

meta valication

Yong Yang

Thursday, July 16, 2015

```
# meta anlalysis validation
# S ~ N(mu0, std0)
# S_i ~ N(mui, stdi)
# mue ~ N(0, stde)

# prepare simulation data

library("metafor", lib.loc="C:/Users/thinkingfly/Documents/R/win-library/3.1")

## Loading 'metafor' package (version 1.9-5). For an overview
## and introduction to the package please type: help(metafor).

library(sm)

## Package 'sm', version 2.2-5.4: type help(sm) for summary information

library(reshape2)
library(colorspace)

randf<-function(x,mu0,sd,N){
  res <- rnorm(N,x+mu0,sd)
}

simulate<-function(U_tot_exp=100,D_tot_exp=1,U_tot_con=100.05,D_tot_con=1,
  U_err=0,D_err=0.1,N_sample=1000,n_sample=50,plot.forest=FALSE,print.value=FALSE){

  s_all_exp=list()
  s_all_con= list()

  ram_seed = rnorm(n_sample,U_err,D_err)
  s_all_exp=lapply(ram_seed,randf,U_tot_exp,sqrt(D_tot_exp^2+D_err^2),N_sample)
  ram_seed = rnorm(n_sample,U_err,D_err)
  s_all_con=lapply(ram_seed,randf,U_tot_con,sqrt(D_tot_con^2+D_err^2),N_sample)
  all_mean_exp = sapply(s_all_exp,mean)
  all_sd_exp = sapply(s_all_exp,sd)
  all_mean_con = sapply(s_all_con,mean)
  all_sd_con = sapply(s_all_con,sd)
  all_n_exp = rep(N_sample,n_sample)
  all_n_con = rep(N_sample,n_sample)
  # meta analysis
  es<-escalc(measure="SMD", m1i=all_mean_exp,m2i=all_mean_con,n1i=all_n_exp,
    n2i=all_n_con,sd1i=all_sd_exp,sd2i=all_sd_con,vtype="UB")
  meta0<-rma(as.numeric(es$yi),as.numeric(es$vi),method="DL") #DL
  #par(mar = rep(2, 4))
  #par(font=1,cex=1,cex.lab=1,cex.main=1,cex.sub=1,cex.axis=1,lwd=1)
```

```

if (plot.forest==TRUE)
  forest(meta0,xlab="SMD",mlab="RE Model for All Sites")
if (print.value==TRUE){
  print("The pvalue is")
  print(meta0$pval)
}
meta0$pval
}

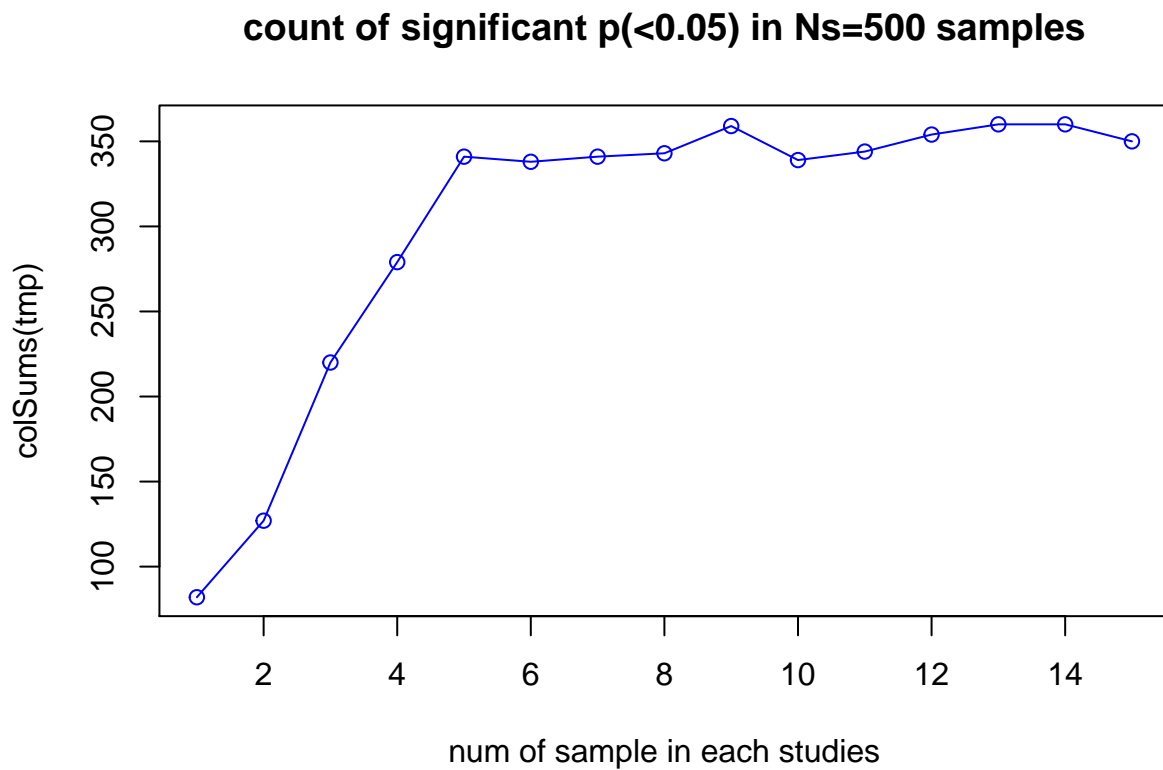
test_N<-function(x,Ns=500){
  pvalue <- replicate(Ns,simulate(N_sample=x))
}

test_n<-function(x,Ns=500){
  pvalue <- replicate(Ns,simulate(n_sample = x))
}

##### test sample size in each study
N_sample<-c(20,50,100,200,500,1000,2000,3000,5000,6000,7000,8000,9000,10000,20000)

test_N_p<-sapply(N_sample,test_N)
colnames(test_N_p)<-as.character(N_sample)
tmp <- apply(test_N_p,c(1,2),(function (x) as.numeric(x<0.05)))
plot(colSums(tmp),type="o",col="blue",xlab="num of sample in each studies")
title(main="count of significant p(<0.05) in Ns=500 samples")

```



```
##### test sample size in each study
n_sample<-c(7,10,15,20,40,60,80,100,150,200,250,300)

test_n_p<-sapply(n_sample,test_n)
colnames(test_n_p)<-as.character(n_sample)
tmp <- apply(test_n_p,c(1,2),(function (x) as.numeric(x<0.05)))
plot(colSums(tmp),type="o",col="blue",xlab="num of studies")
title(main="count of significant p(<0.05) in Ns=500 samples")
```

count of significant $p(<0.05)$ in $N_s=500$ samples

