Assignment 2

Xinyi Lin

10/14/2019

```
library(tidyverse)
```

Question 1

Let trueDLT = true DLT probability, sp = selection probability, anTreat = average number of patients treated, anDLT = average number of patients with DLT. The table of the 3+3 design is shown below

```
# Question 1
get_res = function(i,p){
  res = rbinom(3,1,p)
  res = rbind(rep(i,3),res)
  return(res)
}
dose1 = rbind(c(1:5), c(0.017, 0.043, 0.10, 0.22, 0.41))

sim3p3 = function(dose, N = 1000){
  mtd_v = rep(NA,1000)
  com_trail = c(0,0)
  for (j in 1:N) {
    mtd = 0
    trail = c(0,0)
    for (i in 1:5) {
      res = get_res(dose[1,i], dose[2,i])
      trail = cbind(trail, res)
      if (sum(res[2,])>=2) {
        mtd = i-1
        break
        } else if(sum(res[2,]==1)){
          ext_res = get_res(dose[1,i], dose[2,i])
          trail= cbind(trail,ext_res)
          res = cbind(res, ext_res)
          if(sum(res[2,])>=2) {
            mtd = i-1
            break
          }
        }
      mtd = i
    }
    mtd_v[j] = mtd
    com_trail = cbind(com_trail, trail[,-1])
  }
```

```
  trail_res = t(com_trail[,-1])
  colnames(trail_res) = c("dose", "res")
  return(list(mtd = mtd_v, trail_res = trail_res))
}

show_table = function(sim3p3, dose){
  sp = table(sim3p3$mtd)
  per_m = sim3p3$trail_res %>%
    as.data.frame() %>%
    group_by(dose) %>%
    summarize(n = n(),
              DLT = sum(res)) %>%
    mutate(anTreat = n/1000,
           anDLT = DLT/1000,
           s = as.numeric(sp[c(2:6)]),
           sp = s/1000)
  per_m$trueDLT = as.numeric(dose[2,])
  per_m %>%
    select(dose, trueDLT, sp, anTreat, anDLT) %>%
    knitr::kable()
}

set.seed(123)
sim3p31 = sim3p3(dose1)
show_table(sim3p31,dose1)
```

dose	trueDLT	sp	anTreat	anDLT
1	0.017	0.019	3.132	0.045
2	0.043	0.075	3.354	0.141
3	0.100	0.293	3.609	0.331
4	0.220	0.425	3.828	0.824
5	0.410	0.187	2.628	1.063

Question 2

```
set.seed(123)
# a
dose2 = rbind(c(1:5), c(0.10, 0.22, 0.41, 0.64, 0.81))
sim3p32 = sim3p3(dose2)
show_table(sim3p32,dose2)
```

dose	trueDLT	sp	anTreat	anDLT
1	0.10	0.310	3.660	0.327
2	0.22	0.427	3.819	0.841
3	0.41	0.181	2.640	1.060
4	0.64	0.005	0.687	0.455
5	0.81	NA	0.015	0.014

```r
# b
dose3 = rbind(c(1:5), c(0.043, 0.10,0.22, 0.41, 0.64))
sim3p33 = sim3p3(dose3)
show_table(sim3p33, dose3)
```

dose	trueDLT	sp	anTreat	anDLT
1	0.043	0.077	3.381	0.159
2	0.100	0.321	3.633	0.340
3	0.220	0.404	3.786	0.865
4	0.410	0.159	2.439	0.992
5	0.640	0.012	0.627	0.393

```r
dose4 = rbind(c(1:5), c(0.007, 0.017, 0.043, 0.10, 0.22))
sim3p34 = sim3p3(dose4)
show_table(sim3p34, dose4)
```

dose	trueDLT	sp	anTreat	anDLT
1	0.007	0.003	3.045	0.016
2	0.017	0.023	3.153	0.056
3	0.043	0.113	3.306	0.136
4	0.100	0.251	3.624	0.400
5	0.220	0.609	3.585	0.728

```r
dose5 = rbind(c(1:5), c(0.003, 0.007, 0.017, 0.043, 0.10))
sim3p35 = sim3p3(dose5)
show_table(sim3p35, dose5)
```

dose	trueDLT	sp	anTreat	anDLT
1	0.003	0.001	3.024	0.010
2	0.007	0.021	3.066	0.024
3	0.017	0.074	3.123	0.045
4	0.043	0.902	3.312	0.137
5	0.100	NA	3.597	0.329

Question 3

a)

```r
show_CRM = function(sim, PI){
  res_table = data.frame(dose = c(1:5), trueDLT = PI, sp = sim$MTD, anTreat =
sim$level, anDLT = sim$tox)
  res_table %>%
    knitr::kable()
}
```

