Data prep script 3: Importing and combining ERP data $$^{\rm Template\ Rmd}$$

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About

This script filter and scores the self-report data from BUDS study: Bullying, Unsupportive family/peers, Discrimination, and Social feedback study using data from PREDICT project collaboration between Northwestern (PI: Shankman) and Columbia (PI: Auerbach).

Get Setup

Clear everything & set width

```
knitr::opts_chunk$set(set.seed(312), echo=TRUE, results='hide', message=FALSE)

options(width=80) #Set width
rm(list=ls()) #Remove everything from environment
cat("\014") #Clear Console
```

Load Libraries

Get the Working Directory

Load data

ADI

Import Area Deprivation Index data

A note on the ADI: "Why are some block groups missing ADI ranks? When a Census Block Group falls into one or more of the suppression criteria mentioned above the ADI rank is replaced with a code describing the suppression reason. Three possible codes will appear in the ADI field: PH for suppression due to low population and/or housing, GQ for suppression due to a high group quarters population, and PH-GQ for suppression due to both types of suppression criteria. A code of KVM designates block groups without an ADI due to Key Missing Variables, stemming from missing data in the source ACS data." https://www.neighborhoodatlas.medicine.wisc.edu/#faq-anchor

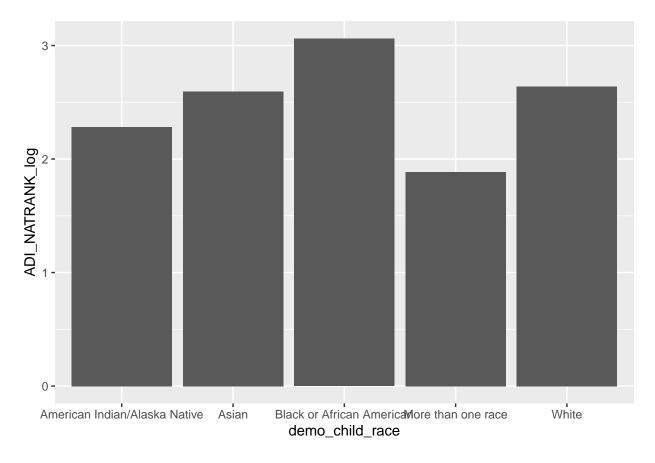
N = are missing data due to one of these fields, and an additional are missing data due to bad addresses.

Compute grand average by ADI median split

Compute scalp topography by ADI median split

Race/Ethnicity and ADI

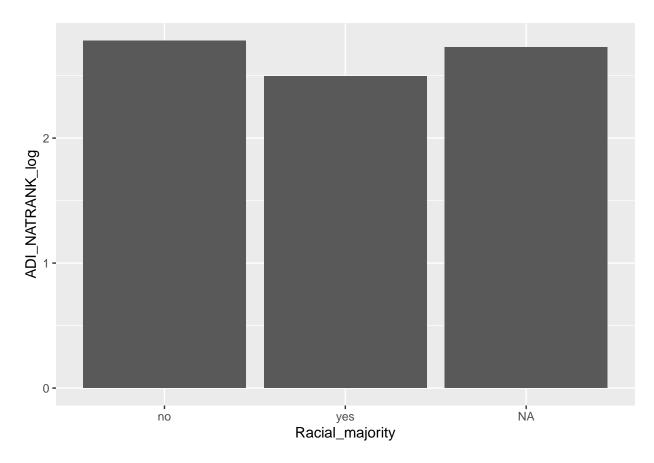
```
anova(lm(formula = ADI_NATRANK_log ~ Racial_minority, data =df_250450_fz))
anova(lm(formula = ADI_NATRANK_log ~ Racial_majority, data =df_250450_fz))
anova(lm(formula = ADI_NATRANK_log ~ demo_child_hispanic, data =df_250450_fz))
anova(lm(formula = ADI_NATRANK_log ~ demo_child_race, data =df_250450_fz))
anova(lm(formula = ADI_NATRANK_log ~ demo_child_race, data = filter(df_250450_fz, demo_child_race=="Whi
              demo child race=="Asian" |
              demo child race=="American Indian/Alaska Native" |
              demo_child_race=="Black or African American" |
              demo_child_race=="More than one race")))
ggplot(filter(df_250450_fz, demo_child_race=="White" |
              demo_child_race=="Asian" |
              demo_child_race=="American Indian/Alaska Native" |
              demo_child_race=="Black or African American" |
              demo_child_race=="More than one race"), aes(x=demo_child_race, y=ADI_NATRANK_log)) +
  geom_bar(stat = "summary", fun.y = "median")
## Warning in geom_bar(stat = "summary", fun.y = "median"): Ignoring unknown
## parameters: 'fun.y'
## Warning: Removed 38 rows containing non-finite values ('stat_summary()').
```



```
ggplot(df_250450_fz, aes(x=Racial_majority, y=ADI_NATRANK_log)) +
  geom_bar(stat = "summary", fun.y = "median")
```

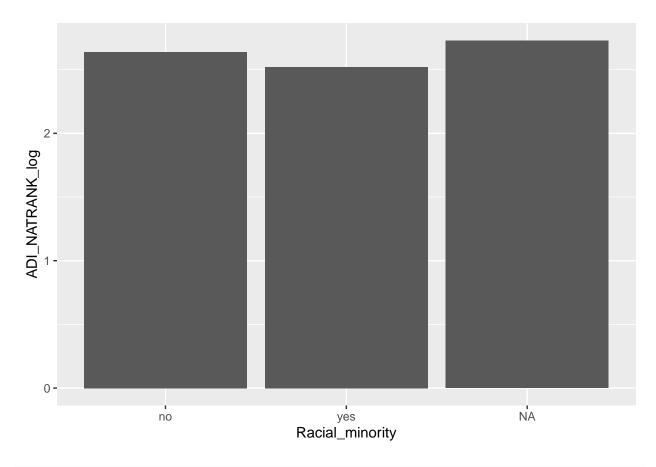
Warning in geom_bar(stat = "summary", fun.y = "median"): Ignoring unknown
parameters: 'fun.y'

Warning: Removed 48 rows containing non-finite values ('stat_summary()').



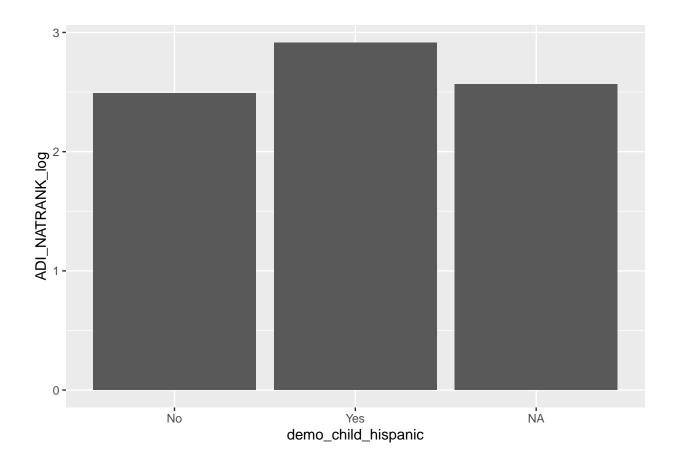
```
ggplot(df_250450_fz, aes(x=Racial_minority, y=ADI_NATRANK_log)) +
geom_bar(stat = "summary", fun.y = "median")
```

Warning in geom_bar(stat = "summary", fun.y = "median"): Ignoring unknown parameters: 'fun.y'
Removed 48 rows containing non-finite values ('stat_summary()').



```
ggplot(df_250450_fz, aes(x=demo_child_hispanic, y=ADI_NATRANK_log)) +
geom_bar(stat = "summary", fun.y = "median")
```

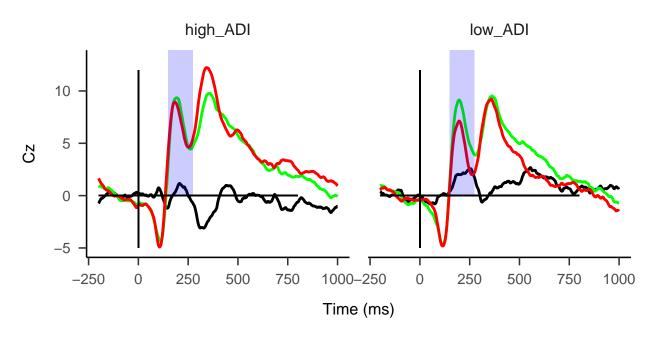
Warning in geom_bar(stat = "summary", fun.y = "median"): Ignoring unknown parameters: 'fun.y'
Removed 48 rows containing non-finite values ('stat_summary()').



