

Antidepressant effects of esketamine in adolescents with major depressive disorder and suicidal ideation: a case series

Reproducible analysis code

Daniela Faria-Guimarães Lucca S. Souza Breno Souza-Marques Flávia Vieira
Igor D. Bandeira Samantha S. Silva Raíza Alves-Pereira Mariana Fontes
Rodrigo P. Mello Gustavo C. Leal Acioly L. T. Lacerda Flávio Kapczinski
Taiane A. Cardoso Aline S. Sampaio Lucas C. Quarantini

Contents

1	Note on reproducibility	2
2	Load the required packages	2
3	Load the dataset	2
4	Assess normality of outcomes	3
4.1	MADRS total score at baseline and 24h post-treatment	3
4.2	MADRS item 10 score at baseline and 24h post-treatment	3
5	Descriptives	4
5.1	MADRS total scores	4
5.2	MADRS item 10 scores	4
6	T-tests	5
6.1	Effect sizes	6
7	Bootstrapped 95% confidence intervals	7
7.1	Create a bootstrap function	7
7.2	Run bootstraps and create ggplot graph objects	8
8	Graphics	10
8.1	Density plots of bootstrapped sample means	10
8.2	Main plots: pre-and post-treatment effects for depressive symptoms and suicidal ideation . .	11

1 Note on reproducibility

This R Markdown file will exactly reproduce our data tidying, transformation, analysis and graphing processes in the R software and produce an illustrative PDF file. Code-only scripts are also available in the Open Science Framework repository for this study, at <https://osf.io/2ujqn/>. The reproduction of this R Markdown file requires that the dataset available in the OSF repository is located in the same directory of this file, and that the user has the necessary dependencies to create a PDF using the `{bookdown}` package. Further information is available at the package website: <https://bookdown.org>. Please refer to the repository for a detailed description of each variable contained herein. All files in the repository, including this one, are licensed under CC-BY-4.0.

The `{renv}` package was used to help with reproducibility. The `renv.lock` file is available and should be imported to the same location on your computer as this script. For further information on how to use these files visit the package website: <https://rstudio.github.io/renv/articles/renv.html>.

2 Load the required packages

```
# Required Packages
library(tidyverse)
library(haven)
library(lsr)
library(rstatix)
library(boot)
library(kableExtra)
library(patchwork)
library(RColorBrewer)
library(ggsci)
library(car)
library(purrr)
library(broom)
library(ggpubr)
```

3 Load the dataset

The first step is to load the dataset into R. You can load the dataset directly from the GitHub repository.

```
set.seed(2509)
## Load from GitHub repository

urlRemote <- "https://raw.githubusercontent.com/"
pathGithub <- "brenosouzamarques/LANP_Esketamine_Adolescents/master/"
fileName <- "Dataset.csv"

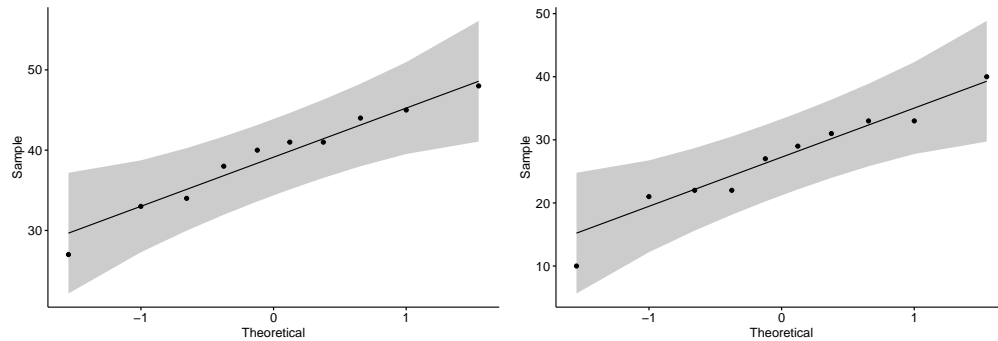
df <- paste0(urlRemote, pathGithub, fileName) %>%
  read.csv()
```

4 Assess normality of outcomes

Q-Q Plots are used to assess the symmetry of dependent variables, that is, **MADRS total score** and **MADRS item 10** at baseline and 24-h post-infusion.

