

The simplest form of the standard 3-stage hierarchical model in the context of MEP size modeling can be described as follows. Let there be  $N_P$  exchange sequences  $\{(x_i^j, y_i^j)_{i=1}^{n_j} \mid j = 1, 2 \dots N_P\}$  of MEP size  $y_i^j$  recorded at stimulus intensity  $x_i^j$  from  $j^{th}$  participant, for a total of  $N_P$  participants.

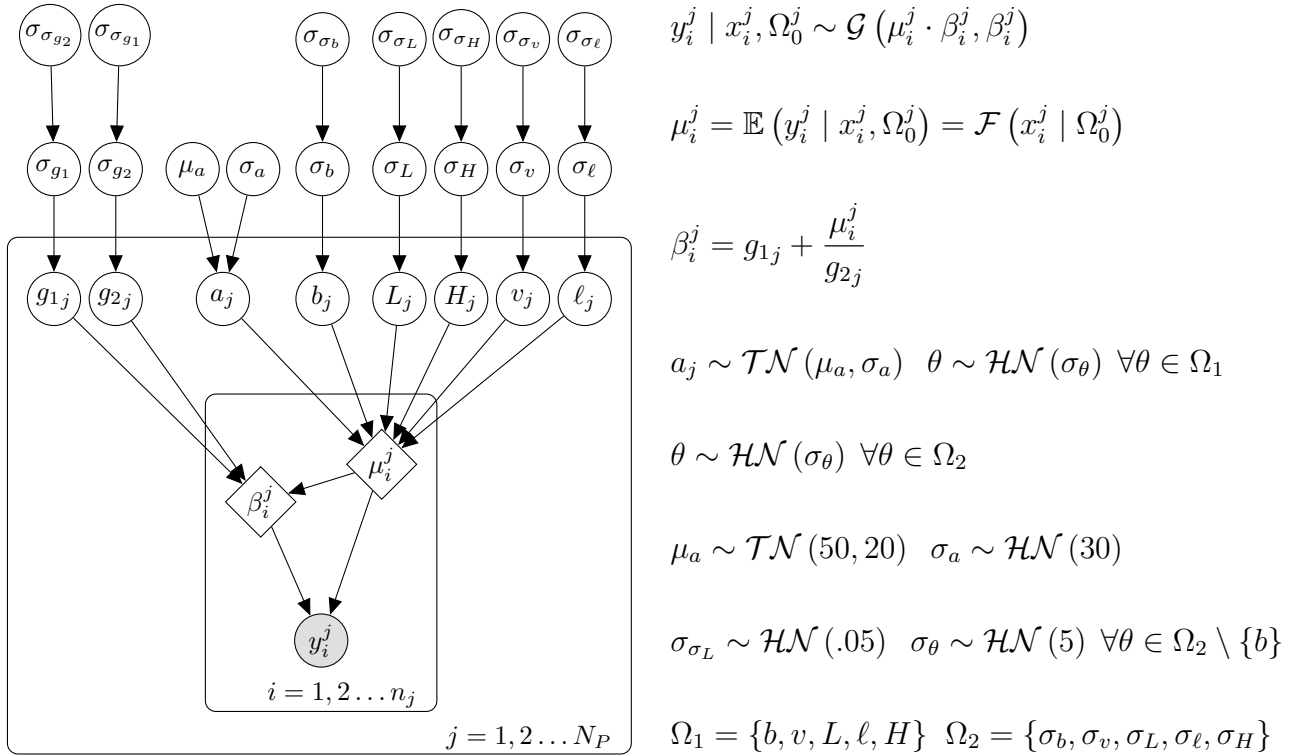
The first stage of hierarchy is the *participant-level* and specifies parametric model  $P(y_i^j \mid x_i^j, \theta_j)$  for each of the  $N_P$  sequences and models the MEP size  $y_i^j$  as a function of stimulus intensity  $x_i^j$  and participant specific parameters  $\theta_j$ . In the second stage,  $\theta_1, \theta_2 \dots \theta_P$  are assumed to be exchangeable and generated from a common distribution  $P(\theta_j \mid \gamma)$  with hyper-parameters  $\gamma$ . In the third stage, the hyper-parameters  $\gamma$  are assumed to be unknown and are assigned a non-informative prior density  $P(\gamma)$ .

$$y_i^j \mid x_i^j, \theta_j, \gamma \sim P(y_i^j \mid x_i^j, \theta_j, \gamma) \quad (4.3.1)$$

$$\theta_j \mid \gamma \sim P(\theta_j \mid \gamma) \quad (4.3.2)$$

$$\gamma \sim P(\gamma) \quad (4.3.3)$$

Figure 4.3.1 shows the graphical representation of the basic hierarchical model implemented by hbmeep (Section 5.1) for recruitment-curve fitting



There are few key details here. Firstly, in (3.2.2), we model the expected observed MEP size as a rectified-logistic function of stimulation intensity. Secondly, the nuisance parameter of the Gamma distribution is a linear combination of this expected value, which

allows for capturing how the spread changes with respect to MEP size. This results in narrower credible intervals for the threshold estimates.