Lab: Learning R

IGF RNA-Seq Workshop 2018 (PLPTH885)

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6/7/2018

Outline

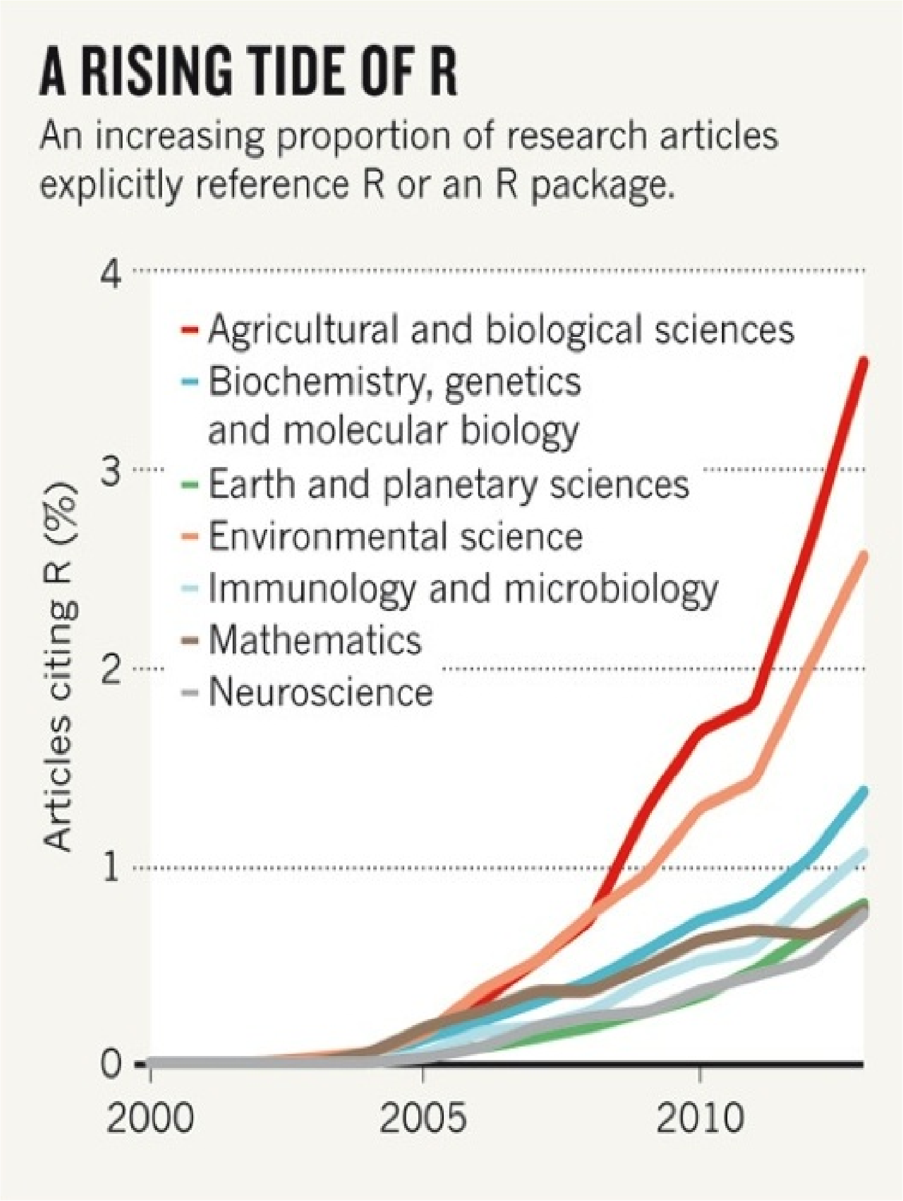
- Introduction of R
- Data structure (vector and data frame)
- Data importing and exporting
- Plotting
- String operations

Lecture assistant

Dr. Cheng He

Why R?

- R is great at statistical computing and graphics
- R is free
- R has great community supports



R example 1 (R for statistics)

Chi-square test

```
d <- c(12, 36, 24, 70)
dm <- matrix(d, nrow=2, byrow=T)
dm
```

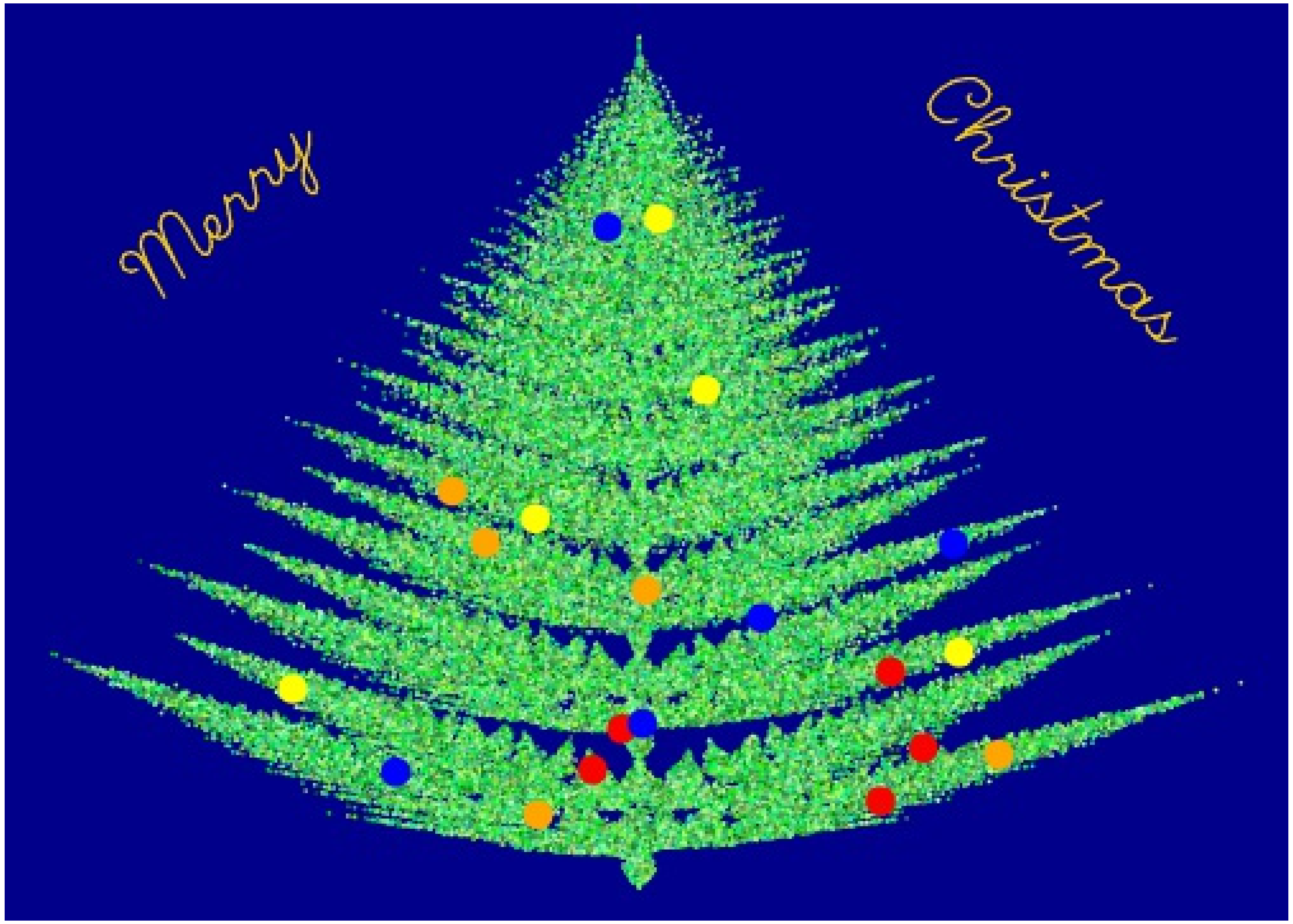
```
     [,1] [,2]
[1,]   12   36
[2,]   24   70
```

```
chisq.test(dm)
```

