

Project 1

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Project information:

Project 1: <http://utdallas.edu/~ammann/stat6341/node10.html>

Yitao: Calucation

Xiao: Confidence interval

Jiwon: Coverage ratio

Xinyu: Verification and extendation

Question 1: No contamination

Setup:

```
p = c(0.5,0.3,0.2)
alpha = 0.05
sampleSizeVector=c(500,1000,1500) # sample size vector

# parameter for method 1
m=3
M = m*(m-1)/2
cv = qchisq(1-alpha/M,M-1) ### critical value
cv
```

```
## [1] 8.188689
```

```
# parameter for method 2
x = seq(1,4,length=1000)
y = 1 - 2*(1 - pnorm(x)) - 4*(m-2)*(1-pnorm(x*sqrt(2)))
a = min(x[y >= 1 - alpha]) ### a value
a
```

```
## [1] 2.036036
```

Generate simulation

For simplicity, only 2 columns of simulated data are demonstrated here:

```
set.seed(321)
df = rbind(rmultinom(2, size = sampleSizeVector[1], prob = p),trialID = 1:2)
df
```

```
##      [,1] [,2]
##      252  259
##      144  145
##      104   96
## trialID   1   2
```

Each column is one poll. You can see the distribtuion is about 0.5, 0.3, 0.2. The trialID is added to record the column location. Later on, we can use this information to calculate the jointed coverage ratio for each poll.

Confidence interval function

The idea is to design the most basic function of all computation.

So this function should input 2 sets of parameters:

- data: one column
- pair difference: the string & positions

```
## singleSample: the one single column you want to calculate
## type: the character string to record the pair difference
## i,j : the locations of the pair elements: p1 means the first element in p,namely p[1]
## a dataframe is returned with complete result

confiFun <- function(singleSample,type,i,j){
  N = sum(singleSample[1:3]) #the column sum; sample size
  phat_i = singleSample[i] / N # the estimated p_i
  phat_j = singleSample[j] / N # the estimated p_j

  delta = phat_i - phat_j #Differences Between Multinomial Proportions
  d_ij = phat_i + phat_j - delta^2 # d_ij for method 1

  # each vector has results from method 1 and method 2
  confiLower = c(delta - sqrt( cv * d_ij /N), delta - a/sqrt(N))
  confiUpper = c(delta + sqrt( cv * d_ij /N), delta + a/sqrt(N))

  ## return a dataframe that named column
  return(data.frame(confiLower = confiLower,confiUpper = confiUpper,
                    type=type,method=c(1L,2L),trueValue = p[i]-p[j],
                    trialID = singleSample[[4]]))
}
```

Let's apply this function to our data. Suppose we want to calculate the delta_12, which is p1-p2.

```
delta_12 = apply(df, 2,confiFun,type="p1-p2",i=1,j=2)
delta_12
```

```
## [[1]]
##   confiLower confiUpper type method trueValue trialID
## 1  0.1055157  0.3264843 p1-p2      1      0.2      1
## 2  0.1249457  0.3070543 p1-p2      2      0.2      1
##
## [[2]]
##   confiLower confiUpper type method trueValue trialID
## 1  0.1167275  0.3392725 p1-p2      1      0.2      2
## 2  0.1369457  0.3190543 p1-p2      2      0.2      2
```

Since we have two column, the result is the length 2 list, where each element is a dataframe.

pair differences for each sample size

To be more efficient, we build a higher level function on top of **confiFun**. It could take one sample size and return all pair difference results from both methods at one shot.

```
confiDataFun <- function(sampleSize,nrep=2){
  set.seed(321)
  df = rbind(rmultinom(nrep, size = sampleSizeVector[1], prob = p),trialID = 1:nrep)
```

```

delta_12 = apply(df, 2, confiFun, type="p1-p2", i=1, j=2)
delta_13 = apply(df, 2, confiFun, type="p1-p3", i=1, j=3)
delta_23 = apply(df, 2, confiFun, type="p2-p3", i=2, j=3)

res = Reduce(rbind, c(delta_12, delta_13, delta_23)) # rbind all dataframe
res$sampleSize = sampleSize # record the sampleSize
return(res)
}

```

Use this function to repeat what we just did.

```
confiDataFun(sampleSize = 500, nrep=2)
```

```

##      confiLower confiUpper  type method trueValue trialID sampleSize
## 1  0.10551570  0.3264843 p1-p2      1      0.2      1      500
## 2  0.12494570  0.3070543 p1-p2      2      0.2      1      500
## 3  0.11672754  0.3392725 p1-p2      1      0.2      2      500
## 4  0.13694570  0.3190543 p1-p2      2      0.2      2      500
## 5  0.19487744  0.3971226 p1-p3      1      0.3      1      500
## 6  0.20494570  0.3870543 p1-p3      2      0.3      1      500
## 7  0.22656451  0.4254355 p1-p3      1      0.3      2      500
## 8  0.23494570  0.4170543 p1-p3      2      0.3      2      500
## 9 -0.00954532  0.1695453 p2-p3      1      0.1      1      500
## 10 -0.01105430  0.1710543 p2-p3      2      0.1      1      500
## 11  0.01004201  0.1859580 p2-p3      1      0.1      2      500
## 12  0.00694570  0.1890543 p2-p3      2      0.1      2      500

