362 CROSSOVER AND REPEATED MEASURES DESIGNS

9.4.1 Williams's Latin-Square Crossover Designs

Balanced designs in t treatments and p = t periods can be created from Latinsquare designs. If there are no carryover effects, then a variance balanced design for direct treatment effects can be achieved by choosing any arbitrary $t \times t$ Latin-square design. If carryover effects are possible, then variance balance can only be achieved when each treatment is preceded by every other treatment an equal number of times. Williams (1949) showed that this property could be achieved with only one particular Latin square if t is an even number, and two particular Latin squares if t is an odd number. An easy algorithm for constructing these particular squares was described by Sheehe and Bross (1961) and is described below.

- 1. Number the treatments from 1 to t.
- 2. Start with a cyclic Latin-square design where the treatments in the *i*th row are $i, i + 1, \ldots, t, 1, \ldots, i 1$.
- 3. Create another Latin square whose rows are the mirror images of the rows in the first Latin square; e.g., the mirror image of (1,2,3,4) is (4,3,2,1).
- 4. Interlace each row of the first Latin square with the corresponding row of the second Latin square to produce a $t \times 2t$ rectangle. For example, interlacing (1, 2, 3, 4) with (4, 3, 2, 1) results in (1, 4, 2, 3, 3, 2, 4, 1).
- 5. Split the $t \times 2t$ rectangle down the middle to form two $t \times t$ Latin squares.
- 6. If t is odd use both Latin squares, if t is even choose either one.

Using this algorithm, the rows of the resulting Latin square(s) are indicators of the sequence groups, and the columns are indicators of the periods. Randomization is accomplished by randomizing the treatments to the level indicators $1, 2, \ldots, t$, and then randomizing one or more subjects to each sequence group.

The williams function in the R package crossdes can also be used to create Willams's crossover Latin-square designs as illustrated in the code below that creates Williams's design for three levels of the treatment factor.

```
> library(crossdes)
> wdes3 <- williams(3)</pre>
> rownames(wdes3) <- paste("seqGroup", 1:6, sep = "")</pre>
> colnames(wdes3) <- paste("Period", 1:3, sep = "")</pre>
> wdes3
           Period1 Period2 Period3
seqGroup1
                  1
                           2
                                    3
                  2
                           3
seqGroup2
                                    1
                  3
                                    2
seqGroup3
                           1
seqGroup4
                  3
                           2
                                    1
                                    2
seqGroup5
                           3
                  1
seqGroup6
                  2
                           1
                                    3
```