Example Use

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Introduction

This R Markdown document shows the usage of the package cino1.

```
# Install local package
install.packages("~/Documents/Masterarbeit/Package/nofone/", repos = NULL, type="source")

## Installing package into '/home/thgaertner/R/x86_64-pc-linux-gnu-library/3.6'

## (as 'lib' is unspecified)

## Warning in install.packages("~/Documents/Masterarbeit/Package/nofone/", :

## installation of package '/home/thgaertner/Documents/Masterarbeit/Package/
## nofone/' had non-zero exit status

# load package
library(cinof1)
```

Data

In this package, a sample data frame is included. It contains data for 300 patients within an n of 1 study. The data has the following structure:

- patient_id: Unique patient identifier
- date: Date of data points
- day: Day in study
- Block: identifies treatment block
- Activity: Dummy variable for steps per day
- treatment: Dummy variable for 2 treatments as factors
- Uncertain Low Back Pain: Dummy variable for Uncertain log back pain on scale 1-15

```
load("data/simpatdat.rda")
# Summarize Data
summary(simpatdat)
```

```
##
      patient_id
                            date
                                          day
                                                            treatment
##
   Min.
          : 0.00
                   2018-01-01: 20
                                                      Treatment_1:1120
                                            : 1.00
   1st Qu.: 4.75
                                20
                                     1st Qu.: 28.75
                   2018-01-02:
                                                      Treatment_2:1120
##
   Median : 9.50
                   2018-01-03:
                                20
                                     Median: 56.50
                                            : 56.50
##
  Mean
          : 9.50
                   2018-01-04:
                                20
                                     Mean
   3rd Qu.:14.25
                   2018-01-05:
                                20
                                     3rd Qu.: 84.25
                                20
##
          :19.00
                   2018-01-06:
                                     Max.
                                            :112.00
##
                             :2120
                    (Other)
## Uncertain_Low_Back_Pain
                               block
                                             Activity
## Min. : 6.000
                                  :1.00
                                          Min.
                                                     45.19
                           Min.
                                                :
## 1st Qu.: 9.000
                           1st Qu.:1.75
                                          1st Qu.: 5563.32
```

```
Median : 9.000
                             Median:2.50
                                             Median: 6910.56
##
    Mean
           : 9.231
                             Mean
                                     :2.50
                                             Mean
                                                    : 6943.34
    3rd Qu.:10.000
                             3rd Qu.:3.25
##
                                             3rd Qu.: 8290.16
           :12.000
                                     :4.00
                                                     :14084.38
##
    Max.
                             Max.
                                             Max.
##
```

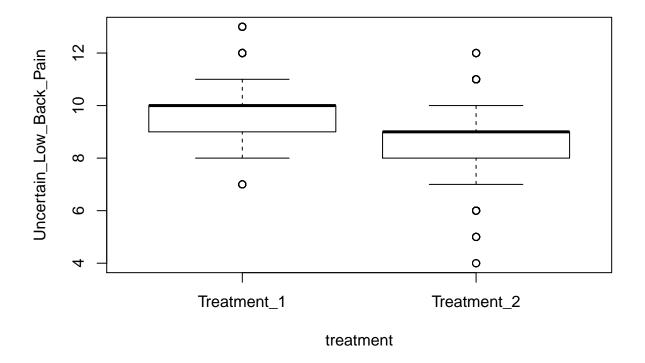
Basic Functions

Basic functions for analyse N-of-1 studys are for example wilcox test or comparative plots. These two functions are provided in this package.

Comparative Plot

To get a first idea about the data and the difference between treatment 1 and treatment 2, a comparative plot could be used. It shows the outcome on the y-Axis against the different treatments on the x-Axis,

```
# Define outcome and exposure column
outcome <- "Uncertain_Low_Back_Pain"
exposure <- "treatment"
# Plot outcome among different exposures
comparative.plot(simpatdat, exposure = exposure, outcome = outcome)</pre>
```



Wilcox Test

To validate, that there is a difference in both treatments, the Wilcox test could be used. It calculates the p-value for the null hypothesis, that there location shift is equal to zero.

```
# Define outcome and exposure column
outcome <- "Uncertain_Low_Back_Pain"
exposure <- "treatment"
# Perform Wilcox test among different exposures
wilcox.nofone(simpatdat, exposure = exposure, outcome = outcome)

##
## Wilcoxon rank sum test
##
## data: Uncertain_Low_Back_Pain by treatment
## W = 1048691, p-value < 2.2e-16
## alternative hypothesis: true location shift is not equal to 0</pre>
```

Bayesian

Bayesian Networks are used to calculated the probability of outcome variables adjusted for confounders. For that, a dag is required, which identifies the relations between the variables. In this implementation, also lags are included and could be specified in the dag by adding .lag= to the variable name.

