Random intercept slope factor (RISF) model is proposed in this study 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 but are yet more parsimonious than multifactor counterparts. Specifically, addition of general random intercept factors to the traditional genetic and environmental factors (slope factors) provides a researcher with a way to model baseline or general individual differences in genetic and environmental components. Exploration of the appropriate factorization proceeds by testing the full model containing both random intercept and slope factor for genetic and environment components. However, when more parsimonious alternatives to the full model constitute the true model, the full model is frequently not empirically identified in Maximum Likelihood (ML) estimation. To remedy this analytic problem, Bayesian estimation is proposed. Moreover, in Bayesian framework all competitive reduced models are compared via Bayes Factors which doesn't require comparing models to be nested as ML framework. The utility of model estimation and comparison under this strategy is examined using a simulation study. The approach is then illustrated with a substantive application in a longitudinal study about female twins' body mass index. Comparisons of the full model with more parsimonious alternatives reveal that random intercept components constitute a parsimonious alternative to the traditional ACE genetic factor model and provide a better model fit in Bayesian estimation framework.