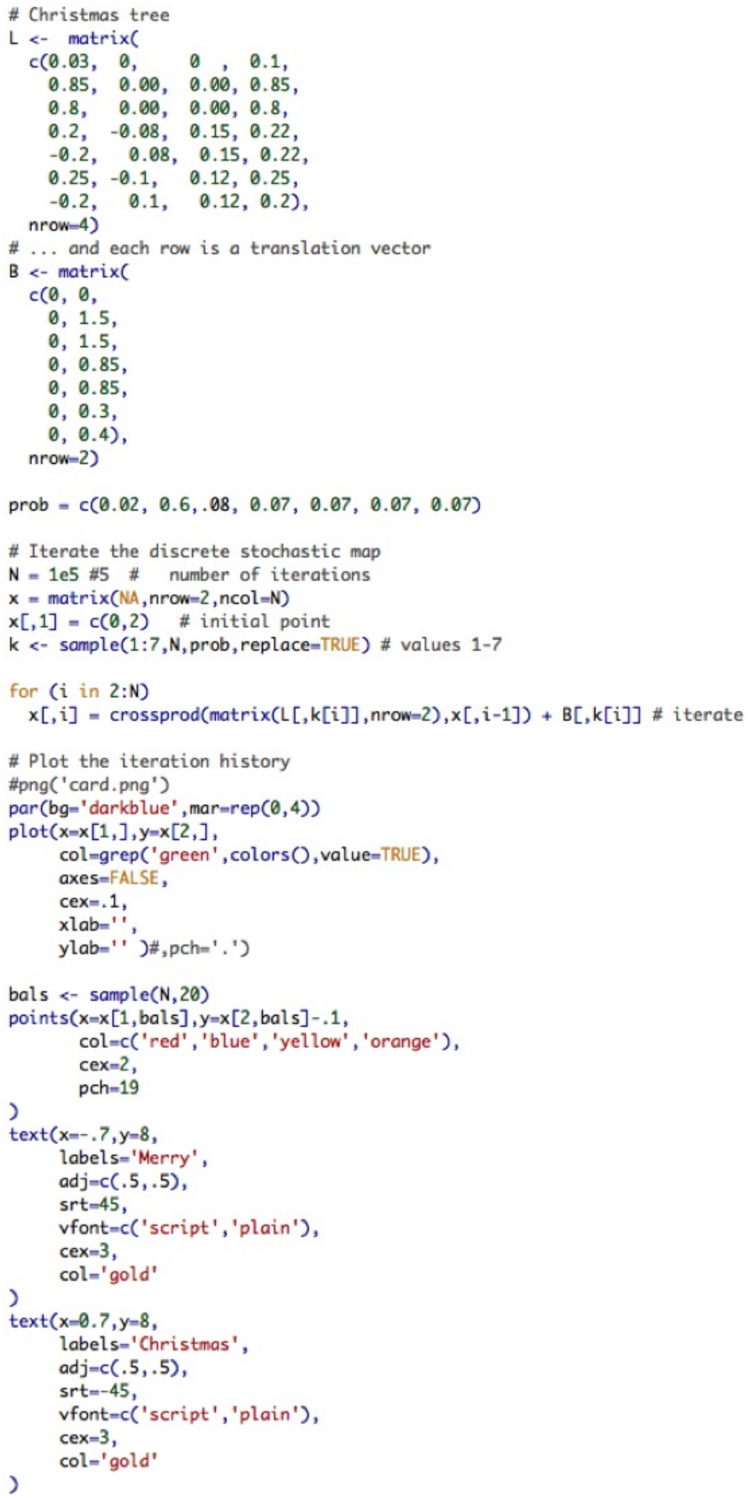
```

    Pearson's Chi-squared test with Yates' continuity correction

data:  dm
X-squared = 7.8894e-31, df = 1, p-value = 1
```

R example 2 (R for graphs)

```
ts="http://129.130.89.83/tmp/public/RNASeq/RNASeq2018/codes/xcard.R"
source(ts)
```



