

Statistical analyses of genotype by environment data
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We introduce in this chapter a series of linear and bilinear models for the study of genotype by environment interaction (GE) and adaptation. These models increasingly incorporate available genetic, physiological, and environmental information for modelling genotype by environment interaction (GE). They are based on analyses of variance and regression and can be formulated in most standard statistical packages. We use the data of a series of trials for 65 barley genotypes (G) grown in 12 environments (E) for illustration and interpretation of the output of such analyses. We aim at identifying key environmental covariables to explain differential phenotypic responses as well as to estimate genotypic sensitivities to these covariables. Using genetic covariables in the form of molecular markers, we partition genotypic main effect terms and GE terms into main effects for quantitative trait loci (QTL) and QTL by environment interaction (QTL.E). The QTL.E estimates can be further regressed on environmental covariables to target differential QTL expression potentially related to environmental factors. We believe that the statistical models that describe GE in direct association to genetic, physiological, and environmental information provide insight in GE and facilitate the development and deployment of new breeding strategies.