

Introduction

Why use R?

Why not use a spreadsheet?

Today's workshop

- A common scenario
- A friend has emailed you her data in a spreadsheet
- Today's workshop is about how to get started.
- It's not about impressing with R code

Why not use a spreadsheet?

- Data manipulation in Excel is VERY risk and time consuming
- A range of software packages are available for Excel
- Large data sets can exceed the size limits of standard programs
- Spreadsheets don't have the inherent understanding of statistics that R has
- For example handling of NA's
- R is hot!

Why use R?

Why use R?

- R is free
- R is available on most operating systems Windows, OS X, Linux
- There are huge numbers of packages available
- Its becoming the international standard for statistics

Getting Started

Some References

References

- [1] James P. Howard. *R Cookbook*. O'Reilly Media, Inc, 2011.
- [2] Phil Spector. *Data Manipulation with R*. Use R series Springer, 2008

Getting Started

Today's Files

Workshop files on Github

<https://github.com/pechang03/SizeDoesMatter>

- The slides. **main.pdf**
- The handouts **handout.pdf**
- The R code **SizeDoesMatterEg.R**
- The spreadsheets
 - 1_RWkshp_dummydata_0TUtable.xlsx
 - 2_RWkshp_dummydata_EnvData_incl2outliersMK.xlsx
 - 3_Followupdatafromcontaminatedsite_MK.xlsx

Getting Started

Installing R!

Download it

- Open <http://www.r-project.org>
- Click CRAN (Under download on Top Left)
- Click <http://cran.ms.unimelb.edu.au/> University of Melbourne

Windows

- Select Windows
- Select Base
- Download R (suggest latest version)

OS X

- Select Select OS X
- Select R-3.2.2.pkg (or the version that matches your OS version)

Getting Started

How about RStudio

- <https://www.rstudio.com/products/rstudio/download/>
- Its also on your thumb drive

Getting Started

Basic steps

```
2+5

## [1] 7

# Create a sequence of numbers
X = 2:10

# Display basic statistical measures
summary(X)

##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
##       2       4       6       6       8      10 

# use q() to quit
```

Getting Started

Help Functions

To access the documentation type

```
help.start()  
help(summary)  
args(summary)  
example(sd)  
??package
```

Help Functions

Search the Web

To search R documentation

- `RSiteSearch("key phrase")`
- `help(adf.test, package="tseries")`
- To search for a tutorial for a package `vignette(package="packagename")`
- For an intro to vignettes see <https://cran.r-project.org/web/packages/sos/vignettes/sos.pdf>
- Examples on the web <http://shiny.rstudio.com/gallery/>

Custom Google search focused on R-specific websites

<http://rseek.org>

Coding Q&A site

<http://stackoverflow.com> <http://stats.stakexchange.com>

Some manners

Iterative development

Working Creatively

Research on how to work creatively based on case studies of successful R&D projects developed into Agile

- Keep the ‘manager’ away
- Work sustainably
- People over process
- Iterative development

Basic R Data types

R Data types

Lists, frames and tables

Vectors

- Vectors $l \leftarrow c(1, 3, 4, 7, 11)$
- Refer to elements using array $l[c(2, 5)]$ 2nd and 5th elements of l

Data Frames

```

a <- c(35,23,24,65)
e <- c("Peter", "John", "Mark", NA)
f <- c(TRUE,TRUE,TRUE,FALSE)
team <- data.frame(a,e,f)
names(team) <- c("Age", "Names", "Passed") # variable names
str(team)

## 'data.frame': 4 obs. of 3 variables:
## $ Age : num 35 23 24 65
## $ Names : Factor w/ 3 levels "John","Mark",...: 3 1 2 NA
## $ Passed: logi TRUE TRUE TRUE FALSE

```

Reading files

Let's read the first table

Check the current directory

Where are we

```

getwd()
setwd("/Users/pcru/SizeDoesMatter1")
dir() #This lists the files
ls() #This lists the variables

```

<http://www.statmethods.net/input/contents.html>

Reading a table from a file

Reading an excel table

To read a csv table as a table try

```

tab1 <- as.matrix(read.csv(file="filetable.csv", sep="," , header=FALSE))

```

But our table is an excel file

- What about a package?
- <http://www.thertrader.com/2014/02/11/a-million-ways-to-connect-r-and-excel/>
- Installing the R package xlsx
- CRAN mirror <http://cran.csiro.au>
- Change in preferences

Getting help on packages

R Packages

CRAN

Where from

- install command
- *install.packages(pkgs)*

Citing Packages

- Citing packages
- Getting the bibtex entry into endnote
- <http://www.lib.uts.edu.au/question/5955/how-can-i-import-bibliography-endnote-bibtex-latex>

```
x←citation()
xl←citation(package="RSQLite")
toBibtex(x)

sessionInfo()
packages_in_use ← c( sessionInfo()$basePkgs, names( sessionInfo()$loadedOnly ) )
the_citations_list ← lapply( X=packages_in_use, FUN=citation )
the_citations_list
```

Reading an excel table

An example

```
table1←read.xlsx2("1_R_Wkshp_dummy_data_OTU_table.xlsx", sheetName =
"Sheet1", header=FALSE, rowNames=FALSE, transpose=TRUE, endRow=18)
```

Loading the xlsx package

```
## Loading required package: xlsx
## Warning: package 'xlsx' was built under R version 3.1.3
## Loading required package: rJava
## Warning: package 'rJava' was built under R version 3.1.3
## Loading required package: methods## Loading required package:
xlsxjars## Loading required package: xtable
```

Reading an excel table

The columns types are wrong

	X1	X2	X3	X4	X5	X6	X7
1	Group	Contaminated					
2	Site	1			2		
3	Sample ID	10000	10001	10002	10003	10004	10005
4	Rep	1	2	3	1	2	3
5	phormidiaceae	24872	24872	5822	7538	7201	7538
6	streptococcaceae	11	7	14	8	10	8

Reading an excel table

Transpose the table

Transposing

We need to transpose the table and set the column names correctly

```
table1t=setNames(data.frame(t(table1[, -1])), table1[, 1])
```

http://rgm3.lab.nig.ac.jp/RGM/R_rdfile?f=Ecdat/man/read.transpose.Rd&d=R_CC <http://stackoverflow.com/questions/17288197/reading-a-csv-file-organized-horizontally>

