<4월 15일 meeting comment 정리>

```
library(boot)
library(tableone)
library(survey)
library(Hmisc)
library(tidyverse)
library(Matching)

delta<-seq(-2,-1,by=0.01) # delta0 sequence
prevalence<-matrix(0,nrow=length(delta),ncol=1)

## prevalence calculate by changing delta0
for(i in 1:length(delta)){
  delta0<-delta[i]
  delta_b<-0.01
  delta_c<-0.01
  #B,C,U,E generating
  set.seed(123*i)
  exposure_hat<-replicate(100000,expr={
    #set.seed(delta0)
    B<-rbinom(1,1,prob=0.5)
    C<-rnorm(1,0,1)
    U<-runif(1)
    p_z<-inv.logit(delta0+delta_b*B+delta_c*C)
    E<-rbinom(1,1,prob=p_z)
    c(B,C,U,E)
    })
  prevalence[i,]<-mean(exposure_hat[4,])
}
# exposure ratio
prevalence
min(prevalence)
[1] 0.11981

## Data generating
delta_rare<-delta[which(prevalence==min(prevalence))] # -2

delta_rare
[1] -2

# sample store
B_sample<-matrix(0,nrow=100,ncol=1000)
```

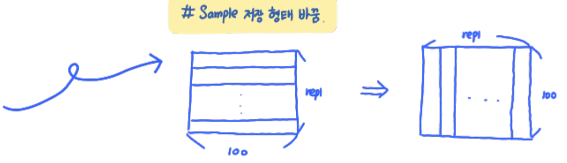
```
C_sample<-matrix(0,nrow=100,ncol=1000)
U_sample<-matrix(0,nrow=100,ncol=1000)
E_sample<-matrix(0,nrow=100,ncol=1000)
Y_sample<-matrix(0,nrow=100,ncol=1000)

effect<-c(log(1.2),log(1.5),log(2),log(2))

# 1000th replication data generating
for(repl in 1:1000){
  delta0<-delta_rare
  delta_b<-0.01
  delta_c<-0.01
  set.seed(123*repl)
  sample<-replicate(100,expr={
    B<-rbinom(1,1,prob=0.5)
    C<-rnorm(1,0,1)
    U<-runif(1)
    p_z<-inv.logit(delta0+delta_b*B+delta_c*C)
    E<-rbinom(1,1,prob=p_z)
    c(B,C,U,E)
    })
  B_sample[,repl]<-sample[1,]
  C_sample[,repl]<-sample[2,]
  U_sample[,repl]<-sample[3,]
  E_sample[,repl]<-sample[4,]
  X_sample<-cbind(B_sample[,repl],C_sample[,repl],U_sample[,repl],E_sample[,repl])

  # Y random sampling - continuous
  Y_sample[,repl]<-as.matrix(X_sample)%*%effect+rnorm(nrow(X_sample),0,1)
}
```

Sample 저장 형태 바꿈.



```
## Data store ##
write.csv(B_sample,file="B_sample.csv",row.names=FALSE)
write.csv(C_sample,file="C_sample.csv",row.names=FALSE)
#write.csv(U_sample,file="U_sample.csv",row.names=FALSE)
write.csv(E_sample,file="E_sample.csv",row.names=FALSE)
write.csv(Y_sample,file="Y_sample.csv",row.names=FALSE)
```

⇒ 생성한 Data
csv file로 저장

```
## Data import ##
```

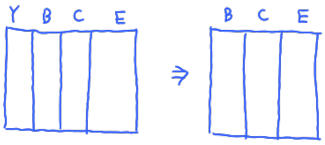
; 저장한 Data Import

```
B_sample<-read.csv("B_sample.csv",header=TRUE)
```

```
C_sample<-read.csv("C_sample.csv",header=TRUE)
#U_sample<-read.csv("U_sample.csv",header=TRUE)
E_sample<-read.csv("E_sample.csv",header=TRUE)
Y_sample<-read.csv("Y_sample.csv",header=TRUE)

## Data export function - treat + covariance ##
#data_export<-function(var_treat,var_cov,data){
#   name<-c(var_treat,var_cov)
#   idx_name<-rep(0,length(name))
#
#   for(n in 1:length(name)){
#      idx_name[n]<-which(colnames(data)==name[n])
#   }
#   mydata<-data[idx_name]
#   return(mydata)
#}
```

문자열로 받음



```
############################################################################
#############
## weight generation function ##
weight_make<-function(var_treat,var_cov,estimate,data){
   result<-list()
   mydata<-data[c(var_treat,var_cov)]
```

Raw Data

String 형태 (treat 변수, confounder 변수명)

