

Supplementary Materials to “Assessment of Bayesian Expected Power via Bayesian Bootstrap”

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1 R codes for the Bayesian bootstrap procedure (BBS)

```
#####  
# pilot: pilot data in data.frame format with subject ID = ID  
# future: future study data  
# n: sample size of pilot data  
# N: sample size of planned future trial  
# post.pi: posterior samples of the probabilities of the sample cases  
# alpha: a vector of hyperparameters of dimensional n in the dirichlet prior  
# (page 5 in the manuscript)  
# m: number of posterior samples on pi  
# t: sets of bootstrapped future data of size N per posterior sample pi  
#####  
library(MCMCpack)  
for(i in 1:m) {  
  post.pi <- rdirichlet(1, rep(1+alpha,n))  
  for(k in 1:t) {  
    future <- NULL  
    count<- c(rmultinom(1,N,post.pi))  
    cum.count<- 0;  
    for(j in 1:n) {  
      if(count[j] != 0) {  
        for(l in 1:count[j]) {  
          cum.count<- cum.count+1;  
          drawY<- pilot[pilot$ID==j,]  
          drawY$ID<- cum.count  
          future<- rbind(future, drawY)  
        }  
      }  
    }  
  }  
  # code the planned analysis on data “future”  
}  
}
```

2 R codes for the double bootstrap procedure (BS2)

```
#####  
# pilot: pilot data in data.frame format with subject ID = ID  
# future: future study data  
# n: sample size of pilot data  
# N: sample size of planned future trial  
# m: sets of bootstrapped pilot data of size n  
# t: sets of bootstrapped future data of size N per bootstrapped sample data  
#####  
for (i in 1:m) {  
  draw.ID<- sample(1:n, n, replace=T)  
  tmp <- NULL  
  for(j in 1:n) {  
    drawY<- pilot[pilot$ID==draw.ID[j],]  
    drawY$ID<- j  
    tmp <- rbind(tmp , drawY)  
  }  
  for(k in 1:t) {  
    draw.ID<- sample(1:n, N, replace=T)  
    future<- NULL  
    for(j in 1:N) {  
      drawY<- tmp[tmp$ID==draw.ID[j],]  
      drawY$ID<- j  
      future <- rbind( future, drawY)  
    }  
    # code the planned analysis on data ‘‘future’’  
  }  
}
```

3 R codes for the power calculation based on multivariate t distribution with co-primary endpoints in equivalence studies

```
#####  
# N: sample size  
# df: degrees of freedom of the multivariate t distribution  
# diff: expected differences on the endpoints  
# Sigma: variance-covariance matrix of the repeated measures;  
# note that the dimension of Sigma is 2 folds of the diff length  
# lower & upper: lower and upper bounds of the equivalence hypotheses  
# that can be different across different endpoints  
# alpha: Type I error rate  
#####  
library(mvtnorm)  
pw.eq.mt<- function(N, df, diff, Sigma, lower=log(0.80),  
                    upper=log(1.25), alpha=0.05)  
{  
  nend<- length(diff)  
  S<- matrix(0,nend,nend)
```

```

cc<- matrix(0,nend, nrow(Sigma))
for(i in 1:nend){
  j<- 2*(i-1)+1;
  cc[i,j:(j+1)]<- c(1,-1)}
S<- cc%%Sigma%%t(cc)/N
crr0<- cov2cor(S);
l<- rep(0,nend)
u<- rep(0,nend)
if (length(lower)==1) lower<- rep(lower,nend)
if (length(upper)==1) upper<- rep(upper,nend)

crr<- diag(2*nend);
for (i in 1:(nend-1)){
  k<- 2*(i-1)+1;
  crr[k:(k+1), k:(k+1)]<- 1
  for (j in (i+1):nend){
    l<- 2*(j-1)+1
    crr[k:(k+1), l:(l+1)]<- crr0[i,j]
    crr[l:(l+1), k:(k+1)]<- crr0[i,j]
  }
}
k<- 2*(nend-1)+1;
crr[k:(k+1), k:(k+1)]<- 1
D<- diag(nend)
for (i in 1:nend) D[i,i]<- 1/sqrt(S[i,i])
delta1<- D%%(diff-lower)
delta2<- D%%(diff-upper)
delta<- rep(0,2*nend)
c<- qt(alpha,df)
Lb<- rep(-c, 2*nend)
Ub<- rep( c, 2*nend)

for(i in 1:nend){
  j<- 2*i-1
  delta[j]<- delta1[i]
  delta[j+1]<- delta2[i]
  Lb[j+1]<- -Inf
  Ub[j]<- Inf
}
crr<- cov2cor(crr)
pw<- pmvt(lower=Lb, upper=Ub, df=df, delta=delta, corr=crr);
pw<- round(pw[1],4)
return(pw)
}
# example (note that the dimension of Sigma is 2 folds of the diff length)
# pw.eq.mt(100, 5, c(0.1,-0.05), 0.16*diag(4))

```