

Package ‘UnitEvents’

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Type Package

Title Multiple Tests Based on a Gaussian Approximation of the Unitary Events Method with Delayed Coincidence Count (MTGAUE) and Permutation Method for Statistical Tests in Neuroscience

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Description Multiple Tests based on a Gaussian Approximation of the Unitary Events method with delayed coincidence count (MTGAUE) and Permutation method. Performs statistical independence tests between two neurons based on coincidence counts. Using C++ neuro-stat code.

License GPL (>=2)

URL <https://github.com/ybouret/neuro-stat>,
<http://math.unice.fr/~malot/liste-MTGAUE.html>

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BH	<i>This function performs Benjamini-Hochberg procedure.</i>
----	---

Description

This function allows to identify the time windows detected by the MTGAUE or permutation procedure.

Usage

```
BH(alpha, p, plot)
```

Arguments

alpha	double; Array of alpha values or maximum values for the false positive. Could be a vector (in case of several tests)
p	double; Array of p-values. Needs to be ordered.
plot	bool; To plot the result or not. Default value is FALSE.

Value

k	The index obtained by Benjamini-Hochberg procedure. Could be an array
---	---

Examples

```
p <- sort(runif(10))
alpha <- 0.05
BH(alpha, p, FALSE)
```

BHbN *BHbN performs Benjamini-Hochberg procedure through functions of neuro-stat code. wink_coincmat function is used here. See <https://github.com/ybouret/neuro-stat>*

Description

BHbN function allows to identify the time windows detected by the test. It calls `wink_coincmat` function of `neuro-stat`

Usage

```
BHbN(TW, level, delay, DataNeur, Rtest, neurostatpath, iperm=FALSE,
      B=10000, num_threads=1, statistical_value="H")
```

Arguments

TW	double; Time window matrix with two rows. Each column is associated to a time window and $A[,i]$ contains the bounds of the i th time window.
level	double; level is the value used in p-value computation
delay	double; delay is the value used in coincidence detection for delay.
DataNeur	A DataNeur e.g. the output of <code>DNeur</code> function. Contains the matrices of spike times
Rtest	Rtest allows to define the type of the test. Possible values are "all", "symmetric", "upper" and "lower".
neurostatpath	It allows to define the path of neuro-stat code if necessary (string). It could be a relative or an absolute path.
iperm	Logical to select permutation method or not. Default is FALSE (it means no permutation, MTGAUE method is chosen)
B	integer; Number of bootstraps. Default is 10000. Only used by the permutation method.
num_threads	integer; Number of threads for neuro-stat computation. Default is 1.
statistical_value	string; Only possible values are "T" or "H". Default is "H". Corresponds to a centered computation or not.

Value

The output is a list with three elements:

- `ndw`: number of detected time windows
- `prange`: a matrix which identifies the detected time windows. The first two rows of this matrix are A . The third row is a sequence of 0, 1 and -1, 0 meaning that the time window is not detected, -1 meaning that the time window is detected and that the average coincidence count is smaller than the expected one, 1 meaning that the time window is detected and that the average coincidence count is bigger than the expected one (in case of independency)

- pvalue: the vector of p-values associated to each test or time window #
- testthe numerator of each GAUE symmetric statistic test

See Also

[BHtest](#)

BHtest	<i>This function is a wrapper to call Benjamini-Hochberg procedure in a general case</i>
--------	--

Description

Benjamini-Hochberg procedure. It calls the function BHbN.

