Advanced data structures, I/O & Control Structures

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Matrix

- There are several ways to make a matrix
- To make a 2x3 (2 rows, 3 columns) matrix of 0's:

```
>mat<-matrix(0,2,3)
```

- To make the following matrix:

71	172
73	169
69	160
65	130

```
>mat2<-rbind(c(71,172),c(73,169),c(69,160),c(65,130))
>mat3<-cbind(c(71,73,69,65),c(172,169,160,130))
```

- To make the following matrix:
  - `mat4<-matrix(1:10,2,5, byrow=T)`

1	2	3	4	5
6	7	8	9	10

Revisit vectors: access data

- Accessing individual observations

```
>whales[2]
```

- Slicing

```
>whales[2:5]
```

- Negative indices

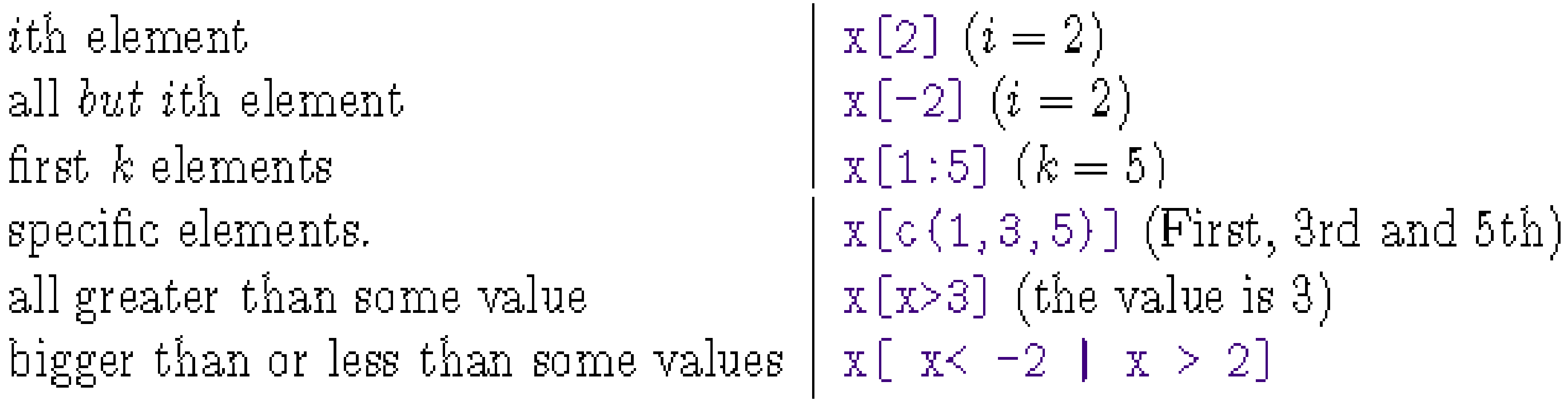
```
>whales[-1]
```

- Logical values

```
>whales[whales>100]
>which(whales>100)
>which.max(whales)
```

Indexing of vector/matrix

- x=1:10



*i*th element	x[2] $(i = 2)$
all *but i*th element	x[-2] $(i = 2)$
first *k* elements	x[1:5] $(k = 5)$
specific elements.	x[c(1,3,5)] (First, 3rd and 5th)
all greater than some value	x[x>3] (the value is 3)
bigger than or less than some values	x[x< -2 | x > 2]

- mat=matrix(1:24, nrow=4)

  mat[,2] # 2nd column

  mat[2,] # 2nd row

  mat[c(2,4),] # 2nd and 4th row

  mat[1:3,1] # 1 to 3 element in column 1

  mat[-c(2,4),] # all but row 2 and 4

New Jersey's Science & Technology University

THE EDGE IN KNOWLEDGE

Create logical vectors by conditions

- Logical operators: <, <=, >, >=, ==, !=
- Comparisons
  - Vectors: AND &; OR |
  - Longer forms &&, ||: return a single value
  - all() and any()
- Examples
  - X=1:5
  - X<5; X>1
  - X >1 & X <5; X >1 | X <5;
  - all(X<5); any(X>1); all(X<5) && any(X>1)
- %in% operator: x %in% c(2,4)

Missing values

- R codes missing values as NA
- is.na(x) is a logical function that assigns a T to all values that are NA and F otherwise

```
>x[is.na(x)]<-0
>mean(x, na.rm=TRUE)
```

