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Correcting for spatial heterogeneity in plant breeding experiments with P-splines

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Abstract

An important aim of the analysis of agricultural field experiments is to obtain good predictions for genotypic performance, by correcting for spatial effects. In practice these corrections turn out to be complicated, since there can be different types of spatial effects; those due to management interventions applied to the field plots and those due to various kinds of erratic spatial trends. This paper explores the use of two-dimensional smooth surfaces to model random spatial variation. We propose the use of anisotropic tensor product P-splines to explicitly model large-scale (global trend) and small-scale (local trend) spatial dependence. On top of this spatial field, effects of genotypes, blocks, replicates, and/or other sources of spatial variation are described by a mixed model in a standard way. Each component in the model is shown to have an effective dimension. They are closely related to variance estimation, and helpful for characterising the importance of model components. An important result of this paper is the formal proof of the relation between several definitions of heritability and the effective dimension associated with the genetic component. The practical value of our approach is illustrated by simulations and analyses of large-scale plant breeding experiments. An R-package, SpATS, is provided.

Keywords: Effective dimension; Field trials; Heritability; Linear mixed model; Spatial analysis; Tensor product P-splines.

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