Package ‘RSCABS’

April 26, 2017

Version 0.9.2
Date 2017-04-24
Title Rao-Scott Cochran-Armitage by Slices Trend Test
Depends R (>= 3.1.0)
SystemRequirements Cairo (>= 1.0.0), ATK (>= 1.10.0), Pango (>= 1.10.0), GTK+ (>= 2.8.0), GLib (>= 2.8.0)
Imports gWidgets, RGtk2, R2HTML, gWidgetsRGtk2, methods
LazyLoad yes
LazyData yes
Description Performs the Rao-Scott Cochran-Armitage by Slices trend test (RSCABS) used in analysis of histopathological endpoints, built to be used with either a GUI or by a command line. The RSCABS method is detailed in “Statistical analysis of histopathological endpoints” by John Green et. al. (2014) <doi:10.1002/etc.2530>.
License CC0
URL https://CRAN.R-project.org/package=RSCABS
Author Joe Swintek [aut, cre],
Kevin Flynn [ctb]
Maintainer Joe Swintek <swintek.joe@epa.gov>
RoxygenNote 5.0.1
NeedsCompilation no
Repository CRAN
Date/Publication 2017-04-26 17:47:29 UTC

R topics documented:

RSCABS-package .................................................. 2
addHistoSpec .................................................... 3
checkPlot ....................................................... 4
checkSelection .................................................. 4
convert2Score ................................................... 5
RSCABS-package

Runs the Rao-Scott adjusted Cochran-Armitage trend test by slices (RSCABS) analysis

Description

This package contains all of the functions necessary to run the RSCABS analysis through the GUI or command line on histopathological data.

Details

- **Package:** RSCABS
- **Type:** Package
- **Version:** 0.01
- **Date:** 2016-04-21
- **License:** CC0
addHistoSpec

Note

The command line version uses runRSCABS (see example below). Use the command Histopath to call the GUI version.

Author(s)

Joe Swintek <swintek.joe@epa.gov> as author and Kevin Flynn as a tester.
Maintainer: Joe Swintek <swintek.joe@epa.gov>

References


Examples

#Take the subset corresponding to F0-females of 16 weeks of age
eexampleHistData.sub<-exampleHistData[which(exampleHistData$Generation=='F2' & exampleHistData$Genotypic_Sex=='Female' & exampleHistData$Age=='16_wk' ), ]
#Run RSCABS
eexampleResults<-runRSCABS(exampleHistData.sub,'Treatment','Replicate',test.type='RS')

---

addHistoSpec Specify data parameters

Description

Calls a tab where you can specify the names of the variables used in Histopath.

Usage

addHistoSpec(Notebook)

Arguments

Notebook The notebook the tab will be added to.

Details

- **Select Gender Variable:** Button used to specify the name of the gender variable.
- **Select Gender Value:** Button used to specify the value of the gender variable.
- **Select Generation Variable:** Button used to specify the name of the generation variable.
- **Select Generation Value:** Button used to specify the value of the generation variable.
- **Select Age Variable:** Button used to specify the name of the age variable.
• **Select Age Value**: Button used to specify the value of the age variable.
• **Select Treatment Variable**: Button used to specify the name of the treatment variable.
• **Select Replicate Variable**: Button used to specify the name of the replicate variable.
• **Confirm Selected Values and Variables**: Press this button when all the values in the data specification form have been selected. Only Treatment must be selected to proceed with the analysis. If all values are selected a pop up message will appear directing you to the main tab.

**Author(s)**
Joe Swintek

**See Also**
runRSCABS, otherPath, Histopath

---

**checkPlot**

*Check the selection for plotting*

**Description**
Checks the selection to find and display errors possible errors. This is called `link{plotPath()}`.

**Usage**
checkPlot()

**Author(s)**
Joe Swintek

---

**checkSelction**

*Checks user inputs*

**Description**
An internal function that checks to see if a variables necessary for Histopath to run has been defined

**Usage**
checkSelction()

**Details**
This function relies on the global variables; GenderVar, GenderVal, GenerationVar, GenerationVal, AgeVar, AgeVal, and TreatmentVar. All of these values are controlled by the GUI.
Value

msg  A message to the user displaying all the values and variables that still need to be declared.