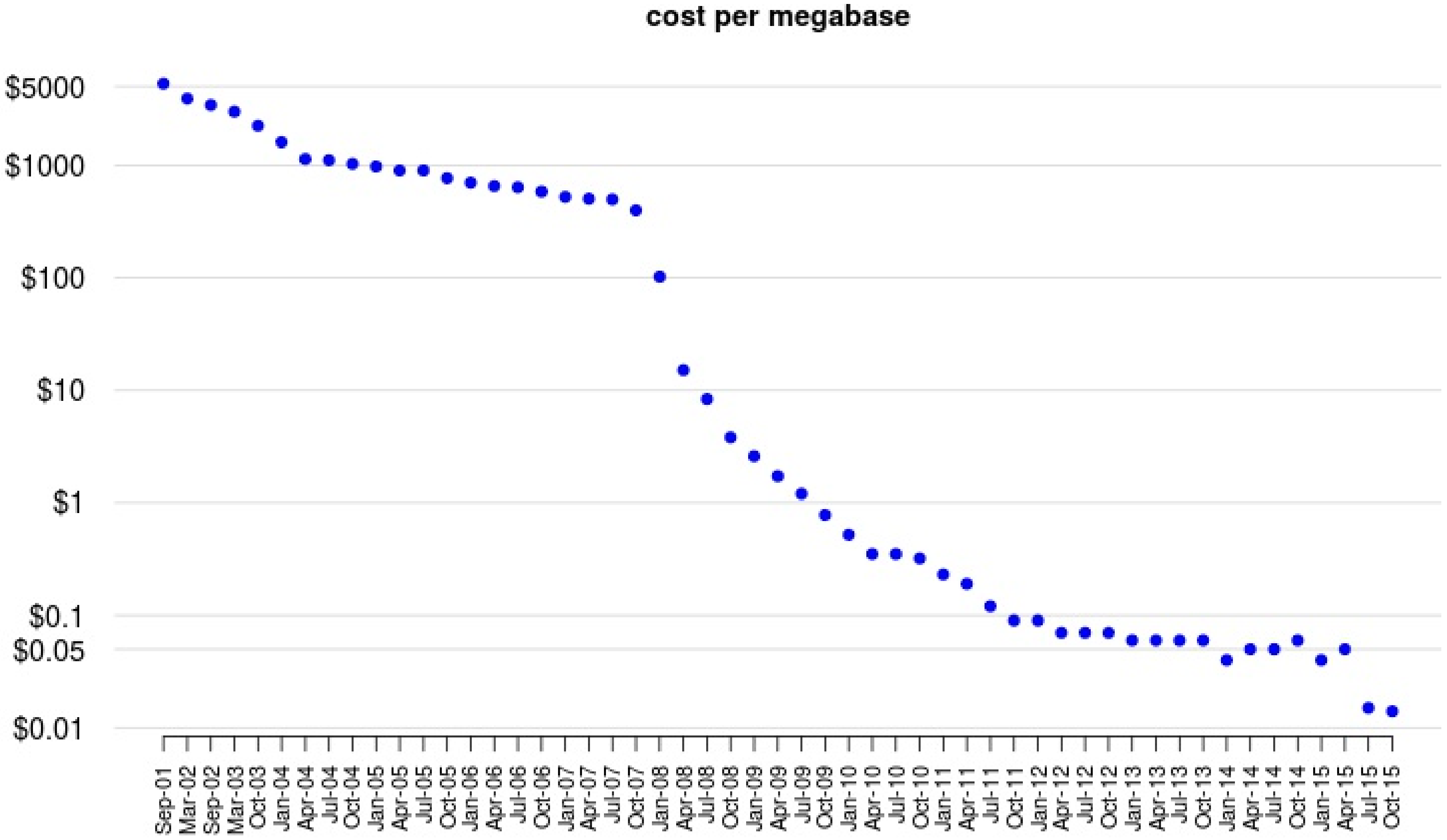
R example 2 code



```
# Christmas tree
L <-  matrix(
  c(0.03,  0,     0  ,  0.1,
    0.85,  0.00,  0.00, 0.85,
    0.8,   0.00,  0.00, 0.8,
    0.2,  -0.08,  0.15, 0.22,
    -0.2,   0.08,  0.15, 0.22,
    0.25, -0.1,   0.12, 0.25,
    -0.2,   0.1,   0.12, 0.2),
  nrow=4)
# ... and each row is a translation vector
B <- matrix(
  c(0, 0,
    0, 1.5,
    0, 1.5,
    0, 0.85,
    0, 0.85,
    0, 0.3,
    0, 0.4),
  nrow=2)

prob = c(0.02, 0.6,.08, 0.07, 0.07, 0.07, 0.07)

# Iterate the discrete stochastic map
N = 1e5 #5  #   number of iterations
x = matrix(NA,nrow=2,ncol=N)
x[,1] = c(0,2)   # initial point
k <- sample(1:7,N,prob,replace=TRUE) # values 1-7

for (i in 2:N)
  x[,i] = crossprod(matrix(L[,k[i]],nrow=2),x[,i-1]) + B[,k[i]] # iterate

# Plot the iteration history
#png('card.png')
par(bg='darkblue',mar=rep(0,4))
plot(x=x[1,],y=x[2,],
     col=grep('green',colors(),value=TRUE),
     axes=FALSE,
     cex=.1,
     xlab='',
     ylab='' )#,pch='.')

bals <- sample(N,20)
points(x=x[1,bals],y=x[2,bals]-.1,
       col=c('red','blue','yellow','orange'),
       cex=2,
       pch=19
)
text(x=-.7,y=8,
     labels='Merry',
     adj=c(.5,.5),
     srt=45,
     vfont=c('script','plain'),
     cex=3,
     col='gold'
)
text(x=0.7,y=8,
     labels='Christmas',
     adj=c(.5,.5),
     srt=-45,
     vfont=c('script','plain'),
     cex=3,
     col='gold'
)
```

R example 3 (R for graphs)

```
cs="http://129.130.89.83/tmp/public/RNASeq/RNASeq2018/codes/trend.R"
source(cs)
```



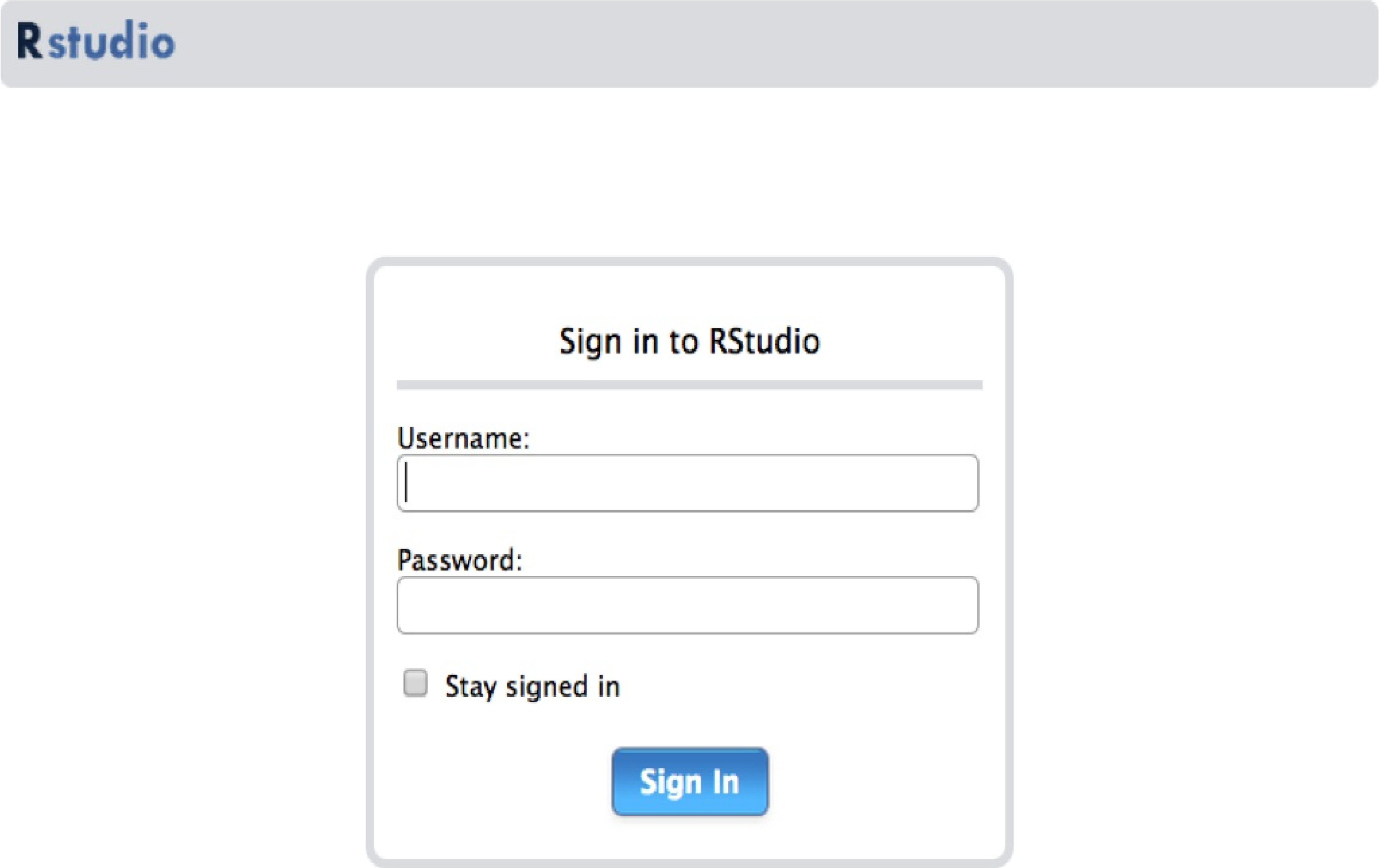
Where can we use R?

