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A NEW METHOD FOR BALANCED INCOMPLETE SEQUENCE CROSSOVER DESIGN

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Abstract

Crossover design is a design in which allocation of different treatment sequences receives by each subject one at a time at different period. It has been useful in the field of clinical trials, animal nutrition and so on. A single algorithm for construction method of Balanced Incomplete Sequence Crossover Design which is universally optimal is presented in this paper, where construction method satisfies primitive root x=2 and x=3 for any number of treatment t which is prime for BISCOD and the number of times each treatment precedes each other treatment increases as number of treatments increase. Each other treatment precede each treatment k-1 times with replicate of k(t-1)times for all number of treatments and pair of treatments occur together k(t-1)/2. Conclusion showed that no treatment allocated more than once per sequence and in the first p-1 period all treatments replicated equally for the estimation of residual effect

Keywords: Balanced Incomplete, Crossover design, Universally Optimal, , Replicate

1. INTRODUCTION

Crossover design is a repeated measure design of allocating sequence of different treatments to each subject at different period one at a time. It is very useful in research area such as clinical trials. A design in which each other treatment preceded every treatment at equal number of time is called balanced design. When all treatments are not in each block, is referred to as incomplete.

An incomplete block design whereby any pair of treatment appear together at an equal number of time is called balanced incomplete block design while balanced incomplete sequence crossover design is a design in which each treatment precedes each other treatment equal number of times but never precedes itself.

Different methods of balanced incomplete sequence crossover design have given by a lot of authors. Adebara and Adeleke (2019) presented two methods of designs for prime number of treatments which are universally optimal for balanced incomplete sequence crossover design (BISCOD) of first order residual effects that satisfy primitive root x=2, and x= 2 or 3 Mithilesh and Archana (2015) presented balanced incomplete sequence crossover design method which is universally optimal of first order residual effect.. Hedayat and Zheng (2010), Bose and Dey(2009), Kunert (1984), Raghavarao and Shah(1984) presented design which is optimal and efficient . Cheng and Wu (1980) discussed universally optimal design for estimation of residual effect over classes of designs

A new method of construction for balanced incomplete sequence crossover design is presented in this paper whereby designs construction were considered for prime numbers that satisfy primitive root x=2 and 3.

2 Methodology

2.1 Material

A new method algorithm for balanced incomplete sequence crossover design is for any prime number of treatment t that satisfies both primitive roots x=2 and 3; whereby t implies number of treatment, x implies primitive root, k implies sequence size and 0 implies treatment t

Algorithm is given below when t= $2k-1$, n= $(t-1)(2k-1)$ and k = $\frac{(t-1)}{2}$

I = 0, x^{k}, x^{2k}, x^{3k},…

2.1.1 Procedure

i multiply the above algorithm with every non-zero element to obtain (t-1) initial sequences

ii develop above (t-1) initial sequences cyclically and balanced incomplete sequence crossover design exists with parameter t= $2k-1$, n= $(t-1)(2k-1)$ and k = $\frac{t+1}{2}$

2.2 Construction for the number of treatment t=5

For t=5, x=2, k=3,

I= 0, x^{k}, x^{2k}

I = 0, 2^{3} 2^{6} (1)

Real value = 0, 8, 64

Mod5 = 0, 3, 4 (1.1)

Therefore the algorithm is (0, 3, 4)

Table 1

Multiply the above algorithm with every non-zero element to obtain (t-1) initial sequences mod 5

0	0	0	0
3	1	4	2
4	3	2	1

Table 1.1

Cyclical development for balanced incomplete sequence crossover design

0	1	2	3	4	0	1	2	3	4	0	1	2	3	4	0	1	2	3	4
3	4	0	1	2	1	2	3	4	0	4	0	1	2	3	2	3	4	0	1
4	0	1	2	3	3	4	0	1	2	2	3	4	0	1	1	2	3	4	0

Each treatment precedes each other treatment two times

Construction for the number of treatment t=7

For V=7, x=3, k=4

I= I= $0, x^{k}, x^{2k}, x^{3k}$

$I_2 = 0, 3^{4}, 3^{8}, 3^{12}$ (2)

Real value = 0, 81, 6561, 531441,

Mod7 = 0, 4, 2, 1 (2.2)

Therefore the algorithm is (0, 4, 2, 1)

Table2

multiply the above algorithm with every non-zero element to obtain (t-1) initial sequences mod 7

0	0	0	0	0	0
4	1	5	2	6	3
2	4	6	1	3	5
1	2	3	4	5	6

Table 2.1

Cyclical development for balanced incomplete sequence crossover design

0	1	2	3	4	5	6	0	1	2	3	4	5	6	0	1	2	3	4	5	6
4	5	6	0	1	2	3	1	2	3	4	5	6	0	5	6	0	1	2	3	4
2	3	4	5	6	0	1	4	5	6	0	1	2	3	6	0	1	2	3	4	5
1	2	3	4	5	6	0	2	3	4	5	6	0	1	3	4	5	6	0	1	2

0	1	2	3	4	5	6	0	1	2	3	4	5	6	0	1	2	3	4	5	6
2	3	4	5	6	0	1	6	0	1	2	3	4	5	3	4	5	6	0	1	2
1	2	3	4	5	6	0	3	4	5	6	0	1	2	5	6	0	1	2	3	4
4	5	6	0	1	2	3	5	6	0	1	2	3	4	6	0	1	2	3	4	5

Each treatment precedes each other treatment three times

3.0 Result and Discussion

The balanced incomplete sequence crossover design constructed for number of treatment, t = 5 in table 1.1 showed that each treatment is being preceded by each other treatment twice, each treatment replicates twelve (12) times, pair of treatments occur together six (6) times; and for number of treatment, t = 7 in table 2.1 showed that each treatment preceded by each other treatment three times, each treatment replicates twenty four (24) times, pair of treatments occur together twelve (12) times

From the above results, it implies that no treatment allocated more than once per sequence and in the first p-1 period all treatments replicated equally for the estimation of residual effect which are universally optimal. Also each replication equals to k(t-1) and pair of treatments occur together k(t-1)/2

4.0 Conclusion

It is concluded that the above construction method satisfies primitive root x=2 and x=3 for any number of treatment t which is prime for BISCOD which is universally optimal and the number of times each treatment precedes each other treatment increases as number of treatments increase. And also, no treatment allocated more than once per sequence and in the first p-1 period all treatments replicated equally for the estimation of residual effect.

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