NHANES cleaning assignment

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Today we are going to look at blood pressure in the NHANES dataset. Our goal is to look at the observed blood pressures and try to predict the unobserved blood pressures. Start by reading in the data set using library(NHANES) and data(NHANES).

- 1) The variables that we are interested in today are ID, Gender, Age, Weight, Height, BPSys1, BPSys2, BPSys3, BPSysAve, BPDia1, BPDia2, BPDia3, TotChol, and Diabetes. Make a new data frame with only these covariates.
- 2) What is the age of the youngest person with a blood pressure reading? Remove all of the people from the data set who are younger than that person.
- 3) Make a new data frame called BP_NA with all of the people who still have NA values for BPSysAve. With your original data frame, remove these people and remove the column BPSysAve.
- 4) gather the columns that start with BPSys into two columns: SysMeasure and BPSys.
- 5) Keep only the numbers in the SysMeasure column. Make sure that they are class numeric.
- 6) Repeat 4 and 5 for the BPDia columns. Then only keep the rows where SysMeasure is the same as DiaMeasure.
- 7) Since systolic and diastolic blood pressures are measured at the same time, we're going to remove the strange values of either. Remove all values of systolic that are greater than 190 or less than 70. Remove all values of diastolic that are greater than 100 or less than 40. Also remove all NA values for both.
- 8) Find the average values of BPSys for each ID while keeping Gender, Age, Weight, Height, TotChol, and Diabetes. Save this as BPSysAve2.
- 9) Fit a linear model for BPSysAve2 using the other covariates (but not ID) and save it to BP_fit. Check out the linear model fit.
- 10) Predict the values in BP_NA using BP_fit and save it to BP_preds.

I-can't-believe-you-made-it-this-far bonus) Compare the values of BPSysAve2 that we generated versus the original values of BPSysAve. Are they the same? We haven't covered this as much, but you can use left_join to combine two data frames by matching variables (such as ID), which easily allows us to compare the averages by person.