

# Package ‘RcmdrPlugin.EZR’

April 2, 2024

**Type** Package

**Title** R Commander Plug-in for the EZR (Easy R) Package

**Version** 1.65

**Date** 2024-4-1

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**Depends** R (>= 4.2.0)

**Imports** Rcmdr (>= 2.8.0), readstata13

**Suggests** abind, aod, aplpack, brant, car, clinfun, cmprsk, consort, foreign, ggplot2, lawstat, meta, metatest, netmeta, multcomp, mvtnorm, Matching, plotly, pROC (>= 1.15.0), survivalROC, survRM2, tableone, readxl, lmerTest, swimplot, currentSurvival, rstatix

**Description** EZR (Easy R) 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 statistical functions, especially for medical statistics. EZR is platform-independent and runs on Windows, Mac OS X, and UNIX. Its complete manual is available only in Japanese (Chugai Igakusha, ISBN: 978-4-498-10918-6, Nankodo, ISBN: 978-4-524-26158-1, Ohmsha, ISBN: 978-4-274-22632-8), but an 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. This report has been cited in more than 10,000 scientific articles.

**Copyright** The functions in EZR package were programmed by Y. Kanda, except for the following functions. dot.plot(), prop.conf(), Cochran.Q.test(), pairwise.prop2.test(), pairwise.pairedt.test(), pairwise.kruskal.test(), pairwise.friedman.test(), pairwise.logrank.test(), pairwise.gray.test(), Steel.Dwass(), Steel(), pdunnet(), Mantel.Byar() were modified from the corresponding functions distributed by professor Aoki (<http://aoki2.si.gunma-u.ac.jp/R>). crr() and cuminc() were derived from cmprsk package. nrisk() was modified from survplot

package (<http://www.cbs.dtu.dk/~eklund/survplot/>). `epi.test()` and `epi.kappa()` were derived from `epiR` package. `jonckheere.test()`, `ph2simon()` and `ph2single()` were derived from `clinfun` package. Functions of meta-analysis were derived from `meta` and `metatest` packages. Functions of matched-pair analysis were derived from `Matching`. Functions of receiver-operating characteristics curve analyses were derived from `pROC` package. Many dialog functions in EZR were modified from the corresponding functions in `Rcmdr` package and `RcmdrPlugin.survivalT` package.

**License** GPL ( $\geq 2$ )

**URL** <https://www.nature.com/articles/bmt2012244.pdf>

<https://www.jichi.ac.jp/saitama-sct/SaitamaHP.files/statmedEN.html>

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2024-04-02 12:42:11 UTC

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EZR	<i>Rcmdr Plug-In Package for the EZR (Easy R especially for medical statistics)</i>
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## 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: <https://www.nature.com/articles/bmt2012244.pdf>). A complete manual of EZR is available only in Japanese (Chugai Igakusha, ISBN: 978-4-498-10918-6, URL: <http://www.chugaiigaku.jp/item/detail.php?id=3342>, Nankodo, ISBN: 978-4-524-26158-1, URL: <https://www.nankodo.co.jp/g/g9784524261581/>, Ohmsha, ISBN: 978-4-274-22632-8, URL: <https://www.ohmsha.co.jp/book/9784274226328/>)

## Details

Package: RcmdrPlugin.EZR  
Type: Package  
Version: 1.65  
Date: 2024-2-28  
License: GPL (>= 2)

## Installation of EZR

See <https://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
- Ordinal logistic regression
- Multinomial 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  
Linear Mixed Model

*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  
Current survival  
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  
Fine-Gray proportional hazard with time-dependent covariate

*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  
ROC curve analysis for time-to-event data  
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  
Network meta-analysis

*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 for selection design in randomized phase II trials  
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 (Waterfall plot)  
Swimmer plot  
Sankey diagram  
Scatterplot  
Scatterplot matrix  
Adjusted survival curve  
Adjusted cumulative incidence 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.tway(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.

## Author(s)

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## References

Its complete manual is available only in Japanese (Chugai Igakusha, ISBN: 978-4-498-10918-6, URL: <http://www.chugaiigaku.jp/item/detail.php?id=3342>, Nankodo, ISBN: 978-4-524-26158-1, URL: <https://www.nankodo.co.jp/g/g9784524261581/>, Ohmsha, ISBN: 978-4-274-22632-8, URL: <https://www.ohmsha.co.jp/book/9784274226328/>), 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: <https://www.nature.com/articles/bmt2012244.pdf>).

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

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EZR dialogs

*EZR dialogs*

---

## Description

EZR dialogs enable point-and-click easy access to a variety of statistical functions.

## Details

EZR dialogs enable point-and-click easy access to a variety of statistical functions.

To select more than one variable in the list box, click on variables pressing Ctrl key, and to de-select one of the selected variables, click on the variable to deselect pressing Ctrl key.



To perform analyses in a subset of the samples, type an R expression into the box labelled "Condition to limit samples for analysis". For example, to perform analysis in male patients aged at least 60 years old, type `Age >= 60 & Sex == "Male"` into the box, assuming that Age and Sex variables indicate age and sex of the patients, respectively.

