

Project 1 function

YL

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Intro

This is an R Markdown document for project 1: <http://utdallas.edu/~ammann/stat6341/node10.html>.

Question 1

Setup:

```
p = c(0.5,0.3,0.2)
alpha = 0.05
sampleSizeVector=c(500,1000,1500)
# parameter for method 1
m=3
M = m*(m-1)/2
cv = qchisq(1-alpha/M,M-1) ### critical value
print(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
print(a)

## [1] 2.036036
```

Generate simulation

Generate 2 simulated data, for example:

```
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 distribution is about 0.5, 0.3, 0.2. Then a function is designed to compute the confidence interval using method 1 and method 2. **This function is going to be the importance one, because it is the most basic part for confidence interval computation regardless what's the distribution or whether it is mixed or not.**

```
## 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 = round(confiLower,4),confiUpper = round(confiUpper,4),
                    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      0.1055      0.3265 p1-p2      1        0.2        1
## 2      0.1249      0.3071 p1-p2      2        0.2        1
##
## [[2]]
##   confiLower confiUpper  type method trueValue trialID
## 1      0.1167      0.3393 p1-p2      1        0.2        2
## 2      0.1369      0.3191 p1-p2      2        0.2        2
```

Since we have two column, the result is the length 2 list, where each element is a dataframe. Looks good. Then we have to try different sample size, which can be done using a function. And we can embed all 3 pair difference to one sampleSize. Check the **apply** build-in function. Check the **Reduce** build-in function.

```
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      0.1055      0.3265 p1-p2      1      0.2      1      500
## 2      0.1249      0.3071 p1-p2      2      0.2      1      500
## 3      0.1167      0.3393 p1-p2      1      0.2      2      500
## 4      0.1369      0.3191 p1-p2      2      0.2      2      500
## 5      0.1949      0.3971 p1-p3      1      0.3      1      500
## 6      0.2049      0.3871 p1-p3      2      0.3      1      500
## 7      0.2266      0.4254 p1-p3      1      0.3      2      500
## 8      0.2349      0.4171 p1-p3      2      0.3      2      500
## 9     -0.0095      0.1695 p2-p3      1      0.1      1      500
## 10    -0.0111      0.1711 p2-p3      2      0.1      1      500
## 11     0.0100      0.1860 p2-p3      1      0.1      2      500
## 12     0.0069      0.1891 p2-p3      2      0.1      2      500
```

Then we have all three pair difference in one shot. The sampleSize column is to distinguish the result from different sampleSize. Let's try two sample size: 500, 1000, 1500. Check the **lapply** build-in function.

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

