**Write-up**

Example 1:

* Assigning completely randomised design (CRD) to randomised block design (RBD).
* The design layout:
* Phase 1:
* 4 animals randomly assigned to 2 treatment groups, animal A and C are assigned to controlled group and animal and D are assigned to diseased group.
* The theoretical ANOVA table for the Phase 1 experiment can be written as

DF Ani

Between Ani

Trt 1 1

Residual 2 1

* The second phase experiment is aiming to assign the animals of the first phase to the block structure of the second phase.
* Suppose the second phase experiment consists of 3 runs and 4-plex iTRAQ tag system.
* The aim of the animal allocation is to minimise the level of confounding between animal effects with both runs and tag effects.
* Another way of describing the above point is to maximise the amount of information in the within runs and tags stratum. Note the second phase design is considered as a row-column design.
* The orthogonal projector for the within runs and tags stratum can be written as
* The information matrix can be written as

where denotes the animal design matrix.

* The aim is to find the that maximised the average efficiency factor and minimised the variance of the canonical efficiency factors of information matrix.
* To find the that match the criteria is first start with a random and swap the first row of the matrix with all other rows of the matrix. Whenever the criteria is met on a specific swap, the new is constructed based on that swap. Once the criteria from the swapping of the first row with the other rows of are checked, then the criteria will check with the with swapping the second row with all the other rows expect the first row of matrix . The Pseudo code is shown in the next point.
* Partial pseudo code of the swapping method:

repeat(10){

for(i in 1:(nrow() - 1)){

for(j in (i+1):nrow()){

= Swapping ([i, ], [j, ])

if( criteria() > criteria()) {

}

}

}

}

* Based on the current example and the criteria described in the previous point, an animal design has found and can be written as

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Run | Tag | | | |
| 1 | 2 | 3 | 4 |
| 1 | B | D | C | A |
| 2 | A | C | B | D |
| 3 | C | A | D | B |

* The treatment design for Phase 2 experiment can be made from the animal and treatment allocation of the Phase 1 experiment.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Run | Tag | | | |
| 1 | 2 | 3 | 4 |
| 1 | Diseased | Diseased | Controlled | Controlled |
| 2 | Controlled | Controlled | Diseased | Diseased |
| 3 | Controlled | Controlled | Diseased | Diseased |

* The theoretical ANOVA table for this two-phase experiment with the animal and treatment allocation described in the previous two points can be written as follow

$ANOVA

DF e Ani Run

Between Run 2 1 0 4

Within

Between Ani

Trt 1 1 3 0

Tag 2 1 3 0

Residual

Tag 3 1 0 0

Residual 3 1 0 0

$EF

Trt Tag eff.Trt eff.Tag

Between Run

Within

Between Ani

Trt 6 1/3 1 1/9

Tag 1/3 1/9

Residual

Tag 8/3 8/9

* The theoretical ANOVA table has shown the tag effects are still confounded with animal effects. The fixed effects table shows the 1/9 of the tag effects is confounded with the animal effects. In addition, one out of three degrees of freedom for the tag is also confounded with the treatment. Hence, the treatment has to be fitted before tag for this model.