```

Let's try all sample size: 500, 1000, 1500.

```
sampleSizeVector
```

```
## [1] 500 1000 1500
```

```
confiList = lapply(sampleSizeVector, confiDataFun)
confiList
```

```

## [[1]]
##      confiLower confiUpper  type method trueValue trialID sampleSize
## 1  0.10551570  0.3264843 p1-p2      1      0.2      1      500
## 2  0.12494570  0.3070543 p1-p2      2      0.2      1      500
## 3  0.11672754  0.3392725 p1-p2      1      0.2      2      500
## 4  0.13694570  0.3190543 p1-p2      2      0.2      2      500
## 5  0.19487744  0.3971226 p1-p3      1      0.3      1      500
## 6  0.20494570  0.3870543 p1-p3      2      0.3      1      500
## 7  0.22656451  0.4254355 p1-p3      1      0.3      2      500
## 8  0.23494570  0.4170543 p1-p3      2      0.3      2      500
## 9 -0.00954532  0.1695453 p2-p3      1      0.1      1      500
## 10 -0.01105430  0.1710543 p2-p3      2      0.1      1      500
## 11  0.01004201  0.1859580 p2-p3      1      0.1      2      500
## 12  0.00694570  0.1890543 p2-p3      2      0.1      2      500
##
## [[2]]
##      confiLower confiUpper  type method trueValue trialID sampleSize
## 1  0.10551570  0.3264843 p1-p2      1      0.2      1     1000
## 2  0.12494570  0.3070543 p1-p2      2      0.2      1     1000
## 3  0.11672754  0.3392725 p1-p2      1      0.2      2     1000

```

```
## 4 0.13694570 0.3190543 p1-p2 2 0.2 2 1000
## 5 0.19487744 0.3971226 p1-p3 1 0.3 1 1000
## 6 0.20494570 0.3870543 p1-p3 2 0.3 1 1000
## 7 0.22656451 0.4254355 p1-p3 1 0.3 2 1000
## 8 0.23494570 0.4170543 p1-p3 2 0.3 2 1000
## 9 -0.00954532 0.1695453 p2-p3 1 0.1 1 1000
## 10 -0.01105430 0.1710543 p2-p3 2 0.1 1 1000
## 11 0.01004201 0.1859580 p2-p3 1 0.1 2 1000
## 12 0.00694570 0.1890543 p2-p3 2 0.1 2 1000
##
## [[3]]
##      confiLower confiUpper type method trueValue trialID sampleSize
## 1 0.10551570 0.3264843 p1-p2 1 0.2 1 1500
## 2 0.12494570 0.3070543 p1-p2 2 0.2 1 1500
## 3 0.11672754 0.3392725 p1-p2 1 0.2 2 1500
## 4 0.13694570 0.3190543 p1-p2 2 0.2 2 1500
## 5 0.19487744 0.3971226 p1-p3 1 0.3 1 1500
## 6 0.20494570 0.3870543 p1-p3 2 0.3 1 1500
## 7 0.22656451 0.4254355 p1-p3 1 0.3 2 1500
## 8 0.23494570 0.4170543 p1-p3 2 0.3 2 1500
## 9 -0.00954532 0.1695453 p2-p3 1 0.1 1 1500
## 10 -0.01105430 0.1710543 p2-p3 2 0.1 1 1500
## 11 0.01004201 0.1859580 p2-p3 1 0.1 2 1500
## 12 0.00694570 0.1890543 p2-p3 2 0.1 2 1500
```

Therefore, we get a list of result for one specific distribtuion. Combine them into one dataframe and save it for plotting.

```
confiData = Reduce(rbind,confiList)
confiData
```

```
##      confiLower confiUpper type method trueValue trialID sampleSize
## 1 0.10551570 0.3264843 p1-p2 1 0.2 1 500
## 2 0.12494570 0.3070543 p1-p2 2 0.2 1 500
## 3 0.11672754 0.3392725 p1-p2 1 0.2 2 500
## 4 0.13694570 0.3190543 p1-p2 2 0.2 2 500
## 5 0.19487744 0.3971226 p1-p3 1 0.3 1 500
## 6 0.20494570 0.3870543 p1-p3 2 0.3 1 500
## 7 0.22656451 0.4254355 p1-p3 1 0.3 2 500
## 8 0.23494570 0.4170543 p1-p3 2 0.3 2 500
## 9 -0.00954532 0.1695453 p2-p3 1 0.1 1 500
## 10 -0.01105430 0.1710543 p2-p3 2 0.1 1 500
## 11 0.01004201 0.1859580 p2-p3 1 0.1 2 500
## 12 0.00694570 0.1890543 p2-p3 2 0.1 2 500
## 13 0.10551570 0.3264843 p1-p2 1 0.2 1 1000
## 14 0.12494570 0.3070543 p1-p2 2 0.2 1 1000
## 15 0.11672754 0.3392725 p1-p2 1 0.2 2 1000
## 16 0.13694570 0.3190543 p1-p2 2 0.2 2 1000
## 17 0.19487744 0.3971226 p1-p3 1 0.3 1 1000
## 18 0.20494570 0.3870543 p1-p3 2 0.3 1 1000
## 19 0.22656451 0.4254355 p1-p3 1 0.3 2 1000
## 20 0.23494570 0.4170543 p1-p3 2 0.3 2 1000
## 21 -0.00954532 0.1695453 p2-p3 1 0.1 1 1000
## 22 -0.01105430 0.1710543 p2-p3 2 0.1 1 1000
## 23 0.01004201 0.1859580 p2-p3 1 0.1 2 1000
```

```
## 24 0.00694570 0.1890543 p2-p3      2      0.1      2      1000
## 25 0.10551570 0.3264843 p1-p2      1      0.2      1      1500
## 26 0.12494570 0.3070543 p1-p2      2      0.2      1      1500
## 27 0.11672754 0.3392725 p1-p2      1      0.2      2      1500
## 28 0.13694570 0.3190543 p1-p2      2      0.2      2      1500
## 29 0.19487744 0.3971226 p1-p3      1      0.3      1      1500
## 30 0.20494570 0.3870543 p1-p3      2      0.3      1      1500
## 31 0.22656451 0.4254355 p1-p3      1      0.3      2      1500
## 32 0.23494570 0.4170543 p1-p3      2      0.3      2      1500
## 33 -0.00954532 0.1695453 p2-p3      1      0.1      1      1500
## 34 -0.01105430 0.1710543 p2-p3      2      0.1      1      1500
## 35 0.01004201 0.1859580 p2-p3      1      0.1      2      1500
## 36 0.00694570 0.1890543 p2-p3      2      0.1      2      1500
```

```
saveRDS(confiData,"YL_Q1a_example.rds") ## R format data type
```