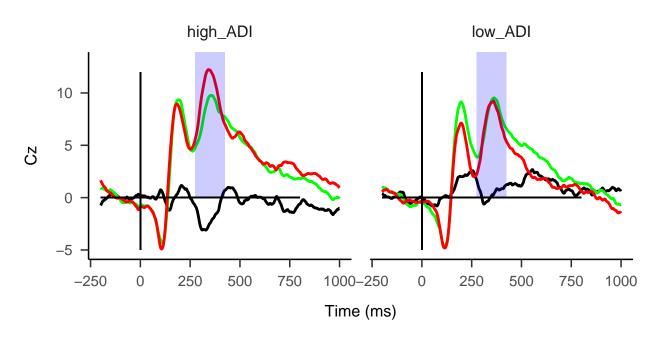
Plots

Grand average



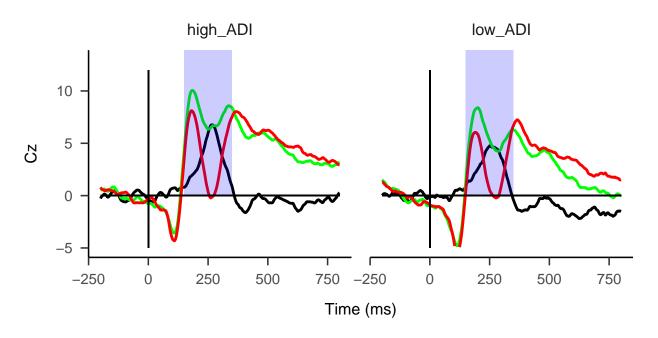




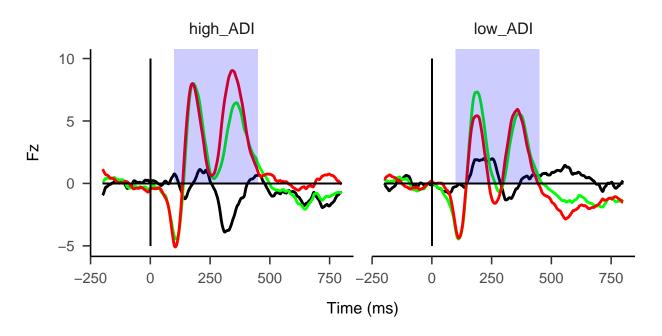


Low value peers



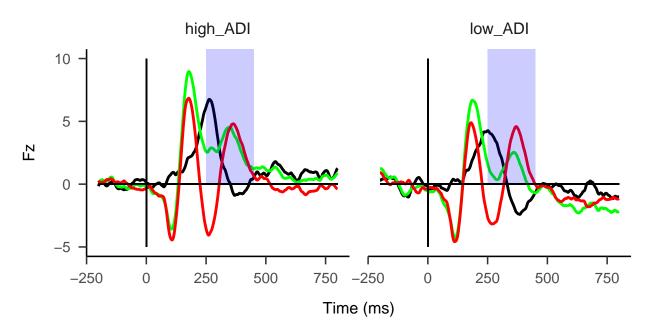




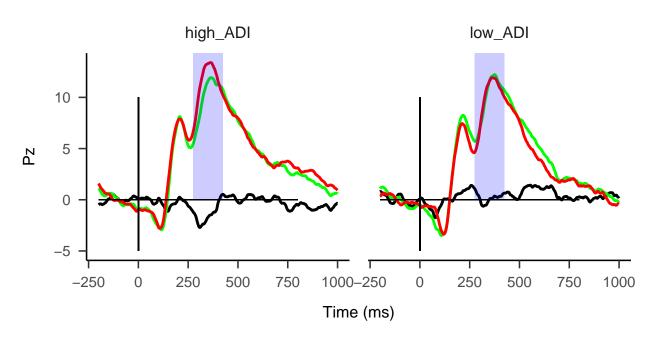


Low value peers

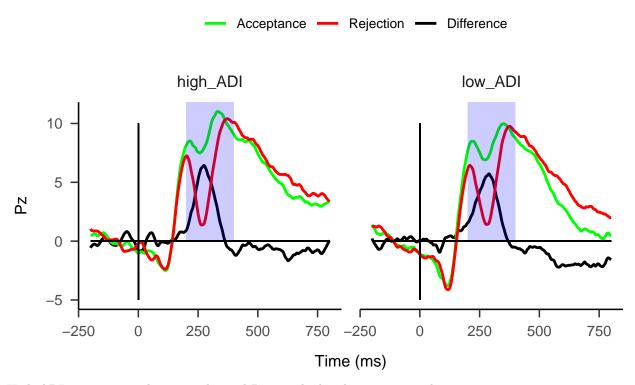








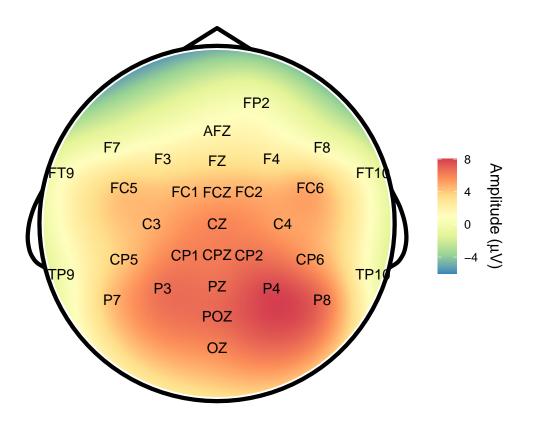
Low value peers



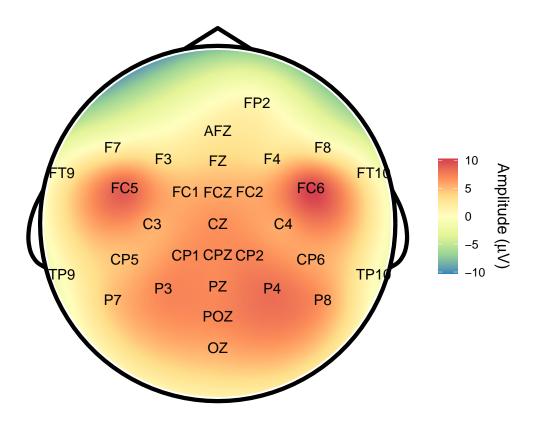
High ADI participants show an enhanced P300 to high value rejection relative to acceptance.

Plot scalp topographies

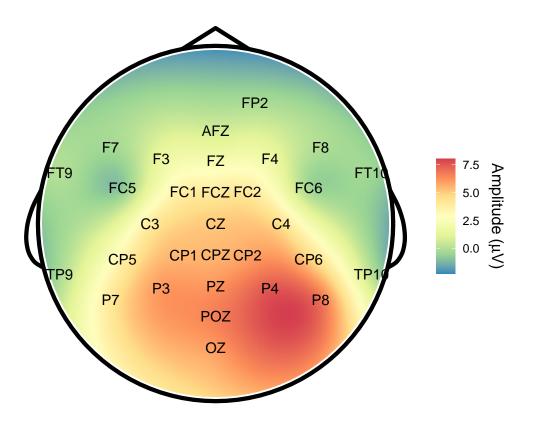
topoplot(eeg.map_for_plotting_adi_150350, palette="Spectral", chanLocs=chanlocs, contour=FALSE, interp_

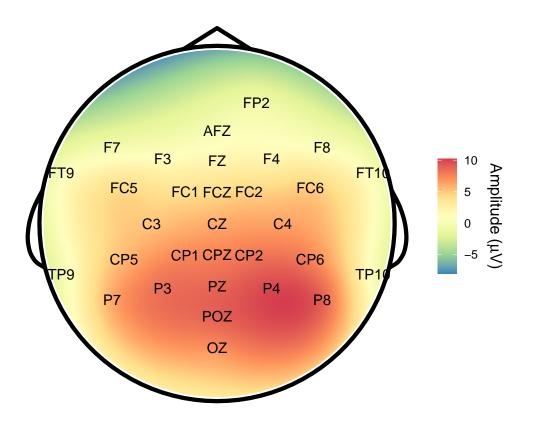


topoplot(filter(eeg.map_for_plotting_adi_150350, adi_median_split=="high_ADI"), palette="Spectral", charge

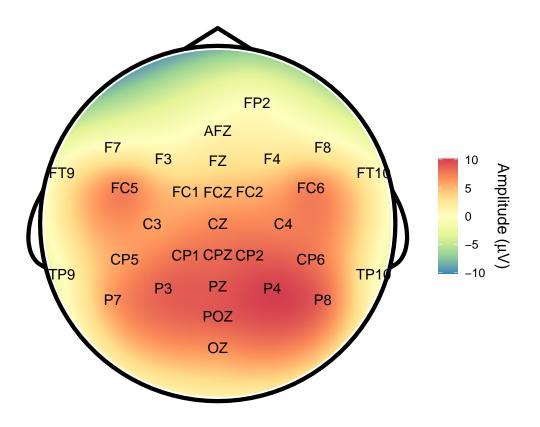


topoplot(filter(eeg.map_for_plotting_adi_150350, adi_median_split=="low_ADI"), palette="Spectral", chan

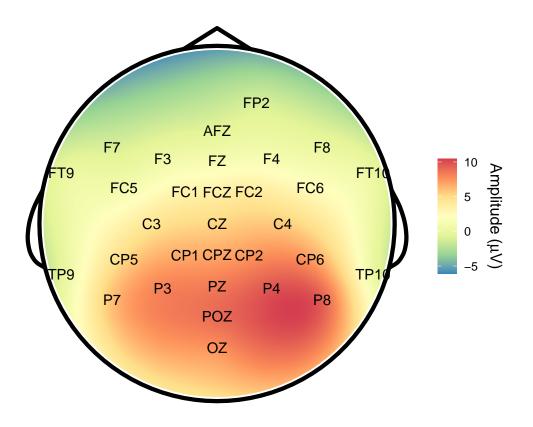




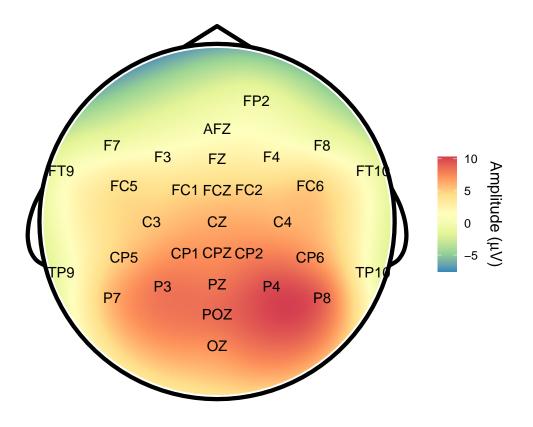
topoplot(filter(eeg.map_for_plotting_adi_250500, adi_median_split=="high_ADI"), palette="Spectral", characteristics."



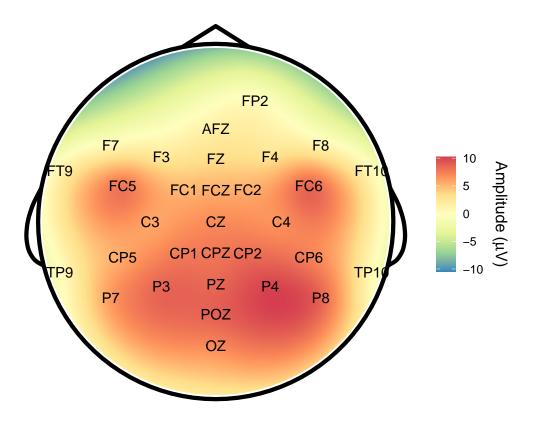
topoplot(filter(eeg.map_for_plotting_adi_250500, adi_median_split=="low_ADI"), palette="Spectral", change



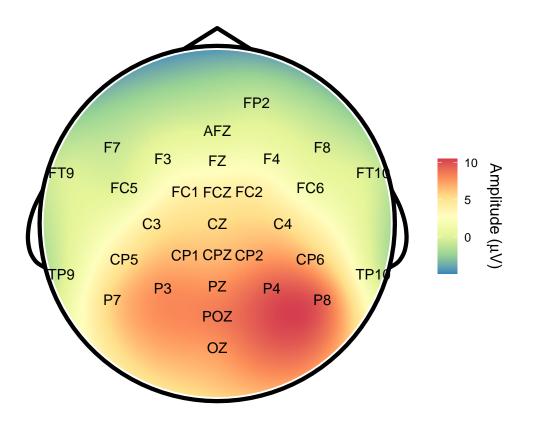
topoplot(eeg.map_for_plotting_adi_200400, palette="Spectral", chanLocs=chanlocs, contour=FALSE, interp_



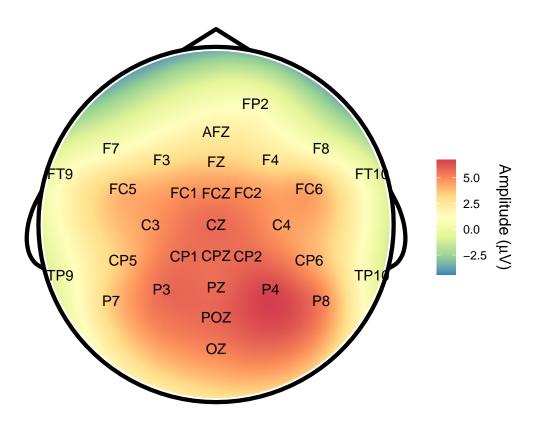
topoplot(filter(eeg.map_for_plotting_adi_200400, adi_median_split=="high_ADI"), palette="Spectral", characteristics."



