# **Momentary Subjective Happiness Analysis**

### **Groundhog Day Project**

Corrado Caudek

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#### **Prelims**

```
# Load necessary library
  suppressPackageStartupMessages({
      library("here")
      library("tidyverse")
      library("mice")
      library("lme4")
      library("brms")
      library("bayesplot")
      library("effectsize")
      library("scales")
      library("sjstats")
      library("sjPlot")
      library("sjmisc")
  })
Source functions
  source(
      here::here("workflows", "scripts", "funs", "funs_instant_mood.R")
  )
```

#### **Import Data**

```
# This script requires the dataframe d from prl_mood.R.
d1 <- readRDS(
    here::here(
        "data", "prep", "groundhog_all_clean.RDS"
    )
)
d1$user_id <- as.numeric(d1$user_id)

# Remove last ema sessions because compliance is too low d <- d1 |>
    dplyr::filter(!is.na(user_id) & ema_number < 13)

length(unique(d$user_id))</pre>
```

### **Data Wrangling**

```
set.seed(123)
# Standardize momentary mood by user_id.
dz <- d |>
    group_by(user_id) |>
    mutate(
      zim = as.vector(scale(instant_mood, center = TRUE, scale = TRUE))
    ) |>
    ungroup()
# Remove participants because of convergence problems.
bad_id_indices <- c(93, 99, 127, 146, 195, 216)
user_id_codes <- unique(dz$user_id)</pre>
bad_codes <- c(</pre>
    user_id_codes[bad_id_indices],
    3338029881, 3665345709, 3248648540
)
good_codes <- setdiff(user_id_codes, bad_codes)</pre>
dz_clean <- dz[dz$user_id %in% good_codes, ]</pre>
```

```
# Get list of unique user_ids
user_id_codes <- unique(dz_clean$user_id)
length(user_id_codes)</pre>
```

[1] 215

### Model of Momentary Subjective Well-Being

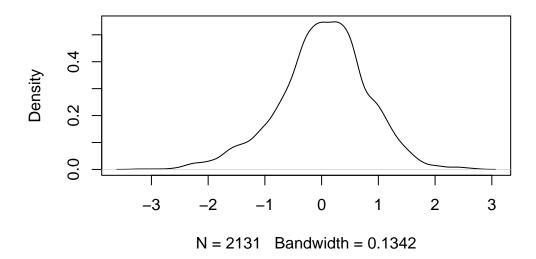
Estimation of the parameters of the Model of subjective well-being (ispired by https://doi.org/10.1073/pnas.

```
# Apply the function process_user() to each user_id.
par_list <- NULL</pre>
results_list <- lapply(user_id_codes, process_user)</pre>
# Bind all data frames together into a single data frame
all_results_df <- bind_rows(results_list)</pre>
# Add mood_pre, mood_post, control.
bysubj_mood_df <- dz_clean |>
    group_by(user_id, ema_number) |>
    summarize(
        mood_pre = mean(mood_pre),
        mood_post = mean(mood_post),
        control = mean(control)
    ) |>
    ungroup()
# Final dataframe.
results_df <- left_join(</pre>
    all_results_df, bysubj_mood_df,
    by = c("user_id", "ema_number")
names(results_df)
```

### **Examine and Clean Parameters**

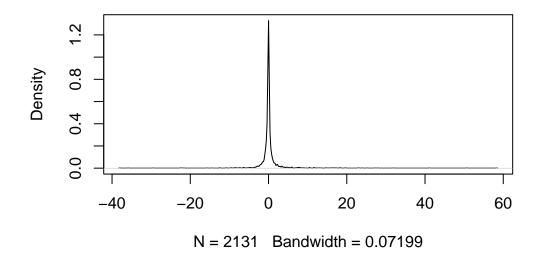
plot(density(results\_df\$w0))

## density(x = results\_df\$w0)



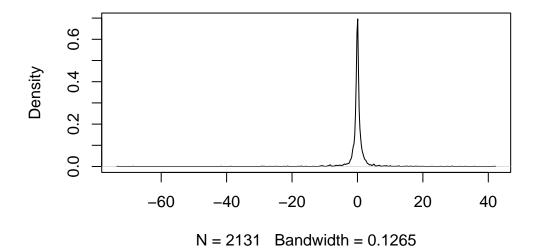
plot(density(results\_df\$w1))

## density(x = results\_df\$w1)

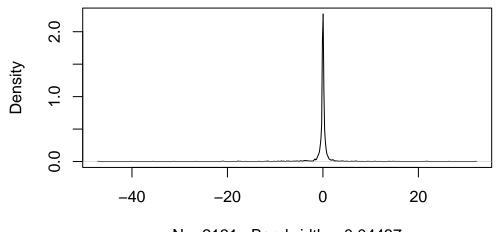


plot(density(results\_df\$w2))

