

“Prediction of genetic values: history, methods and post-genomic challenges”

Daniel Gianola, PhD

Sewall Wright Professor, Department of Animal Sciences,
Department of Biostatistics & Medical Informatics, Department of Dairy Science
University of Wisconsin - Madison

Abstract

A review of statistical methods in quantitative genetics, starting from the seminal contributions of Fisher, Wright and Haldane is presented. Statistical procedures, ranging from path analysis and analysis of variance to Bayesian approaches are presented in a sort of evolutionary framework. Challenges posed by massive phenotypic and genomic data are indicated, and the question of whether or not parametric methods can deal adequately with complexity is raised. The potential of reproducing kernel methods and machine learning approaches is illustrated with animal breeding data, and their possible usefulness in personalized medicine is indicated.