### Cautions in multivariate analyses using EZR

When a categorical variable with more than two categories is to be analyzed in Fine and Gray regression modeling, dummy variables should be created before an analysis, although such dummy variables are automatically created in multiple regression, logistic regression and Cox proportional hazards regression in R. For example, if a user wants to evaluate the effect of three types (A, B, and C) of treatments, information for which is included in the categorical variable Tx as "A", "B" and "C", they would select "Active data set" > "Variables" > "Create dummy variables" from the EZR menu to make three categorical variables named Tx.Dummy.A, Tx.Dummy.B, and Tx.Dummy.C.

Tx.Dummy.A has a value of 1 for patients who received treatment A and 0 for others. Users should choose one of the three categories as a reference and input dummy variables for the other two categories into the regression model.

The stepwise selection function of explanatory variables based on Akaike information criterion and Bayesian information criterion only accepts dummy variables automatically created by R, whereas stepwise selection based on P-value also accepts dummy variables created by a user using EZR. If the option for a "Wald test for overall P-value for factors with >2 levels" is selected in the dialog of the regression analyses, the overall P-value for the categorical variable will be calculated.

Survival curves adjusted for other factors by the mean of covariates method, in which average values of covariates are entered into the Cox proportional hazards model, can be drawn by selecting "Graphs" > "Adjusted survival curve".

### References

Read following article for details. It can be freely downloaded from the journal website as shown below.

Yoshinobu Kanda (2012). Investigation of the freely available easy-to-use software EZR for medical statistics. *Bone Marrow Transplantation* (Open article, URL: <https://www.nature.com/articles/bmt2012244.pdf>).

**Description**

The modified points from the original `hist()` are 1) `hist2()` uses Scott algorithm instead of Sturges. 2) `hist2()` adds a group below the lowest group created by `hist()`.

**Usage**

```
hist2(x, breaks="scott", plot=TRUE, ...)
```

**Arguments**

<code>x</code>	a vector of values for which the histogram is desired.
<code>breaks</code>	see <code>hist()</code> for details.
<code>plot</code>	logical. If TRUE (default), a histogram is plotted.
<code>...</code>	further arguments and graphical parameters passed to <code>plot.histogram</code> and thence to title and axis (if <code>plot = TRUE</code> ).

**Details**

See `hist()` for details.

**See Also**

[hist](#)

---

HistEZR

*Plot a Histogram*

---

**Description**

This function is a wrapper for the [hist](#) function in the base package, permitting percentage scaling of the vertical axis in addition to frequency and density scaling. This function is modified from the `Hist()` function in the Rcmdr package. `HistEZR()` package in RcmdrPlugin.EZR uses `hist2()` instead of `hist()`. In `hist2()`, the method to set breakpoints between histogram cells was changed from "Sturges" to "Scott".

**Usage**

```
HistEZR(x, scale=c("frequency", "percent", "density"), xlab=deparse(substitute(x)),
        ylab=scale, main="", ...)
```

**Arguments**

<code>x</code>	a vector of values for which a histogram is to be plotted.
<code>scale</code>	the scaling of the vertical axis: "frequency" (the default), "percent", or "density".
<code>xlab</code>	x-axis label, defaults to name of variable.
<code>ylab</code>	y-axis label, defaults to value of scale.
<code>main</code>	main title for graph, defaults to empty.
<code>...</code>	arguments to be passed to <code>hist</code> .

**Value**

This function returns NULL, and is called for its side effect — plotting a histogram.

**See Also**

[hist](#)

**Examples**

```
data(iris, package="datasets")
HistEZR(iris$Petal.Length, scale="percent")
```

---

ifelse2

*Conditional Element Selection*

---

**Description**

ifelse2 returns a value with the same shape as test which is filled with elements selected from either yes or no depending on whether the element of test is TRUE or FALSE. Modified from ifelse.

**Usage**

```
ifelse2(test, yes, no)
```

**Arguments**

test	an object which can be coerced to logical mode.
yes	return values for true elements of test.
no	return values for false elements of test.

**Details**

The only difference from ifelse is that, when missing values in test, ifelse gives missing values in the result, whereas ifelse2 gives values for false elements of test.

**See Also**

[ifelse](#)

---

IPTW.ATE	<i>Inverse probability of treatment weighting using stabilized weights based on propensity score</i>
----------	--

---

### Description

Return stabilized weights calculated based on propensity score and assess balance of covariates between the groups.

### Usage

```
IPTW.ATE(GLM)
```

### Arguments

GLM                    an object of class "glm", usually, a result of a call to glm.

### Details

By putting the result of a logistic regression analysis to calculate propensity scores into IPTW.ATE(), this function returns a stabilized weight variable calculated based on propensity scores and assesses the balance of covariates between the groups.

### Value

an object of class "glm"

---

Mantel.Byar	<i>mantel-Byar test</i>
-------------	-------------------------

---

### Description

Performs Mantel-Byar test for comparison of survival data with a time-dependent covariate.

