

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 = rmultinom(2, size = sampleSizeVector[1], prob = p)
df

##      [,1] [,2]
## [1,]  252  259
## [2,]  144  145
## [3,]  104   96
```

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)  #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]))
}

```

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

```

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 = rmultinom(nrep, size = sampleSize, prob = p)

  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 sampleSize

```

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

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

```
##
## [[2]]
##      confiLower confiUpper  type method trueValue sampleSize
## 1 0.07103364 0.2289664 p1-p2      1      0.2     1000
## 2 0.08561489 0.2143851 p1-p2      2      0.2     1000
## 3 0.14186239 0.2981376 p1-p2      1      0.2     1000
## 4 0.15561489 0.2843851 p1-p2      2      0.2     1000
## 5 0.17974708 0.3222529 p1-p3      1      0.3     1000
## 6 0.18661489 0.3153851 p1-p3      2      0.3     1000
## 7 0.22960930 0.3723907 p1-p3      1      0.3     1000
## 8 0.23661489 0.3653851 p1-p3      2      0.3     1000
## 9 0.03557035 0.1664296 p2-p3      1      0.1     1000
## 10 0.03661489 0.1653851 p2-p3      2      0.1     1000
## 11 0.01788663 0.1441134 p2-p3      1      0.1     1000
## 12 0.01661489 0.1453851 p2-p3      2      0.1     1000
```

```
##
## [[3]]
##      confiLower confiUpper  type method trueValue sampleSize
## 1 0.09348744 0.2225126 p1-p2      1      0.2     1500
## 2 0.10542978 0.2105702 p1-p2      2      0.2     1500
## 3 0.15139044 0.2792762 p1-p2      1      0.2     1500
## 4 0.16276311 0.2679036 p1-p2      2      0.2     1500
```

```
## 5 0.20192863 0.3180714 p1-p3 1 0.3 1500
## 6 0.20742978 0.3125702 p1-p3 2 0.3 1500
## 7 0.24250764 0.3588257 p1-p3 1 0.3 1500
## 8 0.24809644 0.3532369 p1-p3 2 0.3 1500
## 9 0.04887767 0.1551223 p2-p3 1 0.1 1500
## 10 0.04942978 0.1545702 p2-p3 2 0.1 1500
## 11 0.03375140 0.1369153 p2-p3 1 0.1 1500
## 12 0.03276311 0.1379036 p2-p3 2 0.1 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 sampleSize
## 1  0.10551570  0.3264843 p1-p2      1      0.2         500
## 2  0.12494570  0.3070543 p1-p2      2      0.2         500
## 3  0.11672754  0.3392725 p1-p2      1      0.2         500
## 4  0.13694570  0.3190543 p1-p2      2      0.2         500
## 5  0.19487744  0.3971226 p1-p3      1      0.3         500
## 6  0.20494570  0.3870543 p1-p3      2      0.3         500
## 7  0.22656451  0.4254355 p1-p3      1      0.3         500
## 8  0.23494570  0.4170543 p1-p3      2      0.3         500
## 9  -0.00954532  0.1695453 p2-p3      1      0.1         500
## 10 -0.01105430  0.1710543 p2-p3      2      0.1         500
## 11  0.01004201  0.1859580 p2-p3      1      0.1         500
## 12  0.00694570  0.1890543 p2-p3      2      0.1         500
## 13  0.07103364  0.2289664 p1-p2      1      0.2        1000
## 14  0.08561489  0.2143851 p1-p2      2      0.2        1000
## 15  0.14186239  0.2981376 p1-p2      1      0.2        1000
## 16  0.15561489  0.2843851 p1-p2      2      0.2        1000
## 17  0.17974708  0.3222529 p1-p3      1      0.3        1000
## 18  0.18661489  0.3153851 p1-p3      2      0.3        1000
## 19  0.22960930  0.3723907 p1-p3      1      0.3        1000
## 20  0.23661489  0.3653851 p1-p3      2      0.3        1000
## 21  0.03557035  0.1664296 p2-p3      1      0.1        1000
## 22  0.03661489  0.1653851 p2-p3      2      0.1        1000
## 23  0.01788663  0.1441134 p2-p3      1      0.1        1000
## 24  0.01661489  0.1453851 p2-p3      2      0.1        1000
## 25  0.09348744  0.2225126 p1-p2      1      0.2        1500
## 26  0.10542978  0.2105702 p1-p2      2      0.2        1500
## 27  0.15139044  0.2792762 p1-p2      1      0.2        1500
## 28  0.16276311  0.2679036 p1-p2      2      0.2        1500
## 29  0.20192863  0.3180714 p1-p3      1      0.3        1500
## 30  0.20742978  0.3125702 p1-p3      2      0.3        1500
## 31  0.24250764  0.3588257 p1-p3      1      0.3        1500
## 32  0.24809644  0.3532369 p1-p3      2      0.3        1500
## 33  0.04887767  0.1551223 p2-p3      1      0.1        1500
## 34  0.04942978  0.1545702 p2-p3      2      0.1        1500
## 35  0.03375140  0.1369153 p2-p3      1      0.1        1500
## 36  0.03276311  0.1379036 p2-p3      2      0.1        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]
## [1,]  252  259
## [2,]  144  145
## [3,]  104   96
```