Author(s)

Joe Swintek

detailedResults2HTML  Saves results as an HTML file

Description

An internal function that prints results from runDetailedResults to an HTML file.

Usage

detailedResults2HTML(Results, k, Dir, Effect)
Arguments

- **Results**: A Results data structure from `runDetailedResults`.
- **k**: The severity score being displayed.
- **Dir**: The name of the new directory to be created.
- **Effect**: The name of the endpoint to be saved.

**Note**
This function will end up creating a new folder.

**Author(s)**
Joe Swintek

**See Also**
- `runDetailedResults, detailedResults2Output`

---

### detailedResults2Output

*Print results to the GUI window*

**Description**
An internal function that prints results from `runDetailedResults` to the window.

**Usage**

detailedResults2Output(Effect, Results, k, ResultsBox, BoolNotebook, Notebook = NULL)

**Arguments**

- **Effect**: The tested endpoint.
- **Results**: A Results data structure from `runDetailedResults`.
- **k**: The severity score being displayed.
- **ResultsBox**: The name of the box the results are displayed in.
- **BoolNotebook**: A bool indicating to add another tab to the current notebook.
- **Notebook**: The current notebook.

**Author(s)**
Joe Swintek

**See Also**
- `runDetailedResults, detailedResults2HTML`
Example histology data

Description

Example Histology data included in StatCharms and RSCABS.

Usage

data(exampleHistData)

Format

A test data set for StatCharms and RSCABS that contains all the necessary identifiers along with 51 histopathological endpoints.

- **Generation** The generation, with three levels F0, F1, and F2.
- **Treatment** The treatment variable, with 6 levels, where 1 represents the controls.
- **Replicate** The replicate variable. Observation within the same generation, treatment, and replicate value belong to the same replicate.
- **Genotypic_Sex** The genotypic sex either Female or Male.
- **Age** The age either 16_wk or 8_wk.

Source

US EPA Duluth MED Lab

References

TBA

Examples

data(exampleHistData)
str(exampleHistData)
filterData  
*Filters problematic data*

**Description**

An internal function called by OtherPath to filter out problematic endpoints for calculating detailed responses.

**Usage**

```r
cleanData(effect, Data)
```

**Arguments**

- `effect` The endpoint under examination
- `Data` Data from Histopath

**Details**

Filter out potential endpoints that do not have a score above 0 or contain values above 20. This will also exclude anything flagged as an identification variable.

**Value**

BOOL Returns a TRUE or FALSE

**Author(s)**

Joe Swintek

---

getDir  
*Attain the name of a directory*

**Description**

An internal function that creates a dialogue box to attain the name of a directory to be created.

**Usage**

```r
cleanDir(window)
```

**Arguments**

- `window` The window the dialogue box resides in.
**Histopath**

**Value**

Dir
The name of a directory.

**Author(s)**

Joe Swintek

---

**Histopath**

*GUI for analysis of histopathological data*

---

**Description**

This is the function call to start the GUI interface for StatCharms

**Usage**

Histopath()

**Details**

- **Load Data Button:** A standard data set in the "tall" format. Every row indicates an organism. The data set must contain columns for the treatment level and every tested histological endpoint. The data must be in .csv to load it into Histopath.

- **Specify Data Button:** This is used to tell Histopath the names of the columns used to specify the data. Pushing the button brings up a new tab that needs to be navigated to. See addHistospec for details.

- **Run RSCABS Button:** Pressing this will perform the RSCABS analysis. The results will replace the current data in the display box.

- **Run Other Analyses Button:** Pressing this will bring up a new window with the ability to perform other relevant analyses. See otherPath for details.

- **Save Result Button:** Used to save the results of the RSCABS analysis.

**Value**

Returns a list with the following values:

Response
The endpoint that is being tested.

Treatment
The treatment level.

R-Score
The severity score from the histology.

Statistic
The test statistic corresponding that row’s endpoint treatment level, and RSCORE.

P-Value
The corresponding p-value.

