Package ‘RSCABS’

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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
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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
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

```r
## 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

```r
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 `plotPath()`.

**Usage**

```r
checkPlot()
```

**Author(s)**

Joe Swintek
checkSelection

Checks user inputs

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

Usage
checkSelection()

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

Converts any object that is not zero or a positive number to NA

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)
**exampleHistData**

---

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Effect</td>
<td>The tested endpoint.</td>
</tr>
<tr>
<td>Results</td>
<td>A Results data structure from <code>runDetailedResults</code>.</td>
</tr>
<tr>
<td>k</td>
<td>The severity score being displayed.</td>
</tr>
<tr>
<td>ResultsBox</td>
<td>The name of the box the results are displayed in.</td>
</tr>
<tr>
<td>BoolNotebook</td>
<td>A bool indicating to add another tab to the current notebook.</td>
</tr>
<tr>
<td>Notebook</td>
<td>The current notebook.</td>
</tr>
<tr>
<td>Inverse</td>
<td>Bool indicating an inverse scale endpoint.</td>
</tr>
</tbody>
</table>

**Author(s)**

Joe Swintek

**See Also**

`runDetailedResults, detailedResults2HTML`

---

**Description**

Example Histology data included in StatCharrms and RSCABS.

**Usage**

```r
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 either 16_wk or 8_wk.

**Source**

US EPA Duluth MED Lab
filterData

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

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

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

getDir(window)

Arguments

window 
The window the dialogue box resides in.

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 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 to the 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.
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

_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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data</td>
<td>Tall formatted data used in Histopath and runRSCABS.</td>
</tr>
<tr>
<td>Effect</td>
<td>The name of endpoint being plotted.</td>
</tr>
<tr>
<td>Treatment</td>
<td>The name of the treatment variable.</td>
</tr>
<tr>
<td>Metric</td>
<td>The value being plotted, either &quot;Total&quot; or as a &quot;Percent&quot;.</td>
</tr>
<tr>
<td>Lowest</td>
<td>Determines whether to &quot;Include&quot; or &quot;Remove&quot; the lowest response. The lowest response should correspond to no effect.</td>
</tr>
<tr>
<td>PlotParms</td>
<td>A list of plotting parameters, see setPlotParms.</td>
</tr>
</tbody>
</table>
popMessage

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
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
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

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 0.01 < p-value <= 0.05, "**" for 0.001 < p-value <= 0.01, and "***" for p-value <= 0.001.
RSCABSMain

Author(s)
Joe Swintek

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  
*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**

```r
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  

**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**

```r
runEffectSelect()
```

**Author(s)**

Joe Swintek

---

runRSCABS  

**Description**

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

**Usage**

```r
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 then 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
# 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
testResults<-runRSCABS(exampleHistData.sub,'Treatment',
'Replicate',test.type='RS')
```

## End(Not run)
**runStdSubset**  
*Subset the data used in Histopath*

### Description
An internal function 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**  
*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**

```r
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**

```r
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

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
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)
```
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

---

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

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
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