## Valid restricted randomization for small experiments

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Joint work with Josh Paik (Penn State University)

## Introductory example

Suppose that scientists at a horticultural research institute are planning an experiment to compare three varieties of tomato, labelled $A, B$ and $C$, to see which gives the biggest yield (in weight of fruit per plant). They propose to use a greenhouse which has room for nine tomato plants in a single row. The initial, systematic layout is shown below.
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variety ("treatment") | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |
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Devil 2: If you keep doing that, differences between regions will contribute more to the estimate of experimental error than they will to the estimates of differences between varieties, so you may fail to detect genuine differences between varieties.
Angel: Can we use a smaller set of potential layouts with the properties that
(a) we never get a series of 3 adjacent plots with the same variety;
(b) we do not get the bias mentioned by Devil 2?

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## Terminology: UK, Australia

[^0]
## Treatment structure How many?

Are they factorial?
Is any factor quantitative?
Is there a control?

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## Randomization

| Plot structure |  |
| :---: | :---: |
| Inherent nuisance factors <br> Maybe none <br> Maybe blocks <br> Maybe rows and columns <br> Small units inside large units | Construct <br> design <br> Which <br> treatment <br> goes on which <br> experimental <br> unit? |

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Restricted randomization means using only a proper subset of the possible layouts.

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From now on, I will continue to use the term restricted randomization in the sense that Yates did.

## Valid randomization

In the context of experiments with a single error term in the analysis of variance,
Fisher and Yates said that a method of randomization should have the property that, averaged over all possible outcomes of the randomization, the expectations of the mean square for treatments and the mean square for error should be equal if there are no differences between treatments.

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If $\alpha \neq \beta$ then we make no assumptions about the relationship between $\varepsilon_{\alpha}$ and $\varepsilon_{\beta}$.
Random choice of layout for the experiment turns all our statistical notions (such as estimators and mean squares) into random variables.

## More technical details

In an unblocked experiment with equal replication, a method of randomization is strongly valid if there are probabilities $p_{1}$ and $p_{2}$ such that, whenever $\alpha$ and $\beta$ are distinct plots,

$$
\begin{equation*}
P(T(\alpha)=T(\beta)=i)=p_{1} \quad \text { for each treatment } i \tag{1}
\end{equation*}
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and

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\begin{equation*}
P(T(\alpha)=i \text { and } T(\beta)=j)=p_{2} \quad \text { whenever } i \neq j \tag{2}
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If a strongly valid method of randomization is used, then all pairs of distinct plots have the same probability $p_{2}$ of contributing to the estimator of the difference between any ordered pair of distinct treatments, and probability $v p_{1}$ of contributing to the mean square for error, where $v$ is the number of treatments.

## Even more technical details

Suppose that there are $v$ treatments, each with replication $r$, so that the number $N$ of plots is given by $N=v r$. If Equations (1) and (2) are satisfied, then

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\begin{equation*}
p_{1}=\frac{1}{v} \frac{r-1}{N-1} \tag{3}
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For a Latin square, there is one such pair for plots in the same row or in the same column, and another such pair for plots which are in different rows and different columns.

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Here we restrict attention to unblocked experiments where the plots form a single line. Denote the design for such an unblocked experiment by $\Delta$.

## First strongly valid method, using permutation groups

A group of permutations of the set of $N$ plots is doubly transitive if, whenever $\alpha, \beta, \gamma$ and $\delta$ are plots with $\alpha \neq \beta$ and $\gamma \neq \delta$, there is a some permutation in the group which takes $\alpha$ to $\gamma$ and $\beta$ to $\delta$.

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In 1976-1978, RAB was employed as a post-doc at the Agricultural Research Council Unit of Statistics (in Edinburgh) because her DPhil thesis was about finite permutation groups. This led to a paper on restricted randomization for Latin squares (and other things) in Biometrika in 1983.

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Given such a rectangle, Youden proposed randomizing by choosing one of the rows with equal probability and then randomizing the actual treatments to the letters in that row.

## An example from Youden's paper

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There are $3 \times 2=6$ columns.
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Suppose that $v=3$ and $r=2$.

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| $A$ | $A$ | $B$ | $C$ | $B$ | $C$ |
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Randomize by choosing one of the 5 rows with equal probability, then randomizing the 3 treatments to $A, B$ and $C$.

## An alternative explanation of Youden's method

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$$
\begin{array}{lll}
\{1,2\} & \{3,5\} & \{4,6\} \\
\{1,3\} & \{2,6\} & \{4,5\} \\
\{1,4\} & \{2,3\} & \{5,6\} \\
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In each row, the letters give the blocks of $\Gamma$.
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| $A$ | $A$ | $B$ | $C$ | $B$ | $C$ |
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1. Choose a row of the $m \times N$ rectangle at random, with probability $1 / m$ for each row.
2. Randomize the allocation of the treatments in our design $\Delta$ to the $v$ letters in that row.

