

Example Use

Thomas Gaertner

4/13/2021

```
devtools::document()

## Warning: [/home/thgaertner/Documents/Masterarbeit/Package/nofone/R/
## adjtreat.R:25] @example spans multiple lines. Do you want @examples?

## Warning: [/home/thgaertner/Documents/Masterarbeit/Package/nofone/R/
## basic_functions.R:64] @example spans multiple lines. Do you want @examples?

## Writing NAMESPACE
## Writing NAMESPACE
## Writing find_optimum_rec.Rd
## Writing find_optimum_iterate.Rd

knitr::opts_chunk$set(echo = TRUE)
```

Introduction

This R Markdown document shows the usage of the package `cinof1`.

```
# Install local package
devtools::document()

## Warning: [/home/thgaertner/Documents/Masterarbeit/Package/nofone/R/
## adjtreat.R:25] @example spans multiple lines. Do you want @examples?

## Warning: [/home/thgaertner/Documents/Masterarbeit/Package/nofone/R/
## basic_functions.R:64] @example spans multiple lines. Do you want @examples?

## Writing NAMESPACE
## Writing NAMESPACE

install.packages("~/Documents/Masterarbeit/Package/nofone/", repos = NULL, type="source")
# load package
library(cinof1)
library(doParallel)
```

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 loq 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  Min.   : 1.00  Treatment_1:1120
## 1st Qu.: 4.75  2018-01-02: 20  1st Qu.: 28.75  Treatment_2:1120
## Median : 9.50  2018-01-03: 20  Median : 56.50
## Mean   : 9.50  2018-01-04: 20  Mean    : 56.50
## 3rd Qu.:14.25  2018-01-05: 20  3rd Qu.: 84.25
## Max.   :19.00  2018-01-06: 20  Max.    :112.00
##              (Other)   :2120
## Uncertain_Low_Back_Pain  block      Activity
## Min.   : 6.000          Min.   :1.00  Min.   : 45.19
## 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
## Max.   :12.000          Max.   :4.00  Max.   :14084.38
##
```

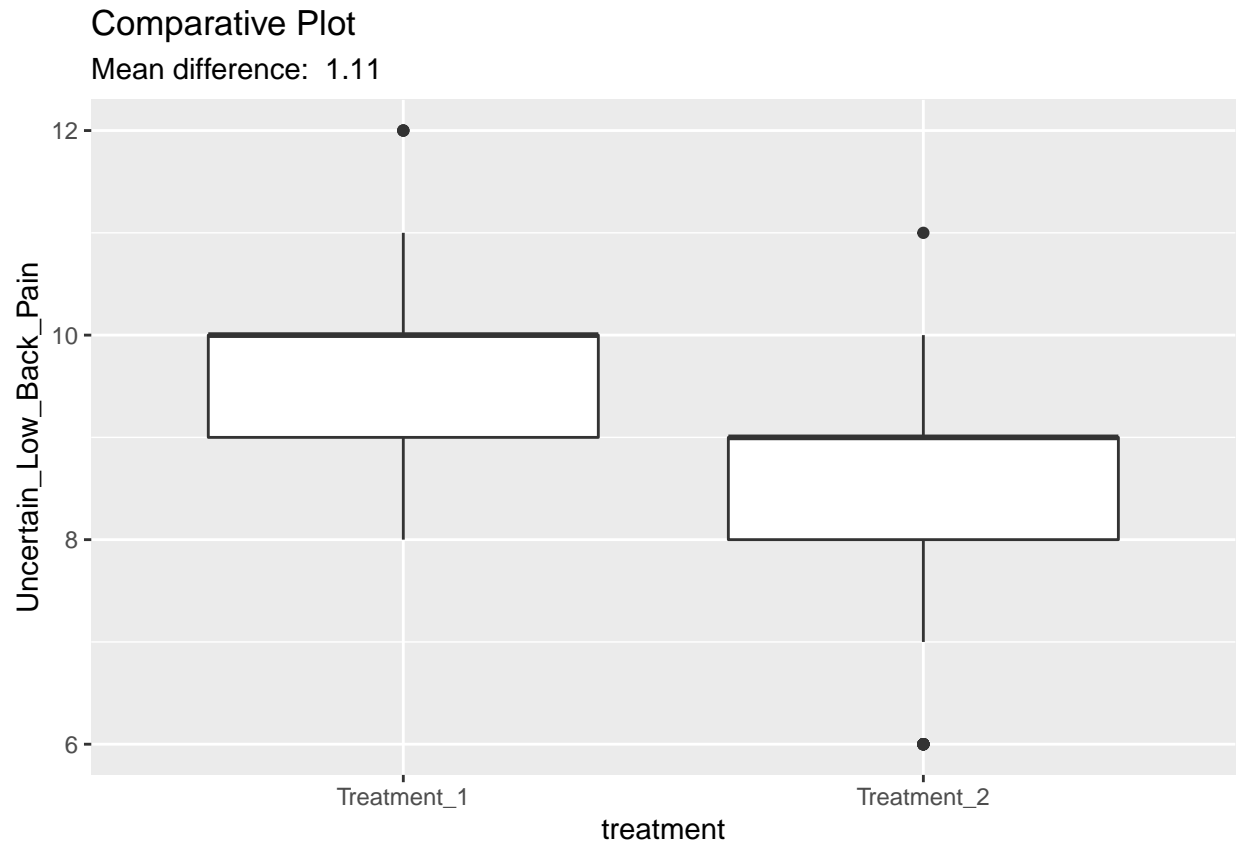
Basic Functions

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)
```