# density(x = results\_df\$w2)



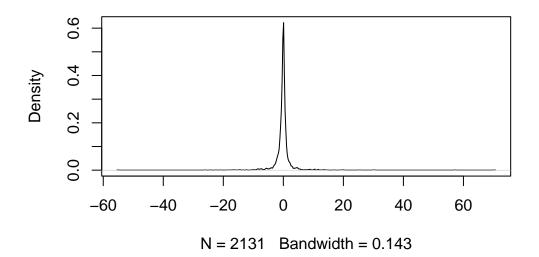
# density(x = results\_df\$w3)



N = 2131 Bandwidth = 0.04437

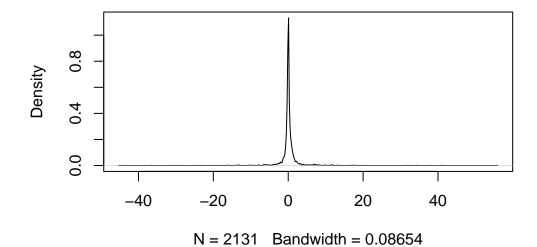
plot(density(results\_df\$w4))

## density(x = results\_df\$w4)

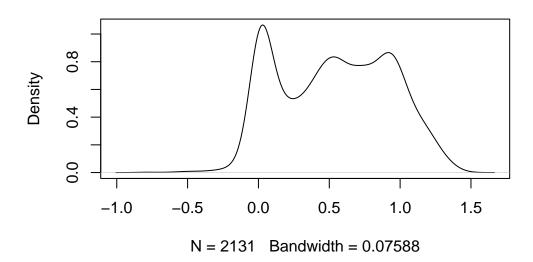


plot(density(results\_df\$w5))

# density(x = results\_df\$w5)

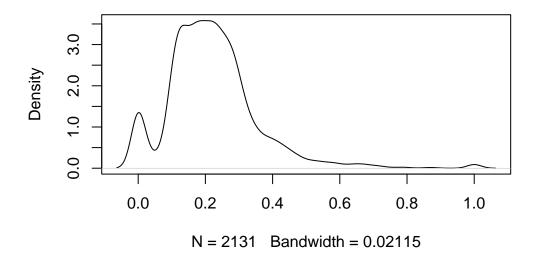


## density(x = results\_df\$gamma)



plot(density(results\_df\$alpha))

### density(x = results\_df\$alpha)



```
remove_outliers <- function(my_vector) {</pre>
    # Calculate mean and standard deviation
    mean_val <- mean(my_vector, na.rm = TRUE)</pre>
    std_dev <- sd(my_vector, na.rm = TRUE)</pre>
    # Calculate Z-scores
    z_scores <- (my_vector - mean_val) / std_dev</pre>
    # Replace outliers with NA
    my_vector[abs(z_scores) > 3.5] <- NA</pre>
    my_vector
}
results_df$cw1 <- remove_outliers(results_df$w1)</pre>
results_df$cw2 <- remove_outliers(results_df$w2)</pre>
results_df$cw3 <- remove_outliers(results_df$w3)</pre>
results_df$cw4 <- remove_outliers(results_df$w4)</pre>
results_df$cw5 <- remove_outliers(results_df$w5)</pre>
results_df$cwg <- remove_outliers(results_df$gamma)</pre>
results_df$cmood_pre <- remove_outliers(results_df$mood_pre)</pre>
results_df$cmood_post <- remove_outliers(results_df$mood_post)</pre>
```

```
# Remove and impute the values alpha = 0 ad alpha = 1
  results_df$calpha <- ifelse(</pre>
    results_df$alpha < 0.00001 | results_df$alpha > 0.99999, NA, results_df$alpha
  # Remove redundant columns
  results_w_df <- results_df |>
      dplyr::select(
         !c(w0, w1, w2, w3, w4, w5, gamma, mood_pre, mood_post, alpha)
      )
Imputation of missing data.
  imputed_cart <- complete(mice(results_w_df, method = "cart"))</pre>
 iter imp variable
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                          cw4
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```

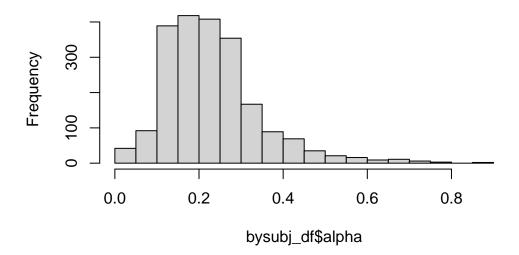
### **Data wrangling**

