Homework1

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```r
library(tidyverse)
```

Part 1

Question 1

```r
Y_obs <- c(8.62,1.48,8.93,9.57,2.65,7.3,.06,1.72,2.19,7.32,7.53,7.62)
Z <- c(rep(0,6), rep(1,6))
```

a)

```r
Y_obs <- c(8.62,1.48,8.93,9.57,2.65,7.3,.06,1.72,2.19,7.32,7.53,7.62)
Z <- c(rep(0,6), rep(1,6))

tstat_obs <- mean(Y_obs[Z == 1]) - mean(Y_obs[Z == 0])

ind_combos <- combn(1:12,6)
tstats <- vector(mode = "double",length = ncol(ind_combos))

for (i in 1:ncol(ind_combos)) {
  Zperm <- rep(0,12)
  Zperm[ind_combos[,i]] = 1
  tstats[i] = mean(Y_obs[Zperm==1]) - mean(Y_obs[Zperm==0])
}

pval <- mean(abs(tstats) >= abs(tstat_obs))
```

The two-tailed p-value is 0.2706.

b)

```r
set.seed(2929)
sampled_tstats <- sample(tstats, size = 1000, replace = TRUE)
pval_1000 <- mean(abs(sampled_tstats) >= abs(tstat_obs))
```

The two-tailed p-value from 1000 samples from the distribution under the Sharp Null Hypothesis is 0.27.

c)

```r
ttest_pval <- t.test(Y_obs[Z==1], Y_obs[Z==0],var.equal = TRUE)$p.value
```

The p-value using a t-test is 0.3368.

d)

(b)'s approximation of (a) is part of the assignment mechanism component of the potential outcome framework as it draws from the distribution of all possible treatment assignments.

(c)'s approximation of (a) falls under the probabilistic model component of the potential outcome framework as it assumes the data in both groups is normally distributed with equal variance.

Question 2

a)

```r
Y_obs_orig <- matrix(Y_obs,nrow = 6)
colnames(Y_obs_orig) <- c("0", "1")

combos <-expand.grid(pair1 = 0:1,pair2 = 0:1, pair3 = 0:1
                     ,pair4 = 0:1,pair5 = 0:1, pair6 = 0:1)
```

```r
tstats <- vector(mode = "double",length = nrow(combos))
for (i in 1:nrow(combos)) {
  Y_obs_perm <- Y_obs_orig
  ind <- which(combos[i,] == 1)
  Y_obs_perm[ind,] = Y_obs_perm[ind,c(2,1)]
  tstats[i] = mean(Y_obs_perm[,2]) - mean(Y_obs_perm[,1])
}
```

```
pval <- mean(abs(tstats) >= abs(tstat_obs))
```

The p-value from randomizing within pairs is 0.375.

b)

```
set.seed(2121)
sampled_tstats <- sample(tstats, size = 1000, replace = TRUE)
pval_1000 <- mean(abs(sampled_tstats) >= abs(tstat_obs))
```

The p-value from sampling is 0.398.

c)

```
ttest_pval <- t.test(Y_obs[Z==1], Y_obs[Z==0], var.equal = TRUE, paired = TRUE)
```

Using a paired t-test the p-value is 0.3652.

d)

Part (2b) is a part of the assignment mechanism as it makes sure $Z \perp X$ through randomization.

Part (2c) is a part of the probabilistic model just like question 1.

Question 3

$$
\begin{aligned}
Y_i^{obs} &= Z_i Y_i(1) + (1 - Z_i) Y_i(0) \\
\hat{\tau} &= \frac{1}{n_1} \sum_{i=1}^{n} Z_i Y_i^{obs} - \frac{1}{n_0} \sum_{i=1}^{n} (1 - Z_i) Y_i^{obs} \\
\hat{\tau} &= \frac{1}{n_1} \sum_{i=1}^{n} Z_i Y_i(1) - \frac{1}{n_0} \sum_{i=1}^{n} (1 - Z_i) Y_i(0) \\
&\text{Under CRE } Z_i \perp Y_i(0), Y_i(1) \text{ and } E[Y(z)] = Y(z) \\
E[\hat{\tau}] &= \frac{1}{n_1} \sum_{i=1}^{n} E[Z_i] Y_i(1) - \frac{1}{n_0} \sum_{i=1}^{n} E(1 - Z_i) Y_i(0) \\
&= \frac{1}{n_1} \sum_{i=1}^{n} \frac{n_1}{n} Y_i(1) - \frac{1}{n_0} \sum_{i=1}^{n} \frac{n_0}{n} Y_i(0) \\
&= \frac{1}{n_1} \sum_{i=1}^{n} Y_i(1) - \frac{1}{n_0} \sum_{i=1}^{n} Y_i(0) = \tau
\end{aligned}
$$

Question 4

Part 2

Question 1