Fields across many columns

Replicating first column

TDD – First do it the easy way first

```
ctridx<-which(table1t$Group=="Control")
table1t$Group[1:48]<-"Contaminated"
table1t$Group[(ctridx+1):48]<-"Control"
```

```
t1t<-table1t$Site
for(i in c(2:length(table1t$Site)))
{
  temp<-as.character(table1t$Site[i])
  tempb<-as.character(t1t[i-1])
  if(table1t$Site[i]=="")
  {
    t1t[i]<-tempb
  }
  if(!table1t$Site[(i)]=="")
  {
    t1t[i]<-temp
  }
}
table1t$Site<-t1t
```

```
## X3
## 1
## Levels: 1 2 3 4 FALSE TRUE
## X4
## 1
## Levels: 1 2 3 4 FALSE TRUE
## X5
## 2
## Levels: 1 2 3 4 FALSE TRUE
## X6
## 2
## Levels: 1 2 3 4 FALSE TRUE
## X7
```

```
## 2
## Levels: 1 2 3 4 FALSE TRUE
## X8
## 1
## Levels: 1 2 3 4 FALSE TRUE
## X9
## 1
## Levels: 1 2 3 4 FALSE TRUE
## X10
## 1
## Levels: 1 2 3 4 FALSE TRUE
## X11
## 2
## Levels: 1 2 3 4 FALSE TRUE
## X12
## 2
## Levels: 1 2 3 4 FALSE TRUE
## X13
## 2
## Levels: 1 2 3 4 FALSE TRUE
## X14
## 1
## Levels: 1 2 3 4 FALSE TRUE
## X15
## 1
## Levels: 1 2 3 4 FALSE TRUE
## X16
## 1
## Levels: 1 2 3 4 FALSE TRUE
## X17
## 2
## Levels: 1 2 3 4 FALSE TRUE
## X18
## 2
## Levels: 1 2 3 4 FALSE TRUE
## X19
## 2
## Levels: 1 2 3 4 FALSE TRUE
## X20
## 1
## Levels: 1 2 3 4 FALSE TRUE
## X21
## 1
## Levels: 1 2 3 4 FALSE TRUE
## X22
```

```

## 1
## Levels: 1 2 3 4 FALSE TRUE
## X23
## 2
## Levels: 1 2 3 4 FALSE TRUE
## X24
## 2
## Levels: 1 2 3 4 FALSE TRUE
## X25
## 2
## Levels: 1 2 3 4 FALSE TRUE
## X26
## 3
## Levels: 1 2 3 4 FALSE TRUE
## X27
## 3
## Levels: 1 2 3 4 FALSE TRUE
## X28
## 3
## Levels: 1 2 3 4 FALSE TRUE
## X29
## 4
## Levels: 1 2 3 4 FALSE TRUE
## X30
## 4
## Levels: 1 2 3 4 FALSE TRUE
## X31
## 4
## Levels: 1 2 3 4 FALSE TRUE
## X32
## 3
## Levels: 1 2 3 4 FALSE TRUE
## X33
## 3
## Levels: 1 2 3 4 FALSE TRUE
## X34
## 3
## Levels: 1 2 3 4 FALSE TRUE
## X35
## 4
## Levels: 1 2 3 4 FALSE TRUE
## X36
## 4
## Levels: 1 2 3 4 FALSE TRUE
## X37

```

```

##      4
## Levels: 1 2 3 4 FALSE TRUE
## X38
##      3
## Levels: 1 2 3 4 FALSE TRUE
## X39
##      3
## Levels: 1 2 3 4 FALSE TRUE
## X40
##      3
## Levels: 1 2 3 4 FALSE TRUE
## X41
##      4
## Levels: 1 2 3 4 FALSE TRUE
## X42
##      4
## Levels: 1 2 3 4 FALSE TRUE
## X43
##      4
## Levels: 1 2 3 4 FALSE TRUE
## X44
##      3
## Levels: 1 2 3 4 FALSE TRUE
## X45
##      3
## Levels: 1 2 3 4 FALSE TRUE
## X46
##      3
## Levels: 1 2 3 4 FALSE TRUE
## X47
##      4
## Levels: 1 2 3 4 FALSE TRUE
## X48
##      4
## Levels: 1 2 3 4 FALSE TRUE
## X49
##      4
## Levels: 1 2 3 4 FALSE TRUE
## rowNames
##      FALSE
## Levels: 1 2 3 4 FALSE TRUE
## transpose
##      TRUE
## Levels: 1 2 3 4 FALSE TRUE

```

Strings

How to work with strings

stringr package

- `require(stringr)`

A look at the stringer package

- `stri_c(str1, str2)`

concatenates two string

- `str_len(str)`

```
require(stringr)
```

```
## Loading required package: stringr
```

```
table1t$Rep<-str_replace(table1t$Rep,"[rep]{3}?", "\\1")  
table1t$Rep<-str_replace(table1t$Rep,"A", "1")  
table1t$Rep<-str_replace(table1t$Rep,"B", "2")  
table1t$Rep<-str_replace(table1t$Rep,"C", "3")  
table1t$Rep<-as.factor(table1t$Rep)
```

Reading Tables

Reading a table of other types

- <http://www.statmethods.net/input/importingdata.html>
- <http://stackoverflow.com/questions/17288197/reading-a-csv-file-organized-horizontally>
- http://rgm3.lab.nig.ac.jp/RGM/R_rdf.html?f=Ecdat/man/read.transpose.Rd&d=R_CC
- Input files from Stata

```
library(foreign)
mydata <- read.dta("c:/mydata.dta")
```

Morning Tea Time

Back in 20min

Need coffee !!

Types

Let's read the next table

Reading a table using xls

```
setwd("/Users/pcru/SizeDoesMatter1")
#dir()
table2<-read.xlsx2("2_R Wkshp_dummy data_Env Data_incl2outliersMK.xlsx", sheetName = "Sheet2", head
```

	Group	Site	Sample.ID	Rep	Spill.date	Sample.collection.date
1	Contaminated	1	10000	1	14-May-14	15.5.14
2	Contaminated	1	10001	2	14-May-14	15.5.14
3	Contaminated	1	10002	3	14-May-14	15.5.14
4	Contaminated	2	10003	1	14-May-14	15.5.14
5	Contaminated	2	10004	2	14-May-14	15.5.14
6	Contaminated	2	10005	3	14-May-14	15.5.14

Reading the next table

Reading a table I

Oh NO

- All columns have been set to factors
- Dates have different formats

```
str(table2[,1:11])
```

```
## 'data.frame': 48 obs. of 11 variables:
## $ Group : Factor w/ 2 levels "Contaminated",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ Site : Factor w/ 4 levels "1","2","3","4": 1 1 1 2 2 2 1 1 1 2 ...
## $ Sample.ID : Factor w/ 18 levels "10000","10001",...: 1 2 3 4 5 6 7 8 9 1 ...
## $ Rep : Factor w/ 9 levels "1","2","3","A",...: 1 2 3 1 2 3 7 8 9 7 ...
## $ Spill.date : Factor w/ 2 levels "14-May-14","N/A": 1 1 1 1 1 1 1 1 1 1 ...
## $ Sample.collection.date: Factor w/ 4 levels "15.5.14","17/5/14",...: 1 1 1 1 1 1 2 2 2 2 ...
## $ labnum : Factor w/ 36 levels "2000","2001",...: 1 2 3 4 5 6 7 8 9 19 ...
## $ phosphate..ppb. : Factor w/ 39 levels "10","105","108",...: 27 30 28 26 25 27 12 15 13 7 .
## $ ammonia..ppb. : Factor w/ 41 levels "10","103","1042",...: 10 14 15 6 7 4 31 34 32 28 ...
## $ chlorophyll..ug.L. : Factor w/ 38 levels "1","10","11",...: 20 23 21 25 17 18 16 14 15 12 ...
## $ DO.... : Factor w/ 31 levels "100","120","31",...: 5 4 3 7 6 5 8 7 9 11 ...
```