```
## [[1]]
##      confiLower confiUpper  type method trueValue trialID sampleSize
## 1      0.1055      0.3265 p1-p2      1      0.2      1      500
## 2      0.1249      0.3071 p1-p2      2      0.2      1      500
## 3      0.1167      0.3393 p1-p2      1      0.2      2      500
## 4      0.1369      0.3191 p1-p2      2      0.2      2      500
## 5      0.1949      0.3971 p1-p3      1      0.3      1      500
## 6      0.2049      0.3871 p1-p3      2      0.3      1      500
## 7      0.2266      0.4254 p1-p3      1      0.3      2      500
## 8      0.2349      0.4171 p1-p3      2      0.3      2      500
## 9     -0.0095      0.1695 p2-p3      1      0.1      1      500
## 10    -0.0111      0.1711 p2-p3      2      0.1      1      500
## 11     0.0100      0.1860 p2-p3      1      0.1      2      500
## 12     0.0069      0.1891 p2-p3      2      0.1      2      500
##
## [[2]]
##      confiLower confiUpper  type method trueValue trialID sampleSize
## 1      0.1055      0.3265 p1-p2      1      0.2      1     1000
## 2      0.1249      0.3071 p1-p2      2      0.2      1     1000
## 3      0.1167      0.3393 p1-p2      1      0.2      2     1000
## 4      0.1369      0.3191 p1-p2      2      0.2      2     1000
## 5      0.1949      0.3971 p1-p3      1      0.3      1     1000
## 6      0.2049      0.3871 p1-p3      2      0.3      1     1000
## 7      0.2266      0.4254 p1-p3      1      0.3      2     1000
## 8      0.2349      0.4171 p1-p3      2      0.3      2     1000
## 9     -0.0095      0.1695 p2-p3      1      0.1      1     1000
## 10    -0.0111      0.1711 p2-p3      2      0.1      1     1000
## 11     0.0100      0.1860 p2-p3      1      0.1      2     1000
## 12     0.0069      0.1891 p2-p3      2      0.1      2     1000
##
## [[3]]
##      confiLower confiUpper  type method trueValue trialID sampleSize
## 1      0.1055      0.3265 p1-p2      1      0.2      1     1500
```

## 2	0.1249	0.3071	p1-p2	2	0.2	1	1500
## 3	0.1167	0.3393	p1-p2	1	0.2	2	1500
## 4	0.1369	0.3191	p1-p2	2	0.2	2	1500
## 5	0.1949	0.3971	p1-p3	1	0.3	1	1500
## 6	0.2049	0.3871	p1-p3	2	0.3	1	1500
## 7	0.2266	0.4254	p1-p3	1	0.3	2	1500
## 8	0.2349	0.4171	p1-p3	2	0.3	2	1500
## 9	-0.0095	0.1695	p2-p3	1	0.1	1	1500
## 10	-0.0111	0.1711	p2-p3	2	0.1	1	1500
## 11	0.0100	0.1860	p2-p3	1	0.1	2	1500
## 12	0.0069	0.1891	p2-p3	2	0.1	2	1500

Therefore, we get the 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	0.1055	0.3265	p1-p2	1	0.2	1	500
## 2	0.1249	0.3071	p1-p2	2	0.2	1	500
## 3	0.1167	0.3393	p1-p2	1	0.2	2	500
## 4	0.1369	0.3191	p1-p2	2	0.2	2	500
## 5	0.1949	0.3971	p1-p3	1	0.3	1	500
## 6	0.2049	0.3871	p1-p3	2	0.3	1	500
## 7	0.2266	0.4254	p1-p3	1	0.3	2	500
## 8	0.2349	0.4171	p1-p3	2	0.3	2	500
## 9	-0.0095	0.1695	p2-p3	1	0.1	1	500
## 10	-0.0111	0.1711	p2-p3	2	0.1	1	500
## 11	0.0100	0.1860	p2-p3	1	0.1	2	500
## 12	0.0069	0.1891	p2-p3	2	0.1	2	500
## 13	0.1055	0.3265	p1-p2	1	0.2	1	1000
## 14	0.1249	0.3071	p1-p2	2	0.2	1	1000
## 15	0.1167	0.3393	p1-p2	1	0.2	2	1000
## 16	0.1369	0.3191	p1-p2	2	0.2	2	1000
## 17	0.1949	0.3971	p1-p3	1	0.3	1	1000
## 18	0.2049	0.3871	p1-p3	2	0.3	1	1000
## 19	0.2266	0.4254	p1-p3	1	0.3	2	1000
## 20	0.2349	0.4171	p1-p3	2	0.3	2	1000
## 21	-0.0095	0.1695	p2-p3	1	0.1	1	1000
## 22	-0.0111	0.1711	p2-p3	2	0.1	1	1000
## 23	0.0100	0.1860	p2-p3	1	0.1	2	1000
## 24	0.0069	0.1891	p2-p3	2	0.1	2	1000
## 25	0.1055	0.3265	p1-p2	1	0.2	1	1500
## 26	0.1249	0.3071	p1-p2	2	0.2	1	1500
## 27	0.1167	0.3393	p1-p2	1	0.2	2	1500
## 28	0.1369	0.3191	p1-p2	2	0.2	2	1500
## 29	0.1949	0.3971	p1-p3	1	0.3	1	1500
## 30	0.2049	0.3871	p1-p3	2	0.3	1	1500
## 31	0.2266	0.4254	p1-p3	1	0.3	2	1500
## 32	0.2349	0.4171	p1-p3	2	0.3	2	1500
## 33	-0.0095	0.1695	p2-p3	1	0.1	1	1500
## 34	-0.0111	0.1711	p2-p3	2	0.1	1	1500
## 35	0.0100	0.1860	p2-p3	1	0.1	2	1500
## 36	0.0069	0.1891	p2-p3	2	0.1	2	1500

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

Question 2

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)

