Package ‘Tendril’

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Type Package
Title Compute and Display Tendril Plots
License GPL-2
Version 2.0.4
Description Compute the coordinates to produce a tendril plot.

In the tendril plot, each tendril (branch) represents a type of events, and the direction of the tendril is dictated by on which treatment arm the event is occurring. If an event is occurring on the first of the two specified treatment arms, the tendril bends in a clockwise direction. If an event is occurring on the second of the treatment arms, the tendril bends in an anti-clockwise direction.


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plot.Tendril  Plot Tendril

Description

Function to plot Tendril results

Usage

## S3 method for class 'Tendril'
plot(x, term = NULL, coloring = "Terms",
     interactive = FALSE, ...)

Arguments

x  An object of class tendril, as made by Tendril()

term  The term to extract.

coloring  Name of column used for coloring tendrils (only basic plots). Available coloring choices are: "Terms" - One tendril one color; "p" - Prop.test; "p.adj" - P-values adjusted using the False discovery rate method within each tendril; "fish" - Fisher.test; "rdiff" - Risk difference; "RR" - Risk Ratio; "OR" - Odds Ratio; "FDR.tot" - P-values adjusted using the False discovery rate method for all tendrils; and "TermsCount" - Total number of events for that specific type of event

interactive  Specifies if the plot must be interactive or not. If interactive == TRUE, plotly will be used to render the plot. Otherwise, (default) the plot will be rendered as a static image using ggplot2.

...  unused

Details

If saving the results of the function to a variable, this will be of class tendril and will contain the data passed to the plot function and the plot itself
plot.TendrilPerm

Examples

# generate data using Tendril()
data <- Tendril(mydata = TendrilData,
rotations = Rotations,
AEfreqThreshold = 9,
Tag = "Comment",
Treatments = c("placebo", "active"),
Unique.Subject.Identifier = "subjid",
Terms = "ae",
Treat = "treatment",
StartDay = "day",
SubjList = SubjList,
SubjList.subject = "subjid",
SubjList.treatment = "treatment"
)

#Do plot
res <- plot(data, coloring = "Terms")
res <- plot(data, coloring = "p.adj")

#To re-do the plot after the first call:
print(res)

plot.TendrilPerm     Plot TendrilPerm

Description

Function to plot TendrilPerm results

Usage

## S3 method for class 'TendrilPerm'
plot(x, coloring = "p.adj", percentile = FALSE,
...

Arguments

x          An object of class TendrilPerm, as made by TendrilPerm()
coloring   Name of column used for coloring tendrils. Available coloring choices are: "Terms" - One tendril one color; "p" - Prop.test; "p.adj" - P-values adjusted using the False discovery rate method within each tendril; "fish" - Fisher.test; "rdiff" - Risk difference; "RR" - Risk Ratio; "OR" - Odds Ratio; "FDR.tot" - P-values adjusted using the False discovery rate method for all tendrils; and "TermsCount" - Total number of events for that specific type of event
percentile Specifies if the plot must show percentile values. Default is FALSE.
...        unused
Examples

```r
# generate data using Tendril()
data <- Tendril(mydata = TendrilData,
rotations = Rotations,
AEfreqThreshold = 9,
Tag = "Comment",
Treatments = c("placebo", "active"),
Unique.Subject.Identifier = "subjid",
Terms = "ae",
Treat = "treatment",
StartDay = "day",
SubjList = SubjList,
SubjList.subject = "subjid",
SubjList.treatment = "treatment"
)
tendril_perm <- TendrilPerm(
tendril = data,
PermTerm="AE40",
n.perm = 200,
perm.from.day = 1)

#Do plot
res <- plot(tendril_perm)
res <- plot(tendril_perm, percentile = TRUE)

#To re-do the plot after the first call:
print(res)
```

---

**plot_timeseries**  
*Plot time series*

**Description**

Plot time series of net events on a second treatment arm

**Usage**

```r
plot_timeseries(tendril, term = NULL)
```

**Arguments**

- **tendril**: An object of class Tendril, as made by Tendril()
- **term**: A character vector describing the value or values of Term to select; defaults to NULL which corresponds to all values
Examples

# generate data using Tendril()
data <- Tendril(
  mydata = TendrilData,
  rotations = Rotations,
  AEfreqThreshold = 9,
  Tag = "Comment",
  Treatments = c("placebo", "active"),
  Unique.Subject.Identifier = "subjid",
  Terms = "ae",
  Treat = "treatment",
  StartDay = "day",
  SubjList = SubjList,
  SubjList.subject = "subjid",
  SubjList.treatment = "treatment"
)

# do plot
plot_timeseries(data, term="AE33")
plot_timeseries(data, term=c("AE33","AE40"))
plot_timeseries(data, term=NULL)

Rotations

Example of Rotations in package Tendril.