Reading the next table

Reading a table II

Break it down

First read a few rows only

```
table2 <- read.xlsx2("2_R Wkshp_dummy data_Env Data_incl2outliersMK.xlsx", sheetName = "Sheet2",
  header = TRUE, rowNames = FALSE, as.Data.frame = FALSE, colIndex = c(1:5),
  stringsAsFactors = FALSE, colClasses = c("character", "numeric", "numeric",
  rep("character", 2)), endRow = 4)
sapply(table2, mode)
```

```
##      Group      Site Sample.ID      Rep      Spill.date
## "character" "numeric" "numeric" "character" "character"
##      rowNames as.Data.frame
##      "logical" "logical"
```

```
sapply(table2, class)
```

```
##      Group      Site Sample.ID      Rep      Spill.date
## "character" "numeric" "numeric" "character" "character"
##      rowNames as.Data.frame
##      "logical" "logical"
```

Reading the next table

Setting the data types

colClasses

- The variable `colClasses` can be used to specify the row types.
- We need to set **stringsAsFactor=FALSE** or all columns will be loaded as factors
- The dates are in a non-standard format so we need to read them as chars first

```
table2b<-read.xlsx2("2_R Wkshp_dummy data_Env Data_incl2outliersMK.xlsx",  
sheetName = "Sheet2",header=TRUE,rowNames=FALSE,as.Data.frame=FALSE,  
colIndex=c(1:11),stringsAsFactors=FALSE,  
colClasses=c("character",rep("numeric",2),"character",rep("character",2),rep("numeric",6)))  
sapply(table2,class)
```

```
##      Group      Site Sample.ID      Rep  Spill.date  
## "character" "numeric" "numeric" "character" "character"  
##      rowNames as.Data.frame  
##      "logical"      "logical"
```


Reading table 2

Setting the Date Type

```
table2f <- table2
table2f$Spill.date <- as.Date(table2f$Spill.date, "%d-%b-%y")
table2f$Sample.collection.date <- as.Date(table2f$Sample.collection.date, "%d.%m.%y")

## Error in as.Date.default(table2f$Sample.collection.date, "%d.%m.%y"):
## do not know how to convert 'table2f$Sample.collection.date' to
## class "Date"

# sapply(table2f,mode)
sapply(table2f, class)

##      Group      Site  Sample.ID      Rep  Spill.date
## "character" "numeric" "numeric" "character" "Date"
##      rowNames as.Data.frame
##      "logical" "logical"
```

Reading table 2

Setting the Date Type Correctly

colClasses

- The as.Date method can take a format string as the second variable
- The format strings are described in help on strptime
- But Spill.date has **two formats**
- We can use the if else function to combine them

```
table2bf<-table2b
table2bf$Spill.date<-as.Date(table2bf$Spill.date,"%d-%b-%y")
cdate1<-as.Date(table2bf$Sample.collection.date,"%d.%m.%y")
cdate2<-as.Date(table2bf$Sample.collection.date,"%d/%m/%y")
table2bf$Sample.collection.date<-as.Date(ifelse
(!is.na(cdate1),as.Date(cdate1),as.Date(cdate2)), origin="1970-01-01")
table2bf$Group<-as.factor(table2bf$Group)
table2bf$Rep<-as.factor(table2bf$Rep)
dated<-table2bf$Sample.collection.date-table2bf$Spill.date
```

Reading table 2

Setting the Date Type Correctly

Count the NAs

```
na_count <-sapply(table2bf, function(y) sum(length(which(is.na(y)))))
na_count
```

```
##           Group           Site      Sample.ID
##           0             0             0
##           Rep      Spill.date Sample.collection.date
##           0             24             0
##           labnum  phosphate..ppb.      ammonia..ppb.
##           0             0             0
## chlorophyll..ug.L.      DO....      rowNames
##           0             0             0
##           as.Date.frame
##           0
```

Strings

Reading table 2

Just fix the Rep column using the stringr package again

```
require(stringr)
table2bf$Rep<-str_replace(table2bf$Rep,"[rep]{3}?", "\\1")
table2bf$Rep<-str_replace(table2bf$Rep,"A","1")
table2bf$Rep<-str_replace(table2bf$Rep,"B","2")
table2bf$Rep<-str_replace(table2bf$Rep,"C","3")
table2bf$Rep<-as.factor(table2bf$Rep)
str(table2bf)

## 'data.frame': 48 obs. of 13 variables:
## $ Group : Factor w/ 2 levels "Contaminated",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ Site : num 1 1 1 2 2 2 1 1 1 2 ...
## $ Sample.ID : num 10000 10001 10002 10003 10004 ...
## $ Rep : Factor w/ 3 levels "1","2","3": 1 2 3 1 2 3 1 2 3 1 ...
## $ Spill.date : Date, format: "2014-05-14" "2014-05-14" ...
## $ Sample.collection.date: Date, format: "2014-05-15" "2014-05-15" ...
## $ labnum : num 2000 2001 2002 2003 2004 ...
## $ phosphate..ppb. : num 3020 3253 3169 2999 2879 ...
## $ ammonia..ppb. : num 13880 14598 14676 10984 11657 ...
## $ chlorophyll..ug.L. : num 302 323 315 352 289 296 254 248 250 220 ...
## $ DO... : num 34 33 31 38 36 34 40 38 41 45 ...
## $ rowNames : logi FALSE FALSE FALSE FALSE FALSE FALSE ...
## $ as.Data.frame : logi FALSE FALSE FALSE FALSE FALSE FALSE ...
```

Merging Tables

How to merge two data sets?

Using the merge command

The inbuilt command merge

- R has a command merge
- To begin, start looking at the first 9 lines of the tables and merge them
- Need to use Group, Site, Sample.ID because otherwise it's not unique

```
merge(x, y, by = intersect(names(x), names(y)),
      by.x = by, by.y = by, all = FALSE, all.x = all, all.y = all,
      sort = TRUE, suffixes = c(".x", ".y"),
      incomparables = NULL, ...)
```

```

tab1c<-table1t[1:9,]
tab2c<-table2b[1:9,]
m1<-merge(tab1c,tab2c,by.x="Sample ID",by.y="Sample.ID")
m2<-merge(table1t,table2bf,by.x=c("Group","Site","Sample ID"),
by.y=c("Group","Site","Sample.ID"))
m3<-merge(table1t,table2bf,by.x=c("Group","Site","Sample ID","Rep"),
by.y=c("Group","Site","Sample.ID","Rep"))

```

Lunch Time

Back in 30 min

Provided

How do I append two data sets?

To begin load the third data set

Follow up data from contaminated site

```

table3<-read.xlsx2("3_Follow up data from contaminated site_MK.xlsx",
  sheetName ="Sheet1",header=TRUE,rowNames=FALSE,
  colClasses=c(rep("character",3),
  rep("character",2),rep("numeric",18)))
table3f<-table3
table3f$Spill.date<-as.Date(table3f$Spill.date,"%d.%m.%y")
table3f$Sample.collection.date<-as.Date(table3f$Sample.collection.date,"%d.%m.%y")
sapply(table3f,mode)
sapply(table3f,class)

```

How do I append two data sets?