Reading in other sources of data

- Use R’ s built-in libraries and data sets

```
>range(lynx) #lynx is a built-in dataset
>library(MASS) # load a library
>data(survey)  # load a dataset in the library
>data(survey, package="MASS")#load just data
>head(survey)
>tail(survey)
```

- Copy and paste by scan()

```
>whales=scan()
1: 74 122 235 111 292 111 211 133 156 79
11:
Read 10 items
```

Read formatted data

- Read data from formatted data files, e.g. a file of numbers from a single file, a table of numbers separated by space, comma, tab etc, with or without header

```
>whale=scan(file="whale.txt")
 "whale.txt" :
74 122 235 111 292 111 211 133 156 79
>whale=read.table(file="whale.txt", header=TRUE)
 "whale.txt" :
    texas florida
1   74     89
2   122    254
3   ....   ....
>read.table(file=file.choose()) # specify the file
>read.table(file="http://statweb.stanford.edu/~rag/stat141/exs/whale.txt",header=T)    # read from internet
```

Data frame

- A "data matrix" or a "data set"
  - it likes a matrix (rectangular grid)
  - But unlike matrix, different columns can be of different types
  - Row names have to be unique
- >alphabet<-data.frame(index=1:26, symbol=LETTERS)
- read.table() stores data in a *data frame*
- Access var in a dataset: $, attach(), with()

```
>library(ISwR)  #load the package that provides thuesen data
>data(thuesen)
>names(thuesen)  #variable names
> blood.glucose # not visible
>length(thuesen$blood.glucose)
>with(thuesen, range(blood.glucose))
```

```
>attach(thuesen)
>range(blood.glucose)
>detach(thuesen)
```

More about data frame

- Indexing of data frames is the same as that of vector and matrix `>energy[energy$stature== "lean",]`
- Sorting rows by order()

```
>energy[order(energy$expend),]
>energy[with(energy, order(stature, expend)),]
```

- Selecting subsets of data by subset()

```
>subset(energy, stature=="lean" & expend>8)
```

