Package 'pro'

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Type Package

Title Point-Process Response Model for Optogenetics

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Author Xi (Rossi) LUO with contributions from Dylan Small and Vikaas Sohal

Maintainer Xi (Rossi) LUO <`xi.rossi.luo@gmail.com`>

Suggests cin

Description Optogenetics is a new tool to study neuronal circuits that have been genetically modified to allow stimulation by flashes of light. This package implements the methodological framework, Point-process Response model for Optogenetics (PRO), for analyzing data from these experiments. This method provides explicit nonlinear transformations to link the flash point-process with the spiking point-process. Such response functions can be used to provide important and interpretable scientific insights into the properties of the biophysical process that governs neural spiking in response to optogenetic stimulation.

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NeedsCompilation no

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`model.pro` *Model matrix for point-process responses*

Description

Constructs a `data.frame` to be fitted using `pro`. Reference: X Luo, S Gee, V Sohal, D Small (In Press). A Point-process Response Model for Optogenetics Experiments on Neural Circuits. _Statistics in Medicine_.

Usage

```
model.pro(spike, flash, fixed = NULL, kv = F)
```

Arguments

`spike`	A binary vector represents spiking (1) or no spiking (0).
`flash`	A binary vector of the same length of `spike`, 1 for flashing and 0 for non-flashing.
`fixed`	Whether a fixed time window of spike/flash history should be used. If it is `NULL`, a varying time window of history will be used as described in the reference. If it is a integer `j`, a fixed window from index `t-j` to `t` will be used.
`kv`	Whether the history dependence model in Kass and Ventura (2001) (A Spike-Train Probability Model, Neural Computation 13, 1713-1720) should be employed. This differs from the history dependence model in the reference.

Value

a `data.frame` of the three response functions (PF, CF, SF) and other intermediate functions (for future modeling use).

Examples

```
n <- 500
set.seed(100)
re <- sim.lif(n, rbinom(n, 1, 0.14), 7, 3)
d <- model.pro(re$sbin, re$I)
d[1:10, ]
```

`pro` *Fit the PRO model*

Description

Fit the PRO model to data. Reference: X Luo, S Gee, V Sohal, D Small (In Press). A Point-process Response Model for Optogenetics Experiments on Neural Circuits. _Statistics in Medicine_.

Usage

```
pro(spike, flash, ...)
```

Arguments

`spike`	A binary vector represents spiking (1) or no spiking (0).
`flash`	A binary vector of the same length of `spike`, 1 for flashing and 0 for non-flashing.
`...`	Additional parameters, see `model.pro`.

Value

a `glm` object of the fitted PRO coefficients.

Examples

```
n <- 500
set.seed(100)
re <- sim.lif(n, rbinom(n, 1, 0.14), 7, 3)
fit.pro <- pro(re$sbin, re$I)
summary(fit.pro)
```

`sim.lif` *Simulate optogenetic stimulation on a leaky-integrate-fire neuron*

Description

Simulate various kinds of neural measures (e.g. membrane potentials and spikes) from a LIF neuron.

Usage

```
sim.lif(n, I, C, R, Vth = 1, V0 = 0, bin = 5, dt = 0.05)
```

Arguments

`n`	Number of time bins. The total time is `n` times `bin`.
`I`	Input stimulus vector of length `n`.
`C`	Membrane capacitance of the simulated neuron.
`R`	Membrane resistance of the simulated neuron.
`Vth`	Membrane potential threshold for spiking.
`V0`	Membrane potential reset value after spiking.
`bin`	Time length for each time bin. Default 5 millisecond.
`dt`	Time length for each simulation step. Default 0.05 millisecond.

Value

a `list` of simulated neural spikes, optogenetic light flashes, and simulation parameters.

Examples

```
n<- 500
set.seed(100)
re <- sim.lif(n, rbinom(n, 1, 0.14), 7, 3)
```

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