Data Analysis Course Outline

Below are the tentative weekly topics to be covered. Also included are selected R functions that we will learn how to use.

Further, there are examples of some code and its output for each week to give you an rough idea about what these topics are covering.

We will learn all of this as we go, so don't be scared by anything. . . it get pretty easy once you have a foundation.

This document was constructed entirely within R as an R-markdown (Rmd) file.

The complete code for this document can be found online HERE

All course documents and data sets can be found on the Course GitHub repository

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WEEK 1

- Why use code!?
- INSTALL R / R-studio
- Familiarize R-studio functions and layout
- Where to look for help

```
# Functions covered (parital list):
help()
```

WEEK 2

- Command-line tools
- BASH
- compression
- grep, sed, find, |, gzip/gunzip, tar, mv, cp, mkdir, etc.

```
# count the number of DNA sequences in a set of fasta files
grep -c "^>" ./Data/Fastq_16S/*.fasta
```

```
## ./Data/Fastq_16S/fq1.fasta:50
## ./Data/Fastq_16S/fq2.fasta:25
```

WEEK 3

- Assigning things to objects
- Get familiar with object types and basic functions
  - values, vectors, lists
  - data frames and matrices
  - boolean, character, numeric, POSIXct
- Accessing elements of objects
- Boolean evaluations
- Data-type conversions

```
# Functions covered (parital list):
=       <-      ->
class()
data.frame()  as.factor()  as.numeric()   as.character()   as.POSIXct()   as.matrix()
==    <   >  <=    >=
+     -   *   /
which()   signif()    ceiling()     floor()       round()
c()       list()      cbind()       rbind()       sum()         mean()        sd()
```

```
vector = c(1,2,3,4,5,6,7,8,9,10) # assign a series of numbers to an object called "vector"
mean(vector) # calculate the mean of the numbers in that object
```

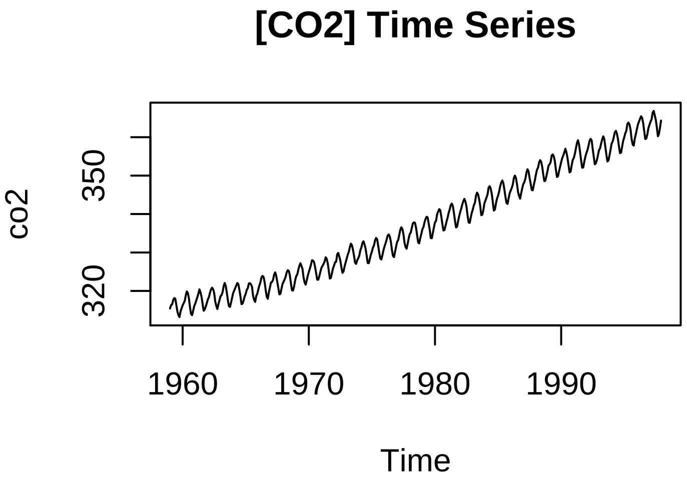
```
## [1] 5.5
```

WEEK 4

- Importing data
- Useful data formats
- Data structure and attributes
- Summary stats and basic visualizations
- Exploring data
    - Sorting, Transposing, Sampling
    - heatmaps, boxplots, barcharts, scatterplots, histograms

```
# Functions covered (parital list):
read.csv()          read.delim()
str()               dim()               names()             attributes()          head()
summary()           min()               max()               range()               quantile()
hist()              boxplot()           barplot()           plot()                heatmap()
sample()            t()                 sort()              tail()                var()
```

```
plot(co2, main = "[CO2] Time Series") # make a simple plot of the data in the object called "co2"
```



```
summary(co2) # generate statistical summaries of those data
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   313.2   323.5   335.2   337.1   350.3   366.8
```

