

# BAYESIAN RANDOM INTERCEPT SLOPE FACTOR MODEL FOR LONGITUDINAL TWIN DATA

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## ABSTRACT

The Random Intercept (RI) factor model is proposed as an alternative to traditional genetic factor models for the analysis of longitudinal twin data. This model constitutes a more factorially complex alternative to the single factor models which is yet more parsimonious than multifactor counterparts. Specifically, addition of general random intercept factors provides a way to model general individual differences in genetic and environmental components. Exploration of the appropriate factorization proceeds by testing the full model containing both a random intercept factor as well as the traditional factor which has freely estimated factor loadings the genetic and environment components of the model. When both of these components are not present for all genetic and environmental components, this model is frequently not empirically identified under Maximum Likelihood (ML) estimation. Bayesian estimation with subsequent model comparison using Bayes Factors is proposed as a remedy of this problem. Feasibility of the approach to model estimation and comparison is illustrated using a simulation study. The approach is then empirically illustrated using prospective longitudinal data from a study of body mass index in young women. Model comparisons indicate that while the estimated additive genetic contribution to body mass appears well modeled by a random intercept factor model that common and unique environmental effects were well-modeled by intercept-only factors. Heritability estimates under the RI appeared markedly different than those obtained under the traditional model.