Rstudio is an open source integrated development environment (IDE) for R

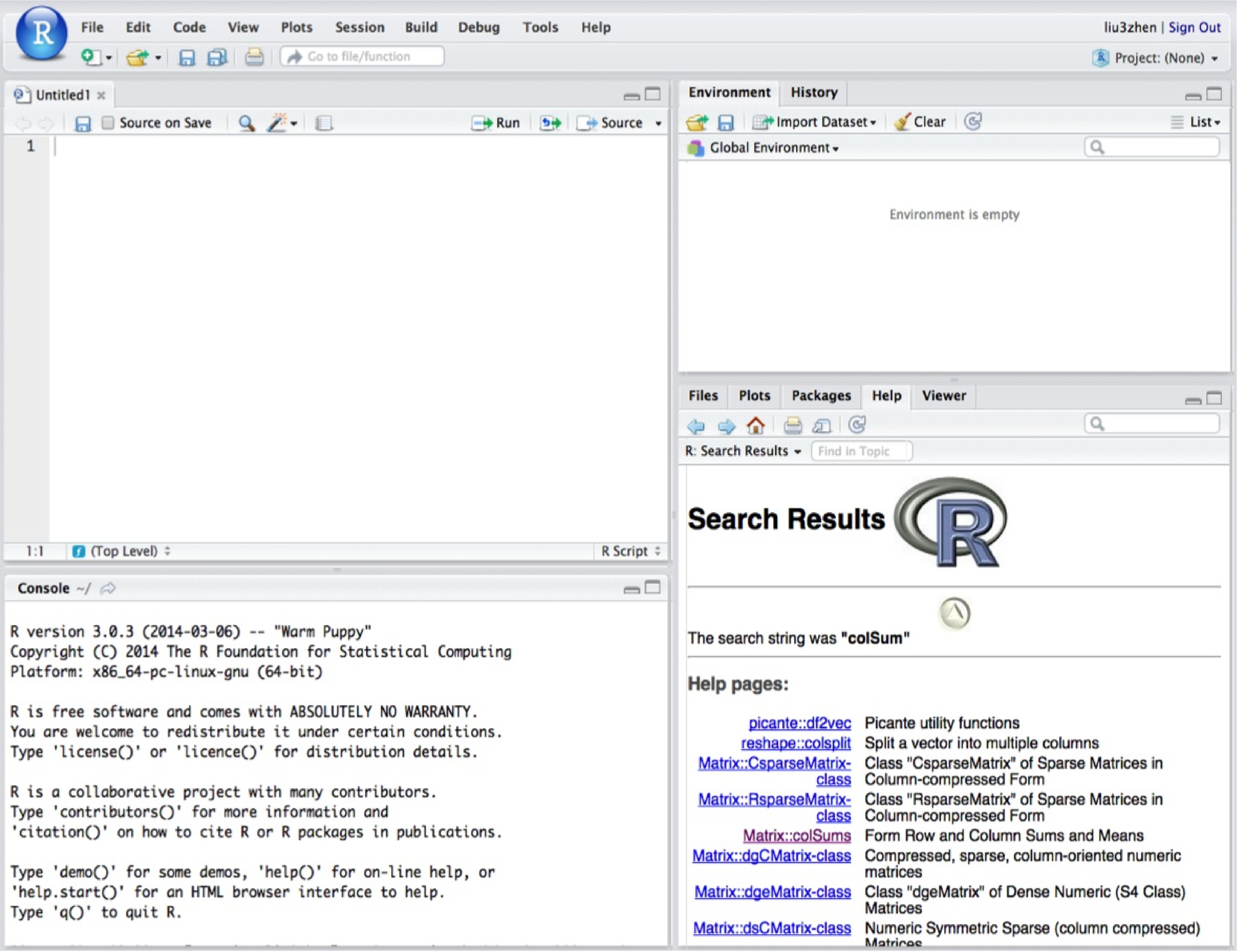
- On your own machine (Rstudio Desktop)
    - Download and install R
    - Download and install Rstudio
- Use Rstudio at Beocat (Rstudio server)
    - rstudio.beocat.cis.ksu.edu
    - Your **KSU ID** and **password** to login

Rstudio at Beocat

rstudio.beocat.cis.ksu.edu



Rstudio interface



```
R version 3.0.3 (2014-03-06) -- "Warm Puppy"
Copyright (C) 2014 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

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.
```

Search Results

The search string was "**colSum**"

Help pages:

picante::df2vec	Picante utility functions
reshape::colsplit	Split a vector into multiple columns
Matrix::CsparseMatrix-class	Class "CsparseMatrix" of Sparse Matrices in Column-compressed Form
Matrix::RsparseMatrix-class	Class "RsparseMatrix" of Sparse Matrices in Column-compressed Form
Matrix::colSums	Form Row and Column Sums and Means
Matrix::dgCMatrix-class	Compressed, sparse, column-oriented numeric matrices
Matrix::dgeMatrix-class	Class "dgeMatrix" of Dense Numeric (S4 Class) Matrices
Matrix::dsCMatrix-class	Numeric Symmetric Sparse (column compressed) Matrices

Getting started, R commands

Expression: evaluated, printed, and the value lost

```r
2 + 4
```

```
[1] 6
```

```r
68 * 0.15
```

```
[1] 10.2
```

Assignment assign values to a variable
evaluated, the value passed to a variable but NOT printed

assignment operator: <- or =

```r
y <- 2
y = 2
info <- "hello world"
cat(info)
```

```
hello world
```

Notes

- Comments (#): Notes to scripts, starting with a hashtag (‘#’), everything to the end of the line is a comment.

