

Phenotypic and marker based analysis of multi-environment data

Identifying the genetic basis of GxE and responses to stress

Fred van Eeuwijk¹, Marcos Malosetti¹ & Ky Mathews²

¹ Wageningen University, Netherlands, ² CSIRO, Australia

Breeding programmes use multi-environment trials (METs) to assess the responses of genotypes in their dependence on the environment. The design of the individual trials within a MET is often complicated by the large sets of genotypes that have to be evaluated under heterogeneous conditions. Special types of designs have been developed that take into account the restrictions imposed by such trials, which can be combined with powerful statistical methodologies to improve the analysis of the data.

For the analysis of METs and the description of genotype by environment interaction (GxE) various approaches exist. Well-known exploratory models for GxE are the Finlay-Wilkinson model and AMMI models. Alternatively, factorial regression models allow the incorporation of explicit genotypic and environmental covariables to describe GxE and therefore are able to reflect better the underlying physiological processes creating GxE. The estimates for the genotypic slopes in the factorial regression models have an interpretation as adaptability parameters. For modelling genetic variances and correlations, mixed model methodology is recommended. Genotypic stability and reliability parameters can be derived from the fit of appropriate mixed models.

Factorial regression within a mixed model context provides a suitable framework for the mapping of quantitative trait loci (QTLs), including extensions to QTL by environment interaction (QTLxE). This modelling framework is equally applicable to the analysis of segregating populations (traditional QTL analysis) and unstructured populations (linkage disequilibrium (LD) analysis).

The objective of the course is to introduce the participants to the analysis of single trials, the modelling of GxE for MET data, modelling of main effect QTLs and QTLxE, multi-trait QTL modelling, and LD mapping. To achieve this objective, lectures will be combined with computer demonstrations and exercises. We will use the statistical package Genstat for the analyses. Genstat has extensive mixed model facilities and its so-called Discovery version is free for non-profit organisations in the developing world (<http://www.vsni.co.uk/products/discovery/>).

Schedule:

Day 1: Analysis of breeding trials (phenotypic);

Analysis of single and multiple environment trials
Models for GxE analysis in METs

Day 2: QTL mapping using mixed models

Single environment QTL mapping
Multiple environment QTL mapping, including the modelling of QTLxE
Multi-trait QTL mapping
LD mapping

References

- Malosetti, M, van der Linden, CG, Vosman, B & van Eeuwijk, FA 2007 A mixed model approach to association mapping using pedigree information with an illustration to resistance for *Phytophthora infestans* in potato. *Genetics* 175, 879-889
- Manneh B, Stam P, Struik PC, Oliver SB, van Eeuwijk FA. 2007 QTL-based analysis of genotype-by-environment interaction for grain yield of rice in stress and non-stress environments. *Euphytica* DOI 10.1007/s10681-007-9368-8
- Hammer, G., M. Cooper, F. Tardieu, S. Welch, B. Walsh, F.A. van Eeuwijk, S. Chapman, and D. Podlich, 2006. Models for navigating biological complexity in breeding improved crop plants. *TRENDS in Plant Science* 11 (12): 1360-1385.
- A.T.W. Kraakman, F. Martínez, B. Mussiraliiev, F.A. van Eeuwijk, R.E. Niks 2006. Linkage disequilibrium mapping of morphological, resistance, and other agronomically relevant traits in modern spring barley cultivars. *Molecular Breeding* 17: 41-58.
- M. Malosetti, R. G. F. Visser, C. Celis-Gamboa, F. A. van Eeuwijk 2006. QTL methodology for response curves on the basis of non-linear mixed models, with an illustration to senescence in potato, *Theor Appl Genet* 113:288–300
- Mateo Vargas, Fred van Eeuwijk, Jose Crossa, and Jean Marcel Ribaut. 2006. Mapping QTLs and QTL×Environment Interaction Using Factorial Regression and Partial Least Squares Methods. *Theoretical and Applied Genetics*, 112: 1009–1023
- Fred A. van Eeuwijk, Marcos Malosetti, Xinyou Yin, Paul C. Struik and Piet Stam. 2005. Statistical models for genotype by environment data; From conventional ANOVA models to eco-physiological QTL models. *Australian Journal of Agricultural Research* 56: 883-894.
- Xinyou Yin, Paul C. Struik, Fred A. van Eeuwijk, Piet Stam and Jianjun Tang. 2005. QTL analysis and QTL-based prediction of flowering phenology in recombinant inbred lines of barley. *Journal of Experimental Botany*, 56, 967-976.
- A. T. W. Kraakman, R. E. Niks, P. M. M. M. Van den Berg, P. Stam & F. A. Van Eeuwijk 2004 Linkage disequilibrium mapping of yield and yield stability in modern spring barley cultivars. *Genetics*: 138: 435-446.
- M Malosetti, J Voltas, I Romagosa, S.E. Ullrich & F.A. van Eeuwijk (2004) Mixed models including environmental variables for studying QTL by environment interaction. *Euphytica* 137: 139-145.
- Eeuwijk, F.A. van, Cooper, M. DeLacy, I.H., Ceccarelli, S. and Grando S. (2001). Some vocabulary and grammar for the analysis of multi-environment trials, as applied to the analysis of FPB and PPB trials. *Euphytica* 122: 477-490.
- Crossa, J., M. Vargas, F. A. van Eeuwijk, C. Jiang, G. O. Edmeades, and D. Hoisington (1999) Interpreting genotype × environment interaction in tropical maize using linked molecular markers and environmental covariables. *Theoretical and Applied Genetics* 99: 611-625.
- Vargas, M., J. Crossa, F.A. van Eeuwijk, M.E. Ramírez & K. Sayre (1999) Using AMMI, factorial regression, and partial least squares regression models for interpreting genotype x environment interaction. *Crop Science*, 39: 955-967.
- Voltas, J., F.A. van Eeuwijk, J.L. Araus & I. Romagosa. (1999) Integrating statistical and ecophysiological analysis of genotype by environment interaction for grain filling of barley in Mediterranean areas. II. Grain growth. *Field Crops Research* 62: 75-84.
- Voltas, J., F.A. van Eeuwijk, A. Sombrero, A. Lafarga, E. Igartua & I. Romagosa. (1999) Integrating statistical and ecophysiological analysis of genotype by environment interaction for grain filling of barley in Mediterranean areas. I. Individual grain weight. *Field Crops Research* 62: 63-74 .