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(simpdat, 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
```

Adjust Wash In and Wash Out

```
outcome <- "Uncertain_Low_Back_Pain"
exposure <- "treatment"
variables <- c("Activity")
id <- "patient_id"
time_col <- "day"
```

```
result <- estimate.gamma.tau(data = simpatdat, outcome = outcome, exposure = exposure, variables = vari
```

```
result
```

```
## $data
```

```
##   treatment.Treatment_1.gamma treatment.Treatment_2.gamma
```

```
## 1           1           1
```

```
## 2           2           1
```

```
## 3           1           2
```

```
## 4           2           2
```

```
##   treatment.Treatment_1.tau treatment.Treatment_2.tau      r2
```

```
## 1           1           1 0.3925277
```

```
## 2           2           1 0.3922651
```

```
## 3           1           2 0.4098408
```

```
## 4           2           2 0.4429989
```

```
##   treatment.Treatment_1.Estimate treatment.Treatment_1.Std..Error
```

```
## 1           1.11654798           0.03050288
```

```
## 2          -0.03097696           0.16987892
```

```
## 3          -0.48246803           0.19819322
```

```
## 4          -3.24965646           0.27524924
```

```
##   treatment.Treatment_2.Estimate treatment.Treatment_2.Std..Error
```

```
## 1           NA           NA
```

```
## 2          -1.145895           0.1638043
```

```
## 3          -1.656651           0.2029606
```

```
## 4          -4.357631           0.2717909
```

```
##
```

```
## $best
```

```
##   treatment.Treatment_1.gamma treatment.Treatment_2.gamma
```

```
## 4           2           2
```

```
##   treatment.Treatment_1.tau treatment.Treatment_2.tau
```

```
## 4           2           2
```

```
fit.adj.lm(data = simpatdat, outcome = outcome, exposure = exposure, variables = variables, effects = r
```

```
## Warning in if (is.na(effects)) {: the condition has length > 1 and only the
## first element will be used
```

