

Package ‘RSCABS’

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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 gWidgets2, RGtk2, R2HTML, gWidgets2RGtk2, 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>.

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URL <https://CRAN.R-project.org/package=RSCABS>

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RSCABS-package	<i>Runs the Rao-Scott adjusted Cochran-Armitage trend test by slices (RSCABS) analysis</i>
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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

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

Green, John W. and Springer, Timothy A. and Saulnier, Amy N. and Swintek, Joe, (2014) Statistical analysis of histopathological endpoints. *Environmental Toxicology and Chemistry*, 33(5), 1108-1116

Examples

```
## Not run:
#Take the subset corresponding to F0-females of 16 weeks of age
## Not run:
data(exampleHistData)
exampleHistData.sub<-exampleHistData[which(exampleHistData$Generation=='F2' &
exampleHistData$Genotypic_Sex=='Female' & exampleHistData$Age=='16_wk' ), ]
#Run RSCABS
exampleResults<-runRSCABS(exampleHistData.sub,'Treatment','Replicate',test.type='RS')

## End(Not run)
```

`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	<i>Checks user inputs</i>
---------------	---------------------------

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

convert2Score	<i>Converts any object that is not zero or a positive number to NA</i>
---------------	--

Description

An internal function for converting any non-whole number in a vector into NA which is excluded from the analysis.

Usage

```
convert2Score(Dvec)
```

Arguments

Dvec	A vector to be converted.
------	---------------------------

Value

Dvec	A vector after conversion.
------	----------------------------

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, Inverse=FALSE)
```

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.
Inverse	Bool indicating an inverse scale endpoint.

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, Inverse=FALSE)
```

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.
Inverse	Bool indicating an inverse scale endpoint.

Author(s)

Joe Swintek

See Also

[runDetailedResults](#), [detailedResults2HTML](#)

exampleHistData	<i>Example histology data</i>
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Description

Example Histology data included in StatCharrms and RSCABS.

Usage

```
data(exampleHistData)
```

Format

A test data set for StatCharrms 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 ether 16_wk or 8_wk.

Source

US EPA Duluth MED Lab

References

TBA

Examples

```
data(exampleHistData)
str(exampleHistData)
```

filterData	<i>Filters problematic data</i>
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Description

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

Usage

```
filterData(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	<i>Attain the name of a directory</i>
--------	---------------------------------------

Description

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

Usage

```
getDir(window)
```

Arguments

window	The window the dialogue box resides in.
--------	---

Value

Dir	The name of a directory.
-----	--------------------------

Author(s)

Joe Swintek

Histopath	<i>GUI for analysis of histopathological data</i>
-----------	---

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 bring 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 perform the 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

Green, John W., Springer, Timothy A., Saulnier, Amy N., and Swintek, Joe (2014) Statistical analysis of histopathological endpoints. *Environmental Toxicology and Chemistry*, 33(5), 1108-1116

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 ran. 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	<i>Plot histopathological data</i>
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Description

GUI for plotting histopathological data.

Usage

```
plotPath()
```

Details

See [plotRSCABS](#) or [setPlotParms](#) for further details.

Author(s)

Joe Swintek

See Also

[plotRSCABS](#)

plotRSCABS	<i>Plots histopathological data.</i>
------------	--------------------------------------

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 .

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 k th 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 through 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 *Attain detailed results on an endpoint*

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

```
runDetailedResults(Data, GroupVar = "", ReplicateVar = "", effect = "", Inverse=FALSE)
```

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.
Inverse	Bool, indicating that this effect is an inverse scale effect.

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	<i>Runs a detailed analysis on an endpoint</i>
-----------------	--

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	<i>Runs RSCABS</i>
-----------	--------------------

Description

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

Usage

```
runRSCABS(Data, Treatment, Replicate='', 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 [checkSelction](#). 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

Green, John W. and Springer, Timothy A. and Saulnier, Amy N. and Swintek, Joe, (2014) Statistical analysis of histopathological endpoints. *Environmental Toxicology and Chemistry*, 33(5), 1108-1116

Examples

```
## Not run:
## Not run:
#Take the subset corresponding to F0-females of 16 weeks of age
data(exampleHistData)
exampleHistData.sub<-exampleHistData[which(exampleHistData$Generation=='F2' &
exampleHistData$Genotypic_Sex=='Female' & exampleHistData$Age=='16_wk' ), ]
#Run RSCABS
exampleResults<-runRSCABS(exampleHistData.sub,'Treatment',
'Replicate',test.type='RS')

## End(Not run)
```

runStdSubset	<i>Subset the data used in Histopath</i>
--------------	--

Description

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

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	<i>Attain the name of a file to be saved</i>
--------	--

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	<i>Saves a data set</i>
----------	-------------------------

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	<i>Window to declare the names of variables and values</i>
------------	--

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	<i>Sets the default plotting parameters for RSCABS</i>
--------------	--

Description

An internal function for setting the plotting parameters not defined by the prior to function call. This is called by [plotRSCABS](#).

Usage

```
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 <code>Metric</code> .
main	The title.
legend.text	The legend text defaults to name of the rows of <code>Out</code> .
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 <code>ColorFunction</code> .

Note

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

Author(s)

Joe Swintek

See Also

[plotRSCABS](#)

stepDownRSCABS	<i>Performs the step down aspect of RSCABS</i>
----------------	--

Description

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

Usage

```
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

Result.K	An intermediary result.
----------	-------------------------

Author(s)

Joe Swintek

stepKRSCABS	<i>Steps through the severity score for a given effect</i>
-------------	--

Description

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

Usage

```
stepKRSCABS(Effect, Data.Prepare, Treatment, Replicate, test.type)
```

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

```
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

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