원하는 추정치

만 가지고 오도록,,

```
   trt<-mydata[,var_treat]
   ps<-glm(trt~.,data=mydata,family='binomial')$fitted.values
   #ps<-predict(psmodel,type='response')
```

; 성향점수 get

myformula = as.formula(sprintf("%s ~ .")) 생성 ⇒ glm에 myformular 대입

var_treat

이렇게 작성하면 error의 위험이 있을수 있음!

```
   if(estimate=="ATE"){
      weight<-ifelse(trt==1,1/ps,1/(1-ps))
   }
   else if(estimate=='ATT'){
      weight<-ifelse(trt==1,1,ps/(1-ps))
   }
   else{
      weight<-ifelse(trt==1,(1-ps)/ps,1)
   }
```

이 변수 대신 data[, var_treat] 이용!

이전에 잘못 작성한 부분 수정.

```
   resul~~t[[1]]~~<-weight
result~~[[2]]~~<-ifelse(weight>quantile(weight,prob=0.99),quantile(weight,prob=0.99),weight)
   return(result)}
```

result$untrimmed ← weight

result$trimmed ← ~

name 부여!

truncation 적용한 weight 와 하지 않은 weight 2가지 version list에 저장

```
## weighted data export ##
weighteddata<-function(data,weight){
  require(survey)
  data<-svydesign(ids=~1,data=data,weights=~weight)
  mydata<-data[[7]]
  return(mydata)
}
```

가중치 부여해주는 function

result가 list 형태

⇒ 7th에 weighted Data가 있음.

함수사용보다는 계산한 Weight 값을 Data의 한 열로 추가 ⇒ Hardcoding으로 가중평균, 분산 계산 ⇒ SMD 공식 생성해 Balance check!

```
## balance check function - no function ##
#balance_check<-function(var_treat,var_cov,weight,data){
#   before_table<-matrix(0,nrow=length(var_cov),ncol=2)
#   rownames(before_table)<-var_cov
#
colnames(before_table)<-c("IPTW_before_mean_difference","IPTW_before_variance_rati
o")
#
#   after_table<-matrix(0,nrow=length(var_cov),ncol=2)
#   rownames(after_table)<-var_cov
#
colnames(after_table)<-c("IPTW_after_mean_difference","IPTW_after_variance_ratio")
#
#   ind_treat<-which(colnames(data)==var_treat)
#   treat<-data[,ind_treat]
#   cov<-data[-ind_treat]
#   for(i in 1:length(cov)){
#     var_cov<-cov[,i]
#     std_var_cov = (var_cov - mean(var_cov))/sd(var_cov)
#     simple_M1 = mean(std_var_cov[treat==1])
#     simple_M0 = mean(std_var_cov[treat==0])
#     simple_V1 = var(std_var_cov[treat==1])
#     simple_V0 = var(std_var_cov[treat==0])
#     wgted_M1 = Hmisc::wtd.mean(x=std_var_cov[treat==1],weights=weight[treat==1])
#     wgted_M0 = Hmisc::wtd.mean(x=std_var_cov[treat==0],weights=weight[treat==0])
#     wgted_V1 = Hmisc::wtd.var(x=std_var_cov[treat==1],weights=weight[treat==1])
#     wgted_V0 = Hmisc::wtd.var(x=std_var_cov[treat==0],weights=weight[treat==0])
#     before_table[i,1] = simple_M1 - simple_M0
#     before_table[i,2] = simple_V1/simple_V0
#     after_table[i,1] = wgted_M1 - wgted_M0
#     after_table[i,2] = wgted_V1/wgted_V0
#   }
#   result<-cbind(before_table,after_table)
#   return(result)
#}

## balance check function - function yes ##
balance_check<-function(var_treat,var_cov,data){
```

String 형태   raw Data

```
  require(tableone)
  table<-CreateTableOne(vars=var_cov,strata=var_treat,data=data,test=FALSE)
  print(table,smd=TRUE)
}
```

Balance Check 할수 있는 table 생성

SMD도 같이 제시

```
## check ##
```

; 함수 결과 확인하는 Example

```
E<-E_sample[,1]
B<-B_sample[,1]
#U<-U_sample[,1]
C<-C_sample[,1]
Y<-Y_sample[,1]
data<-data.frame("E"=E,"B"=B,"C"=C,"Y"=Y)
cov<-c("B","C")
#mydata<-data_export("E",cov,data)
#head(mydata)
tableone_before<-balance_check(var_treat="E",var_cov=cov,data=data)
```

