

Extending the Hierarchical Model for Antibody Kinetics

Kwan Ho Lee

UC Davis

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- Incorporates feedback from Dr. Morrison and Dr. Aiemjoy
- Focus exclusively on (Teunis and Eijkeren 2016) model
- Clarifies model dynamics: growth, clearance, decay
- Uses updated parameter notation: μ_y , μ_b , γ , α , ρ
- Assumes block-diagonal covariance structure across biomarkers

Two-phase within-host antibody kinetics:

$$\frac{dy}{dt} = \begin{cases} \mu_y y(t), & t \leq t_1 \\ -\alpha y(t)^\rho, & t > t_1 \end{cases} \quad \text{with} \quad \frac{db}{dt} = \mu_b b(t) - \gamma y(t) \quad (1)$$

Initial conditions: $y(0) = y_0$, $b(0) = b_0$

Key transition: t_1 is the time when $b(t_1) = 0$

Derived quantity: $y_1 = y(t_1)$

Closed-Form Solutions

Antibody concentration $y(t)$

- $t \leq t_1$:

$$y(t) = y_0 e^{\mu_y t}$$

- $t > t_1$:

$$y(t) = y_1 \left(1 + (\rho - 1) \alpha y_1^{\rho-1} (t - t_1) \right)^{-\frac{1}{\rho-1}}$$

Pathogen load $b(t)$

- $t \leq t_1$:

$$b(t) = b_0 e^{\mu_b t} - \frac{\gamma y_0}{\mu_y - \mu_b} (e^{\mu_y t} - e^{\mu_b t})$$

- $t > t_1$:

Time of Peak Response

Peak Time t_1

$$t_1 = \frac{1}{\mu_y - \mu_b} \log \left(1 + \frac{(\mu_y - \mu_b)b_0}{\gamma y_0} \right) \quad (2)$$

Peak Antibody Level y_1

$$y_1 = y_0 e^{\mu_y t_1} \quad (3)$$

Parameter Summary

Table 1: Parameter summary for antibody kinetics model.

| Symbol | Description |
|----------|---|
| μ_y | Antibody production rate (growth phase) |
| μ_b | Pathogen replication rate |
| γ | Clearance rate (by antibodies) |
| α | Antibody decay rate |
| ρ | Shape of antibody decay (power-law) |
| t_1 | Time of peak response |
| y_1 | Peak antibody concentration |

Note: Only the first 6 are typically estimated. y_1 is derived from the ODE solution at t_1 .

Model Comparison: (Teunis and Eijkeren 2016) vs This Presentation

Table 2: Comparison of Teunis (2016) model and this presentation's model assumptions.

| Component | (Teunis and Eijkeren 2016) | This Presentation |
|--------------------------------|--------------------------------|----------------------------|
| Pathogen ODE | $\mu_0 b(t) - cy(t)$ | $\mu_b b(t) - \gamma y(t)$ |
| Antibody ODE (pre- t_1) | $\mu y(t)$ | $\mu_y y(t)$ |
| Antibody ODE (post- t_1) | $-\alpha y(t)^r$ | $-\alpha y(t)^\rho$ |
| Antibody growth type | Pathogen-driven | Self-driven exponential |
| Antibody rate name | μ | μ_y |
| t_1 formula | Uses μ_0, μ, b_0, c, y_0 | Uses μ_b, μ_y , etc. |

Full Parameter Model (7 Parameters)

Subject-level parameters:

$$\theta_{ij} \sim \mathcal{N}(\mu_j, \Sigma_j), \quad \theta_{ij} = \begin{bmatrix} y_{0,ij} \\ b_{0,ij} \\ \mu_{b,ij} \\ \mu_{y,ij} \\ \gamma_{ij} \\ \alpha_{ij} \\ \rho_{ij} \end{bmatrix}$$

Hyperparameters – Means:

- μ_j : population-level mean vector for biomarker j
- Prior on μ_j :

$$\mu_j \sim \mathcal{N}(\mu_{\text{hyp},j}, \Omega_{\text{hyp},j})$$

Core Parameters Used for Curve Drawing

In this presentation, we focus on **5 key parameters** required to draw antibody curves:

- y_0 : initial antibody level
- t_1 : time of peak antibody response
- y_1 : peak antibody level
- α : decay rate
- ρ : shape of decay

Note: t_1 and y_1 are **derived from the full model** - These 5 are sufficient for prediction and plotting

Classifying Model Parameters ((Teunis and Eijkeren 2016) Structure)

Estimated Parameters (7 total):

- **Core model parameters (5):** $\mu_b, \mu_y, \gamma, \alpha, \rho$
- **Initial conditions (2):** y_0, b_0

Derived Quantity (not estimated):

- y_1 : peak antibody level computed as $y(t_1)$

Time of Pathogen Clearance t_1

Definition: t_1 is the time when the pathogen is cleared, i.e., $b(t_1) = 0$

Analytic expression:

$$t_1 = \frac{1}{\mu_y - \mu_b} \log \left(1 + \frac{(\mu_y - \mu_b)b_0}{\gamma y_0} \right)$$

Key observations: t_1 depends on μ_b , μ_y , b_0 , y_0 , and $y_1 = y(t_1)$ is computed based on this time point

Why It's a Seven-Parameter Model

- Our model estimates **7 parameters**:
 - 5 biological parameters: $\mu_b, \mu_y, \gamma, \alpha, \rho$
 - 2 initial conditions: y_0, b_0
- But we often refer to an 8th quantity: y_1
- So why isn't y_1 a parameter?