y <- 2 + 4 # an example of the assignment

- Variable names are case senstive

```
y <- 2
Y <- 3
y
```

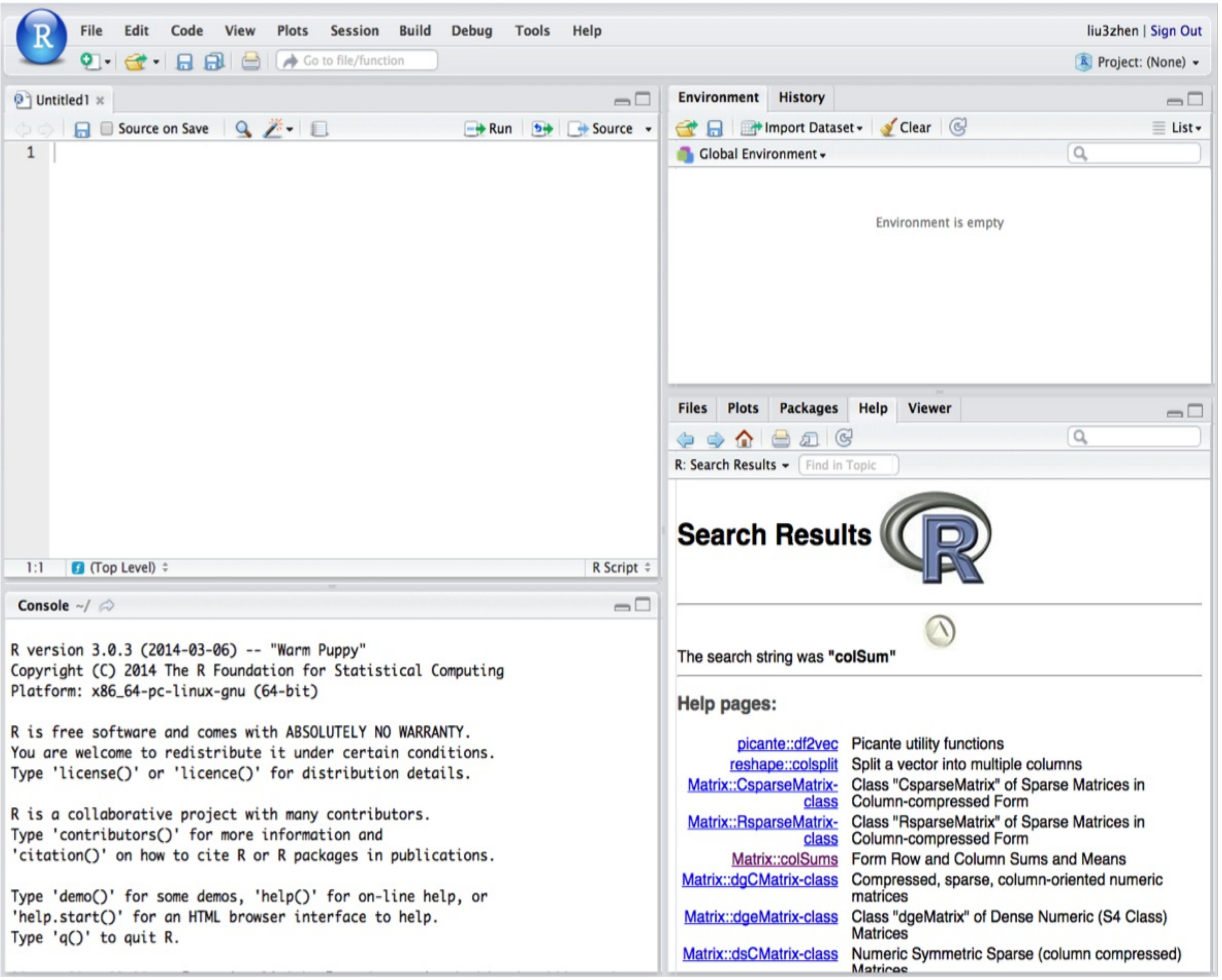
```
[1] 2
```

```
Y
```

```
[1] 3
```

Executing commands

- PC window: control + return (enter)
- Apple MAC: command + return (enter)



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vector: multiple elements

A vector is a single entity consisting of an ordered collection of numbers, characters, logical quantities, etc.

concatenate command: **c()**

- Numeric vector
  c(10.4, 5.6, 3.1, 6.4, 21.7)

- Logical vector
  c(TRUE, FALSE, TRUE, TRUE)

- Character vector
  c("a", "b", "c")

- Missing value (NA, not available)
  c("a", "b", "c", NA)

vector manipulation (I)

```
# Numeric vector
x <- c(10.4, 5.6, 3.1, 6.4, 21.7)
sum(x)
```

```
[1] 47.2
```

```
2*x
```

```
[1] 20.8 11.2  6.2 12.8 43.4
```

```
### extract 2nd elements
x[2]
```

```
[1] 5.6
```

vector manipulation (II)

Logical vector

lv <- c(TRUE, FALSE, TRUE, TRUE) !lv lv == FALSE

vector manipulation (III)

```r
# Character vector
cv <- c("a", "b", "c")
cv2 <- paste(cv, 1:3, sep="")
cv2
```

```
[1] "a1" "b2" "c3"
```

```r
# Missing value
mvv <- c("a", "b", "c", NA)
is.na(mvv)
```

```
[1] FALSE FALSE FALSE  TRUE
```

vector manipulation (IV)

Vectors must have their values with the same mode, either numeric, character, logical, or other types.

conversion to other modes

```
z <- 0:9
is.numeric(z)
```

```
[1] TRUE
```

```
digits <- as.character(z) # convert to character
d <- as.numeric(digits) # convert to numeric
```

vector manipulation (V)

- Select a subset of a vector

```
x <- c(4, 5, 7, 3, 9)
x[c(2, 3)]
```

```
[1] 5 7
```

```
x[x>6]
```

```
[1] 7 9
```

```
x[-c(1, 5)]
```

```
[1] 5 7 3
```

- Modify a vector

```
x[3] <- 23.1
c(x, 10.9)
```

```
[1]  4.0  5.0 23.1  3.0  9.0 10.9
```

Question 1

Can a vector contain different types of elements?

```
c(1, "a")
c(1, TRUE)
c(TRUE, "a")
c(1, "a", TRUE)
```

Data frame

A data frame may be regarded as a matrix (table) with columns possibly of differing modes

- Making data frames

```
df <- data.frame(name=c("Josh", "rose"), age=c(23, 35))
df
```

```
  name age
1 Josh  23
2 rose  35
```

Working with a data frame

```
df
```

```
  name age
1 Josh  23
2 rose  35
```

Trying these commands:

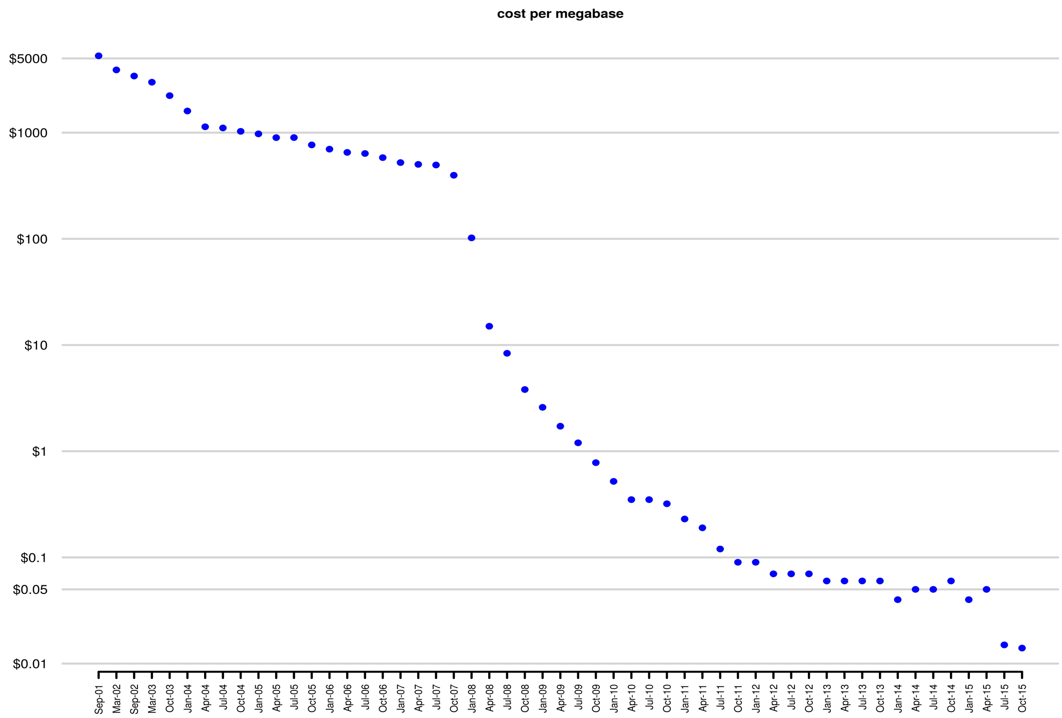
```
head(df, 1)
tail(df, 1)
str(df)
df[2, 1]
df[2, 2]
df[2]
df[, 2]
```

Importing data

read.table(): to read a data frame (table)
read.delim, **read.csv**

```
cpm="http://129.130.89.83/tmp/public/RNASeq/RNASeq2018/data/cs.txt"
d <- read.delim(cpm)
head(d, 3)
```

```
    Date Cost.per.Mb Cost.per.Genome
1 Sep-01     5292.39        95263072
2 Mar-02     3898.64        70175437
3 Sep-02     3413.80        61448422
```