```
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 at question 1. We can just simply apply the 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   -0.0697    0.1697 p1-p2      1      0.02      1
## 2   -0.0411    0.1411 p1-p2      2      0.02      1
##
## [[2]]
##   confiLower confiUpper type method trueValue trialID
## 1   -0.2044    0.0364 p1-p2      1      0.02      2
## 2   -0.1751    0.0071 p1-p2      2      0.02      2
```

Then we can design a function that generate mix data and calculate the pair difference, which is similar to confiDataFun.

```
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      -0.0885    0.1525 p1-p2      1      0.02      1      500
## 2      -0.0591    0.1231 p1-p2      2      0.02      1      500
## 3      -0.0888    0.1488 p1-p2      1      0.02      2      500
## 4      -0.0611    0.1211 p1-p2      2      0.02      2      500
## 5       0.2621    0.4339 p1-p3      1     0.36      1      500
## 6       0.2569    0.4391 p1-p3      2     0.36      1      500
## 7       0.2185    0.3975 p1-p3      1     0.36      2      500
## 8       0.2169    0.3991 p1-p3      2     0.36      2      500
## 9       0.2311    0.4009 p2-p3      1     0.34      1      500
## 10      0.2249    0.4071 p2-p3      2     0.34      1      500
## 11      0.1896    0.3664 p2-p3      1     0.34      2      500
## 12      0.1869    0.3691 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      -0.0885    0.1525 p1-p2      1      0.02      1      500
## 2      -0.0591    0.1231 p1-p2      2      0.02      1      500
## 3      -0.0888    0.1488 p1-p2      1      0.02      2      500
## 4      -0.0611    0.1211 p1-p2      2      0.02      2      500
## 5       0.2621    0.4339 p1-p3      1     0.36      1      500
## 6       0.2569    0.4391 p1-p3      2     0.36      1      500
## 7       0.2185    0.3975 p1-p3      1     0.36      2      500
## 8       0.2169    0.3991 p1-p3      2     0.36      2      500
## 9       0.2311    0.4009 p2-p3      1     0.34      1      500
## 10      0.2249    0.4071 p2-p3      2     0.34      1      500
## 11      0.1896    0.3664 p2-p3      1     0.34      2      500
## 12      0.1869    0.3691 p2-p3      2     0.34      2      500
## 13     -0.0362    0.1322 p1-p2      1      0.02      1     1000
## 14     -0.0164    0.1124 p1-p2      2      0.02      1     1000
## 15     -0.0916    0.0796 p1-p2      1      0.02      2     1000
## 16     -0.0704    0.0584 p1-p2      2      0.02      2     1000
## 17      0.2631    0.3889 p1-p3      1     0.36      1     1000
## 18      0.2616    0.3904 p1-p3      2     0.36      1     1000
## 19      0.2783    0.3977 p1-p3      1     0.36      2     1000
## 20      0.2736    0.4024 p1-p3      2     0.36      2     1000
## 21      0.2163    0.3397 p2-p3      1     0.34      1     1000
## 22      0.2136    0.3424 p2-p3      2     0.34      1     1000
## 23      0.2841    0.4039 p2-p3      1     0.34      2     1000
## 24      0.2796    0.4084 p2-p3      2     0.34      2     1000
```