```
# Difference post - pre on the raw mood data.
bysubj_df <- imputed_cart |>
    mutate(
        # Approximately centered:
        ema_number_c = ema_number - 4,
        # The mood_pre and mood_post outliers have been replaced
        # with NAs and then imputed.
        mood_dif = cmood_post - cmood_pre
    )
bysubj_df_renamed <- dplyr::rename(</pre>
  bysubj_df,
  mood_pre = cmood_pre,
  mood_post = cmood_post,
  alpha = calpha
bysubj_df$environment <- ifelse(</pre>
  bysubj_df$is_reversal == 1, "Volatile", "Stable"
bysubj_df$alpha <- bysubj_df$calpha</pre>
bysubj_df$calpha <- NULL</pre>
```

### **Effect of Environment on Alpha**

```
bysubj_df$alpha |> hist()
```

### Histogram of bysubj\_df\$alpha



```
m <- brm(
    alpha ~ environment +
        (environment | user_id / ema_number),
    family = asym_laplace(),
    algorithm = "meanfield",
    data = bysubj_df,
    refresh = 0
)</pre>
```

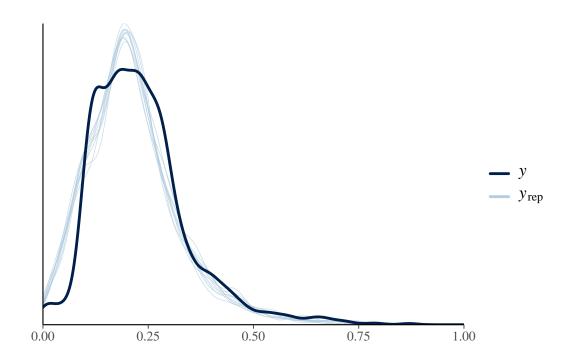
```
Running /Library/Frameworks/R.framework/Resources/bin/R CMD SHLIB foo.c using C compiler: 'Apple clang version 15.0.0 (clang-1500.0.40.1)' using SDK: 'MacOSX14.0.sdk' clang -arch arm64 -I"/Library/Frameworks/R.framework/Resources/include" -DNDEBUG -I"/Library In file included from <br/>
In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/R In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/R In file included from /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/R
```

/Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/namespace Eigen {

/Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/library/RcppEigen/include/Eigen/namespace Eigen {

Using 10 posterior draws for ppc type 'dens\_overlay' by default.

Warning: Removed 552 rows containing non-finite values (`stat\_density()`).



summary(m)

Family: asym\_laplace

Links: mu = identity; sigma = identity; quantile = identity
Formula: alpha ~ environment + (environment | user\_id/ema\_number)

Data: bysubj\_df (Number of observations: 2131)

Draws: 1 chains, each with iter = 1000; warmup = 0; thin = 1;

total post-warmup draws = 1000

#### Group-Level Effects:

~user\_id (Number of levels: 215)

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat
sd(Intercept)	0.00	0.00	0.00	0.00	1.00
<pre>sd(environmentVolatile)</pre>	0.01	0.00	0.01	0.02	1.00
<pre>cor(Intercept,environmentVolatile)</pre>	-0.45	0.13	-0.68	-0.17	1.00
	Bulk_ESS	Tail_ESS			
sd(Intercept)	882	787			
<pre>sd(environmentVolatile)</pre>	937	941			
<pre>cor(Intercept,environmentVolatile)</pre>	921	1026			

~user\_id:ema\_number (Number of levels: 2131)

	Estimate	Est.Error	1-95% CI	u-95% CI Rhat
sd(Intercept)	0.00	0.00	0.00	0.01 1.00
<pre>sd(environmentVolatile)</pre>	0.00	0.00	0.00	0.01 1.00
<pre>cor(Intercept,environmentVolatile)</pre>	-0.05	0.50	-0.89	0.85 1.00
	Bulk_ESS	Tail_ESS		
sd(Intercept)	906	952		
<pre>sd(environmentVolatile)</pre>	1011	903		
<pre>cor(Intercept,environmentVolatile)</pre>	977	981		

#### Population-Level Effects:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	0.09	0.01	0.08	0.10	1.00	975	914
environmentVolatile	0.10	0.01	0.09	0.11	1.00	940	981

### Family Specific Parameters:

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
sigma	0.03	0.00	0.03	0.04	1.00	933	990
quantile	0.36	0.01	0.34	0.37	1.00	770	856

Draws were sampled using variational (meanfield).

bayes\_R2(m)

Estimate Est.Error Q2.5 Q97.5 R2 0.1549301 0.01496497 0.1261506 0.1843055

conditional\_effects(m, "environment")