Weight 부여 전 confounder 간 Balance check,,

```
                 Stratified by E
                  0             1             SMD
  n                 88            12
  B (mean (SD))   0.56 (0.50) 0.33 (0.49)   0.451
  C (mean (SD))  -0.04 (0.99) 0.31 (1.10)   0.335

weight_result<-weight_make("E",cov,estimate='ATE',data=data)

weight_result
[[1]]
```

; Question) Weight가 모두 1이라는 것은 PS-score 가 매우 작다는 것을 의미 ⇒ how to Solve ?

```
  [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 [63] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

[[2]]
  [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 [63] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
```

```
# weighted data #
weighteddata1<-weighteddata(data=data,weight=weight_result[[1]]) #weighteddata[[7]]
weighteddata2<-weighteddata(data=data,weight=weight_result[[2]])
tableone_after1<-balance_check(var_treat="E",var_cov=cov,data=weighteddata1)
               Stratified by E
                0             1           SMD
  n                88           12
  B (mean (SD))  0.56 (0.50) 0.33 (0.49)  0.451
  C (mean (SD)) -0.04 (0.99) 0.31 (1.10)  0.335

tableone_after2<-balance_check(var_treat="E",var_cov=cov,data=weighteddata2)
               Stratified by E
                0             1           SMD
  n                88           12
  B (mean (SD))  0.56 (0.50) 0.33 (0.49)  0.451
  C (mean (SD)) -0.04 (0.99) 0.31 (1.10)  0.335

#### IPTW ATE & ATT ####
result_ATE<-matrix(0,nrow=1000,ncol=2)
colnames(result_ATE)<-c("before_truncation_ATE","after_truncation_ATE")
result_ATE<-as.data.frame(result_ATE)

result_ATT<-matrix(0,nrow=1000,ncol=2)
colnames(result_ATT)<-c("before_truncation_ATT","after_truncation_ATT")
result_ATT<-as.data.frame(result_ATT)
```

추정한 값
저장 위해
matrix 생성

```
## 1000th simulated ##
for(j in 1:1000){
  E<-E_sample[,j]
  B<-B_sample[,j]
  C<-C_sample[,j]
  #U<-U_sample[,j]
  Y<-Y_sample[,j]
```

각 replication 마다
Data 가져오기

DataFrame 생성

```
  data<-data.frame("E"=E,"B"=B,"C"=C,"Y"=Y)
  cov<-c("B","C")
```

Confounder 변수명 지정

```
  #mydata<-data_export("E",cov,data)
  weight_ATE<-weight_make("E",cov,estimate='ATE',data=data)
  weight_ATT<-weight_make("E",cov,estimate='ATT',data=data)
```

weight
생성

```
  weighteddata1_ATE<-weighteddata(data=data,weight=weight_ATE[[1]])
```

truncation 안한 weight 이용해

pseudo-population 생성

```
  weighteddata2_ATE<-weighteddata(data=data,weight=weight_ATE[[2]])
  weighteddata1_ATT<-weighteddata(data=data,weight=weight_ATT[[1]])
  weighteddata2_ATT<-weighteddata(data=data,weight=weight_ATT[[2]])
```

truncation 한 weight 이용해 pseudo-population 생성

```
  result_ATE[j,1]<-lm(Y~E,data=weighteddata1_ATE)$coef['E']
  result_ATE[j,2]<-lm(Y~E,data=weighteddata2_ATE)$coef['E']

  result_ATT[j,1]<-lm(Y~E,data=weighteddata1_ATT)$coef['E']
  result_ATT[j,2]<-lm(Y~E,data=weighteddata1_ATT)$coef['E']
```

생성한 Pseudo-Population 이용해 ATE, ATT 추정

weighted Data 사용대신 weight option 이용해 lm 적합!

```
}

mean(result_ATE[,1])
[1] 0.6957256
mean(result_ATE[,2])
[1] 0.6957256

mean(result_ATT[,1])
[1] 0.6957256

mean(result_ATT[,2])
[1] 0.6957256
log(2)
[1] 0.6931472

# plotting - ATE #
par(mfrow=c(2,1))
plot(result_ATE[,1],main="ATE estimators using IPTW")
abline(h=log(2),col='red')
plot(result_ATE[,2],main="ATE estimators using IPTW_truncated version")
abline(h=log(2),col='red')
```