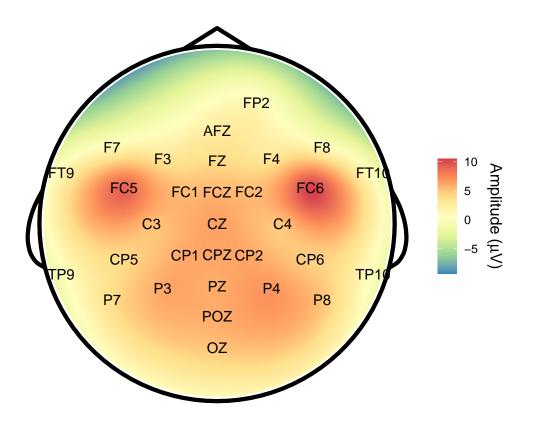
topoplot(filter(eeg.map_for_plotting_adi_200400, adi_median_split=="low_ADI"), palette="Spectral", change



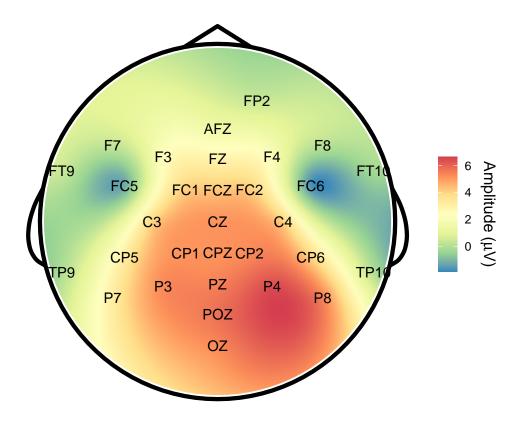
topoplot(eeg.map_for_plotting_adi_150275, palette="Spectral", chanLocs=chanlocs, contour=FALSE, interp_



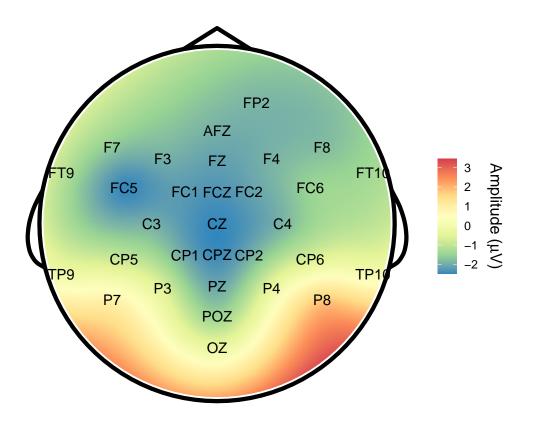
topoplot(filter(eeg.map_for_plotting_adi_150275, adi_median_split=="high_ADI"), palette="Spectral", charge



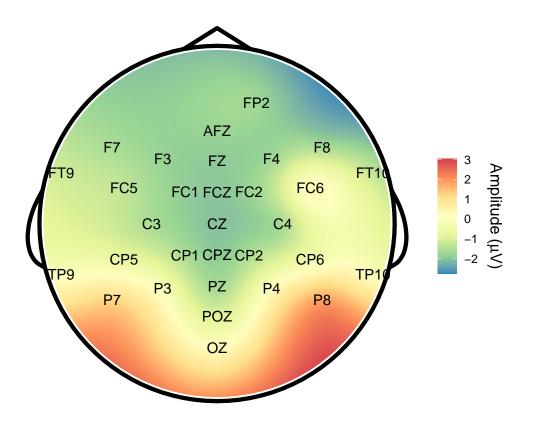
topoplot(filter(eeg.map_for_plotting_adi_150275, adi_median_split=="low_ADI"), palette="Spectral", chan



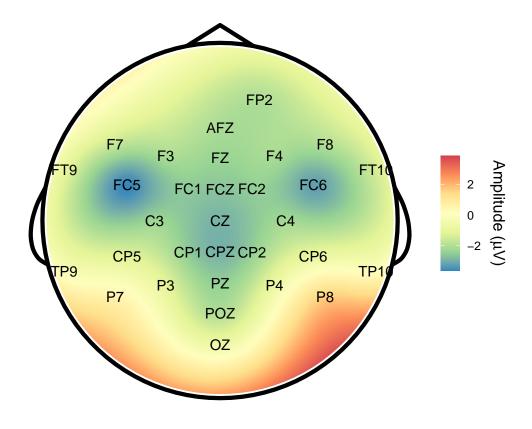
 ${\tt topoplot(eeg.map_for_plotting_adi_50150,\ palette="Spectral",\ chanLocs=chanlocs,\ contour=FALSE,\ interp_location of the contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour=contour$



topoplot(filter(eeg.map_for_plotting_adi_50150, adi_median_split=="high_ADI"), palette="Spectral", chan



topoplot(filter(eeg.map_for_plotting_adi_50150, adi_median_split=="low_ADI"), palette="Spectral", chanL



STRAIN

```
load(here("data/BUDS_cleaning02_with_strain.RData"))
BUDS_cleaning02_with_strain$ID <- as.integer(as.character(BUDS_cleaning02_with_strain$id_1_i))

df_275425_pooled_strain <- df_275425_pooled %>%
    full_join(BUDS_cleaning02_with_strain, by="ID")

df_275425_cz_strain <- df_275425_cz %>%
    full_join(BUDS_cleaning02_with_strain, by="ID")

df_150350_cz_strain <- df_150350_cz %>%
    full_join(BUDS_cleaning02_with_strain, by="ID")

df_250450_fz_strain <- df_250450_fz %>%
    full_join(BUDS_cleaning02_with_strain, by="ID")

df_200400_pz_strain <- df_200400_pz %>%
    full_join(BUDS_cleaning02_with_strain, by="ID")

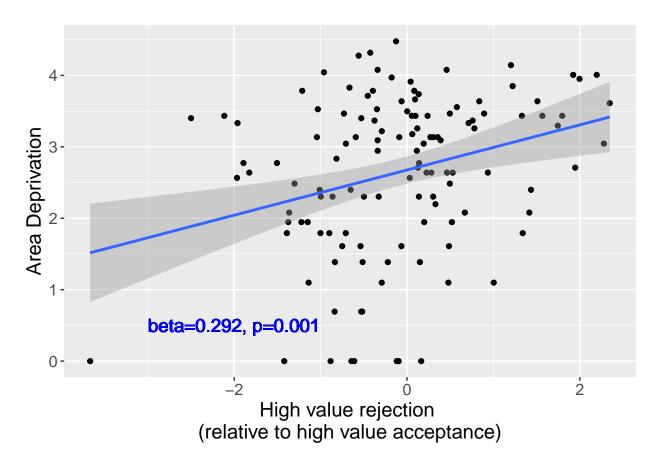
df_150275_cz_strain <- df_150275_cz %>%
    full_join(BUDS_cleaning02_with_strain, by="ID")
```

```
df_50150_cz_strain <- df_50150_cz %>%
  full join(BUDS cleaning02 with strain, by="ID")
# df 4001000 pz strain <- df 4001000 pz %>%
   full_join(BUDS_cleaning02_with_strain, by="ID")
# df_6001500_pz_strain <- df_6001500_pz %>%
   full join(BUDS cleaning02 with strain, by="ID")
df 150350 cz long strain <- df 150350 cz long %>%
 full_join(BUDS_cleaning02_with_strain, by="ID", relationship = "many-to-many")
df_200400_pz_long_strain <- df_200400_pz_long %>%
  full_join(BUDS_cleaning02_with_strain, by="ID", relationship = "many-to-many")
df_250450_fz_long_strain <- df_250450_fz_long %>%
  full_join(BUDS_cleaning02_with_strain, by="ID", relationship = "many-to-many")
df 275425_pooled_long_strain <- df_275425_pooled_long %>%
  full_join(BUDS_cleaning02_with_strain, by="ID", relationship = "many-to-many")
df_275425_cz_long_strain <- df_275425_cz_long %>%
 full_join(BUDS_cleaning02_with_strain, by="ID", relationship = "many-to-many")
df 150275 cz long strain <- df 150275 cz long %>%
  full_join(BUDS_cleaning02_with_strain, by="ID", relationship = "many-to-many")
df_50150_cz_long_strain <- df_50150_cz_long %>%
 full_join(BUDS_cleaning02_with_strain, by="ID", relationship = "many-to-many")
```

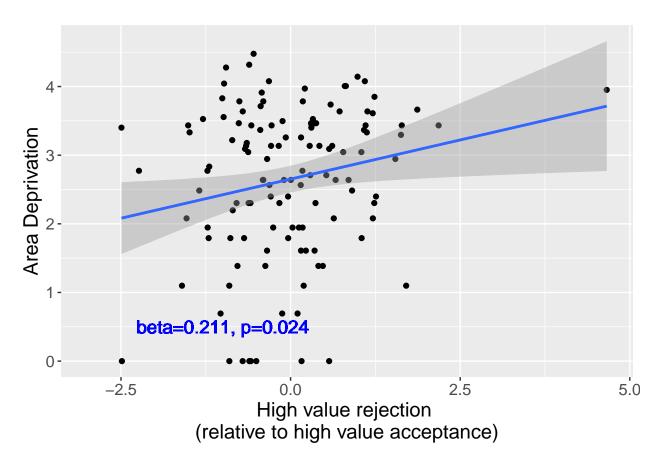
Stressors and ADI

```
lm(formula = ADI_NATRANK_log_z ~ CRDiffTH, data = df_150350_cz_strain)
lm(formula = ADI_NATRANK_log_z ~ CRAllTH, data = df_150350_cz_strain)
# Housing related stressors
lm(formula = ADI_NATRANK_log_z ~ DHEvntCT, data = df_150350_cz_strain)
lm(formula = ADI_NATRANK_log_z ~ DHAllCT, data = df_150350_cz_strain)
lm(formula = ADI_NATRANK_log_z ~ DHEvntTH, data = df_150350_cz_strain)
# Domain: Treatment/Health - Count of Chronic Difficulties
lm(formula = ADI_NATRANK_log_z ~ DTDiffCT, data = df_150350_cz_strain)
summary(lm(AR_AA ~ ADI_NATRANK_log_z + StressCT + StressTH + Age + Sex, df_150350_cz_strain))
summary(lm(AR AA ~ ADI NATRANK log z + StressCT + StressTH + Age + Sex, df 250450 fz strain))
summary(lm(AR_AA ~ ADI_NATRANK_log_z + StressCT + StressTH + Age + Sex, df_200400_pz_strain))
for (p in STRAIN_scales) {
 for (data in c("df_150350_cz_strain","df_250450_fz_strain","df_200400_pz_strain")) {
 for (comp in c("RR_RA")) {
      eval(parse(text=paste0('print(summary(lm(',comp,' ~ ',p,', ',data,'))$call)
                             print(summary(lm(',comp,' ~ ',p,', ',data,'))$coef[2,4])')))
 }}}
lm(formula = AR_AA ~ DMDiffCT, data = df_250450_fz_strain)
lm(formula = AR_AA ~ DMDiffTH, data = df_250450_fz_strain)
lm(formula = AR AA ~ DGEvntCT, data = df 200400 pz strain)
```