Signif
The significance flag where "." is a p-value > 0.05, "*" is a 0.01 < p-value <= 0.05, "**" for 0.001 < p-value <= 0.01, and "***" for p-value <= 0.001.
Note

See the vignette for a full tutorial on how to use this function.

Author(s)

Joe Swintek

References


See Also

runRSCABS, otherPath, addHistoSpec

---

openCB

Open a csv file

Description

An internal function that creates a dialogue box used to open a file with a csv extension.

Usage

openCB(window)

Arguments

window

The window the dialogue box resides in.

Value

df

The data frame that is opened.

Author(s)

Joe Swintek
**otherPath**

*Other analyses for histopathological endpoints*

**Description**

This window is used to calculate the Cochran-Armitage trend test by slices(SCABS), the chi-squared test for homogeneity, and a frequency table for each end point.

**Usage**

`otherPath()`

**Details**

- **Run SCABS Button:** Run SCABS on all end points.
- **Get Details on a Response Button:** Attains values for the chi-squared test for homogeneity, frequency tables, and a RSCABS analysis for a single endpoint.
- **Get Details on all Responses Button:** Attains values for the chi-squared test for homogeneity, frequency tables, and a RSCABS analysis for all endpoints. This will prompt the creation of a new directory and fill that directly with html files containing tables for each endpoint.
- **Save Button:** Saves the results from the last analysis run. SCABS analyses are saved as csv files, while detailed on a Responses are saved as html files.

**Author(s)**

Joe Swintek

**See Also**

`runrscabs, addhistospec, Histopath`

---

**plotPath**

*Plot histopathological data*

**Description**

GUI for plotting histopathological data.

**Usage**

`plotPath()`

**Details**

See `plotRSCABS` or `setPlotParms` for further details.
Author(s)

Joe Swintek

See Also

plotRSCABS

plotRSCABS. Plots histopathological data.

Description

Plots histopathological data used in the RSCABS analysis as stacked bar graphs.

Usage

plotRSCABS(Data, Effect, Treatment, Metric = "Percent", Lowest = "Remove",
       PlotParms = NULL, Format = NULL, File = NULL,...)

Arguments

Data Tall formatted data used in Histopath and runRSCABS.
Effect The name of endpoint being plotted.
Treatment The name of the treatment variable.
Metric The value being plotted, either "Total" or as a "Percent".
Lowest Determines whether to "Include" or "Remove" the lowest response. The lowest
       response should correspond to no effect.
PlotParms A list of plotting parameters, see setPlotParms.
Format The name (as a string) of the function that saves the plot to a file. Use NULL to
       print the plot to the screen.
File The name of the file the plot is saved to.
... Other arguments to be passed to barplot.

Author(s)

Joe Swintek
**popMessage**  
*Pops up a message*

**Description**

An internal function that creates a window to display a message.

**Usage**

```r
popMessage(Message)
```

**Arguments**

- **Message**
  A message to be displayed.

**Author(s)**

Joe Swintek

---

**prepDataRSCABS**  
*Prepares data for an RSCABS analysis*

**Description**

An internal function that takes tall formatted data and converts it to a form usable for the RSCABS analysis.

**Usage**

```r
prepDataRSCABS(Effect = "", Data = {}, Treatment = "", Replicate = "")
```

**Arguments**

- **Effect**
  The endpoint being converted.
- **Data**
  The tall formatted data set.
- **Treatment**
  The name of the treatment variable.
- **Replicate**
  The name of the replicate variable.

**Value**

Returns a list containing:

- **x.i.j**
  matrix containing the number of observed "successes" for replicate i on treatment j.
- **n.i.j**
  matrix containing the number of observations for replicate i on treatment j.
- **m.i**
  matrix of number replicates in each treatment-replicate combination.
- **K.max**
  The maximum severity score for the endpoint.
Author(s)
Joe Swintek

RSCABK  Runs the kth slice of RSCABS

Description
An internal function that calculates the RSCABS or SCABS test statistic with the associated p-value.