WEEK 5

- Finding/Installing/Loading packages
- Extending functionality of R
- Subsetting and manipulating raw data
- Output options

```
# Functions covered (parital list):
install.packages()
library()
cor()
write.table()       sink()        tiff/jpeg/png() / dev.off()
```

```
data # show original data
```

```
##    Plant        Type  Treatment conc uptake
## 1    Qn1      Quebec nonchilled   95   16.0
## 43   Mn1 Mississippi nonchilled   95   10.6
## 44   Mn1 Mississippi nonchilled  175   19.2
## 2    Qn1      Quebec nonchilled  175   30.4
## 3    Qn1      Quebec nonchilled  250   34.8
## 45   Mn1 Mississippi nonchilled  250   26.2
## 4    Qn1      Quebec nonchilled  350   37.2
## 46   Mn1 Mississippi nonchilled  350   30.0
## 5    Qn1      Quebec nonchilled  500   35.3
## 47   Mn1 Mississippi nonchilled  500   30.9
```

```
data[data$Type == "Quebec",] # subset data to only include samples from "Quebec"
```

```
##   Plant   Type  Treatment conc uptake
## 1   Qn1 Quebec nonchilled   95   16.0
## 2   Qn1 Quebec nonchilled  175   30.4
## 3   Qn1 Quebec nonchilled  250   34.8
## 4   Qn1 Quebec nonchilled  350   37.2
## 5   Qn1 Quebec nonchilled  500   35.3
```

```
  Skills Test 1:

  * Import data set
  * Convert elements to new data type
  * Subset based on values
  * Calculate summary statistics
  * Create basic summary figures
  * Export summary statistics to text file
```

WEEK 6

- Data estimations
  - point estimates
  - interval estimates
- Hypothesis testing / Model fitting

    - t-test (paired/unpaired)
    - chi-square
    - ANOVA
    - LM/GLM
    - HEAD
    - Mixed-effect models (lme4)
    - rpart

```
# Functions covered (parital list):
lm()        glm()         aov()
t.test()    chisq.test()  rpart()     gmodel()
```

```
ANOVA = aov(uptake ~ conc, data = CO2) # model CO2 uptake by plants, predicted by CO2 concentration
summary(ANOVA) # show summary ANOVA table and P-value
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)    
## conc         1   2285  2285.0   25.25 2.91e-06 ***
## Residuals   82   7422    90.5                     
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# T-test comparing mean CO2 uptake in two groups
t.test(CO2$uptake[CO2$Type == "Quebec"],CO2$uptake[CO2$Type == "Mississippi"])
```

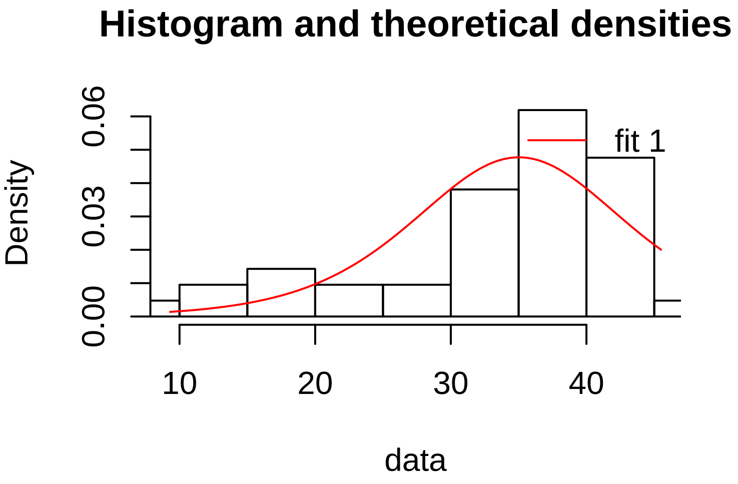
```
## 
##  Welch Two Sample t-test
## 
## data:  CO2$uptake[CO2$Type == "Quebec"] and CO2$uptake[CO2$Type == "Mississippi"]
## t = 6.5969, df = 78.533, p-value = 4.451e-09
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   8.839475 16.479572
## sample estimates:
## mean of x mean of y 
##  33.54286  20.88333
```