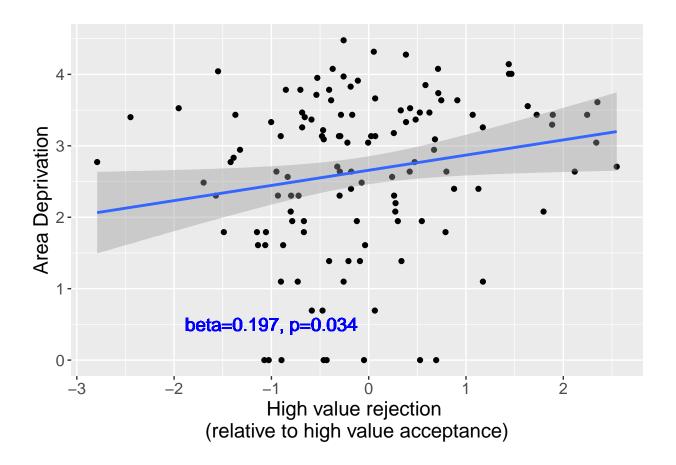
Significant regression results



```
## Warning: Removed 68 rows containing non-finite values ('stat_smooth()').
## Removed 68 rows containing missing values ('geom_point()').
```



```
## Warning: Removed 68 rows containing non-finite values ('stat_smooth()').
## Removed 68 rows containing missing values ('geom_point()').
```

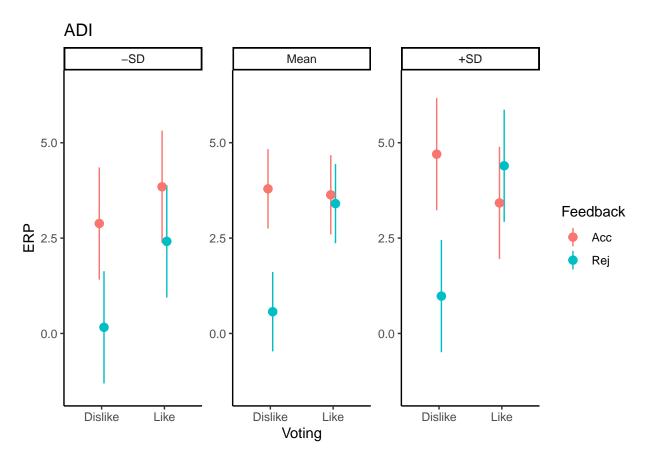


Interactions

ADI

150-350 Cz

```
lmer(formula = ERP ~ Feedback*Voting*ADI_NATRANK_log + (Voting | ID), data = df_150350_cz_long))
summary(lmer(formula = ERP ~ Feedback*Voting*ADI_NATRANK_log + (Voting | ID), data = df_150350_cz_long)
bbmle::AICtab(lm(formula = ERP ~ Feedback*Voting*ADI_NATRANK_log, data = df_150350_cz_long),
      lme4::lmer(formula = ERP ~ Feedback*Voting*ADI_NATRANK_log + (1 | ID), data = df_150350_cz_long,
models_150350_cz_table <- lmer_adi_interaction_table(df_150350_cz_long)</pre>
models 150350 cz table$component <- "150350 cz"
model_150350_cz <- lmer(formula = ERP ~ Voting*Feedback*ADI_NATRANK_log + (1 | ID), data = df_150350_cz
plot_cap(
    model_150350_cz,
    condition = list(
              "Voting",
        "Feedback",
        "ADI_NATRANK_log" = "threenum")) +
  scale_y_continuous(limits=c(-1.5,6.5)) +
  labs(title="ADI") +
    theme_classic()
```

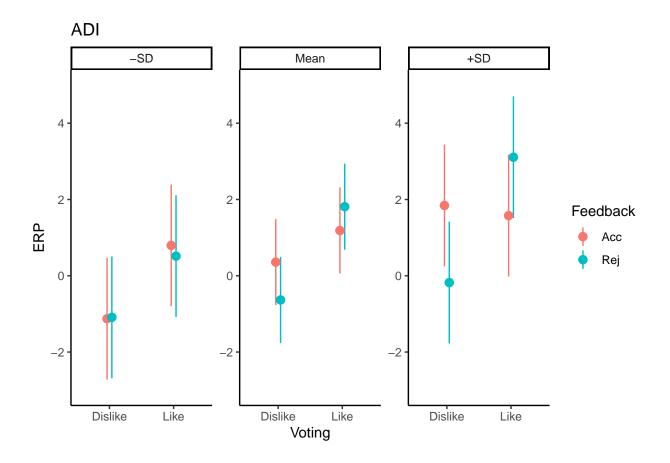


200-400 Pz

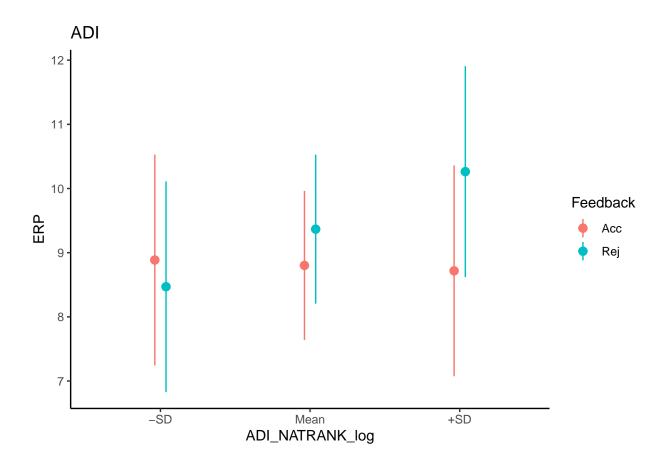
```
models_200400_pz_table <- lmer_adi_interaction_table(df_200400_pz_long)
models_200400_pz_table$component <- "200400_pz"</pre>
```

250-350 Fz

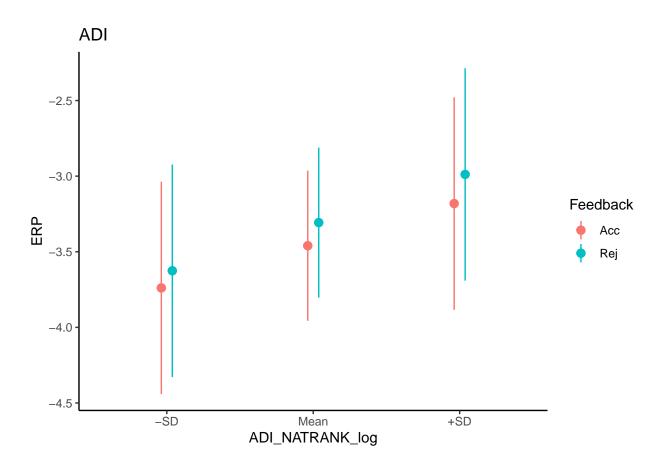
```
anova(lmer(formula = ERP ~ Feedback*Voting*ADI_NATRANK_log + (1 | ID), data = df_250450_fz_long),
      lmer(formula = ERP ~ Feedback*Voting*ADI_NATRANK_log + (Feedback | ID), data = df_250450_fz_long)
anova(lmer(formula = ERP ~ Feedback*Voting*ADI_NATRANK_log + (1 | ID), data = df_250450_fz_long),
      lmer(formula = ERP ~ Feedback*Voting*ADI_NATRANK_log + (Voting | ID), data = df_250450_fz_long))
bbmle::AICtab(lm(formula = ERP ~ Feedback*Voting*ADI_NATRANK_log, data = df_250450_fz_long),
      lme4::lmer(formula = ERP ~ Feedback*Voting*ADI_NATRANK_log + (1 | ID), data = df_250450_fz_long,
models_250450_fz_table <- lmer_adi_interaction_table(df_250450_fz_long)</pre>
models_250450_fz_table$component <- "250450_fz"</pre>
model_250450_fz <- lmer(formula = ERP ~ Feedback*Voting*ADI_NATRANK_log + (1 | ID), data = df_250450_fz
plot_cap(
   model_250450_fz,
    condition = list(
        "Voting",
        "Feedback",
        "ADI NATRANK log" = "threenum")) +
  scale_y_continuous(limits=c(-3,5)) +
  labs(title="ADI") +
   theme_classic()
```



