

# Package ‘nof1’

August 13, 2018

**Type** Package

**Title** Single Subject (N-Of-1) Designs to Answer Patient-Identified Research Questions

**Version** 0.5.0

**Depends** R (>= 2.10)

**Imports** rjags (>= 4-6), splines, combinat, MASS, jsonlite, ggplot2, scales, coda (>= 0.13)

**Description** A package for running N of 1 study trials. Runs Bayesian linear regression, ordinal/logistic regression, and poisson regression. Includes different plots to visualize the results.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.0.1

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kernel_plot	<i>Kernel density of the posterior distribution for odds ratio</i>
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**Description**

Kernel density of the posterior distribution for odds ratio

**Usage**

```
kernel_plot(result, xlim_value = c(0, 10), title = NULL)
```

**Arguments**

result	nof1 result object created using nof1.run
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nof1.binomial.simulation	<i>Binomial simulation</i>
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**Description**

Binomial simulation

**Usage**

```
nof1.binomial.simulation(Base.size = 14, Treat.size = 56, alpha = 0.5,
  beta_A = -0.1, beta_B = -0.05)
```

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nof1.data	<i>Make a nof1 object containing data, priors, and a jags model file</i>
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**Description**

Make a nof1 object containing data, priors, and a jags model file

**Usage**

```
nof1.data(Y, Treat, baseline = "baseline", ncat = NULL, response = NULL,
  Time = NULL, knots = NULL, alpha.prior = NULL, beta.prior = NULL,
  dc.prior = NULL, c1.prior = NULL, rho.prior = NULL, hy.prior = NULL)
```

## Arguments

Y	Outcome of the study. This should be a vector with length of total number of observations.
Treat	Treatment indicator vector with same length as the outcome.
baseline	baseline Treatment name. This serves as a baseline/placebo when comparing different treatments.
ncat	Number of categories. Used in ordinal models.
response	Type of outcome. Can be normal, binomial, poisson or ordinal.
Time	parameter used for modelling splines. Still under development.
knots	parameter used for modelling splines. Still under development.
alpha.prior	Prior for the intercept of the model.
beta.prior	Prior for the treatment coefficient.
dc.prior	Prior for the length between cutpoints. Used only for ordinal logistic models.
c1.prior	Prior for the first cutpoint. Used only for ordinal logistic models.
rho.prior	Prior for the correlated error model. Still under development.
hy.prior	Prior for the heterogeneity parameter. Supports uniform, gamma, and half normal for normal and binomial response and wishart for multinomial response. It should be a list of length 3, where first element should be the distribution (one of dunif, dgamma, dlnorm, dwish) and the next two are the parameters associated with the distribution. For example, list("dunif", 0, 5) give uniform prior with lower bound 0 and upper bound 5 for the heterogeneity parameter. For wishart distribution, the last two parameter would be the scale matrix and the degrees of freedom.
gamma.prior	Prior for modelling splines. Still under development.

## Value

Creates list of variables that are used to run the model using `nof1.run`

Y	Outcome
Treat	Treatment
baseline	Baseline variable
ncat	Number of categories for ordinal response
nobs	Total number of observations in a study
Treat.name	Treatment name besides baseline treatment
response	The type of response variable
priors	Priors that the code will be using
code	Rjags model file code that is generated using information provided by the user. To view model file inside R, use <code>cat(nof1\$code)</code> .

## Examples

```
###Blocker data example
laughter
Y <- laughter$Y
Treat <- laughter$Treat
nof1 <- nof1.data(Y, Treat, ncat = 11, baseline = "Usual Routine", response = "ordinal")
str(nof1)
cat(nof1$code)
```

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nof1.inits	<i>Generate initial values</i>
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**Description**

Generate initial values

**Usage**

```
nof1.inits(nof1, n.chains)
```

**Arguments**

n.chains	number of chains you want
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nof1.normal.simulation	<i>Normal simulation</i>
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**Description**

Normal simulation

**Usage**

```
nof1.normal.simulation(Base.size = 2, Treat.size = 8, prec = 0.5,  
  alpha = 50, beta_A = -3, beta_B = -1)
```

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nof1.ordinal.simulation	<i>Ordinal simulation</i>
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**Description**