Question 2: Contamination

Generating data

```
q = 0.1 # mixing probabilities
p = c(0.46,0.44,0.1)
r = c(0.34,0.33,0.33)
df
```

```
##      [,1] [,2]
##      252 259
##      144 145
##      104  96
## trialID   1   2
```

Back to our earlier example. The sample size is 500. (Column sum). nrep=2. (Column number).

Using **rbinom** to separate people into not going to vote and going to vote. In this way, their sum is still 500.

```
sampleSize = 500
nrep = 2
sampleSize_NV = rbinom(nrep, sampleSize, q)
sampleSize_NV # the number of people not going to vote, for column 1 and column 2
```

```
## [1] 57 48
```

```
sampleSize_V = sampleSize - sampleSize_NV
sampleSize_V # the number of people going to vote, for column 1 and column 2
```

```
## [1] 443 452
```

Then, we want to generate data according to each sample size (each column would have different sample size for people vote and not vote)

```
VList = lapply(sampleSize_V,function(x){
  rmultinom(1, size = x, prob = p)
})

Vmat = Reduce(cbind,VList) # transfer to matrix format
Vmat #the exact number for people vote for p1 p2 p3
```

```
##      [,1] [,2]
## [1,]  216  184
## [2,]  185  222
## [3,]   42   46
```

```
NVList = lapply(sampleSize_NV,function(x){
  rmultinom(1, size = x, prob = r)
})
NVmat = Reduce(cbind,NVList) #transfer to matrix format
NVmat #the exact number for people not vote but said would vote for p1 p2 p3
```

```
##      [,1] [,2]
## [1,]   16  18
## [2,]   22  22
## [3,]   19   8
```

Add these two matrix together gives us the mixed data. Each column sum is still 500

```
dfmix = Vmat + NVmat
dfmix
```

```
##      [,1] [,2]
## [1,]  232  202
## [2,]  207  244
## [3,]   61   54
```

```
colSums(dfmix)
```

```
## [1] 500 500
```

Once we have the similar data structure at question 1. We can simply apply defined functions.

```
dfmix = rbind(dfmix,trialID=1:2) # add trial id as last row
tmp = apply(dfmix, 2,confiFun,type="p1-p2",i=1,j=2)
tmp
```

```
## [[1]]
##      confiLower confiUpper  type method trueValue trialID
## 1 -0.06974304  0.1697430 p1-p2      1      0.02      1
## 2 -0.04105430  0.1410543 p1-p2      2      0.02      1
##
## [[2]]
##      confiLower confiUpper  type method trueValue trialID
## 1 -0.2043871  0.03638714 p1-p2      1      0.02      2
## 2 -0.1750543  0.00705430 p1-p2      2      0.02      2
```

Then we can design another higher level function that taking given sample size and mix ratio to do:

1. Generate mix data
2. calculate the pair difference using **confiFun**.

```
confiMixDataFun <- function(sampleSize,q,r = c(0.34,0.33,0.33),nrep=2){
  set.seed(321)

  sampleSize_NV = rbinom(nrep, sampleSize, q)
  sampleSize_V = sampleSize - sampleSize_NV

  VList = lapply(sampleSize_V,function(x){
    rmultinom(1, size = x, prob = p)
  })
```

```

Vmat = Reduce(cbind,VList) # transfer to matrix format

NVList = lapply(sampleSize_NV,function(x){
  rmultinom(1, size = x, prob = r)
})
NVmat = Reduce(cbind,NVList)
dfmix = Vmat+ NVmat
dfmix = rbind(dfmix,trialID=1:nrep)

delta_12 = apply(dfmix, 2,confiFun,type="p1-p2",i=1,j=2)
delta_13 = apply(dfmix, 2,confiFun,type="p1-p3",i=1,j=3)
delta_23 = apply(dfmix, 2,confiFun,type="p2-p3",i=2,j=3)

res = Reduce(rbind,c(delta_12,delta_13,delta_23))
res$sampleSize = sampleSize
return(res)
}

confiMixDataFun(sampleSize = 500,q=0.1)