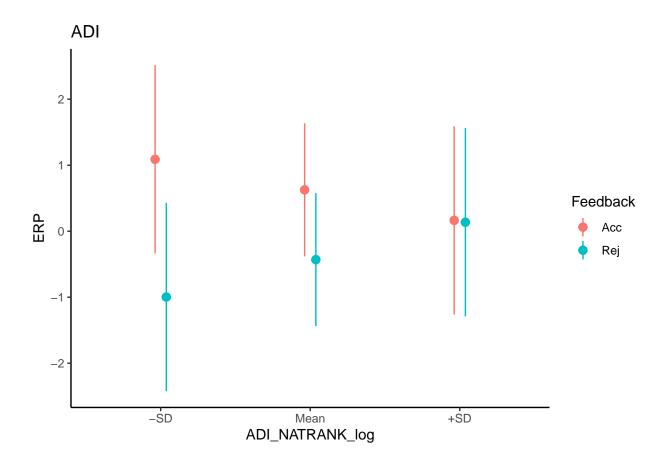
275-425 Pooled



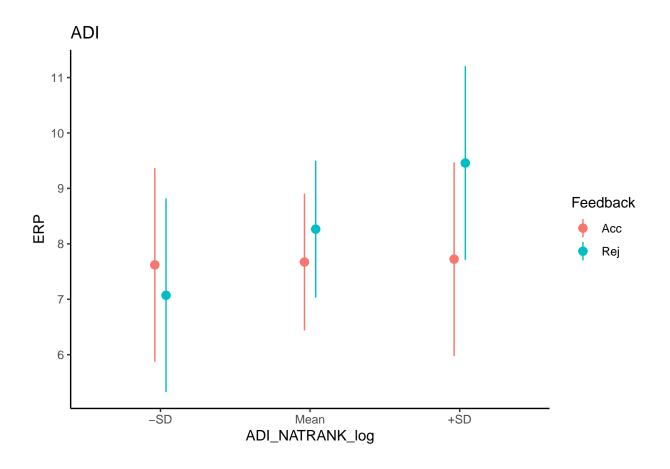
50-150 Cz



150-275 Cz



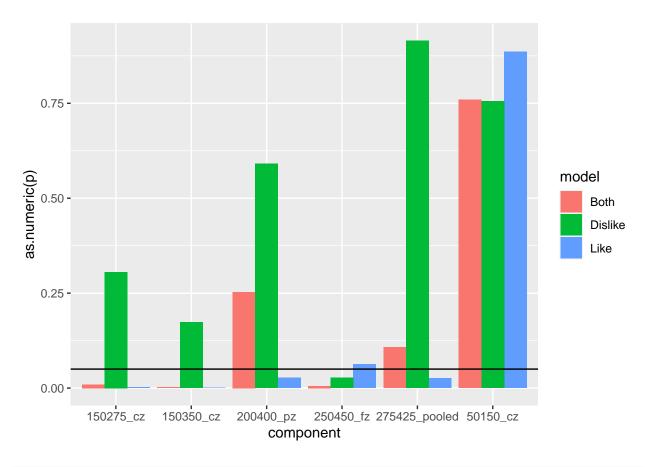
275-425 Cz



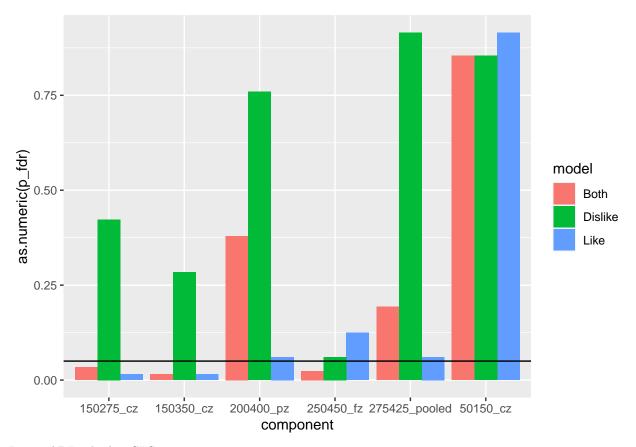
All components

```
models_table <- rbind(models_150275_cz_table, models_50150_cz_table, models_275425_pooled_table, models_table$p_fdr <- p.adjust(models_table$p, method="fdr")

ggplot(models_table, aes(x=component, fill=model, y=as.numeric(p))) +
    geom_col(position="dodge") +
    geom_hline(yintercept=0.05)</pre>
```



```
ggplot(models_table, aes(x=component, fill=model, y=as.numeric(p_fdr))) +
geom_col(position="dodge") +
geom_hline(yintercept=0.05)
```



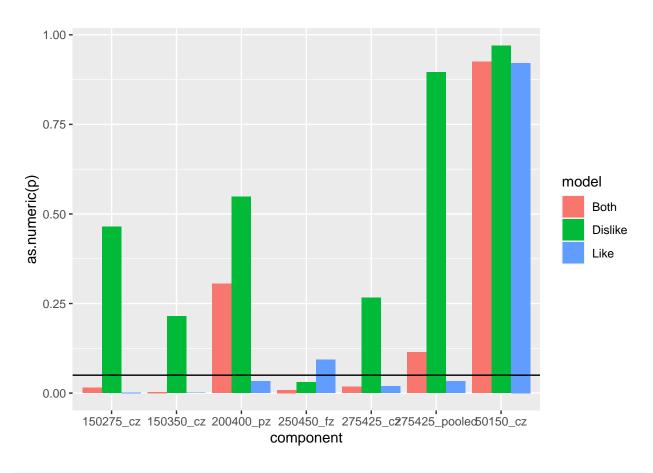
Lower ADI is higher SES

Race and Ethnicity

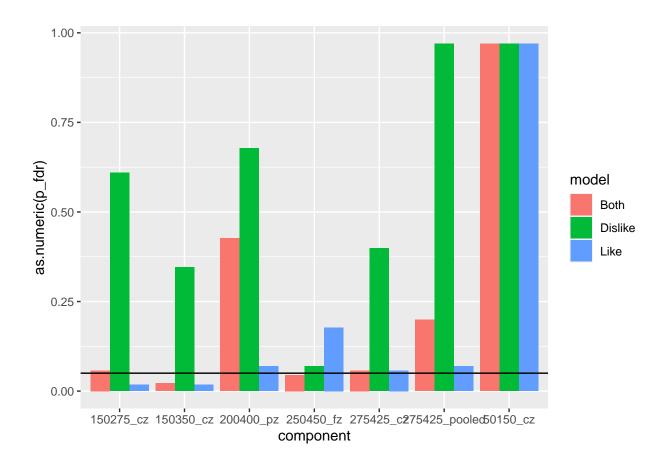
```
# 150-350 Cz
summary(lmer(formula = ERP ~ Feedback*Voting*Racial_minority + (1 | ID), data = df_150350_cz_long))
summary(lmer(formula = ERP ~ Feedback*Voting*Racial_majority + (1 | ID), data = df_150350_cz_long))
summary(lmer(formula = ERP ~ Feedback*Voting*demo_child_hispanic + (1 | ID), data = df_150350_cz_long))
# 200-400 Pz
summary(lmer(formula = ERP ~ Feedback*Voting*Racial_minority + (1 | ID), data = df_200400_pz_long))
summary(lmer(formula = ERP ~ Feedback*Voting*Racial_majority + (1 | ID), data = df_200400_pz_long))
summary(lmer(formula = ERP ~ Feedback*Voting*demo_child_hispanic + (1 | ID), data = df_200400_pz_long))
# 250-350 Fz
summary(lmer(formula = ERP ~ Feedback*Voting*Racial_minority + (1 | ID), data = df_250450_fz_long))
summary(lmer(formula = ERP ~ Feedback*Voting*Racial_majority + (1 | ID), data = df_250450_fz_long))
summary(lmer(formula = ERP ~ Feedback*Voting*demo_child_hispanic + (1 | ID), data = df_250450_fz_long))
# 275-425 Fz
summary(lmer(formula = ERP ~ Feedback*Voting*Racial_minority + (1 | ID), data = df_275425_pooled_long))
summary(lmer(formula = ERP ~ Feedback*Voting*Racial_majority + (1 | ID), data = df_275425_pooled_long))
summary(lmer(formula = ERP ~ Feedback*Voting*demo_child_hispanic + (1 | ID), data = df_275425_pooled_lo.
```

Covaring for age, sex, hispanic, stress, IDAS

```
lmer_adi_interaction_table_cov <- function(data, Component) {</pre>
  new_model <- data.frame(model = c("Both","Like","Dislike"),</pre>
                            beta = NA,
                            p = NA,
                           component = Component)
new_model$beta <- c(broom.mixed::tidy(lmer(formula = ERP ~ Feedback*Voting*ADI_NATRANK_log_z + Age + Se
                    broom.mixed::tidy(lmer(formula = ERP ~ Feedback*ADI_NATRANK_log_z + Age + Sex + dem
                    broom.mixed::tidy(lmer(formula = ERP ~ Feedback*ADI_NATRANK_log_z + Age + Sex + dem
new_model$p <- c(broom.mixed::tidy(lmer(formula = ERP ~ Feedback*Voting*ADI_NATRANK_log_z + Age + Sex +</pre>
                    broom.mixed::tidy(lmer(formula = ERP ~ Feedback*ADI_NATRANK_log_z + Age + Sex + dem
                    broom.mixed::tidy(lmer(formula = ERP ~ Feedback*ADI_NATRANK_log_z + Age + Sex + dem
new_model
}
models_table_cov <- rbind(lmer_adi_interaction_table_cov(df_150275_cz_long_strain, "150275_cz"),</pre>
        lmer_adi_interaction_table_cov(df_50150_cz_long_strain, "50150_cz"),
        lmer_adi_interaction_table_cov(df_275425_cz_long_strain, "275425_cz"),
        lmer_adi_interaction_table_cov(df_275425_pooled_long_strain, "275425_pooled"),
        lmer_adi_interaction_table_cov(df_250450_fz_long_strain, "250450_fz"),
        lmer_adi_interaction_table_cov(df_200400_pz_long_strain, "200400_pz"),
        lmer_adi_interaction_table_cov(df_150350_cz_long_strain, "150350_cz"))
models_table_cov$p_fdr <- p.adjust(models_table_cov$p, method="fdr")</pre>
ggplot(models_table_cov, aes(x=component, fill=model, y=as.numeric(p))) +
  geom col(position="dodge") +
  geom_hline(yintercept=0.05)
```



```
ggplot(models_table_cov, aes(x=component, fill=model, y=as.numeric(p_fdr))) +
  geom_col(position="dodge") +
  geom_hline(yintercept=0.05)
```



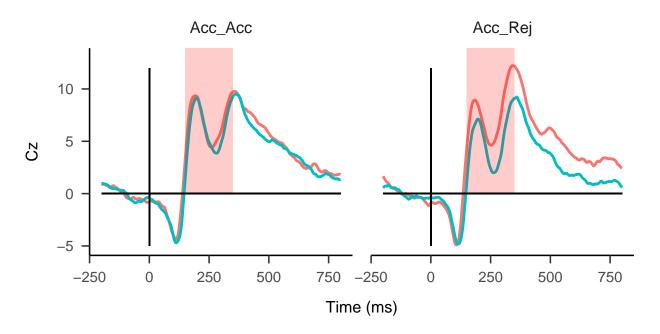
Exaggerated response to rejection

```
ggplot(data=filter(df_ga_Cz_adi_wide, Condition=="Acc_Acc" | Condition=="Acc_Rej"), aes(x=Time, y=grand
facet_wrap(~ Condition) +
    xlim(-200, 800) +
    ylim( -5, 13) +
    geom_line(linewidth=1) +
    annotate("rect", xmin=150, xmax=350, ymin=0, ymax=Inf, alpha=0.2, fill="red") +
    geom_rect(aes(xmin=0, xmax=0, ymin=-5, ymax=12), color="black") +
    geom_rect(aes(xmin=-200, xmax=800, ymin=0, ymax=0), color="black") +
    labs(x="Time (ms)", y="Cz", title="High value peers") +
    theme_apa(base_size = 12) + theme(legend.position="top")
```

Warning: Removed 1198 rows containing missing values ('geom_line()').

