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Copula Integration for Genetic Selection Parameter Estimation in Bivariate Linear Mixed Models

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In animal genetics, linear mixed models are pivotal in determining the genetic and environmental impacts on animal traits, which is critical for designing effective breeding strategies. Traditional approaches, such as restricted maximum likelihood, rely on the assumption of multi-normality in trait distributions. However, this assumption often fails in practice due to the non-Gaussian nature of the joint distribution of multiple traits, resulting in biased estimations.

In this study, a novel method was introduced by incorporating functions known as copulas, which describe the specific dependence structures. This was achieved using a stochastic gradient algorithm, where genetic parameters were estimated by maximizing a likelihood function that includes copulas.

Following validation with simulated Gaussian data, the method was applied to other dependence structures, such as the Clayton copula, demonstrating its functionality.

The findings indicate that accounting for the actual joint distribution of traits can lead to more precise estimations of genetic parameters, thereby enhancing the effectiveness of breeding programs.

Auteurs principaux: KUHN, Estelle (INRAE, MaIage);   ROHMER, Tom (Inrae);   BRUNING, Victoria (IN-RAE)

Orateur: BRUNING, Victoria (INRAE)

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