Description

Example of Rotations in package Tendril.

Usage

Rotations

Format

A numeric vector with 1000 number 3s:

SubjList

Example of SubjList in package Tendril.

Description

Example of SubjList in package Tendril.

Usage

SubjList
Format

A data frame with 500 rows and 2 variables:

- **subjId**: The subject IDs
- **treatment**: The two treatments causing the tendrils to bend left or right

Description

Function to calculate coordinates and statistical measures used to create a tendril plot

Usage

```r
```

Arguments

- **mydata**: A dataframe containing the data for the tendril calculations
- **rotations**: a vector of same length as mydata containing the rotation factors for all the events
- **AEfreqThreshold**: The minimum frequency threshold of events to be included in the analysis. Default is 50
- **Tag**: A tag or comment associated with the analysis
- **Treatments**: The names of the two treatments to be included in the tendril. The first treatment bends to the right and second treatment bends to the left. Must be a vector of two elements and the two elements must be found in the Treatment column
- **Unique.Subject.Identifier**: The name of the column containing the unique patients IDs
- **Terms**: The name of the column containing the name of the tendrils (e.g. adverse event terms)
- **Treat**: The name of the column containing the name of the treatments
- **StartDay**: The name column containing the days of the events
- **SubjList**: A dataframe containing subject IDs and treatments
- **SubjList.subject**: The name of the columns in SubjList containing the subjects IDs
SubjList.treatment
   The name of the columns in SubjList containing the treatments
SubjList.dropoutday
   The name of the column in SubjList containing the dropoutday
compensate_imbalance_groups
   Boolean Whether the rotation factors have been compensated for imbalance in the groups
filter_double_events
   Boolean whether to filter out events duplicated in subject id and adverse effect
suppress_warnings
   Boolean whether to suppress warnings from chi squared approximation may be incorrect

Details
   The function accepts a dataframe with at least 4 columns named as the arguments Unique.Subject.Identifier, Terms, Treat and StartDay.
   Two treatments must be given as arguments, and at least one of the two treatments must be found in the Treatment column
   The function returns an object of class tendril. The object contains the coordinates for the tendril plot and the arguments of the tendril function
   The result of the function can be plotted with plot()
   The result can be saved to file using write.table() with argument row.names = FALSE

Value
   The function return an object of class tendril. The object contains the original dataset added with the tendril coordinates, all the function arguments and a dataframe with the results from statistical analysis
   - data$data : Dataframe of orginal data, coordinates and stat results
   - data$Unique.Subject.Identifier : Column containing subject IDs
   - data$Terms : Column containing the name of the tendrils
   - data$Treat : Column containing the name of the treatments
   - data$StartDay : Column containing the days of the events
   - data$Treatments : The names of the treatments causing the tendrils to bend
   - data$AEfreqThreshold : The frequency threshold for the events to be included in the analysis
   - data$Tag : A tag or comment associated with the analysis
   - data$n.tot : A dataframe with the total number of events for each treatment. Used in the statistical calculations
   - data$SubjList : A dataframe containing subject IDs and treatments
   - data$SubjList.subject : The name of the columns in SubjList containing the subjects IDs
   - data$SubjList.treatment : The name of the columns in SubjList containing the treatments
   - data$SubjList.dropoutday : The name of the column in SubjList containing the dropoutday
• data$rotation_vector: Rotation vector used to generate the tendril
• data$compensate_imbalance_groups: Boolean Whether the rotation factors have been compensated for imbalance in the groups

Examples

```r
data <- Tendril(mydata = TendrilData,
rotations = Rotations,
AEfreqThreshold = 9,
Tag = "Comment",
Treatments = c("placebo", "active"),
Unique.Subject.Identifier = "subjid",
Terms = "ae",
Treat = "treatment",
StartDay = "day",
SubjList = SubjList,
SubjList.subject = "subjid",
SubjList.treatment = "treatment"
)

plot(data)
```

Tendril.perm.res

Example object Tendril as generated by Tendril() and Tendril.perm().