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.

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

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

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

  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	sampleSize
## 1	-0.08852527	0.1525253	p1-p2	1	0.02	500
## 2	-0.05905430	0.1230543	p1-p2	2	0.02	500
## 3	-0.08875420	0.1487542	p1-p2	1	0.02	500
## 4	-0.06105430	0.1210543	p1-p2	2	0.02	500
## 5	0.26206692	0.4339331	p1-p3	1	0.36	500
## 6	0.25694570	0.4390543	p1-p3	2	0.36	500
## 7	0.21849712	0.3975029	p1-p3	1	0.36	500
## 8	0.21694570	0.3990543	p1-p3	2	0.36	500
## 9	0.23109768	0.4009023	p2-p3	1	0.34	500
## 10	0.22494570	0.4070543	p2-p3	2	0.34	500
## 11	0.18964074	0.3663593	p2-p3	1	0.34	500
## 12	0.18694570	0.3690543	p2-p3	2	0.34	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	sampleSize	mixRatio
## 1	-0.08852527	0.15252527	p1-p2	1	0.02	500	0.1
## 2	-0.05905430	0.12305430	p1-p2	2	0.02	500	0.1
## 3	-0.08875420	0.14875420	p1-p2	1	0.02	500	0.1
## 4	-0.06105430	0.12105430	p1-p2	2	0.02	500	0.1
## 5	0.26206692	0.43393308	p1-p3	1	0.36	500	0.1
## 6	0.25694570	0.43905430	p1-p3	2	0.36	500	0.1
## 7	0.21849712	0.39750288	p1-p3	1	0.36	500	0.1
## 8	0.21694570	0.39905430	p1-p3	2	0.36	500	0.1
## 9	0.23109768	0.40090232	p2-p3	1	0.34	500	0.1
## 10	0.22494570	0.40705430	p2-p3	2	0.34	500	0.1
## 11	0.18964074	0.36635926	p2-p3	1	0.34	500	0.1
## 12	0.18694570	0.36905430	p2-p3	2	0.34	500	0.1
## 13	-0.03619570	0.13219570	p1-p2	1	0.02	1000	0.1
## 14	-0.01638511	0.11238511	p1-p2	2	0.02	1000	0.1
## 15	-0.09155930	0.07955930	p1-p2	1	0.02	1000	0.1
## 16	-0.07038511	0.05838511	p1-p2	2	0.02	1000	0.1
## 17	0.26306300	0.38893700	p1-p3	1	0.36	1000	0.1
## 18	0.26161489	0.39038511	p1-p3	2	0.36	1000	0.1
## 19	0.27826500	0.39773500	p1-p3	1	0.36	1000	0.1
## 20	0.27361489	0.40238511	p1-p3	2	0.36	1000	0.1
## 21	0.21631196	0.33968804	p2-p3	1	0.34	1000	0.1
## 22	0.21361489	0.34238511	p2-p3	2	0.34	1000	0.1
## 23	0.28413436	0.40386564	p2-p3	1	0.34	1000	0.1
## 24	0.27961489	0.40838511	p2-p3	2	0.34	1000	0.1
## 25	-0.02743581	0.11010247	p1-p2	1	0.02	1500	0.1
## 26	-0.01123689	0.09390356	p1-p2	2	0.02	1500	0.1
## 27	-0.06754685	0.07154685	p1-p2	1	0.02	1500	0.1
## 28	-0.05057022	0.05457022	p1-p2	2	0.02	1500	0.1

```

## 29 0.27134107 0.37399227 p1-p3      1      0.36      1500      0.1
## 30 0.27009644 0.37523689 p1-p3      2      0.36      1500      0.1
## 31 0.28048542 0.37951458 p1-p3      1      0.36      1500      0.1
## 32 0.27742978 0.38257022 p1-p3      2      0.36      1500      0.1
## 33 0.23088572 0.33178095 p2-p3      1      0.34      1500      0.1
## 34 0.22876311 0.33390356 p2-p3      2      0.34      1500      0.1
## 35 0.27852314 0.37747686 p2-p3      1      0.34      1500      0.1
## 36 0.27542978 0.38057022 p2-p3      2      0.34      1500      0.1
##
## [[2]]
##      confiLower confiUpper  type method trueValue sampleSize mixRatio
## 1  -0.09865072 