

Welcome to Statistics Workshop!

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1:00-3:15 Experimental Design and Mixed model using SAS (Alissa)

3:20-3:50 Introduction to R: How to avoid command lines... (Mizuho)

INTRODUCTION TO R: HOW TO AVOID COMMAND LINES...

Mizuho Nita, Virginia Tech

For APS Potomac Division Statistic workshop 2015



What is R?

- R is a system for statistical computation and graphics developed initially by Ross Ihaka and Robert Gentleman at the Department of Statistics of the University of Auckland in Auckland, New Zealand Ihaka and Gentleman (1996).
- R offers facilities for data manipulation, calculation and graphical display either through build-in functions or add-on packages contributed by users.
- It is distributed freely under the GNU General Public License (www.gnu.org/copyleft/gpl.html) and can be used for commercial purposes.

R: Pros

- Free (vs several thousand \$ for SAS commercial license)
 - ▣ Do you need to pay for SAS to run simple ANOVA?
- Can run on many platforms
 - ▣ Windows, Mac, Linux and Unix
- Powerful. Variety of packages and very active development of different packages that may fit your need.
 - ▣ Very strong graphic capability

R: Pros

- Flexible. E.g., data input from different formats. A very good integration with database languages too.
- Gaining popularity very quickly
 - ▣ Becoming an universal language for many data analysis communities

R: Cons

- Documentations are available, but many of them are as cryptic as SAS manual...
 - ▣ E.g. No phone tech support
- As with other software, it is not error-free
 - ▣ SAS has been very good about fixing errors.
 - ▣ R itself has been updated frequently, but if there is an error in a specific package you use, it may or may not be fixed. (but it is the same with macros for SAS)

R: Cons

- “Graphical” interface is not really graphical
 - ▣ Esp. compared with other stats packages such as JMP or Minitab
- Commands
 - ▣ In SAS, you define everything and submit.
 - ▣ In R, you type in a command at a time, then move on to different command(s) to get what you want.
 - E.g., `summary(yourdata)` for parameter estimates then `anova(yourdata)` to obtain ANOVA table
- I hate command-line operation...
- Is there any way to get around in R?

Install R

- To download R itself, go to the Comprehensive R Archive Network (CRAN) at
<http://cran.r-project.org/>
- Choose your operating system under the web page heading, Download and Install R.

Install R



CRAN

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About R

[R Homepage](#)

[The R Journal](#)

Software

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[Contributed](#)

The Comprehensive R Archive Network

Download and Install R

Precompiled binary distributions of the base system and contributed packages, **Windows and Mac** users most likely want one of these versions of R:

- [Download R for Linux](#)
- [Download R for \(Mac\) OS X](#)
- [Download R for Windows](#)

R is part of many Linux distributions, you should check with your Linux package management system in addition to the link above.

Source Code for all Platforms

Windows and Mac users most likely want to download the precompiled binaries listed in the upper box, not the source code. The sources have to be compiled before you can use them. If you do not know what this means, you probably do not want to do it!

- The latest release (2014-10-31, Pumpkin Helmet) [R-3.1.2.tar.gz](#), read [what's new](#) in the latest version.
- Sources of [R alpha and beta releases](#) (daily snapshots, created only in time periods before a planned release).
- Daily snapshots of current patched and development versions are [available here](#). Please read about [new features and bug fixes](#) before filing corresponding feature requests or bug reports.
- Source code of older versions of R is [available here](#).
- Contributed extension [packages](#)

Questions About R

- If you have questions about R like how to download and install the software, or what the license terms are, please read our [answers to frequently asked questions](#) before you send an email.

In the case of my Mac...

Files:

[R-3.1.2-snowleopard.pkg](#)

MD5-hash: 8a093200b567282932992decff5daf1d
SHA1-hash: e8aee3cc4d3d97d8e5237fb50afaede38e1fb993
(ca. 68MB)

R 3.1.2 binary for Mac OS X 10.6 (Snow Leopard) and higher, signed package. Contains R 3.1.2 framework, R.app GUI 1.65 in 64-bit for Intel Macs. The above file is an Installer package which can be installed by double-clicking. Depending on your browser, you may need to press the control key and click on this link to download the file.

This package contains the R framework, 64-bit GUI (R.app) and Tcl/Tk 8.6.0 X11 libraries. The latter component is optional and can be omitted when choosing "custom install", it is only needed if you want to use the `tcltk` R package. GNU Fortran is **NOT** included (needed if you want to compile packages from sources that contain FORTRAN code) please see [the tools directory](#).

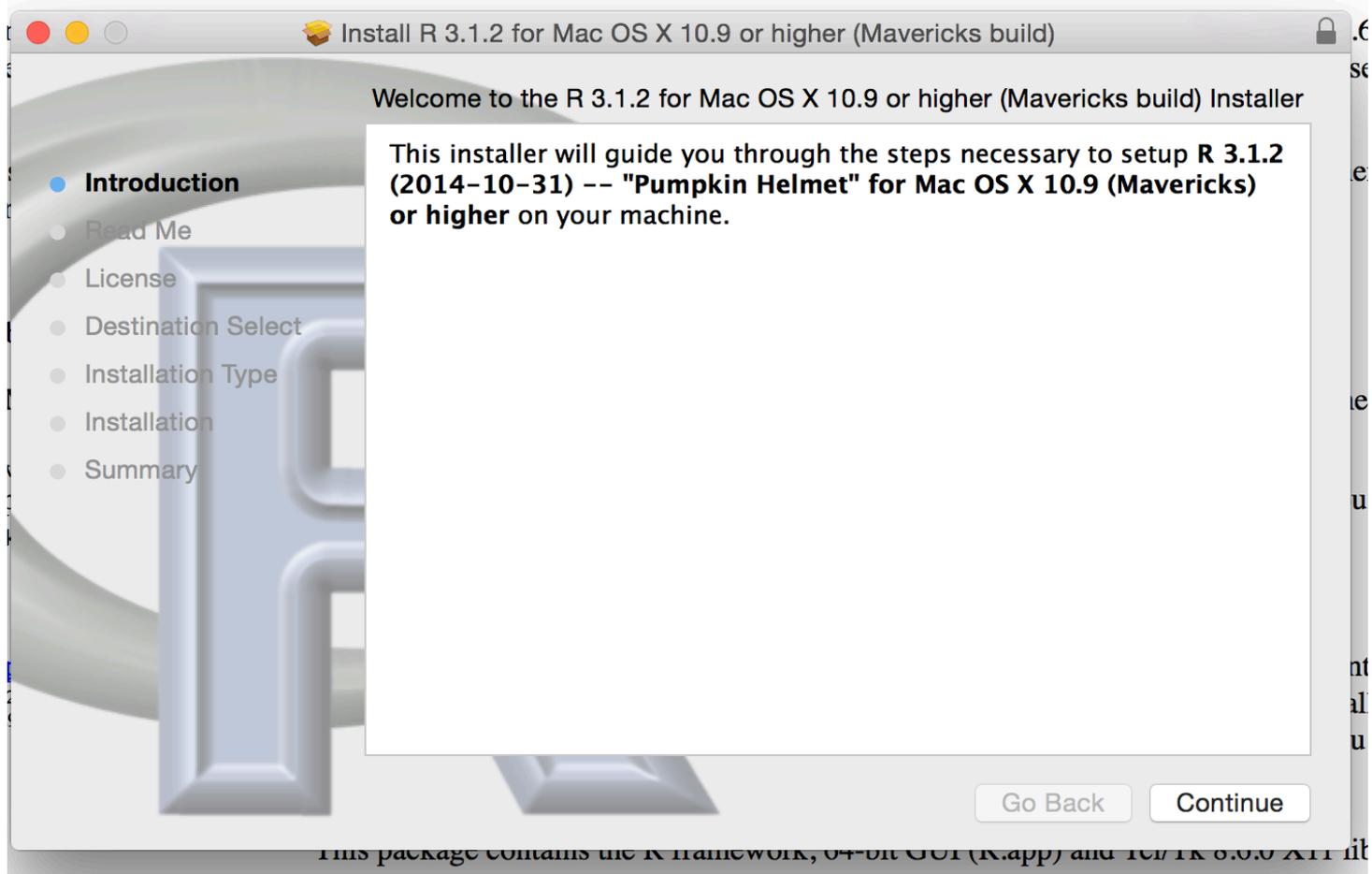
[R-3.1.2-mavericks.pkg](#)

