Static PID-5 and EMA Self-Compassion

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Le misure "basali" corrispondenti ai 5 domini del PID-5 sono state calcolate **escludendo** i 15 item che vengono usati nelle notifiche EMA.

```
# Read and process 'esi_bf' data
esi_bf <- rio::import(
  here::here(
    "data",
    "processed",
    "esi_bf.csv"
  )
) |>
  dplyr::distinct(user_id, .keep_all = TRUE) |> # Keep only distinct user_id
  dplyr::select(user_id, esi_bf) # Select relevant columns

# Read and process 'pid5' data
pid5 <- rio::import(
  here::here(
    "data",
    "processed",
    "pid5.csv"
  )
) |>
  dplyr::distinct(user_id, .keep_all = TRUE) |>  # Keep only distinct user_id
  dplyr::select(user_id, starts_with("domain_")) # Select domain variables

# Merge 'esi_bf' and 'pid5' data by user_id
df <- left_join(esi_bf, pid5, by = "user_id")

# Define list of user IDs with careless responding
user_id_with_careless_responding <- c(
  "ma_se_2005_11_14_490",
  "reve20041021036",
  "di_ma_2005_10_20_756",
  "pa_sc_2005_09_10_468",
  "il_re_2006_01_18_645",
  "so_ma_2003_10_13_804",
  "lo_ca_2005_05_07_05_437",
  "va_ma_2005_05_31_567",
  "no_un_2005_06_29_880",
  "an_bo_1988_08_24_166",
  "st_ma_2004_04_21_426",
  "an_st_2005_10_16_052",
  "vi_de_2002_12_30_067",
```

```
  "gi_ru_2005_03_08_033",
  "al_mi_2005_03_05_844",
  "la_ma_2006_01_31_787",
  "gi_lo_2004_06_27_237",
  "ch_bi_2001_01_28_407",
  "al_pe_2001_04_20_079",
  "le_de_2003_09_05_067",
  "fe_gr_2002_02_19_434",
  "ma_ba_2002_09_09_052",
  "ca_gi_2003_09_16_737",
  "an_to_2003_08_06_114",
  "al_se_2003_07_28_277",
  "ja_tr_2002_10_06_487",
  "el_ci_2002_02_15_057",
  "se_ti_2000_03_04_975",
  "co_ga_2003_10_29_614",
  "al_ba_2003_18_07_905",
  "bi_ro_2003_09_07_934",
  "an_va_2004_04_08_527",
  "ev_cr_2003_01_27_573"
)

# Filter out users with careless responses
df1 <- df[!(df$user_id %in% user_id_with_careless_responding), ]
```

```
# Read EMA data and rename 'subj_code' to 'user_id'
ema_raw <- readRDS(
  here::here(
    "data",
    "raw",
    "ema",
    "ema_data_scoring.RDS"
  )
) |>
  dplyr::rename(
    user_id = subj_code
  )

# Merge EMA data with filtered main data
df2 <- left_join(df1, ema_raw, by = "user_id")

# Verify number of unique users
length(unique(df2$user_id))
```

```
[1] 429
```

Compliance

Escludiamo i soggetti che hanno risposto a meno di 10 notifiche.

```
# Conta quante risposte EMA ha fornito ciascun soggetto
user_counts <- df2 %>%
  group_by(user_id) %>%
```

```
  summarise(n_responses = n()) %>%
  ungroup()

# Tieni solo i soggetti con almeno 10 risposte
valid_users <- user_counts %>%
  filter(n_responses >= 10) %>%
  pull(user_id)

# Filtra il dataframe originale
df2 <- df2 %>%
  dplyr::filter(user_id %in% valid_users)
```

```
length(unique(df2$user_id))
```

```
[1] 379
```

Generate negative instant mood

```
# Costruisce una misura media dell'affetto negativo momentaneo

# Seleziona solo le colonne rilevanti (per velocità)
items <- c("sad", "angry", "happy", "satisfied")

# Imputa i missing (1 solo imputazione, dato che i NA sono pochi)
imputed <- mice(df2[, items], m = 1, maxit = 10, seed = 123)
```

```

 iter imp variable
  1   1  sad  angry  happy  satisfied
  2   1  sad  angry  happy  satisfied
  3   1  sad  angry  happy  satisfied
  4   1  sad  angry  happy  satisfied
  5   1  sad  angry  happy  satisfied
  6   1  sad  angry  happy  satisfied
  7   1  sad  angry  happy  satisfied
  8   1  sad  angry  happy  satisfied
  9   1  sad  angry  happy  satisfied
  10   1  sad  angry  happy  satisfied
```

```
# Estrai il dataset imputato e sostituisci le colonne originali
df2_imputed <- complete(imputed)
df2[, items] <- df2_imputed[, items]

df2 <- df2 %>%
  mutate(
    happy_reversed = 100 - happy, # Scala 0-100
    satisfied_reversed = 100 - satisfied,
    neg_aff_ema = rowMeans(
      cbind(sad, angry, happy_reversed, satisfied_reversed),
      na.rm = TRUE
    )
  )
```

