

# Homework1

Jon Campbell

```
library(tidyverse)
```

## Part 1

### Question 1

```
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)

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

ind_combos <- combn(12,6, simplify = FALSE)
tstats = c()
for (i in seq_along(ind_combos)) {
  Y_treat_mean <- mean(Y_obs[ind_combos[[i]]])
  Y_notreat_mean <- mean(Y_obs[-ind_combos[[i]]])
  tstats <- c(tstats, Y_treat_mean - Y_notreat_mean)
}

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

```
[1] 0.2705628
```

b)

```
sampld_tstats <- sample(tstats, size = 1000, replace = TRUE)
pval_1000 <- mean(abs(sampld_tstats) >= abs(tstat_obs))
pval_1000
```

```
[1] 0.252
```

c)

```
t.test(Y_treat, Y_notreat, var.equal = TRUE)$p.value
```

```
[1] 0.3367792
```

d)

## Question 2

a)

```
X <- c(1:6, 1:6)
taus = c()
for (i in unique(X)) {
  tau = Y_obs[Z == 1 & X == i] - Y_obs[Z == 0 & X == i]
  taus = c(taus, tau)
}
tstat_obs = mean(taus)

tstats <- c()
for (i in seq_along(ind_combos)) {
  Z_perm = rep(0, 12)
  Z_perm[ind_combos[[i]]] = 1

  taus = c()
  for (j in unique(X)) {
    tau = Y_obs[Z_perm == 1 & X == j] - Y_obs[Z_perm == 0 & X == j]
    taus = c(taus, tau)
  }
  tstats = c(tstats, mean(taus))
}
```

```

}

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

```

[1] NA

b)

```
ind_combos[[70]]
```

[1] 1 2 3 7 9 11

c)

```

t.test(Y_treat, Y_notreat
       , var.equal = TRUE, paired = TRUE)

```

Paired t-test

```

data: Y_treat and Y_notreat
t = -0.99559, df = 5, p-value = 0.3652
alternative hypothesis: true mean difference is not equal to 0
95 percent confidence interval:
 -7.229626  3.192959
sample estimates:
mean difference
 -2.018333

```

d)

### Question 3

$$Y_i^{obs} = Z_i Y_i(1) + (1 - Z_i) Y_i(0) \hat{\tau} = \frac{1}{n_1} \sum_{i=1}^n Z_i Y_i^{obs} - \frac{1}{n_0} \sum_{i=1}^n (1 - Z_i) Y_i^{obs} \hat{\tau} = \frac{1}{n_1} \sum_{i=1}^n Z_i Y_i(1) - \frac{1}{n_0} \sum_{i=1}^n (1 - Z_i) Y_i(0) \text{ Under } \tau = 0$$

## 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, 30, 40, 45, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100), nrow = 12, ncol = 4)
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)

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

```
[1] 228.9755
```

```
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_pot"] - mean(pot_outcomes[, "Y0_pot"])))^2) / 12

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

```
[1] 75.42614
```

## Question 2

```
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])
}
```

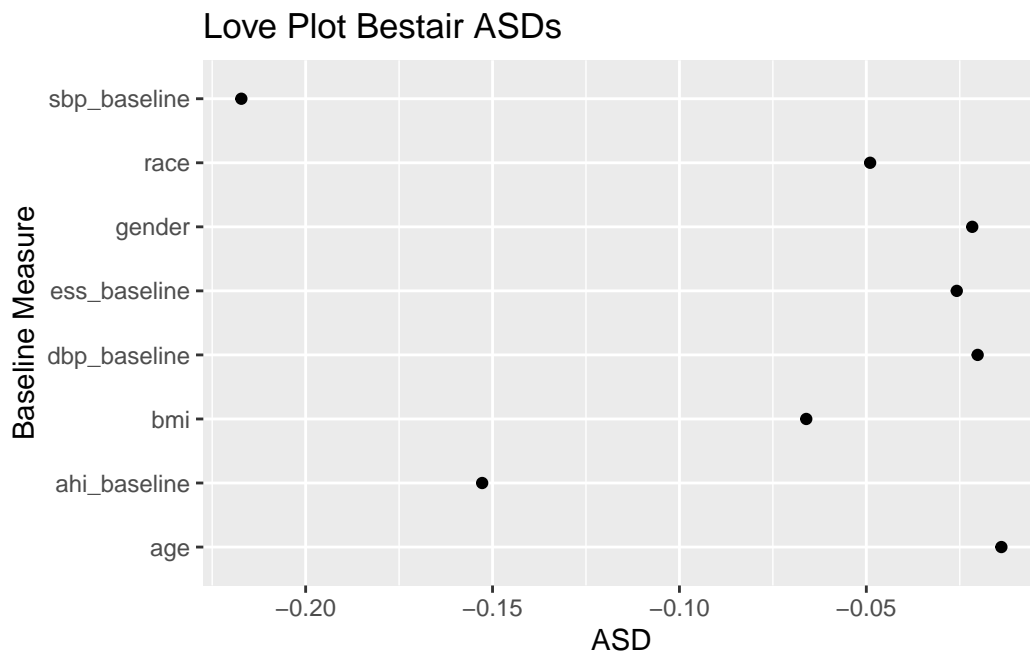
```

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
```

```
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

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

a)

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

```
[1] -0.2083442
```

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

```
treatment_arm
-0.1299632
```

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

```
treatment_arm
-0.08518287
```

b)