MD5-hash: d8fb6eaf80357dd058aa1691c684e091
SHA1-hash: 61c78cbb3024bf648032006fe19d8421c52ac8ba
(ca. 55MB)

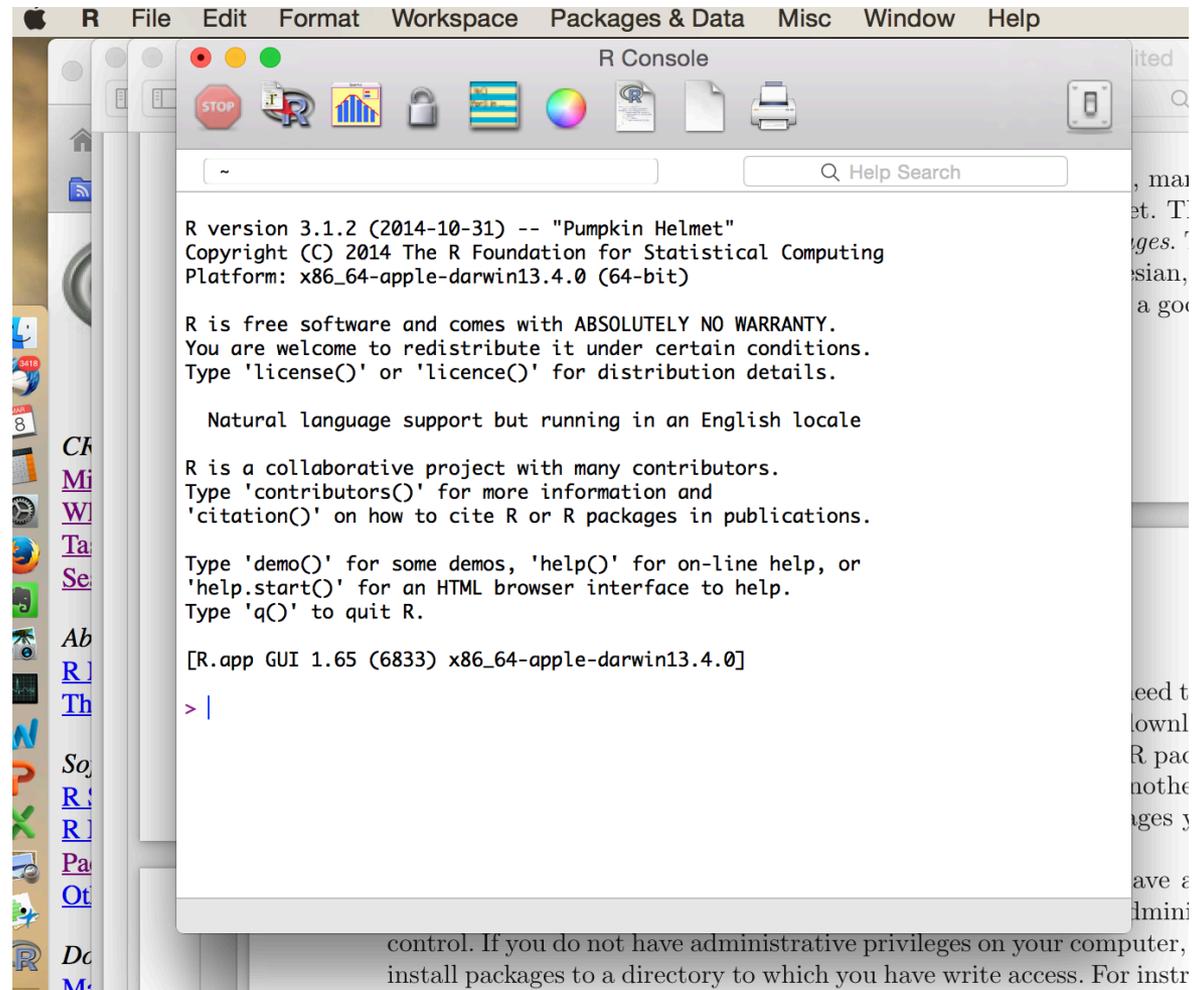
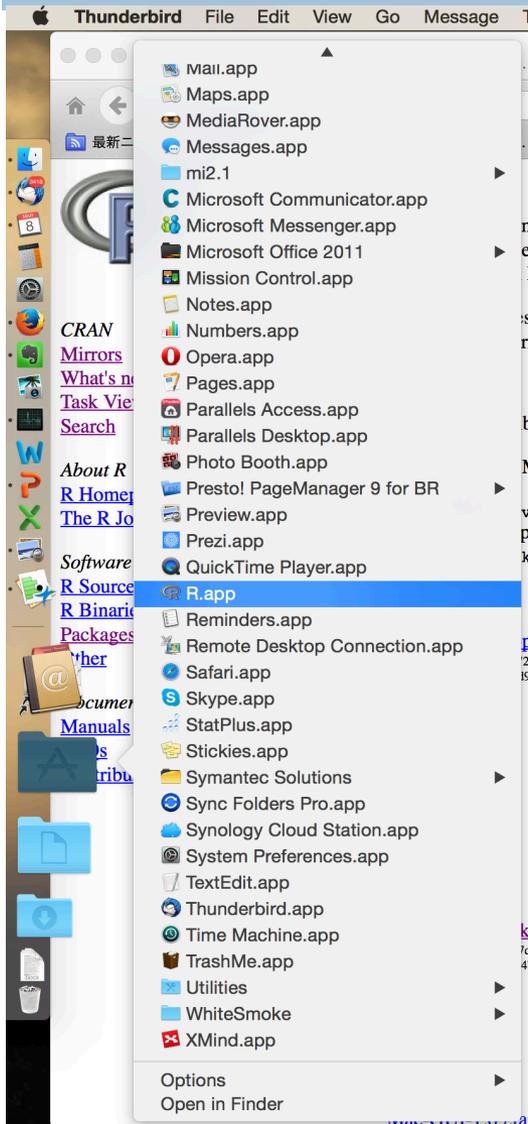
R 3.1.2 binary for Mac OS X 10.9 (Mavericks) and higher, signed package. It contains the same software versions as above, but this R build has been built with Xcode 5 to leverage new compilers and functionalities in Mavericks not available in earlier OS X versions.

Note: the use of X11 (including `tcltk`) requires [XQuartz](#) to be installed since it is no longer part of OS X. Always re-install XQuartz when upgrading your OS X to a new major version.