Exporting data

write.table() or **write.csv()**

To write a tab-delimited file

```
x <- data.frame(a = "pi", b = pi)
write.table(x, file="foo.txt", sep="\t", row.names=FALSE)
```

- file="foo.txt": foo.txt is the ouput file name
- sep="\t": separated by a tab (\t)
- row.names=FALSE: row names are not included in the output

Practice by your own

- Create a data frame

  three columns: 1. Name 2. Major 3. Gender
  three rows (entries): your neighbors and you

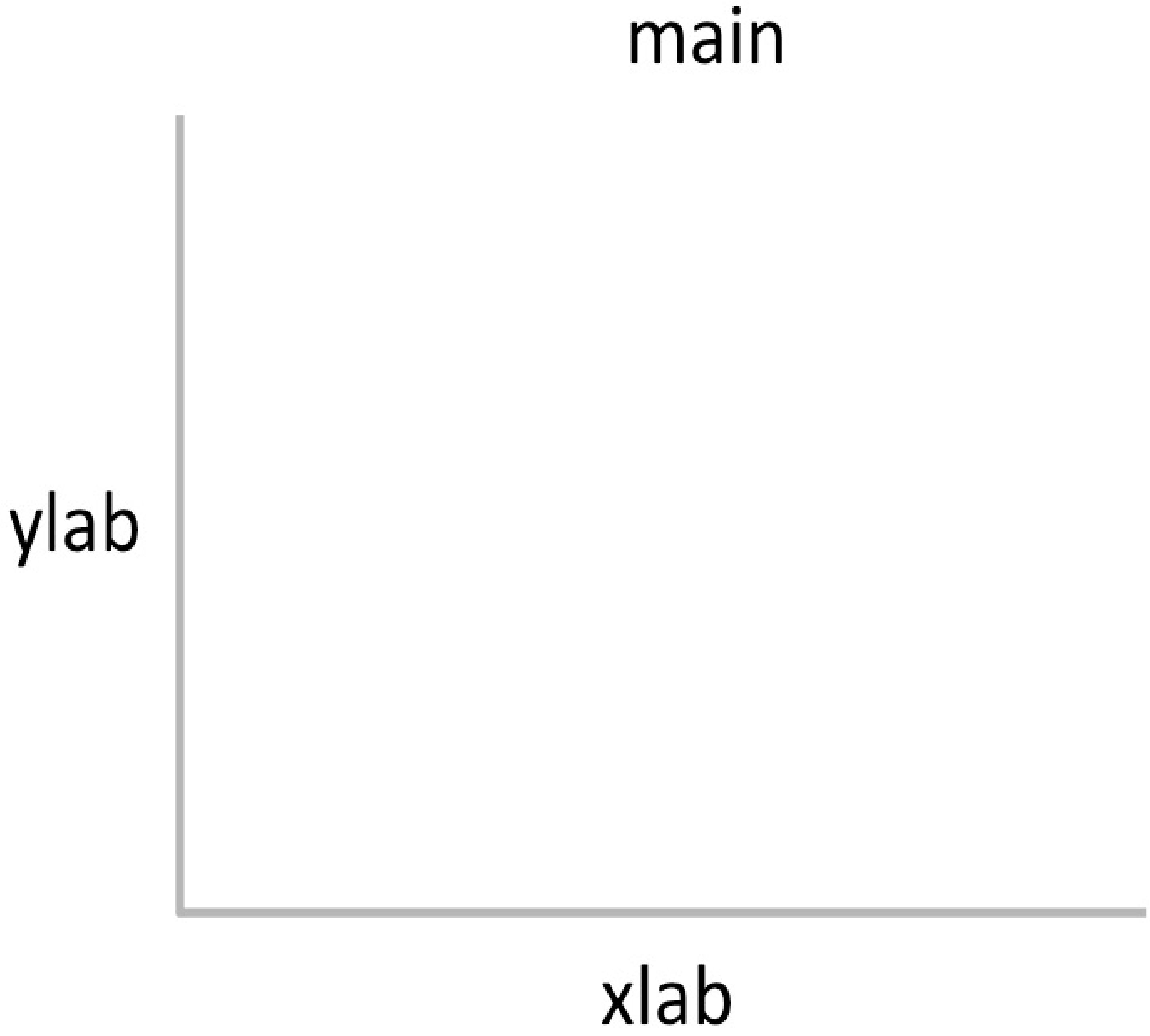
- Write the data frame to an output file

- Read the file to R and add one more column (e.g., favorite color)

Plotting: plot()

High-level plot: create a new plot

plot(x, y, xlab, ylab, main, …)