```
##
```

```
## Call:
```

```
## lm(formula = formula(str_formula), data = data, na.action = na.omit)
```

```
##
```

```
## Coefficients:
```

```
##           (Intercept) treatment.Treatment_1.gamma.2.tau.2
```

```
##           1.360e+01           -3.250e+00
```

```
##           Activity treatment.Treatment_2.gamma.2.tau.2
```

```
##           -8.569e-05           -4.358e+00
```

Bayesian

Bayesian Networks are used to calculate 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.

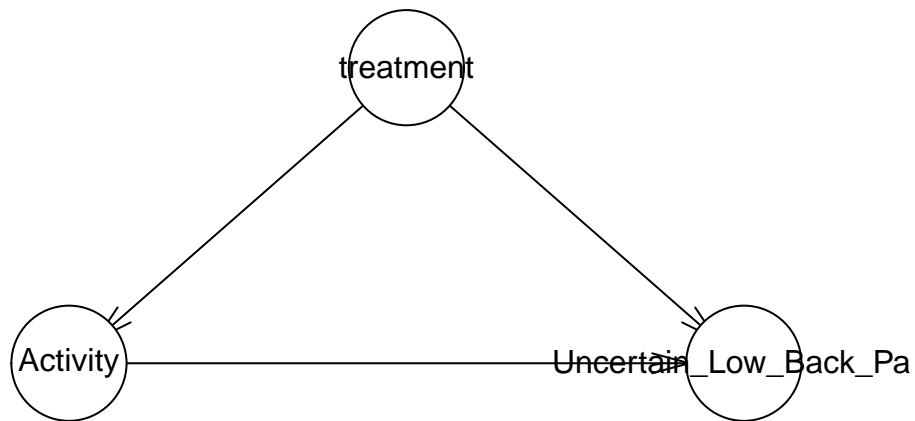
Preprocess Data

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

# Load data
load("data/simpatdag.rda")
load("data/simpatdat.rda")

# Dag preprocessing
bn.dag <- bn.prep.dag(simpatdag)
```

Transformed Bn DAG



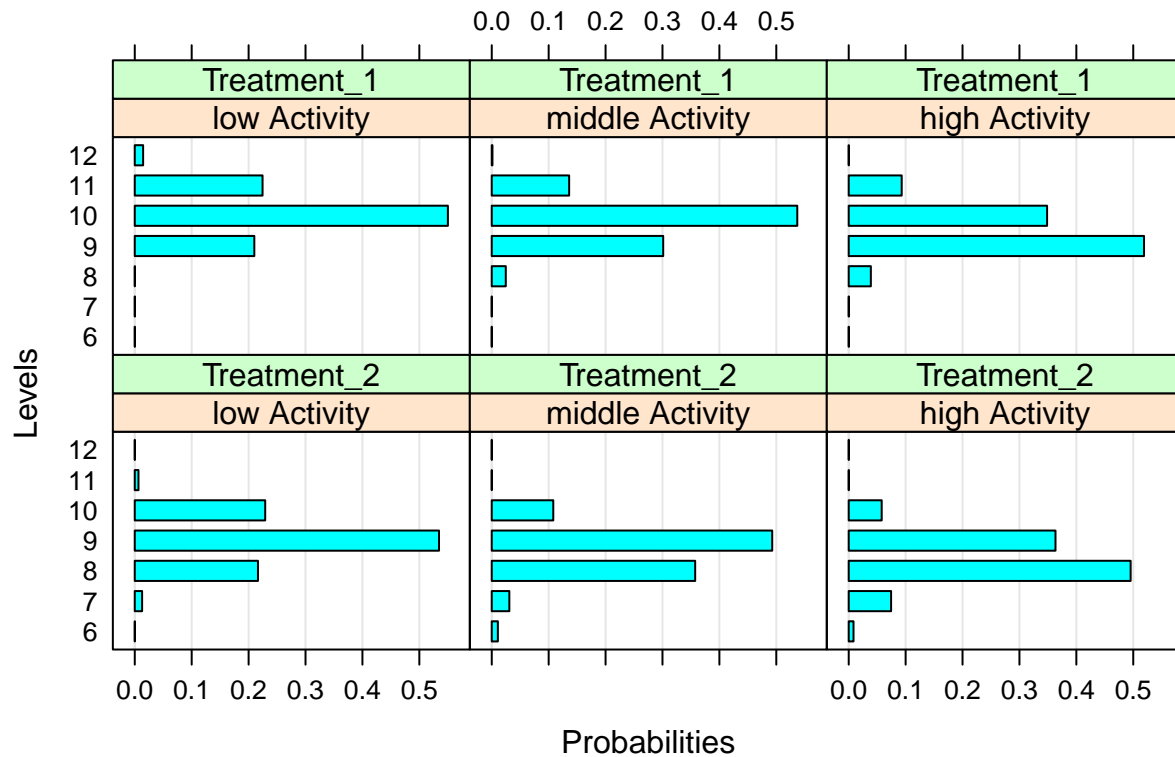
```
# Data Preprocessing (Factorization)
simpatdat$Uncertain_Low_Back_Pain <- as.factor(simpatdat$Uncertain_Low_Back_Pain)
simpatdat$Activity <- cut(simpatdat$Activity, 3, labels=c("low Activity", "middle Activity", "high Activity"))
bn.data <- bn.prep.data(bn.dag, simpatdat, id, time_col)
bn.data <-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

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)
```

