

Rcmdr Plug-In Package for the EZR (Easy R especially for medical statistics)

Description

This package provides an R Commander plug-in EZR (Easy R), which adds a variety of statistical functions, including survival analyses, ROC analyses, metaanalyses, sample size calculation, and so on, to the R commander. EZR enables point-and-click easy access to a variety of statistical functions as shown below, especially for medical statistics. A report that introduced the investigation of EZR was published in *Bone Marrow Transplantation* (Nature Publishing Group) as an Open article. This report can be used as a simple manual. It can be freely downloaded from the journal website (URL:

<http://www.nature.com/bmt/journal/vaop/ncurrent/pdf/bmt2012244a.pdf>). A complete manual of EZR is available only in Japanese (Chugai Igakusha, ISBN: 978-4-498-10901-8, URL: <http://www.chugaiigaku.jp/item/detail.php?id=1660> or Nankodo, ISBN: 978-4-524-26158-1, URL: <http://www.nankodo.co.jp/g/g9784524261581/>)

Details

Package: RcmdrPlugin.EZR

Type: Package

Version: 1.41

Date: 2019-10-01

License: GPL (>= 2)

Installation of EZR

See <http://www.jichi.ac.jp/saitama-sct/SaitamaHP.files/statmedEN.html> for detailed information. Briefly, EZR is platform-independent. RcmdrPlugin.EZR should be installed with R commander (Rcmdr) and the other packages that Rcmdr or EZR depends on. Packages required by EZR can be easily installed at the same time with the installation of EZR by copying and pasting the following command to the R console window after "`>`".

```
install.packages(pkgs="RcmdrPlugin.EZR", dependencies=TRUE)
```

After installation, R commander can be started by the command, `library(Rcmdr)` from the R console. Packages required by Rcmdr are installed at the first start-up of R commander. EZR can be loaded by selecting RcmdrPlugin.EZR from the "Tools" > "Load Rcmdr plug-in(s)" menu. Answer "Yes" to "Restart now?".

On Windows, EZR plugin package will be loaded when R commander is started, if the following sentence is added to the Rprofile.site file in etc folder in the R folder (C:\Program Files\R\R-X.XX.X\etc).

```
options(Rcmdr=list(plugins="RcmdrPlugin.EZR"))
```

In addition, if the following phrase is added to the command in "Target:" column on the "Shortcut" tab of the "Property" of "R" shortcut on the desktop (which can be opened by right-clicking on the shortcut), R commander will start at the same time with launching R.

```
R_DEFAULT_PACKAGES="Rcmdr"
```

Therefore, if these two options were added, EZR can be started just by double-clicking on the "R" shortcut on the desktop.

In OS X, these can be done by opening the Terminal.app located in the Utilities folder, followed by copying and pasting the following command.

```
echo "options(Rcmdr=list(plugins='RcmdrPlugin.EZR'))" >> ~/.Rprofile
echo "library(Rcmdr)" >> ~/.Rprofile
echo "local({" >> ~/.Rprofile
echo "old <- getOption('defaultPackages')" >> ~/.Rprofile
echo "options(defaultPackages = c(old, 'Rcmdr'))" >> ~/.Rprofile
echo "})" >> ~/.Rprofile
```

The default data folder of Windows EZR can be changed by right-clicking on this "R" shortcut on the desktop, selecting "Properties", and replacing the folder name in the "Start in:" column on the "Shortcut" tab.

EZR statistical functions

EZR includes following statistical functions.

For discrete variables

Frequency distributions/cr Confidence interval for a proportion
One sample proportion test
Confidence interval for a difference between two proportions
Confidence interval for a ratio of two proportions
Compare two proportions (Fisher's exact test and Chi-square test)
Compare proportions of two paired samples (McNemar test)
Compare proportions of more than two paired samples (Cochran Q test)
Cochran-Armitage test for trend in proportions
Logistic regression

For continuous variables

Numerical summaries
Smirnov-Grubbs test for outliers
Kolmogorov-Smirnov test for normal distribution
Confidence interval for a mean
Single-sample t-test
Two-variances F-test
Two-sample t-test
Paired t-test
Bartlett's test
One-way ANOVA
Repeated-measures ANOVA
Multi-way ANOVA
ANCOVA
Test for Pearson's correlation
Linear regression

For nonparametric tests for continuous variables

Mann-Whitney U test
Wilcoxon's signed rank test
Kruskal-Wallis test
Friedman test
Jonckheere-Terpstra test
Spearman's rank correlation test

For survival analysis

Kaplan-Meier survival curve and logrank test
Logrank trend test
Cox proportional hazard regression

Cox proportional hazard regression with time-dependent covariate
Cumulative incidence of competing events and Gray test
Fine-Gray proportional hazard regression for competing events