Usage
RSCABK(x.i.j, n.i.j, m.i, testK, test.type)

Arguments
x.i.j   matrix containing the number of observed "successes" for replicate i on treatment j.
n.i.j   matrix containing the number of observations for replicate i on treatment j.
m.i    matrix of number units in each treatment/replicate combination.
TestK   The kth severity score being tested.
test.type    Indicate the type of analysis to be performed. Use "RS" to select the Rao-Scott adjustment to the Cochran-Armitage test and "CA" to ignore the adjustment.

Value
Returns a list with the following values:
Response   The endpoint that is being tested.
Treatment   The treatment level.
R-Score    The severity score from the histology.
Statistic   The test statistic corresponding to that row’s endpoint treatment level and R-Score.
P-Value    The corresponding p-value
Signif    The significance flag where "." is a p-value > 0.05, "*" is a 0.01 < p-value <= 0.05, "**" for 0.001 < p-value <= 0.01, and "***" for p-value <= 0.001.

Author(s)
Joe Swintek
RSCABSMain

Cleans data and runs RSCABS when called from the GUI interface

Description

This is an internal function called though the GUI to prepare data for input into `runRSCABS`.

Usage

RSCABSMain(Data, GroupVar = "", ReplicateVar = "", BoScabs = FALSE)

Arguments

Data A standard data set in the tall format. Every row indicates an organism. The data set must contain columns for the treatment level and every tested histological endpoint.

GroupVar The name of the column that contain the information about the treatment level. Increasing values indicate higher treatments.

ReplicateVar The name of the column that contain the information about the replicate structure. This is optional, if this is not declared at function call, BoScabs will be set to FALSE.

BoScabs Indicate the type of analysis to be performed. Use FALSE to select the Rao-Scott adjustment to the Cochran-Armitage test and TRUE to ignore the adjustment.

Value

Returns a list with the following values:

Response The endpoint that is being tested.

Treatment The treatment level.

R-Score The severity score from the histology.

Statistic The test statistic corresponding that row’s endpoint treatment level, and R-Score.

P-Value The corresponding p-value

Signif The significance flag with "." is a p-value > 0.05, "*" is a 0.01 < p-value <= 0.05, "**" for 0.001 < p-value <= 0.01, and "***" for p-value <= 0.001.

Author(s)

Joe Swintek
runDetailedResults  

**Description**

An internal function called by OtherPath to attain detailed results on an endpoint. This function performs a chi-squared test for homogeneity, calculates a frequency table, and recalculates RSCABS.

**Usage**

```r
rundetailedresults(data, groupvar = "", replicatevar = "", effect = ")
```

**Arguments**

- `Data` Tall formatted data from Histopath.
- `GroupVar` The name of the treatment variable.
- `ReplicateVar` The name of the replicate variable.
- `effect` The effect being tested.

**Value**

Returns a list containing:

- `Numeric` The top level of the list is a numeric key associated with the severity score.
- `ChiResults` Chi square results.
- `Step$Row` The results from the RSCABS analysis.
- `Step$FreqTable` The frequency table associated with each treatment level.

**Author(s)**

Joe Swintek

**See Also**

detailedResults2HTML, detailedResults2Output
**runEffectSelect**

*Runs a detailed analysis on an endpoint*

**Description**

An internal function called when the "Get Details on a Response" button is pushed. This function sanitizes the user's input, performs a detailed analysis on an endpoint, then prints them to the display.

**Usage**

`runEffectSelect()`

**Author(s)**

Joe Swintek

---

**runRSCABS**

*Runs RSCABS*

**Description**

Runs the Rao-Scott adjusted Cochran-Armitage trend by slices (RSCABS) analysis.