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")
```

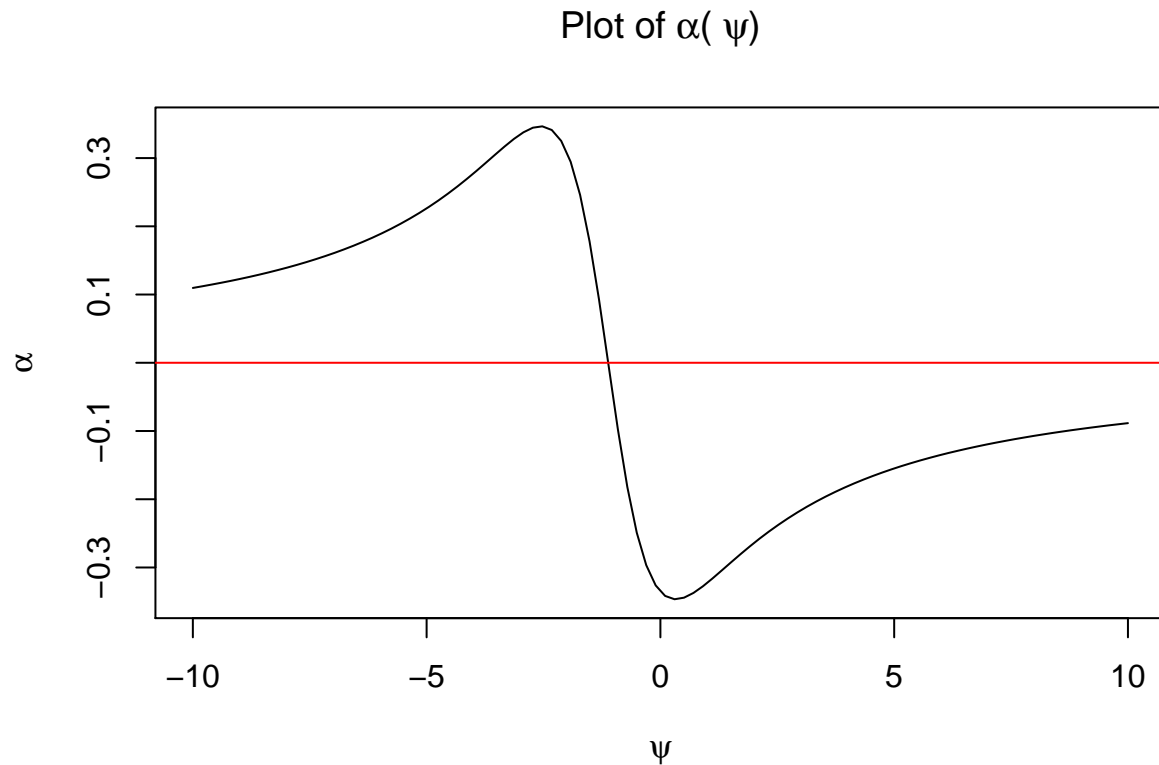
Fit G-Estimation by Iteration

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_psi=1)
```

