Introduction to R software for statistical computing

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Overview



- 2 Demonstration
- Getting started
- 4 knitr: Integrating R into a reproducible workflow





Introduction

R

- Statistical programming language
- Software environment
- Developed by Ihaka and Gentleman, R Development Core Team
- Appeared in 1993
- Decendent of S, influenced by C
- http://www.r-project.org



Introduction

Capabilities of R

- Data management
- Analysis
- Computation comparable to MATLAB
- Graphics



Introduction

Characteristics of R

- Command line
- Functions, objects
- Data stuctures: (rectangular) data frame, list, vector, matrix



Introduction

Advantages of R

- Freely available
- Can easily write your own functions
- Intuitive to use
- Flexible
- Fast implementation of new methods
- Users have access to source code



Introduction

Disadvantages of R

- Contributed packages should be used with caution
- Limited capacity for working with very large datasets. Data must fit into RAM



Demonstration

Demo to illustrate

- Basic variable assignment and some structures
- Reading in a text file
- Data manipulation: subsets, re-categorizing variables
- Calculate non-parametric survival estimates
- Examine the stucture of R objects
- Extract individual items from R objects



Getting started

Installing R

- cran.r-project.org
- Windows intallation:

cran.r-project.org/bin/windows/base/



Getting started

Editing your R code

You can use your favorite text ditor/IDE (integrated development environment) or use the one that is built-in.

R's editor very basic

- R Studio More features like highlighting and matching brackets
 - Easy to use
 - Includes a built-in terminal
 - Freely available at

http://www.rstudio.com/ide/download/

- Textmate Available only on Mac
 - Even more features and funcitonality



• Freely available at http://macromates.com JoAnn Alvarez Introduction to R

Getting started

Reading and writing files

- Functions read.table(), read.csv(), read.fwf()
- Do not have to specify details as in SAS
- Example:

```
myData <- read.table(file = "filename.csv", header
= TRUE, sep = ",")
```

• Can read other types of files with foreign package

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Getting started

Installing and using packages All R functions and datasets are in packages.

- CRAN cran.r-project.org, bioconductor
- Install: install.packages("Hmisc")
- Load: library(Hmisc)
- Update: update.packages()
- See all currently loaded packages: SessionInfo()





Using the R documentation

- apropos()
- help()



- Reproducible research
- \bullet Combines R code and $\ensuremath{{\ensuremath{\mathbb E}}} T_E\!Xmarkup$ into one report document
- Enables raw output, tables, graphics, and report text to be dynamically updated



knitr

Example report made in knitr

Aim 1 analyses for microhematuria R03

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Contents

1	Written summary	1
2	Demographic and univariate association tables	3
3	Model results	11
4	Mechanism of gender disparity in cystoscopy use in microhematuria work up	13
5	Raw model entput 51. Saw unskipte. 52. Procedum 53. Insights. 54. Complete exclusion. 54. Occupiete exclusion. 55. Working entputy (enthud).	15 15 15 16 17 18
G	Supplementary material 6.1 Check of proportional odds assumption for workup intensity	20 20

1 Written summary

Research aim: Determine the association between race and receipt of a timely and complete evaluation of hematuris in a ration-wide 5% sample of Medicare patients. We hypothesise that Africar-Americane with hematuria receive sub-optimal workup of hematuria compared to Whites, and that controlling for socio-cosmole status will attenuate the scala differences.

Data considerations: Data from areas other than the fifty US states or the District of Columbia were excluded. There were 21 such observations.

Variable dightifiame: Pointas were condeted to have a cancer disposed if they had any of the finding disposed proceds, renal cacker, blocker cacke, out excit, poststabelangi, blocker hengin, other hengin. Base was entoprind as black, white. Hispatia, Astas, or other. For lattice whose race was block or "anknown" in the data were transition at hengin and posttice of automarkan medication. The start of th



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Introduction to R

knitr Example

example.Rnw

\documentclass{article} \begin{document}

<<echo=FALSE>>= data <- rexp(100, 1/7) meandata <- mean(data) @

\noindent The mean of the data was
\Sexpr{round(meandata, 2)}.

<<ceho=FAISE>>= boxplot(data, boxvex = 0.5, boxplot(data, boxvex = 0.5, las = 1, outline = FAISE, ylim = c(0, max(data))) stripchart(data, method = "jitter", pch = 19, vertical = TRUE, add = TRUE) @

\end{document}

knit("example.Rnw")

example.tex

\documentclass{article}
\usepackage{graphicx, color}
\begin{document}

\noindent The mean of the data was 7.12.

\begin{kmitrout}
\definecolor{shadecolor}{rgb}{0.969, 0.969, 0.969}\col
\includegraphics[vidth=\maxvidth]{figure/unnamed-chunk
\end{figure}
\end{kmitrout}
\end{kmitrout}



Simple knitr Example





Figure 1: This is my figure caption

The mean of the data was 7.12.

Resources for learning R

R resources

- Terri Scott's teaching materials http://biostat.mc. vanderbilt.edu/wiki/Main/TheresaScott
- Robert Meunchen's *R* for SAS and SPSS Users http://r4stats.com/books/r4sas-spss/
- Robert Meunchen's https://science.nature.nps.gov/im/datamgmt/ statistics/R/documents/R_for_SAS_SPSS_users.pdf



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Resources for learning R

More resources

- Nashville R Users Group http://www.meetup.com/Nashville-R-Users-Group/
- UCLA's website: http://www.ats.ucla.edu/stat/r/
- R manuals http://cran.r-project.org/manuals.html http://cran.r-project.org/doc/manuals/r-patched/ R-intro.pdf
- Vanderbilt Department of Biostatistics wiki http://biostat.mc.vanderbilt.edu/wiki/Main/RS





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