ok!

```
# plotting - ATT #
par(mfrow=c(2,1))
plot(result_ATT[,1],main="ATT estimators using IPTW")
abline(h=log(2),col='red')
plot(result_ATT[,2],main="ATT estimators using IPTW_truncated version")
abline(h=log(2),col='red')

##########################################################################
###########
```

```
## matched data export ##   ; Matching 후 matching 된 Data return 해주는 function
matcheddata<-function(var_treat,var_cov,data,PSM,M){
                       String 형태             ps Matching    → 한개의 treated subject에
                                               시행여부          대해 몇 개의 control subject
                                                                matching 할 것인지 지정
  require(Matching)
  if(PSM==TRUE){
    mydata<-data[c(var_treat,var_cov)]
    trt<-~~mydata[,var_treat]~~  → IPTW 처럼 myformula 이용!
    ps<-glm(~~trt~~~.,data=mydata,family='binomial')$fitted.values  # ps 계산
    m.out<-Match(Tr=data[,var_treat],M=M,X=~~logit~~(ps),replace=FALSE)
                                            그냥 ps 이용!
  }
  else{
    m.out<-Match(Tr=data[,var_treat],M=M,X=data[,var_cov],replace=FALSE)
  }
  matched<-data[unlist(m.out[c("index.treated","index.control")]),]
  return(~~matched~~)
}  → matched 된 Data 말고, index.treated, index control
                만 return ⇒ Data에 column으로 추가 (matching 이면 1,
                                                  아니면 0으로 coding)

> ## check ##   ; 함수 확인 위한 Example
E<-E_sample[,1]
B<-B_sample[,1]
#U<-U_sample[,1]
C<-C_sample[,1]
Y<-Y_sample[,1]
data<-data.frame("E"=E,"B"=B,"C"=C,"Y"=Y)
cov<-c("B","C")

# matched data #
matchdata_greedy<-matcheddata("E",cov,data=data,PSM=FALSE,M=1) )
matchdata_PSM<-matcheddata("E",cov,data=data,PSM=TRUE,M=1)     )  모두 1:1로 가정

# matched data balance check #
balance_PSM<-balance_check("E",cov,matchdata_PSM)
                 Stratified by E
                  0              1              SMD
  n               12             12
  B (mean (SD))   0.50 (0.52)  0.33 (0.49)   0.328
  C (mean (SD))  -0.48 (0.80)  0.31 (1.10)   0.825

balance_greedy<-balance_check("E",cov,matchdata_greedy)
                 Stratified by E
                  0              1              SMD
  n               12             12
```

ok!

```
  B (mean (SD)) 0.33 (0.49) 0.33 (0.49) <0.001
  C (mean (SD)) 0.21 (0.86) 0.31 (1.10)  0.105
```

↳ greedy matching 통해 group 간 balance 정도 맞추어진것 확인!

```
#### PSM matching & greedy matching ####
PSM_ATE<-c()
greedy_ATE<-c()
```

↳ 결과 저장 위한 변수 생성

```
## 1000th simulated ##
for(j in 1:1000){
  E<-E_sample[,j]
  B<-B_sample[,j]
  C<-C_sample[,j]
  #U<-U_sample[,j]
  Y<-Y_sample[,j]
  data<-data.frame("E"=E,"B"=B,"C"=C,"Y"=Y)
  cov<-c("B","C")

  # matched data generation #
  matchdata_greedy<-matcheddata("E",cov,data=data,PSM=FALSE,M=1)
  matchdata_PSM<-matcheddata("E",cov,data=data,PSM=TRUE,M=1)


PSM_ATE[j]<-matchdata_PSM$Y[matchdata_PSM$E==1]-matchdata_PSM$Y[matchdata
_PSM$E==0]
```

; E[Y|E=1] - E[Y|E=0] 계산

```
greedy_ATE[j]<-matchdata_greedy$Y[matchdata_greedy$E==1]-matchdata_greedy$Y[
matchdata_greedy$E==0]

}

plot(PSM_ATE,main="ATE estimators using PSM")
abline(h=log(2),col='red')
plot(PSM_ATE,main="ATE estimators using greedy matching")
abline(h=log(2),col='red')

################################################################
#### Regression ####
ATE_regression<-c()

for(j in 1:1000){
  E<-E_sample[,j]
  B<-B_sample[,j]
  C<-C_sample[,j]
  #U<-U_sample[,j]
  Y<-Y_sample[,j]
  data<-data.frame("E"=E,"B"=B,"C"="C,"Y"=Y)
  cov<-c("B","C")

  #mydata<-data_export("E",cov,data)
  ATE_regression[j]<-lm(Y~.,data=data)$coef['E']
}

par(mfrow=c(1,1))
plot(ATE_regression,main="ATE estimators using regression")
abline(h=log(2),col='red')
```

; Regression 결과 회귀계수 저장.

⇒ 성능은 주로 Bias 와 Variance로 평가 / 수정한 code 마다 저장, 맨 위에
주석으로 무엇을 바꾸었는지 간단하게 작성,,