Self-compassion negativa

Consideriamo solo le notifiche dove Self-Compassion è stata misurata.

```
df_self_comp_ema <- df2 %>%
  dplyr::filter(!is.na(ucs_neg) & !is.na(cs_pos))

length(unique(df_self_comp_ema$user_id))
```

```
[1] 379
```

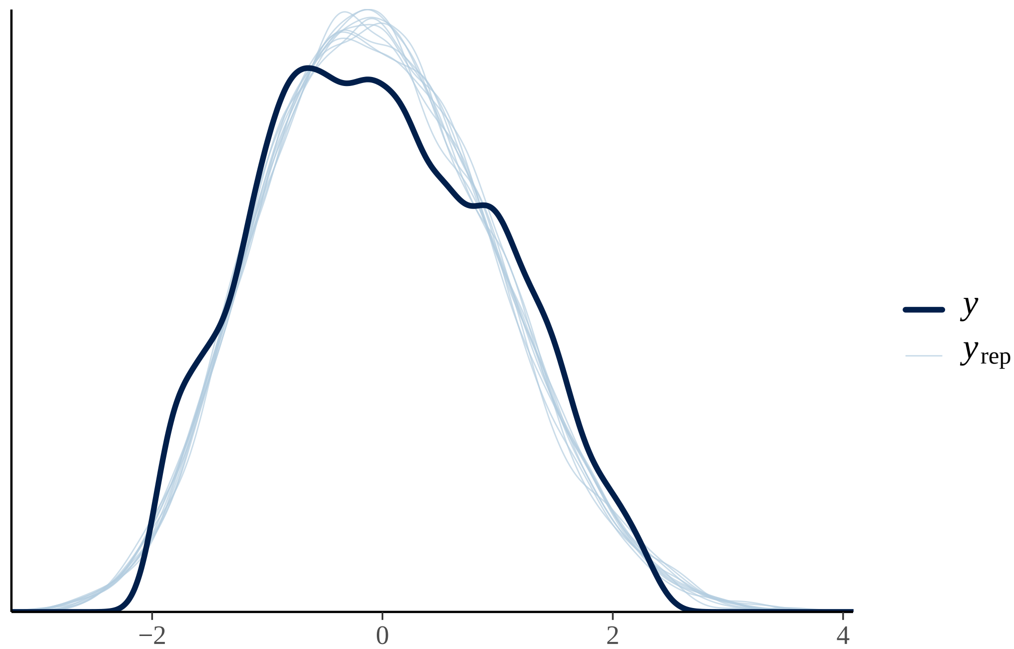
```
dim(df_self_comp_ema)
```

```
[1] 6229   92
```

```
df_self_comp_ema_scaled <- df_self_comp_ema %>%
  dplyr::select(
    ucs_neg,
    domain_negative_affect,
    domain_detachment,
    domain_antagonism,
    domain_disinhibition,
    domain_psychoticism,
    neg_aff_ema,
    pid5_negative_affectivity,
    pid5_detachment,
    pid5_antagonism,
    pid5_disinhibition,
    pid5_psychoticism,
    user_id # Mantiene user_id così com'è
  ) %>%
  dplyr::mutate(
    # Applica la standardizzazione (scale) a tutte le colonne selezionate
    # tranne user_id. as.vector() è usato per assicurare che l'output sia un vettore.
    dplyr::across(
      c(
        ucs_neg,
        neg_aff_ema,
        domain_negative_affect,
        domain_detachment,
        domain_antagonism,
        domain_disinhibition,
        domain_psychoticism,
        pid5_negative_affectivity,
        pid5_detachment,
        pid5_antagonism,
        pid5_disinhibition,
        pid5_psychoticism
      ),
      ~ as.vector(scale(.))
    )
  )

model_base <- brm(
  ucs_neg ~ 1 +
```

```
    domain_negative_affect + domain_detachment +
    domain_antagonism + domain_disinhibition + domain_psychoticism +
    (1 + neg_aff_ema | user_id),
  data = df_self_comp_ema_scaled,
  family = skew_normal(),
  prior = c(
    prior(normal(0, 1), class = "Intercept"),
    prior(normal(0, 1), class = "b"),
    prior(exponential(1), class = "sd"),
    prior(exponential(1), class = "sigma")
  ),
  chains = 4,
  cores = 4,
  iter = 2000,
  seed = 123,
  backend = "cmdstanr",
  save_pars = save_pars(all = TRUE)
)

# Posterior predictive check for the baseline model
pp_check(model_base)
```

```
Using 10 posterior draws for ppc type 'dens_overlay' by default.
```




```
print(model_base)
```

```
 Family: skew_normal
  Links: mu = identity; sigma = identity; alpha = identity
Formula: ucs_neg ~ 1 + domain_negative_affect + domain_detachment + domain_antagonism + doma
   Data: df_self_comp_ema_scaled (Number of observations: 5757)
  Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup draws = 4000

Multilevel Hyperparameters:
```