```

```

##      confiLower confiUpper  type method trueValue trialID sampleSize
## 1 -0.08852527  0.1525253 p1-p2      1      0.02      1      500
## 2 -0.05905430  0.1230543 p1-p2      2      0.02      1      500
## 3 -0.08875420  0.1487542 p1-p2      1      0.02      2      500
## 4 -0.06105430  0.1210543 p1-p2      2      0.02      2      500
## 5  0.26206692  0.4339331 p1-p3      1      0.36      1      500
## 6  0.25694570  0.4390543 p1-p3      2      0.36      1      500
## 7  0.21849712  0.3975029 p1-p3      1      0.36      2      500
## 8  0.21694570  0.3990543 p1-p3      2      0.36      2      500
## 9  0.23109768  0.4009023 p2-p3      1      0.34      1      500
## 10 0.22494570  0.4070543 p2-p3      2      0.34      1      500
## 11 0.18964074  0.3663593 p2-p3      1      0.34      2      500
## 12 0.18694570  0.3690543 p2-p3      2      0.34      2      500

```

Apply to different sampleSize and q

```

resMix = lapply(seq(0.1,0.5,by=0.1), function(q){
  resList = lapply(sampleSizeVector, confiMixDataFun,q=q)
  resDF = Reduce(rbind,resList)
  resDF$mixRatio = q # Record q
  return(resDF)
})

resMix

```

```

## [[1]]
##      confiLower confiUpper  type method trueValue trialID sampleSize
## 1 -0.08852527  0.15252527 p1-p2      1      0.02      1      500
## 2 -0.05905430  0.12305430 p1-p2      2      0.02      1      500
## 3 -0.08875420  0.14875420 p1-p2      1      0.02      2      500
## 4 -0.06105430  0.12105430 p1-p2      2      0.02      2      500
## 5  0.26206692  0.43393308 p1-p3      1      0.36      1      500
## 6  0.25694570  0.43905430 p1-p3      2      0.36      1      500
## 7  0.21849712  0.39750288 p1-p3      1      0.36      2      500
## 8  0.21694570  0.39905430 p1-p3      2      0.36      2      500

