

# Package: Tendril (via r-universe)

September 12, 2024

**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. Ref: Karpefors, M and Weatherall, J., ``The Tendril Plot - a novel visual summary of the incidence, significance and temporal aspects of adverse events in clinical trials" - JAMIA 2018; 25(8): 1069-1073 <doi:10.1093/jamia/ocy016>

**URL** <https://github.com/Karpefors/Tendril>

**BugReports** <https://github.com/Karpefors/Tendril/issues>

**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 3.5)

**Imports** ggplot2, dplyr, plyr, reshape2, magrittr, scales, graphics, grDevices, plotly

**RoxygenNote** 6.1.1

**Suggests** testthat, knitr, rmarkdown, devtools

**VignetteBuilder** knitr

**NeedsCompilation** no

**Repository** <https://astrazeneca.r-universe.dev>

**RemoteUrl** <https://github.com/astrazeneca/tendril>

**RemoteRef** HEAD

**RemoteSha** a82ac87a6b4d887b7fbe6239270c60e03c75883f

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plot.Tendrill	<i>Plot Tendrill</i>
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## Description

Function to plot Tendrill results

## Usage

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

## Arguments

x	An object of class tendrill, as made by Tendrill()
term	The term to extract.
coloring	Name of column used for coloring tendrills (only basic plots). Available coloring choices are: "Terms" - One tendrill one color; "p" - Prop.test; "p.adj" - P-values adjusted using the False discovery rate method within each tendrill; "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 tendrills; 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 tendrill and will contain the data passed to the plot function and the plot itself

**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)
```

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plot.TendrilPerm	<i>Plot TendrilPerm</i>
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**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

```
# 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"
)
tendrill_perm <- TendrilPerm(
  tendrill = data,
  PermTerm="AE40",
  n.perm = 200,
  perm.from.day = 1)

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

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

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plot\_timeseries

*Plot time series*

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## Description

Plot time series of net events on a second treatment arm

## Usage

```
plot_timeseries(tendrill, term = NULL)
```

## Arguments

tendrill	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)
```

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Rotations

*Example of Rotations in package Tendril.*

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**Description**

Example of Rotations in package Tendril.

**Usage**

Rotations

**Format**

A numeric vector with 1000 number 3s:

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SubjList

*Example of SubjList in package Tendril.*

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**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

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Tendril	<i>Tendril</i>
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**Description**

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

**Usage**

```
Tendril(mydata, rotations, AEFreqThreshold = 50, Tag = "Comment",
        Treatments = c("Active", "Placebo"),
        Unique.Subject.Identifier = "Unique.Subject.Identifier",
        Terms = "Dictionary.Derived.Term", Treat = "Actual.Treatment...DB",
        StartDay = "Analysis.Start.Relative.Day", SubjList = NULL,
        SubjList.subject = NULL, SubjList.treatment = NULL,
        SubjList.dropoutday = NULL, compensate_imbalance_groups = FALSE,
        filter_double_events = FALSE, suppress_warnings = FALSE)
```

**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

<code>SubjList.treatment</code>	The name of the columns in <code>SubjList</code> containing the treatments
<code>SubjList.dropoutday</code>	The name of the column in <code>SubjList</code> containing the dropoutday
<code>compensate_imbalance_groups</code>	Boolean Whether the rotation factors have been compensated for imbalance in the groups
<code>filter_double_events</code>	Boolean whether to filter out events duplicated in subject id and adverse effect
<code>suppress_warnings</code>	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$data` : Dataframe of original data, coordinates and stat results
- `data$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

```
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 original 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.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().*


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### Description

The object contains the following 12 items:

### Usage

Tendril.res

### Format

A list of 12 elements:

- Tendril.res\$data** : Dataframe of original 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

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TendrilData	<i>Example dataframe in package Tendril.</i>
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### 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

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TendrilPerm	<i>Tendril permutations</i>
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### 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="AE40",
  n.perm = 200,
  perm.from.day = 1)

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

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