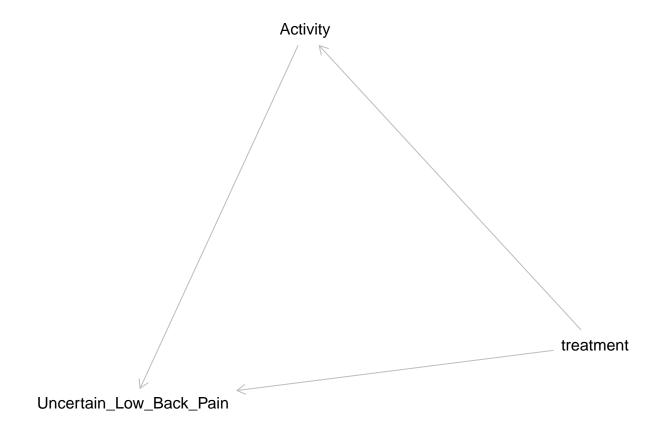
Preprocess Data

```
# specify column names
id <- "patient_id"
time_col <- "day"

# Load data
load("data/ex.dag.rda")
load("data/simpatdat.rda")

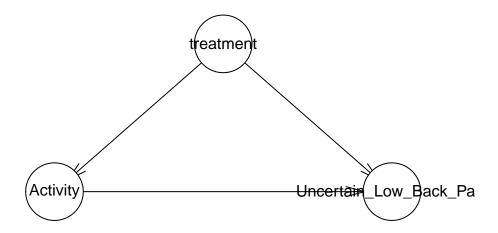
plot(ex.dag)</pre>
```

Plot coordinates for graph not supplied! Generating coordinates, see ?coordinates for how to set you



Dag preprocessing
bn.dag <- bn.prep.dag(ex.dag)</pre>

Transformed Bn DAG

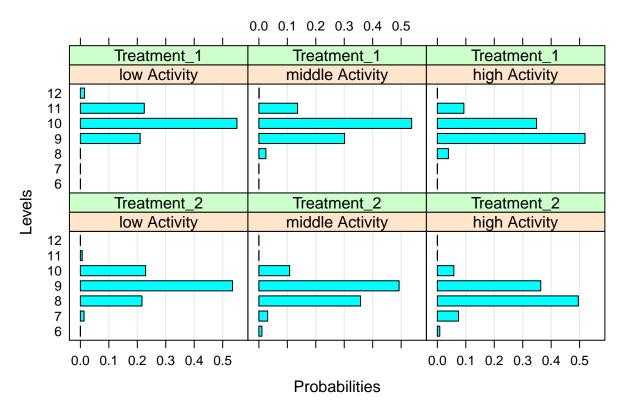


```
# Data Preprocessing (Factorization)
simpatdat$Uncertain_Low_Back_Pain <- as.factor(simpatdat$Uncertain_Low_Back_Pain)
simpatdat$Activity <- cut(simpatdat$Activity, 3, labels=c("low Activity", "middle Activity", "high Activity bn.data <- bn.prep.data(bn.dag, simpatdat, id, time_col)
bn.data <- na.omit(bn.data)</pre>
```

Fit and Plot Results

```
fitted.bn <- bn.fit.dag(bn.data, bn.dag, method="bayes")
library(bnlearn)
bn.fit.barchart(fitted.bn$Uncertain_Low_Back_Pain)</pre>
```

Conditional Probabilities for Node Uncertain_Low_Back_Pain



G-Estimation

G-Estimation is used to adjust the analysis for causal inferences. For that, three different methods are implemented

Load Data

```
load("data/simpatdat.rda")
```

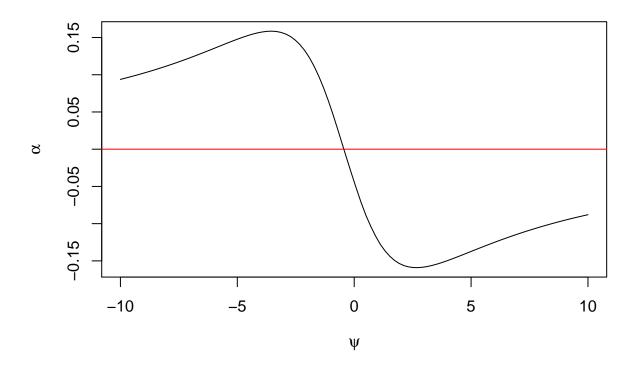
Fit G-Estimation by Iteration

It iterates over several values for ψ and returns a data frame with ψ and corresponding α

```
outcome <- "Uncertain_Low_Back_Pain"
exposure <- "treatment"
confounder <- c("Activity")
id <- "patient_id"
df <- nofgest(simpatdat, outcome, exposure, confounder, id, method="iterate", steps=100, upper_bound_ps</pre>
```

This function is useful to plot a curve for α and ψ .

Plot of $\alpha(\psi)$



Fit G-Estimation by Recursive Mean

This function approximate ψ by an interval search.

```
outcome <- "Uncertain_Low_Back_Pain"</pre>
exposure <- "treatment"</pre>
confounder <- c("Activity")</pre>
id <- "patient_id"</pre>
nofgest(simpatdat, outcome, exposure, confounder, id, method="rec_mean")
## [1] "Converged! Optimal Psi: -0.443288747439986"
## [1] "Number of iterations: 50"
## $upper_psi
## [1] -0.4432887
##
## $upper_beta
## [1] -6.491118e-16
##
## $lower_psi
## [1] -0.4432887
##
## $lower_beta
## [1] 1.881633e-16
##
## $n_it
## [1] 50
```

Fit G-Estimation by Recursive Improved

This function approximate ψ by an optimized interval search.

```
outcome <- "Uncertain_Low_Back_Pain"</pre>
exposure <- "treatment"</pre>
confounder <- c("Activity")</pre>
id <- "patient_id"</pre>
nofgest(simpatdat, outcome, exposure, confounder, id, method="rec")
## [1] "Converged! Optimal Psi: -0.443288747439985"
## [1] "Number of iterations: 8"
## $upper_psi
## [1] -0.4432887
##
## $upper_beta
## [1] -1.980295e-16
##
## $lower_psi
## [1] -0.490945
##
## $lower_beta
## [1] 0.004872248
##
## $n_it
## [1] 8
```