Usage

```
BHtest(TW, level, delay, DataNeur, neurostatpath = "",
Rtest="all", iperm=FALSE, B=10000, num_threads=1, statistical_value='H')
```

Arguments

TW	TW is a matrix for the definition of time windows. The matrix has two rows, each column corresponds to a small time window. The number of columns of TW is equal to the number of time windows.
level	double; level is the value used in p-value computation, level is the maximum value for the false positive.
delay	double; delay is the value used in coincidence detection.
DataNeur	A DataNeur e.g. the output of DNeur function. Contains the matrices of spike times
neurostatpath	string; It allows to define the path of neuro-stat code if necessary. It could be a relative or an absolute path. Default value is empty.
Rtest	string; Rtest allows to define the type of the test. Only possible values are "symmetric", "upper", "lower".
iperm	Logical to select permutation method or not. Default is FALSE - it means no permutation and MTGAUE method is chosen
B	integer; Number of bootstraps used in permutation method. Default is 10000.
num_threads	integer; Number of threads for neuro-stat computation. Default is 1.
statistical_value	string; Only possible values are "T" or "H". Default is "H". Corresponds to a centered computation or not.

Value

The detected time windows after Benjamini-Hochberg procedure.

See Also[BHbN](#)

check_input	<i>To check if input spike files exist. Returns a list of names of existing spike files and a chain of words as a figure title</i>
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Description

To check if input spike files exist. Returns a list of names of existing spike files and a chain of words as a figure title. If the first neuron file does not exist, the default file is chosen.

Usage

```
check_input(neur1file, neur2file)
```

Arguments

neur1file	string; Input file name given by the user containing spikes for the first neuron
neur2file	string; Input file name given by the user containing spikes for the second neuron

Value

The output is a list with 2 elements:

- ndf: list of strings; The list contains the names of existing neuron files (after verification). The first item is equal to neur1file if it exists
- titlename: string; It will be used as the title of some figures

Examples

```
out <- check_input('UnitEvents/data/Neur1_c13.txt', 'UnitEvents/data/Neur2_c13.txt')
```

compute_pvalues	<i>Computation of the p-values associated to the GAUE symmetric test</i>
-----------------	--

Description

This function computes the p-values associated to the GAUE symmetric test and the numerator of this test.

Usage

```
compute_pvalues(C, ntrials, a, b, delay, test)
```

Arguments

C	matrix with 3 rows. It corresponds to the output of the function wink_coincmat
ntrials	int; the number of trials of the datasets used to compute the average coincidence count with delay
a	lower bound of the time window
b	upper bound of the time window
delay	double; value used in coincidence detection
test	string; To define the test; only possible values are "all", "symmetric", "upper" and "lower". Default value is "all" (upper values appear in red, while lower ones appear in blue)

Value

The output of this function is a list with two elements, the first one is the p-value associated to the GAUE symmetric test and the second one is the numerator of the statistic test.

Examples

```
a <- 0 # lowest time
b <- 2 # highest time
ntrials <- 1
delay <- 0.02
C <- matrix(ncol=1,c(0,1,0.5))
test <- "symmetric"
compute_pvalues(C, ntrials, a, b, delay, test)
```

compute_time_windows *To create time windows*

Description

To create time windows.

Usage

```
compute_time_windows(a, b, height, spacing)
```

Arguments

a	Starting time of observation
b	End time of observation
height	Length of a time window. Identical for every time window.
spacing	Value to define a shift. If spacing=height, there is no overlap.

Value

Returns a list containing time windows.

- A: Matrix of time windows with two rows and (len-1) columns. Each column is a time window
- L: Time step or spacing between the starts of two consecutive time windows. Equal to input argument spacing.
- len: length of the sequence. Equal to the number of time windows plus one

Examples

```
# L = 0.01, no overlapping
TW1 <- compute_time_windows(a=0, b=1, height=0.01, spacing=0.01)

# with overlapping
TW2 <- compute_time_windows(a=0, b=1, height=0.1, spacing=0.05)
```

data_treatment	<i>Treatment of the input spike data, possibly modified.</i>
----------------	--

Description

Treatment of the input spike data, possibly modified (multiplied by a factor). Matrices of spike times are obtained from input files.

Usage

```
data_treatment(neufiles)
```

Arguments

neufiles List of input spike files

Value

The output is a list with 3 elements:

- ntrials: number of trials
- N1: First neuron. Contains the number of spikes per trial and spike data.
- N2: Second neuron. Contains number of spikes per trial and spike data.