```

| | | | | | | | |
|-------|-------------|------------|-------|---|------|---|------|
| ## 9 | 0.23109768 | 0.40090232 | p2-p3 | 1 | 0.34 | 1 | 500 |
| ## 10 | 0.22494570 | 0.40705430 | p2-p3 | 2 | 0.34 | 1 | 500 |
| ## 11 | 0.18964074 | 0.36635926 | p2-p3 | 1 | 0.34 | 2 | 500 |
| ## 12 | 0.18694570 | 0.36905430 | p2-p3 | 2 | 0.34 | 2 | 500 |
| ## 13 | -0.03619570 | 0.13219570 | p1-p2 | 1 | 0.02 | 1 | 1000 |
| ## 14 | -0.01638511 | 0.11238511 | p1-p2 | 2 | 0.02 | 1 | 1000 |
| ## 15 | -0.09155930 | 0.07955930 | p1-p2 | 1 | 0.02 | 2 | 1000 |
| ## 16 | -0.07038511 | 0.05838511 | p1-p2 | 2 | 0.02 | 2 | 1000 |
| ## 17 | 0.26306300 | 0.38893700 | p1-p3 | 1 | 0.36 | 1 | 1000 |
| ## 18 | 0.26161489 | 0.39038511 | p1-p3 | 2 | 0.36 | 1 | 1000 |
| ## 19 | 0.27826500 | 0.39773500 | p1-p3 | 1 | 0.36 | 2 | 1000 |
| ## 20 | 0.27361489 | 0.40238511 | p1-p3 | 2 | 0.36 | 2 | 1000 |
| ## 21 | 0.21631196 | 0.33968804 | p2-p3 | 1 | 0.34 | 1 | 1000 |
| ## 22 | 0.21361489 | 0.34238511 | p2-p3 | 2 | 0.34 | 1 | 1000 |
| ## 23 | 0.28413436 | 0.40386564 | p2-p3 | 1 | 0.34 | 2 | 1000 |
| ## 24 | 0.27961489 | 0.40838511 | p2-p3 | 2 | 0.34 | 2 | 1000 |
| ## 25 | -0.02743581 | 0.11010247 | p1-p2 | 1 | 0.02 | 1 | 1500 |
| ## 26 | -0.01123689 | 0.09390356 | p1-p2 | 2 | 0.02 | 1 | 1500 |
| ## 27 | -0.06754685 | 0.07154685 | p1-p2 | 1 | 0.02 | 2 | 1500 |
| ## 28 | -0.05057022 | 0.05457022 | p1-p2 | 2 | 0.02 | 2 | 1500 |
| ## 29 | 0.27134107 | 0.37399227 | p1-p3 | 1 | 0.36 | 1 | 1500 |
| ## 30 | 0.27009644 | 0.37523689 | p1-p3 | 2 | 0.36 | 1 | 1500 |
| ## 31 | 0.28048542 | 0.37951458 | p1-p3 | 1 | 0.36 | 2 | 1500 |
| ## 32 | 0.27742978 | 0.38257022 | p1-p3 | 2 | 0.36 | 2 | 1500 |
| ## 33 | 0.23088572 | 0.33178095 | p2-p3 | 1 | 0.34 | 1 | 1500 |
| ## 34 | 0.22876311 | 0.33390356 | p2-p3 | 2 | 0.34 | 1 | 1500 |
| ## 35 | 0.27852314 | 0.37747686 | p2-p3 | 1 | 0.34 | 2 | 1500 |
| ## 36 | 0.27542978 | 0.38057022 | p2-p3 | 2 | 0.34 | 2 | 1500 |
| ## | mixRatio | | | | | | |
| ## 1 | 0.1 | | | | | | |
| ## 2 | 0.1 | | | | | | |
| ## 3 | 0.1 | | | | | | |
| ## 4 | 0.1 | | | | | | |
| ## 5 | 0.1 | | | | | | |
| ## 6 | 0.1 | | | | | | |
| ## 7 | 0.1 | | | | | | |
| ## 8 | 0.1 | | | | | | |
| ## 9 | 0.1 | | | | | | |
| ## 10 | 0.1 | | | | | | |
| ## 11 | 0.1 | | | | | | |
| ## 12 | 0.1 | | | | | | |
| ## 13 | 0.1 | | | | | | |
| ## 14 | 0.1 | | | | | | |
| ## 15 | 0.1 | | | | | | |
| ## 16 | 0.1 | | | | | | |
| ## 17 | 0.1 | | | | | | |
| ## 18 | 0.1 | | | | | | |
| ## 19 | 0.1 | | | | | | |
| ## 20 | 0.1 | | | | | | |
| ## 21 | 0.1 | | | | | | |
| ## 22 | 0.1 | | | | | | |
| ## 23 | 0.1 | | | | | | |
| ## 24 | 0.1 | | | | | | |
| ## 25 | 0.1 | | | | | | |


```

## 26      0.1
## 27      0.1
## 28      0.1
## 29      0.1
## 30      0.1
## 31      0.1
## 32      0.1
## 33      0.1
## 34      0.1
## 35      0.1
## 36      0.1
##
## [[2]]
##      confiLower confiUpper  type method trueValue trialID sampleSize
## 1 -0.09865072  0.13865072 p1-p2      1      0.02      1      500
## 2 -0.07105430  0.11105430 p1-p2      2      0.02      1      500
## 3 -0.06378376  0.17178376 p1-p2      1      0.02      2      500
## 4 -0.03705430  0.14505430 p1-p2      2      0.02      2      500
## 5  0.21041811  0.38958189 p1-p3      1      0.36      1      500
## 6  0.20894570  0.39105430 p1-p3      2      0.36      1      500
## 7  0.21053690  0.39346310 p1-p3      1      0.36      2      500
## 8  0.21094570  0.39305430 p1-p3      2      0.36      2      500
## 9  0.19118927  0.36881073 p2-p3      1      0.34      1      500
## 10 0.18894570  0.37105430 p2-p3      2      0.34      1      500
## 11 0.15873898  0.33726102 p2-p3      1      0.34      2      500
## 12 0.15694570  0.33905430 p2-p3      2      0.34      2      500
## 13 -0.05032634  0.11632634 p1-p2      1      0.02      1     1000
## 14 -0.03138511  0.09738511 p1-p2      2      0.02      1     1000
## 15 -0.03004481  0.13604481 p1-p2      1      0.02      2     1000
## 16 -0.01138511  0.11738511 p1-p2      2      0.02      2     1000
## 17  0.22550942  0.35449058 p1-p3      1      0.36      1     1000
## 18  0.22561489  0.35438511 p1-p3      2      0.36      1     1000
## 19  0.22889877  0.35910123 p1-p3      1      0.36      2     1000
## 20  0.22961489  0.35838511 p1-p3      2      0.36      2     1000
## 21  0.19346558  0.32053442 p2-p3      1      0.34      1     1000
## 22  0.19261489  0.32138511 p2-p3      2      0.34      1     1000
## 23  0.17746764  0.30453236 p2-p3      1      0.34      2     1000
## 24  0.17661489  0.30538511 p2-p3      2      0.34      2     1000
## 25 -0.04476428  0.09143095 p1-p2      1      0.02      1     1500
## 26 -0.02923689  0.07590356 p1-p2      2      0.02      1     1500
## 27 -0.02861704  0.10728371 p1-p2      1      0.02      2     1500
## 28 -0.01323689  0.09190356 p1-p2      2      0.02      2     1500
## 29  0.23418745  0.33914589 p1-p3      1      0.36      1     1500
## 30  0.23409644  0.33923689 p1-p3      2      0.36      1     1500
## 31  0.23782338  0.34350996 p1-p3      1      0.36      2     1500
## 32  0.23809644  0.34323689 p1-p3      2      0.36      2     1500
## 33  0.21140311  0.31526355 p2-p3      1      0.34      1     1500
## 34  0.21076311  0.31590356 p2-p3      2      0.34      1     1500
## 35  0.19942891  0.30323776 p2-p3      1      0.34      2     1500
## 36  0.19876311  0.30390356 p2-p3      2      0.34      2     1500
##      mixRatio
## 1      0.2
## 2      0.2
## 3      0.2

