## BAYESIAN META-ANALYSIS MODELS FOR GENETIC ASSOCIATIONS

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We describe univariate and multivariate Bayesian hierarchical meta-analysis models for combining estimates of genetic association across studies. The appeal of these models lies in their flexibility, including the ability to accommodate mixed fixed and random effects, partial exchangeability, diverse distributional assumptions and prior information. Moreover, the Bayesian approach delivers posterior point and interval estimates, predictions and probabilities that meet a range of estimation and hypothesis testing aims.

We demonstrate these features through two case studies. The first involves the association between marbling, or intramuscular fat, and a polymorphism in the 5' promoter region of the bovine Thyroglobulin gene (TG5). A Bayesian hierarchical model was developed to combine the 19 relevant estimates identified from 14 studies, incorporating four breed groups and four different measures of marbling. Overall, there is substantial support for an additive association between the TG5 marker and marbling. The marker effect was also assessed across various breed groups.

The second case study involves combining multiple indicators of beef tenderness. Here, individual studies report on one or both of the indicators of interest. A multivariate metaanalysis model is suggested in which 'strength is borrowed' across both studies and indicators. The impact of the multivariate assessment on the individual indicators in such a metaanalysis is of particular methodological interest.