For diagnostic test analysis

Accuracy of qualitative test
Kappa statistics for agreement of two tests
Compute positive and negative predictive values
ROC curve analysis for quantitative test
Compare two ROC curves
Cronbach's alpha coefficient for reliability

For matched-pair analysis

Extract matched controls
Mantel-Haenzel test for matched proportions
Conditional logistic regression for matched-pair analysis
Stratified Cox proportional hazard regression for matched-pair analysis

For meta-analysis and meta-regression test

Meta-analysis and meta-regression test for proportions
Meta-analysis and meta-regression test for means
Meta-analysis and meta-regression test for hazard ratios

For sample size and power calculation

Calculate sample size from control and desired response rates
Calculate sample size from proportion and confidence interval
Calculate sample size or power for comparison with specified proportion
Calculate sample size or power for comparison between two proportions
Calculate sample size for non-inferiority trial of two proportions
Calculate sample size from standard deviation and confidence interval
Calculate sample size or power for comparison between two means
Calculate sample size for non-inferiority trial of two means
Calculate sample size or power for comparison between two paired means
Calculate sample size or power for comparison between two survival curves
Calculate sample size for non-inferiority trial of two survival curves

For drawing graphs

Bar graph(Frequencies)
Pie chart(Frequencies)
Stem-and-leaf display
Histogram
QQ plot
Bar graph(Means)
Line graph(Means)
Line graph(Repeated measures)
Boxplot
Dot chart
Ordered chart
Scatterplot
Scatterplot matrix
Adjusted survival curve
Stacked cumulative incidences

Statistical functions from original R commander

Principal-components analysis
Factor analysis
k-means cluster analysis
Hierarchical cluster analysis
Summarize hierarchical clustering
Add hierarchical clustering to data set
Linear hypothesis
Variance-inflation factor
Breusch-Pagan test for heteroscedasticity
Durbin-Watson test for autocorrelation
RESET test for nonlinearity
Bonferroni outlier test
Basic diagnostic plots
Residual quantile-comparison plot
Component+residual plots
Added-variable plots
Influence plot
Effect plots

Basic operations in EZR

These EZR functions can be started by point-and-click access using the items on the menu bar. See EZRdialogs for details. R commander automatically creates and executes corresponding R commands that appear in the "Script window". Results

are shown in the "Output window". If any errors or warnings are noted, messages will appear in the "Message window". The created commands can be saved by selecting "File" > "Save script" on the menu bar. The output can be saved by selecting "File" > "Save output". By saving the commands, users can reproduce the analyses and can also share the procedure with the other investigators.

The following EZR functions can be executed by typing the commands in the "Script window" and clicking on the "Submit" button.

Following functions are built to create a formatted table for presentation.

`w.twoway(table, filename)` function copies the results of two-way table analyses to the clipboard or text file.

`w.ttest(table, filename)` function copies the results of t-test to the clipboard or text file.

`w.survival(table, filename)` function copies the results of survival analyses to the clipboard or text file.

`w.ci(table, filename)` function copies the results of cumulative incidence analyses to the clipboard or text file.

`w.multi(table, filename)` function copies the results of multivariate regression analyses to the clipboard or text file.

"table" can be omitted except for logistic regression analysis and Fine & Gray proportional hazard regression analysis, in which "odds" and "crr.table" should be specified for "table" (default is "cox.table" to copy the results of Cox proportional hazard regression analysis).

If "filename" is omitted, the formatted table will be copied to the clipboard, which can be pasted into a spreadsheet.

`Mantel.Byar()` function is for Mantel-Byar test and Simon and Makuch plot, which should be performed after executing "Cox proportional hazard modeling with time-dependent covariate".

`rmean.table()` function is for restricted mean survival time analysis, that should be used after "Kaplan-Meier survival curve and logrank test" analysis.

`rmean.table.adjusted()` function is for adjusted restricted mean survival time analysis, that should be used after "Adjusted survival curve" analysis.

Translations

EZR comes with translations from English into Japanese.

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References

Its complete manual is available only in Japanese (Chugai Igakusha, ISBN: 978-4-498-10901-8, URL: <http://www.chugaiigaku.jp/item/detail.php?id=1660> or Nankodo, ISBN: 978-4-524-26158-1, URL: <http://www.nankodo.co.jp/g/g9784524261581/>), but a report that introduced the investigation of EZR was published in *Bone Marrow Transplantation* (Nature Publishing Group) as an Open article. This report can be used as a simple manual. It can be freely downloaded from the journal website as shown below.

Yoshinobu Kanda (2013). Investigation of the freely available easy-to-use software EZR for medical statistics. *Bone Marrow Transplantation* (Open article, URL: <http://www.nature.com/bmt/journal/vaop/ncurrent/pdf/bmt2012244a.pdf>).

EZR web site: Division of Hematology, Saitama Medical Center, Jichi Medical University. URL: <http://www.jichi.ac.jp/saitama-sct/SaitamaHP.files/statmedEN.html>