- Splitting data

```
>split(energy$expend, energy$stature)
```

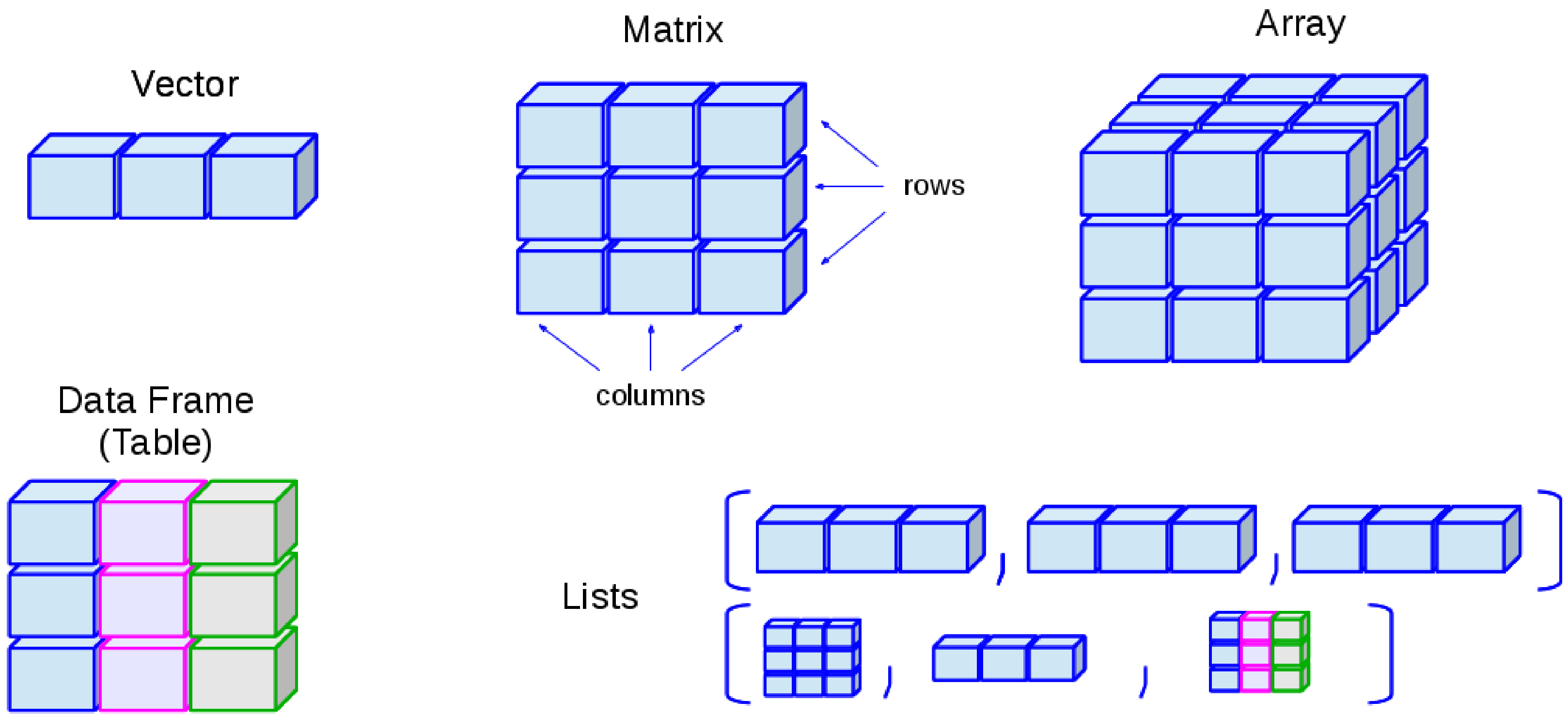
Lists

- A larger composite object for combining a collection of objects
  - Different from data frame, each object can be of different length, in additional to being of different types

```
>a=list(whales=c(74,122,235,111,292,111,211,133,16,79),
 simpsons=c("Homer", "Marge", "Bart", "Lisa", "Maggie"))
```

  - Access by $ or [[]]: a$simpsons or a[[2]]

Summary of data structures



Manage the work environment

- What if there are more variables defined than can be remembered?
- ls() list all the objects(var, fun, etc) in a given environment
- rm(a, b): delete variables a and b
  - rm(list=ls()) will ?
- Get and set working directory

```
>getwd()
>setwd("working/directory/path")
```

- Save and load working environment

```
>save.image(file="filename.RData")
>load(file="filename.RData")
```

scripting

- Edit your commands using your favorite text editors
- How to run

Inside R: >source(filename)

  - Takes the input and runs them
  - Do syntax-check before anything is executed
  - Set echo=T to print executed commands

  OR copy & paste

Outside R: R CMD BATCH filename

output is in *.Rout

Or: Rscript filename

How to install packages

- To install CRAN packages, execute from the R console the following command:

  ```
  > install.packages( 'UsingR' )
  ```

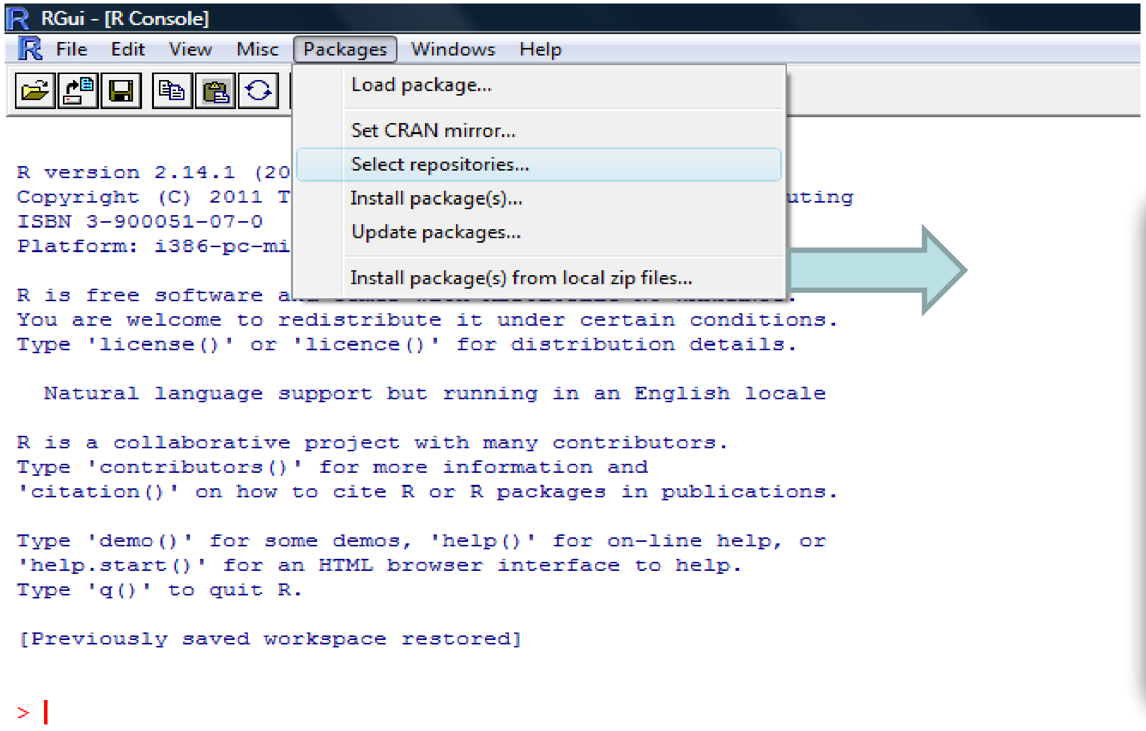
  OR download the package and install it directly

  ```
  R CMD INTALL aPackage_0.1.tar.gz
  ```

