

Genotype-environment interaction: a comparison of two basic models

Jean-Pierre Masson¹ and Denys Pommeret²

¹Agrocampus Rennes, France

² Université de la Méditerranée IML, Campus de Luminy, Marseille, France

Abstract

In the classic mixed models the marginal variance of a phenotypic trait Y is not dependent on the environment. Here we are comparing two basic models on which heteroscedasticity on marginal distributions is introduced.

The first model was presented in SanCristobal et al. (1998). In the second model we suppose that genotype (u, v) and environment η are acting in the following way:

$$Y = \mu + u + \eta.v.e + \epsilon$$

where $(u, v), e, \epsilon$ are independent, $\epsilon \sim N(0, \sigma_\epsilon^2)$, $e \sim N(0, 1)$ and (u, v) normally distributed with 0 means, $var(u) = \sigma_u^2$, $var(v) = \sigma_v^2$ and $Cov(u, v) = \rho.\sigma_u.\sigma_v$.

On the second model we prove that $Y = X_1 + X_2$ where X_1 and X_2 are independent, X_1 is Gaussian distributed and X_2 is the product of two independent Gaussian variables. Deconvolution and estimation procedures are illustrated through simulations.

Keywords

Genotype-environment interaction, Deconvolution, Density estimation, Inverse transform, Plasticity.

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