High value peers



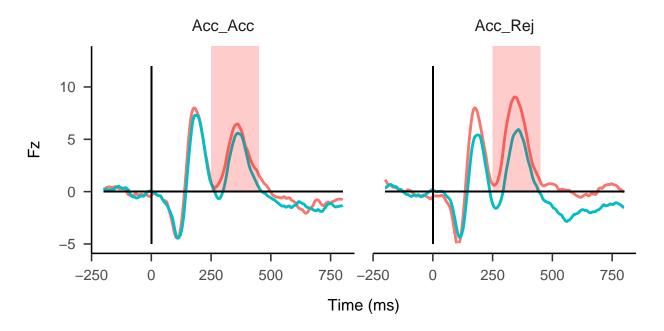


```
ggplot(data=filter(df_ga_Fz_adi_wide, Condition=="Acc_Acc" | Condition=="Acc_Rej"), aes(x=Time, y=grand
facet_wrap(~ Condition) +
    xlim(-200, 800) +
    ylim(-5, 13) +
    geom_line(linewidth=1) +
    annotate("rect", xmin=250, xmax=450, ymin=0, ymax=Inf, alpha=0.2, fill="red") +
    geom_rect(aes(xmin=0, xmax=0, ymin=-5, ymax=12), color="black") +
    geom_rect(aes(xmin=-200, xmax=800, ymin=0, ymax=0), color="black") +
    labs(x="Time (ms)", y="Fz", title="High value peers") +
    theme_apa(base_size = 12) + theme(legend.position="top")
```

Warning: Removed 1198 rows containing missing values ('geom_line()').

High value peers



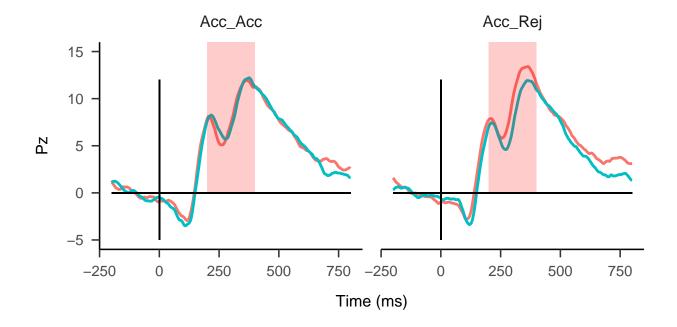


```
ggplot(data=filter(df_ga_Pz_adi_wide, Condition=="Acc_Acc" | Condition=="Acc_Rej"), aes(x=Time, y=grand facet_wrap(~ Condition) +
    xlim(-200, 800) +
    ylim(-5, 15) +
    geom_line(linewidth=1) +
    annotate("rect", xmin=200, xmax=400, ymin=0, ymax=Inf, alpha=0.2, fill="red") +
    geom_rect(aes(xmin=0, xmax=0, ymin=-5, ymax=12), color="black") +
    geom_rect(aes(xmin=-200, xmax=800, ymin=0, ymax=0), color="black") +
    labs(x="Time (ms)", y="Pz", title="High value peers") +
    theme_apa(base_size = 12) + theme(legend.position="top")
```

Warning: Removed 1198 rows containing missing values ('geom_line()').

High value peers





66 99

66 99

66 99

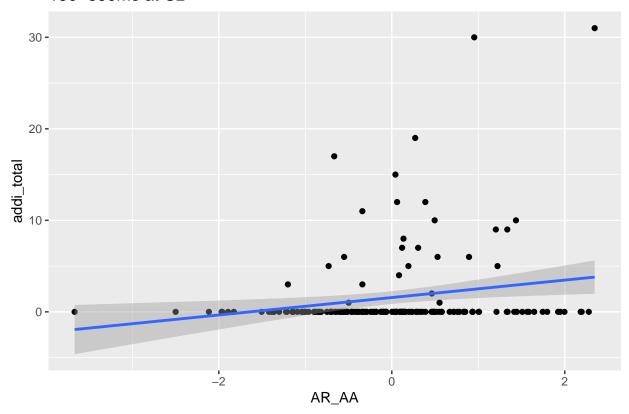
Regressions with ADDI

Significant results

```
summary(zeroinfl(formula = addi_total ~ AA_AR, data = df_150350_cz))
summary(zeroinfl(formula = addi_educ ~ AA_AR, data = df_150350_cz))
summary(zeroinfl(formula = addi_distress ~ AA_AR, data = df_200400_pz))
summary(zeroinfl(formula = addi_total ~ AA_AR, data = df_275425_pooled))
summary(zeroinfl(formula = addi_educ ~ AA_AR, data = df_275425_pooled))
summary(zeroinfl(formula = addi_distress ~ AA_AR, data = df_275425_pooled))
summary(glm(addi_01 ~ AA_AR, data=df_150350_cz, family="binomial"))
summary(glm(addi_01 ~ AA_AR, data=df_275425_pooled, family="binomial"))
summary(zeroinfl(formula = addi_total ~ AA_AR, data = df_150350_cz %% filter(df_150350_cz$addi_total<2
summary(zeroinfl(formula = addi_educ ~ AA_AR, data = df_150350_cz %>% filter(df_150350_cz$addi_educ<8))</pre>
summary(zeroinfl(formula = addi_distress ~ AA_AR, data = df_200400_pz %>% filter(df_200400_pz$addi_dist
m1 <- zeroinfl(formula = addi_total ~ AR_AA, data = df_150350_cz)</pre>
mnull <- update(m1, . ~ 1)</pre>
pchisq(2 * (logLik(m1) - logLik(mnull)), df = 3, lower.tail = FALSE)
ggplot(df_150350_cz, aes(x=AR_AA, y=addi_total)) +
  geom_point() +
  stat_smooth(method="lm") +
 labs(title="150-350ms at Cz")
```

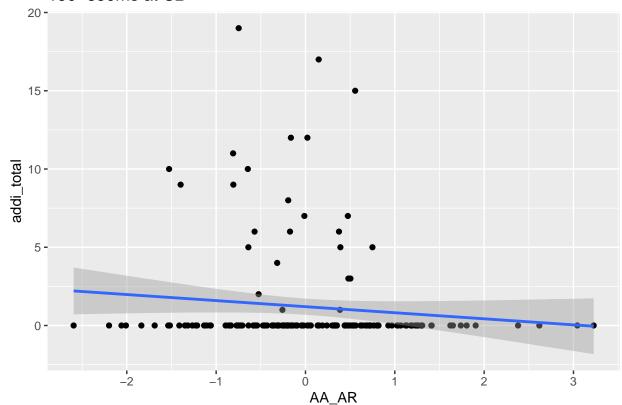
- ## Warning: Removed 28 rows containing non-finite values ('stat_smooth()').
- ## Warning: Removed 28 rows containing missing values ('geom_point()').

150-350ms at Cz



```
ggplot(df_150350_cz %>% filter(df_150350_cz$addi_total<20), aes(x=AA_AR, y=addi_total)) +
  geom_point() +
  stat_smooth(method="lm") +
  labs(title="150-350ms at Cz")</pre>
```

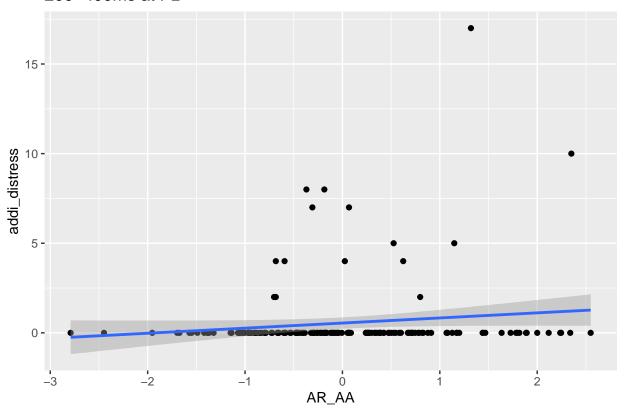
150-350ms at Cz



```
summary(zeroinfl(formula = addi_distress ~ AR_AA, data = df_200400_pz))
ggplot(df_200400_pz, aes(x=AR_AA, y=addi_distress)) +
  geom_point() +
  stat_smooth(method="lm") +
  labs(title="200-400ms at Pz")
```

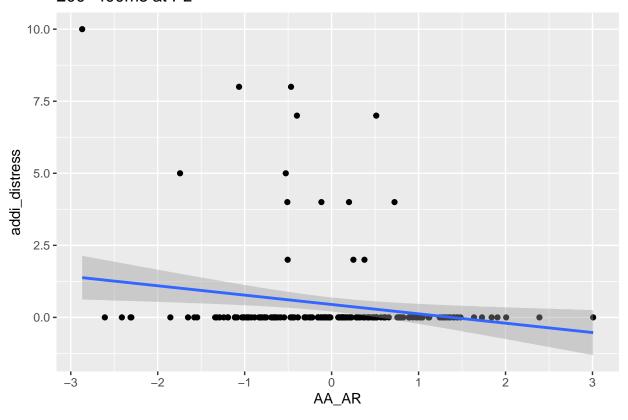
Warning: Removed 28 rows containing non-finite values ('stat_smooth()').
Removed 28 rows containing missing values ('geom_point()').

200-400ms at Pz



```
ggplot(df_200400_pz %>% filter(df_200400_pz$addi_distress<15), aes(x=AA_AR, y=addi_distress)) +
geom_point() +
stat_smooth(method="lm") +
labs(title="200-400ms at Pz")</pre>
```





Regressions with BCS-A

```
for (p in c("bcs_physical_vic", "bcs_physical_vic_01", "bcs_verbal_vic", "bcs_rel_vic", "bcs_cyber_vic", "bc
      eval(parse(text=paste0('hist(',data,'$',p,')')))
for (data in c("df_150350_cz","df_250450_fz","df_200400_pz")) {
  for (comp in c("A_all")) {
    for (p in c("bcs_physical_vic","bcs_physical_vic_01","bcs_verbal_vic","bcs_rel_vic","bcs_cyber_vic"
      eval(parse(text=paste0('print(zeroinfl(',p,' ~ ',comp,', ',data,')$call)
                             print(round(summary(zeroinfl(',p,' ~ ',comp,', ',data,'))$coefficients$cou.
    }}}
for (data in c("df_150350_cz")) {
  for (comp in c("RA_RR")) {
    for (p in c("bcs_physical_vic","bcs_physical_vic_01","bcs_verbal_vic","bcs_rel_vic","bcs_cyber_vic"
      eval(parse(text=paste0('print(zeroinfl(',p,' ~ ',comp,', ',data,')$call)
                             print(round(summary(zeroinfl(',p,' ~ ',comp,', ',data,'))$coefficients$cour
    }}}
for (data in c("df_250450_fz")) {
  for (comp in c("AA_AR")) {
```

```
for (p in c("bcs_physical_vic","bcs_physical_vic_01","bcs_verbal_vic","bcs_rel_vic","bcs_cyber_vic",
      eval(parse(text=paste0('print(zeroinfl(',p,' ~ ',comp,', ',data,')$call)
                             print(round(summary(zeroinfl(',p,' ~ ',comp,', ',data,'))$coefficients$cou
  }}}
for (data in c("df_200400_pz")) {
  for (comp in c("AR_RR","RA_RR","RA_AA")) {
    for (p in c("bcs_physical_vic", "bcs_physical_vic_01", "bcs_verbal_vic", "bcs_rel_vic", "bcs_cyber_vic"
      eval(parse(text=paste0('print(zeroinfl(',p,' ~ ',comp,', ',data,')$call)
                             print(round(summary(zeroinfl(',p,' ~ ',comp,', ',data,'))$coefficients$count
   }}}
# for (data in c("df_4001000_pz")) {
   for (comp in c("RR_RA", "AA_RA")) {
      for (p in c("bcs_physical_vic", "bcs_physical_vic_01", "bcs_verbal_vic", "bcs_rel_vic", "bcs_cyber_vi
#
        eval(parse(text=paste0('print(zeroinfl(',p,' ~ ',comp,', ',data,')$call)
#
                               print(round(summary(zeroinfl(',p,' ~ ',comp,', ',data,'))$coefficients$c
     }}}
```