```
pot_outcomes <- matrix(c(35, 40, 45 ,55, 55 ,55, 65, 70, 25, 30, 45, 55, 60, 65, 75, 80, 3
colnames(pot_outcomes) <- c("Y1_pot","Y0_pot")
sample_ind = combn(1:12, m =4, simplify = FALSE)
rand_assign_ind = combn(1:4, m =2, simplify = FALSE)
```

```
diffs <- matrix(NA, nrow = length(sample_ind), ncol = length(rand_assign_ind))

for (samp in seq_along(sample_ind)) {
  sample <- pot_outcomes[sample_ind[[samp]],]

  for (i in seq_along(rand_assign_ind)) {

    Y1_obs <- sample[rand_assign_ind[[i]],"Y1_pot"]
    Y0_obs <- sample[-rand_assign_ind[[i]],"Y0_pot"]

    difference <- mean(Y1_obs) - mean(Y0_obs)
```

```r
    diffs[samp,i] <- difference
  }
}
var(as.vector(diffs))
```

```
[1] 228.9755
```

```r
var1 = var(pot_outcomes[,"Y1_pot"])
var0 = var(pot_outcomes[,"Y0_pot"])

var01 = sum((pot_outcomes[,"Y1_pot"] -pot_outcomes[,"Y0_pot"] - (mean(pot_outcomes[,"Y1_po

var0/6+var1/6-var01/12
```

```
[1] 75.42614
```

Question 2

```r
diffs <- matrix(NA, nrow = length(sample_ind), ncol = length(rand_assign_ind))

for (samp in seq_along(sample_ind)) {
  for (i in seq_along(rand_assign_ind)) {

    sample <- pot_outcomes[sample_ind[[samp]],]
    Y1_obs <- sample[rand_assign_ind[[i]],"Y1_pot"]
    Y0_obs <- sample[-rand_assign_ind[[i]],"Y0_pot"]
    difference <- mean(Y1_obs) - mean(Y0_obs)

    diffs[samp,i] <- difference
  }
}
var(apply(diffs, MARGIN = 1,FUN = sum))
```

```
[1] 94.50911
```

Part 3

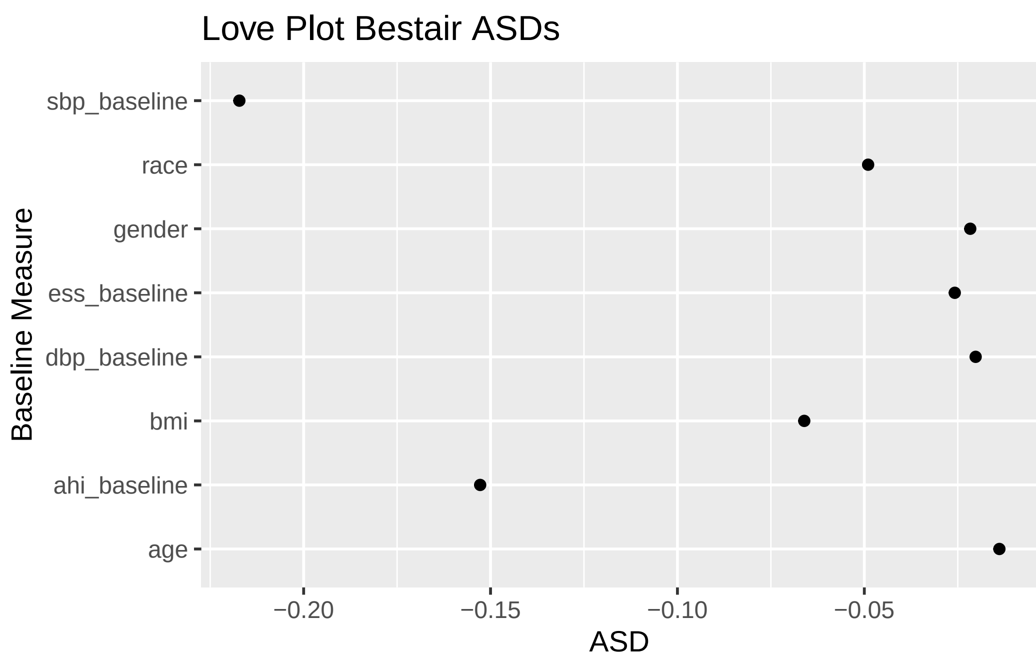
```
bestair <- readxl::read_xlsx("bestair640-1.xlsx", sheet = "data")
for (i in seq_along(bestair)) {
  y = pull(bestair[,i])
  m = mean(y, na.rm = TRUE)
  y = ifelse(is.na(y), m, y)
  bestair[,i] = y
}
```

Question 1

