

Appendix

Load libraries

```
library(brms)
library(dplyr)
library(data.table)
library(stringr)
library(reshape2)
library(ggplot2)
library(ggpubr)
```

Subsetting the data to include Latino vs White only

psychotherapy

```
load("brms_pt3a_output_rr_subset.RData")
summary(brms.pt3a)
```

```
## Family: bernoulli
## Links: mu = logit
## Formula: ptadhere90 ~ race_num + gra.cent.priorAD + gra.cent.priorMH + lowincome + (race_num | MS_ProviderID)
## Data: kp10.wh.hi (Number of observations: 204709)
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##           total post-warmup samples = 4000
##
## Group-Level Effects:
## ~MS_ProviderID (Number of levels: 4394)
##           Estimate Est.Error 1-95% CI u-95% CI Rhat
## sd(Intercept)          0.72    0.01    0.69    0.75 1.00
## sd(race_num1)           0.23    0.02    0.20    0.27 1.00
## cor(Intercept,race_num1) -0.80    0.04   -0.88   -0.72 1.00
##           Bulk_ESS Tail_ESS
## sd(Intercept)          1347    2162
## sd(race_num1)           1025    1994
## cor(Intercept,race_num1) 1232    1800
##
## Population-Level Effects:
##           Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS
## Intercept          -0.03    0.02   -0.06    0.00 1.00    1426
## race_num1           -0.14    0.01   -0.16   -0.11 1.00    3615
## gra.cent.priorAD    -0.15    0.01   -0.17   -0.13 1.00   10051
## gra.cent.priorMH     0.06    0.01    0.04    0.09 1.00    7826
## lowincome           -0.05    0.01   -0.07   -0.03 1.00    9039
##           Tail_ESS
## Intercept           1861
## race_num1            3020
## gra.cent.priorAD    3222
## gra.cent.priorMH    3264
## lowincome            3233
##
```

```
## Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample
## is a crude measure of effective sample size, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

proportion by REM interaction

```
load("brms_pt3a_int_output_rr_subset.RData")
summary(brms.pt3a.int)
```

```
## Family: bernoulli
## Links: mu = logit
## Formula: ptadhere90 ~ race_num + gra.cent.priorAD + gra.cent.priorMH + rem.prop + rem.prop * race_num
## Data: kp10.wh.hi (Number of observations: 204709)
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##           total post-warmup samples = 4000
##
## Group-Level Effects:
## ~MS_ProviderID (Number of levels: 4394)
##           Estimate Est.Error 1-95% CI u-95% CI Rhat
## sd(Intercept)          0.68    0.01    0.66    0.71 1.00
## sd(race_num1)          0.22    0.02    0.18    0.25 1.00
## cor(Intercept,race_num1) -0.79    0.04   -0.88   -0.70 1.00
##           Bulk_ESS Tail_ESS
## sd(Intercept)          1222    2284
## sd(race_num1)          1249    2424
## cor(Intercept,race_num1) 1197    1405
##
## Population-Level Effects:
##           Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS
## Intercept             0.42    0.03    0.36    0.48 1.00    1316
## race_num1             -0.29    0.03   -0.36   -0.22 1.00    2842
## gra.cent.priorAD      -0.15    0.01   -0.17   -0.13 1.00    9158
## gra.cent.priorMH       0.06    0.01    0.04    0.08 1.00    7464
## rem.prop              -1.06    0.06   -1.19   -0.94 1.00    1620
## lowincome             -0.04    0.01   -0.06   -0.02 1.00    9227
## race_num1:rem.prop     0.41    0.06    0.28    0.53 1.00    2878
##           Tail_ESS
## Intercept             2535
## race_num1             2998
## gra.cent.priorAD      3135
## gra.cent.priorMH      3173
## rem.prop              2243
## lowincome             3282
## race_num1:rem.prop     2585
##
## Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample
## is a crude measure of effective sample size, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

medication

```
load("brms_ad3a_output_rr_subset.RData")
summary(brms.ad3a)
```

```

## Family: bernoulli
## Links: mu = logit
## Formula: adadhere ~ race_num + gra.cent.priorAD + gra.cent.priorMH + lowincome + (race_num | MS_Prov
## Data: kp10.wh.hi (Number of observations: 246209)
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
## total post-warmup samples = 4000
##
## Group-Level Effects:
## ~MS_ProviderID (Number of levels: 4443)
## Estimate Est.Error 1-95% CI u-95% CI Rhat
## sd(Intercept) 0.36 0.01 0.34 0.38 1.00
## sd(race_num1) 0.08 0.04 0.01 0.15 1.08
## cor(Intercept,race_num1) 0.17 0.23 -0.20 0.70 1.03
## Bulk_ESS Tail_ESS
## sd(Intercept) 1518 2343
## sd(race_num1) 46 290
## cor(Intercept,race_num1) 267 955
##
## Population-Level Effects:
## Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS
## Intercept 1.09 0.01 1.07 1.11 1.00 3944
## race_num1 -0.69 0.01 -0.71 -0.67 1.00 5926
## gra.cent.priorAD 0.23 0.01 0.21 0.25 1.00 8141
## gra.cent.priorMH 0.18 0.01 0.16 0.20 1.00 6300
## lowincome -0.14 0.01 -0.15 -0.12 1.00 7772
## Tail_ESS
## Intercept 3425
## race_num1 3311
## gra.cent.priorAD 3341
## gra.cent.priorMH 2819
## lowincome 3252
##
## Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample
## is a crude measure of effective sample size, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).

```

proportion by REM interaction

```

load("brms_ad3a_int_output_rr_subset.RData")
summary(brms.ad3a.int)

```

```

## Family: bernoulli
## Links: mu = logit
## Formula: adadhere ~ race_num + gra.cent.priorAD + gra.cent.priorMH + rem.prop + rem.prop * race_num
## Data: kp10.wh.hi (Number of observations: 246209)
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
## total post-warmup samples = 4000
##
## Group-Level Effects:
## ~MS_ProviderID (Number of levels: 4443)
## Estimate Est.Error 1-95% CI u-95% CI Rhat
## sd(Intercept) 0.35 0.01 0.34 0.37 1.00
## sd(race_num1) 0.05 0.03 0.00 0.12 1.06
## cor(Intercept,race_num1) -0.08 0.30 -0.65 0.62 1.02

```

```

##                               Bulk_ESS Tail_ESS
## sd(Intercept)                 1817    2730
## sd(race_num1)                  98     352
## cor(Intercept,race_num1)      2309    1382
##
## Population-Level Effects:
##           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## Intercept          1.27    0.02    1.23    1.31 1.00    2767
## race_num1          -0.45    0.03   -0.50   -0.39 1.00    2994
## gra.cent.priorAD    0.23    0.01    0.21    0.25 1.00    7019
## gra.cent.priorMH    0.18    0.01    0.17    0.21 1.00    6046
## rem.prop           -0.43    0.04   -0.51   -0.35 1.00    2506
## lowincome          -0.12    0.01   -0.14   -0.10 1.00    8941
## race_num1:rem.prop -0.37    0.05   -0.47   -0.27 1.00    2808
##           Tail_ESS
## Intercept          2600
## race_num1          2760
## gra.cent.priorAD   2869
## gra.cent.priorMH   2934
## rem.prop           3068
## lowincome          3104
## race_num1:rem.prop 2867
##
## Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample
## is a crude measure of effective sample size, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).

```