No significant results

Regressions with PROMIS

```
for (p in c("promis_peer_sumraw","promis_fam_sumraw","promis_peer_tscore","promis_fam_tscore")) {
      eval(parse(text=paste0('hist(',data,'$',p,')')))
    }
for (data in c("df_150350_cz","df_250450_fz","df_200400_pz")) {
  for (comp in c("A_all")) {
    for (p in c("promis_peer_sumraw", "promis_fam_sumraw", "promis_peer_tscore", "promis_fam_tscore")) {
      eval(parse(text=paste0('print(summary(lm(',comp,' ~ ',p,', ',data,'))$coefficients)')))
    }}}
for (data in c("df_150350_cz","df_250450_fz","df_200400_pz")) {
  for (comp in c("A_all")) {
    for (p in c("promis_peer_sumraw","promis_fam_sumraw","promis_peer_tscore","promis_fam_tscore")) {
      eval(parse(text=paste0('print(summary(lm(',comp,' ~ ',p,', ',data,'))$coefficients)')))
}}}
for (data in c("df_150350_cz")) {
  for (comp in c("RA_RR")) {
    for (p in c("promis_peer_sumraw","promis_fam_sumraw","promis_peer_tscore","promis_fam_tscore")) {
      eval(parse(text=paste0('print(summary(lm(',comp,' ~ ',p,', ',data,'))$coefficients)')))
}}}
for (data in c("df_250450_fz")) {
  for (comp in c("AA_AR")) {
    for (p in c("promis_peer_sumraw","promis_fam_sumraw","promis_peer_tscore","promis_fam_tscore")) {
      eval(parse(text=paste0('print(summary(lm(',comp,' ~ ',p,', ',data,'))$coefficients)')))
}}}
```

```
for (data in c("df_200400_pz")) {
   for (comp in c("AR_RR","RA_RR","RA_AA")) {
     for (p in c("promis_peer_sumraw","promis_fam_sumraw","promis_peer_tscore","promis_fam_tscore")) {
        eval(parse(text=pasteO('print(summary(lm(',comp,' ~ ',p,', ',data,'))$coefficients)')))
     }}}

# for (data in c("df_4001000_pz")) {
     # for (comp in c("RR_RA","AA_RA")) {
        for (p in c("promis_peer_sumraw","promis_fam_sumraw","promis_peer_tscore","promis_fam_tscore")) {
        eval(parse(text=pasteO('print(summary(lm(',comp,' ~ ',p,', ',data,'))$coefficients)')))
     # }}}
```

No significant results

Regressions with romantic relationship

```
load(here("data/BUDS_cleaning02_with_strain.RData"))
BUDS_cleaning02_with_strain$ID <- as.integer(as.character(BUDS_cleaning02_with_strain$id_1_i))
BUDS_cleaning02_with_strain <- BUDS_cleaning02_with_strain %>%
  distinct(ID, .keep_all=TRUE) %>%
  mutate(RelationshipStatus_named = case_match(RelationshipStatus, 1 ~ "I've never had a boyfriend or g
                                        2 ~ "I've had a boyfriend or girlfriend, but I'm not dating any
                                        3 ~ "I'm dating someone, but it's not very serious",
                                        4 ~ "I have a serious boyfriend or girlfriend",
                                        5 ~ "I am married"),
         Never_dated = case_when(RelationshipStatus == 1 ~ "never_dated",
                                  RelationshipStatus > 1 & RelationshipStatus!=2 ~ "dated"),
         RelationshipStatus_named_no4 = case_match(RelationshipStatus, 1 ~ "I've never had a boyfriend
                                        2 ~ "I've had a boyfriend or girlfriend, but I'm not dating any
                                        3 ~ "I'm dating someone, but it's not very serious",
                                        4 ~ NA,
                                        5 ~ "I am married"),
         RelationshipStatus_named_no2 = case_match(RelationshipStatus, 1 ~ "I've never had a boyfriend
                                        2 ~ NA,
                                        3 ~ "I'm dating someone, but it's not very serious",
                                        4 ~ "I have a serious boyfriend or girlfriend",
                                        5 ~ "I am married"))
df_150350_cz_strain <- df_150350_cz %>%
  full_join(BUDS_cleaning02_with_strain, by="ID")
df_250450_fz_strain <- df_250450_fz %>%
  full_join(BUDS_cleaning02_with_strain, by="ID")
df_200400_pz_strain <- df_200400_pz %>%
  full_join(BUDS_cleaning02_with_strain, by="ID")
# df 4001000 pz strain <- df 4001000 pz %>%
  full_join(BUDS_cleaning02_with_strain, by="ID")
```

```
# df_6001500_pz_strain <- df_6001500_pz %>%
     full join(BUDS cleaning02 with strain, by="ID")
table(df_150350_cz_strain$RelationshipStatus_named)
table(df_150350_cz_strain$Never_dated)
# Acceptance from a liked peer relative to acceptance from a disliked peer is greater for youth who hav
# summary(lm(AA_RA ~ Never_dated, data = df_4001000_pz_strain))
# summary(lm(A_all ~ Never_dated, data = df_4001000_pz_strain))
\# ggplot(filter(df\_4001000\_pz\_strain, complete.cases(Never\_dated)), aes(y=A\_all, x=Never\_dated)) +
    # geom_bar(stat="summary", position = "dodge", fun.y = "mean")
# df_4001000_pz_hcs_strain <- df_4001000_pz_hcs %>%
    # full_join(BUDS_cleaning02_with_strain, by="ID")
\# anova(lm(call = AA_RA ~ Never_dated, data = df_4001000_pz_hcs_strain))
# t.test(A_all ~ Never_dated, df_4001000_pz_strain)
# t.test(AA_RA ~ Never_dated, df_4001000_pz_hcs_strain)
# for (data in c("df_200400_pz_strain")) {
     for (comp in c("AR_RR", "RA_RR", "RA_AA")) {
            for (p in c("RelationshipStatus", "Never_dated")) {
#
                eval(parse(text=paste0('print(summary(lm(',comp,' ~ ',p,', ',data,')))')))
#
           }}}
\tt df\_4001000\_pz\_strain\_idas \begin{tabular}{l} \b
for (var in c(15,18,20,41,47,99,
                            3,10,23,27,50,53,59,64)) {
  eval(parse(text=paste0('
   df_4001000_pz_strain_idas$idas_',var,' <- dplyr::recode_factor(df_4001000_pz_strain_idas$idas_',var,'
    "Not at all"=1,
    "A little bit"=2.
   "Moderately"=3,
   "Quite a bit"=4,
   "Extremely"=5,
    `1`=1, `2`=2, `3`=3, `4`=4,`5`=5)
   df_4001000_pz_strain_idas$idas_',var,' <- as.integer(df_4001000_pz_strain_idas$idas_',var,')')))</pre>
for (var in c(1:17)) {
  eval(parse(text=paste0('
    df_4001000_pz_strain_idas$acips_',var,' <- dplyr::recode_factor(df_4001000_pz_strain_idas$acips_',var
    "Very false for me"=1,
    "Moderately false for me"=2,
    "Slightly false for me"=3,
    "Slightly true for me"=4,
    "Moderately true for me"=5,
    "Very true for me"=6,
    1=1, 2=2, 3=3, 4=4,5=5, 6=6
    df_4001000_pz_strain_idas$acips_',var,' <- as.integer(df_4001000_pz_strain_idas$acips_',var,')')))
```

```
df_4001000_pz_strain_idas\das_idas_sa <- rowMeans(df_4001000_pz_strain_idas[,c("idas_15","idas_18",
                                                                         "idas_20","idas_41",
                                                                         "idas_47", "idas_99")], na.rm=T)
df_4001000_pz_strain_idas$idas_wellbeing <- rowMeans(df_4001000_pz_strain_idas[,c("idas_3","idas_10",
                                                                         "idas_23","idas_27",
                                                                         "idas 50", "idas 53",
                                                                         "idas 59", "idas 64")], na.rm=T)
df_4001000_pz_strain_idas$acips <- rowMeans(df_4001000_pz_strain_idas[,c("acips_1","acips_2",
                                                                         "acips_3", "acips_4",
                                                                         "acips_5", "acips_6",
                                                                        "acips_7", "acips_8",
                                                                        "acips_9", "acips_10"
                                                                        "acips_11", "acips_12",
                                                                        "acips_13", "acips_14",
                                                                        "acips_15", "acips_16", "acips_17"
df_4001000_pz_strain_idas$idas_sa_norm <- bestNormalize(df_4001000_pz_strain_idas$idas_sa)$x.t
hist(df_4001000_pz_strain_idas$idas_sa_norm)
df_4001000_pz_strain_idas\sacips_norm <- bestNormalize(df_4001000_pz_strain_idas\sacips)\sx.t
hist(df_4001000_pz_strain_idas$acips_norm)
t.test(idas_sa_norm ~ Never_dated, df_4001000_pz_strain_idas)
t.test(idas_wellbeing ~ Never_dated, df_4001000_pz_strain_idas)
t.test(acips ~ Never_dated, df_4001000_pz_strain_idas)
summary(lm(AA_RA ~ idas_sa_norm + acips_norm + idas_wellbeing, df_4001000_pz_strain_idas))
summary(lm(AA_RA ~ idas_sa_norm*Never_dated, df_4001000_pz_strain_idas))
# SEND THIS TO STEW
summary(lm(AA_AR ~ idas_sa_norm + idas_wellbeing, df_4001000_pz_strain_idas))
df_4001000_pz_strain_idas_complete <- df_4001000_pz_strain_idas %>%
  filter(complete.cases(AA_AR) & complete.cases(idas_sa_norm) & complete.cases(idas_wellbeing))
fit.1 <- lm(AA_AR ~ idas_sa_norm, data=df_4001000_pz_strain_idas_complete)</pre>
fit.2 <- lm(AA_AR ~ idas_wellbeing, data=df_4001000_pz_strain_idas_complete)
df_4001000_pz_strain_idas_complete$residual2 <- residuals(fit.2)</pre>
df_4001000_pz_strain_idas_complete$residual1 <- residuals(lm(idas_sa_norm ~ idas_wellbeing, df_4001000_
# Check and make sure these lead to the same effect as the regular multiple regression model
round(summary(lm(AA_AR ~ idas_sa_norm + idas_wellbeing, df_4001000_pz_strain_idas))$coefficients[2,],3)
round(summary(lm(residual2 ~ residual1, df_4001000_pz_strain_idas_complete))$coefficients[2,],3)
# yea, these are basically the same except for some slight change due to rounding and the fact that the
ggplot(df_4001000_pz_strain_idas_complete, aes(x=residual1, y=residual2)) +
  geom_point() +
  stat_smooth(method="lm", color="black", se=TRUE) +
  labs(x="Social anxiety symptoms", y="Response to high-value peer acceptance") +
  papaja::theme_apa() +
  theme(text = element_text(size = 16))
```

```
ggplot(df_4001000_pz_strain_idas_complete, aes(x=idas_sa_norm, y=AA_AR)) +
geom_point() +
stat_smooth(method="lm") +
papaja::theme_apa()
```