Loading the third data set

Joining table 3 to the other merged tables

- We need to be careful to match everything
- Install the **plyr** package This has lots of useful functions for renaming var etc
- This means we need columns for corynebacteriaceae and porphyromonadaceae
- Should these values be NA or 0?
- We will do one of each.
- Generally we would use NA but in this case 0 is better as its likely the rows were missing as none were detected

How do I append two data sets?

Appending the third set

```
require(plyr)
Sample.ID←rep(20000,3)
table3fi←cbind(table3f,Sample.ID)
#how many columns I can't count
ncol(table3fi)
ncol(m3)
#now get the cols all right
table3fii←table3fi[c(1,2,24,3,4:23)]
m3i←m3[c(1:4,19:20,5:18,21:26)]
setdiff(names(m3i),names(table3fii))
m3ii←rename(m3i,c("Sample ID"="Sample.ID"))
corynebacteriaceae←rep(0,nrow(table3fii))
porphyromonadaceae←rep(NA,nrow(table3fii))
table3fiii←cbind(table3fii, corynebacteriaceae, porphyromonadaceae)
setdiff(names(m3ii),names(table3fiii))

m3ii[,c(7:24)] ← sapply(m3ii[,c(7:24)],as.numeric)
m3ii[,c(1:4)] ←sapply(m3ii[,c(1:4)],as.character)
#m3ii[,c(" Site ")] ←sapply(m3ii[,c(" Site ")],as.character)

table3fiii[,c(1:4)] ← sapply(table3fiii[,c(1:4)],as.character)
table3fiii[,c(7:24)] ← sapply(table3fiii[,c(7:24)],as.numeric)
table4←rbind(m3ii,table3fiii)
table4[,1] ← sapply(table4[,1],as.factor)
```

```
## Loading required package: plyr
```

```
## [1] 24
```

```
## [1] 27
```

```
## [1] "Sample ID"          "corynebacteriaceae" "porphyromonadaceae"
```

```
## character(0)
```

Another Break

Fat or wide

Reshaping Tables

reshape2

reshape2

- vignette(reshape) doesn't work
- try <http://had.co.nz/reshape/>
- and <http://seananderson.ca/2013/10/19/reshape.html>

A small example for melt

- Suppose we want a box plot to see if there are outliers

- We will use ggplot2 box plot
- The box plot needs data in long format.
- To use this first **melt** the data
- We need to specify the unique key, the variable name and the value name
- The key is not unique.
- Then plot it

Reshaping Tables

melt and boxplot

The code

```
matable4<-melt(table4[,c(1:4,6:25)],variable.name = "microbe",
value.name ="abundance", id=c("Group","Site","Sample.ID","Rep"),
factorsAsStrings=FALSE,rm.na=TRUE)
```

```
require(reshape2)
```

```
## Loading required package: reshape2
```

```
matable4<-melt(table4[,c(1:4,7:25)],variable.name = "microbe",
value.name ="abundance", id=c("Group","Site","Sample.ID","Rep"),
factorsAsStrings=FALSE,rm.na=TRUE)
```

Reshaping Tables

Boxplot cont

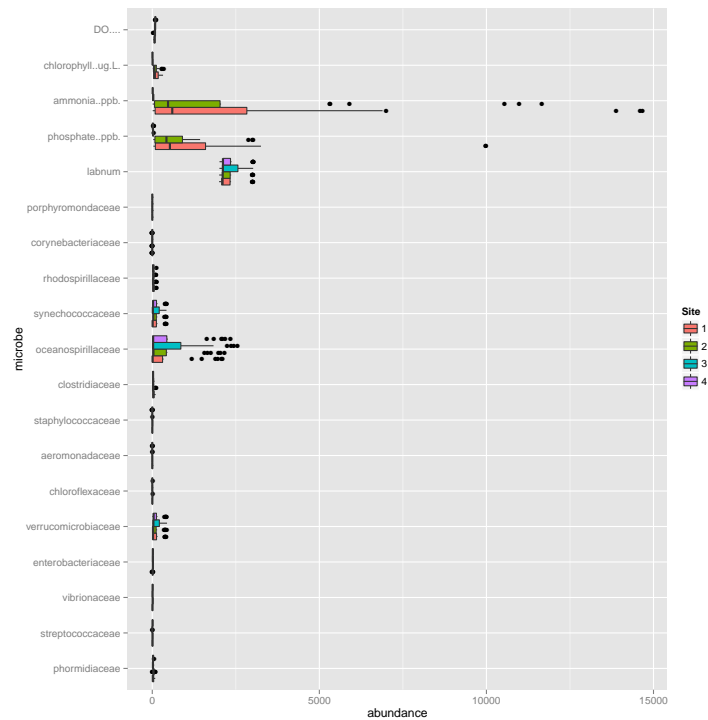
Using ggplot

- As we have keys we need to specify the x and y
- Let's make the sites different colors
- The variable names are long so flip it with *coord_flip()*
- Looks like we have outliers...hmm

```
require(ggplot2)
```

```
## Loading required package: ggplot2
```

```
ggplot(matable4,aes(x=microbe,y=abundance,fill=Site)) + geom_boxplot() + coord_flip()
## Warning: Removed 24 rows containing non-finite values (stat_boxplot).
```



Finding Outliers

Interquartile range

Finding Outliers

- Outliers are defined 1.5 times the interquartile range above the upper quartile
- Assume that rows 12 and 14 in phosphate are errors as the 9 is typed twice
- Still issues with ammonia to explore

```
phosphate<-table4[, "phosphate..ppb."]
upper.limit <- quantile(phosphate)[4] + 1.5*IQR(phosphate)
lower.limit <- quantile(phosphate)[2] - 1.5*IQR(phosphate)
#table4[phosphate> upper.limit,c("Site", "phosphate..ppb.")]
```

Reshaping Tables

Finding Outliers

Removing Outliers

	Site	phosphate..ppb.
1	1	3020.00
2	1	3253.00
3	1	3169.00
12	1	9982.00
14	1	9982.00
16	1	1542.00