Installation on a Mac

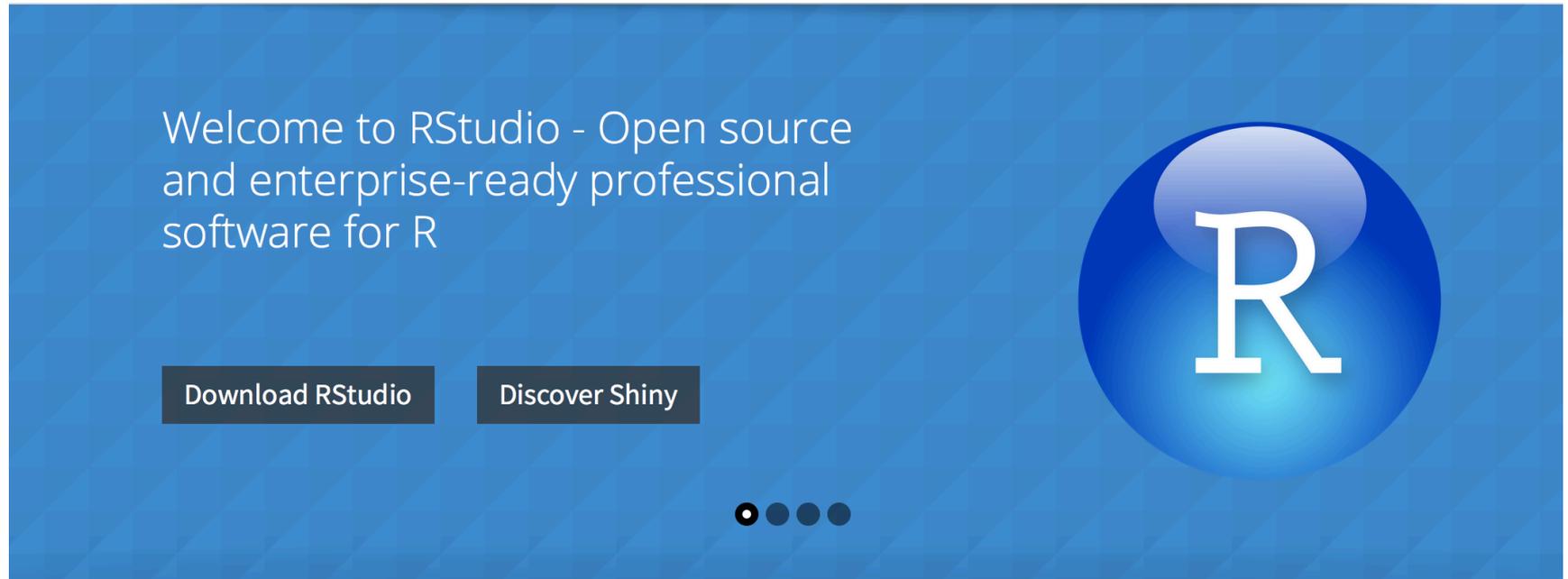


Installation takes 2-3 min



control. If you do not have administrative privileges on your computer, install packages to a directory to which you have write access. For instr