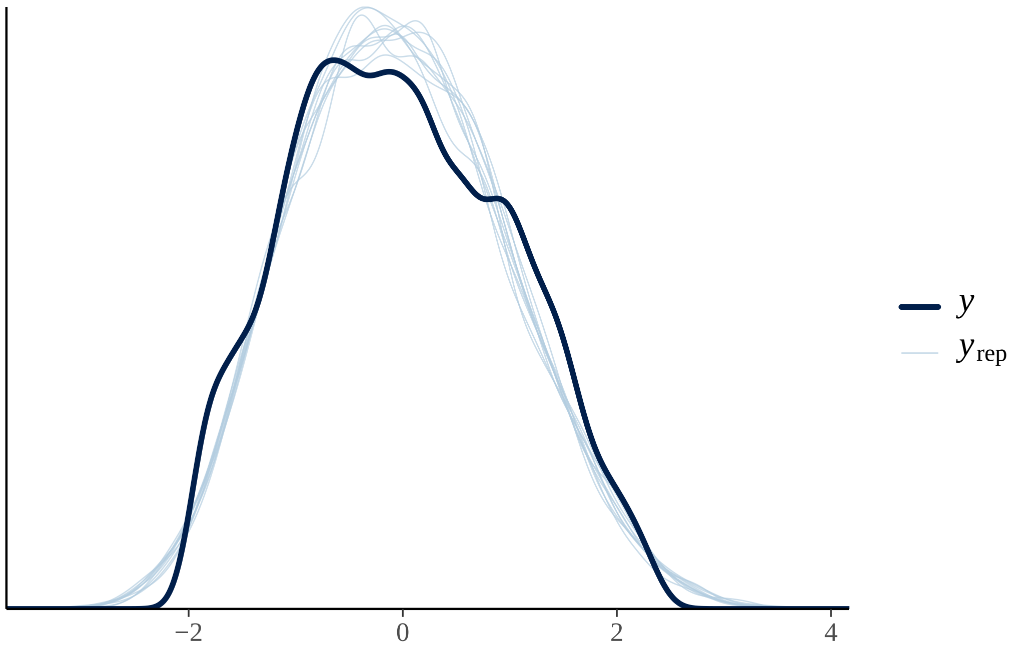
```
~user_id (Number of levels: 350)
                             Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
sd(Intercept)                    0.55      0.02     0.50     0.60 1.00      699
sd(neg_aff_ema)                  0.42      0.02     0.38     0.46 1.00     1135
cor(Intercept,neg_aff_ema)       0.24      0.09     0.06     0.42 1.03      176
                             Tail_ESS
sd(Intercept)                    1109
sd(neg_aff_ema)                  1739
cor(Intercept,neg_aff_ema)        386

Regression Coefficients:
                         Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
Intercept                   -0.13      0.05    -0.22    -0.04 1.04      157
domain_negative_affect       0.32      0.04     0.25     0.40 1.01      318
domain_detachment            0.06      0.03    -0.01     0.13 1.00      649
domain_antagonism           -0.00      0.03    -0.07     0.07 1.01      417
domain_disinhibition         0.09      0.04     0.02     0.17 1.01      503
domain_psychoticism          0.02      0.04    -0.06     0.10 1.01      595
                         Tail_ESS
Intercept                     285
domain_negative_affect        924
domain_detachment            1150
domain_antagonism             535
domain_disinhibition          791
domain_psychoticism          1100

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     0.57      0.01     0.56     0.59 1.00     4255     2986
alpha     1.39      0.11     1.17     1.62 1.00     3270     3077

Draws were sampled using sample(hmc). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
# Fit augmented Bayesian model with interaction effects
model_alt <- brm(
  ucs_neg ~
    domain_negative_affect * pid5_negative_affectivity +
    domain_detachment * pid5_detachment +
    domain_antagonism * pid5_antagonism +
    domain_disinhibition * pid5_disinhibition +
    domain_psychoticism * pid5_psychoticism +
    (1 + pid5_negative_affectivity + pid5_detachment + pid5_antagonism +
       pid5_disinhibition + pid5_psychoticism | user_id),
  data = df_self_comp_ema_scaled,
  family = skew_normal(),
  prior = c(
    prior(normal(0, 1), class = "Intercept"),
    prior(normal(0, 1), class = "b"),
    prior(exponential(1), class = "sd"),
    prior(exponential(1), class = "sigma")
```

```r
  ),
  chains = 4,
  cores = 4,
  iter = 2000,
  # seed = 123,
  backend = "cmdstanr",
  save_pars = save_pars(all = TRUE)
)
```

```r
pp_check(model_alt)
```

```
Using 10 posterior draws for ppc type 'dens_overlay' by default.
```




```r
print(model_alt)
```

```
Warning: There were 2 divergent transitions after warmup. Increasing
adapt_delta above 0.8 may help. See
http://mc-stan.org/misc/warnings.html#divergent-transitions-after-warmup
```

```
 Family: skew_normal
  Links: mu = identity; sigma = identity; alpha = identity
Formula: ucs_neg ~ domain_negative_affect * pid5_negative_affectivity + domain_detachment *
   Data: df_self_comp_ema_scaled (Number of observations: 5757)
  Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup draws = 4000

Multilevel Hyperparameters:
~user_id (Number of levels: 350)
                                                  Estimate Est.Error l-95% CI
sd(Intercept)                                         0.38      0.02     0.35
sd(pid5_negative_affectivity)                         0.15      0.02     0.12
sd(pid5_detachment)                                   0.13      0.02     0.08
sd(pid5_antagonism)                                   0.11      0.02     0.06
sd(pid5_disinhibition)                                0.14      0.02     0.11
```

```
sd(pid5_psychoticism)                                 0.07      0.03     0.01
cor(Intercept,pid5_negative_affectivity)              0.18      0.11    -0.04
cor(Intercept,pid5_detachment)                       -0.09      0.13    -0.34
cor(pid5_negative_affectivity,pid5_detachment)       -0.08      0.19    -0.43
cor(Intercept,pid5_antagonism)                       -0.09      0.14    -0.35
cor(pid5_negative_affectivity,pid5_antagonism)        0.45      0.19     0.04