```
baselines <- c("gender","age","bmi",
 "race","sbp_baseline","dbp_baseline","ahi_baseline","ess_baseline")
ASDs = matrix(NA, nrow = 1, ncol = 8)
colnames(ASDs) <- baselines
Z <- bestair$treatment_arm
for (bl in baselines) {
  X <- pull(bestair[,bl])
  s1 <- var(X[Z==1])
  s0 <- var(X[Z==0])
  diff_sum <- sum(X*Z)/sum(Z)-sum(X*(1-Z))/sum(1-Z)
  asd <- diff_sum/sqrt(s1+s0)
  ASDs[,bl] <- asd

}
```

```
#love plot
asd_dat <- tibble(
  bls = baselines,
  asd = ASDs[1,]
)
ggplot(asd_dat,aes(x = asd, y = bls)) +
  geom_point() +
  labs(title = "Love Plot Bestair ASDs"
       ,y = "Baseline Measure"
       ,x = "ASD")
```



Question 2

```
Z <- bestair$treatment_arm
Y <- bestair$sbp_6mo
tau_unadj <- mean(Y[Z==1]) - mean(Y[Z==0])
tau_unadj
```

```
[1] -4.907177
```

```
bestair_centered <- bestair|>
  mutate(across(gender:ess_baseline, ~ .x-mean(.x)))

ancova1 <- lm(formula = sbp_6mo~.,data = bestair_centered)
tau_adj_anc1 <- ancova1$coefficients["treatment_arm"]

ancova2 <- lm(formula = sbp_6mo~.^2,data = bestair_centered)
tau_adj_anc2 <- ancova2$coefficients["treatment_arm"]
```

```
X_mat <- as.matrix(bestair_centered[,2:9])
as.vector(ancova1$residuals)
```

```
  [1]   0.72418463   5.87782418   2.02205186  -0.67970961   5.48543941
  [6]  11.12333493  22.03036046  10.40373557  16.00880076  -7.49903245
 [11]  21.83336401   0.34417092  -2.77587678  -5.46146113   6.29798214
 [16]   1.53501748  -1.69504331  -6.45803092 -15.68243254   8.21399912
 [21] -15.30960343  -5.04025508  -7.17155008  -3.46508683  -5.34078380
 [26]  -6.00645577  15.48489652  -1.73139629   4.81205921 -11.89994057
 [31]  -1.35631817  -0.12539863 -10.92493221  -7.45379837   1.61531145
 [36]   1.98766286 -11.96707802   4.32947706  -5.46926497   4.36435506
 [41]   4.13981194 -13.31440187  -2.16750693   2.99973369  -1.26475631
 [46]  -3.99403619 -16.52478518  -2.76970803   1.49838183   3.89688930
 [51]   0.25809623   1.64161358   5.82966726  21.09775063  -9.38553208
 [56]   9.00219896 -11.07159488  11.15178012   0.53924690 -13.11086054
 [61]  11.47154172 -12.43857882   6.84561827  -5.95813641  12.80801506
 [66] -13.32132353  -4.58483058 -21.71124152   4.51179466  15.55032001
 [71]   6.38077123  -3.86445816  11.24286990   0.81960655  -2.86280479
 [76]   2.69471525  22.96781764   5.77082371   0.11695790  -0.06314628
 [81]   5.75139807  -5.22485105   1.18023905  -9.62798032   1.56231069
 [86]   1.06411549   2.79881359   3.35448165   0.39576589  11.42904196
 [91] -15.40328838   7.23520472   4.86064081   6.39067383  -6.70689714
 [96]  -9.12434444  11.34250922  -3.65727973   0.41435408  -9.10183514
[101] -12.54239142  -8.50610473  11.93262901   3.60166708 -13.79882297
[106]   9.35128949  -6.79121015  -0.92039034  -6.78934590   1.15694232
[111]   0.35542314   4.09807003   0.68423875   3.10956405   5.76107354
[116]  -0.34215833  12.44204229   1.56215718  -5.82690642  -5.81474801
[121] -16.27646759  -6.91003448   4.11894404  -8.39743233
```

```r
hw_se_anc1 <-sqrt(car::hccm(ancova1
                            ,type = "hc2")["treatment_arm","treatment_arm"])
#sqrt(car::hccm(ancova2, type = "hc0")["treatment_arm","treatment_arm"])
```

Question 3

```r
bestair_hyperten <- bestair_centered |>
  mutate(resist_hyperten = if_else(sbp_6mo>=130,1,0)) |>
  select(treatment_arm:ess_baseline,resist_hyperten)
```

a)

```r
Z <- bestair$treatment_arm
Y <- bestair_hyperten$resist_hyperten
mean(Y[Z==1]) - mean(Y[Z==0])
```

```
[1] -0.2083442
```

```r
bin_ols <- lm(resist_hyperten~., data = bestair_hyperten)
bin_ols$coefficients["treatment_arm"]
```

```
treatment_arm
   -0.1299632
```

```r
bin_ols_inter <- lm(resist_hyperten~.^2, data = bestair_hyperten)
bin_ols_inter$coefficients["treatment_arm"]
```

```
treatment_arm
  -0.08518287
```

b)