Regressions with STRAIN

All stressors

```
stressors <- c("StressCT","StressTH","EvntCT","DiffCT","EvntTH","DiffTH")</pre>
# RewP, P3, LPP
for (data in c("df_150350_cz_strain","df_250450_fz_strain","df_200400_pz_strain",
               "df_4001000_pz_strain","df_6001500_pz_strain")) {
 for (comp in c("A_all","AA_AR","RA_RR")) {
   for (p in stressors) {
      eval(parse(text=paste0('print(summary(lm(',comp,' ~ ',p,', ',data,'))$coef[2,4])')))
   }}}
# LPP
for (data in c("df 4001000 pz strain","df 6001500 pz strain")) {
  for (comp in c("RR_RA","AA_RA")) {
   for (p in stressors) {
      eval(parse(text=paste0('print(summary(lm(',comp,' ~ ',p,', ',data,'))$coef[2,4])')))
   }}}
# P3
for (data in c("df_200400_pz_strain")) {
  for (comp in c("AR_RR","RA_AA")) {
    for (p in stressors) {
      eval(parse(text=paste0('print(summary(lm(',comp,' ~ ',p,', ',data,'))$coef[2,4])')))
   }}}
```

Interpersonal Loss

```
for (data in c("df_4001000_pz_strain","df_6001500_pz_strain")) {
   for (comp in c("RR_RA","AA_RA")) {
     for (p in interpersonal_loss) {
        eval(parse(text=paste0('print(summary(lm(',comp,' ~ ',p,', ',data,'))$coef[2,4])')))
     }}}

# P3
for (data in c("df_200400_pz_strain")) {
   for (comp in c("AR_RR","RA_AA")) {
     for (p in interpersonal_loss) {
        eval(parse(text=paste0('print(summary(lm(',comp,' ~ ',p,', ',data,'))$coef[2,4])')))
     }}}
```

Humiliation

Full sample

```
humiliation <- c("CHEvntCT", "CHDiffCT", "CHAllCT", "CHEvntTH", "CHDiffTH", "CHAllTH")
# RewP, P3, LPP
for (data in c("df_150350_cz_strain","df_250450_fz_strain","df_200400_pz_strain",
              "df_4001000_pz_strain","df_6001500_pz_strain")) {
 for (comp in c("A_all","AA_AR","RA_RR")) {
   for (p in humiliation) {
     eval(parse(text=paste0('print(summary(lm(',comp,' ~ ',p,', ',data,'))$coef[2,4])')))
   }}}
# LPP
for (data in c("df_4001000_pz_strain","df_6001500_pz_strain")) {
 for (comp in c("RR_RA","AA_RA")) {
   for (p in humiliation) {
     eval(parse(text=paste0('print(summary(lm(',comp,' ~ ',p,', ',data,'))$coef[2,4])')))
   }}}
# P3
for (data in c("df_200400_pz_strain")) {
 for (comp in c("AR_RR","RA_AA")) {
   for (p in humiliation) {
     eval(parse(text=paste0('print(summary(lm(',comp,' ~ ',p,', ',data,'))$coef[2,4])')))
   }}}
for (data in c("df_250450_fz_strain")) {
 for (comp in c("AA_AR")) {
   for (p in humiliation) {
     eval(parse(text=paste0('print(summary(lm(',comp,' ~ ',p,', ',data,')))')))
   }}}
summary(lm(formula = AA_AR ~ CHAllCT, data = df_250450_fz_strain)) #Characteristic: Humiliation - Total
summary(lm(formula = AA_AR ~ CHAllTH, data = df_250450_fz_strain)) #Characteristic: Humiliation - Total
```

```
summary(lm(formula = AA_AR ~ CHEvntCT, data = df_250450_fz_strain)) #Characteristic: Humiliation - Coun
summary(lm(formula = AA_AR ~ CHEvntTH, data = df_250450_fz_strain)) #~ Characteristic: Humiliation - Se

ggplot(df_250450_fz_strain, aes(x=CHAllCT, y=AA_AR)) +
    geom_point() +
    stat_smooth(method="lm")

ggplot(df_250450_fz_strain, aes(x=CHAllTH, y=AA_AR)) +
    geom_point() +
    stat_smooth(method="lm")

ggplot(df_250450_fz_strain, aes(x=CHEvntCT, y=AA_AR)) +
    geom_point() +
    stat_smooth(method="lm")
```

These findings are specific to humiliation type stressors from the STRAIN.

The direction suggests that greater experience with humiliating life events is related to a enhanced response to acceptance relative to rejection. However, since rejection appears to elicits a greater ERP than rejection in this time window (i.e., negative difference), it is more interpretable as greater experience with humiliating life events is related to a less negative net response to rejection (right?).

Financial

```
financial <- c("DFEvntCT", "DFDiffCT", "DFAllCT", "DFEvntTH", "DFDiffTH", "DFAllTH")</pre>
for (p in financial) {
 for (data in c("df 150350 cz strain","df 250450 fz strain","df 200400 pz strain")) {
  for (comp in c("RR RA")) {
      eval(parse(text=paste0('print(summary(lm(',comp,' ~ ',p,', ',data,'))$call)
                             print(summary(lm(',comp,' ~ ',p,', ',data,'))$coef[2,4])')))
   }}}
summary(lm(formula = ADI_NATRANK_log_z ~ DFDiffCT, data = df_150350_cz_strain))
summary(lm(formula = ADI_NATRANK_log_z ~ DFDiffTH, data = df_150350_cz_strain))
# Domain: Financial - Count of Chronic Difficulties
summary(lm(formula = DFDiffCT ~ RR_RA, data = df_150350_cz_strain))
summary(lm(formula = DFDiffCT ~ RR_RA, data = df_250450_fz_strain))
summary(lm(formula = RR_RA ~ DFAllCT, data = df_250450_fz_strain))
# Domain: Financial - Severity of Chronic Difficulties
summary(lm(formula = RR_RA ~ DFDiffTH, data = df_150350_cz_strain))
summary(lm(formula = RR_RA ~ DFDiffTH, data = df_250450_fz_strain))
summary(lm(formula = RR_RA ~ DFAllTH, data = df_250450_fz_strain))
df_150350_cz_strain$DFDiffCT_z <- scale(df_150350_cz_strain$DFDiffCT, scale=T, center=T)
df_150350_cz_strain$DFDiffTH_z <- scale(df_150350_cz_strain$DFDiffTH, scale=T, center=T)
```

```
df 250450 fz strain$DFDiffCT z <- scale(df 250450 fz strain$DFDiffCT, scale=T, center=T)
df_250450_fz_strain$DFDiffTH_z <- scale(df_250450_fz_strain$DFDiffTH, scale=T, center=T)
ggplot(df 150350 cz strain, aes(x=DFDiffCT z, y=RR RA)) +
 geom_point() +
  stat smooth(method="lm") +
  geom_text(x=2, y=-2.5, color="blue", size=5, label=paste0("beta=",
      round(tidy(lm(formula = RR RA ~ DFDiffCT z, data = df 150350 cz strain))[2,c(2)],3),
       round(tidy(lm(formula = RR_RA ~ DFDiffCT_z, data = df_150350_cz_strain))[2,c(5)],3))) +
   labs(x="Low value rejection \n(relative to low value acceptance)",
       y="STRAIN financial chronic stressors (count)",
      title="150-350 ms at Cz")
ggplot(df_250450_fz_strain, aes(x=DFDiffCT_z, y=RR_RA)) +
  geom_point() +
  stat_smooth(method="lm") +
  geom_text(x=3, y=-2.5, color="blue", size=5, label=paste0("beta=",
       round(tidy(lm(formula = RR_RA ~ DFDiffCT_z, data = df_250450_fz_strain))[2,c(2)],3),
       ", p=",
      round(tidy(lm(formula = RR_RA ~ DFDiffCT_z, data = df_250450_fz_strain))[2,c(5)],3))) +
   labs(x="Low value rejection \n(relative to low value acceptance)",
      y="STRAIN financial chronic stressors (count)",
      title="250-450 ms at Fz")
ggplot(df_150350_cz_strain, aes(x=DFDiffTH_z, y=RR_RA)) +
  geom_point() +
  stat_smooth(method="lm") +
  geom_text(x=14, y=-2.5, color="blue", size=5, label=paste0("beta=",
       round(tidy(lm(formula = RR_RA ~ DFDiffTH_z, data = df_150350_cz_strain))[2,c(2)],3),
       ", p=",
       round(tidy(lm(formula = RR_RA ~ DFDiffTH_z, data = df_150350_cz_strain))[2,c(5)],3))) +
   labs(x="Low value rejection \n(relative to low value acceptance)",
       y="STRAIN financial chronic stressors (severity)",
      title="150-350 ms at Cz")
ggplot(df 250450 fz strain, aes(x=DFDiffTH z, y=RR RA)) +
  geom point() +
  stat_smooth(method="lm") +
  geom_text(x=14, y=-3, color="blue", size=5, label=paste0("beta=",
       round(tidy(lm(formula = RR_RA ~ DFDiffTH_z, data = df_250450_fz_strain))[2,c(2)],3),
       ", p=",
       round(tidy(lm(formula = RR_RA ~ DFDiffTH_z, data = df_250450_fz_strain))[2,c(5)],3))) +
   labs(x="Low value rejection \n(relative to low value acceptance)",
      y="STRAIN financial chronic stressors (severity)",
       title="250-450 ms at Fz")
```

save(BUDS_cleaning04, file=here("data/BUDS_cleaning04.RData"))