cor(pid5_detachment,pid5_antagonism)                 -0.14      0.25    -0.58
cor(Intercept,pid5_disinhibition)                    -0.06      0.11    -0.26
cor(pid5_negative_affectivity,pid5_disinhibition)    -0.18      0.16    -0.47
cor(pid5_detachment,pid5_disinhibition)              -0.28      0.20    -0.63
cor(pid5_antagonism,pid5_disinhibition)              -0.30      0.20    -0.68
cor(Intercept,pid5_psychoticism)                     -0.24      0.23    -0.64
cor(pid5_negative_affectivity,pid5_psychoticism)     -0.32      0.27    -0.76
cor(pid5_detachment,pid5_psychoticism)               -0.14      0.31    -0.70
cor(pid5_antagonism,pid5_psychoticism)                0.19      0.29    -0.43
cor(pid5_disinhibition,pid5_psychoticism)             0.04      0.28    -0.50
                                                  u-95% CI Rhat Bulk_ESS
sd(Intercept)                                         0.42 1.00     1393
sd(pid5_negative_affectivity)                         0.19 1.00     1315
sd(pid5_detachment)                                   0.17 1.01      686
sd(pid5_antagonism)                                   0.15 1.00      642
sd(pid5_disinhibition)                                0.17 1.00     1115
sd(pid5_psychoticism)                                 0.13 1.01      368
cor(Intercept,pid5_negative_affectivity)              0.39 1.00     2118
cor(Intercept,pid5_detachment)                        0.16 1.00     2510
cor(pid5_negative_affectivity,pid5_detachment)        0.31 1.00     1021
cor(Intercept,pid5_antagonism)                        0.19 1.00     2454
cor(pid5_negative_affectivity,pid5_antagonism)        0.79 1.00     1009
cor(pid5_detachment,pid5_antagonism)                  0.38 1.01      637
cor(Intercept,pid5_disinhibition)                     0.16 1.00     2726
cor(pid5_negative_affectivity,pid5_disinhibition)     0.16 1.00      938
cor(pid5_detachment,pid5_disinhibition)               0.14 1.01      452
cor(pid5_antagonism,pid5_disinhibition)               0.11 1.01      453
cor(Intercept,pid5_psychoticism)                      0.29 1.00     2807
cor(pid5_negative_affectivity,pid5_psychoticism)      0.31 1.00     1545
cor(pid5_detachment,pid5_psychoticism)                0.51 1.00     1061
cor(pid5_antagonism,pid5_psychoticism)                0.73 1.00     1313
cor(pid5_disinhibition,pid5_psychoticism)             0.58 1.00     1839
                                                  Tail_ESS
sd(Intercept)                                         2602
sd(pid5_negative_affectivity)                         2326
sd(pid5_detachment)                                    763
sd(pid5_antagonism)                                    838
sd(pid5_disinhibition)                                2449
sd(pid5_psychoticism)                                  990
cor(Intercept,pid5_negative_affectivity)              2690
cor(Intercept,pid5_detachment)                        2803
cor(pid5_negative_affectivity,pid5_detachment)        1378
cor(Intercept,pid5_antagonism)                        2685
cor(pid5_negative_affectivity,pid5_antagonism)        1768
cor(pid5_detachment,pid5_antagonism)                  1441
```

```
cor(Intercept,pid5_disinhibition)                          2861
cor(pid5_negative_affectivity,pid5_disinhibition)          1608
cor(pid5_detachment,pid5_disinhibition)                     742
cor(pid5_antagonism,pid5_disinhibition)                    1132
cor(Intercept,pid5_psychoticism)                           1836
cor(pid5_negative_affectivity,pid5_psychoticism)           2095
cor(pid5_detachment,pid5_psychoticism)                     1877
cor(pid5_antagonism,pid5_psychoticism)                     2077
cor(pid5_disinhibition,pid5_psychoticism)                  2895

Regression Coefficients:
                                                  Estimate Est.Error l-95% CI
Intercept                                            -0.02      0.03    -0.06
domain_negative_affect                                0.23      0.03     0.17
pid5_negative_affectivity                             0.34      0.02     0.31
domain_detachment                                     0.03      0.03    -0.02