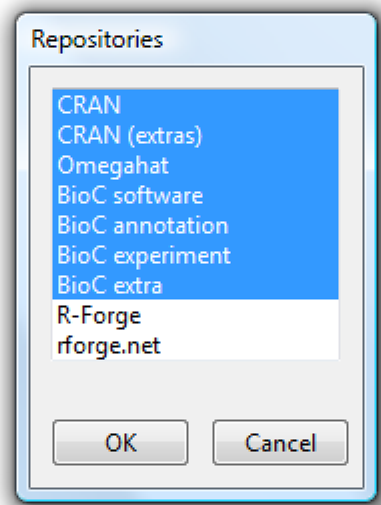
- Load a library

  ```
  >library("UsingR")
  or
  >library(UsingR)
  ```

Windows: Set repositories



```
R version 2.14.1 (20
Copyright (C) 2011 T                                   uting
ISBN 3-900051-07-0
Platform: i386-pc-mi

R is free software a
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

[Previously saved workspace restored]

>
```

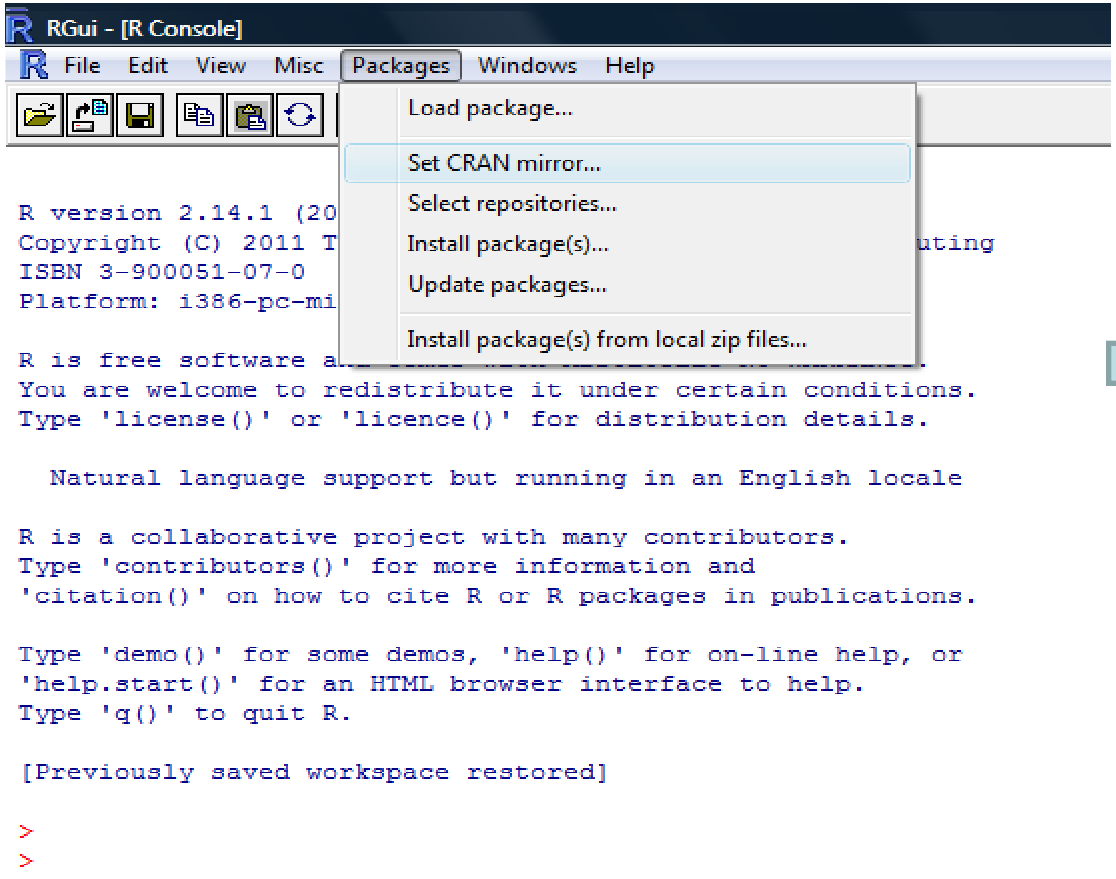


Repositories (selected: CRAN, CRAN (extras), Omegahat, BioC software, BioC annotation, BioC experiment, BioC extra):