**Usage**

`runRSCABS(Data, Treatment, Replicate='CA', Effects = '', test.type = "RS")`

**Arguments**

- **Data**: A standard data set in the tall format. Every row indicates an organism. The data set must contain columns for the treatment level and every tested histological endpoint.
- **Treatment**: The name of the column that contains the information about the treatment level. Increasing values indicate higher treatments.
- **Replicate**: The name of the column that contains the information about the replicate structure. If the replicate is not specified this will default to running "CA" as the test type.
- **Effects**: The endpoint to be tested. Defaults to all columns that have integers less than 20. The analysis assumes that higher scores indicate a worse outcome.
- **test.type**: Indicate the type of analysis to be performed. Use "RS" to select the Rao-Scott adjustment to the Cochran-Armitage test and "CA" to ignore the adjustment.
Value

Returns a list with the following values:

- **Response**: The endpoint that is being tested.
- **Treatment**: The treatment level.
- **R-Score**: The severity score from the histology.
- **Statistic**: The test statistic corresponding to that row's endpoint treatment level, and R-Score.
- **P-Value**: The corresponding p-value
- **Signif**: The significance flag where "." is a p-value > 0.05, "*" is a 0.01 < p-value <= 0.05, "**" for 0.001 < p-value <= 0.01, and "***" for p-value <= 0.001.

Note

The outputted data frame will not show results for endpoints that did not meet selection criteria as determined by `checkSelection`. Also note that RSCABS is a step down procedure so analysis for an effect at an RSCORE will stop when a non-significant result is found.

Author(s)

Joe Swintek

References


Examples

```r
#Take the subset corresponding to F0-females of 16 weeks of age
dakeHistData.sub <- exampleHistData[which(exampleHistData$Generation=='F2' &
                                   exampleHistData$Genotypic_Sex=='Female' &
                                   exampleHistData$Age=='16_wk'), ] #Run RSCABS
dakeResults <- runRSCABS(exampleHistData.sub, "Treatment",
                          'Replicate', test.type= 'RS')
```

runStdSubset

Subset the data used in Histopath

Description

An internal function that that will subset data for Histopath based on the global variables; GenderVar, GenderVal, GenerationVar, GenerationVal, AgeVar, and AgeVal.
saveCB

Usage
	runStdSubset(Data)

Arguments

Data Data that has been formatted for use in Histopath.

Details

This function relies on the global variables; GenderVar, GenderVal, GenerationVar, GenerationVal, AgeVar, and AgeVal. All of these values are controlled through GUI.

Value

UseData Sub-setted data that will be used in the RSCABS calculation.

Author(s)

Joe Swintek

saveCB Attain the name of a file to be saved

Description

An internal function used to call a dialogue box to name a file to be saved.

Usage

saveCB(window, OutData)

Arguments

window The window the dialogue box resides in.
OutData Data to be saved.

Author(s)

Joe Swintek
saveFile  Saves a data set

Description
An internal function that save a data set as csv file.

Usage
saveFile(File, OutData)

Arguments
File  Name of the file to be saved.
OutData  Data to be saved.

Author(s)
Joe Swintek

selectPara  Window to declare the names of variables and values

Description
This internal function brings up a window to declare a variable or value. The function then assigns the names in global variables and updates the corresponding labels on the OtherPath window.

Usage
selectPara(VarName, LabelName=NULL, Enviro, What=NULL, Mult=FALSE, Display=NULL)

Arguments
VarName  The name (as a string) of the variable or value to be specified in the data set.
LabelName  The name (as a string) of the label that will be updated. The default is to not update a label.
What  A vector that can can be selected from.
Enviro  The name (as a string) of the environment that containing the variables and labels.
Mult  Bool for determining if multiple values can be selected.
Display  Indicates what is displayed in the window title.

Author(s)
Joe Swintek
setPlotParms

---

**setPlotParms**

Sets the default plotting parameters for RSCABS

---

**Description**

An internal function for setting the plotting parameters not defined by the prior to function call. This is called by `plotRSCABS`.

**Usage**

```r
setPlotParms(PlotParms, Out, Effect, Metric, Lowest,...)
```

**Arguments**

- `PlotParms`: A list that contains values for the plotting parameters for `barplot`.
- `Out`: A matrix of values that will be plotted.
- `Effect`: The name of the endpoint being plotted.
- `Metric`: The value being plotted and be "Total" or "Percent".
- `Lowest`: Determines whether to "Include" or "Remove" the lowest response. The lowest response should correspond to no effect.
- `...`: Other arguments to be passed to `barplot`.

**Value**

The values of PlotParms have the same name as the plotting parameters of `barplot`.