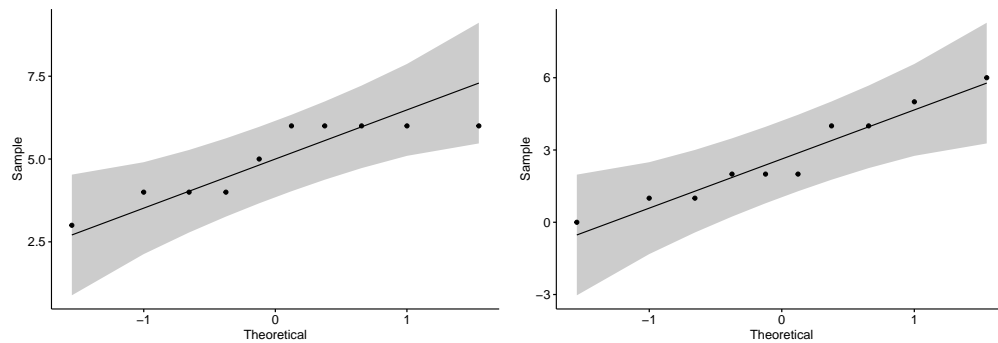
4.1 MADRS total score at baseline and 24h post-treatment

```
ggqqplot(df$MADRS_pré)
ggqqplot(df$MADRS_24h)
```



4.2 MADRS item 10 score at baseline and 24h post-treatment

```
ggqqplot(df$Item10_PréMADRS)
ggqqplot(df$Item10_24hMADRS)
```



5 Descriptives

Total depressive symptoms and suicidal ideation scores are presented as means and standard deviations.

5.1 MADRS total scores

```
madsr_total <- c(df$MADRS_pré, df$MADRS_24h)
time <- rep(c("baseline", "post"), each = 10)
data_madsr_total <- tibble(time, madsr_total)
kbl(data_madsr_total %>% group_by(time) %>%
  summarise(
    Mean = mean(madsr_total),
    "Std dev" = sd(madsr_total),
    Maximum = max(madsr_total),
    Minimum = min(madsr_total),
    Median = median(madsr_total)),
  caption = "MADRS total score",
  booktabs = T) %>% kable_styling(latex_options = c("hold_position"))
```

Table 1: MADRS total score

time	Mean	Std dev	Maximum	Minimum	Median
baseline	39.1	6.297266	48	27	40.5
post	26.8	8.403703	40	10	28.0

5.2 MADRS item 10 scores

```
item_10_total <- c(df$Item10_PréMADRS, df$Item10_24hMADRS)
time <- rep(c("baseline", "post"), each = 10)
data_madsr_total <- tibble(time, item_10_total)
kbl(
  data_madsr_total %>%
  group_by(time) %>%
  summarise(
    Mean = mean(item_10_total),
    "Std dev" = sd(item_10_total),
    Maximum = max(item_10_total),
    Minimum = min(item_10_total),
    Median = median(item_10_total)),
  caption = "MADRS item 10 score",
  booktabs = T) %>% kable_styling(latex_options = c("hold_position"))
```

Table 2: MADRS item 10 score

time	Mean	Std dev	Maximum	Minimum	Median
baseline	5.0	1.154700	6	3	5.5
post	2.7	1.946507	6	0	2.0

6 T-tests

We aimed to determine if a single 0.5mg/kg dose of esketamine can reduce depressive symptoms and suicidal ideation in adolescents. We test this hypothesis with a paired-samples t-test.

```
### T-test - MADRS Total Scores
```

```
ttest_total_madrs <- t.test(x = df$MADRS_pré,  
                           y = df$MADRS_24h,  
                           paired = T,  
                           alternative = "two.sided")  
  
ttest_item10_madrs <- t.test(x = df$Item10_PréMADRS,  
                             y = df$Item10_24hMADRS,  
                             paired = T,  
                             alternative = "two.sided")  
  
table_madrs <- map_df(list(ttest_total_madrs, ttest_item10_madrs), tidy)  
  
table_madrs$'Outcome' <- c("MADRS total score",  
                           "MADRS item 10")  
  
table_madrs <- table_madrs %>% rename(  
  "Mean Difference" = estimate,  
  "T statistic" = statistic,  
  "DF" = parameter,  
  "95% CI lower" = conf.high,  
  "95% CI higher" = conf.low,  
  "P-value" = p.value)  
  
kbl(table_madrs[c(9, 4, 2, 3, 1, 5, 6)],  
     caption = "T-tests", booktabs = T) %>%  
  kable_styling(latex_options = c("hold_position"))
```

Table 3: T-tests

Outcome	DF	T statistic	P-value	Mean Difference	95% CI higher	95% CI lower
MADRS total score	9	4.221349	0.0022350	12.3	5.708616	18.891384
MADRS item 10	9	3.146129	0.0118109	2.3	0.646234	3.953766