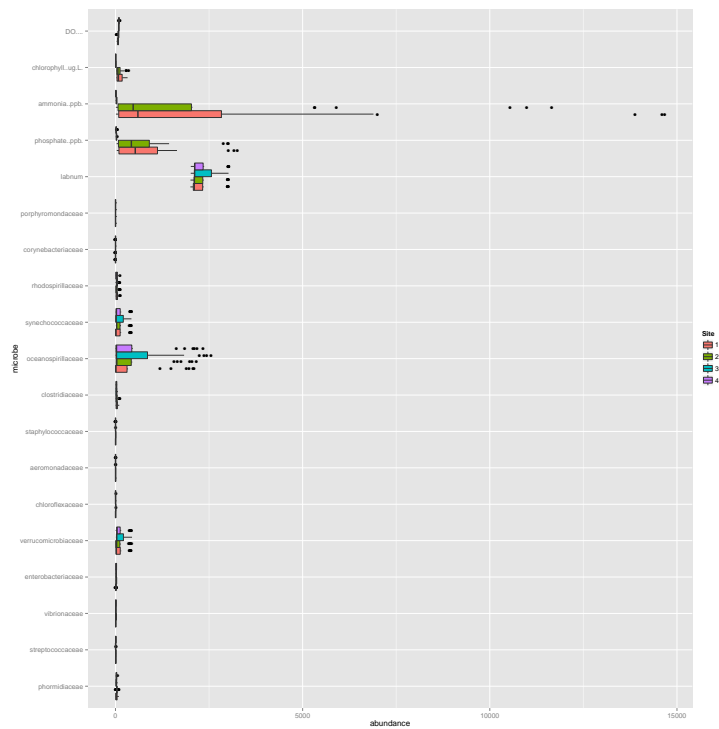
```
table4[12,"phosphate..ppb."]<-982
table4[14,"phosphate..ppb."]<-982
```

Outliers check

Redo the boxplot

Look again ggplot

```
## Warning: Removed 24 rows containing non-finite values (stat.boxplot).
```



R package

RSQLite

RSQLite

- Suppose merge is not enough? I know about SQL and want to do joins
- Install RSQLite
- We also need to install DBI

```
## Loading required package: RSQLite
```

```
db <- dbConnect(SQLite(), dbname="Test.sqlite")
#getConfig()$staged.queries
# sqldf(attach "Test1.sqlite" as new)
dbBegin(db)
```

```
## [1] TRUE
```

```
dbWriteTable(db, "table1", table1t, overwrite=TRUE)
```

```
## [1] TRUE
```

```
dbReadTable(db, "table1")
```

```
##           Group Site Sample.ID Rep phormidiaceae
## X2      Contaminated     1   10000     1      24872
## X3      Contaminated     1   10001     2      24872
## X4      Contaminated     1   10002     3       5822
## X5      Contaminated     2   10003     1       7538
## X6      Contaminated     2   10004     2       7201
## X7      Contaminated     2   10005     3       7538
## X8      Contaminated     1   10006     1       8467
## X9      Contaminated     1   10007     2       7340
## X10     Contaminated     1   10008     3       8467
## X11     Contaminated     2   10000     1       2000
## X12     Contaminated     2   10001     2       2083
## X13     Contaminated     2   10002     3       1899
## X14     Contaminated     1   10003     1       1947
## X15     Contaminated     1   10004     2       2733
## X16     Contaminated     1   10005     3       2385
## X17     Contaminated     2   10006     1        800
## X18     Contaminated     2   10007     2        738
## X19     Contaminated     2   10008     3        800
## X20     Contaminated     1   10003     1        200
```

##	X21	Contaminated	1	10004	2	189
##	X22	Contaminated	1	10005	3	271
##	X23	Contaminated	2	10006	1	46
##	X24	Contaminated	2	10007	2	62
##	X25	Contaminated	2	10008	3	94
##	X26	Contaminated	3	10009	1	24
##	X27	Control	3	10010	2	64
##	X28	Control	3	10011	3	21
##	X29	Control	4	10012	1	56
##	X30	Control	4	10013	2	27
##	X31	Control	4	10014	3	53
##	X32	Control	3	10015	1	115
##	X33	Control	3	10016	2	97
##	X34	Control	3	10017	3	45
##	X35	Control	4	10009	1	33
##	X36	Control	4	10010	2	51
##	X37	Control	4	10011	3	47
##	X38	Control	3	10012	1	105
##	X39	Control	3	10013	2	72
##	X40	Control	3	10014	3	115
##	X41	Control	4	10015	1	18
##	X42	Control	4	10016	2	54
##	X43	Control	4	10017	3	33
##	X44	Control	3	10012	1	36
##	X45	Control	3	10013	2	58
##	X46	Control	3	10014	3	36
##	X47	Control	4	10015	1	60
##	X48	Control	4	10016	2	164
##	X49	Control	4	10017	3	79
##	rowNames	FALSE	FALSE	FALSE	F1LSE	FALSE
##	transpose	TRUE	TRUE	TRUE	TRUE	TRUE
##		streptococcaceae	vibrionaceae	enterobacteriaceae		
##	X2	11	33	131		
##	X3	7	40	200		
##	X4	14	40	200		
##	X5	8	95	151		
##	X6	10	83	140		
##	X7	8	95	151		
##	X8	5	29	132		
##	X9	5	51	168		
##	X10	5	29	132		
##	X11	10	34	97		
##	X12	17	38	91		
##	X13	27	31	51		
##	X14	0	0	2		

## X15	1	0	1
## X16	0	0	2
## X17	26	33	34
## X18	22	58	42
## X19	26	33	34
## X20	6	5	39
## X21	2	3	23
## X22	5	1	39
## X23	3	9	55
## X24	1	5	95
## X25	3	0	55
## X26	2	6	36
## X27	3	3	36
## X28	0	4	30
## X29	1	30	79
## X30	5	9	129
## X31	1	1	124
## X32	0	10	52
## X33	4	6	13
## X34	0	2	9
## X35	4	4	11
## X36	0	10	41
## X37	0	3	29
## X38	10	39	288
## X39	10	29	413
## X40	12	34	481
## X41	5	2	43
## X42	3	5	50
## X43	4	5	86
## X44	10	4	28
## X45	12	1	28
## X46	1	0	44
## X47	4	7	48
## X48	2	11	111
## X49	3	5	88
## rowNames	FALSE	FALSE	FALSE
## transpose	TRUE	TRUE	TRUE
##	verrucomicrobiaceae	chloroflexaceae	aeromonadaceae
## X2	977	351	20
## X3	1500	246	76
## X4	844	246	76
## X5	1006	41	1
## X6	1112	83	6
## X7	1195	41	0
## X8	1805	23	0

## X9	1906	28	0
## X10	1902	23	0
## X11	1244	40	1
## X12	1933	40	1
## X13	1244	80	0
## X14	251	1	0
## X15	271	0	1
## X16	299	0	0
## X17	1348	209	1
## X18	3612	205	0
## X19	1348	209	3
## X20	176	1	0
## X21	211	0	3
## X22	183	1	0
## X23	544	0	9
## X24	611	1	0
## X25	544	0	1
## X26	471	0	0
## X27	500	0	1
## X28	541	0	0
## X29	1405	3	1
## X30	1678	1	1
## X31	1360	0	0
## X32	1590	0	0
## X33	398	0	0
## X34	195	1	0
## X35	1213	7	2
## X36	3461	12	1
## X37	1688	3	0
## X38	590	1	1
## X39	598	0	0
## X40	639	1	0
## X41	949	0	0
## X42	974	0	0
## X43	662	0	0
## X44	267	0	0
## X45	249	2	0
## X46	337	0	0
## X47	625	0	0
## X48	886	0	0
## X49	791	0	0
## rowNames	FALSE	FALSE	FALSE
## transpose	TRUE	TRUE	TRUE
##	staphylococcaceae	clostridiaceae	oceanospirillaceae
## X2	115	274	1438