WEEK 7

- Experimental design
- Common designs and analysis options
- Quantitative vs qualitative data
- Probability distributions
- Fitting distributions
- Type I and Type II errors
- Post-hoc tests

```
# Packages used (partial list):
fitdistrplus
MASS
# Functions covered (parital list):
plotdist()      descdist()
fitdist()       denscomp()        cdfcomp()
TukeyHSD()
```

```
# Fit CO2 uptake data from Quebec samples to a logistic probability distribution
fit.logistic = fitdist(CO2$uptake[CO2$Type == "Quebec"], distr = "logis")
denscomp(fit.logistic) # Plot comparison between logistic distribution and actual data
```



WEEK 8

- Non-parametric alternatives
- Mann-Whitney-Wilcoxin
- Kruskal-Wallace
- Apply functions

```
# Packages used (partial list):

# Functions covered (parital list):
wilcox.test()     kruskal.test()

apply()     sapply()      lapply()      tapply()
```

```
data[,4:5] # look at columns 4 and 5 from object called "data"
```

```
##    conc uptake
## 1    95   16.0
## 43   95   10.6
## 44  175   19.2
## 2   175   30.4
## 3   250   34.8
## 45  250   26.2
## 4   350   37.2
## 46  350   30.0
## 5   500   35.3
## 47  500   30.9
```

```
apply(data[,4:5], 2, sum) # Apply the 'sum' function to those columns
```

```
##   conc uptake
## 2740.0  270.6
```

WEEK 9

- Other peoples' data
- Principles of tidy data
- Intuitive manipulations and group functions
  - filter
  - arrange
  - select
  - mutate
  - group_by
  - summarize
  - %>%
- Tidy data transformations
  - gather
  - spread

```
# Packages used (partial list):
dplr      plyr      tidyr
# Functions covered (parital list):
filter()      arrange()       select()        mutate()
group_by()    summarize()     %>%
gather()      spread()
```

```
# Get specific summary data for defined groups from the object called "data" and save as object called
group.summaries = data %>%
  group_by(Type) %>%
  summarize(Samples = n(), Mean.uptake = mean(uptake), Total.uptake = sum(uptake), StDev.uptake = sd(up

as.data.frame(group.summaries) # display summary info for different locations (groups) as a data frame
```

```
##          Type Samples Mean.uptake Total.uptake StDev.uptake
## 1      Quebec       5       30.74        153.7     8.608020
## 2 Mississippi       5       23.38        116.9     8.501882
```

```
  Skills Test 2:

  * Import messy data
  * Convert to tidy format
  * Plot data distribution
  * Rearrange and mutate data set
  * Summary stats on grouped data
  * Test hypothesis / post-hoc tests
```

WEEK 10

- Predicting data
- Intro to ggplot

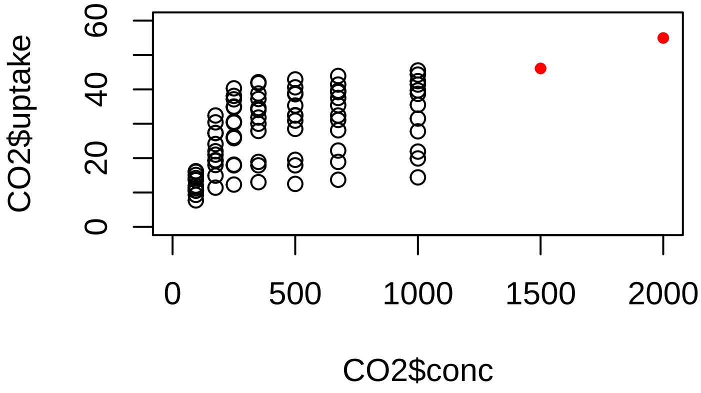
```
# Packages used (partial list):
ggplot2

# Functions covered (parital list):
predict()
qplot()
```

```
ggplot()
    aes()
```

```
library(ggplot2) # load ggplot2 package

new.data = data.frame(conc = c(1500,2000)) # give new predictor values (CO2 concentration)
predicted = predict(ANOVA, newdata = new.data) # predict plant uptake for those values based on previou
predicted # Look at predictions based on our ANOVA model
```

```
##        1        2
## 46.09617 54.96146
```

```
plot(CO2$conc,CO2$uptake,xlim=c(0,2000),ylim=c(0,60)) # simple plot of CO2 data
points(x=c(1500,2000),y=predicted[1:2],pch=20,col="Red") # Add our predicted uptake values for higher C
```