0.13865072 p1-p2      1      0.02        500      0.2
## 2  -0.07105430 0.11105430 p1-p2      2      0.02        500      0.2
## 3  -0.06378376 0.17178376 p1-p2      1      0.02        500      0.2
## 4  -0.03705430 0.14505430 p1-p2      2      0.02        500      0.2
## 5   0.21041811 0.38958189 p1-p3      1      0.36        500      0.2
## 6   0.20894570 0.39105430 p1-p3      2      0.36        500      0.2
## 7   0.21053690 0.39346310 p1-p3      1      0.36        500      0.2
## 8   0.21094570 0.39305430 p1-p3      2      0.36        500      0.2
## 9   0.19118927 0.36881073 p2-p3      1      0.34        500      0.2
## 10  0.18894570 0.37105430 p2-p3      2      0.34        500      0.2
## 11  0.15873898 0.33726102 p2-p3      1      0.34        500      0.2
## 12  0.15694570 0.33905430 p2-p3      2      0.34        500      0.2
## 13 -0.05032634 0.11632634 p1-p2      1      0.02       1000      0.2
## 14 -0.03138511 0.09738511 p1-p2      2      0.02       1000      0.2
## 15 -0.03004481 0.13604481 p1-p2      1      0.02       1000      0.2
## 16 -0.01138511 0.11738511 p1-p2      2      0.02       1000      0.2
## 17  0.22550942 0.35449058 p1-p3      1      0.36       1000      0.2
## 18  0.22561489 0.35438511 p1-p3      2      0.36       1000      0.2
## 19  0.22889877 0.35910123 p1-p3      1      0.36       1000      0.2
## 20  0.22961489 0.35838511 p1-p3      2      0.36       1000      0.2
## 21  0.19346558 0.32053442 p2-p3      1      0.34       1000      0.2
## 22  0.19261489 0.32138511 p2-p3      2      0.34       1000      0.2
## 23  0.17746764 0.30453236 p2-p3      1      0.34       1000      0.2
## 24  0.17661489 0.30538511 p2-p3      2      0.34       1000      0.2
## 25 -0.04476428 0.09143095 p1-p2      1      0.02       1500      0.2
## 26 -0.02923689 0.07590356 p1-p2      2      0.02       1500      0.2
## 27 -0.02861704 0.10728371 p1-p2      1      0.02       1500      0.2
## 28 -0.01323689 0.09190356 p1-p2      2      0.02       1500      0.2
## 29  0.23418745 0.33914589 p1-p3      1      0.36       1500      0.2
## 30  0.23409644 0.33923689 p1-p3      2      0.36       1500      0.2
## 31  0.23782338 0.34350996 p1-p3      1      0.36       1500      0.2
## 32  0.23809644 0.34323689 p1-p3      2      0.36       1500      0.2
## 33  0.21140311 0.31526355 p2-p3      1      0.34       1500      0.2
## 34  0.21076311 0.31590356 p2-p3      2      0.34       1500      0.2
## 35  0.19942891 0.30323776 p2-p3      1      0.34       1500      0.2
## 36  0.19876311 0.30390356 p2-p3      2      0.34       1500      0.2
##
## [[3]]
##      confiLower confiUpper  type method trueValue sampleSize mixRatio
## 1  -0.102576215 0.13057622 p1-p2      1      0.02        500      0.3
## 2  -0.077054300 0.10505430 p1-p2      2      0.02        500      0.3
## 3  -0.045680404 0.18568040 p1-p2      1      0.02        500      0.3
## 4  -0.021054300 0.16105430 p1-p2      2      0.02        500      0.3