##	25	-0.0274	0.1101	p1-p2	1	0.02	1	1500						
##	26	-0.0112	0.0939	p1-p2	2	0.02	1	1500						
##	27	-0.0675	0.0715	p1-p2	1	0.02	2	1500						
##	28	-0.0506	0.0546	p1-p2	2	0.02	2	1500						
##	29	0.2713	0.3740	p1-p3	1	0.36	1	1500						
##	30	0.2701	0.3752	p1-p3	2	0.36	1	1500						
##	31	0.2805	0.3795	p1-p3	1	0.36	2	1500						
##	32	0.2774	0.3826	p1-p3	2	0.36	2	1500						
##	33	0.2309	0.3318	p2-p3	1	0.34	1	1500						
##	34	0.2288	0.3339	p2-p3	2	0.34	1	1500						
##	35	0.2785	0.3775	p2-p3	1	0.34	2	1500						
##	36	0.2754	0.3806	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	-0.0987	0.1387	p1-p2	1	0.02	1	500						
##	2	-0.0711	0.1111	p1-p2	2	0.02	1	500						

## 3	-0.0638	0.1718	p1-p2	1	0.02	2	500
## 4	-0.0371	0.1451	p1-p2	2	0.02	2	500
## 5	0.2104	0.3896	p1-p3	1	0.36	1	500
## 6	0.2089	0.3911	p1-p3	2	0.36	1	500
## 7	0.2105	0.3935	p1-p3	1	0.36	2	500
## 8	0.2109	0.3931	p1-p3	2	0.36	2	500
## 9	0.1912	0.3688	p2-p3	1	0.34	1	500
## 10	0.1889	0.3711	p2-p3	2	0.34	1	500
## 11	0.1587	0.3373	p2-p3	1	0.34	2	500
## 12	0.1569	0.3391	p2-p3	2	0.34	2	500
## 13	-0.0503	0.1163	p1-p2	1	0.02	1	1000
## 14	-0.0314	0.0974	p1-p2	2	0.02	1	1000
## 15	-0.0300	0.1360	p1-p2	1	0.02	2	1000
## 16	-0.0114	0.1174	p1-p2	2	0.02	2	1000
## 17	0.2255	0.3545	p1-p3	1	0.36	1	1000
## 18	0.2256	0.3544	p1-p3	2	0.36	1	1000
## 19	0.2289	0.3591	p1-p3	1	0.36	2	1000
## 20	0.2296	0.3584	p1-p3	2	0.36	2	1000
## 21	0.1935	0.3205	p2-p3	1	0.34	1	1000
## 22	0.1926	0.3214	p2-p3	2	0.34	1	1000
## 23	0.1775	0.3045	p2-p3	1	0.34	2	1000
## 24	0.1766	0.3054	p2-p3	2	0.34	2	1000
## 25	-0.0448	0.0914	p1-p2	1	0.02	1	1500
## 26	-0.0292	0.0759	p1-p2	2	0.02	1	1500
## 27	-0.0286	0.1073	p1-p2	1	0.02	2	1500
## 28	-0.0132	0.0919	p1-p2	2	0.02	2	1500
## 29	0.2342	0.3391	p1-p3	1	0.36	1	1500
## 30	0.2341	0.3392	p1-p3	2	0.36	1	1500
## 31	0.2378	0.3435	p1-p3	1	0.36	2	1500
## 32	0.2381	0.3432	p1-p3	2	0.36	2	1500
## 33	0.2114	0.3153	p2-p3	1	0.34	1	1500
## 34	0.2108	0.3159	p2-p3	2	0.34	1	1500
## 35	0.1994	0.3032	p2-p3	1	0.34	2	1500
## 36	0.1988	0.3039	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      -0.1026    0.1306 p1-p2      1      0.02      1      500
## 2      -0.0771    0.1051 p1-p2      2      0.02      1      500
## 3      -0.0457    0.1857 p1-p2      1      0.02      2      500
## 4      -0.0211    0.1611 p1-p2      2      0.02      2      500
## 5       0.1590    0.3450 p1-p3      1      0.36      1      500
## 6       0.1609    0.3431 p1-p3      2      0.36      1      500
## 7       0.1729    0.3631 p1-p3      1      0.36      2      500
## 8       0.1769    0.3591 p1-p3      2      0.36      2      