## X3	342	288	1789
## X4	342	258	1789
## X5	4	365	5
## X6	9	365	2
## X7	4	365	9
## X8	1	643	14
## X9	1	941	14
## X10	1	711	14
## X11	0	204	93
## X12	0	229	72
## X13	0	285	93
## X14	0	8	1080
## X15	0	12	1633
## X16	1	12	1080
## X17	4	400	747
## X18	7	733	636
## X19	2	299	747
## X20	1	76	256
## X21	0	63	263
## X22	2	85	256
## X23	1	136	284
## X24	20	643	293
## X25	1	136	293
## X26	0	31	189
## X27	1	59	510
## X28	0	42	215
## X29	0	143	2096
## X30	0	124	834
## X31	0	100	426
## X32	0	34	263
## X33	0	33	1095
## X34	0	18	523
## X35	0	96	273
## X36	0	100	1432
## X37	0	74	330
## X38	1	119	4584
## X39	1	181	3811
## X40	0	202	3165
## X41	0	38	380
## X42	0	29	548
## X43	0	56	403
## X44	0	62	394
## X45	0	58	311
## X46	0	66	376
## X47	0	66	773

## X48	0	167	1778
## X49	0	40	1289
## rowNames	FALSE	FALSE	FALSE
## transpose	TRUE	TRUE	TRUE
##	synechococcaceae	rhodospirillaceae	corynebacteriaceae
## X2	471	1267	0
## X3	498	1597	0
## X4	692	1844	0
## X5	20	70	0
## X6	20	82	0
## X7	48	70	0
## X8	27	97	0
## X9	83	97	0
## X10	27	97	0
## X11	61	579	0
## X12	61	603	0
## X13	61	579	0
## X14	245	2245	0
## X15	245	2001	0
## X16	142	2834	0
## X17	95	1432	0
## X18	70	1834	0
## X19	95	1432	0
## X20	101	786	0
## X21	104	844	0
## X22	101	826	0
## X23	65	1833	0
## X24	53	2528	0
## X25	65	2999	0
## X26	67	568	0
## X27	128	1877	0
## X28	152	582	0
## X29	769	1699	0
## X30	954	3145	0
## X31	555	1171	0
## X32	45	323	0
## X33	164	911	0
## X34	513	485	0
## X35	75	732	0
## X36	414	3101	0
## X37	298	1262	0
## X38	807	3586	0
## X39	1916	5757	0
## X40	1120	4168	0
## X41	276	821	0

## X42	394	489	0
## X43	498	611	0
## X44	212	1001	0
## X45	301	889	0
## X46	330	943	0
## X47	521	1300	0
## X48	1220	3013	0
## X49	383	1255	0
## rowNames	FALSE	FALSE	FALSE
## transpose	TRUE	TRUE	TRUE
##	porphyromonadaceae		
## X2	0		
## X3	0		
## X4	0		
## X5	0		
## X6	0		
## X7	0		
## X8	0		
## X9	0		
## X10	0		
## X11	0		
## X12	0		
## X13	0		
## X14	0		
## X15	0		
## X16	0		
## X17	0		
## X18	0		
## X19	0		
## X20	0		
## X21	0		
## X22	0		
## X23	0		
## X24	0		
## X25	0		
## X26	0		
## X27	0		
## X28	0		
## X29	0		
## X30	0		
## X31	0		
## X32	0		
## X33	0		
## X34	0		
## X35	0		

```

## X36      0
## X37      0
## X38      0
## X39      0
## X40      0
## X41      0
## X42      0
## X43      0
## X44      0
## X45      0
## X46      0
## X47      0
## X48      0
## X49      0
## rowNames FALSE
## transpose TRUE

dbListFields(db,"table1")

## [1] "row_names"      "Group"          "Site"
## [4] "Sample ID"      "Rep"            "phormidiaceae"
## [7] "streptococcaceae" "vibrionaceae"   "enterobacteriaceae"
## [10] "verrucomicrobiaceae" "chloroflexaceae" "aeromonadaceae"
## [13] "staphylococcaceae" "clostridiaceae" "oceanospirillaceae"
## [16] "synechococcaceae" "rhodospirillaceae" "corynebacteriaceae"
## [19] "porphyromondaceae"

dbListTables(db)

## [1] "table1"

dbGetQuery(db, "SELECT * from table1")

##   row_names      Group Site Sample ID  Rep phormidiaceae
## 1      X2 Contaminated   1    10000    1      24872
## 2      X3 Contaminated   1    10001    2      24872
## 3      X4 Contaminated   1    10002    3       5822
## 4      X5 Contaminated   2    10003    1       7538
## 5      X6 Contaminated   2    10004    2       7201
## 6      X7 Contaminated   2    10005    3       7538
## 7      X8 Contaminated   1    10006    1       8467
## 8      X9 Contaminated   1    10007    2       7340
## 9     X10 Contaminated   1    10008    3       8467
## 10     X11 Contaminated   2    10000    1       2000
## 11     X12 Contaminated   2    10001    2       2083
## 12     X13 Contaminated   2    10002    3       1899
## 13     X14 Contaminated   1    10003    1       1947

```


## 14	X15 Contaminated	1	10004	2	2733
## 15	X16 Contaminated	1	10005	3	2385
## 16	X17 Contaminated	2	10006	1	800
## 17	X18 Contaminated	2	10007	2	738
## 18	X19 Contaminated	2	10008	3	800
## 19	X20 Contaminated	1	10003	1	200
## 20	X21 Contaminated	1	10004	2	189
## 21	X22 Contaminated	1	10005	3	271
## 22	X23 Contaminated	2	10006	1	46
## 23	X24 Contaminated	2	10007	2	62
## 24	X25 Contaminated	2	10008	3	94
## 25	X26 Contaminated	3	10009	1	24
## 26	X27 Control	3	10010	2	64
## 27	X28 Control	3	10011	3	21
## 28	X29 Control	4	10012	1	56
## 29	X30 Control	4	10013	2	27
## 30	X31 Control	4	10014	3	53
## 31	X32 Control	3	10015	1	115
## 32	X33 Control	3	10016	2	97
## 33	X34 Control	3	10017	3	45
## 34	X35 Control	4	10009	1	33
## 35	X36 Control	4	10010	2	51
## 36	X37 Control	4	10011	3	47
## 37	X38 Control	3	10012	1	105
## 38	X39 Control	3	10013	2	72
## 39	X40 Control	3	10014	3	115
## 40	X41 Control	4	10015	1	18
## 41	X42 Control	4	10016	2	54
## 42	X43 Control	4	10017	3	33
## 43	X44 Control	3	10012	1	36
## 44	X45 Control	3	10013	2	58
## 45	X46 Control	3	10014	3	36
## 46	X47 Control	4	10015	1	60
## 47	X48 Control	4	10016	2	164
## 48	X49 Control	4	10017	3	79
## 49	rowNames	FALSE FALSE	FALSE FALSE	FALSE	FALSE
## 50	transpose	TRUE TRUE	TRUE TRUE	TRUE	TRUE
##	streptococcaceae	vibrionaceae	enterobacteriaceae	verrucomicrobiaceae	
## 1	11	33	131	977	
## 2	7	40	200	1500	
## 3	14	40	200	844	
## 4	8	95	151	1006	
## 5	10	83	140	1112	
## 6	8	95	151	1195	
## 7	5	29	132	1805	