```



```

## 5 0.158965711 0.34503429 p1-p3 1 0.36 500 0.3
## 6 0.160945700 0.34305430 p1-p3 2 0.36 500 0.3
## 7 0.172904284 0.36309572 p1-p3 1 0.36 500 0.3
## 8 0.176945700 0.35905430 p1-p3 2 0.36 500 0.3
## 9 0.145596297 0.33040370 p2-p3 1 0.34 500 0.3
## 10 0.146945700 0.32905430 p2-p3 2 0.34 500 0.3
## 11 0.106179475 0.28982053 p2-p3 1 0.34 500 0.3
## 12 0.106945700 0.28905430 p2-p3 2 0.34 500 0.3
## 13 -0.062123105 0.10212310 p1-p2 1 0.02 1000 0.3
## 14 -0.044385113 0.08438511 p1-p2 2 0.02 1000 0.3
## 15 -0.038800951 0.12480095 p1-p2 1 0.02 1000 0.3
## 16 -0.021385113 0.10738511 p1-p2 2 0.02 1000 0.3
## 17 0.179657786 0.31234221 p1-p3 1 0.36 1000 0.3
## 18 0.181614887 0.31038511 p1-p3 2 0.36 1000 0.3
## 19 0.182920311 0.31707969 p1-p3 1 0.36 1000 0.3
## 20 0.185614887 0.31438511 p1-p3 2 0.36 1000 0.3
## 21 0.160312735 0.29168727 p2-p3 1 0.34 1000 0.3
## 22 0.161614887 0.29038511 p2-p3 2 0.34 1000 0.3
## 23 0.141360934 0.27263907 p2-p3 1 0.34 1000 0.3
## 24 0.142614887 0.27138511 p2-p3 2 0.34 1000 0.3
## 25 -0.012498212 0.12183155 p1-p2 1 0.02 1500 0.3
## 26 0.002096442 0.10723689 p1-p2 2 0.02 1500 0.3
## 27 -0.042610395 0.09061040 p1-p2 1 0.02 1500 0.3
## 28 -0.028570224 0.07657022 p1-p2 2 0.02 1500 0.3
## 29 0.217086545 0.32558012 p1-p3 1 0.36 1500 0.3
## 30 0.218763109 0.32390356 p1-p3 2 0.36 1500 0.3
## 31 0.177129616 0.28687038 p1-p3 1 0.36 1500 0.3
## 32 0.179429776 0.28457022 p1-p3 2 0.36 1500 0.3
## 33 0.163847004 0.26948633 p2-p3 1 0.34 1500 0.3
## 34 0.164096442 0.26923689 p2-p3 2 0.34 1500 0.3
## 35 0.153802322 0.26219768 p2-p3 1 0.34 1500 0.3
## 36 0.155429776 0.26057022 p2-p3 2 0.34 1500 0.3
##
## [[4]]
##      confiLower confiUpper type method trueValue sampleSize mixRatio
## 1 -0.09184480 0.13984480 p1-p2 1 0.02 500 0.4
## 2 -0.06705430 0.11505430 p1-p2 2 0.02 500 0.4
## 3 -0.12286806 0.11086806 p1-p2 1 0.02 500 0.4
## 4 -0.09705430 0.08505430 p1-p2 2 0.02 500 0.4
## 5 0.14765989 0.33634011 p1-p3 1 0.36 500 0.4
## 6 0.15094570 0.33305430 p1-p3 2 0.36 500 0.4
## 7 0.15585009 0.34014991 p1-p3 1 0.36 500 0.4
## 8 0.15694570 0.33905430 p1-p3 2 0.36 500 0.4
## 9 0.12479160 0.31120840 p2-p3 1 0.34 500 0.4
## 10 0.12694570 0.30905430 p2-p3 2 0.34 500 0.4
## 11 0.16158495 0.34641505 p2-p3 1 0.34 500 0.4
## 12 0.16294570 0.34505430 p2-p3 2 0.34 500 0.4
## 13 -0.02764356 0.13364356 p1-p2 1 0.02 1000 0.4
## 14 -0.01138511 0.11738511 p1-p2 2 0.02 1000 0.4
## 15 -0.08998442 0.07198442 p1-p2 1 0.02 1000 0.4
## 16 -0.07338511 0.05538511 p1-p2 2 0.02 1000 0.4
## 17 0.15316015 0.29083985 p1-p3 1 0.36 1000 0.4
## 18 0.15761489 0.28638511 p1-p3 2 0.36 1000 0.4
## 19 0.12951315 0.26448685 p1-p3 1 0.36 1000 0.4

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## 20 0.13261489 0.26138511 p1-p3      2      0.36      1000      0.4
## 21 0.10210741 0.23589259 p2-p3      1      0.34      1000      0.4
## 22 0.10461489 0.23338511 p2-p3      2      0.34      1000      0.4
## 23 0.13818796 0.27381204 p2-p3      1      0.34      1000      0.4
## 24 0.14161489 0.27038511 p2-p3      2      0.34      1000      0.4
## 25 -0.04683578 0.08683578 p1-p2      1      0.02      1500      0.4
## 26 -0.03257022 0.07257022 p1-p2      2      0.02      1500      0.4
## 27 -0.04736724 0.08603391 p1-p2      1      0.02      1500      0.4
## 28 -0.03323689 0.07190356 