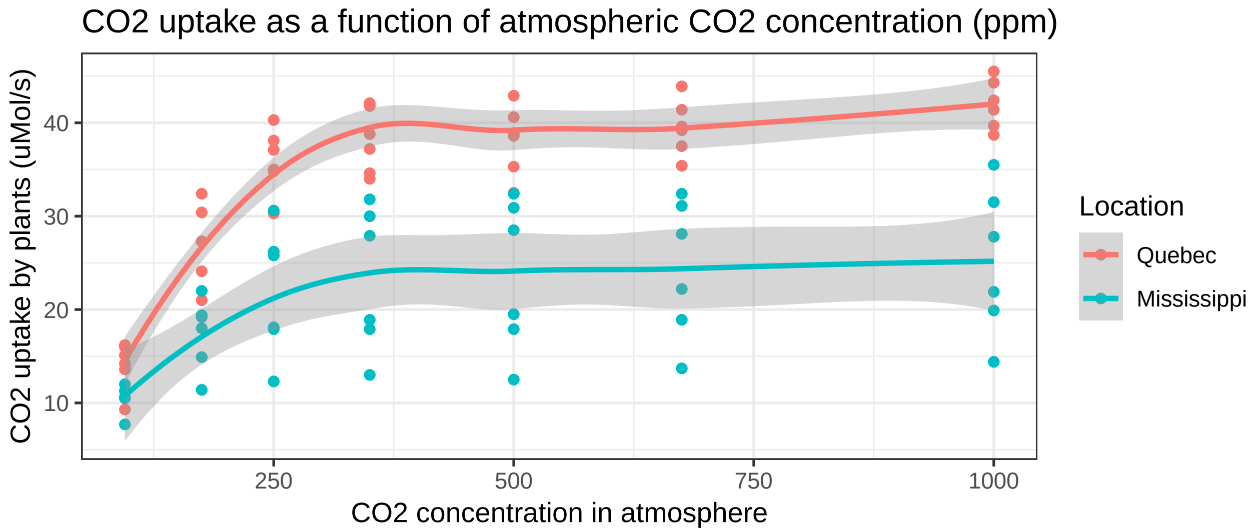
WEEK 11

- Figure generation
- Figure export

```
# Packages used (partial list):
ggplot2

# Functions covered (parital list):
ggplot()
geom_point()       geom_boxplot()      geom_bar()      geom_violin()
labs()             ggsave()
```

```
library(ggplot2) # load ggplot2 package

# Create ggplot and save as abject called "CO2.plot"
CO2.plot = ggplot(CO2, aes(x=conc, y=uptake, col=Type))+
  geom_point() +
  geom_smooth(method = "loess") +
  labs(x="CO2 concentration in atmosphere", y="CO2 uptake by plants (uMol/s)") +
  ggtitle("CO2 uptake as a function of atmospheric CO2 concentration (ppm)") +
  theme_bw() +
  scale_color_discrete(name = "Location")

# Display plot
```

```
CO2.plot
```

