PSY652, Unit 7, In class activity – Exploring a 3-Way Interaction
Dataframe: sleep.csv

Build inside your Sleep Notebook for this activity. Here, we will continue to explore the hygiene by anxiety interaction effect, but now consider the effect for females as well.

At the point where we left off:

1. Create a third level header called "Explore the model for females." Add a code chunk. Use a pipe to create a new dataset called slp_females (based on the slp dataset) where you select only females (use the filter function) and then center hygiene and anxiety at the mean (use the mutate function). Next, fit a linear regression model in which sleep is regressed on the centered versions of hygiene and anxiety, as well as the interaction between hygiene and anxiety. Don't include any other control variables. Interpret the model – does there seem to be an interaction between hygiene and anxiety for females?

2. Now, determine if the interaction effect between hygiene and anxiety significantly differs between males and females. Create a fourth level header called "Fit a 3-way interaction to determine if the hygiene*anxiety effect is significantly different by sex." Create a new dataset called slp_3way (based on the slp dataset), we'll keep males and females, so no need to filter. However, we need to center hygiene and anxiety at the mean in the whole sample, use mutate to accomplish this task. Now, fit a model with a three-way interaction. When fitting a 3-way interaction, you must include all 2-way interactions, so regress sleep on hygiene_m, anxiety_m, female, hygiene_m*anxiety_m, hygiene_m*female, anxiety_m*female, and hygiene_m*anxiety_m*female.

3. Use the output from the model in Step 2 to write two reduced forms of the equation – one that represents the relationship between hygiene and sleep when anxiety is 1 standard deviation above the mean in the entire sample for males, and one that represents the relationship between hygiene and sleep when anxiety is 1 standard deviation above the mean in the entire sample for females. Note that to get the standard deviation, I used: sd(slp_3way$anxiety_m). To get started, use the equation below and plug in the known values (e.g., for the male equation, plug in 0 for female and .9047863 for anxiety_m), solve, combine likes, and reduce to a final intercept and slope.

Y-hat$_i$ = 66.971 + 5.248*hygiene_m$_i$ + -3.299*anxiety_m$_i$ + 4.924*female$_i$ + -.945*hygiene_m$_i$*anxiety_m$_i$ + -.307*hygiene_m$_i$*female$_i$ + .748*anxiety_m$_i$*female$_i$ + .861*hygiene_m$_i$*anxiety_m$_i$*female$_i$

For males when anxiety_m is 1 SD above the mean: Y-hat$_i$ = _____ + _____ * hygiene_m$_i$

For females when anxiety_m is 1 SD above the mean: Y-hat$_i$ = _____ + _____ * hygiene_m$_i$

4. In the model for Step 2, the slope for hygiene_m:anxiety_m is the interaction effect for males – because they are the group coded 0 for female. The slope for the 3 way interaction (hygiene_m:anxiety_m:female) is the DIFFERENCE in the hygiene_m:anxiety_m interaction effect for females compared to males. Therefore, the predicted interaction effect for females is obtained by taking the male interaction effect and adding the 3-way interaction effect (-.945 + .861 = -.084). Take a look at the output from Step 1, do you see this value somewhere? Is this what you expected?

5. Use the jtools package to plot the 3-way interaction using the code in the last code chunk on the back of this sheet. Talk through the plots with your partner.

6. Take a look at the simple slopes produced by jtools – note the simple slopes for males and females when anxiety is 1 standard deviation above the mean. Do they match what you obtained in Step 3?

Explore the model for females
```{r}

slp_females <- slp %>%
  filter(female == 1) %>%
  mutate(hygiene_m = hygiene - mean(hygiene),
         anxiety_m = anxiety - mean(anxiety))

cont1_female <- lm(data=slp_females, sleep ~ hygiene_m + anxiety_m + hygiene_m*anxiety_m)
ols_regress(cont1_female)


```

Fit a 3-Way interaction to determine if the hygiene*anxiety effect is significantly different by sex
```{r}

slp_3way <- mutate(slp,
                   hygiene_m = hygiene - mean(hygiene),
                   anxiety_m = anxiety - mean(anxiety))

mod3way <- lm(data = slp_3way, sleep ~ hygiene_m + anxiety_m + female +
                hygiene_m*anxiety_m + hygiene_m*female + anxiety_m*female + hygiene_m*anxiety_m*female)
ols_regress(mod3way)

#note that as a shortcut, you can write the following, which will create all interaction terms for you
#mod3way <- lm(data = slp_3way, sleep ~ hygiene_m*anxiety_m*female)
#ols_regress(mod3way)

sd(slp_3way$anxiety_m)

```

Plot the results of the 3-Way Interaction
```{r}
#install.packages("cowplot")
library(cowplot)

threeway.jn <- lm(data=slp_3way, sleep ~  hygiene*anxiety*female.f)

probe_interaction(threeway.jn, pred = hygiene, modx = anxiety, mod2 = female.f,
                  jnplot = TRUE,
                  x.label = "Sleep Hygiene",
                  y.label = "Sleep Efficiency",
                  main.title = "Differential effect of hygiene on sleep efficiency by anxiety",
                  legend.main = "Level of Anxiety")

```