RStudio: provides more visual aids to R



Powerful IDE for R

RStudio IDE is a powerful and



R Packages

Our developers and expert



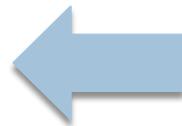
Bring R to the web

Shiny is an elegant and powerful

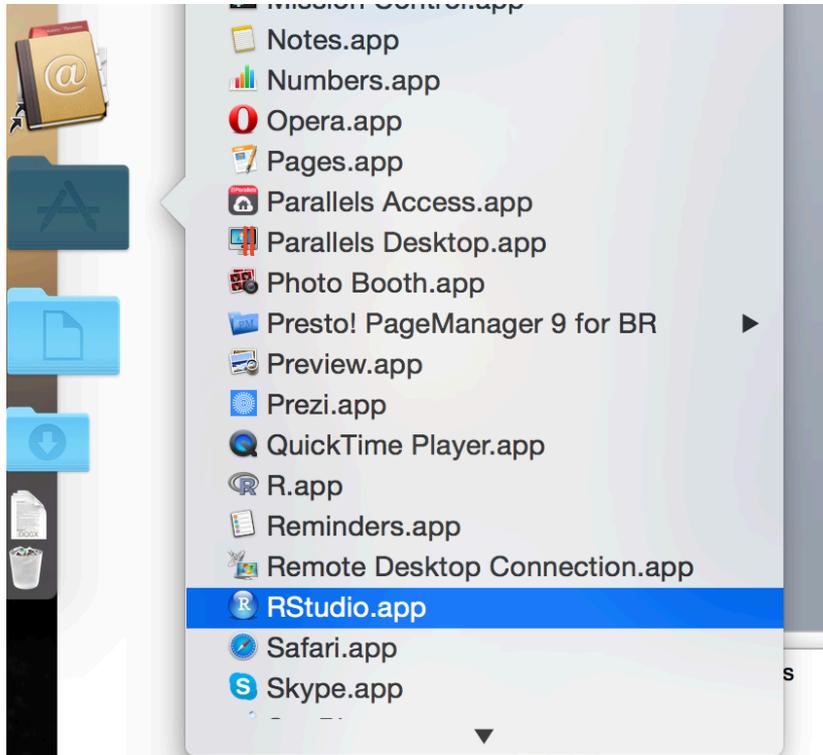
Install RStudio

Installers for ALL Platforms

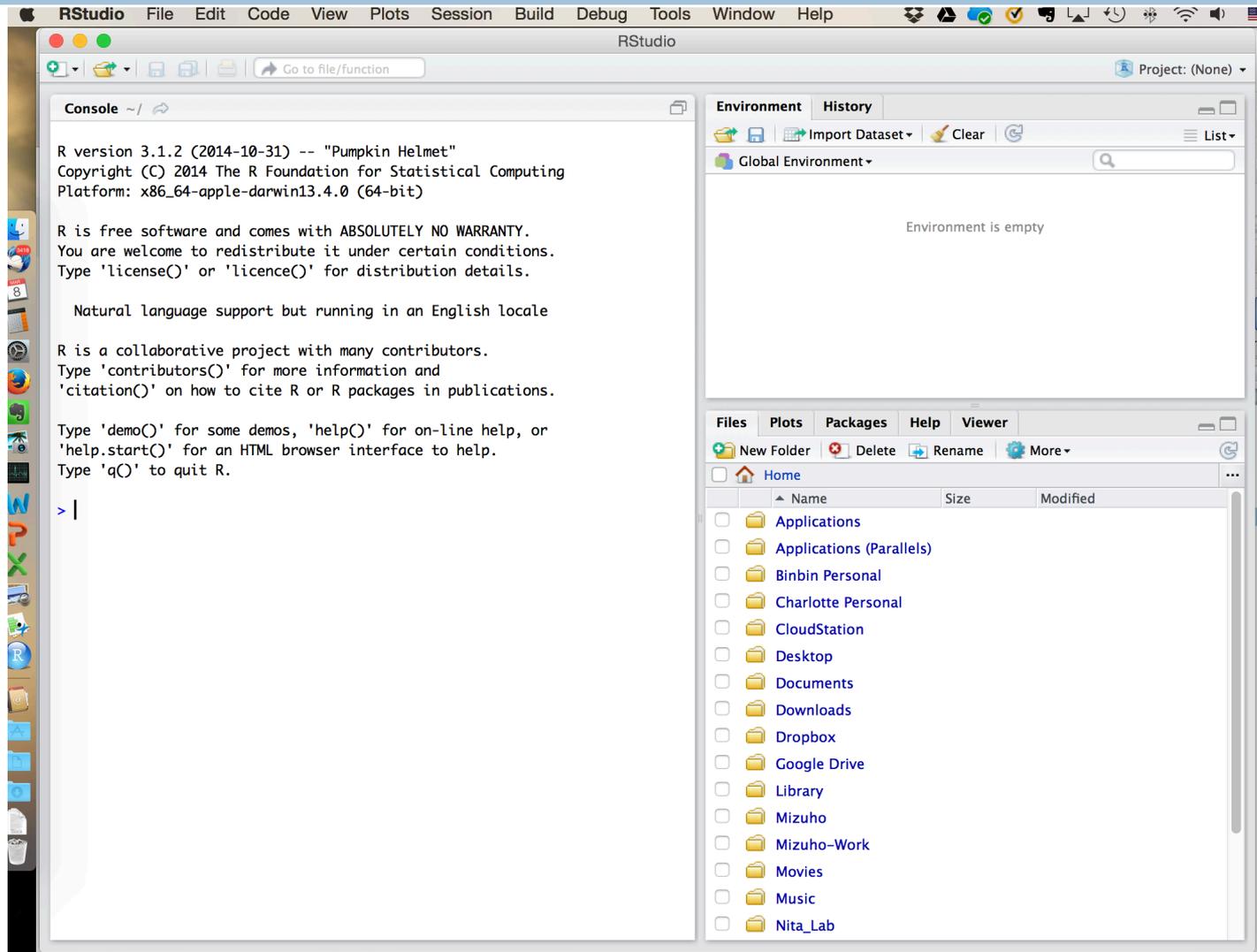
Installers	Size	Date	MD5
RStudio 0.98.1103 - Windows XP/Vista/7/8	47.4 MB	2015-03-07	65b22a3836cbba7117c131c2efa489ac
RStudio 0.98.1103 - Mac OS X 10.6+ (64-bit)	43.7 MB	2015-03-07	94d897bdd3e954473654ec7a67dd4e83
RStudio 0.98.1103 - Debian 6+/Ubuntu 10.04+ (32-bit)	49.5 MB	2015-03-07	723fdcb28dac8cd004c06855d1421c24
RStudio 0.98.1103 - Debian 6+/Ubuntu 10.04+ (64-bit)	51.4 MB	2015-03-07	4426d2797e27c7b6dd0394c180685a8e
RStudio 0.98.1103 - Fedora 13+/RedHat 7+/openSUSE 11.4+ (32-bit)	49.9 MB	2015-03-07	c3c286b2d29edbd9b6b8c01585c7531d
RStudio 0.98.1103 - Fedora 13+/RedHat 7+/openSUSE 11.4+ (64-bit)	51.5 MB	2015-03-07	e39c8ec071df40eb7a567db819246001



Running Rstudio



RStudio interface

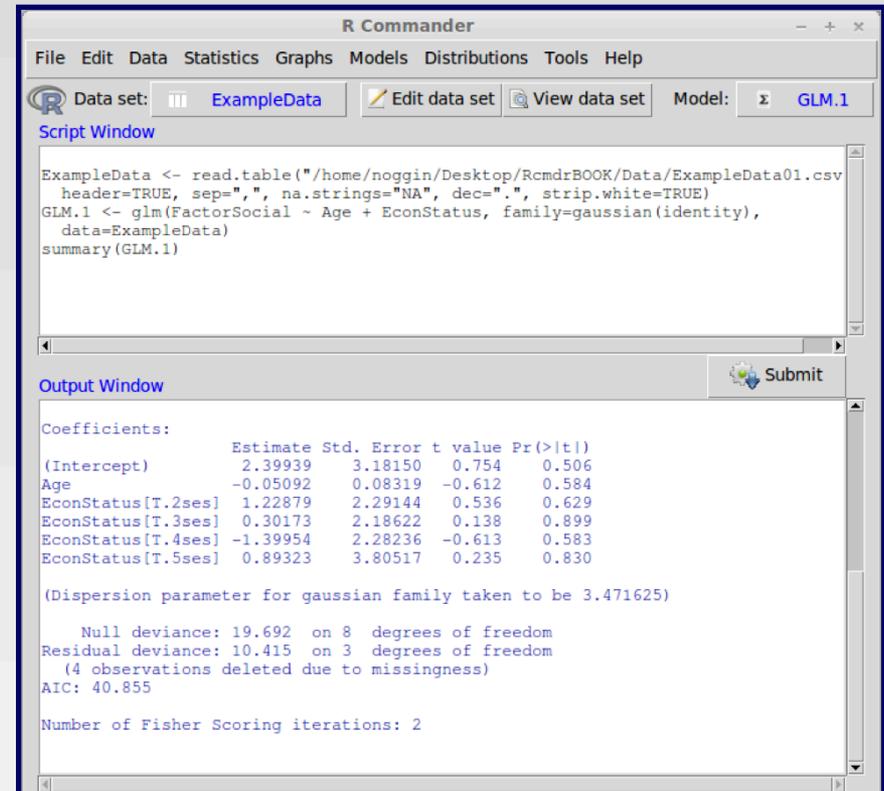


R Commander: GUI for R

R commander (Rcmdr)

R provides a powerful and comprehensive system for analysing data and when used in conjunction with the R-commander (a graphical user interface, commonly known as Rcmdr) it also provides one that is easy and intuitive to use. Basically, R provides the engine that carries out the analyses and Rcmdr provides a convenient way for users to input commands. The Rcmdr program enables analysts to access a selection of commonly-used R commands using a simple interface that should be familiar to most computer users. It also serves the important role of helping users to implement R commands and develop their knowledge and expertise in using the command line --- an important skill for those wishing to exploit the full power of the program.

Information about installing R can be found on the web at the R homepage <http://www.r-project.org/> which provides lots of information about the R project and also directs users to one of the CRAN sites (the Comprehensive R Archive Network) that have been set up on many servers across the world in order for users to download the software. CRAN provides all files necessary to install R on a number of different computing platforms (Linux, MacOS X and Windows) along with detailed information about installation and also offers manuals and contributed documentation in a number of languages and for a number of specific disciplines.



The screenshot shows the R Commander interface. The 'Data set' is 'ExampleData' and the 'Model' is 'GLM.1'. The 'Script Window' contains the following R code:

```
ExampleData <- read.table("/home/noggin/Desktop/RcmdrBOOK/Data/ExampleData01.csv"
  header=TRUE, sep=";", na.strings="NA", dec=".", strip.white=TRUE)
GLM.1 <- glm(FactorSocial ~ Age + EconStatus, family=gaussian(identity),
  data=ExampleData)
summary(GLM.1)
```

The 'Output Window' displays the following results:

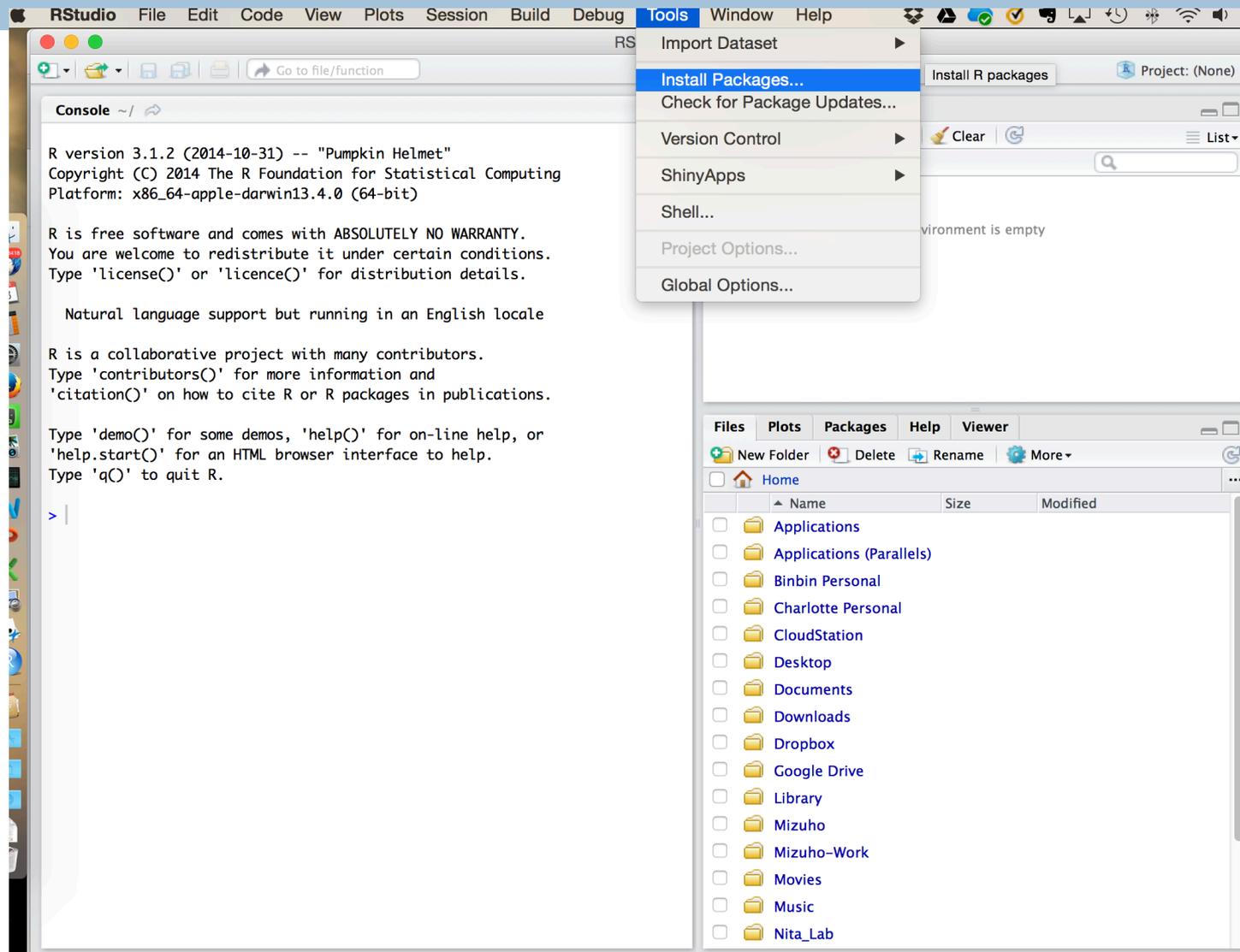
```
Coefficients:
      Estimate Std. Error t value Pr(>|t|)
(Intercept)  2.39939    3.18150   0.754  0.506
Age          -0.05092    0.08319  -0.612  0.584
EconStatus[T.2ses]  1.22879    2.29144   0.536  0.629
EconStatus[T.3ses]  0.30173    2.18622   0.138  0.899
EconStatus[T.4ses] -1.39954    2.28236  -0.613  0.583
EconStatus[T.5ses]  0.89323    3.80517   0.235  0.830

(Dispersion parameter for gaussian family taken to be 3.471625)

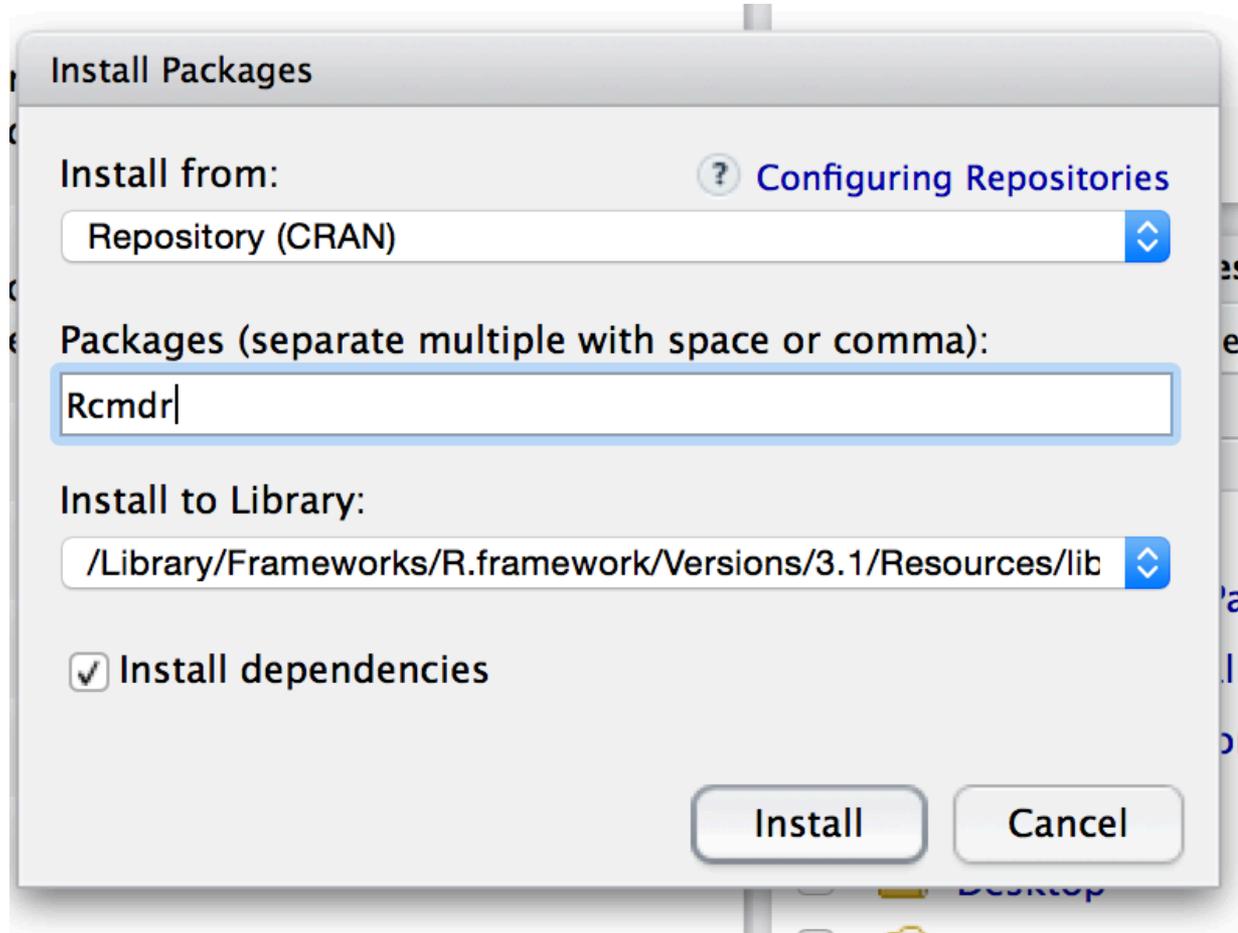
Null deviance: 19.692  on 8  degrees of freedom
Residual deviance: 10.415  on 3  degrees of freedom
(4 observations deleted due to missingness)
AIC: 40.855

Number of Fisher Scoring iterations: 2
```

