

# Package: closeloop (via r-universe)

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**Type** Package

**Title** Integrate Single-Arm Observational Data in Network Meta Analysis

**Version** 0.1.0

**Date** 2024-08-07

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**Description** This package Calculates distance between single-arm observational studies by using co-variates information to remove heterogeneity in Network Meta-Analysis in Randomized clinical trials. This package will facilitate the inclusion of observational data in Network Meta ANalysis, thereby enhancing the comprehensiveness and robustness of comparative effectiveness research. The proposed R package will provide researchers with a powerful tool to systematically adjust for heterogeneity in single-arm observational studies, enabling their integration into NMAs. This will improve the accuracy and reliability of comparative effectiveness research, ultimately informing better healthcare decisions. Schmitz S et. al. The use of single armed observational data to closing the gap in otherwise disconnected evidence networks: a network meta-analysis in multiple myeloma. BMC Med Res Methodol. 2018 Jun 28;18(1):66. doi: 10.1186/s12874-018-0509-7. PMID: 29954322; PMCID: PMC6022299.

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**Encoding** UTF-8

**LazyData** true

**Imports** combinat

**RoxygenNote** 7.3.1

**Depends** R (>= 3.5.0)

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**URL** <https://github.com/heorlytics/closeloop>

**Repository** <https://heorlytics.r-universe.dev>  
**RemoteUrl** <https://github.com/heorlytics/closeloop>  
**RemoteRef** HEAD  
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<i>calc_dist</i>	<i>Title</i> To calculate distance between two studies using covariate information
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### Description

**Title** To calculate distance between two studies using covariate information

### Usage

```
calc_dist(df, col_names, Study = "Study", Treat = "Treatment", weights, digits)
```

### Arguments

<b>df</b>	A data frame consists of columns namely "Study", "Treatment", and at least one covariate.
<b>col_names</b>	A vector of column names specifying covariate names.
<b>Study</b>	A column name in a data frame named as "Study" specifying study names.
<b>Treat</b>	A column name in a data frame named as "Treatment" specifying treatment names.
<b>weights</b>	A variable in which the results of <i>specify_weight()</i> function was stored.
<b>digits</b>	A numeric value indicating the number of decimal places in the Distance calculated.

### Value

Data frame

### Author(s)

Shubhram Pandey <shubhram1992@gmail.com>

## Examples

```
attach(exampleData)
var = c("Male","Age")
weights = specify_weight(var, weights = c(0.5,0.5))
weights
dist = calc_dist(df = exampleData, col_names = var, weights = weights,digits = 4)
dist
```

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check\_data

*Function to check if all values are numeric in data*

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## Description

Function to check if all values are numeric in data

## Usage

```
check_data(df, col_names = NULL)
```

## Arguments

df	A data frame contains columns that represent covariates
col_names	A numeric vector of covariates that can be binary or continuous

## Value

logical

## Author(s)

Shubhram Pandey <shubhram1992@gmail.com>

## Examples

```
attach(exampleData)
var = c("Age","Male")
x = check_data(df = exampleData, col_names = var)
x
```

`exampleData` *This is a simulated data*

## Description

Data were extracted from the studies included.

## Usage

`exampleData`

## Format

A data frame with with the 4 following variables (columns).

**Study** This character vector represents number of the study.

**Male** This vector represents the proportion of males.

**Age** This vector represents the average age in each study.

**Treatment** This vector represents the treatment. ...

## Details

A simulated data were created to run examples.

## Author(s)

Shubhram Pandey <shubhram.pandey@heorlytics.com>

`is_prop` *Function to check if columns are proportions*

## Description

Function to check if columns are proportions

## Usage

`is_prop(df, col_names)`

## Arguments

<code>df</code>	a data frame to be checked
<code>col_names</code>	column names to be checked

**Value**

list

**Author(s)**

Shubhram Pandey <shubhram1992@gmail.com>

**Examples**

```
#' attach(exampleData)
result <- is_prop(exampleData,c("Male","Age"))
result
```

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**specify\_weight**      *Title specify\_weight*

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**Description**

Title `specify_weight`

**Usage**

```
specify_weight(var, weights)
```

**Arguments**

<code>var</code>	Variables for which weights can be assigned
<code>weights</code>	weights in same sequence as variables

**Value**

list

**Author(s)**

Shubhram Pandey <shubhram1992@gmail.com>

**Examples**

```
var = c("Male","Age")
weights = specify_weight(var, weights = c(0.5,0.5))
weights
```

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