500
## 9       0.1456    0.3304 p2-p3      1      0.34      1      500
## 10      0.1469    0.3291 p2-p3      2      0.34      1      500
## 11      0.1062    0.2898 p2-p3      1      0.34      2      500
## 12      0.1069    0.2891 p2-p3      2      0.34      2      500
## 13     -0.0621    0.1021 p1-p2      1      0.02      1     1000
## 14     -0.0444    0.0844 p1-p2      2      0.02      1     1000
## 15     -0.0388    0.1248 p1-p2      1      0.02      2     1000
## 16     -0.0214    0.1074 p1-p2      2      0.02      2     1000
## 17      0.1797    0.3123 p1-p3      1      0.36      1     1000
## 18      0.1816    0.3104 p1-p3      2      0.36      1     1000
## 19      0.1829    0.3171 p1-p3      1      0.36      2     1000
## 20      0.1856    0.3144 p1-p3      2      0.36      2     1000
## 21      0.1603    0.2917 p2-p3      1      0.34      1     1000
## 22      0.1616    0.2904 p2-p3      2      0.34      1     1000
## 23      0.1414    0.2726 p2-p3      1      0.34      2     1000
## 24      0.1426    0.2714 p2-p3      2      0.34      2     1000
## 25     -0.0125    0.1218 p1-p2      1      0.02      1     1500
## 26      0.0021    0.1072 p1-p2      2      0.02      1     1500
## 27     -0.0426    0.0906 p1-p2      1      0.02      2     1500
## 28     -0.0286    0.0766 p1-p2      2      0.02      2     1500
## 29      0.2171    0.3256 p1-p3      1      0.36      1     1500
## 30      0.2188    0.3239 p1-p3      2      0.36      1     1500
## 31      0.1771    0.2869 p1-p3      1      0.36      2     1500
## 32      0.1794    0.2846 p1-p3      2      0.36      2     1500
## 33      0.1638    0.2695 p2-p3      1      0.34      1     1500
## 34      0.1641    0.2692 p2-p3      2      0.34      1     1500

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## 35      0.1538      0.2622 p2-p3      1      0.34      2      1500
## 36      0.1554      0.2606 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      -0.0918      0.1398 p1-p2      1      0.02      1        500
## 2      -0.0671      0.1151 p1-p2      2      0.02      1        500
## 3      -0.1229      0.1109 p1-p2      1      0.02      2        500
## 4      -0.0971      0.0851 p1-p2      2      0.02      2        500
## 5       0.1477      0.3363 p1-p3      1      0.36      1        500
## 6       0.1509      0.3331 p1-p3      2      0.36      1        500
## 7       0.1559      0.3401 p1-p3      1      0.36      2        500
## 8       0.1569      0.3391 p1-p3      2      0.36      2        500
## 9       0.1248      0.3112 p2-p3      1      0.34      1        500
## 10      0.1269      0.3091 p2-p3      2      0.34      1        500
## 11      0.1616      0.3464 p2-p3      1      0.34      2        500
## 12      0.1629      0.3451 p2-p3      2      0.34      2        500