Install R commander from RStudio



Type in “Rcmdr”, check the box for dependencies



Run R commander from RStudio

The screenshot shows the RStudio interface with the following components:

- Console:** Shows the process of downloading several R packages from CRAN. The packages are: `Misc_1.0-2.tgz` (87 Kb), `car_2.0-25.tgz` (1.3 Mb), `tcltk_2.1.2-11.tgz` (855 Kb), `abind_1.4-0.tgz` (32 Kb), and `Rcmdr_2.1-7.tgz` (5.1 Mb). The console also shows the path where the packages are downloaded: `/var/folders/nf/3v3p1xs50cz4bm519qj82dj00000gn/T//Rtmp2Mi57/downloaded_packages`.
- Environment pane:** Shows "Global Environment" and "Environment is empty". A blue arrow points down from this pane towards the Packages pane.
- Packages pane:** Shows a list of installed and available packages. A blue arrow points to the `Rcmdr` package in the list.

Name	Description	Version
<code>minqa</code>	Derivative-free optimization algorithms by quadratic approximation	1.2-4
<code>munsell</code>	Munsell colour system	0.4.2
<code>nlme</code>	Linear and Nonlinear Mixed Effects Models	3.1-118
<code>nloptr</code>	R interface to NLOpt	1.0.4
<code>nnet</code>	Feed-forward Neural Networks and Multinomial Log-Linear Models	7.3-8
<code>parallel</code>	Support for Parallel computation in R	3.1.2
<code>pbkrtest</code>	Parametric bootstrap and Kenward-Roger-based methods for mixed model comparison	0.4-2
<code>plyr</code>	Tools for splitting, applying and combining data	1.8.1
<code>proto</code>	Prototype object-based programming	0.3-10
<code>quantreg</code>	Quantile Regression	5.11
<code>Rcmdr</code>	R Commander	2.1-7
<code>RcmdrMisc</code>	R Commander Miscellaneous Functions	1.0-2
<code>RColorBrewer</code>	ColorBrewer Palettes	1.1-2
<code>Rcpp</code>	Seamless R and C++ Integration	0.11.5

If you install on a Mac, it may ask you to install Xcode-related files

- + Xquartz from xquartz.macosforge.org
- + Java update for OSX
- I don't think there is additional files required for Windows (at least for 8.1)

XQuartz

A version of the [X.Org X Window System](#) that runs on OS X

The XQuartz project is an open-source effort to develop a version of the [X.Org X Window System](#) that runs on OS X. Together with supporting libraries and applications, it forms the X11.app that Apple has shipped with OS X since version 10.5.

Quick Download

<u>Download</u>	<u>Version</u>	<u>Released</u>	<u>Info</u>
 XQuartz-2.7.7.dmg	2.7.7	2014-08-18	For OS X 10.6 or later (including Mavericks)

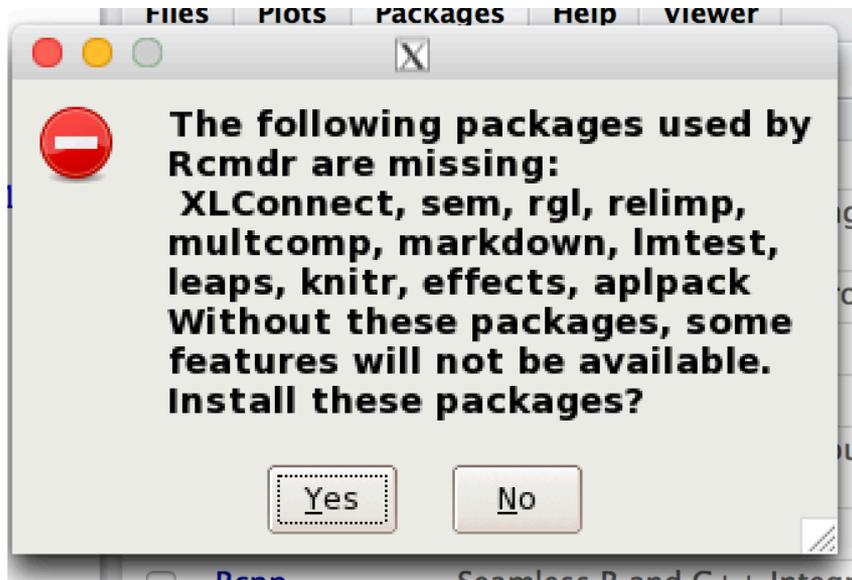
A list of all available XQuartz releases can be found [here](#).
(Development "beta" releases, if available, are [here](#).)



Java for OS X 2014-001

[Download](#)

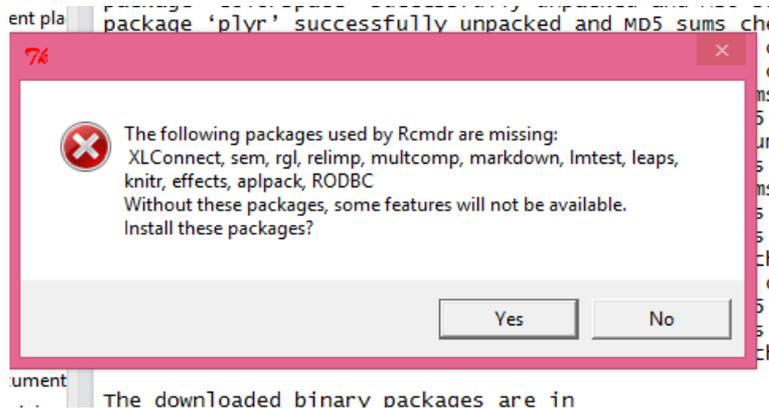
It may ask to install several packages at the first run



← Warning message on a Mac. It took about 2-3 min to load.

For PC, I did not get any message at the first run. However, on the second run, R commander did not load...

I ended up installing some of missing packages manually, then suddenly a pop-up warning message came up... It took about 10 min from start to finish for PC



Finally! R commander is running!

The screenshot displays the R Commander application window on a Mac OS X desktop. The window title is 'R Commander' and it has a menu bar with 'File', 'Edit', 'Data', 'Statistics', 'Graphs', 'Models', 'Distributions', 'Tools', and 'Help'. Below the menu bar, there are buttons for 'Data set: <No active dataset>', 'Edit data set', and 'View data set', along with a 'Model: <No active model>' button. The main workspace is divided into two panes: 'R Script' and 'R Markdown', both of which are currently empty. At the bottom of the window, there is a 'Submit' button and a terminal window.

The terminal window shows the following output:

```
ts_3.0-3.tgz'  
Content type 'application/x-gzip' length 225216 bytes (219 Kb)  
opened URL  
=====  
downloaded 219 Kb  
  
trying URL 'http://cran.rstudio.com/bin/macosx/mavericks/contrib/3.1/aplpac  
k_1.3.0.tgz'  
Content type 'application/x-gzip' length 3158954 bytes (3.0 Mb)  
opened URL  
=====  
downloaded 3.0 Mb  
  
The downloaded binary packages are in  
  
/var/folders/nf/3v3p1xs50cz4bm519qj82dj00000gn/T/Rtmp2mZnjI/downloaded_pa  
ckages  
RcmdrMsg: [1] NOTE: R Commander Version 2.1-7: Sun Mar 8 16:50:33 2015  
  
Rcmdr Version 2.1-7  
  
Warning message:  
package 'car' was built under R version 3.1.3  
>
```

On the right side of the window, there is a 'Project: (None)' dropdown menu and a 'List' button. Below this, there is a search bar and a table of installed and available packages.