6.1 Effect sizes

Effect sizes allow further interpretation of changes from baseline to 24 hours post-ketamine treatment.

```
effectsize_madrs <- lsr::cohensD(df$MADRS_pré,  
                                df$MADRS_24h,  
                                method = "paired")  
  
effectsize_item10 <- lsr::cohensD(df$Item10_PréMADRS,  
                                  df$Item10_24hMADRS,  
                                  method = "paired")  
  
kbl(tribble(~Outcome, ~"Effect Size (Cohen's D)",  
            "MADRS total score", effectsize_madrs,  
            "MADRS item 10", effectsize_item10),  
     caption = "Effect sizes",  
     booktabs = T) %>% kable_styling(latex_options = c("hold_position"))
```

Table 4: Effect sizes

Outcome	Effect Size (Cohen's D)
MADRS total score	1.3349078
MADRS item 10	0.9948934

7 Bootstrapped 95% confidence intervals

7.1 Create a bootstrap function

This functions creates a main element, the `data_dens` data frame. It stores the bootstrapped samples of means as they are calculated using the bias-corrected and accelerated (Bca) method. These are later used to plot density graphs that compare bootstrapped distributions of pre-and post-treatment symptoms.

```
boot_funs <- function(df, f1, f2){  
  a <- df[[f1]]  
  b <- df[[f2]]  
  boot_a <- boot(a,  
    function(x, j) mean(x[j], na.rm = T), #Boot baseline variable  
    R = 10000)  
  boot_b <- boot(b,  
    function(x, j) mean(x[j], na.rm = T), #Boot 7 days variable  
    R = 10000)  
  boot_ci_a <- boot.ci(boot.out = boot_a, #Calculate baseline CI  
    conf = 0.95,  
    type = "bca")  
  boot_ci_b <- boot.ci(boot.out = boot_b, #Calculate post-treatment CI  
    conf = 0.95,  
    type = "bca")  
  print(boot_ci_a) # Return baseline bootstrapped CI  
  print(boot_ci_b) # Return post-treatment bootstrapped CI  
  
  ## Code to extract bootstrapped sample means  
  densitiy_a <- boot_a$t  
  densitiy_b <- boot_b$t  
  dens <- c(densitiy_a, densitiy_b)  
  time <- rep(c("Baseline", "Post-Treatment"), each = 10000)  
  data_dens <-< data.frame(dens, time)  
  data_dens$time <- factor(data_dens$time)  
}
```

7.2 Run bootstraps and create ggplot graph objects

7.2.1 Bootstrap - MADRS total score

```
### Bootstrap CI - MADRS total score
boot_funs(df, "MADRS_pré", "MADRS_24h")

## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 10000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = boot_a, conf = 0.95, type = "bca")
##
## Intervals :
## Level      BCa
## 95%   (34.9, 42.4 )
## Calculations and Intervals on Original Scale
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 10000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = boot_b, conf = 0.95, type = "bca")
##
## Intervals :
## Level      BCa
## 95%   (21.2, 31.1 )
## Calculations and Intervals on Original Scale

plot_madrs <- ggplot(data_dens)+
  geom_density(aes(x = dens, fill = time),
               color = "white",
               alpha = 0.9)+
  labs(x = "Total MADRS scores")+
  scale_fill_brewer(name = "Time of assessment:",
                   palette = "Dark2")+
  theme_classic()+
  theme(text = element_text(family = "serif"),
        axis.text.x = element_text(size = 14),
        axis.title.x = element_text(size = 14),
        axis.text.y = element_text(size = 14),
        axis.title.y = element_text(size = 14),
        legend.text = element_text(size = 13),
        legend.title = element_text(size = 13)) ##ggplot2 graph
```


7.2.2 Bootstrap - MADRS item 10

```
### Bootstrap CI - MADRS item 10

boot_funs(df, "Item10_PréMADRS", "Item10_24hMADRS")

## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 10000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = boot_a, conf = 0.95, type = "bca")
##
## Intervals :
## Level      BCa
## 95%      ( 4.1,  5.5 )
## Calculations and Intervals on Original Scale
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 10000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = boot_b, conf = 0.95, type = "bca")
##
## Intervals :
## Level      BCa
## 95%      ( 1.5,  3.8 )
## Calculations and Intervals on Original Scale

plot_madrs10 <- ggplot(data_dens)+
  geom_density(aes(x = dens, fill = factor(time)),
               color = "white",
               alpha = 0.9)+
  labs(x = "Item 10 MADRS scores",
       y = element_blank())+
  scale_fill_brewer(name = "Time of assessment:",
                    palette = "Dark2")+
  theme_classic()+
  theme(text = element_text(family = "serif"),
        axis.text.x = element_text(size = 14),
        axis.title.x = element_text(size = 14),
        axis.text.y = element_text(size = 14),
        axis.title.y = element_text(size = 14),
        legend.text = element_text(size = 13),
        legend.title = element_text(size = 13)) ##ggplot2 graph
```