pid5_detachment                                       0.21      0.02     0.18
domain_antagonism                                     0.02      0.03    -0.03
pid5_antagonism                                      -0.11      0.02    -0.14
domain_disinhibition                                  0.03      0.03    -0.03
pid5_disinhibition                                    0.19      0.01     0.16
domain_psychoticism                                  -0.04      0.03    -0.11
pid5_psychoticism                                     0.02      0.02    -0.01
domain_negative_affect:pid5_negative_affectivity      0.06      0.01     0.04
domain_detachment:pid5_detachment                    -0.01      0.01    -0.04
domain_antagonism:pid5_antagonism                     0.01      0.01    -0.01
domain_disinhibition:pid5_disinhibition              -0.02      0.01    -0.04
domain_psychoticism:pid5_psychoticism                -0.01      0.01    -0.04
                                                  u-95% CI Rhat Bulk_ESS
Intercept                                             0.03 1.00     1605
domain_negative_affect                                0.28 1.00     1363
pid5_negative_affectivity                             0.37 1.00     3982
domain_detachment                                     0.08 1.00     1917
pid5_detachment                                       0.24 1.00     3938
domain_antagonism                                     0.08 1.00     1649
pid5_antagonism                                      -0.08 1.00     4286
domain_disinhibition                                  0.09 1.00     1418
pid5_disinhibition                                    0.22 1.00     4528
domain_psychoticism                                   0.02 1.00     1291
pid5_psychoticism                                     0.05 1.00     3686
domain_negative_affect:pid5_negative_affectivity      0.09 1.00     4054
domain_detachment:pid5_detachment                     0.01 1.00     3884
domain_antagonism:pid5_antagonism                     0.04 1.00     3657
domain_disinhibition:pid5_disinhibition               0.01 1.00     3206
domain_psychoticism:pid5_psychoticism                 0.01 1.00     3959
                                                  Tail_ESS
Intercept                                             2312
domain_negative_affect                                1717
pid5_negative_affectivity                             3299
domain_detachment                                     2205
pid5_detachment                                       2932
```

```
domain_antagonism                                    2178
pid5_antagonism                                      3088
domain_disinhibition                                 2600
pid5_disinhibition                                   3066
domain_psychoticism                                  1796
pid5_psychoticism                                    2996
domain_negative_affect:pid5_negative_affectivity     3218
domain_detachment:pid5_detachment                    2666
domain_antagonism:pid5_antagonism                    2675
domain_disinhibition:pid5_disinhibition              2869
domain_psychoticism:pid5_psychoticism                3051

Further Distributional Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma     0.53      0.01     0.52     0.54 1.00     2675     2890
alpha     1.45      0.12     1.20     1.69 1.00     3844     2913

Draws were sampled using sample(hmc). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
loo0 <- loo(model_base, save_psis = TRUE)
```

```
Warning: Found 24 observations with a pareto_k > 0.7 in model 'model_base'. We
recommend to set 'moment_match = TRUE' in order to perform moment matching for
problematic observations.
```

```
loo1 <- loo(model_alt, save_psis = TRUE)
```

```
Warning: Found 20 observations with a pareto_k > 0.7 in model 'model_alt'. We
recommend to set 'moment_match = TRUE' in order to perform moment matching for
problematic observations.
```

```
loo_compare(loo0, loo1)
```

```
           elpd_diff se_diff
model_alt     0.0       0.0
model_base -416.8      55.7
```

