# Lecture 12 - MCMC application: modelling PRRS viremia


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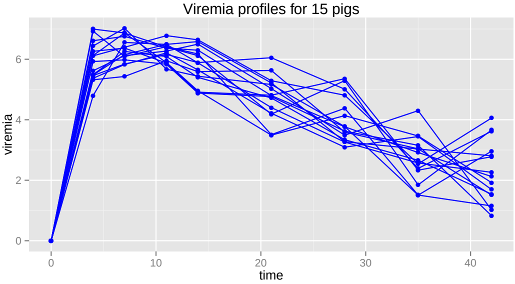
# Bayesian Inference for the parameters of the Woods function (Islam et al., 2013)




- Data were obtained from a in-vivo challenge study
- viremia profiles suggest different host responses to PRRSV infections

## potential sources of variation

- within host variation (dynamic variation of each pig's viremia)
- between host variation (difference between pigs)

## model first stage: within host variation

$y_{i,j}$ viral load of pig $i$ at time $j$

**first stage: within host variation:**

$$y_{i,j} = f(a_i, b_i, c_i, t_{i,j}) + \epsilon_{i,j}$$

- $f(a_i, b_i, c_i, t_{i,j}) = a_i t_{i,j}^{b_i} \exp(-c_i t_{i,j})$ (Woods function)
- $\epsilon \sim \mathrm{N}(0, \sigma_\epsilon^2)$ - constant variance over time - **strong assumption!**

**Distribution for the viremia profiles based on model first stage:**

$$y_{i,j} \sim \mathrm{N}(f(a_i, b_i, c_i, t_{i,j}), \sigma_\epsilon^2)$$

## model second stage: between host variation:

- problem: for the Woods function, $a$ must be larger than 0 and both $b$ and $c$ must be between 0 and 1
- we can use transformations to allow the paramters to vary on the real line - makes inference easier

**example:** $\boldsymbol{\theta}_i = [\log(a_i) \;\; \text{logit}(b_i) \;\; \text{logit}(c_i)]$

- a probability distribution can be considered to account for random variation in each parameter for each pig i

$$\log(a_i) = \mu_a + e_{i,a}$$

$$\text{logit}(b_i) = \mu_b + e_{i,b}$$

$$\text{logit}(c_i) = \mu_c + e_{i,b}$$

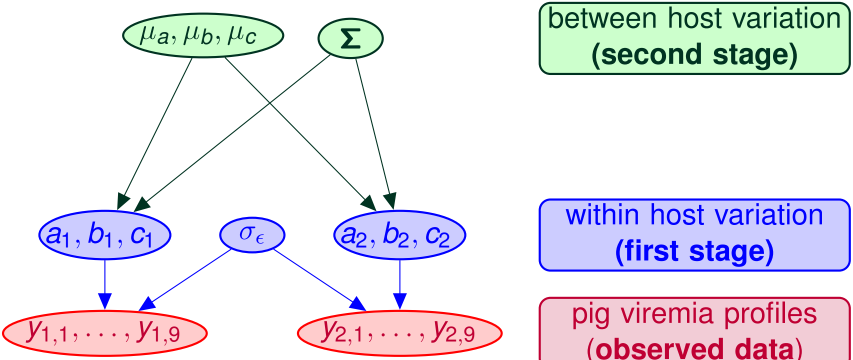
$$\boldsymbol{\theta}_i \sim \text{MultiNormal}([\mu_a \;\; \mu_b \;\; \mu_c]^\top, \boldsymbol{\Sigma})$$

$\boldsymbol{\Sigma}$ is a variance-covariance matrix

**other covariates could be included to account for systematic variation (eg. pig's age)**

## what we have so far..

$y_{i,j}$ viral load of pig $i$ at time $j$, $i = 1, 2$, $j = 1, \ldots, 9$



# prior uncertainty about parameters (model 3 rd stage) and Bayesian inference

## prior uncertainty about parameters of first and second stages

$$\boldsymbol{\mu} = [\mu_a \;\; \mu_b \;\; \mu_c]^\top \sim \text{MultiNormal}(\mathbf{0}, \boldsymbol{\Sigma}_\mu)$$

($\Sigma_\mu$ components must be high values for a non-informative prior distribution)

$$\sigma_\epsilon^2 \sim \text{InverseGamma}(a, b) \qquad \text{and} \qquad \Sigma \sim \text{InverseWishart}(k, \mathbf{D})$$