- CRAN
- CRAN (extras)
- Omegahat
- BioC software
- BioC annotation
- BioC experiment
- BioC extra
- R-Forge
- rforge.net

- Make sure you include necessary repositories (you may simply select all of them)

Windows: Set CRAN mirror



```
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[Previously saved workspace restored]

>
>
```
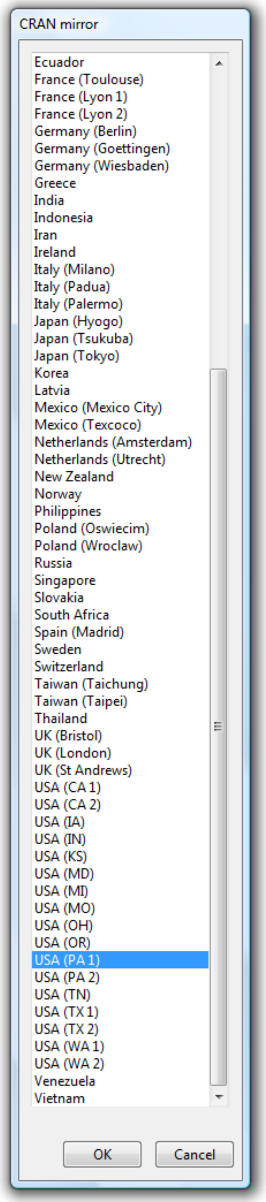
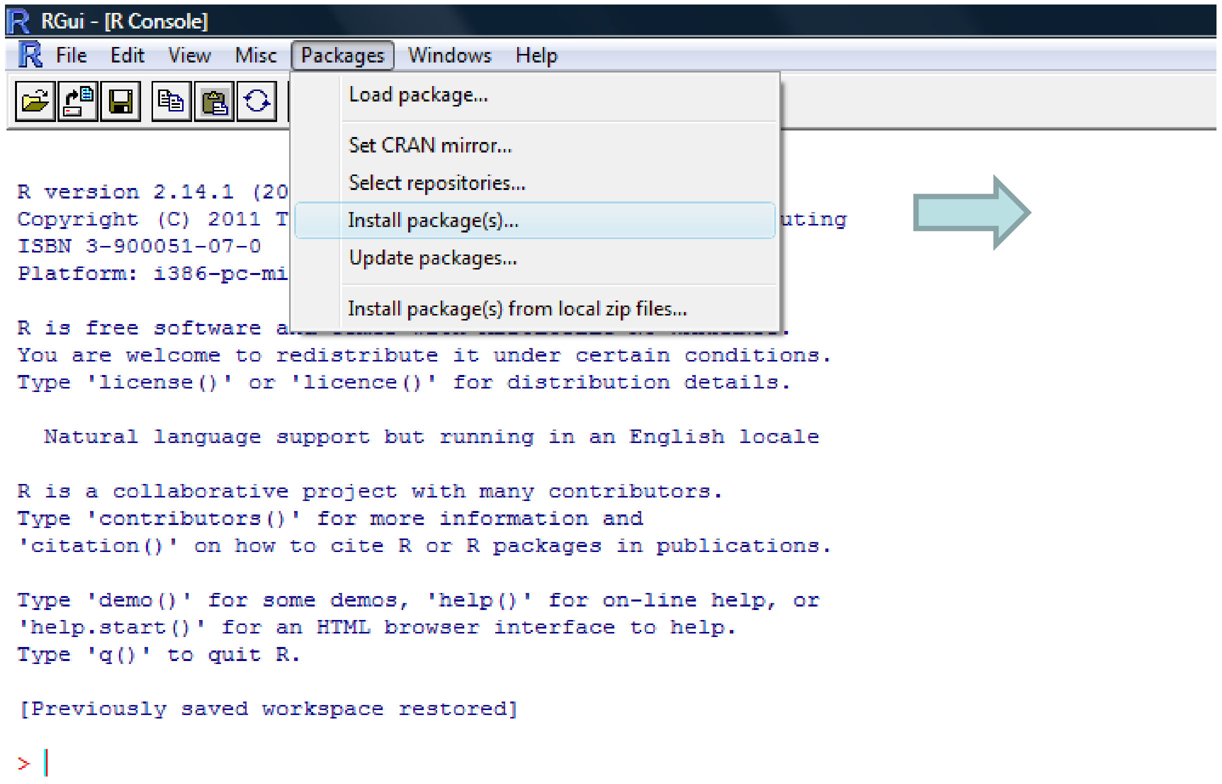