Visualizzare ELPD_diff

Visualizzare dove il modello alternativo (model_alt) migliora la predizione rispetto al modello di base (model_base), a livello di soggetto.

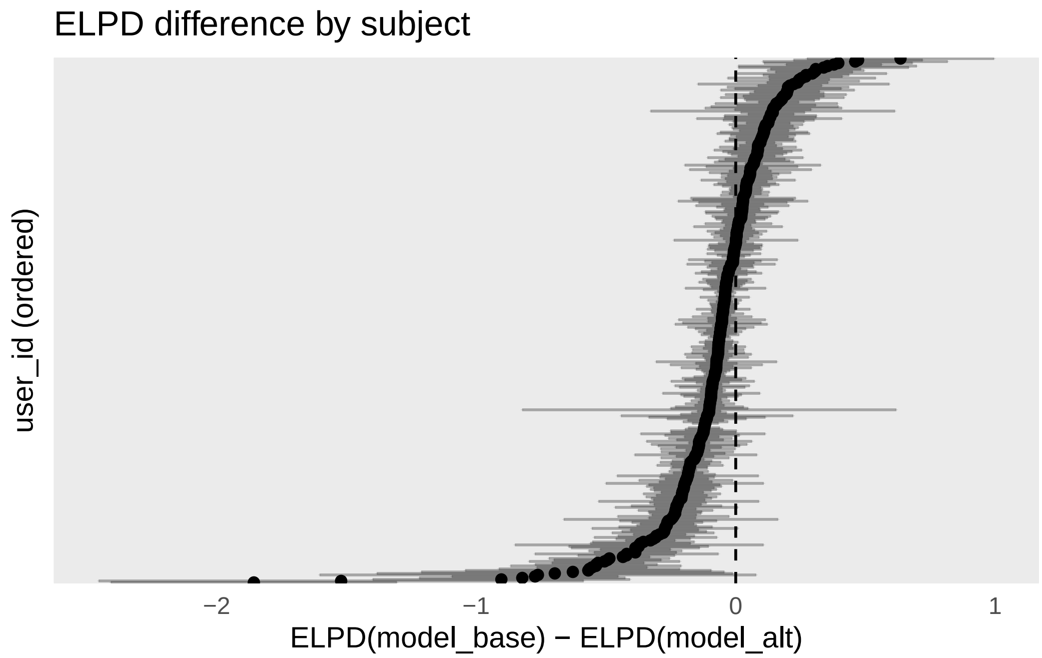
```
# Differenza pointwise tra i due modelli
elpd_diff <- loo0$pointwise[, "elpd_loo"] - loo1$pointwise[, "elpd_loo"]
```

```
# Recupera i dati usati nel modello
model_data <- model_base$data

# Aggiungi la colonna con la differenza di ELPD
model_data$elpd_diff <- elpd_diff
```

```
subject_diffs <- model_data %>%
  group_by(user_id) %>%
  summarise(
```

```
    mean_elpd_diff = mean(elpd_diff, na.rm = TRUE),
    se = sd(elpd_diff, na.rm = TRUE) / sqrt(n())
  ) %>%
  arrange(mean_elpd_diff)
```

```
ggplot(subject_diffs, aes(x = reorder(user_id, mean_elpd_diff), y = mean_elpd_diff)) +
  geom_point() +
  geom_errorbar(aes(ymin = mean_elpd_diff - se, ymax = mean_elpd_diff + se),
                width = 0.2, alpha = 0.3) +
  geom_hline(yintercept = 0, linetype = "dashed") +
  coord_flip() +
  labs(title = "ELPD difference by subject",
       x = "user_id (ordered)",
       y = "ELPD(model_base) - ELPD(model_alt)") +
  theme_minimal() +
  scale_x_discrete(labels = NULL)
```



Ogni punto rappresenta un soggetto. L'asse y mostra la differenza di ELPD tra i modelli: ELPD_base − ELPD_alt. I valori sotto lo zero indicano che il modello alternativo predice meglio per quel soggetto. Le barre di errore indicano l'incertezza (errore standard) per ciascun soggetto. Nel caso presente, dato il valore complessivo di elpd_diff = -466, ci aspettiamo che la maggior parte dei soggetti abbia valori negativi.