```

## 13	-0.0276	0.1336	p1-p2	1	0.02	1	1000
## 14	-0.0114	0.1174	p1-p2	2	0.02	1	1000
## 15	-0.0900	0.0720	p1-p2	1	0.02	2	1000
## 16	-0.0734	0.0554	p1-p2	2	0.02	2	1000
## 17	0.1532	0.2908	p1-p3	1	0.36	1	1000
## 18	0.1576	0.2864	p1-p3	2	0.36	1	1000
## 19	0.1295	0.2645	p1-p3	1	0.36	2	1000
## 20	0.1326	0.2614	p1-p3	2	0.36	2	1000
## 21	0.1021	0.2359	p2-p3	1	0.34	1	1000
## 22	0.1046	0.2334	p2-p3	2	0.34	1	1000
## 23	0.1382	0.2738	p2-p3	1	0.34	2	1000
## 24	0.1416	0.2704	p2-p3	2	0.34	2	1000
## 25	-0.0468	0.0868	p1-p2	1	0.02	1	1500
## 26	-0.0326	0.0726	p1-p2	2	0.02	1	1500
## 27	-0.0474	0.0860	p1-p2	1	0.02	2	1500
## 28	-0.0332	0.0719	p1-p2	2	0.02	2	1500
## 29	0.1835	0.2925	p1-p3	1	0.36	1	1500
## 30	0.1854	0.2906	p1-p3	2	0.36	1	1500
## 31	0.1780	0.2874	p1-p3	1	0.36	2	1500
## 32	0.1801	0.2852	p1-p3	2	0.36	2	1500
## 33	0.1641	0.2719	p2-p3	1	0.34	1	1500
## 34	0.1654	0.2706	p2-p3	2	0.34	1	1500
## 35	0.1592	0.2675	p2-p3	1	0.34	2	1500
## 36	0.1608	0.2659	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      -0.0466    0.1786 p1-p2      1      0.02      1      500
## 2      -0.0251    0.1571 p1-p2      2      0.02      1      500
## 3      -0.0970    0.1290 p1-p2      1      0.02      2      500
## 4      -0.0751    0.1071 p1-p2      2      0.02      2      500
## 5       0.1005    0.2995 p1-p3      1      0.36      1      500
## 6       0.1089    0.2911 p1-p3      2      0.36      1      500
## 7       0.0800    0.2760 p1-p3      1      0.36      2      500
## 8       0.0869    0.2691 p1-p3      2      0.36      2      500
## 9       0.0382    0.2298 p2-p3      1      0.34      1      500
## 10      0.0429    0.2251 p2-p3      2      0.34      1      500
## 11      0.0649    0.2591 p2-p3      1      0.34      2      500
## 12      0.0709    0.2531 p2-p3      2      0.34      2      500
## 13     -0.0778    0.0858 p1-p2      1      0.02      1     1000
## 14     -0.0604    0.0684 p1-p2      2      0.02      1     1000
## 15     -0.0936    0.0656 p1-p2      1      0.02      2     1000
## 16     -0.0784    0.0504 p1-p2      2      0.02      2     1000
## 17      0.1625    0.2955 p1-p3      1      0.36      1     1000
## 18      0.1646    0.2934 p1-p3      2      0.36      1     1000
## 19      0.0849    0.2231 p1-p3      1      0.36      2     1000
## 20      0.0896    0.2184 p1-p3      2      0.36      2     1000
## 21      0.1586    0.2914 p2-p3      1      0.34      1     1000
## 22      0.1606    0.2894 p2-p3      2      0.34      1     1000
## 23      0.0984    0.2376 p2-p3      1      0.34      2     1000
## 24      0.1036    0.2324 p2-p3      2      0.34      2     1000
## 25     -0.0512    0.0806 p1-p2      1      0.02      1     1500
## 26     -0.0379    0.0672 p1-p2      2      0.02      1     1500
## 27     -0.0430    0.0883 p1-p2      1      0.02      2     1500
## 28     -0.0299    0.0752 p1-p2      2      0.02      2     1500
## 29      0.1456    0.2571 p1-p3      1      0.36      1     1500
## 30      0.1488    0.2539 p1-p3      2      0.36      1     1500
## 31      0.1412    0.2535 p1-p3      1      0.36      2     1500
## 32      0.1448    0.2499 p1-p3      2      0.36      2     1500
## 33      0.1314    0.2419 p2-p3      1      0.34      1     1500
## 34      0.1341    0.2392 p2-p3      2      0.34      1     1500
## 35      0.1192    0.2301 p2-p3      1      0.34      2     1500
## 36      0.1221    0.2272 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')
```