- You can choose anyone but physically close ones are preferred

Windows: install packages



```
R version 2.14.1 (20
Copyright (C) 2011 T                                   uting
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'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

[Previously saved workspace restored]

> |
```

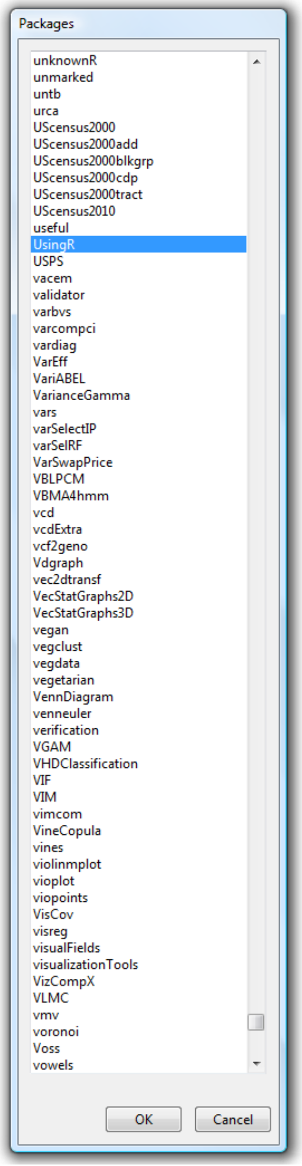

```
unknownR
unmarked
untb
urca
UScensus2000
UScensus2000add
UScensus2000blkgrp
UScensus2000cdp
UScensus2000tract
UScensus2010
useful
UsingR
USPS
vacem
validator
varbvs
varcompci
vardiag
VarEff
VariABEL
VarianceGamma
vars
varSelectIP
varSelRF
VarSwapPrice
VBLPCM
VBMA4hmm
vcd
vcdExtra
vcf2geno
Vdgraph
vec2dtransf
VecStatGraphs2D
VecStatGraphs3D
vegan
vegclust
vegdata
vegetarian
VennDiagram
venneuler
verification
VGAM
VHDClassification
VIF
VIM
vimcom
VineCopula
vines
violinmplot
vioplot
viopoints
VisCov
visreg
visualFields
visualizationTools
VizCompX
VLMC
vmv
voronoi
Voss
vowels
```

Additional references

- Beginners should print out the R Reference Card

http://cran.r-project.org/doc/contrib/Short-refcard.pdf

- The R-FAQ (Frequently Asked Questions on R)

http://cran.r-project.org/doc/FAQ/R-FAQ.html

- A rather terse introduction to R online

http://cran.r-project.org/doc/manuals/R-intro.html

- Bioconductor

http://www.bioconductor.org/

- A useful online manual for R & Bioconductor

http://manuals.bioinformatics.ucr.edu/home/R_BioCondManual

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- Jeff Solka: for some of the slides adapted or modified from his lecture slides at George Mason University
- Brian Healy: for some of the slides adapted or modified from his lecture slides at Harvard University

Getting Data In and Out of R

Principal functions reading data

- read.table, read.csv, for reading tabular data
- readLines, for reading lines of a text file
- source, for reading in R code files (inverse of dump)
- dget, for reading in R code files (inverse of dput)
- load, for reading in saved workspaces
- unserialize, for reading single R objects in binary form

Principal functions writing data

- write.table, for writing tabular data to text files (i.e. CSV) or connections
- writeLines, for writing character data line-by-line to a file or connection
- dump, for dumping a textual representation of multiple R objects
- dput, for outputting a textual representation of an R object
- save, for saving an arbitrary number of R objects in binary format (possibly compressed) to a file.
- serialize, for converting an R object into a binary format for outputting to a connection (or file).