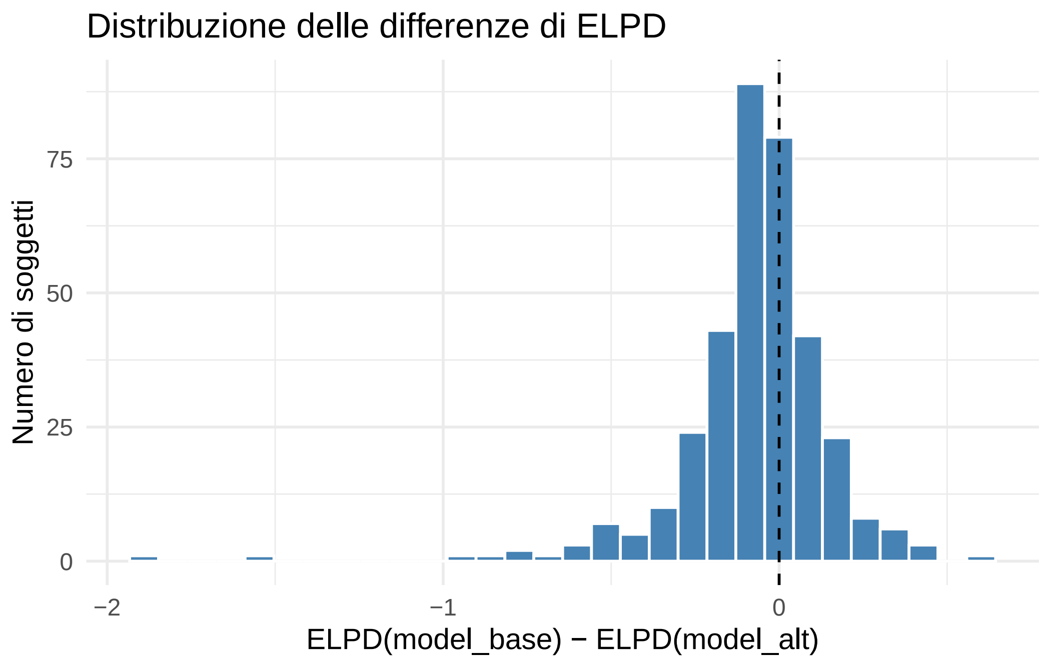
```
subject_diffs %>%
  summarise(
    n = n(),
    n_better_alt = sum(mean_elpd_diff < 0),
    proportion = n_better_alt / n,
    percent = proportion * 100
  )
```

```
# A tibble: 1 x 4
      n n_better_alt proportion percent
  <int>        <int>      <dbl>   <dbl>
```

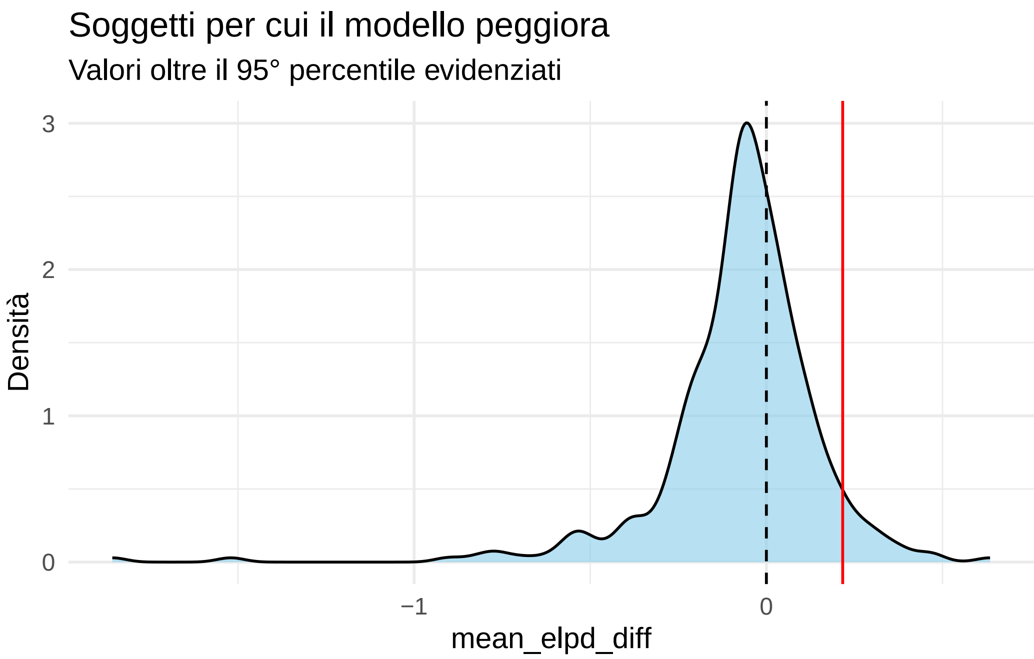
```
1    350           226       0.646     64.6
```