## Our approach, continued

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p_{1}=\frac{1}{v} \frac{\lambda}{m}=\frac{1}{v} \frac{r-1}{N-1},
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Likewise, $P(T(\alpha) \neq T(\beta))=(m-\lambda) / m$, and this probability is equally split between the $v(v-1)$ ordered pairs of distinct treatments in $\Delta$, and so

$$
p_{2}=\frac{1}{v(v-1)} \frac{m-\lambda}{m}=\frac{1}{v(v-1)} \frac{(N-r)}{N-1}=\frac{1}{v} \frac{r}{N-1},
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so that Equations (2) and (4) are satisfied.

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so that Equations (2) and (4) are satisfied.
As with the first method, the task now is to find a permutation of the columns of the $m \times N$ rectangle such none of the $m$ rows gives a bad pattern.

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There are three treatments, each replicated three times, so $v=r=3$ and $N=9$.

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| $A$ | $B$ | $C$ | $B$ | $B$ | $C$ | $A$ | $A$ | $C$ |


| $\{1,3,5\}$ | $\{2,8,9\}$ | $\{4,6,7\}$ |
| :--- | :--- | :--- |
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Each row contains exactly two adjacent pairs of columns with the same letter.
Moreover, no row has all three occurrences of any letter in either the first or last four columns.

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In this case we cannot avoid the layout $A A B B$, and so there is no method of valid restricted randomization.
When $v=2$ and $r=3$, then $\Gamma$ must be a resolved balanced incomplete-block design for 6 treatments in blocks of size 3 . The smallest such design consists of all triples of treatments, and so we cannot avoid the layout $A A A B B B$.

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For example, here is a valid restricted randomization scheme for $v=5$ and $r=3$.

| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| $A$ | $C$ | $E$ | $B$ | $E$ | $B$ | $D$ | $D$ | $A$ | $E$ | $C$ | $C$ | $D$ | $A$ | $B$ |
| $A$ | $A$ | $C$ | $B$ | $D$ | $C$ | $D$ | $A$ | $B$ | $B$ | $E$ | $D$ | $E$ | $C$ | $E$ |
| $B$ | $A$ | $D$ | $B$ | $A$ | $E$ | $E$ | $C$ | $E$ | $C$ | $C$ | $D$ | $B$ | $A$ | $D$ |
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| $D$ | $E$ | $E$ | $B$ | $A$ | $D$ | $C$ | $A$ | $A$ | $C$ | $D$ | $B$ | $E$ | $B$ | $C$ |
| $A$ | $D$ | $B$ | $B$ | $A$ | $D$ | $E$ | $B$ | $C$ | $D$ | $E$ | $C$ | $C$ | $E$ | $A$ |
| $C$ | $A$ | $C$ | $B$ | $B$ | $E$ | $C$ | $E$ | $A$ | $D$ | $B$ | $E$ | $D$ | $D$ | $A$ |

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For example, here is a valid restricted randomization scheme for $v=5$ and $r=3$.

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| $B$ | $A$ | $D$ | $B$ | $A$ | $E$ | $E$ | $C$ | $E$ | $C$ | $C$ | $D$ | $B$ | $A$ | $D$ |
| $E$ | $B$ | $D$ | $B$ | $C$ | $C$ | $B$ | $A$ | $D$ | $E$ | $D$ | $E$ | $C$ | $A$ | $A$ |
| $D$ | $E$ | $E$ | $B$ | $A$ | $D$ | $C$ | $A$ | $A$ | $C$ | $D$ | $B$ | $E$ | $B$ | $C$ |
| $A$ | $D$ | $B$ | $B$ | $A$ | $D$ | $E$ | $B$ | $C$ | $D$ | $E$ | $C$ | $C$ | $E$ | $A$ |
| $C$ | $A$ | $C$ | $B$ | $B$ | $E$ | $C$ | $E$ | $A$ | $D$ | $B$ | $E$ | $D$ | $D$ | $A$ |

Two identical duads per row.

## Progress so far

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| $E$ | $B$ | $D$ | $B$ | $C$ | $C$ | $B$ | $A$ | $D$ | $E$ | $D$ | $E$ | $C$ | $A$ | $A$ |
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| $A$ | $D$ | $B$ | $B$ | $A$ | $D$ | $E$ | $B$ | $C$ | $D$ | $E$ | $C$ | $C$ | $E$ | $A$ |
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Two identical duads per row. No identical triads in any row.


[^0]:    Plot structure
    Inherent nuisance factors
    Maybe none
    Maybe blocks
    Maybe rows and columns Small units inside large units

