

## Genomic Tools to find the best cows for each environment

### Problem

Resilient genotypes are able to better cope with environmental perturbations, which is very important when genotype by environment interactions (GxE) exist. Traditional genomic GxE models assume that GxE effects are similarly expressed across the genome. This assumption is not correct because specific regions in the genome harbor quantitative trait loci (QTL) and others do not, and loci may have different effects in different environments.

### Solution

We have developed a protocol and analysis pipelines for genomic GxE models in which individual single nucleotide polymorphisms (SNP) effects may differ across environments. The method relies on readily available Best Linear Unbiased Prediction (BLUP) software packages that use a statistical model that ensures best and unbiased estimation of breeding values. The use of readily available software allows easy and quick uptake by genetic evaluation centres.

### Outcome

The analysis protocol consists of several steps and can be applied to dairy or beef cattle or other species. The data set of interest is split in two subsets and then follow a two-step approach: (1) estimate SNP effects in the first data set and calculate SNP (co)variances based on the estimated SNP effects and (2) weigh the SNP genotypes using the estimated (co)variances in (1) and simultaneously compute SNP effects and (co)variances in the second data set. The approach has been tested in simulated data showing a slight increase in accuracy of genomic breeding values of young selection candidates when allowing SNP (co)variances across the genome to be heterogeneous. Applied to real data of Irish dairy and beef crossbred population we did not see any advantage of modeling heterogeneous SNP (co)variances.

### Practical recommendations

The analysis protocol can be applied to genomic GxE models like multi-trait or reaction norm models. The use of this protocol by genetic evaluation centres will aid in the selection of genotypes suited to their environment. The analysis protocol delivers genomic breeding values for animals in different environments, which are valuable selection tools for farmers to select the best animals for their environment.

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### Keywords

Genotype by environment interaction; Genomic prediction

### Illustrations

#### Analysis protocol

Split data set in two subsets

Estimate SNP-effects assuming equal (co)variances in subset 1

Weigh SNP genotypes using estimated (co)variances in subset 1 and compute SNP effects and (co)variances in subset 2



*“GENomic management Tools to Optimize Resilience and Efficiency - GenTORE” is an H2020 project which aims to develop innovative genome-enabled selection and management tools to empower farmers to optimize cattle resilience and efficiency in different and changing environments.*  
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