brms-modeling-figure

Dan Spakowicz

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```
load("data/model-output.RData")

m <- brm
rm(brm)

# Change `days` back to numeric
m[["data"]]$days <-
  m[["data"]]$days %>%
  as.character() %>%
  as.numeric()
```

Model evaluation based on [the brms vignette https://cran.r-project.org/web/packages/brms/vignettes/brms_nonlinear.html]

```
summary(m)
```

```
##  Family: negbinomial
##   Links: mu = log; shape = identity
## Formula: Akkermansia ~ days + (1 | SubjectID) + cluster * IL17F
##    Data: x (Number of observations: 314)
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup samples = 4000
##
## Group-Level Effects:
## ~SubjectID (Number of levels: 23)
##               Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## sd(Intercept)     2.91      0.60     1.96     4.28        955 1.00
##
## Population-Level Effects:
##                Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## Intercept          4.43      0.79     2.81     5.95        817 1.00
## days              -0.00      0.00    -0.00    -0.00       4550 1.00
## cluster3           1.43      1.59    -1.68     4.67       1148 1.00
## IL17F              1.04      0.92    -0.69     2.94       1629 1.00
## cluster3:IL17F    -1.13      0.99    -3.16     0.79       1624 1.00
##
## Family Specific Parameters:
##       Estimate Est.Error l-95% CI u-95% CI Eff.Sample Rhat
## shape     0.33      0.03     0.28     0.39       3574 1.00
##
## 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).
```

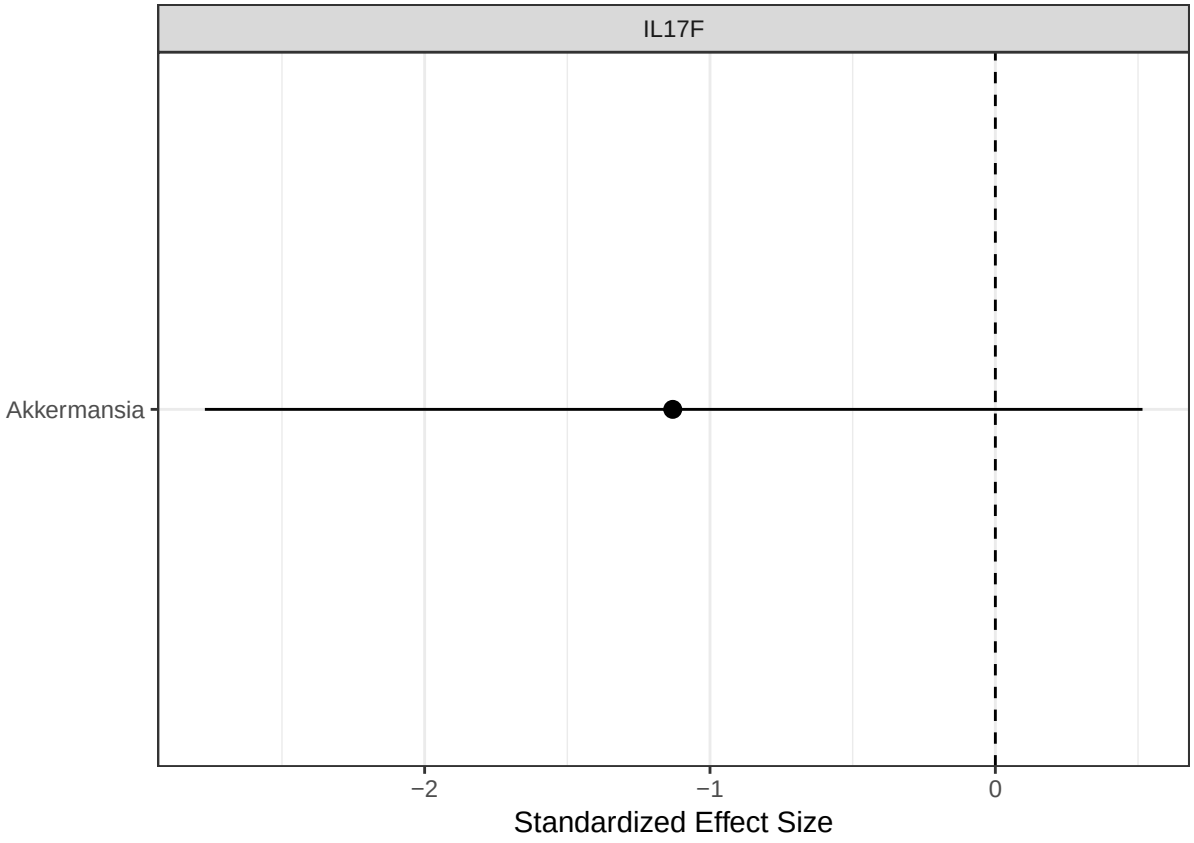
The goal of this is to visualize the result of this model in a way that displays the effect size.

Version 1: Forest plot style

```
# Regenerating a table like the output from the modeling
c3 <- broom::tidy(m) %>%
  filter(grepl("cluster3:", term)) %>%
  mutate(cytokine = str_remove(term, "b_cluster3:")) %>%
  mutate(genus = m$formula$resp)
```

After completing this for all models `bind_rows` together, filter to significant interactions and plot

```
c3 %>%
  ggplot(aes(x = genus, y = estimate, ymin = lower, ymax = upper)) +
  geom_pointrange() +
  coord_flip() +
  theme_bw() +
  geom_hline(yintercept = 0, linetype = "dashed") +
  labs(x = "", y = "Standardized Effect Size") +
  facet_wrap(~cytokine)
```



Version 2: ggridges style

```
# Grab interaction term
vars <- get_variables(m)
```

```
term <- vars[grep("b_cluster3:", vars)]
tsub <- gsub("b_cluster3:", "", term)
genus <- "Akkermansia"

genus.vec <-
  m %>%
  spread_draws(!!sym(term)) %>%
  select(!!sym(term)) %>%
  mutate(genus = !!m$formula$resp) %>%
  rename(value = !!sym(term)) %>%
  mutate(cytokine = tsub)
```

After completing this for all models `bind_rows` together, and plot

```
genus.vec %>%
  ggplot(aes(x = value, y = genus)) +
  geom_density_ridges() +
  labs(x = "Standardized Effect Size",
       y = "") +
  facet_wrap(~cytokine) +
  geom_vline(xintercept = 0, linetype = "dashed") +
  theme_bw()
```

```
## Picking joint bandwidth of 0.17
```