```

```
## 4      0.2
## 5      0.2
## 6      0.2
## 7      0.2
## 8      0.2
## 9      0.2
## 10     0.2
## 11     0.2
## 12     0.2
## 13     0.2
## 14     0.2
## 15     0.2
## 16     0.2
## 17     0.2
## 18     0.2
## 19     0.2
## 20     0.2
## 21     0.2
## 22     0.2
## 23     0.2
## 24     0.2
## 25     0.2
## 26     0.2
## 27     0.2
## 28     0.2
## 29     0.2
## 30     0.2
## 31     0.2
## 32     0.2
## 33     0.2
## 34     0.2
## 35     0.2
## 36     0.2
```

```
##
```

```
## [[3]]
```

| ## | confiLower | confiUpper | type | method | trueValue | trialID | sampleSize |
|-------|--------------|------------|-------|--------|-----------|---------|------------|
| ## 1 | -0.102576215 | 0.13057622 | p1-p2 | 1 | 0.02 | 1 | 500 |
| ## 2 | -0.077054300 | 0.10505430 | p1-p2 | 2 | 0.02 | 1 | 500 |
| ## 3 | -0.045680404 | 0.18568040 | p1-p2 | 1 | 0.02 | 2 | 500 |
| ## 4 | -0.021054300 | 0.16105430 | p1-p2 | 2 | 0.02 | 2 | 500 |
| ## 5 | 0.158965711 | 0.34503429 | p1-p3 | 1 | 0.36 | 1 | 500 |
| ## 6 | 0.160945700 | 0.34305430 | p1-p3 | 2 | 0.36 | 1 | 500 |
| ## 7 | 0.172904284 | 0.36309572 | p1-p3 | 1 | 0.36 | 2 | 500 |
| ## 8 | 0.176945700 | 0.35905430 | p1-p3 | 2 | 0.36 | 2 | 500 |
| ## 9 | 0.145596297 | 0.33040370 | p2-p3 | 1 | 0.34 | 1 | 500 |
| ## 10 | 0.146945700 | 0.32905430 | p2-p3 | 2 | 0.34 | 1 | 500 |
| ## 11 | 0.106179475 | 0.28982053 | p2-p3 | 1 | 0.34 | 2 | 500 |
| ## 12 | 0.106945700 | 0.28905430 | p2-p3 | 2 | 0.34 | 2 | 500 |
| ## 13 | -0.062123105 | 0.10212310 | p1-p2 | 1 | 0.02 | 1 | 1000 |
| ## 14 | -0.044385113 | 0.08438511 | p1-p2 | 2 | 0.02 | 1 | 1000 |
| ## 15 | -0.038800951 | 0.12480095 | p1-p2 | 1 | 0.02 | 2 | 1000 |
| ## 16 | -0.021385113 | 0.10738511 | p1-p2 | 2 | 0.02 | 2 | 1000 |
| ## 17 | 0.179657786 | 0.31234221 | p1-p3 | 1 | 0.36 | 1 | 1000 |
| ## 18 | 0.181614887 | 0.31038511 | p1-p3 | 2 | 0.36 | 1 | 1000 |

