicolor", ]$Sepal.Length,
    data[data$Species == "versicolor", ]$Sepal.Width,
    col = 'yellow')

points(data[data$Species == "virginica", ]$Sepal.Length,
    data[data$Species == "virginica", ]$Sepal.Width, col = 'blue')

coefs = coef(ols)
abline(coefs[1],coefs[2])
abline(coefs[3] + coefs[1],coefs[2],col='yellow')
abline(coefs[4] +coefs[1],coefs[2],col='blue')
```

General Syntax: Factors

Scatter plot of sepal length vs sepal width



Advanced Syntax: Nonlinear Regression

The 1m function can be extended to nonlinear functions. For example, it possible include a quadratic term in our model.

Sepal.Width =
$$\beta_1$$
Sepal.Length + β_2 Sepal.Length² + ε

To add a quadratic term to the model, add I(Sepal.Length^2) to the left side of the tilde, ~. It is also possible to include higher order nonlinear terms, such as cubic, quintic, etc.

Advanced Syntax: Nonlinear Regression

```
ols_quadratic <- lm(Sepal.Width - Sepal.Length + I(Sepal.Length^2), data = data)
summary(ols_quadratic)</pre>
```

```
##
## Call:
## lm(formula = Sepal.Width ~ Sepal.Length + I(Sepal.Length^2).
      data = data)
##
## Residuals:
       Min
                10 Median 30
##
                                         Max
## -1.13070 -0.26310 -0.02446 0.25728 1.38725
##
## Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
##
## (Intercept)
                  6.41584 1.58499 4.048 8.33e-05 ***
## Sepal.Length
                 -1.08556 0.53625 -2.024 0.0447 *
## I(Sepal.Length^2) 0.08571 0.04476 1.915 0.0574 .
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4304 on 147 degrees of freedom
## Multiple R-squared: 0.03783, Adjusted R-squared: 0.02474
## F-statistic: 2.89 on 2 and 147 DF, p-value: 0.05877
```

Advanced Syntax: Interaction term

It is also possible to include model interaction between explanatory variables.

Sepal.Width
$$= eta_1$$
Sepal.Length $+ eta_2$ Petal.Length $+ eta_3$ Sepal.Length $imes$ Petal.Length $+ arepsilon$

Sepal.Length \times Petal.Length models simple interaction between Sepal.Length and Petal.Length.

Advanced Syntax: Interaction term

```
ols_interaction <- lm(Sepal.Width - Sepal.Length + Petal.Length + Sepal.Length*Petal.Length, data = data) summary(ols_interaction)
```

```
##
## Call:
## lm(formula = Sepal.Width ~ Sepal.Length + Petal.Length + Sepal.Length *
      Petal.Length, data = data)
##
##
## Residuals:
##
       Min
                1Q Median
                                          Max
## -0.86960 -0.19846 0.00743 0.20704 0.72871
##
## Coefficients:
                           Estimate Std. Error t value Pr(>|t|)
##
## (Intercept)
                           1.51011 0.64336 2.347 0.020257 *
## Sepal.Length
                           0.46940 0.12954 3.624 0.000400 ***
## Petal.Length
                          -0.42907 0.11832 -3.626 0.000397 ***
## Sepal.Length:Petal.Length 0.01795 0.02186 0.821 0.413063
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3239 on 146 degrees of freedom
## Multiple R-squared: 0.4589, Adjusted R-squared: 0.4478
## F-statistic: 41.28 on 3 and 146 DF, p-value: < 2.2e-16
```

Advanced Syntax: Interaction term

Note that using the formula Sepal.Width ~ Sepal.Length*Petal.Length produces the same result as Sepal.Length + Petal.Length + Sepal.Length*Petal.Length.

```
ols_interaction <- lm(Sepal.Width - Sepal.Length*Petal.Length, data = data)
summary(ols_interaction)</pre>
```

```
##
## Call:
## lm(formula = Sepal.Width ~ Sepal.Length * Petal.Length, data = data)
##
## Residuals:
       Min
               10 Median
                                 30
                                         Max
## -0.86960 -0.19846 0.00743 0.20704 0.72871
##
## Coefficients:
##
                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)
                          1.51011 0.64336 2.347 0.020257 *
## Sepal.Length
                         0.46940 0.12954 3.624 0.000400 ***
## Petal.Length
                          -0.42907 0.11832 -3.626 0.000397 ***
## Sepal.Length:Petal.Length 0.01795 0.02186 0.821 0.413063
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3239 on 146 degrees of freedom
## Multiple R-squared: 0.4589, Adjusted R-squared: 0.4478
## F-statistic: 41.28 on 3 and 146 DF. p-value: < 2.2e-16
```

Advanced Syntax: Non-linear regression and Interaction term

```
ols_q_i <- lm(Sepal.Width - Sepal.Length*as.factor(Species) + I(Sepal.Length^2), data = data) summary(ols_q_i)
```

```
##
## Call:
## lm(formula = Sepal.Width ~ Sepal.Length * as.factor(Species) +
##
      I(Sepal.Length^2), data = data)
##
## Residuals:
##
       Min
                    Median
                 10
                                   30
                                           Max
## -0.71404 -0.15888 0.01535 0.16089 0.61676
##
## Coefficients:
##
                                            Estimate Std. Error t value
## (Intercept)
                                            -2.17766 1.59715 -1.363
## Sepal.Length
                                             1.44156 0.60909 2.367
## as.factor(Species)versicolor
                                             0.79275 0.93445 0.848
## as.factor(Species)virginica
                                             0.84269 1.29009 0.653
## I(Sepal.Length^2)
                                            -0.06397 0.05959 -1.073
## Sepal.Length:as.factor(Species)versicolor -0.35909
                                                      0.17402 -2.064
## Sepal.Length:as.factor(Species)virginica -0.36224
                                                       0.22839 -1.586
                                            Pr(>|t|)
##
## (Intercept)
                                              0.1749
## Sepal.Length
                                              0.0193 *
## as.factor(Species)versicolor
                                              0.3977
## as.factor(Species)virginica
                                              0.5147
## I(Sepal.Length^2)
                                              0.2849
## Sepal.Length:as.factor(Species)versicolor
                                              0.0409 *
## Sepal.Length:as.factor(Species)virginica
                                              0.1149
```

Obtaining the residuals

Recall it is possible the measure the error between the model and response variables. Given least squares fit,

$$r_i = y_i - \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \dots + \beta_n X_{ni}$$

r is the residual vector and $\sum_{i=1}^{m} r_i^2$ is the residual standard error.

Obtaining the residuals

It is possible to obtain residuals from the output of ${\tt lm}$

```
res <- ols*residuals
head(data.frame(res=res))
```

```
## res
## 1 0.03911127
## 2 -0.39091271
## 3 -0.12093668
## 4 -0.18594867
## 5 0.17409928
## 6 0.33414723
```