Video

- https://youtu.be/Z_dc_FADyi4
- ?read.table

read.table(file="http://statweb.stanford.edu/~rag/stat141/exs/whale.txt"),header=T) # read from internet

- ?readLines

readLines("http://statweb.stanford.edu/~rag/stat141/exs/whale.txt")

Using dput() and dump()

- dput()/dget()
  - y <- **data.frame**(a = 1, b = "a")
  - dput(y)
  - dput(y, file = "y.R")
- dump()/source()
  - x <- "foo"; y <- **data.frame**(a = 1L, b = "a")
  - dump(c("x", "y"), file = "data.R")
  - **rm**(x, y)
  - **source**("data.R")
  - str(y)

Difference between dput() and dump()

- dump can be used to output multiple objects
- dump adds the object name and can be source()'d

Binary Formats save()/load()

- a <- **data.frame**(x = rnorm(100), y = runif(100))
- b <- **c**(3, 4.4, 1 / 3)
- *## Save 'a' and 'b' to a file*
- **save**(a, b, file = "mydata.rda")
- *## Load 'a' and 'b' into your workspace*
- **load**("mydata.rda")
- *## Save everything to a file*
- **save.image**(file = "mydata.RData")
- *## load all objects in this file*
- **load**("mydata.RData")

Reading in Larger Datasets with read.table

- Video https://youtu.be/BJYYIJO3UFI
- A tip

```
> initial <- read.table("datatable.txt", nrows = 100)
> classes <- sapply(initial, class)
> tabAll <- read.table("datatable.txt", colClasses = classes)
```

Summary

- write.csv() and write.table() are used when you want to exchange data in tabular text format.
- dput() saves single data object in R code
- dump() saves multiple data objects and their metadata in R code
- save() is similar to dump() but saves in binary format or ASCII
- save.image() saves workspace in binary format

Calculating Memory Requirements for R Objects

- An example: a data frame with 1,500,000 rows and 120 columns, all of which are numeric data.
  - 1,500,000 × 120 × 8 bytes/numeric

Control Structures

Commonly used control structures

- if and else: testing a condition and acting on it
- for: execute a loop a fixed number of times
- while: execute a loop *while* a condition is true
- repeat: execute an infinite loop (must break out of it to stop)
- break: break the execution of a loop
- next: skip an iteration of a loop

if-else

- **if**(<condition>) {

## do something

}

## Continue with rest of code

- **if**(<condition>) {

## do something

}

else {

## do something else

}

if-else {if-else}

```
if(<condition1>) {
## do something
} else if(<condition2>) {
## do something different
} else {
## do something different
}
#------------------------
if(<condition1>) {
}
if(<condition2>) {
}
```

Example

```
x <- runif(1, 0, 10)
```

-
  ```
  if(x > 3) {
   y <- 10
  } else {
   y <- 0
  }
  ```

-
  ```
  y <- if(x > 3) {
    10
   } else {
     0
   }
  ```
- `y <- ifelse(x>3, 10, 0)`

ifelse()

- x <- c(6:-4)
- sqrt(x) #- gives warning
- sqrt(ifelse(x >= 0, x, NA)) # no warning
- ## Note: the following also gives the warning !
- ifelse(x >= 0, sqrt(x), NA)

- ## example of different return modes:

```
yes <- 1:3
no <- pi^(0:3)
typeof(ifelse(NA,    yes, no)) # logical
typeof(ifelse(TRUE,  yes, no)) # integer
typeof(ifelse(FALSE, yes, no)) # double
```

for Loops

- **for**(i **in** 1:10) {

 print(i)

}

x <- **c**("a", "b", "c", "d")

- **for**(i **in** 1:4) {

## Print out each element of 'x'

 print(x[i])

}

for Loops (cont’ d)

- seq_along() function is commonly used in conjunction with for loops

```
for(i in seq_along(x)) {
    print(x[i])
}
```

- It is not necessary to use an index-type variable

```
for(letter in x) {
    print(letter)
}
```

- One line loops (curly braces are not required)

```
for(i in 1:4) print(x[i])
```

Nested for loops

```
x <- matrix(1:6, 2, 3)
for(i in seq_len(nrow(x))) {
    for(j in seq_len(ncol(x))) {
       print(x[i, j])
    }
}
```

while Loops

```
while (<condition>) {
    ## do something
}
```

Example:

```
count <- 0
while(count < 10) {
  print(count)
  count <- count + 1
}
```

While loops can potentially result in infinite loops if not written properly. Use with care!

repeat

```
x0 <- 1
tol <- 1e-8
repeat {
    x1 <- computeEstimate()
    if(abs(x1 - x0) < tol) { ## Close enough?
      break
    } else {
      x0 <- x1
    }
}
```

next, break

- next is used to skip an iteration of a loop.

```
for(i in 1:100) {
  if(i <= 20) {
    ## Skip the first 20 iterations
    next
  }
## Do something here
}
```