Name	Description	Version
<input type="checkbox"/> plyr	model comparison Tools for splitting, applying and combining data	1.8.1
<input type="checkbox"/> proto	Prototype object-based programming	0.3-10
<input type="checkbox"/> quantreg	Quantile Regression	5.11
<input checked="" type="checkbox"/> Rcmdr	R Commander	2.1-7
<input checked="" type="checkbox"/> RcmdrMisc	R Commander Miscellaneous Functions	1.0-2
<input type="checkbox"/> RColorBrewer	ColorBrewer Palettes	1.1-2
<input type="checkbox"/> Rcpp	Seamless R and C++ Integration	0.11.5
<input type="checkbox"/> reshape2	Flexibly Reshape Data: A Reboot of the Reshape Package.	1.4.1
<input type="checkbox"/> rpart	Recursive Partitioning and Regression Trees	4.1-8
<input type="checkbox"/> rstudio	Tools and Utilities for RStudio	0.98.110
<input type="checkbox"/> rstudioapi	Safely access the RStudio API.	0.2
<input checked="" type="checkbox"/> sandwich	Robust Covariance Matrix Estimators	2.3-2
<input type="checkbox"/> scales	Scale functions for graphics.	0.2.4
<input type="checkbox"/> SparseM	Sparse Linear Algebra	1.6
<input type="checkbox"/> spatial	Functions for Kriging and Point Pattern Analysis	7.3-8

Demonstration 1

- R, R studio, and R commander
- Simple ANOVA in R commander

- Create a new data table “Bot.Example” by importing a sample Excel file
- Create a Box-plot
- Run 1-way ANOVA

What R commander does for you

- `Rcmdr> .Workbook <- loadWorkbook("/Users/mizuho/Mizuho/APS/Stats workshop/Bot example APS.xls")`
 - ▣ Importing into a temporary file
- `Rcmdr> Bot.Example <- readWorksheet(.Workbook, "Bot 8.26.2014", header=TRUE, rownames=NULL)`
 - ▣ Selecting a sheet from Excel, telling there is heading on the columns, storing information into file "Bot.Example"
- `Rcmdr> remove(.Workbook)`
 - ▣ Removing the temporary file
- `Rcmdr> Bot.Example[, c(1, 2)] <- lapply(Bot.Example[, c(1, 2), drop=FALSE], as.factor)`
 - ▣ Applying a Function over a List or Vector

Output from R commander (ANOVA)

```
Rcmdr> AnovaModel.Bot <- aov(Botrytis ~ Treatment, data=Bot.Example)
```

```
Rcmdr> summary(AnovaModel.Bot)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Treatment	5	494	98.80	9.075	2.97e-08 ***
Residuals	474	5161	10.89		

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Rcmdr> with(Bot.Example, numSummary(Botrytis, groups=Treatment,  
Rcmdr+   statistics=c("mean", "sd")))
```

	mean	sd	data:n
BioBot	1.5250	3.9393343	80
Check	1.8250	5.2162720	80
IsoF	0.1000	0.5867741	80
Kilbot	2.6625	4.6740429	80
Lune	0.0000	0.0000000	80
Standard	0.1875	0.6383077	80

Simultaneous Confidence Intervals

Multiple Comparisons of Means: Tukey Contrasts

```
Fit: aov(formula = Botrytis ~ Treatment, data = Bot.Example)
```

```
Quantile = 2.8616
```

```
95% family-wise confidence level
```

Linear Hypotheses:

	Estimate	lwr	upr
Check - BioBot == 0	0.30000	-1.19293	1.79293
IsoF - BioBot == 0	-1.42500	-2.91793	0.06793
Kilbot - BioBot == 0	1.13750	-0.35543	2.63043
Lune - BioBot == 0	-1.52500	-3.01793	-0.03207
Standard - BioBot == 0	-1.33750	-2.83043	0.15543
IsoF - Check == 0	-1.72500	-3.21793	-0.23207
Kilbot - Check == 0	0.83750	-0.65543	2.33043
Lune - Check == 0	-1.82500	-3.31793	-0.33207
Standard - Check == 0	-1.63750	-3.13043	-0.14457
Kilbot - IsoF == 0	2.56250	1.06957	4.05543
Lune - IsoF == 0	-0.10000	-1.59293	1.39293
Standard - IsoF == 0	0.08750	-1.40543	1.58043
Lune - Kilbot == 0	-2.66250	-4.15543	-1.16957
Standard - Kilbot == 0	-2.47500	-3.96793	-0.98207
Standard - Lune == 0	0.18750	-1.30543	1.68043

BioBot
"bc"

Check
"c"

IsoF
"ab"

Kilbot
"c"

Lune
"a"

Standard
"ab"

lme4 package

- Bates, et al., (2014) “Linear Mixed Models with lme4”, Journal of Statistical Software
- The lme4 package for R provides functions to fit and analyze linear mixed models, generalized linear mixed models and nonlinear mixed models.
- It seems that this package has been gaining a popularity against other mixed model packages

Other packages can be used

- lmerTest (by Alexandra Kuznetsova <alku@dtu.dk>, Per Bruun Brockhoff, Rune Haubo Bojesen Christensen)
 - ▣ The package provides anova function, that gives data frame similar to what gives lme4 package but with p-values calculated from F statistics of type 3/type 1 hypotheses. There are two options for denominator degrees of freedom of F statistics: "Satterthwaite" and "Kenward-Roger".
- lsmeans (by Russell V. Lenth, The University of Iowa)
 - ▣ Provides a simple way of obtaining least-squares means and contrasts

SAS code example

```
Proc mixed data = Bot;
title 'Mixed model example';
title2 'Fake Botrytis Trial

class treatment block;
  model Botrytis = treatment block;
  random block;
  lsmeans treatment / adjust=none
  */ods output statements for
lettering!*/;
ods output diffs=ppp lsmeans=ppp;
ods exclude diffs lsmeans;
run;
/** Since Proc Mixed won't
separation,
I am using a macro that has
%include 'C:\Users\Mizuho\Documents\
\pdmix800.sas';
%pdmix800(ppp,mmm,alpha=0.05);
quit;
```

Covariance Parameter Estimates	
Cov Parm	Estimate
Block	0.2024
Residual	11.9102

Fit Statistics	
-2 Res Log Likelihood	2549.1
AIC (smaller is better)	2553.1
AICC (smaller is better)	2553.1
BIC (smaller is better)	2551.8

Type 3 Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
Treatment	5	471	18.33	<.0001

Mixed model example Fake Botrytis Trial data, Disease severity

Effect=Treatment Method=Tukey-Kramer(P<0.05) Set=1

Obs	Treatment	Estimate	Standard Error	Letter Group
1	KillerBot	4.1500	0.4466	A
2	Check	2.3750	0.4466	B
3	BioBot	1.5250	0.4466	BC
4	Standard	0.1875	0.4466	C
5	IsoF	0.1000	0.4466	C
6	Lune	1.11E-16	0.4466	C

Demonstration 2: lme4 package etc.