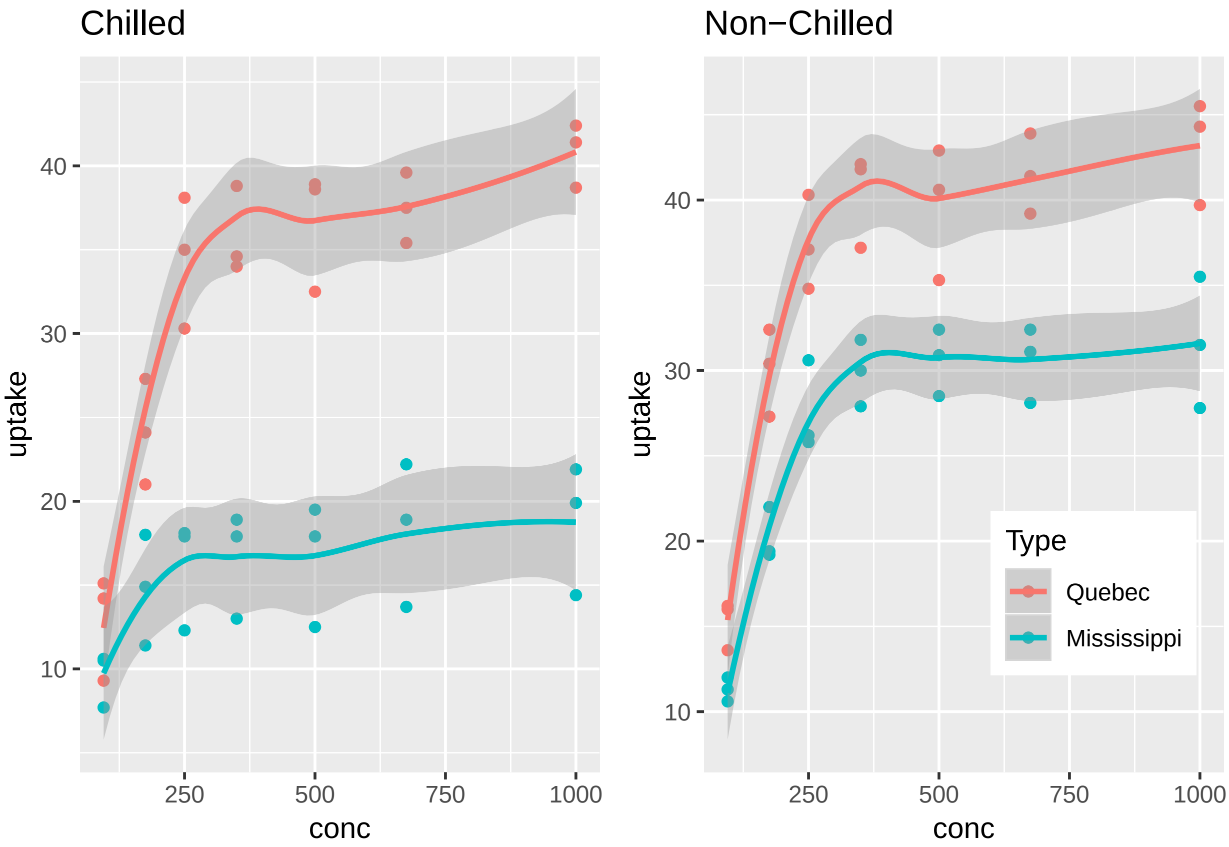


WEEK 12

- Figure generation continued

```
# Packages used (partial list):
ggplot2
gridExtra

# Functions covered (parital list):
grid.arrange()
ggplot()
scale_*()
```

```
# Make two separate plots - One for each temperature treatment
CO2.plot.1 = ggplot(CO2[CO2$Treatment == "chilled",], aes(x=conc, y=uptake, col=Type)) +
  geom_point() +
  geom_smooth(method = "loess") +
  ggtitle("Chilled") +
  theme(legend.position="none")

CO2.plot.2 = ggplot(CO2[CO2$Treatment == "nonchilled",], aes(x=conc, y=uptake, col=Type)) +
  geom_point() +
  geom_smooth(method = "loess") +
  ggtitle("Non-Chilled") +
  theme(legend.position=c(.75,.25))

# Combine the two plots into one image
grid.arrange(CO2.plot.1, CO2.plot.2, nrow = 1)
```