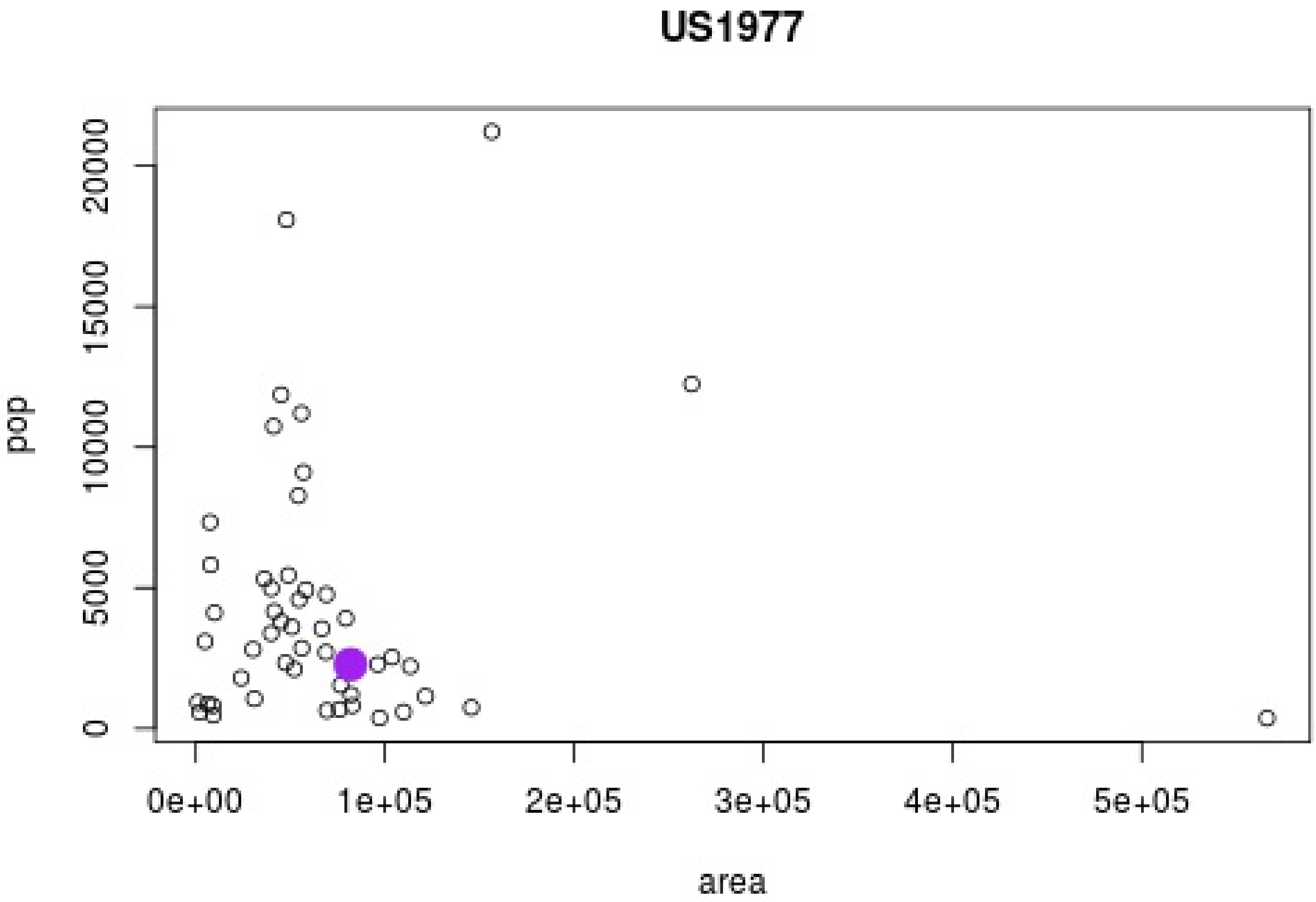
Adding contents to a plot

Low-level plot: add to an existing plot

- add points
  points()
- add lines
  lines()
- add text or legend
  text()
  legend()

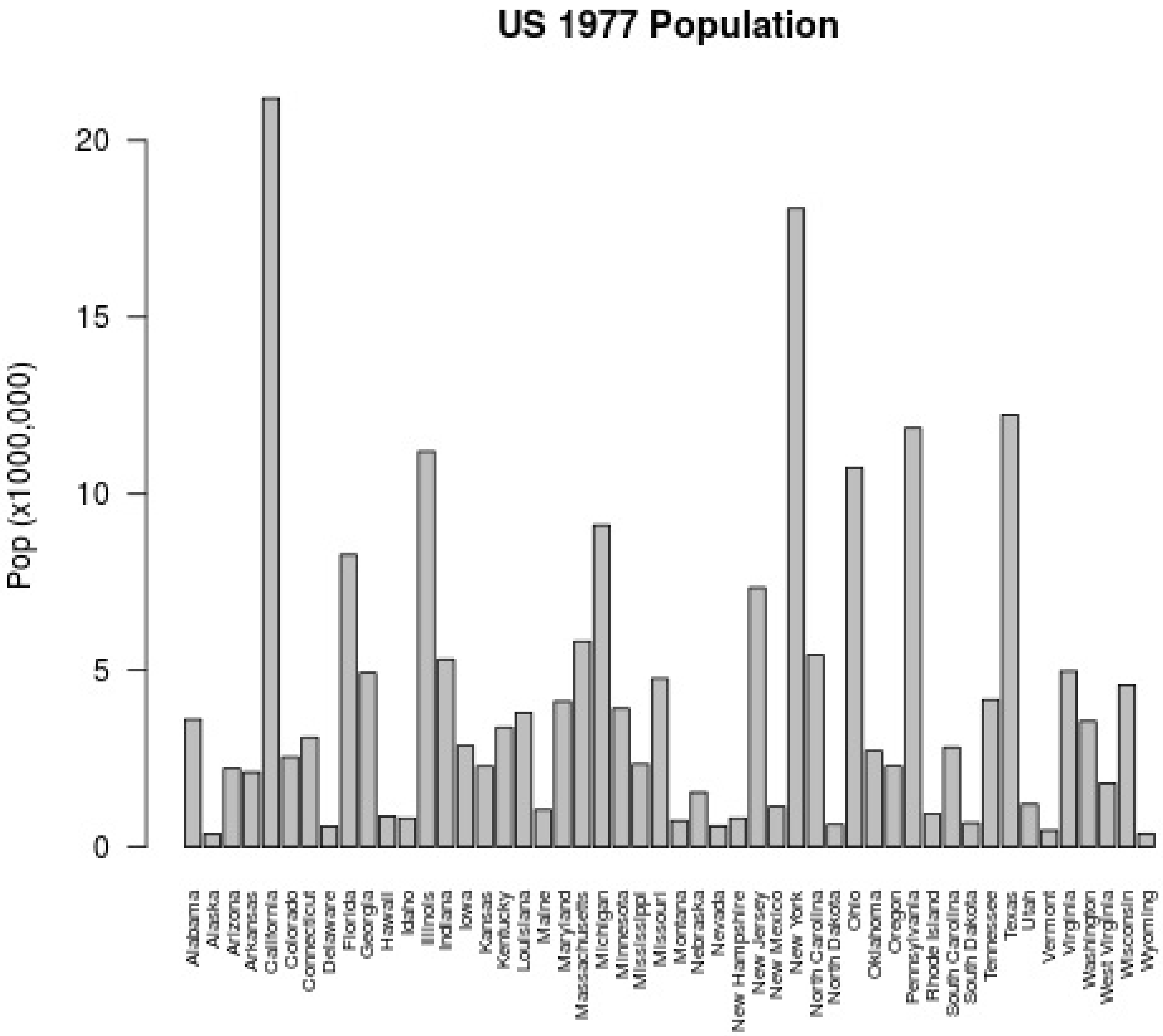
Scatter plot

```
area <- state.x77[, "Area"]
pop <- state.x77[, "Population"]
# scatter plot
plot(area, pop, main="US1977")
# label points
points(area["Kansas"], pop["Kansas"], col="purple",
       lwd=2, pch=19, cex=2)
```



