

Mixed model based QTL mapping in GenStat

Presenters: Fred van Eeuwijk, Hans Jansen & Marcos Malosetti

Organization: Biometris, Wageningen University

When: Monday 14th - Wednesday 16th May, 2012

Where: Hotel Hof van Wageningen, Wageningen

Who should attend

MSc and PhD students, post docs, and researchers from private and public organisations interested in a flexible map construction and QTL mapping approach. Map construction and QTL mapping tools will be offered for a wide spectrum of populations. QTL mapping theory and facilities will be presented for single and multiple traits, as well single and multiple environments. It is recommended that attendees have some familiarity with analysis of variance, regression, mixed models and basic quantitative genetic concepts.

Overview

QTL mapping is introduced as an extension of phenotypic analysis by linear (mixed) model analysis of single traits. Effectively, on a genomic grid, genetic covariates are fitted to phenotypic responses. These genetic covariates represent contrasts in unobserved QTL genotype probabilities given marker information. The calculation of these genetic covariates will be explained for various types of populations: inbreeders, outbreeders and association panels. After mixed model QTL analysis for single traits in single trials, extensions will be described for multiple trials and multiple traits. Hands on QTL analyses will utilize Windows menus in GenStat.

Learning Objectives

By the end of the course you should be able to:

- Construct a genetic map from marker scores on different types of breeding populations
- Perform a QTL analysis for a wide array of breeding populations, for single and multiple environments, and single and multiple traits
- Use various inference procedures for assessing QTL evidence
- Report QTL locations and effects

Instruction methods and time table

Theory will be presented in the form of lectures. Supervised practicals will allow attendants to become familiar with the details of the actions required to perform a QTL analysis in GenStat using Windows' dialogues. These practicals will also serve to learn how to interpret QTL mixed model analysis output. Participants are requested to bring their own laptops.

Time schedule	
Day	Contents
Day 1 morning 9.00-12.00	Lectures: General introduction Linkage analysis Construction of genetic maps Practical: Construction of genetic maps
Day 1 afternoon 13.30-17.00	Lectures: Phenotypic analysis of single trials Marker regression Simple and composite interval mapping Practical: Single trait QTL detection
Day 2 morning 9.00-12.00	Lectures: Phenotypic analysis of multiple trials (environments) Genotype by environment interaction QTL analysis of multiple environments (QTL by environment interaction) Practical: QTL analysis of multiple environments
Day 2 afternoon 13.30-17.00	Lecture: QTL analysis of multiple traits Practical: QTL analysis of multiple traits
Day 3 morning 9.00-12.00	Lectures: Association mapping QTL analysis for multi-parental populations Practical: Association mapping
Day 3 afternoon 13.30-15.00	Lectures: Further developments in QTL mapping

Registration details

The registration for this course is open until May 7th, 2012.

Fee:	Graduate school students:	€200
	Academics (WUR and others):	€300
	Non-academics	€750

The registration fee includes course materials, morning coffee/tea, lunch and afternoon coffee/tea. Registration also includes an evening dinner on Tuesday 15th May.

To register send an email to BIOMETRIS@wur.nl. Details for payment will be sent by reply to your email.

Venue

The workshop will be held in Hotel Hof van Wageningen, Lawickse Allee 9, 6701 AN, Wageningen, The Netherlands, <http://www.hofvanwageningen.nl/>.

Accommodation

Participants can conveniently stay at the hotel Hof van Wageningen. Alternatives are

Hotel de Wageningsche Berg: <http://www.hoteldewageningseberg.nl/>

Hotel de Wereld: <http://www.hoteldewereld.nl/>

Hotel de Nieuwe Wereld: <http://www.denieuwewereld.nl/>

Some selected papers

- Xueqing Huang, Maria-João Paulo, Martin Boer, Sigi Effgen, Paul Keizer, Maarten Koornneef and Fred A. van Eeuwijk. (2011). Analysis of natural allelic variation in Arabidopsis using a multiparent recombinant inbred line population. *PNAS* 108, 11: 4488-4493
- Marcos Malosetti, Fred A. van Eeuwijk, Martin P. Boer, Ana M. Casas, Mónica Elía, Marian Moralejo, Prasanna R. Bhat, Luke Ramsay, José-Luis Molina-Cano. (2011). Gene and QTL detection in a three-way barley cross under selection by a mixed model with kinship information using SNPs. *Theoretical and Applied Genetics* 122:1605–1616
- Fred A. van Eeuwijk, Marco C.A.M. Bink, Karine Chenu and Scott C. Chapman (2010) Detection and use of QTL for complex traits in multiple environments – Current Opinion in Plant Biology 13:193-205
- Van Eeuwijk FA, Boer MP, *et al.* (2010) Mixed model approaches for the identification of QTLs within a maize hybrid breeding program *Theor Appl Genet* 120: 429-440
- Pinto RS, Reynolds MP, Mathews KL, McIntyre CL, Olivares-Villegas J, Chapman SC (2010) Heat and drought adaptive QTL in a wheat population designed to minimize confounding agronomic effects. *Theoretical and Applied Genetics* DOI 10.1007/s00122-010-1351-4
- Chenu K, Chapman SC, Tardieu F, McLean G, Welcker C and Hammer GL (2009) Revealing the yield impacts of organ-level quantitative trait loci associated with drought response in maize - A gene-to-phenotype modeling approach. *Genetics* 183: 1507–1523.
- Mark Cooper - Fred A van Eeuwijk - Graeme L Hammer - Dean W Podlich (2009) Modeling QTL for complex traits: detection and context for plant breeding *Current Opinion in Plant Biology*, 12, 231-240.
- Wang J, Chapman SC, Bonnett DG and Rebetzke GJ (2009). Simultaneous selection of major and minor genes: use of QTL to increase selection efficiency of coleoptile length of wheat (*Triticum aestivum* L.). *Theor Appl Genet* 119:65–74
- Malosetti, M., Ribaut, J. M., Vargas, M., Crossa, J., & Van Eeuwijk, F. A. (2008). A multi-trait multi-environment QTL mixed model with an application to drought and nitrogen stress trials in maize (*zea mays* L.). *Euphytica*, 161(1-2), 241-257.
- Boer MP, Wright D, Feng L, Podlich D, Luo L, Cooper M., and FA van Eeuwijk (2007) A Mixed-Model Quantitative Trait Loci (QTL) Analysis for Multiple-Environment Trial Data Using Environmental Covariables for QTL-by-Environment Interactions, With an Example in Maize. *Genetics* 177: 1801-1813.
- Malosetti, M., Van Der Linden, C. G., Vosman, B., & Van Eeuwijk, F. A. (2007). A mixed-model approach to association mapping using pedigree information with an illustration of resistance to *phytophthora infestans* in potato. *Genetics*, 175(2), 879-889.
- Wang, J., Chapman, S.C., Bonnett, D.G., Rebetzke, G.J, Crouch, J. (2007). Application of population genetic theory and simulation models to efficiently pyramid multiple genes via marker-assisted selection. *Crop Science* 47(2): 582-588.
- Hammer G, Cooper M, Tardieu F, Welch S, Walsh B, van Eeuwijk FA, Chapman S, Podlich D, (2006) Models for navigating biological complexity in breeding improved crop plants. *Trends in Plant Science* 11 (12): 1360-1385.
- 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.
- Malosetti, M., Voltas, J., Romagosa, I., Ullrich, S. E., & Eeuwijk, F. A. V. (2004). Mixed models including environmental covariables for studying QTL by environment interaction. *Euphytica*, 137(1), 139-145.
- 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.