- Use the data imported using R commander (Bot.Example)
- You can access to it from RStudio!
- Load 1) lme4, 2) lmerTest, and 3) lsmeans packages

Demonstration 2 (cont.)

- `Mixed.Bot <- lmer(Botrytis ~ Treatment + (1 | Block), Bot.Example)`
 - `1 | Rep` specifies “Block” as a random factor
 - Each level of the grouping factor, Block, has its own random intercept.
- `anova(Mixed.Bot)`
 - Provide ANOVA table for type-III test (with `lmerTest` package)
- `lsmeans(Mixed.Bot, pairwise ~ Treatment, adjust = "tukey")`
 - Post-hoc (mean separation) using Tukey-Kramer

Results comparison

```
> anova(Mixed.Bot)
Analysis of Variance Table of type 3 with Satterthwaite
approximation for degrees of freedom
      Sum Sq Mean Sq NumDF DenDF F.value    Pr(>F)
Treatment 1091.9  218.37     5   471  18.335 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Type 3 Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
Treatment	5	471	18.33	<.0001

There are many other ways to do the post-hoc analysis in R...

- Please note that the example is one of the simpler methods.
- For example, you can do the same using package “multicomp”
- ```
> Bot.Out2 <- glht(Mixed.Bot, linfct =
 mcp("Treatment" = "Tukey"))
```
- ```
> summary(Bot.Out2)
```

Output from “multicomp”

Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

Fit: lme4::lmer(formula = Botrytis ~ Treatment + (1 | Rep), data = Bot2.Dataset)

Linear Hypotheses:

	Estimate	Std. Error	z value	Pr(> z)	
Check - Botector == 0	-0.6451	0.5296	-1.218	0.82814	
IsofetamidH - Botector == 0	-2.3701	0.5296	-4.475	< 0.001	***
LunaT - Botector == 0	-2.4701	0.5296	-4.664	< 0.001	***
Rovral - Botector == 0	-2.2826	0.5296	-4.310	< 0.001	***
Tavano - Botector == 0	-0.9451	0.5296	-1.785	0.47550	
IsofetamidH - Check == 0	-1.7250	0.5107	-3.378	0.00960	**
LunaT - Check == 0	-1.8250	0.5107	-3.573	0.00472	**
Rovral - Check == 0	-1.6375	0.5107	-3.206	0.01694	*
Tavano - Check == 0	-0.3000	0.5107	-0.587	0.99189	
LunaT - IsofetamidH == 0	-0.1000	0.5107	-0.196	0.99996	
Rovral - IsofetamidH == 0	0.0875	0.5107	0.171	0.99998	
Tavano - IsofetamidH == 0	1.4250	0.5107	2.790	0.05905	.
Rovral - LunaT == 0	0.1875	0.5107	0.367	0.99913	
Tavano - LunaT == 0	1.5250	0.5107	2.986	0.03367	*
Tavano - Rovral == 0	1.3375	0.5107	2.619	0.09276	.

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Adjusted p values reported -- single-step method)

MNBU plug-in in R commander

- Install RcmdrPlugin.NMBU from RStudio
 - ▣ With the previous version, you were able to install from R commander, but I was not able to do so with a newer versions
 - ▣ It will add function to run linear mixed model
 - It looks like it is `lm()` function, but output is the similar to `lmer()`...
 - `Rcmdr> Bot.Mixed.NMBU <- lm(Botrytis ~ Treatment + r(Block), data=Bot.Example, REML=TRUE)`
 - `> summary(Bot.Mixed.NMBU)`
 - Linear mixed model fit by REML ['lmerMod']
 - Formula: `Botrytis ~ Treatment + (1 | Block)`

R Commander

File Edit Data **Statistics** Graphs Models Distributions Tools Help

Example Edit data set View data set Model: Σ AnovaModel.Bot

- Summaries
- Contingency tables
- Means
- Proportions
- Variations
- Nonparametric tests
- Dimensional analysis
- Fit models**
 - Linear regression...
 - Linear model...
 - Generalized linear model...
 - Multinomial logit model...
 - Ordinal regression model...

```

AnovaModel.Bot, linfct = mcp(Treatment = "Tukey"))
  lrs) # pairwise tests
  lra) # confidence intervals
  lay
old.oma <- par(om
plot(confint(.Pa
par(old.oma)
})

```

Submit

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 licence(') for distribution details

object with many contributors:
 or more information and
 cite R or R packages in publications

demos, 'help()' for on-line
 HTML browser interface to help

- Linear regression...
- Simplex mixture model...
- Multinomial logit model...
- Ordinal regression model...
- Generalized linear model...
- Principal-components analysis...
- Multivariate regression...
- Linear model...

45 warnings.
 + 5 warnings:

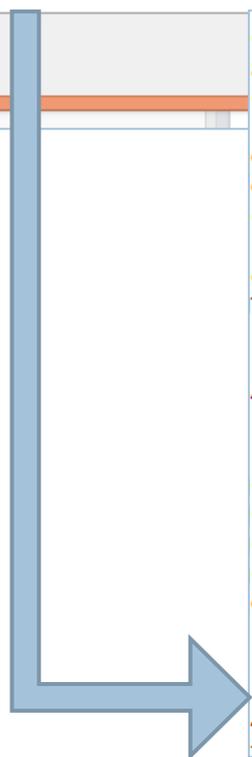
R Commander

File Edit Data **Statistics** Graphs Models Distributions Tools Help

Example Edit data set View data set Model: Σ <No active model>

- Summaries
- Contingency tables
- Means
- Proportions
- Variations
- Nonparametric tests
- Dimensional analysis
- Fit models**
 - Discriminant analysis (NMBU)

Submit



Demonstration 3: MNBU plug-in in R commander

- Install RcmdrPlugin.NMBU from RStudio
 - ▣ With the previous version, you were able to install from R commander, but I was not able to do so with a newer versions
 - ▣ It will add function to run linear mixed model
 - Uses `lm()` function, but output to `lmer()`?

Agricolae package

- It offers many functions that we could use
 - ▣ Experimental design aid
 - ▣ Options on ad-hoc analysis, including LSD, Tukey, Dunnet, etc.
 - ▣ Plus, it will do a lettering for us!
- However, it cannot read outputs from lmer directly.

Using agricolae to come up with a randomized complete block design with 5 treatments and 4 blocks

```
> require(stats);
> str(design.rcbd)
function (trt, r, serie = 2, seed = 0, kinds = "Super-Duper",
  first = TRUE, continue = FALSE)
> trt <- c("A", "B", "C", "D", "E")
> repeticion <- 4
> outdesign <- design.rcbd(trt, r=repeticion, seed=-513, serie=2)
> # book2 <- outdesign$book
> book2 <- zigzag(outdesign) # zigzag numeration
> print(t(matrix(book2[,3], c(5,4))))
```

← Random number generator

```
  [,1] [,2] [,3] [,4] [,5]
[1,] "D" "B" "C" "E" "A"
[2,] "E" "A" "D" "B" "C"
[3,] "E" "D" "B" "A" "C"
[4,] "A" "E" "C" "B" "D"
> print(t(matrix(book2[,1], c(5,4))), digits=0)
```

← A constant that is used to set numerical tag blocks , eg number = 2, the labels will be : 101

```
  [,1] [,2] [,3] [,4] [,5]
[1,] 101 102 103 104 105
[2,] 205 204 203 202 201
[3,] 301 302 303 304 305
[4,] 405 404 403 402 401
```

That's it for today!

- Thank you very much for your attention!
- Please give us your feedback!