Pease Replication List

1. Open **PeaseReplicationNotebook** and run the first three code chunks (Provided)
   1. # Load libraries
   2. # Read in the original datafiles
   3. # Read in the saved datafiles
2. Use pipes to assign the following changes to the ***midus2*** dataframeto a new dataframe called ***midus2.subset***
   1. Filter the data to contain only cases where ***SAMPLMAJ*** is equal to 1.
   2. Subset the data to contain only the following variables
      1. M2ID
      2. B1PRSEX
      3. B1PF7A
      4. All variables that contain "***B1SE6***" in their name
      5. B1PAGE\_M2
      6. B1SE7I
      7. B1SE7T
      8. B1SE7BB
      9. B1SE7EE
      10. B1SNEURO
      11. B1SEXTRA
      12. B1SOPEN
      13. B1SCONS2
      14. B1SAGREE
      15. B1SMPQAG
   3. Filter the data to include only participants with no missing data for any of the following variables:
      1. B1SNEURO
      2. B1SEXTRA
      3. B1SOPEN
      4. B1SCONS2
      5. B1SAGREE
      6. B1SMPQAG
      7. B1PRSEX
      8. B1PAGE\_M2
      9. B1PF7A
   4. Create a new flag variable called ***IN\_MIDUS2*** that is equal to 1 for every participant in the dataset.
3. Use pipes to assign the following changes to the ***bio*** dataframeto a new dataframe called ***bio.subset***
   1. Subset the data to contain only the following variables
      1. M2ID
      2. All variables that contain “***B4Q4***" in their name
      3. All variables that contain “***B4Q5***" in their name
      4. All variables that contain “***B4Q6***" in their name
      5. B4QTA\_AG
      6. B4QTA\_AT
      7. B4QTA\_AR
      8. B4QAE\_AI
      9. B4QAE\_AO
      10. B4QAE\_AC
   2. Filter the data to include only participants with no missing data for any of the following variables:
      1. B4QTA\_AG
      2. B4QTA\_AT
      3. B4QTA\_AR
      4. B4QAE\_AI
      5. B4QAE\_AO
      6. B4QAE\_AC
   3. Create a new flag variable called ***IN\_BIO*** that is equal to 1 for every participant in the dataset.
4. Use pipes to assign the following to a new dataframe called ***combine***
   1. Use a joining function to merge the ***midus2.subset*** and ***bio.subset*** data such that all cases from ***midus2.subset*** are retained and any cases in ***bio.subset*** that don’t have a corresponding case in ***midus2.subset*** are dropped.
      1. Use M2ID number as the key
   2. Use select() to move all of the following variables to the front of the dataframe, followed by all remaining variables
      1. M2ID
      2. B1PF7A
      3. B1SNEURO
      4. B1SAGREE
      5. B1SEXTRA
      6. B1SOPEN
      7. B1SCONS2
      8. B4QTA\_AG
      9. B4QTA\_AT
      10. B4QTA\_AR
      11. B4QAE\_AI
      12. B4QAE\_AO
      13. B4QAE\_AC
      14. B1SMPQAG
      15. B1PF7A
      16. B1PAGE\_M2
      17. B1PRSEX
5. ***# create dataset for analysis*** (provided)
6. Reproduction of correlation matrix from article (w/ apaTables)
7. Insert a new code chunk with the first-level header ***“# Center all of the continuous variables***” and make the following changes to the analyze data:
   1. Create a new variable called ***B1SNEURO.C*** that is the mean-centered version of ***B1SNEURO***.
   2. Create a new variable called ***B1SAGREE.C*** that is the mean-centered version of ***B1SAGREE***.
   3. Create a new variable called ***B1SEXTRA.C*** that is the mean-centered version of ***B1SEXTRA***.
   4. Create a new variable called ***B1SOPEN.C*** that is the mean-centered version of ***B1SOPEN***.
   5. Create a new variable called ***B1SCONS2.C*** that is the mean-centered version of ***B1SCONS2***.
   6. Create a new variable called ***B1PAGE\_M2.C*** that is the mean-centered version of ***B1PAGE\_M2***.
8. Get descriptive statistics for the analyze data and confirm that your new variables all have a mean of 0.
9. Estimate a series of 7 regression models: ***m1 – m7.*** For each model, the independent variables will be the same: Neuroticism, Agreeableness, Extraversion, Openness, Conscientiousness, Age, and Gender (“***FEMALE***”). Be sure to use the mean-centered versions for everything but Gender.
   1. The Dependent variable for each model is listed below.
      1. ***m1:*** Trait Anger
      2. ***m2:*** Trait Anger: Angry Temperament
      3. ***m3***: Trait Anger: Angry Reaction
      4. ***m4***: Anger Expression: Anger-In
      5. ***m5***: Anger Expression: Anger-Out
      6. ***m6***: Anger Expression: Anger-Control
      7. ***m7***: Aggression