Ordinal simulation

**Usage**

```
nof1.ordinal.simulation(Base.size = 100, Treat.size = 100, alpha = 0,  
  beta_A = -0.1, beta_B = -0.3, cut = c(0.5, 1, 1.5, 2), ncat = 5)
```

### Ordinal simulation for WNYC

### Ordinal simulation for WNYC

```
nof1.ordinal.simulation2(alpha = 0, beta_B = 1, cut = c(-2, -1.5, -1,
-0.5, 0, 0.5, 1, 1.5, 2, 2.1, 2.3), ncat = 11)
```

### Poisson simulation

## Poisson simulation

```
nof1.poisson.simulation(Base.size = 14, Treat.size = 56, alpha = 1,
  beta_A = -0.1, beta_B = -0.05)
```

Run *nofl* model

## Run nof1 model

```
nof1.run(nof1, inits = NULL, n.chains = 3, max.run = 1e+05,
  setsize = 10000, n.run = 50000, conv.limit = 1.05,
  extra.pars.save = NULL)
```

nof1                      nof1 object created using nof1.data

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odds_ratio_plot	<i>Odds ratio plot for the raw data</i>
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**Description**

Odds ratio plot for the raw data

**Usage**

```
odds_ratio_plot(result.list, result.name = NULL, level = 0.95,  
  title = NULL)
```

**Arguments**

result.list	list of nofl results created using nofl.run
level	confidence interval level (default is 0.95)
name	of the outcomes. If left unspecified, it numbers each result in order of how it is stored in result.list

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probability_barplot	<i>Plot showing probability certain treatment is better than the other one</i>
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**Description**

Plot showing probability certain treatment is better than the other one

**Usage**

```
probability_barplot(result.list, result.name = NULL)
```

**Arguments**

result.list	list of nofl results created using nofl.run
result.name	name of the outcomes. If left unspecified, it numbers each result in order of how it is stored in result.list

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raw_table	<i>Summary data table for nofl</i>
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**Description**

Summary data table for nofl

**Usage**

```
raw_table(nof1)
```

**Arguments**

nof1	nofl object created using nofl.data
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read_input_data	<i>Read json data in as an R object</i>
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**Description**

Read json data in as an R object

**Usage**

```
read_input_data(data, metadata)
```

**Arguments**

data	input data. see sample input.json in the github repo
metadata	metadata. see sample input.json in the github repo

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stacked_percent_barplot	<i>Stacked_percent_barplot for raw data (for ordinal or binomial data)</i>
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**Description**

Stacked\_percent\_barplot for raw data (for ordinal or binomial data)

**Usage**

```
stacked_percent_barplot(nof1, title = NULL)
```

**Arguments**

nof1	nof1 object created using nof1.data
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summarize_nof1	<i>Summarizes the result from the model into json format</i>
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**Description**

Summarizes the result from the model into json format

**Usage**

```
summarize_nof1(nof1, result)
```



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time_series_plot	<i>Time series plot for the raw data</i>
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**Description**

Draw time series plot

**Usage**

```
time_series_plot(nof1, time = NULL, timestamp = NULL,
  timestamp.format = "%m/%d/%Y %H:%M")
```

**Arguments**

nof1	nof1 object created using nof1.data
time	can manually specify time variable
timestamp	or instead provide timestamp information for the all the outcomes
timestamp.format	format of timestamp used. See default format.

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time_series_plot2	<i>time series plot across different interventions</i>
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**Description**

time series plot across different interventions

**Usage**

```
time_series_plot2(nof1, time = NULL, timestamp = NULL,
  timestamp.format = "%m/%d/%Y %H:%M", Outcome.name = "")
```

**Arguments**

nof1	nof1 object created using nof1.data
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wrap	<i>Wrapper function that runs the n-of-1 model</i>
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**Description**

Wrapper function that runs the n-of-1 model

**Usage**

```
wrap(data, metadata)
```

**Arguments**

json.file	input json data
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`wrap2`*Wrapper function for afib study that runs the n-of-1 model*

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**Description**

Wrapper function for afib study that runs the n-of-1 model

**Usage**

```
wrap2(data, metadata)
```

**Arguments**

`json.file`      input json data

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