See Also

[check_input](#)

Examples

```
neur1file = "UnitEvents/data/Neur1_c13.txt"; neur2file = "UnitEvents/data/Neur2_c13.txt"
I = check_input(neur1file, neur2file) # to check input files
neufiles = I[[1]]
T = data_treatment(neufiles)
```

DNeur

To create DataNeur from input neuron files.

Description

To create DataNeur from input neuron files. A DataNeur contains matrices of size ntrials-by-(nmax+1) containing spike times. nmax is the maximum number of spikes over the trials for each neuron. The first column of the matrix is the number of spikes for each trial. For a missing value, 0 is used to fill the matrix.

Usage

```
DNeur(neur1file, neur2file)
```

Arguments

neur1file	string; Input file name given by the user containing spike times for the first neuron
neur2file	string; Input file name given by the user containing spike times for the second neuron.

Value

The output is a list with four elements:

- DN: list of two matrices, one for each neuron. Each matrix contains spike times of the corresponding neuron. Each matrix has a size ntrials-by-(nmax+1) where nmax is the maximum number of spikes over the trials, specific to each neuron. The first column of the matrix is the number of spikes for each trial.
- titlename: string; It will be used as a title of figures
- xrange: Time interval - typically minimum and maximum values of spike times
- ntrials: Number of trials. Should be the same for each neuron

See Also

[data_treatment](#)

Examples

```
out <- DNeur('UnitEvents/data/Neur1_c13.txt', 'UnitEvents/data/Neur2_c13.txt')
```

draw_windows	<i>To draw time windows. To highlight detected windows after test.</i>
--------------	--

Description

To draw time windows. Called after Benjamin-Hochberg procedure. Fill and border colors and density can be modified (see polygon function). Default values are "yellow" for fill color, "black" for border and no density.

Usage

```
draw_windows(A1t, xrange, yrange, col="yellow", density="", border="black")
```

Arguments

A1t	double; Time window matrix (with two rows). For example it is the matrix of detected windows after Benjamini-Hochberg procedure
xrange	Double; Numeric vector of length two to define the x-coordinate range in the plot.
yrange	Double; Numeric vector of length two to define the y-coordinate range in the plot
col	string; Fill color in the call to polygon function.. Default value is "yellow".
density	string; Density in the call to polygon function. No density by default.
border	string; Border color in the call to polygon function. Default value is "black".

Examples

```
par(mfrow=c(1,2))
s = seq(0.001, 0.9, 0.1)
A = matrix(ncol=length(s), nrow=2)
A[1,] = s
A[2,] = s+0.1
xrange = c(0,max(A))
yrange = c(-25,0)
draw_windows(A, xrange, yrange)
draw_windows(A, xrange, yrange, col="lightgreen", border=NA, density=c(11))
```

findUE	<i>To find Unitary Events in detected time windows with a given delay</i>
--------	---

Description

To find Unitary Events in detected time windows with a given delay

Usage

```
findUE(A, DataNeur, delay)
```

Arguments

A	Matrix of detected time windows. Contains two rows. It should contain detected time windows after Benjamini-Hochberg procedure.
DataNeur	A DataNeur e.g. the output of DNeur function. List which contains spike time matrices
delay	double; delay is the value for delay used in coincidence detection.

Value

The output is a list with 2 elements:

- N1: Detected indices for the first neuron
- N2: Detected indices for the second neuron

Examples

```
TW = compute_time_windows(a=1e-3, b=2.1, height=1e-1, spacing=0.05)
neur1file = "UnitEvents/data/Neur1_c13.txt"
neur2file = "UnitEvents/data/Neur2_c13.txt"
DataNeur = DNeur(neur1file, neur2file)
delay = 0.02
A = matrix(nrow = 3, ncol=0)
A[1:2,] = TW$A
T = findUE(A, DataNeur, delay)
```

get_nspath	<i>To get the correct path of the neuro-stat code checking if files exist.</i>
------------	--

Description

To get the correct path of the neuro-stat code. Checks if the dynamic library already exists, otherwise neuro-stat is cloned again.

