Linear variance structures for modelling temporal and spatial correlations in biological data and data from agricultural field trials

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Abstract

Plant breeding and variety testing relies heavily on field experiment conducted in multiple environments. This talk will cover mainly the analysis of individual trials, which is the basis for the joint analysis of series of trials.

Most agricultural field trials involve a layout of plots in incomplete blocks (one-dimensional blocking) or rows and columns (two-dimensional blocking). Resolvable incomplete block and row-column designs have proven effective in obtaining efficient estimates of treatment effects. Further improvement may be possible by post-blocking or by inclusion of spatial model components.

This paper reviews options for augmenting a baseline block or row-column model for individual trials by the addition of spatial components (Lee and Piepho, 2007; Piepho and Williams, 2007), including separable linear variance models and simple state-space models such as random walks (Piepho and Ogutu, 2007). The usefulness of linear variance models is assessed by analysing a number of field trials, most of which are uniformity trials.

Relationship to nearest-neighbour methods based on first and second differences as well as the Papadakis method will be discussed (Piepho and Richter, 2007). We specifically study the properties of the nearest neighbour methods proposed by Wilkinson et al. (1983) and Schwarzbach (1984), which are quite popular among plant breeders.

In connection with random walk models to represent field trend, we will also briefly mention options to fit state-space models for biological time series in a mixed model framework.

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