- `xlab`: The label for the x axis, defaults to 'Treatment Group'.
- `ylab`: The label for the y axis, defaults to the value of `Metric`.
- `main`: The title.
- `legend.text`: The legend text defaults to name of the rows of `Out`.
- `args.legend`: Extra parameters to be passed to `legend`. Defaults to placing the legend in the right margin.
- `ColorFunction`: The code pallet used to color the bar plots. Defaults to using `heat.colors`.
- `Colors`: The colors used in the bar plot. Defaults to using the pallet determined by `ColorFunction`.

**Note**

This function only changes item in PlotParms that have a NULL value.

**Author(s)**

Joe Swintek

**See Also**

`plotRSCABS`
**stepDownRSCABS**

*Performs the step down aspect of RSCABS*

**Description**

An internal function that performs the step down aspect of RSCABS.

**Usage**

```r
stepDownRSCABS(TestK, x.i.j, n.i.j, m.i, Effect, test.type)
```

**Arguments**

- `TestK`: The severity score being tested
- `x.i.j`: Matrix containing the number of observed "successes" for replicate i on treatment j.
- `n.i.j`: Matrix containing the number of observations for replicate i on treatment j.
- `m.i`: Matrix of number units in each treatment/replicate combination.
- `Effect`: The the end point to be tested.
- `test.type`: Indicate the type of analysis to be performed. Use "RS" to select the Rao-Scott adjustment to the Cochran-Armitage test and "CA" to ignore the adjustment.

**Value**


**Author(s)**

Joe Swintek

---

**stepKRSCABS**

*Steps through the severity score for a given effect*

**Description**

An internal function for stepping through each severity score of an endpoint.

**Usage**

```r
stepKRSCABS(Effect, Data.Prep, Treatment, Replicate, test.type)
```
subsetDataKeep

Arguments

- **Effect**: Endpoint being tested.
- **Data.Prep**: Data prepared by prep.data.RSCABS.
- **Treatment**: Name of the treatment variable.
- **Replicate**: Name of the replicate variable.
- **test.type**: Indicate the type of analysis to be performed. Use "RS" to select the Rao-Scott adjustment to the Cochran-Armitage test and "CA" to ignore the adjustment.

Value

- **Results.Effect**: An intermediary step for results.

Author(s)

Joe Swintek

---

**subsetDataKeep**  
*Subsets data*

Description

An internal function used to subset data and sanitize inputs.

Usage

```r
subsetDataKeep(Data, Var, Val)
```

Arguments

- **Data**: Tall formatted data used in Histopath.
- **Var**: The variable used for sub-setting.
- **Val**: The value of the variable being sub-setted on.

Value

- **Subset**: Post subset data
Index

*Topic **Plotting**
  - checkPlot, 4
  - plotPath, 11
  - plotRSCABS, 12
  - setPlotParms, 21

*Topic **RSCABS**
  - addHistoSpec, 3
  - Histopath, 9
  - otherPath, 11
  - RSCABS-package, 2
  - runRSCABS, 17

*Topic **datasets**
  - exampleHistData, 7

addHistoSpec, 3, 9–11
barplot, 12, 21
checkPlot, 4
checkSelction, 4, 18
convert2Score, 5
detailedResults2HTML, 5, 6, 16
detailedResults2output, 6, 6, 16
deprecated
exampleHistData, 7
filterData, 8
getDir, 8
heat.colors, 21
Histopath, 3, 4, 9, 11, 12
legend, 21
openCB, 10
otherPath, 4, 9, 10, 11
plotPath, 11
plotRSCABS, 11, 12, 12, 21
popMessage, 13
prepDataRSCABS, 13
RSCABK, 14
RSCABS (RSCABS-package), 2
RSCABS-package, 2
RSCABSMain, 15
runDetailedResults, 5, 6, 16
runEffectSelect, 17
runRSCABS, 3, 4, 10–12, 15, 17
runStdSubset, 18
saveCB, 19
saveFile, 20
selectPara, 20
setPlotParms, 11, 12, 21
stepDownRSCABS, 22
stepKRSRSCABS, 22
subsetDataKeep, 23