*Stat 622/422 (Dr. Baron) Advanced Biostatistics*

**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 |