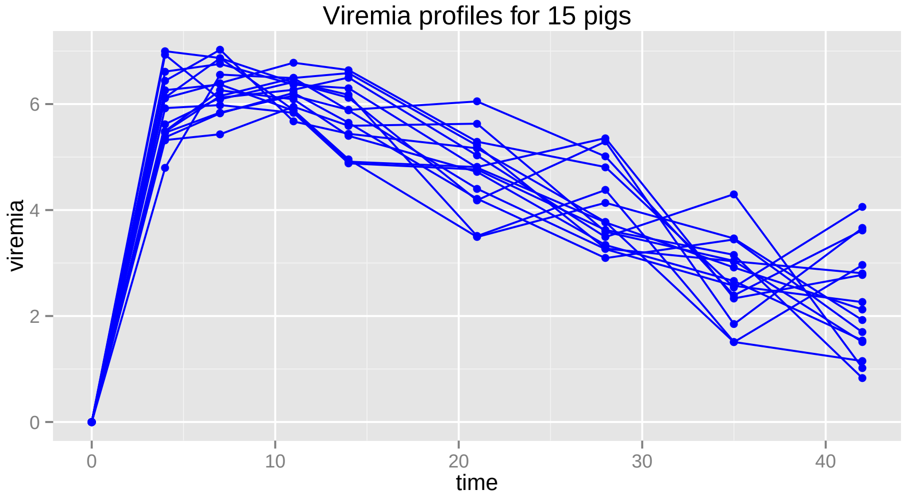
- **parameters:** $\boldsymbol{\theta}^\top = [\boldsymbol{\theta}_1^\top, \ldots \; \boldsymbol{\theta}_k^\top], \sigma^2, \boldsymbol{\mu}, \Sigma$
- **data:** viremia profiles of the pigs

## Posterior distribution

$$\begin{aligned} \text{posterior} \quad &\propto \quad \text{prior} \times \text{likelihood} \\ g(\boldsymbol{\theta}, \sigma^2, \boldsymbol{\mu}, \Sigma | \textbf{data}) \quad &\propto \quad g(\boldsymbol{\theta}) g(\boldsymbol{\sigma}^2) g(\boldsymbol{\mu}) g(\boldsymbol{\Sigma}) f(data | \boldsymbol{\theta}, \sigma^2, \boldsymbol{\Sigma}) \end{aligned}$$

**MCMC must be used to sample from this posterior**

# Now we have a model for this data



## graphical representation of the model for two pigs observed 9 times each

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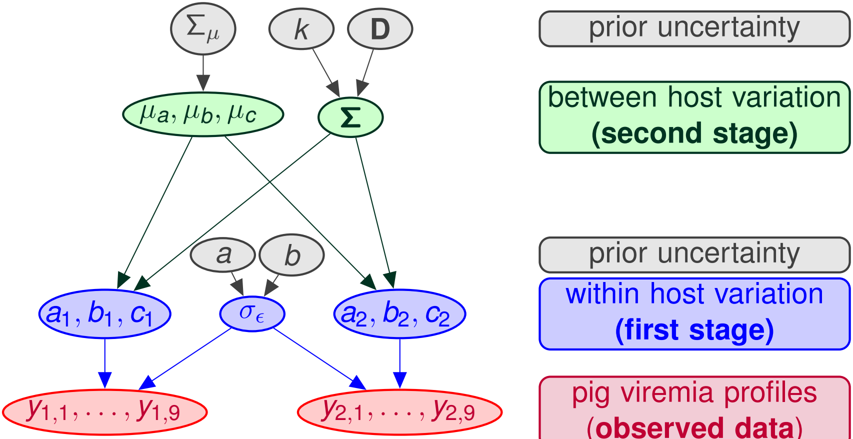

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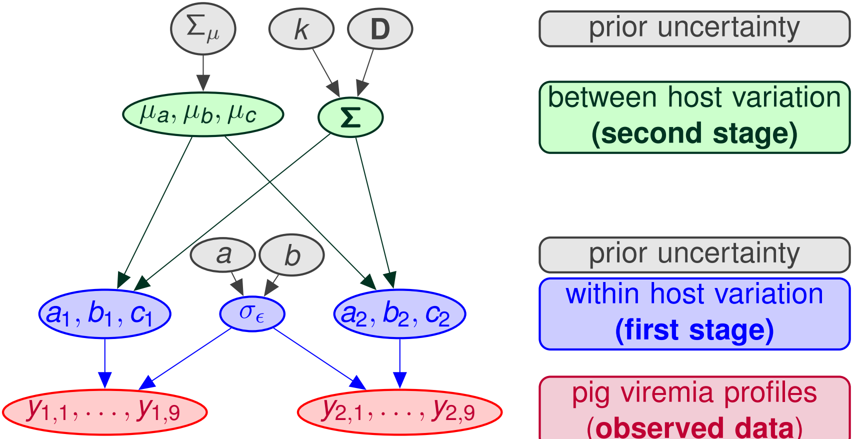