Usage

```
get_nspath(neurostatpath)
```

Arguments

neurostatpath string; It contains the path of the neuro-stat code. For example, 'NEURO/neuro-stat' (on Linux or Mac)

Value

Returns a string containing the path of neuro-stat code

Examples

```
rpath <- get_nspath('neuro-stat')
```

isequalUE	<i>To check if two UEs are equal.</i>
-----------	---------------------------------------

Description

To check if two UEs are equal. To be equal, they should have the same detected time windows.

Usage

```
isequalUE(xns, xpaf)
```

Arguments

xns First set of Unitary Events. Should be a list with fields A and UE.
xpaf Second set of Unitary Events. Should be a list with fields A and UE.

Value

The output is a logical = TRUE if equality false elsewhere.

load_neurostatpath	<i>This function allows to the dynamic library of neuro-stat code and source the required R file of neuro-stat.</i>
--------------------	---

Description

It loads the dynamic library of neuro-stat code and source the required R file of neuro-stat.

Usage

```
load_neurostatpath(neurostatpath)
```

Arguments

neurostatpath string; It contains the path of the neuro-stat code. For example, 'NEURO/neuro-stat' (on Linux or Mac)

maxtime	<i>Function to compute the maximum time value for the plot. Specific user function for Neur1_c13.txt example.</i>
---------	---

Description

Function to compute the maximum time value for the plot. Specific user function for Neur1_c13.txt example. Here the value is in the last column of the neuron data files (in seconds)

Usage

```
maxtime(NeuDataFiles)
```

Arguments

NeuDataFiles List of filenames for neuron data. Each file only contains the number of spikes and spike values.

Value

double; Maximum time value for the plot

Examples

```
maxtime(list('UnitEvents/data/Neur1_c13.txt', 'UnitEvents/data/Neur2_c13.txt'))
```

spikes.plot *To plot spikes of each neuron*

Description

To plot spikes of each neuron. Spikes of the first neuron are represented at the bottom in grey color, while spikes of the second neuron are represented at the top in green color. There is a red dividing line.

Usage

```
spikes.plot(DataNeur, xrange, yrange, titlename)
```

Arguments

DataNeur	A DataNeur e.g. the output of DNeur function - Contains the matrices of spike times
xrange	Double; Numeric vector of length two to define the x-coordinate range in the plot.
yrange	Double; Numeric vector of length two to define the y-coordinate range in the plot
titlename	string; Title of the figure. Default value is an empty string.

Examples

```
# creation of spikes
lambda <- 50 #firing rate
a <- 0; b <- 2 # times
p=lambda*(b-a)
trials <- 10; N <- 20
ntops <- rpois(N,p)
M <- matrix(data=0,nrow=N,ncol=max(ntops)+1)
M[,1] <- ntops
for (i in 1:N) # for each trial
{
  r <- ntops[i] # depending on ntops
  if (r!=0)
  { x <- runif(r,a,b) # uniform law
    M[i,2:(r+1)] <- sort(x) # sorting
  }
}
F1 <- M[1:trials,]
F2 <- M[(trials+1):(2*trials),]
xrange <- c(0,max(F1[,-1],F2[,-1])) #maximum spike value
yrange <- c(-50,2*nrow(F1[,-1])+2) # number of trials
DNeur <- list(DN=list(F1, F2), ntrials= nrow(F1[,-1]))
titlename <- "Neuro"
spikes.plot(DNeur, xrange, yrange, titlename)
```

UE.plot	<i>Function for plotting unitary events (coincident spikes and detected windows)</i>
---------	--

Description

Function for plotting coincident spikes and detected windows

Usage

```
UE.plot(A1t, UE, xrange, yrange)
```

Arguments

A1t	Time window matrix. It should contain detected time windows after Benjamini-Hochberg procedure.
UE	List of Unitary Events. Contains fields N1 (first neuron) and N2 (second neuron). UE\$N1 is a 3-by-ntrials matrix.
xrange	Double; Numeric vector of length two to define the x-coordinate range in the plot.
yrange	Double; Numeric vector of length two to define the y-coordinate range in the plot