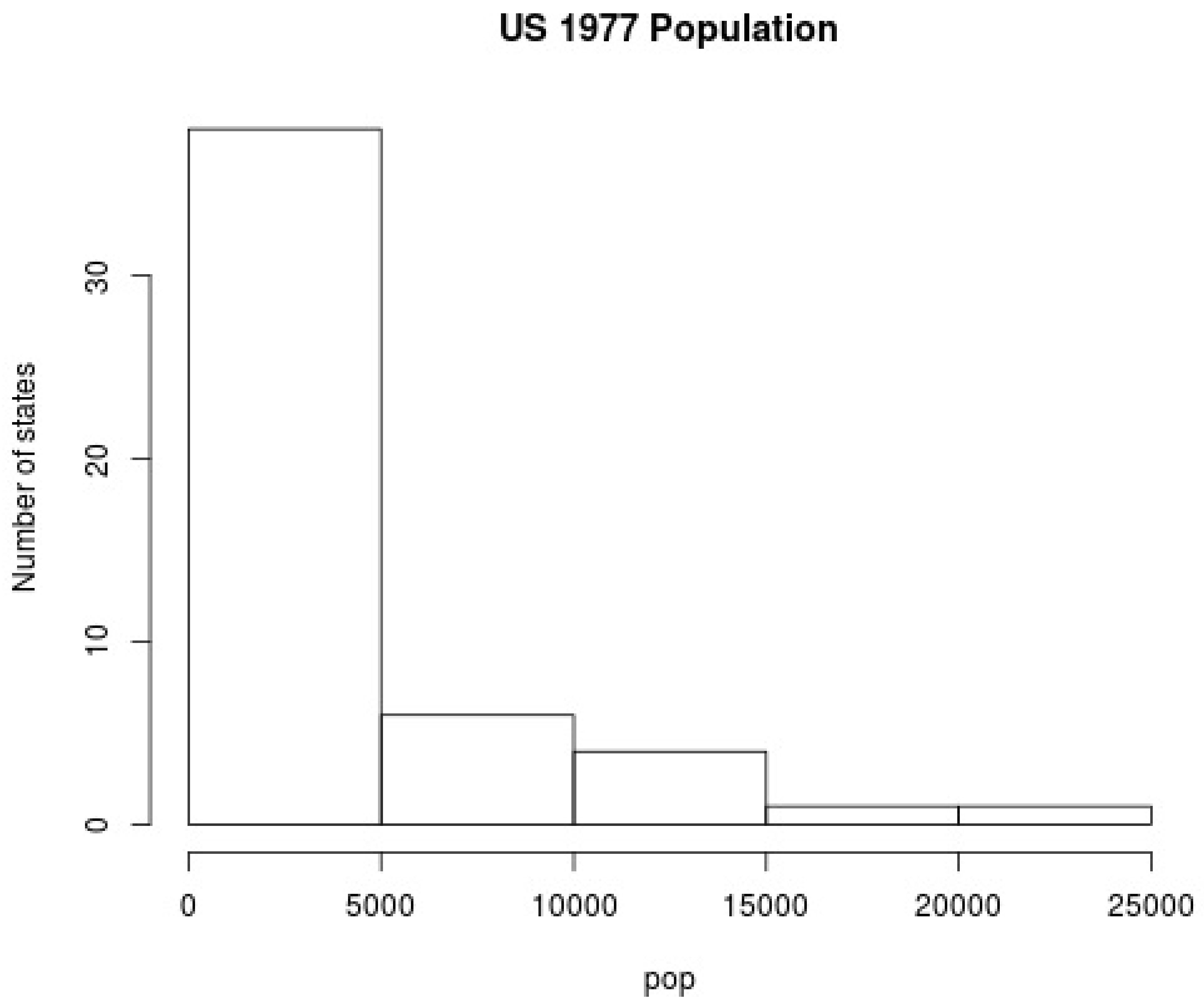
Boxplot

```
barplot(pop/1000, las=2, cex.names=0.65, ylab="Pop (x1000,000)",
        main="US 1977 Population")
```



Histogram

```
hist(pop, ylab="Number of states", main="US 1977 Population")
```



String operations - nchar

nchar() nchar the sizes of the corresponding elements of a vector.

```r
cvec <- c("google", "hello", "the", "world")
nchar(cvec)
```

```
[1] 6 5 3 5
```

String operations - grep

grep() grep searches for matches to argument pattern within each element of a character vector

```
cvec
```

```
[1] "google" "hello"  "the"    "world"
```

```
grep("o", cvec)
```

```
[1] 1 2 4
```

String operations – sub and gsub

sub() and **gsub()** sub and gsub perform replacement of the first and all matches respectively.

```
cvec
```

```
[1] "google" "hello"  "the"    "world"
```

```
sub("o", "O", cvec)
```

```
[1] "gOogle" "hellO"  "the"    "wOrld"
```

```
gsub("o", "O", cvec)
```

```
[1] "gOOgle" "hellO"  "the"    "wOrld"
```

Package installation

Prepare for the next Lab: RNA-Seq DE analysis

```
# DESeq2
source("http://bioconductor.org/biocLite.R")
biocLite("DESeq2")

# GOSeq
biocLite("goseq")

# GO.db
biocLite("GO.db")
```

Getting help

Usage of commands

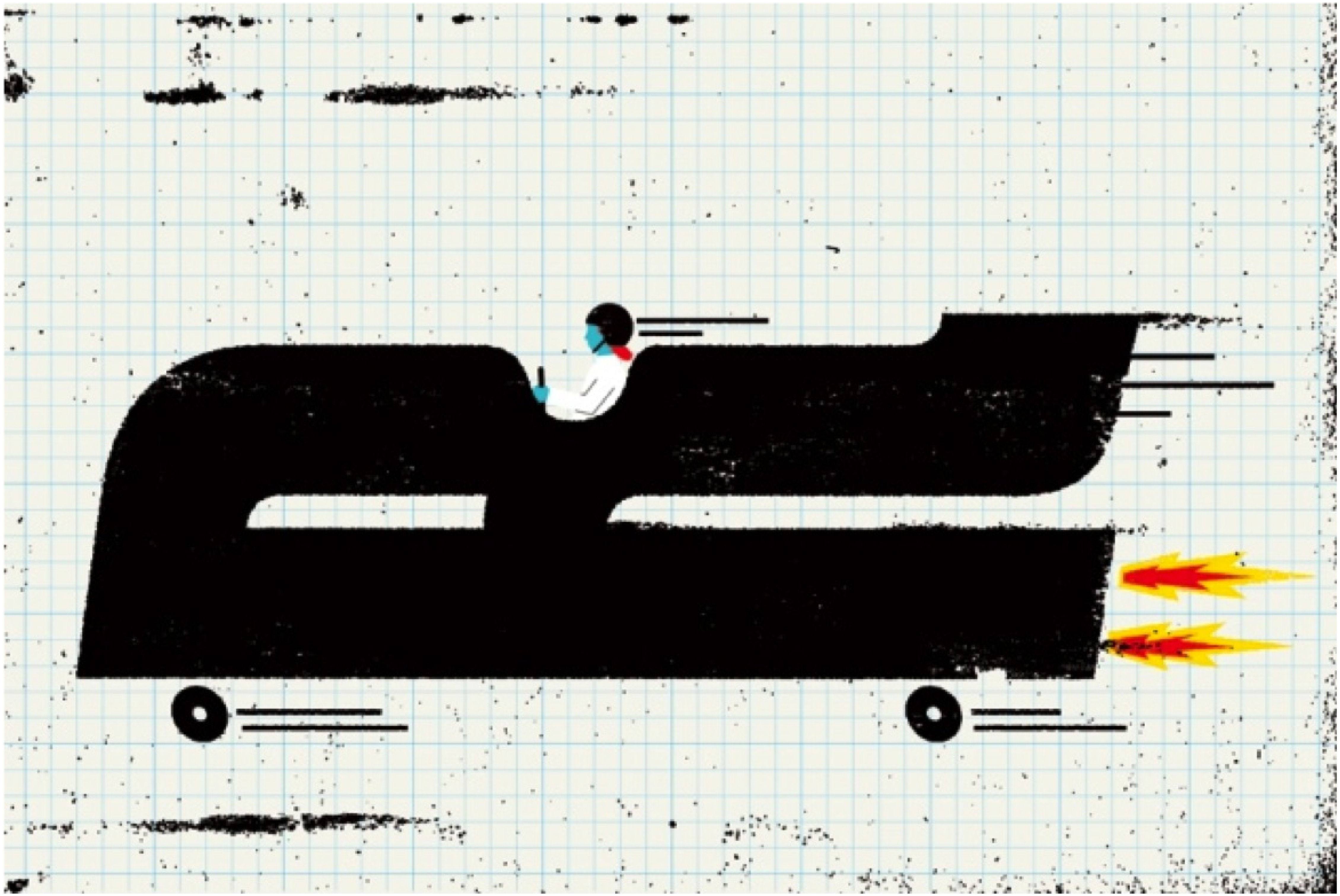
- help(nchar)
- ?nchar
- ??colsum

R Reference Card

- stack overflow
- google

Learning R at swirlstats

Adventure with R



http://www.nature.com/news/programming-tools-adventures-with-r-1.16609