- break is used to exit a loop immediately, regardless of what iteration the loop may be on.

```
for(i in 1:100) {
   print(i)
   if(i > 20) {
    ## Stop loop after 20 iterations
    break
   }
}
```

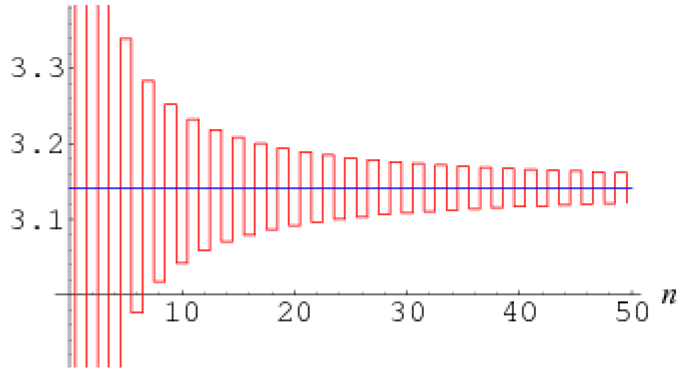
Summary

- Control structures like if, while, and for allow you to control the flow of an R program
- Infinite loops should generally be avoided, even if (you believe) they are theoretically correct.
- Control structures mentioned here are primarily useful for writing programs; for commandline interactive work, the "apply" functions are more useful (will cover later)
- It is more efficient to use built-in functions or vectorization rather than control structures whenever possible.

Computing Lab Ex.

- Compute pi by Gregory series.
  - Let n = 100
  - Use loop
  - Challenge: write one line R
    - by using vectorization

$$4\sum_{k=1}^{n}\frac{(-1)^{k+1}}{2k-1}$$



- Stock Volume Analysis
  - Download IBM historical daily data of the entire 2018 from Yahoo.
  - Find the "Download Data" link to download the csv file to you local disk. https://finance.yahoo.com/quote/IBM/history?period1=1514782800&period2=1546232400&interval=1d&filter=history&frequency=1d
  - Load csv file into a data frame
  - Return all rows where the Close is greater than Open (bull market)
  - Return all rows where the Close is less than Open (bear market)
  - For the above two subsets, compute the average Volume for each.
  - In which market condition is the average Volume higher?

CS636 Homework 1

- Due on midnight June 5, 2020
- Submit electronic copy in Canvas

For the following questions, please use R commands to find solutions when applicable. Please use Jupyter Notebook and submit IPython Notebook File (.ipynb) of your notebook, including all code and results.

1.20 The built-in data set islands contains the size of the world's land masses that exceed 10,000 square miles. Use sort() with the argument decreasing=TRUE to find the seven largest land masses.

For Example, the expected solution is

```
> sort(islands, decreasing=TRUE)[1:7]
     Asia       Africa North America South America    Antarctica        Europe     Australia
    16988        11506          9390          6795          5500          3745          2968
```

1.21 Load the data set primes (UsingR). This is the set of prime numbers in [1,2003]. How many are there? How many in the range [1,100]? [100,1000]?

1.22 Load the data set primes (UsingR). We wish to find all the twin primes. These are numbers *p* and *p*+2, where both are prime.

1. Explain what primes[−1] returns.
2. If you set n=length (primes), explain what primes[−n] returns.
3. Why might primes [−1]—primes [−n] give clues as to what the twin primes are? How many twin primes are there in the data set?

1.23 For the data set treering, which contains tree-ring widths in dimension-less units, use an R function to answer the following:

1. How many observations are there?
2. Find the smallest observation.
3. Find the largest observation.
4. How many are bigger than 1.5?

1.24 The data set mandms (UsingR) contains the targeted color distribution in a bag of M&Ms as percentages for varies types of packaging. Answer these questions.

1. Which packaging is missing one of the six colors?
2. Which types of packaging have an equal distribution of colors?
3. Which packaging has a single color that is more likely than all the others? What color is this?

1.25 The t imes variable in the data set nym. 2002 (UsingR) contains the time to finish for several participants in the 2002 New York City Marathon. Answer these questions.

1. How many times are stored in the data set?
2. What was the fastest time in minutes? Convert this into hours and minutes using R.
3. What was the slowest time in minutes? Convert this into hours and minutes using R.

1.26 For the data set rivers, which is the longest river? The shortest?

1.27 The data set uspop contains decade-by-decade population figures for the United States from 1790 to 1970.

1. Use names() and seq() to add the year names to the data vector.
2. Use diff() to find the inter-decade differences. Which decade had the greatest increase?
3. Explain why you could reasonably expect that the difference will always increase with each decade. Is this the case with the data?