Description

The object contains the following 15 items:

Usage

Tendril.perm.res

Format

A list of 15 elements:

- **Tendril.perm.res$data**: Dataframe of orginal data and coordinates
- **Tendril.perm.res$Terms**: Column containing the name of the tendrils
- **Tendril.perm.res$Unique.Subject.Identifier**: Columns containing subject IDs
- **Tendril.perm.res$Treat**: Column containing the name of the treatments
- **Tendril.perm.res$StartDay**: Column containing the start days of the events
- **Tendril.perm.res$Treatments**: The names of the treatments causing the tendrils to bend
- **Tendril.perm.res$AEfreqThreshold**: The frequency threshold for the events to be included in the analysis
- **Tendril.perm.res$Tag**: A tag or comment associated with the analysis
**Tendril.res**

- **Tendril.perm.res$SubjList**: A dataframe containing subject IDs and treatments
- **Tendril.perm.res$SubjList.subject**: The name of the column in SubjList containing the subjects IDs
- **Tendril.perm.res$SubjList.treatment**: The name of the columns in SubjList containing the treatments
- **Tendril.perm.res$n.tot**: A data frame of 2 variables for number of subjects in each treatment
- **Tendril.perm.res$PermTerm**: Name of the tendril used for the permutations
- **Tendril.perm.res$perm.data**: A dataframe containing the permutation results
- **Tendril.perm.res$tendril.pi**: A list of permutation percentile calculation results

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**Tendril.res**

**Example object Tendril as generated by Tendril().**

**Description**

The object contains the following 12 items:

**Usage**

Tendril.res

**Format**

A list of 12 elements:

- **Tendril.res$data**: Dataframe of orginal data and coordinates
- **Tendril.res$Terms**: Column containing the name of the tendrils
- **Tendril.res$Unique.Subject.Identifier**: Columns containing subject IDs
- **Tendril.res$Treat**: Column containing the name of the treatments
- **Tendril.res$StartDay**: Column containing the start days of the events
- **Tendril.res$Treatments**: The names of the treatments causing the tendrils to bend
- **Tendril.res$AEfreqThreshold**: The frequency threshold for the events to be included in the analysis
- **Tendril.res$Tag**: A tag or comment associated with the analysis
- **Tendril.res$SubjList**: A dataframe containing subject IDs and treatments
- **Tendril.res$SubjList.subject**: The name of the column in SubjList containing the subjects IDs
- **Tendril.res$SubjList.treatment**: The name of the columns in SubjList containing the treatments
- **Tendril.res$SubjList.dropoutday**: The name of the column in SubjList containing the dropout-day
- **Tendril.res$rotation_vector**: The rotation vector used for the tendril analysis
- **Tendril.res$compensate_imbalance**: Boolean indicating whether the imbalance in the groups is compensated
- **Tendril.res$n.tot**: A data frame of 2 variables for number of subjects in each treatment
TendrilData

Example dataframe in package Tendril.

Description
A dataset containing the minimal 4 columns required to produce a Tendril plot

Usage
TendrilData

Format
A data frame with 1000 rows and 4 variables:

- **subjID**: The subject IDs
- **treatment**: The two treatments causing the tendrils to bend right or left, respectively
- **ae**: The names of the tendrils
- **day**: The day of the event relative to the treatment start date

TendrilPerm

**Tendril permutations**

Description
Function to compute the permutations of one specified tendril, starting from a specific day. Permutations are simulated under the null hypothesis. Thus, on average, there will be an equal number of events on each treatment arm.

Usage
TendrilPerm(tendril, PermTerm, n.perm = 100, perm.from.day = 1,
pi.low = 0.1, pi.high = 0.9)

Arguments
- **tendril**: an object of class tendril as produced by Tendril()
- **PermTerm**: the name of the type of event (tendril) to calculate permutations on
- **n.perm**: the number of permutations. Default 100
- **perm.from.day**: the starting day for the permutation calculations. Default 1
- **pi.low**: percentile low value. Default 0.1
- **pi.high**: percentile high value. Default 0.9
Details

Make permutation analysis to a specific type of event, as specified in PermTerm.

Value

The function return an object of class TendrilPerm containing all the input data and a dataframe of permutation results. Use:

data$perm.data

and

data$tendril.pi

and

data$tendril

to access the permutations, percentiles dataframes, and tendril data respectively

Examples

# Create tendril
tendril <- Tendril(mydata = TendrilData,
    rotations = Rotations,
    AEFreqThreshold = 9,
    Tag = "Comment",
    Treatments = c("placebo", "active"),
    Unique.Subject.Identifier = "subjID",
    Terms = "ae",
    Treat = "treatment",
    StartDay = "day",
    SubjList = SubjList,
    SubjList.subject = "subjID",
    SubjList.treatment = "treatment"
)

# Compute permutations
perm.data <- TendrilPerm(tendril = tendril,
    PermTerm="AE48",
    n.perm = 200,
    perm.from.day = 1)

# Plot results
plot(perm.data)
plot(perm.data, percentile = TRUE)
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