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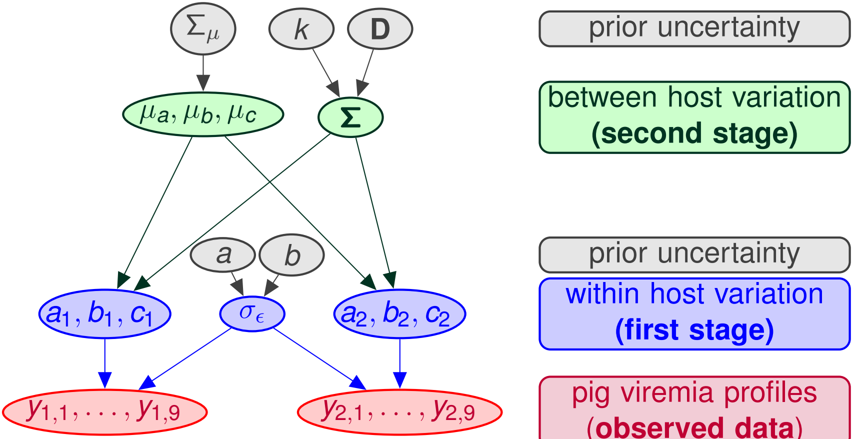

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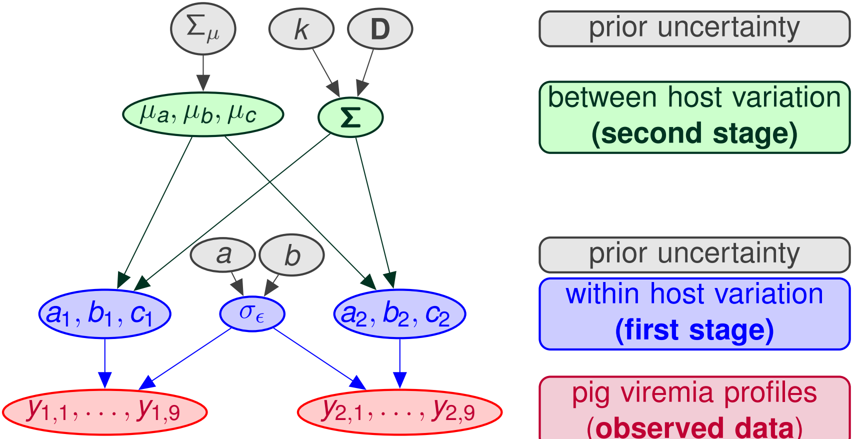

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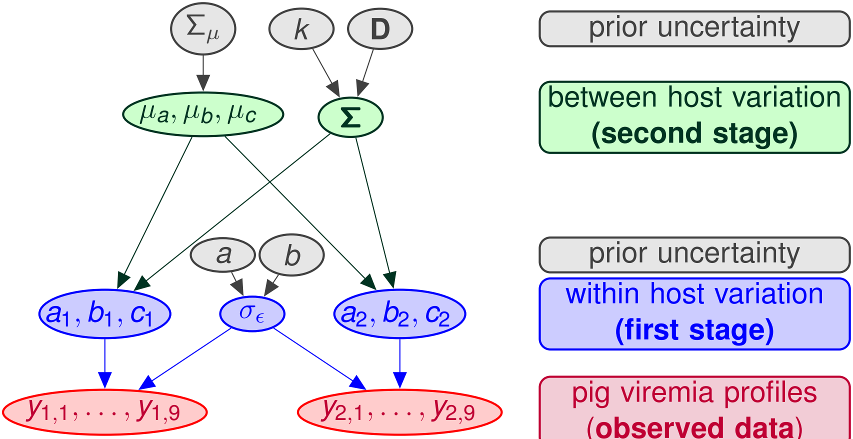


This is a Bayesian hierarchical non-linear model

# Tutorial 12:

## Estimating parameters of the Woods function

- Analyse results of the Hierarchical model fitted to the pigs viremia data
- compare estimates from different pigs