Perfomance metrics of 3+3 design and CRM with different does-toxicity curves are shown below.

```
library(dfcrm)
set.seed(123)
p0 = c(0.08, 0.14, 0.25, 0.37, 0.52)
# 1
PI1 = c(0.017, 0.043, 0.010, 0.22, 0.41)
sim1 = crmsim(PI1, p0, 0.1, 31, x0=3, nsim = 1000, count = FALSE)
show_CRM(sim1, PI1)
```

dose	trueDLT	sp	anTreat	anDLT
1	0.017	0.014	1.069	0.018
2	0.043	0.038	2.822	0.132
3	0.010	0.545	16.021	0.155
4	0.220	0.395	9.587	2.101
5	0.410	0.008	1.501	0.662

```
show_table(sim3p31,dose1)
```

dose	trueDLT	sp	anTreat	anDLT
1	0.017	0.019	3.132	0.045
2	0.043	0.075	3.354	0.141
3	0.100	0.293	3.609	0.331
4	0.220	0.425	3.828	0.824
5	0.410	0.187	2.628	1.063

```
# 2
PI2 = c(0.10, 0.22, 0.41, 0.64, 0.81)
sim2 = crmsim(PI2, p0, 0.1, 31, x0=3, nsim = 1000, count = FALSE)
show_CRM(sim2, PI2)
```

dose	trueDLT	sp	anTreat	anDLT
1	0.10	0.859	23.800	2.395
2	0.22	0.139	4.599	1.041
3	0.41	0.002	2.291	0.957
4	0.64	0.000	0.280	0.183
5	0.81	0.000	0.030	0.025

```
show_table(sim3p32,dose2)
```

dose	trueDLT	sp	anTreat	anDLT
1	0.10	0.310	3.660	0.327
2	0.22	0.427	3.819	0.841
3	0.41	0.181	2.640	1.060

4	0.64	0.005	0.687	0.455
5	0.81	NA	0.015	0.014

```
# 3
PI3 = c(0.043, 0.10, 0.22, 0.41, 0.64)
sim3 = crmsim(PI3, p0, 0.1, 31, x0=3, nsim = 1000, count = FALSE)
show_CRM(sim3, PI3)
```

dose	trueDLT	sp	anTreat	anDLT
1	0.043	0.317	11.956	0.516
2	0.100	0.545	11.075	1.135
3	0.220	0.135	6.579	1.423
4	0.410	0.003	1.104	0.453
5	0.640	0.000	0.286	0.185

```
show_table(sim3p33,dose3)
```

dose	trueDLT	sp	anTreat	anDLT
1	0.043	0.077	3.381	0.159
2	0.100	0.321	3.633	0.340
3	0.220	0.404	3.786	0.865
4	0.410	0.159	2.439	0.992
5	0.640	0.012	0.627	0.393

```
# 4
PI4 = c(0.007, 0.017, 0.043, 0.10, 0.22)
sim4 = crmsim(PI4, p0, 0.1, 31, x0=3, nsim = 1000, count = FALSE)
show_CRM(sim4, PI4)
```

dose	trueDLT	sp	anTreat	anDLT
1	0.007	0.004	1.034	0.011
2	0.017	0.040	2.738	0.040
3	0.043	0.285	10.217	0.413
4	0.100	0.535	11.523	1.124
5	0.220	0.136	5.488	1.239

```
show_table(sim3p34,dose4)
```

dose	trueDLT	sp	anTreat	anDLT
1	0.007	0.003	3.045	0.016
2	0.017	0.023	3.153	0.056
3	0.043	0.113	3.306	0.136
4	0.100	0.251	3.624	0.400
5	0.220	0.609	3.585	0.728

```r
# 5
PI5 = c(0.003, 0.007, 0.017, 0.043, 0.10)
sim5 = crmsim(PI5, p0, 0.1, 31, x0=3, nsim = 1000, count = FALSE)
show_CRM(sim5, PI5)
```

dose	trueDLT	sp	anTreat	anDLT
1	0.003	0.000	0.288	0.000
2	0.007	0.002	0.916	0.005
3	0.017	0.051	5.835	0.094
4	0.043	0.339	9.336	0.383
5	0.100	0.608	14.625	1.518

```r
show_table(sim3p35,dose5)
```

dose	trueDLT	sp	anTreat	anDLT
1	0.003	0.001	3.024	0.010
2	0.007	0.021	3.066	0.024
3	0.017	0.074	3.123	0.045
4	0.043	0.902	3.312	0.137
5	0.100	NA	3.597	0.329

By comparing performance metrics of 3+3 design and CRM design we can find that

1) The selection probability of true MTD in CRM design is always the highest among 5 doses, while the dose with the highest selection probability in 3+3 design is always the dose near MTD.

2) Average numbers of patients treated in 3+3 design is similar among each dose while in CRM, more people treated with MTD.

3) Average numbers of patients with DLT in CRM overall are larger than those in 3+3 design.

b)

```r
PCS = c(sim1$MTD[3], sim2$MTD[1], sim3$MTD[2], sim4$MTD[4], sim5$MTD[5])
mean(PCS)
```

```
## [1] 0.6184
```

The probability of correctly selecting(PCS) the MTD average over the five scenarios is 0.6184.