| | | | | | | | |
|-------|--------------|------------|-------|---|------|---|------|
| ## 19 | 0.182920311 | 0.31707969 | p1-p3 | 1 | 0.36 | 2 | 1000 |
| ## 20 | 0.185614887 | 0.31438511 | p1-p3 | 2 | 0.36 | 2 | 1000 |
| ## 21 | 0.160312735 | 0.29168727 | p2-p3 | 1 | 0.34 | 1 | 1000 |
| ## 22 | 0.161614887 | 0.29038511 | p2-p3 | 2 | 0.34 | 1 | 1000 |
| ## 23 | 0.141360934 | 0.27263907 | p2-p3 | 1 | 0.34 | 2 | 1000 |
| ## 24 | 0.142614887 | 0.27138511 | p2-p3 | 2 | 0.34 | 2 | 1000 |
| ## 25 | -0.012498212 | 0.12183155 | p1-p2 | 1 | 0.02 | 1 | 1500 |
| ## 26 | 0.002096442 | 0.10723689 | p1-p2 | 2 | 0.02 | 1 | 1500 |
| ## 27 | -0.042610395 | 0.09061040 | p1-p2 | 1 | 0.02 | 2 | 1500 |
| ## 28 | -0.028570224 | 0.07657022 | p1-p2 | 2 | 0.02 | 2 | 1500 |
| ## 29 | 0.217086545 | 0.32558012 | p1-p3 | 1 | 0.36 | 1 | 1500 |
| ## 30 | 0.218763109 | 0.32390356 | p1-p3 | 2 | 0.36 | 1 | 1500 |
| ## 31 | 0.177129616 | 0.28687038 | p1-p3 | 1 | 0.36 | 2 | 1500 |
| ## 32 | 0.179429776 | 0.28457022 | p1-p3 | 2 | 0.36 | 2 | 1500 |
| ## 33 | 0.163847004 | 0.26948633 | p2-p3 | 1 | 0.34 | 1 | 1500 |
| ## 34 | 0.164096442 | 0.26923689 | p2-p3 | 2 | 0.34 | 1 | 1500 |
| ## 35 | 0.153802322 | 0.26219768 | p2-p3 | 1 | 0.34 | 2 | 1500 |
| ## 36 | 0.155429776 | 0.26057022 | p2-p3 | 2 | 0.34 | 2 | 1500 |
| ## | mixRatio | | | | | | |
| ## 1 | 0.3 | | | | | | |
| ## 2 | 0.3 | | | | | | |
| ## 3 | 0.3 | | | | | | |
| ## 4 | 0.3 | | | | | | |
| ## 5 | 0.3 | | | | | | |
| ## 6 | 0.3 | | | | | | |
| ## 7 | 0.3 | | | | | | |
| ## 8 | 0.3 | | | | | | |
| ## 9 | 0.3 | | | | | | |
| ## 10 | 0.3 | | | | | | |
| ## 11 | 0.3 | | | | | | |
| ## 12 | 0.3 | | | | | | |
| ## 13 | 0.3 | | | | | | |
| ## 14 | 0.3 | | | | | | |
| ## 15 | 0.3 | | | | | | |
| ## 16 | 0.3 | | | | | | |
| ## 17 | 0.3 | | | | | | |
| ## 18 | 0.3 | | | | | | |
| ## 19 | 0.3 | | | | | | |
| ## 20 | 0.3 | | | | | | |
| ## 21 | 0.3 | | | | | | |
| ## 22 | 0.3 | | | | | | |
| ## 23 | 0.3 | | | | | | |
| ## 24 | 0.3 | | | | | | |
| ## 25 | 0.3 | | | | | | |
| ## 26 | 0.3 | | | | | | |
| ## 27 | 0.3 | | | | | | |
| ## 28 | 0.3 | | | | | | |
| ## 29 | 0.3 | | | | | | |
| ## 30 | 0.3 | | | | | | |
| ## 31 | 0.3 | | | | | | |
| ## 32 | 0.3 | | | | | | |
| ## 33 | 0.3 | | | | | | |
| ## 34 | 0.3 | | | | | | |
| ## 35 | 0.3 | | | | | | |

```

## 36      0.3
##
## [[4]]
##      confiLower confiUpper  type method trueValue trialID sampleSize
## 1  -0.09184480 0.13984480 p1-p2      1      0.02      1      500
## 2  -0.06705430 0.11505430 p1-p2      2      0.02      1      500
## 3  -0.12286806 0.11086806 p1-p2      1      0.02      2      500
## 4  -0.09705430 0.08505430 p1-p2      2      0.02      2      500
## 5   0.14765989 0.33634011 p1-p3      1      0.36      1      500
## 6   0.15094570 0.33305430 p1-p3      2      0.36      1      500
## 7   0.15585009 0.34014991 p1-p3      1      0.36      2      500
## 8   0.15694570 0.33905430 p1-p3      2      0.36      2      500
## 9   0.12479160 0.31120840 p2-p3      1      0.34      1      500
## 10  0.12694570 0.30905430 p2-p3      2      0.34      1      500
## 11  0.16158495 0.34641505 p2-p3      1      0.34      2      500
## 12  0.16294570 0.34505430 p2-p3      2      0.34      2      500
## 13 -0.02764356 0.13364356 p1-p2      1      0.02      1     1000
## 14 -0.01138511 0.11738511 p1-p2      2      0.02      1     1000
## 15 -0.08998442 0.07198442 p1-p2      1      0.02      2     1000
## 16 -0.07338511 0.05538511 p1-p2      2      0.02      2     1000
## 17  0.15316015 0.29083985 p1-p3      1      0.36      1     1000
## 18  0.15761489 0.28638511 p1-p3      2      0.36      1     1000
## 19  0.12951315 0.26448685 p1-p3      1      0.36      2     1000
## 20  0.13261489 0.26138511 p1-p3      2      0.36      2     1000
## 21  0.10210741 0.23589259 p2-p3      1      0.34      1     1000
## 22  0.10461489 0.23338511 p2-p3      2      0.34      1     1000
## 23  0.13818796 0.27381204 p2-p3      1      0.34      2     1000
## 24  0.14161489 0.27038511 p2-p3      2      0.34      2     1000
## 25 -0.04683578 0.08683578 p1-p2      1      0.02      1     1500
## 26 -0.03257022 0.07257022 p1-p2      2      0.02      1     1500
## 27 -0.04736724 0.08603391 p1-p2      1      0.02      2     1500
## 28 -0.03323689 0.07190356 p1-p2      2      0.02      2     1500
## 29  0.18350332 0.29249668 p1-p3      1      0.36      1     1500
## 30  0.18542978 0.29057022 p1-p3      2      0.36      1     1500
## 31  0.17797781 0.28735552 p1-p3      1      0.36      2     1500
## 32  0.18009644 0.28523689 p1-p3      2      0.36      2     1500
## 33  0.16405101 0.27194899 p2-p3      1      0.34      1     1500
## 34  0.16542978 0.27057022 p2-p3      2      0.34      1     1500
## 35  0.15918170 0.26748497 p2-p3      1      0.34      2     1500
## 36  0.16076311 0.26590356 p2-p3      2      0.34      2     1500
##      mixRatio
## 1      0.4
## 2      0.4
## 3      0.4
## 4      0.4
## 5      0.4
## 6      0.4
## 7      0.4
## 8      0.4
## 9      0.4
## 10     0.4
## 11     0.4
## 12     0.4
## 13     0.4