WEEK 13

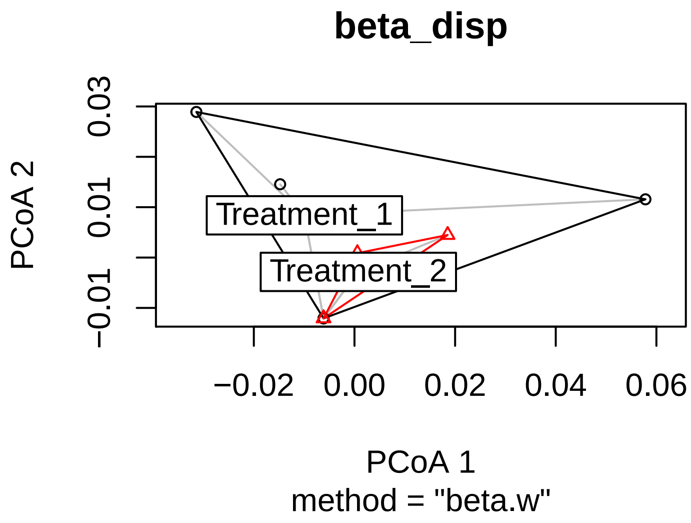
- Data standardization / normalization
- Ecology examples
  - Ordinations / NMDS
  - PermANOVA
  - Distance measures
  - Diversity measures

```r
# Packages used (partial list):
vegan

# Functions covered (parital list):
decostand()       rrarefy()         dist()         betadiver()
metaMDS()         adonis()          diversity()    betadisper()
```

```r
head(community_matrix)[,1:10] # Take a look at the community composition (observed counts) for differen
```

```
##          Species_1 Species_2 Species_3 Species_4 Species_5 Species_6
## Sample_1       548       883       480       357        64       832
## Sample_2       218        67       815       726       974       740
## Sample_3         0       306       199       991       933       244
## Sample_4       792       321       405        35       808       863
## Sample_5       560       460         0       863       794       921
## Sample_6        74       766       573       715       853       453
##          Species_7 Species_8 Species_9 Species_10
## Sample_1       942       434         0        735
## Sample_2       410       294       252        895
## Sample_3       624       378       387        665
## Sample_4       793       749       918        223
## Sample_5       175       478       228         94
## Sample_6       984        63       447        952
```

```
# Look at the beta diversity between two randomly-generated communities

beta_div = betadiver(community_matrix, method = "w")
beta_disp = betadisper(beta_div, treat)
plot(beta_disp)
```



```
Skills Test 3:

* Import data set
* Fit appropriate model
* Use model to predict new response values from new predictors
* Generate and export plots from data sets
```

WEEK 14

- Importing and manipulating DNA sequence data
  - Bioconductor
  - Sequence data
  - Biostrings
- Phylogenetics examples
  - Sequence alignment
  - Tree building
  - Taxonomic assignment

```
# Packages used (partial list):
Bioconductor
ape
biostrings
```

```
# Functions covered (parital list):

To be decided...
```

```r
# Assign a DNA sequence to a special DNAString object
Seq_1 = DNAString("TCTCTTCTGCCCTGTCACCACTGAGGGTGACTACGTCTGG")

reverseComplement(Seq_1) # Gives reverse-compliment of a DNA sequence
```

```
##   40-letter "DNAString" instance
## seq: CCAGACGTAGTCACCCTCAGTGGTGACAGGGCAGAAGAGA
```

WEEK 15

- Data management
- Reporting
- Rmd

  ```
  Skills Test 4 (final):

  * Command-line data access and manipulation
  * Writing a script to
      + import specific data
      + tidy and normalize data
      + subset and group
      + test hypotheses
      + create intuitive plots that include test statistics
  * Save script as readable report
  ```

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