Answer: y_1 is a **computed value**, not directly estimated.

Why y_1 Is Not Fit Directly

- y_1 is the antibody level at the time the pathogen is cleared:

$$y_1 = y(t_1) \quad \text{where } b(t_1) = 0$$

- y_1 is not an “input” — it is **computed** from:
 - $\mu_y, y_0, b_0, \mu_b, \gamma$
 - via solution of ODEs to find t_1 and compute $y(t_1)$

In other words: y_1 is a **derived output**, not a fit parameter.

How y_1 Is Computed

- y_1 is computed by solving the ODE system:

$$\frac{dy}{dt} = \mu_y y(t), \quad \frac{db}{dt} = \mu_b b(t) - \gamma y(t)$$

- Evaluate $y(t)$ at $t = t_1$ using ODE solution:

$$y_1 = y(t_1; \mu_y, y_0, b_0, \mu_b, \gamma)$$

Recap: What We Estimate

Seven model parameters (7-parameter model for full dynamics):

- $\mu_b, \mu_y, \gamma, \alpha, \rho$ (biological process)
- y_0, b_0 (initial state)

Derived quantity:

- $y_1 = y(t_1)$ — not directly estimated, computed

5-parameter subset for curve visualization:

- $y_0, y_1, t_1, \alpha, \rho$

Hierarchical Bayesian Structure

Individual parameters:

$$\theta_{ij} = \begin{bmatrix} y_{0,ij} \\ b_{0,ij} \\ \mu_{b,ij} \\ \mu_{y,ij} \\ \gamma_{ij} \\ \alpha_{ij} \\ \rho_{ij} \end{bmatrix} \sim \mathcal{N}(\mu_j, \Sigma_j)$$

Hyperparameters:

- μ_j : population-level means (per biomarker j)
- Σ_j : 7×7 covariance matrix over parameters

Subject-Level Parameters: θ_{ij}

$$\theta_{ij} \sim \mathcal{N}(\mu_j, \Sigma_j), \quad \theta_{ij} \in \mathbb{R}^7$$

Where:

$$\theta_{ij} = \begin{bmatrix} y_{0,ij} \\ b_{0,ij} \\ \mu_{b,ij} \\ \mu_{y,ij} \\ \gamma_{ij} \\ \alpha_{ij} \\ \rho_{ij} \end{bmatrix}, \quad \Sigma_j \in \mathbb{R}^{7 \times 7}$$

Each subject i has a unique 7-parameter vector per biomarker j , capturing individual-level variation in antibody dynamics.

Hyperparameters: Priors on Population Means

Population-level means:

$$\mu_j \sim \mathcal{N}(\mu_{\text{hyp},j}, \Omega_{\text{hyp},j})$$

Interpretation:

- μ_j : average parameter vector for biomarker j
- $\mu_{\text{hyp},j}$: prior guess (e.g., vector of zeros)
- $\Omega_{\text{hyp},j}$: covariance matrix encoding uncertainty

Example:

$$\mu_{\text{hyp},j} = 0, \quad \Omega_{\text{hyp},j} = 100 \cdot I_7$$

Hyperparameters: Priors on Covariance

Covariance across parameters:

$$\Sigma_j^{-1} \sim \mathcal{W}(\Omega_j, \nu_j)$$

- Σ_j : variability/covariance in subject-level parameters
- Ω_j : prior scale matrix
- ν_j : degrees of freedom

Example:

$$\Omega_j = 0.1 \cdot I_7, \quad \nu_j = 8$$

Observed antibody levels:

$$\log(y_{\text{obs},ij}) \sim \mathcal{N}(\log(y_{\text{pred},ij}), \tau_j^{-1})$$

Precision prior:

$$\tau_j \sim \text{Gamma}(a_j, b_j)$$

- τ_j : shared measurement precision for biomarker j
- Gamma prior allows flexible noise modeling

Let $K = 7$ (parameters), J biomarkers. Then:

$$\Theta_i = [\theta_{i1} \quad \theta_{i2} \quad \cdots \quad \theta_{iJ}] \in \mathbb{R}^{K \times J}$$

Assume:

$$\text{vec}(\Theta_i) \sim \mathcal{N}(\text{vec}(M), \Sigma_K \otimes I_J)$$

Matrix Algebra – Simplified Structure

Setup: $\Theta_i \in \mathbb{R}^{7 \times J}$

Model:

$$\text{vec}(\Theta_i) \sim \mathcal{N}(\text{vec}(M), \Sigma_K \otimes I_J)$$

- Σ_K : 7×7 covariance (same across biomarkers)
- I_J : biomarkers assumed uncorrelated
- Block-diagonal covariance

