



# Multi-environment (multi-trait) QTL mapping using mixed models

## Applications to drought stress trials in maize and wheat

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### QTL analysis based on mixed models

- Greater flexibility to model complex data (with GxE and multiple traits and environments) than standard QTL mapping procedures
- More realistic models by accounting for heterogeneity of variances and correlations for trait-environment combinations
- Easily extendable: more complex interaction models (epistasis) and inclusion of climatic info

### QTL detection approach

1. Find an appropriate model for the variance-covariance structure (VCOV) in the data, i.e., accounting for heterogeneity of variances and correlations in the linear mixed model
2. Model QTLs in relation to genetic predictors (QTL genotype probabilities given marker information) within the model of step 1

## 1. Find appropriate VCOV

$$y_{-ij} = \mu + E_j + GE_{ij}$$

Schematic representation of VCOV models (variances in the diagonal, covariances off diagonals). Different colours means different values, white means = 0. Below number of parameters, deviance and LR with simpler model.



Model	# parameters	deviance	LR
DIAG	6	14084	
XFA1	12	13949	135
XFA2	18	13919	30

$y_{ij}$ : response  
 $\mu$ : mean  
 $E_j$ : environment effect  
 $GE_{ij}$ : polygenic effect (GGE) + error

Based on a loglikelihood ratio (LR) tests the most suitable VCOV is chosen.

## 2. Creating genetic predictors from marker data:

$$\begin{aligned} QQ &\rightarrow x_i = 1 \\ \text{Genetic predictors } x_i: Qq &\rightarrow x_i = 0 \\ qq &\rightarrow x_i = -1 \end{aligned}$$

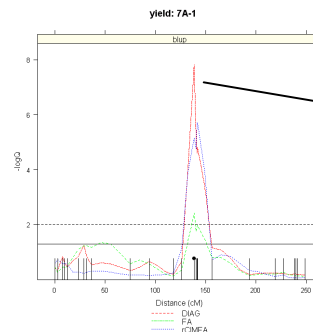
### Illustration with two examples

- Multi-environment QTL mapping
  - Wheat yield in 6 environments (Australia)
- Multi-trait multi-environment QTL mapping
  - Maize: 2 traits (yield and ASI), 11 environments (Mexico and Zimbabwe)

## Multi-environment QTL mapping (wheat)

response for genotype  $i$  in env.  $j$  =  
mean + env + gen.pred. \* env. spec. QTL effect + residual

$$y_{-ij} = \mu + E_j + x_i \alpha_j + GE_{ij}$$



Estimated QTL effects ( $\alpha_j$ ) in each of 6 environments (significant ones in red).

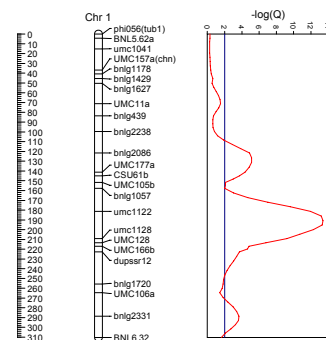
Trial	yield
1512-SB	5.359
4503-SB-Bikoela	4.637
4504-SB-Lundevira	9.604
4505-SB-Narrabri	17.187
sbg02	7.639
sbw04	4.614

Test profile for a QTL effect in at least 1 of the environments

## Multi-trait multi-environment QTL mapping (maize)

response for genotype  $i$ , env.  $j$ , and trait  $t$  =  
trait mean + trait \* env + gen.pred. \* (env.- trait) spec. QTL effect + residual

$$y_{-ijt} = \mu_t + E_{jt} + x_i \alpha_{jt} + GE_{ijt}$$



Estimated QTL effects ( $\alpha_{jt}$ ) on yield and ASI in each of 11 environments (significant ones in red).

environment	yield	ASI
TL01AIS	0.072	-0.304
TL01ASS	0.163	-1.117
TL02AIS	0.353	-2.455
TL02ASS	0.318	-1.453
TL02BWW	0.011	-0.391
TL04BWW	0.439	-0.215
ZW00BIS	0.271	-1.915
ZW00BSS	0.205	-0.758
ZW01AWW	-0.015	-0.186
ZW01BIS	0.397	-0.361
ZW01BSS	0.207	-0.399

Test profile for a QTL effect for at least 1 trait in at least 1 environment

## Conclusion

- We developed a mixed model framework for studying many forms of QTLxE that does not require specialized software
- The present mixed model framework that we employ contains
  - Powerful test for QTLxE
  - Modelling of QTLxE in relation to environmental characterizations
  - Modelling of QTLxE for multiple traits (= changing genetic correlation across environments)