Level-1 variance in HGLM models

In the case of a multilevel model for a dichotomous outcome, there is no unique decomposition or variance at level-1. The level-1 variance depends on the covariates even if you have a single random effect.

Consider the example of a binomial model shown in the HLM manual with the THAI data, using a cross-classification of students by gender and preprimary education and $m_{ij} > 1$, where m_{ij} denotes the number of trials. This implies four cells, each with unique cell size and cell count y_{ij} . The study can be considered to have four level-1 units (cells), with the outcome y_{ij}, given the cell probability ϕ_{ij} , distributed as $B\left(m_{ij}, \phi_{ij}\right)$.

In the metric of the linearized dependent variable, the level-1 variance is the reciprocal of the binomial variance,

$$\text{Level-1 variance} = 1/\left[\phi_{ij}(1 - \phi_{ij})\right]$$

It is possible to rewrite such a model as a threshold model with a latent continuous variable, and then to calculate the decomposition of variance with respect to the latent variable. See Hedeker & Gibbons (1994) in Biometrics for more on random effect thresholds.

It is also possible to calculate a rough estimate. For example, if the model is true, it is assumed that the level-1 error variance is equal to $\pi^2/3$ = 3.29895 for the logistic link function (see, *e.g.*, Hedeker & Gibbons (2006), p. 157), where π represents the constant 3.141592654.