## 8	5	51	168	1906
## 9	5	29	132	1902
## 10	10	34	97	1244
## 11	17	38	91	1933
## 12	27	31	51	1244
## 13	0	0	2	251
## 14	1	0	1	271
## 15	0	0	2	299
## 16	26	33	34	1348
## 17	22	58	42	3612
## 18	26	33	34	1348
## 19	6	5	39	176
## 20	2	3	23	211
## 21	5	1	39	183
## 22	3	9	55	544
## 23	1	5	95	611
## 24	3	0	55	544
## 25	2	6	36	471
## 26	3	3	36	500
## 27	0	4	30	541
## 28	1	30	79	1405
## 29	5	9	129	1678
## 30	1	1	124	1360
## 31	0	10	52	1590
## 32	4	6	13	398
## 33	0	2	9	195
## 34	4	4	11	1213
## 35	0	10	41	3461
## 36	0	3	29	1688
## 37	10	39	288	590
## 38	10	29	413	598
## 39	12	34	481	639
## 40	5	2	43	949
## 41	3	5	50	974
## 42	4	5	86	662
## 43	10	4	28	267
## 44	12	1	28	249
## 45	1	0	44	337
## 46	4	7	48	625
## 47	2	11	111	886
## 48	3	5	88	791
## 49	FALSE	FALSE	FALSE	FALSE
## 50	TRUE	TRUE	TRUE	TRUE
##	chloroflexaceae	aeromonadaceae	staphylococcaceae	clostridiaceae
## 1	351	20	115	274

## 2	246	76	342	288
## 3	246	76	342	258
## 4	41	1	4	365
## 5	83	6	9	365
## 6	41	0	4	365
## 7	23	0	1	643
## 8	28	0	1	941
## 9	23	0	1	711
## 10	40	1	0	204
## 11	40	1	0	229
## 12	80	0	0	285
## 13	1	0	0	8
## 14	0	1	0	12
## 15	0	0	1	12
## 16	209	1	4	400
## 17	205	0	7	733
## 18	209	3	2	299
## 19	1	0	1	76
## 20	0	3	0	63
## 21	1	0	2	85
## 22	0	9	1	136
## 23	1	0	20	643
## 24	0	1	1	136
## 25	0	0	0	31
## 26	0	1	1	59
## 27	0	0	0	42
## 28	3	1	0	143
## 29	1	1	0	124
## 30	0	0	0	100
## 31	0	0	0	34
## 32	0	0	0	33
## 33	1	0	0	18
## 34	7	2	0	96
## 35	12	1	0	100
## 36	3	0	0	74
## 37	1	1	1	119
## 38	0	0	1	181
## 39	1	0	0	202
## 40	0	0	0	38
## 41	0	0	0	29
## 42	0	0	0	56
## 43	0	0	0	62
## 44	2	0	0	58
## 45	0	0	0	66
## 46	0	0	0	66

## 47	0	0	0	167
## 48	0	0	0	40
## 49	FALSE	FALSE	FALSE	FALSE
## 50	TRUE	TRUE	TRUE	TRUE
##	oceanospirillaceae	synechococcaceae	rhodospirillaceae	
## 1	1438	471	1267	
## 2	1789	498	1597	
## 3	1789	692	1844	
## 4	5	20	70	
## 5	2	20	82	
## 6	9	48	70	
## 7	14	27	97	
## 8	14	83	97	
## 9	14	27	97	
## 10	93	61	579	
## 11	72	61	603	
## 12	93	61	579	
## 13	1080	245	2245	
## 14	1633	245	2001	
## 15	1080	142	2834	
## 16	747	95	1432	
## 17	636	70	1834	
## 18	747	95	1432	
## 19	256	101	786	
## 20	263	104	844	
## 21	256	101	826	
## 22	284	65	1833	
## 23	293	53	2528	
## 24	293	65	2999	
## 25	189	67	568	
## 26	510	128	1877	
## 27	215	152	582	
## 28	2096	769	1699	
## 29	834	954	3145	
## 30	426	555	1171	
## 31	263	45	323	
## 32	1095	164	911	
## 33	523	513	485	
## 34	273	75	732	
## 35	1432	414	3101	
## 36	330	298	1262	
## 37	4584	807	3586	
## 38	3811	1916	5757	
## 39	3165	1120	4168	
## 40	380	276	821	

## 41	548	394	489
## 42	403	498	611
## 43	394	212	1001
## 44	311	301	889
## 45	376	330	943
## 46	773	521	1300
## 47	1778	1220	3013
## 48	1289	383	1255
## 49	FALSE	FALSE	FALSE
## 50	TRUE	TRUE	TRUE
##	corynebacteriaceae	porphyromonadaceae	
## 1	0	0	
## 2	0	0	
## 3	0	0	
## 4	0	0	
## 5	0	0	
## 6	0	0	
## 7	0	0	
## 8	0	0	
## 9	0	0	
## 10	0	0	
## 11	0	0	
## 12	0	0	
## 13	0	0	
## 14	0	0	
## 15	0	0	
## 16	0	0	
## 17	0	0	
## 18	0	0	
## 19	0	0	
## 20	0	0	
## 21	0	0	
## 22	0	0	
## 23	0	0	
## 24	0	0	
## 25	0	0	
## 26	0	0	
## 27	0	0	
## 28	0	0	
## 29	0	0	
## 30	0	0	
## 31	0	0	
## 32	0	0	
## 33	0	0	
## 34	0	0	

```
## 35      0      0
## 36      0      0
## 37      0      0
## 38      0      0
## 39      0      0
## 40      0      0
## 41      0      0
## 42      0      0
## 43      0      0
## 44      0      0
## 45      0      0
## 46      0      0
## 47      0      0
## 48      0      0
## 49      FALSE  FALSE
## 50      TRUE   TRUE

#dbDisconnect(db)
```

R package

RQLlite

RSQLite

- Some links to RSQL ideas
- <http://stackoverflow.com/questions/12307685/join-more-than-2-tables-in-r-using-rsqlite>
- <https://support.rstudio.com/hc/en-us/articles/201057987-Quick-list-of-useful-R-packages>
- <https://cran.rstudio.com/web/packages/dplyr/vignettes/introduction.html>

```
select coalesce(fileA ,fileB ),valA ,valB
      from t1 LEFT OUTER JOIN t2 On t1.fileA= t2.fileB
UNION select coalesce(fileA ,fileB ),valA ,valB
      from t2 LEFT OUTER JOIN t1 ON t1.fileA= t2.fileB
(CREATE TABLE all_files AS SELECT fileA FROM t1 UNION SELECT fileB from t2 UNION ...).
```