Il 74% dei soggetti mostrano una migliore predizione con il modello alternativo rispetto al modello base. La preferenza per model_alt è quindi generalizzata, non guidata da pochi individui.

```
ggplot(subject_diffs, aes(x = mean_elpd_diff)) +
  geom_histogram(bins = 30, fill = "steelblue", color = "white") +
  geom_vline(xintercept = 0, linetype = "dashed") +
  labs(
    title = "Distribuzione delle differenze di ELPD",
    x = "ELPD(model_base) - ELPD(model_alt)",
    y = "Numero di soggetti"
  ) +
  theme_minimal()
```




```
ggplot(subject_diffs, aes(x = mean_elpd_diff)) +
  geom_density(fill = "skyblue", alpha = 0.6) +
  geom_vline(xintercept = 0, linetype = "dashed") +
  geom_vline(xintercept = quantile(subject_diffs$mean_elpd_diff, 0.95), color = "red") +
  labs(title = "Soggetti per cui il modello peggiora",
       subtitle = "Valori oltre il 95° percentile evidenziati",
       x = "mean_elpd_diff", y = "Densità") +
  theme_minimal()
```




```
bayes_R2(model_base)
```

```
    Estimate   Est.Error      Q2.5     Q97.5
R2 0.6737426 0.004556891 0.6645596 0.6823755
```

```
bayes_R2(model_alt)
```

```
    Estimate   Est.Error      Q2.5     Q97.5
R2 0.7216953 0.004324445 0.7131141 0.7298307
```

```
# K-fold cross-validation (e.g., 10 folds)
# kfold_base <- kfold(model_base, K = 5, seed = 123)
# kfold_alt  <- kfold(model_alt,  K = 5, seed = 123)
# kfold_compare(kfold_base, kfold_alt)
# Se elpd_diff è negativo per model_base, vuol dire che model_alt predice meglio
# anche in validazione k-fold.
```

```
subject_diffs <- subject_diffs %>%
  mutate(benefit_score = scale(-mean_elpd_diff))
# valori alti = miglioramento maggiore
subject_diffs
```

```
# A tibble: 350 x 4
   user_id                mean_elpd_diff    se benefit_score[,1]
   <chr>                           <dbl> <dbl>             <dbl>
 1 so_li_2004_10_29_776           -1.86  0.551              7.71
 2 ch_va_2003_04_08_010           -1.52  0.935              6.25
 3 el_ca_2003_06_14_053           -0.903 0.496              3.59
 4 ca_fo_2002_08_30_071           -0.822 0.397              3.24
 5 el_bu_2003_09_24_545           -0.773 0.321              3.02
 6 mi_lo_2005_03_17_960           -0.762 0.841              2.98
 7 an_gr_2003_02_23_266           -0.697 0.686              2.70
 8 gi_ma_2004_01_10_447           -0.628 0.584              2.40
 9 ir_mo_2005_02_23_157           -0.568 0.475              2.14
10 al_ne_2005_11_07_247           -0.564 0.349              2.12
```

```
# i 340 more rows
```

Discussione dei risultati: impatto delle misure dinamiche sui modelli predittivi

L'obiettivo principale di questa analisi era valutare se l'integrazione delle **misure dinamiche dei tratti disadattivi di personalità** (ovvero, le valutazioni settimanali del PID-5 tramite EMA) migliorasse la capacità di prevedere l'intensità della **self-compassion negativa** in risposta ad affetti negativi momentanei.

Per testare questa ipotesi, abbiamo confrontato due modelli:

- un **modello base**, in cui la self-compassion negativa (UCS) era spiegata da indicatori EMA dell'affetto negativo e dai tratti PID-5 valutati una sola volta all'inizio dello studio;
- un **modello alternativo**, in cui gli stessi predittori interagivano con le **misure EMA dei cinque domini PID-5**, raccolte in parallelo ai dati di affetto negativo.

I risultati dell'analisi bayesiana con confronto via ELPD (Expected Log Predictive Density) indicano un chiaro miglioramento nella predizione per il modello che include le **interazioni con i tratti EMA**. In particolare, la differenza complessiva di ELPD tra i modelli è di **ΔELPD = -466**, a favore del modello alternativo. Questo effetto non è guidato da pochi casi estremi: in oltre il **74% dei soggetti**, il modello con i tratti EMA ha fornito predizioni migliori, e la distribuzione soggetto-specifica delle differenze di ELPD è fortemente sbilanciata a favore del modello dinamico.

Anche la **varianza spiegata a posteriori (Bayes R^2)** è maggiore nel modello alternativo (R^2 = 0.52 vs. 0.41), suggerendo che la variabilità intra-individuale nei tratti di personalità è un moderatore cruciale della reattività affettiva momentanea.

Dal punto di vista teorico, questi risultati forniscono supporto all'ipotesi che la relazione tra affetto negativo e self-compassion negativa non sia una funzione stabile e fissa, ma **una funzione modulata dai tratti di personalità così come si esprimono nel momento**. L'uso delle misure EMA del PID-5 cattura queste **fluttuazioni disposizionali contestuali**, che non sono accessibili tramite la sola somministrazione statica del PID-5 a inizio studio.

In linea con un approccio **idionomico**, che mira a comprendere il funzionamento individuale nel suo contesto situato, l'evidenza raccolta suggerisce che **combinare misure di stato (affetto negativo momentaneo) con misure di tratto dinamiche (PID-5 EMA)** permette una modellazione più sensibile delle vulnerabilità psicopatologiche. Questi risultati rafforzano l'idea che le valutazioni EMA non siano semplicemente misure rumorose, ma rappresentino un valore aggiunto per comprendere **quando** e **per chi** si attivano risposte maladattive, come la self-compassion negativa.