See Also

[draw_windows](#)

Examples

```
# time window
#TW$A is a time window matrix
TW <- compute_time_windows(0.001, 0.901, 0.1, 0.1)

# creation of spikes
lambda <- 50 #firing rate
a <- 0; b <- 2 # times
p = lambda*(b-a)
trials <- 10; N <- 20
ntops <- rpois(N,p)
M <- matrix(data=0, nrow=N, ncol=max(ntops)+1)
M[,1] <- ntops
for (i in 1:N) # for each trial
{
  r <- ntops[i] # depending on ntops
  if (r!=0)
  { x <- runif(r,a,b) # uniform law
    M[i,2:(r+1)] <- sort(x) # sorting
  }
}
```

```

}
F1 <- M[1:trials,]
F2 <- M[(trials+1):(2*trials),]
UE <-list(N1=F1, N2=F2)

xrange <- c(0,max(F1[,-1],F2[,-1])) #maximum spike value
yrange <- c(-50,2*nrow(F1[,-1])+2) # number of trials

t <- UE.plot(TW$A, UE, xrange, yrange)

```

UnitEvents	<i>Multiple Tests based on a Gaussian Approximation of the Unitary Events method with delayed coincidence count (MTGAUE) or on the permutation method.</i>
------------	--

Description

Multiple Tests based on a Gaussian Approximation of the Unitary Events method with delayed coincidence count (MTGAUE) or on the permutation method. Currently works for two neurons.

Usage

```

UnitEvents(neurostatpath="", DataNeur, delay=0.005, level=0.05,
rasterPlot=TRUE, export=FALSE, Rtest="all", TW,
iperm=FALSE, B=10000, num_threads=1, statistical_value="T")

```

Arguments

neurostatpath	string; It allows to define the path of neuro-stat code if necessary. It could be a relative or an absolute path. Default value is empty which means that default path is used (for example '~/R/x86_64-pc-linux-gnu-library/3.2' on Linux)
DataNeur	A DataNeur e.g. the output of DNeur function. Contains the matrices of spike times.
delay	double; delay is the value used in coincidence detection
level	double; level is the value used in p-value computation, level is the maximum value for the false positive.
rasterPlot	bool; To plot spikes in the window. Default is TRUE.
export	bool; To export the raster to png format. Default is FALSE.
Rtest	string; Rtest allows to define the type of the test. Only possible values are "all", "symmetric", "upper", "lower". Default values is "all" which means that upper and lower tests are performed and discernible.
TW	To define time windows on which statistical tests are performed; Contains fields A, L and len.
iperm	Logical to select permutation method or not. Default value is FALSE - it means no permutation and MTGAUE method is chosen

B	integer; Number of bootstraps used in permutation method. Default is 10000.
num_threads	integer; Number of threads for neuro-stat computation. Default is 1.
statistical_value	string; Only possible values are "T" or "H". Default is "H". Corresponds to a centered computation or not.

Value

The output is a two-field list containing

- A: list of all detected time windows as a three-row matrix (the last row contains the detection sign)
- UE: list of unitary events as a two-row matrix with spike time and trial number for each unitary event

References

Multiple Tests based on a Gaussian Approximation of the Unitary Events method with delayed coincidence count. Tuleau-Malot C., Rouis A., Grammont F. and Reynaud-Bouret P., *Neural Computation*, **26**(7), pp1408–1454, 2014.

Surrogate Data Methods Based on a Shuffling of the Trials for Synchrony Detection: the Centering Issue. Albert M., Bouret Y., Fromont M., and Reynaud-Bouret P., *Neural Computation*, **28**(11), pp2352–2392, 2016.

See Also

[DNeur](#)

Examples

```
DataNeur = DNeur(neur1file = "UnitEvents/data/Neur1_c13.txt",
neur2file = "UnitEvents/data/Neur2_c13.txt")
res = UnitEvents(DataNeur = DataNeur,
TW = compute_time_windows(a=1e-3, b=2.1, 1e-1, 0.05))
```


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