### Usage

```
Mantel.Byar(Group = NULL, Event = TempTD$endpoint_td,
StartTime = TempTD$start_td, StopTime = TempTD$stop_td,
method = c("SAS", "Tominaga"), plot=0, landmark=0)
```

**Arguments**

Group	the name of the time-dependent covariate. If NULL, the last column name of the TempTD dataset will be used.
Event	a vector for event.
StartTime	a vector for starting time.
StopTime	a vector for stopping time.
method	method for analysis. "SAS" or "Tominaga"
plot	plot=1, 2, or 3 to plot Simon and Makuch survival curves. Line discrimination with colors (plot=1), line types (plot=2), or width (plot=3).
landmark	landmark for Simon and Makuch plot.

**Details**

Performs Mantel-Byar test for comparison of survival data with a time-dependent covariate. This function should be performed just after executing "Cox proportional hazard modeling with time-dependent covariate" from the EZR menu. If plot is set to 1, Simon and Makuch plot is drawn with a landmark as specified.

---

rmean.table	<i>caluculation of restricted mean survival</i>
-------------	---

---

**Description**

Caluculate and compare restricted mean survival.

**Usage**

```
rmean.table(x=km, tau=NULL, plot=0)
rmean.table.adjusted(x=coxmodel, tau=NULL)
```

**Arguments**

x	survfit object
tau	specify a value of the truncation time point for the restricted mean survial caluculation, e.g.,tau=365. When tau=NULL, the default value (i.e., the minimum of the largest observed "event" time in each of the two groups) is used.
plot	plot=1 to plot estimated area.

**Details**

rmean.table() function calculates restricted mean survival with a truncation time point as specified by tau option. Also tests the difference in the restricted mean survival, if there are only two groups. This function should be performed after "Kaplan-Meier survival curve and logrank test" function of EZR (or after executing survfit() command). rmean.table() function does not support stratified analysis. rmean.table.adjusted() function calculates adjusted restricted mean survival. This function should be performed after "Adjusted survival curve" function of EZR.

---

 ShipWeight

*Ship weight data for linear regression*


---

**Description**

Weights of ships with males, females, cats, and ants on them.

**Usage**

```
data(ShipWeight)
```

**Format**

Weight_Kg:	Weight of each ship
Male:	Number of males on each ship
Female:	Number of females on each ship
Cat:	Number of cats on each ship
Ant:	Number of ants on each ship

**Note**

Sample file for linear regression.

---

 st.diff

*Calculate standardized difference to assess balance of covariates in unweighted and weighted dataset.*


---

**Description**

Calculate standardized difference to assess balance of covariates in unweighted and weighted dataset.

**Usage**

```
st.diff.binom(factor, group)
st.diff.multinom(factor, group)
st.diff.categor(factor, group)
st.diff.numeric(numeric, group)
st.diff.binom.w(factor, weight, group)
st.diff.multinom.w(factor, weight, group)
st.diff.categor.w(factor, weight, group)
st.diff.numeric.w(numeric, weight, group)
```

**Arguments**

factor	factor variable in vector for balace assessment.
numeric	numeric variable in vector for balace assessment.
group	group variable in vector for balace assessment.
weight	weight variable in vector for balace assessment of weighted dataset.

**Details**

st.diff.binom(), st.diff.multinom(), st.diff.categor() and st.diff.numeric() functions calculate standardized difference of factor variables and numeric variables, respectively, in unweighted dataset. st.diff.binom.w(), st.diff.multinom.w(), st.diff.categor.w() and st.diff.numeric.w() functions calculate standardized difference of factor variables and numeric variables, respectively, in weighted dataset. st.diff.binom() and st.diff.binom.w() are for binomial factors, st.diff.multinom() and st.diff.multinom.w() are for multinomial factors, and st.diff.categor() and st.diff.categor.w() are for factors irrespective of levels.

---

w.multi

---

*Create a formatted table for presentation*


---

**Description**

Creates a formatted table for presentation and outputs to a file or clipboard.

**Usage**

```
w.multireg(table = multireg.table, filename = "clipboard", CI = 0, signif = 0, en = 1)
w.multi(table = cox.table, filename = "clipboard", CI = 0, signif = 0, en = 1)
w.twoway(table = Fisher.summary.table, filename = "clipboard", en = 1)
w.ttest(table = summary.ttest, filename = "clipboard", en = 1)
w.survival(table = km.summary.table, filename = "clipboard", en = 1)
w.ci(table = ci.summary.table, filename = "clipboard", en = 1)
```

**Arguments**

table	a table to output.
filename	a filename for output. If omitted, a formatted table is copied to the clipboard.
CI	If 0, confidence intervals are shown in parentheses.
signif	Number of significant digits.
en	If 1, creat a table in English.

**Details**

`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.multireg(table, filename)` function copies the results of multiple regression 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.

These functions should be performed after executing corresponding analyses from the EZR menu.



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