R package

svUnit

Another important component of TDD is refactoring and unit tests

- Refactoring <http://refactoring.com/>
- <http://www.r-bloggers.com/my-experience-of-learning-r-from-basic-graphs-to-performance-tuning/>
- TDD in R <http://www.slideserve.com/andrew/test-driven-development-in-r>
- Version Control tortoiseSVN <http://tortoisesvn.net/> \itemGitHub\url{<https://github.com/>}

Cleaning things up

Dropping row and columns

Dropping selected variables

Dropping Row and Columns with too many NAs

```
numNAs_inData4_rows <- apply(rawData4, 1, function(z) sum(is.na(z)))
numNAs_inData4_col <- apply(table4, 2, function(z) sum(is.na(z))) # count NAs in Data4
lessThan20 <- table4[!(numNAs_inData4_rows > 20),] #only select the rows contain less Than 20 N
lessThan20col <- table4[,!(numNAs_inData4_col > 20)]
```

Dropping row and columns

Dropping selected variables

Tidy Data

In tidy data:

- Each variable forms a column.
- Each observation forms a row.
- Each type of observational unit forms a table.
- <https://cran.r-project.org/web/packages/tidyr/vignettes/tidy-data.html>
- <http://pj.freefaculty.org/R/Rtips.html#toc-Subsection-1.11>

Spit out the dates and numbers

```
dates4<-table4[,c(5,6)]
abundance<-table4[,c(7:25)]
```

Adding a new column

Calculating the number of days

Calculating the number of days

We can just subtract as.Date fields

```
dates4<-table4[,c(5,6)]
abundance<-table4[,c(7:25)]
days<-dates4[,2]-dates4[,1]
```

Setting the relative abundance

Setting the relative abundance

Normalizing data

sapply

- Also known as centring the data
- Ecological percentage of the sum of the variables
- We can use sweep to centre the data
- *options(digits = 1)* Just to make things pretty

```
sweepOutContinu←sweep(abundance,2,apply(abundance,2,min,na.rm=TRUE))
afterSweepContinu←sweep(sweepOutContinu,2,apply(sweepOutContinu,2,max,na.rm=TRUE),"/")
table5←cbind(table4[,c(1:6)],afterSweepContinu,days)
options(digits=1)
sweep(abundance, 2, colSums(abundance), FUN="/")
scale(abundance, center=FALSE, scale=colSums(abundance))
```

Now let's have some fun

Graphics in R

R has nice graphs

- A graphical output
- <http://rcharts.io/gallery/>
- R Graph gallery currently down try <http://rgraphgallery.blogspot.com/>
- A reference on where to go R thumbnails
- ggplot2 (scatter plot of 2 var and then 3 plots)
- To create a correlation heat map

```
library(corrplot)
abuncor←cor(t5lessThan20col[,c(6:22)])
require(corrplot)
corrplot(abuncor, method = "circle")
```

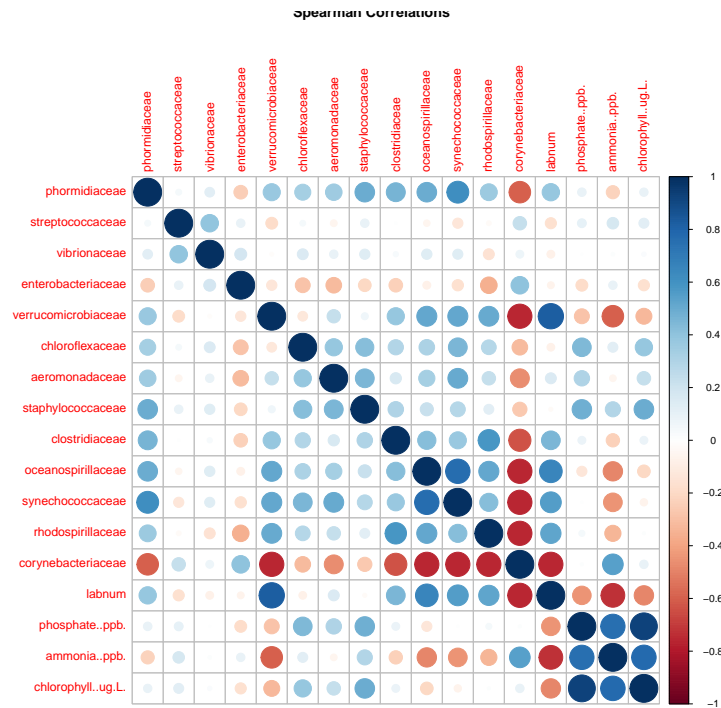
```
## [1] 23
```

```
## Loading required package: corrplot
```


Now let's have some fun

Making a heat map

A heat map



Simple Tests

ttests

t tests

There are many *t* – *tests* available in R <http://www.statmethods.net/stats/ttest.html>

```
# independent 2-group t-test
t.test(t5lessThan20col[,12],t5lessThan20col[,8])

##
## Welch Two Sample t-test
##
## data:  t5lessThan20col[, 12] and t5lessThan20col[, 8]
## t = -3.4052, df = 180.441, p-value = 0.0008149
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
```

```
## -0.20589367 -0.05481872
## sample estimates:
## mean of x mean of y
## 0.2725146 0.4028708
```

What next

Proposed future talks

Help is on the way

- Parameterized Complexity Research Unit (PCRU) PhD students
- PhD student in Bioinformatics from Central South Uni

Your feedback on some ideas

- Using Sweave or Knitr
- Advanced Data Cleaning
- Network Centric data analysis

Resources

If you want to improve this style

References

- [1] LaTeX Beamer <http://latex-beamer.sourceforge.net/>
- [2] Sharelatex Site <https://www.sharelatex.com>
- [3] A Data Cleaning Mooc <https://www.sharelatex.com>

R Packages Used

Session Info

Output of sessionInfo

```
sessionInfo()

## R version 3.1.2 (2014-10-31)
## Platform: x86_64-apple-darwin13.4.0 (64-bit)
##
## locale:
## [1] C
```

```
##
## attached base packages:
## [1] methods stats graphics grDevices utils datasets base
##
## other attached packages:
## [1] corrplot_0.73 RSQlite_1.0.0 DBI_0.3.1 ggplot2_1.0.0
## [5] reshape2_1.4.1 plyr_1.8.1 stringr_0.6.2 xtable_1.7-4
## [9] xlsx_0.5.7 xlsxjars_0.6.1 rJava_0.9-7 knitr_1.11
##
## loaded via a namespace (and not attached):
## [1] MASS_7.3-39 Rcpp_0.11.5 colorspace_1.2-6 digest_0.6.8
## [5] evaluate_0.7.2 formatR_1.2 grid_3.1.2 gtable_0.1.2
## [9] highr_0.5 labeling_0.3 munsell_0.4.2 proto_0.3-10
## [13] scales_0.2.4 tools_3.1.2

# packages_in_use <- c( sessionInfo()$basePkgs, names( sessionInfo()$loadedOnly ) )
#the_citations_list <- lapply( X=packages_in_use, FUN=citation)
#the_citations_list
```