Understanding $\text{vec}(\Theta_i)$

Each $\theta_{ij} \in \mathbb{R}^7$:

$$\theta_{ij} = \begin{bmatrix} y_0 \\ b_0 \\ \mu_0 \\ \mu_1 \\ c \\ \alpha \\ r \end{bmatrix}$$

Flattening:

$$\text{vec}(\Theta_i) \in \mathbb{R}^{7J \times 1}$$

Understanding $\text{vec}(M)$

Let $M = [\mu_1 \mu_2 \cdots \mu_J] \in \mathbb{R}^{7 \times J}$

Example for $J = 3$:

$$M = \begin{bmatrix} \mu_{1,1} & \mu_{1,2} & \mu_{1,3} \\ \mu_{2,1} & \mu_{2,2} & \mu_{2,3} \\ \mu_{3,1} & \mu_{3,2} & \mu_{3,3} \\ \mu_{4,1} & \mu_{4,2} & \mu_{4,3} \\ \mu_{5,1} & \mu_{5,2} & \mu_{5,3} \\ \mu_{6,1} & \mu_{6,2} & \mu_{6,3} \\ \mu_{7,1} & \mu_{7,2} & \mu_{7,3} \end{bmatrix}$$

Covariance Structure: $\Sigma_K \otimes I_J$

$$\text{Cov}(\text{vec}(\Theta_i)) = \Sigma_K \otimes I_J$$

- Σ_K : parameter covariance matrix
- I_J : biomarker-wise independence
- Kronecker product yields block-diagonal matrix

Example: Kronecker Product with $K = 2, J = 3$

Let:

$$\Sigma_K = \begin{bmatrix} \sigma_{11} & \sigma_{12} \\ \sigma_{21} & \sigma_{22} \end{bmatrix}, \quad I_3 = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

Then:

$$\Sigma_K \otimes I_3 \in \mathbb{R}^{6 \times 6}$$

Expanded Matrix: $\Sigma_K \otimes I_3$

$$\Sigma_K \otimes I_3 = \begin{bmatrix} \sigma_{11} & 0 & 0 & \sigma_{12} & 0 & 0 \\ 0 & \sigma_{11} & 0 & 0 & \sigma_{12} & 0 \\ 0 & 0 & \sigma_{11} & 0 & 0 & \sigma_{12} \\ \sigma_{21} & 0 & 0 & \sigma_{22} & 0 & 0 \\ 0 & \sigma_{21} & 0 & 0 & \sigma_{22} & 0 \\ 0 & 0 & \sigma_{21} & 0 & 0 & \sigma_{22} \end{bmatrix}$$

Next Steps: Modeling Correlation Across Biomarkers

Current Limitation:

- Biomarkers assumed independent: I_J

Planned Extension:

- Use full covariance Σ_J :

$$\text{Cov}(\text{vec}(\Theta_i)) = \Sigma_K \otimes \Sigma_J$$

Extending to Correlated Biomarkers

Assume $K = 3$, $J = 3$

Define:

$$\Sigma_K = \begin{bmatrix} \sigma_{11} & \sigma_{12} & \sigma_{13} \\ \sigma_{21} & \sigma_{22} & \sigma_{23} \\ \sigma_{31} & \sigma_{32} & \sigma_{33} \end{bmatrix}, \quad \Sigma_J = \begin{bmatrix} \tau_{11} & \tau_{12} & \tau_{13} \\ \tau_{21} & \tau_{22} & \tau_{23} \\ \tau_{31} & \tau_{32} & \tau_{33} \end{bmatrix}$$

Kronecker Product Structure: $\Sigma_K \otimes \Sigma_J$

$$\Sigma_K \otimes \Sigma_J = \begin{bmatrix} \sigma_{11}\Sigma_J & \sigma_{12}\Sigma_J & \sigma_{13}\Sigma_J \\ \sigma_{21}\Sigma_J & \sigma_{22}\Sigma_J & \sigma_{23}\Sigma_J \\ \sigma_{31}\Sigma_J & \sigma_{32}\Sigma_J & \sigma_{33}\Sigma_J \end{bmatrix}$$

Now biomarkers and parameters can be correlated.

Expanded Form: $\Sigma_K \otimes \Sigma_J$ (3x3)

The 9×9 matrix contains all combinations $\sigma_{ab}\tau_{cd}$

Not block-diagonal — includes cross-biomarker correlation

Practical To-Do List (for Chapter 2)

Model Implementation:

- Define full Σ_J and prior: $\Sigma_J^{-1} \sim \mathcal{W}(\Psi, \nu)$
- Implement $\Sigma_K \otimes \Sigma_J$ in JAGS

Simulation + Validation:

- Simulate individuals with correlated biomarkers
- Fit both block-diagonal and full-covariance models
- Compare fit: DIC, WAIC, predictive checks

Teunis, Peter F. M., and J. C. H. van Eijkeren. 2016. "Linking the Seroresponse to Infection to Within-Host Heterogeneity in Antibody Production." *Epidemics* 16: 33–39.
<https://doi.org/10.1016/j.epidem.2016.04.001>.