```

```
## 14      0.4
## 15      0.4
## 16      0.4
## 17      0.4
## 18      0.4
## 19      0.4
## 20      0.4
## 21      0.4
## 22      0.4
## 23      0.4
## 24      0.4
## 25      0.4
## 26      0.4
## 27      0.4
## 28      0.4
## 29      0.4
## 30      0.4
## 31      0.4
## 32      0.4
## 33      0.4
## 34      0.4
## 35      0.4
## 36      0.4
```

```
##
```

```
## [[5]]
```

| ## | confiLower | confiUpper | type | method | trueValue | trialID | sampleSize |
|-------|-------------|------------|-------|--------|-----------|---------|------------|
| ## 1 | -0.04656225 | 0.17856225 | p1-p2 | 1 | 0.02 | 1 | 500 |
| ## 2 | -0.02505430 | 0.15705430 | p1-p2 | 2 | 0.02 | 1 | 500 |
| ## 3 | -0.09700514 | 0.12900514 | p1-p2 | 1 | 0.02 | 2 | 500 |
| ## 4 | -0.07505430 | 0.10705430 | p1-p2 | 2 | 0.02 | 2 | 500 |
| ## 5 | 0.10054179 | 0.29945821 | p1-p3 | 1 | 0.36 | 1 | 500 |
| ## 6 | 0.10894570 | 0.29105430 | p1-p3 | 2 | 0.36 | 1 | 500 |
| ## 7 | 0.08000858 | 0.27599142 | p1-p3 | 1 | 0.36 | 2 | 500 |
| ## 8 | 0.08694570 | 0.26905430 | p1-p3 | 2 | 0.36 | 2 | 500 |
| ## 9 | 0.03822917 | 0.22977083 | p2-p3 | 1 | 0.34 | 1 | 500 |
| ## 10 | 0.04294570 | 0.22505430 | p2-p3 | 2 | 0.34 | 1 | 500 |
| ## 11 | 0.06489504 | 0.25910496 | p2-p3 | 1 | 0.34 | 2 | 500 |
| ## 12 | 0.07094570 | 0.25305430 | p2-p3 | 2 | 0.34 | 2 | 500 |
| ## 13 | -0.07784263 | 0.08584263 | p1-p2 | 1 | 0.02 | 1 | 1000 |
| ## 14 | -0.06038511 | 0.06838511 | p1-p2 | 2 | 0.02 | 1 | 1000 |
| ## 15 | -0.09360176 | 0.06560176 | p1-p2 | 1 | 0.02 | 2 | 1000 |
| ## 16 | -0.07838511 | 0.05038511 | p1-p2 | 2 | 0.02 | 2 | 1000 |
| ## 17 | 0.16246828 | 0.29553172 | p1-p3 | 1 | 0.36 | 1 | 1000 |
| ## 18 | 0.16461489 | 0.29338511 | p1-p3 | 2 | 0.36 | 1 | 1000 |
| ## 19 | 0.08494826 | 0.22305174 | p1-p3 | 1 | 0.36 | 2 | 1000 |
| ## 20 | 0.08961489 | 0.21838511 | p1-p3 | 2 | 0.36 | 2 | 1000 |
| ## 21 | 0.15860282 | 0.29139718 | p2-p3 | 1 | 0.34 | 1 | 1000 |
| ## 22 | 0.16061489 | 0.28938511 | p2-p3 | 2 | 0.34 | 1 | 1000 |
| ## 23 | 0.09838772 | 0.23761228 | p2-p3 | 1 | 0.34 | 2 | 1000 |
| ## 24 | 0.10361489 | 0.23238511 | p2-p3 | 2 | 0.34 | 2 | 1000 |
| ## 25 | -0.05124456 | 0.08057790 | p1-p2 | 1 | 0.02 | 1 | 1500 |
| ## 26 | -0.03790356 | 0.06723689 | p1-p2 | 2 | 0.02 | 1 | 1500 |
| ## 27 | -0.04301091 | 0.08834424 | p1-p2 | 1 | 0.02 | 2 | 1500 |
| ## 28 | -0.02990356 | 0.07523689 | p1-p2 | 2 | 0.02 | 2 | 1500 |

```

## 29 0.14560954 0.25705713 p1-p3      1      0.36      1      1500
## 30 0.14876311 0.25390356 p1-p3      2      0.36      1      1500
## 31 0.14120633 0.25346034 p1-p3      1      0.36      2      1500
## 32 0.14476311 0.24990356 p1-p3      2      0.36      2      1500
## 33 0.13138430 0.24194903 p2-p3      1      0.34      1      1500
## 34 0.13409644 0.23923689 p2-p3      2      0.34      1      1500
## 35 0.11923624 0.23009709 p2-p3      1      0.34      2      1500
## 36 0.12209644 0.22723689 p2-p3      2      0.34      2      1500
##      mixRatio
## 1      0.5
## 2      0.5
## 3      0.5
## 4      0.5
## 5      0.5
## 6      0.5
## 7      0.5
## 8      0.5
## 9      0.5
## 10     0.5
## 11     0.5
## 12     0.5
## 13     0.5
## 14     0.5
## 15     0.5
## 16     0.5
## 17     0.5
## 18     0.5
## 19     0.5
## 20     0.5
## 21     0.5
## 22     0.5
## 23     0.5
## 24     0.5
## 25     0.5
## 26     0.5
## 27     0.5
## 28     0.5
## 29     0.5
## 30     0.5
## 31     0.5
## 32     0.5
## 33     0.5
## 34     0.5
## 35     0.5
## 36     0.5

```

Combine and save.

```
saveRDS(Reduce(rbind,resMix),'YL_Q2_example.rds')
```