Randomized Designs

R example 1 – completely randomized design

Assign 30 patients to treatments A, B, and C, according to a completely randomized design with equal allocation.

```
> Schedule = rmultinom(30,1,c(1/3,1/3,1/3))
> Schedule
     [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14] [,15] [,16]
[1,]    1    0    1    0    1    1    1    1    0     1     0     0     0     1     0     0
[2,]    0    0    0    1    0    0    0    0    0     0     0     1     0     0     1     1
[3,]    0    1    0    0    0    0    0    0    1     0     1     0     1     0     0     0
     [,17] [,18] [,19] [,20] [,21] [,22] [,23] [,24] [,25] [,26] [,27] [,28] [,29] [,30]
[1,]     0     1     0     0     1     0     0     1     0     1     0     0     0     0
[2,]     0     0     1     1     0     0     0     0     0     0     0     1     0     0
[3,]     1     0     0     0     0     1     1     0     1     0     1     0     1     1
> colSums(Schedule)
 [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
> rowSums(Schedule)
[1] 12  7 11
```

Every patient is assigned to one treatment, but the sample sizes are not equal.

Prepare the treatment schedule:

```
> for (k in 1:30){
+ if(Schedule[1,k]==1){Treatment[k] = "Treatment A"}
+ if(Schedule[2,k]==1){Treatment[k] = "Treatment B"}
+ }
> Schedule
     [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14] [,15] [,16]
[1,]    1    0    1    0    1    1    1    1    0     1     0     0     0     1     0     0
[2,]    0    0    0    1    0    0    0    0    0     0     0     1     0     0     1     1
[3,]    0    1    0    0    0    0    0    0    1     0     1     0     1     0     0     0
     [,17] [,18] [,19] [,20] [,21] [,22] [,23] [,24] [,25] [,26] [,27] [,28] [,29] [,30]
[1,]     0     1     0     0     1     0     0     1     0     1     0     0     0     0
[2,]     0     0     1     1     0     0     0     0     0     0     0     1     0     0
[3,]     1     0     0     0     0     1     1     0     1     0     1     0     1     1
> Treatment
 [1] "Treatment A" "Placebo"     "Treatment A" "Treatment B"
"Treatment A" "Treatment A"
 [7] "Treatment A" "Treatment A" "Placebo"     "Treatment A" "Placebo"
"Treatment B"
```

```
[13] "Placebo"     "Treatment A" "Treatment B" "Treatment B" "Placebo"
"Treatment A"
[19] "Treatment B" "Treatment B" "Treatment A" "Placebo"     "Placebo"
"Treatment A"
[25] "Placebo"     "Treatment A" "Placebo"     "Treatment B" "Placebo"
"Placebo"
```

R Example 2 – block randomization

Create a block randomization with 2 treatments and 10 patients.
First, install package "blockrand".

```
> utils:::menuInstallPkgs()
> library(blockrand)

> blockrand(n=10)
   id block.id block.size treatment
1   1        1          2         A
2   2        1          2         B
3   3        2          6         A
4   4        2          6         A
5   5        2          6         A
6   6        2          6         B
7   7        2          6         B
8   8        2          6         B
9   9        3          4         B
10 10        3          4         A
11 11        3          4         A
12 12        3          4         B
```

Create a block randomization with 3 treatments and 15 patients.

```
> blockrand(n=15, num.levels=3)
   id block.id block.size treatment
1   1        1          6         C
2   2        1          6         B
3   3        1          6         B
4   4        1          6         A
5   5        1          6         C
6   6        1          6         A
```

```
7   7        2          3         A
8   8        2          3         C
9   9        2          3         B
10 10        3          6         C
11 11        3          6         B
12 12        3          6         A
13 13        3          6         A
14 14        3          6         C
15 15        3          6         B
```

R example 3 – stratification by gender

```
> male <- blockrand(n=12, num.levels=3, id.prefix='M',
block.prefix='M',stratum='Male')
> female <- blockrand(n=12, num.levels=3, id.prefix='F',
block.prefix='F',stratum='Female')
> my.study <- rbind(male,female)
> my.study
    id stratum block.id block.size treatment
1  M01    Male       M1          6         A
2  M02    Male       M1          6         C
3  M03    Male       M1          6         A
4  M04    Male       M1          6         B
5  M05    Male       M1          6         C
6  M06    Male       M1          6         B
7  M07    Male       M2          3         A
8  M08    Male       M2          3         B
9  M09    Male       M2          3         C
10 M10    Male       M3          9         C
11 M11    Male       M3          9         B
12 M12    Male       M3          9         B
13 M13    Male       M3          9         C
14 M14    Male       M3          9         A
15 M15    Male       M3          9         C
16 M16    Male       M3          9         A
17 M17    Male       M3          9         B
18 M18    Male       M3          9         A
19 F01  Female       F1          6         A
20 F02  Female       F1          6         A
21 F03  Female       F1          6         B
22 F04  Female       F1          6         C
```

23	F05	Female	F1	6	B
24	F06	Female	F1	6	C
25	F07	Female	F2	6	A
26	F08	Female	F2	6	A
27	F09	Female	F2	6	C
28	F10	Female	F2	6	C
29	F11	Female	F2	6	B
30	F12	Female	F2	6	B