p1-p2      2      0.02      1500      0.4
## 29 0.18350332 0.29249668 p1-p3      1      0.36      1500      0.4
## 30 0.18542978 0.29057022 p1-p3      2      0.36      1500      0.4
## 31 0.17797781 0.28735552 p1-p3      1      0.36      1500      0.4
## 32 0.18009644 0.28523689 p1-p3      2      0.36      1500      0.4
## 33 0.16405101 0.27194899 p2-p3      1      0.34      1500      0.4
## 34 0.16542978 0.27057022 p2-p3      2      0.34      1500      0.4
## 35 0.15918170 0.26748497 p2-p3      1      0.34      1500      0.4
## 36 0.16076311 0.26590356 p2-p3      2      0.34      1500      0.4
##
## [[5]]
##      confiLower confiUpper  type method trueValue sampleSize mixRatio
## 1  -0.04656225 0.17856225 p1-p2      1      0.02      500      0.5
## 2  -0.02505430 0.15705430 p1-p2      2      0.02      500      0.5
## 3  -0.09700514 0.12900514 p1-p2      1      0.02      500      0.5
## 4  -0.07505430 0.10705430 p1-p2      2      0.02      500      0.5
## 5   0.10054179 0.29945821 p1-p3      1      0.36      500      0.5
## 6   0.10894570 0.29105430 p1-p3      2      0.36      500      0.5
## 7   0.08000858 0.27599142 p1-p3      1      0.36      500      0.5
## 8   0.08694570 0.26905430 p1-p3      2      0.36      500      0.5
## 9   0.03822917 0.22977083 p2-p3      1      0.34      500      0.5
## 10  0.04294570 0.22505430 p2-p3      2      0.34      500      0.5
## 11  0.06489504 0.25910496 p2-p3      1      0.34      500      0.5
## 12  0.07094570 0.25305430 p2-p3      2      0.34      500      0.5
## 13 -0.07784263 0.08584263 p1-p2      1      0.02      1000     0.5
## 14 -0.06038511 0.06838511 p1-p2      2      0.02      1000     0.5
## 15 -0.09360176 0.06560176 p1-p2      1      0.02      1000     0.5
## 16 -0.07838511 0.05038511 p1-p2      2      0.02      1000     0.5
## 17  0.16246828 0.29553172 p1-p3      1      0.36      1000     0.5
## 18  0.16461489 0.29338511 p1-p3      2      0.36      1000     0.5
## 19  0.08494826 0.22305174 p1-p3      1      0.36      1000     0.5
## 20  0.08961489 0.21838511 p1-p3      2      0.36      1000     0.5
## 21  0.15860282 0.29139718 p2-p3      1      0.34      1000     0.5
## 22  0.16061489 0.28938511 p2-p3      2      0.34      1000     0.5
## 23  0.09838772 0.23761228 p2-p3      1      0.34      1000     0.5
## 24  0.10361489 0.23238511 p2-p3      2      0.34      1000     0.5
## 25 -0.05124456 0.08057790 p1-p2      1      0.02      1500     0.5
## 26 -0.03790356 0.06723689 p1-p2      2      0.02      1500     0.5
## 27 -0.04301091 0.08834424 p1-p2      1      0.02      1500     0.5
## 28 -0.02990356 0.07523689 p1-p2      2      0.02      1500     0.5
## 29  0.14560954 0.25705713 p1-p3      1      0.36      1500     0.5
## 30  0.14876311 0.25390356 p1-p3      2      0.36      1500     0.5
## 31  0.14120633 0.25346034 p1-p3      1      0.36      1500     0.5
## 32  0.14476311 0.24990356 p1-p3      2      0.36      1500     0.5
## 33  0.13138430 0.24194903 p2-p3      1      0.34      1500     0.5
## 34  0.13409644 0.23923689 p2-p3      2      0.34      1500     0.5

```

```
## 35  0.11923624 0.23009709 p2-p3      1      0.34      1500      0.5
## 36  0.12209644 0.22723689 p2-p3      2      0.34      1500      0.5
```

Combine and save

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