

S2 Appendix: Technical expressions for the three models \mathcal{M}_1 , \mathcal{M}_2 , and \mathcal{M}_3 for

*Estimation of COVID-19 spread curves integrating global data
and borrowing information*

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S.1 Technical expressions for the three models \mathcal{M}_1 , \mathcal{M}_2 , and \mathcal{M}_3

Technical expressions for the three models, \mathcal{M}_1 , \mathcal{M}_2 , and \mathcal{M}_3 , compared Subsection “**Benefits from the information borrowing**” in the main manuscript are given as follows:

\mathcal{M}_1 is an individual country-based model (non-hierarchical model) that uses infection trajectory for a single country $\mathbf{y} = (y_1, \dots, y_T)^\top$. The model is given by

$$y_t = f(t; \theta_1, \theta_2, \theta_3, \xi) + \epsilon_t, \epsilon_t \sim \mathcal{N}(0, \sigma^2), \theta_l \sim \mathcal{N}(\alpha_l, \sigma_l^2), \\ \xi \sim \log \mathcal{N}(0, 1), (t = 1, \dots, T, l = 1, 2, 3),$$

where $f(t; \theta_1, \theta_2, \theta_3)$ is the Richards growth curve ((1) in the main manuscript), and improper priors are used for error variances and intercept terms as (6).

\mathcal{M}_2 is a Bayesian hierarchical model without using covariates, which uses infection trajectories from N countries, $\{\mathbf{y}_i\}_{i=1}^N$. This model is equivalent to BHRM (2) – (6) with removed covariates terms in (3).

\mathcal{M}_3 is the BHRM (2) – (6).