THE ANALYSIS (AND DESIGN) OF SELECTION EXPERIMENTS USING LINEAR MIXED MODELS

TNM079, DESIGN TABLEAU, MODEL FITTING, MODEL CHECKING AND MODEL SUMMARIES

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Monday 10th November 2025

The aim of this workshop considers a range of topics which underpin the methods of analysis (and design) for data-sets arising from selection experiments in plant and animal genetic improvement programs and/or studies using a linear mixed model. The features which are common to across all applications is the use of genetic relatedness via either ancestral and/or genomic information. The workshop is application driven and will rely heavily on using real examples to illustrate the ideas.

Methods of analysis of selection experiments has changed dramatically in recent times. Analysis of variance (ANOVA) techniques are often no longer applicable, while LMMs offer a flexible alternative with many key benefits. These include the ability to accommodate unbalanced data-sets, to allow more complex variance models for both genetic and non-genetic effects, and using models to accommodate dependence in the error component.

Key developments in LMM theory and software have led to universal usage of the method of Residual Maximum Likelihood (REML) (Patterson & Thompson 1971), which can be fitted using the Average Information (AI) algorithm (Gilmour, Thompson & Cullis, 1995) in ASReml-r (Butler et al. 2017) and DWReml (Butler et al. 2025).

Despite the potential benefits of using LMMs for the analysis of selection experiments, the move away from ANOVA has come at a cost.

The literature is full of examples of the misuse of LMMs for selection experiments. Some common flaws/misunderstandings include: failing to recognise pseudo (or false) replication, testing/dropping model terms that define strata, providing standard errors for means (not treatment contrasts) when there is no valid framework for inference, and failing to recognise the need for negative estimates of variance components which reproduces the appropriate estimate of error in multi-strata experiments.

Hence the driving philosophy of the workshop will be to provide a toolbox that attempts to "ensure the use of LMMs for the analysis (and design) of selection experiments honours the fundamental principles of design and analysis, as developed by Sir R. A. Fisher and perpetuated by John Nelder and Rosemary Bailey."

The have been chosen to illustrate commonly used techniques such as pedigree and genomic best linear unbiased prediction using a fully-efficient single-step approach, which incorporates terms associated with peripheral effects and the plots structure of the selection experiment. All models will be fitted using DWReml.