8 Graphics

8.1 Density plots of bootstrapped sample means

Creates an annotated plot using the {ggplot2} density plots for the bootstrapped sample means and the {patchwork} package.

```
## Density plots of bootstrapped sample means

## Creates patchwork object
graficos <- plot_madrs + plot_madrs10 &
  theme(legend.position = "bottom",
        text = element_text(family = "serif"),
        title = element_text(size = 12),
        legend.title = element_text(size = 12))

## Creates guided patchwork object
graficos_f <- graficos + plot_layout(guides = "collect")

## Edits and annotates patchwork object
plota <- graficos_f + plot_annotation(
  title = 'Supp. Fig. 1 - Bootstrapped sample means for total and item 10 MADRS scores',
  subtitle = 'Density plots of results at baseline and 24 hours post-treatment')

## Saves plot in high resolution
ggsave("density_plot.png", plota, width=25, height=15, units="cm", dpi=450)
```

8.2 Main plots: pre-and post-treatment effects for depressive symptoms and suicidal ideation

This next part uses a long formatted dataset to plot pre-and post-infusion scores for each patient.

```
## Create dataset for total MADRS scores
madr_total <- c(df$MADRS_pré, df$MADRS_24h)
time <- rep(c("baseline", "post"), each = 10)
id <- rep(1:10, 2)
id <- factor(id)
madr_data_plot <- tibble(id, time, madrs_total)

## plot total MADRS scores
madr_plot <- madrs_data_plot %>% ggplot()+
  geom_boxplot(aes(x = time, y = madrs_total),
    width = .3,
    alpha = .3,
    color = "grey")+
  scale_y_continuous(breaks = seq(from = 10,
    to = 50,
    by = 5))+
  scale_x_discrete(labels = c("Baseline", "24 hours post-infusion"))+
  geom_point(aes(x = time, y = madrs_total,
    color = id,
    group = id),
    size = 1.5)+
  geom_line(aes(x = time, y = madrs_total,
    color = id,
    group = id,
    alpha = .4),
    size = 1.5)+
  scale_color_npg()+
  theme_classic()+
  labs(x = "Time of assessment",
    y = "Total MADRS scores")+
  theme(axis.title.x = element_text(size = 14,
    face = "bold"),
    axis.text.x = element_text(size = 13),
    axis.title.y = element_text(size = 15,
    face = "bold"),
    axis.text.y = element_text(size = 13),
    legend.position = "none")

## Create dataset for MADRS Item 10
si_pre <- df$Item10_PréMADRS
si_post <- df$Item10_24hMADRS

madr_item10 <- c(si_pre, si_post)
time <- rep(c("baseline", "post"), each = 10)
id <- rep(1:10, 2)
id <- factor(id)
madr_item_plot <- tibble(id, time, madrs_item10)

item10_plot <- madrs_item_plot %>% ggplot()+
```

```

geom_boxplot(aes(x = time, y = madsr_item10),
             width = .3,
             alpha = .3,
             color = "grey")+
scale_y_continuous(breaks = c(0, 1, 2, 3, 4, 5, 6))+
scale_x_discrete(labels = c("Baseline", "24 hours post-infusion"))+
geom_point(aes(x = time, y = madsr_item10,
               color = id,
               group = id),
           size = 1.5,
           position = position_dodge(0.08))+
geom_line(aes(x = time, y = madsr_item10,
              color = id,
              group = id,
              alpha = .4),
          size = 1.5,
          position = position_dodge(0.08))+
scale_color_npg()+
theme_classic()+
labs(x = "Time of assessment",
     y = "MADRS item 10 scores")+
theme(axis.title.x = element_text(size = 14,
                                   face = "bold"),
      axis.text.x = element_text(size = 13),
      axis.title.y = element_text(size = 15,
                                   face = "bold"),
      axis.text.y = element_text(size = 13),
      legend.position = "none",
      text = element_text(family = "serif"))

```

8.2.1 Code to join plots and produce the final image using {patchwork}.

```

## Creates patchwork object
graficos_i10 <- madsr_plot + item10_plot &
  theme(text = element_text(family = "serif"),
        title = element_text(size = 16),
        legend.title = element_text(size = 14))

## Edits and annotates patchwork object
graficos_i10 <- graficos_i10 + plot_annotation(
  title = 'Total and item 10 MADRS scores at baseline and 24h post-treatment',
  subtitle = 'Scores are given for each patient') &
  theme()

## Saves plot in high resolution
ggsave("MADRS_plot.png", graficos_i10, width=20, height=10, units="cm", dpi=450)
ggsave("MADRS_plot.tiff", graficos_i10, width=20, height=10, units="cm", dpi=450)

```