

Depression State Analysis with Sensor Data

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Loading libraries that we are going to need

```
library(rmarkdown)
library(SimDesign)
library(janitor)
```

```
##
## Attaching package: 'janitor'
## The following objects are masked from 'package:stats':
##
##   chisq.test, fisher.test
```

```
library(tidyverse) #helps wrangle data
```

```
## -- Attaching packages ----- tidyverse 1.3.2 --
## v ggplot2 3.3.6      v purrr  0.3.4
## v tibble  3.1.8      v dplyr  1.0.9
## v tidyr   1.2.0      v stringr 1.4.0
## v readr   2.1.2      v forcats 0.5.1
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(lubridate) #helps wrangle date attributes
```

```
##
## Attaching package: 'lubridate'
##
## The following objects are masked from 'package:base':
##
##   date, intersect, setdiff, union
```

```
library(ggplot2) #helps visualize data
getwd() #displays your working directory
```

```
## [1] "/cloud/project"
```

```
library(readr)
```

The dataset was downloaded from <https://datasets.simula.no/depresjon/>

```
scores <- read_csv("dataset/scores.csv")
```

```
## Rows: 55 Columns: 12
```

```
## -- Column specification -----
## Delimiter: ",",
```

```
## chr (3): number, age, edu
## dbl (9): days, gender, afftype, melanch, inpatient, marriage, work, madsr1, ...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

Prepare data process The data's integrity can be verified at (<https://bmcrenotes.biomedcentral.com/articles/10.1186/1756-0500-3-149>). An actigraph watch was worn on the right wrist to track motor activity (Actiwatch, Cambridge Neurotechnology Ltd, England, model AW4).

It contains the following columns; number (patient identifier), days (number of days of measurements), gender (1 or 2 for female or male), age (age in age groups), afftype (1: bipolar II, 2: unipolar depressive, 3: bipolar I), melanch (1: melancholia, 2: no melancholia), inpatient (1: inpatient, 2: outpatient), edu (education grouped in years), marriage (1: married or cohabiting, 2: single), work (1: working or studying, 2: unemployed/sick leave/pension), madsr1 (MADRS score when measurement started), madsr2 (MADRS when measurement stopped).

View(scores)

Process data

```
# Inspect the dataframes and look for incongencies
str(scores)
(scores <- rename(scores
  ,condition_number = number
  ,disease_type = afftype))
# Remove "bad" data
# The dataframe includes non-applicable entries. we will remove bad data for this column
# We will create a new version of the dataframe (v2) since data is being removed
names(scores)
#remove not applicable columns
scores_v2 <- na.omit(scores)
View(scores_v2)
#find mean value of of madsr score
scores_v2$new_means <- rowMeans(scores_v2[, c(11,12)])
#transform data
#standardise madsr value respective with number of days measured
scores_v2$standard_madsr <- scores_v2$new_means / scores_v2$days
#cleaningnames of columns
clean_names(scores_v2)
```

Analyse the data

```
ggplot(data = scores_v2, aes(x = disease_type, y = standard_madsr, color = inpatient)) +
  geom_point()
ggplot(data = scores_v2, aes(x = disease_type, y = standard_madsr, color = inpatient)) +
  geom_point() +
  facet_wrap(~inpatient)
ggplot(data = scores_v2, aes(x = disease_type, y = standard_madsr, color = edu)) +
  geom_point()

ggplot(data = scores_v2, aes(x = disease_type, y = standard_madsr, color = edu)) +
  geom_line()

ggplot(data = scores_v2, aes(x = disease_type, y = standard_madsr, color = edu)) +
  geom_point() +
  facet_wrap(~edu)
```

```
ggplot(data = scores_v2, aes(x = disease_type, y = standard_madrs, color = work)) +  
  geom_point()
```

```
ggplot(data = scores_v2, aes(x = disease_type, y = standard_madrs, color = work)) +  
  geom_point() +  
  facet_wrap(~work)
```

```
ggplot(data = scores_v2, aes(x = disease_type, y = standard_madrs, color = marriage)) +  
  geom_point()
```

```
ggplot(data = scores_v2, aes(x = disease_type, y = standard_madrs, color = marriage)) +  
  geom_point() +  
  facet_wrap(~marriage)
```

```
ggplot(data = scores_v2, aes(x = age, y = standard_madrs, color = inpatient)) +  
  geom_point()
```

```
ggplot(data = scores_v2, aes(x = age, y = melanch, color = inpatient)) +  
  geom_point()
```

```
ggplot(data = scores_v2, aes(x = standard_madrs, y = condition_number, color = inpatient)) +  
  geom_point()
```