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

```
plot(df$PSI, df$Beta, type="l", main=expression(paste("Plot of ", alpha, "( ", psi, ")")),
     xlab=expression(psi),
     ylab=expression(alpha))
# Add a second line
lines(c(-100,100), c(0,0), type="l", col="red")
```



Fit G-Estimation by Recursive Mean

This function approximate ψ by an interval search.

```
outcome <- "Uncertain_Low_Back_Pain"
exposure <- "treatment"
confounder <- c("Activity")
id <- "patient_id"
nofgest(simpdat, outcome, exposure, confounder, id, method="rec_mean", max_number_it = 10, verbose=FALSE)
```

```
## [1] "Max Iterations:"
```

```
##      upper_psi  upper_beta  upper_se lower_psi  lower_beta  lower_se
## 1 -1.109375 -0.003446206 0.040946897 -1.117188 0.0003072594 0.03584373
## 2 -1.109375 -0.003446206 0.040946897 -1.117188 0.0003072594 0.03584373
## 3 -1.109375 -0.003446206 0.040946897 -1.125000 0.0040606711 0.03584373
## 4 -1.093750 -0.010950659 0.040608006 -1.125000 0.0040606711 0.03584373
## 5 -1.062500 -0.025931203 0.039908527 -1.125000 0.0040606711 0.03584373
## 6 -1.000000 -0.055632933 0.038450862 -1.125000 0.0040606711 0.03584373
## 7 -1.000000 -0.055632933 0.038450862 -1.250000 0.0635736508 0.03584373
## 8 -1.000000 -0.055632933 0.038450862 -1.500000 0.1720752047 0.03584373
## 9 -1.000000 -0.055632933 0.038450862 -2.000000 0.3086996366 0.03584373
## 10 0.000000 -0.335496982 0.025465297 -2.000000 0.3086996366 0.03584373
## 11 2.000000 -0.264243363 0.008784946 -2.000000 0.3086996366 0.03584373
##      iteration
## 1           10
## 2            9
```

```
## 3      8
## 4      7
## 5      6
## 6      5
## 7      4
## 8      3
## 9      2
## 10     1
## 11     0
```

Fit G-Estimation by Recursive Improved

This function approximate ψ by an optimized interval search.

```
outcome <- "Uncertain_Low_Back_Pain"
exposure <- "treatment"
confounder <- c("Activity")
id <- "patient_id"
nofgest(simpdat, outcome, exposure, confounder, id, method="rec", max_number_it = 10, verbose=FALSE)
```

```
## [1] "Converged! Optimal Psi: -1.1165479816877"

##   upper_psi   upper_beta   upper_se lower_psi   lower_beta   lower_se
## 1 -1.1165480 -1.179378e-17 0.041099672 -1.116548 9.698380e-08 0.03584373
## 2 -1.1165480 -1.179378e-17 0.041099672 -1.116548 9.698380e-08 0.03584373
## 3 -1.1165480 -1.915311e-15 0.041099672 -1.116548 9.698380e-08 0.03584373
## 4 -1.1162943 -1.219032e-04 0.041094300 -1.116548 9.698380e-08 0.03584373
## 5 -1.1162943 -1.219032e-04 0.041094300 -1.157368 1.959637e-02 0.03584373
## 6 -0.9804303 -6.482132e-02 0.037986401 -1.157368 1.959637e-02 0.03584373
## 7 -0.9804303 -6.482132e-02 0.037986401 -2.000000 3.086996e-01 0.03584373
## 8 0.1551857 -3.438355e-01 0.024008679 -2.000000 3.086996e-01 0.03584373
## 9 2.0000000 -2.642434e-01 0.008784946 -2.000000 3.086996e-01 0.03584373
##   iteration
## 1          8
## 2          7
## 3          6
## 4          5
## 5          4
## 6          3
## 7          2
## 8          1
## 9          0
```