Table 1: Summary of parameters, definitions, and priors/posteriors in the mediator and outcome submodels

		Mediator Submodel
Symbol	**Definition / Role**	**Distribution / Prior**
M_{ij}	Log relative abundance of the jth microbial feature for subject i.	$M_{ij} \mid \alpha_j, \phi_j, t_i, \theta_j, X_i, \sigma_M^2 \sim N\Big(\alpha_j + \phi_j\, t_i + \sum_{p=1}^{P} \theta_{jp}\, X_{ip},\, \sigma_M^2\Big)$
α_j	Taxon-specific intercept for feature j.	$\alpha_j \sim N\big(0, \sigma_\alpha^2\big)$
ϕ_j	Effect of the treatment in the mediator model.	$\phi_j \mid \zeta_j, \sigma_j^2 \sim \zeta_j\, N(0,\, \sigma_j^2)\ +\ (1-\zeta_j)\, \delta_0(\phi_j)$
θ_{jp}	Effect of covariate X_{ip} in the mediator model.	$\theta_{jp} \mid \eta_{jp}, \sigma_j^2 \sim \eta_{jp}\, N(0,\, \sigma_j^2)\ +\ (1-\eta_{jp})\, \delta_0(\theta_{jp})$
ζ_j	Inclusion indicator for ϕ_j (spike-and-slab).	$\zeta_j \sim$ Beta-Bernoulli(a_j, b_j)
η_{jp}	Inclusion indicator for θ_{jp} (spike-and-slab).	$\eta_{jp} \sim$ Beta-Bernoulli(a_{jp}, b_{jp})
σ_M^2	Error variance in the mediator model.	$\sigma_M^2 \sim$ InvGamma$(a_0,\, b_0)$
		Outcome Submodel
Symbol	**Definition / Role**	**Distribution / Prior**
y_i	Observed outcome for subject i.	$y_i \mid \Delta, t_i, \kappa, X_i, \beta, M_i, \sigma_Y^2 \sim N\Big(\Delta\, t_i + \sum_{p=1}^{P} \kappa_p\, X_{ip} + \sum_{j=1}^{J} \beta_j\, M_{ij},$
Δ	Direct effect of treatment t_i on outcome y_i.	
κ_p	Effect of covariate X_{ip} on outcome y_i.	
β_j	Effect of microbial feature M_{ij} on outcome y_i.	The sum of selected microbial feature coefficients follows: $$\sum_{j \in \gamma_\beta} \beta_j \sim N\left(0, \frac{p_{\gamma_\beta}\sigma^2}{1 + c^2 p_{\gamma_\beta}}\right).$$ Also, the compositional constraint: $\sum_{j=1}^{J} \beta_j = 0$ applies.
σ_Y^2	Error variance in the outcome model.	$\sigma_Y^2 \sim$ InvGamma$(a_0^Y,\, b_0^Y)$
		Additional Priors and Structures
γ	Vector of selection indicators. $\gamma = (1, \gamma_\kappa, \gamma_\beta)$.	$P(\gamma) \propto \exp\Big(a_\kappa^T \gamma_\kappa + b\gamma_\kappa^T \gamma_\kappa + a_\beta^T \gamma_\beta + \gamma_\beta^T Q_\beta \gamma_\beta\Big)$

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	Mediator Submodel (Continued)	
Symbol	**Definition / Role**	**Distribution / Prior**
Q_β	Inverse of phylogeny-induced correlation matrix C.	$Q_\beta = C^{-1}$. E.g. $c_{pq} = \exp(-2\rho\, d_{pq})$
T	Transformation matrix ensuring $\sum \beta_j = 0$.	$T'_\gamma T_\gamma$ is designed as a block matrix: $$(T'_\gamma T_\gamma)^{-1} = \begin{bmatrix} I_{p_{\gamma_\kappa}+1} & \mathbf{0} \\ \mathbf{0} & (T'_{\gamma_\beta} T_{\gamma_\beta})^{-1} \end{bmatrix},$$ where $$(T'_{\gamma_\beta} T_{\gamma_\beta})^{-1} = I_{p_{\gamma_\beta}} - \frac{c^2}{1 + c^2 p_{\gamma_\beta}} \mathbf{1}_{p_{\gamma_\beta}} \mathbf{1}'_{p_{\gamma_\beta}}.$$
T_β	Specific transformation matrix for microbial feature constraints.	$T_\beta = \left(I_J \mid c\mathbf{1}_J^T\right)$, where large c enforces the sum-to-zero constraint.
$\Delta,\ \kappa_\gamma,\ \beta_\gamma$	Coefficients (outcome submodel) under M_γ; z-prior form.	$\Delta,\ \kappa_\gamma,\ \beta_\gamma \,\big\vert\, M_\gamma,\ \sigma^2 \ \sim\ N\Big(0,\ \sigma^2 \left(T_\gamma^T\, T_\gamma\right)^{-1}\Big)$