Section 8

# Hierarchical models

# Hierarchical models

- Hierarchical modeling provides a framework for building complex and high-dimensional models from simple and low-dimensional building blocks
- Of course, it is possible to analyze these models using non-Bayesian methods
- However, this modeling framework is popular in the Bayesian literature because MCMC is conducive to hierarchical models
- Both “divide and conquer” big problems by splitting them into a series of smaller problems in the same way

# Outline

These notes cover Chapter 6

- Building a hierarchical model through layes
- Directed acyclic graphs
- Several examples

# Hierarchical models

Often Bayesian models can we written in the following layers of the hierarchy

1. **Data layer**: $[\mathbf{Y}|\theta, \alpha]$ is the likelihood for the observed data **Y** given the model parameters

2. **Process layer**: $[\theta|\alpha]$ is the model for the parameters $\theta$ that define the latent data generating process

3. **Prior layer**: $[\alpha]$ prior for hyperparameters

# Epidemiology example - Data layer

- Let $S_t$ and $I_t$ be the number of susceptible and infected individuals in a population, respectively, at time $t$
- The data $Y_t$ is the number of observed cases at time $t$
- The data layer models our ability to measure the process $I_t$
- **Data layer**: $Y_t | I_t \sim \text{Binomial}(I_t, p)$
- This assumes no false positives and false negative probability $p$

# Epidemiology example - Process layer

- Scientific understanding of the disease is used to model disease propagation
- We might select the simple Reed-Frost model

$$\textbf{Process layer}: \quad I_{t+1} \sim \text{Binomial}\left[S_t, 1-(1-q)^{I_t}\right]$$
$$S_{t+1} = S_t - I_{t+1}$$

- This assumes all infected individuals are removed from the population before the next time step
- Also that $q$ is the probability of a non-infected person coming into contact with and contracting the disease from an infected individual

# Epidemiology example - Prior layer

- The epidemiological process-layer model expresses the disease dynamics up to a few unknown parameters
- The Bayesian model is completed using priors, say,
- **Prior layer:**

$$\begin{aligned} I_1 &\sim \text{Poisson}(\lambda_1) \\ S_1 &\sim \text{Poisson}(\lambda_2) \\ p, q &\sim \text{beta}(a, b) \end{aligned}$$

# When to stop adding layers?

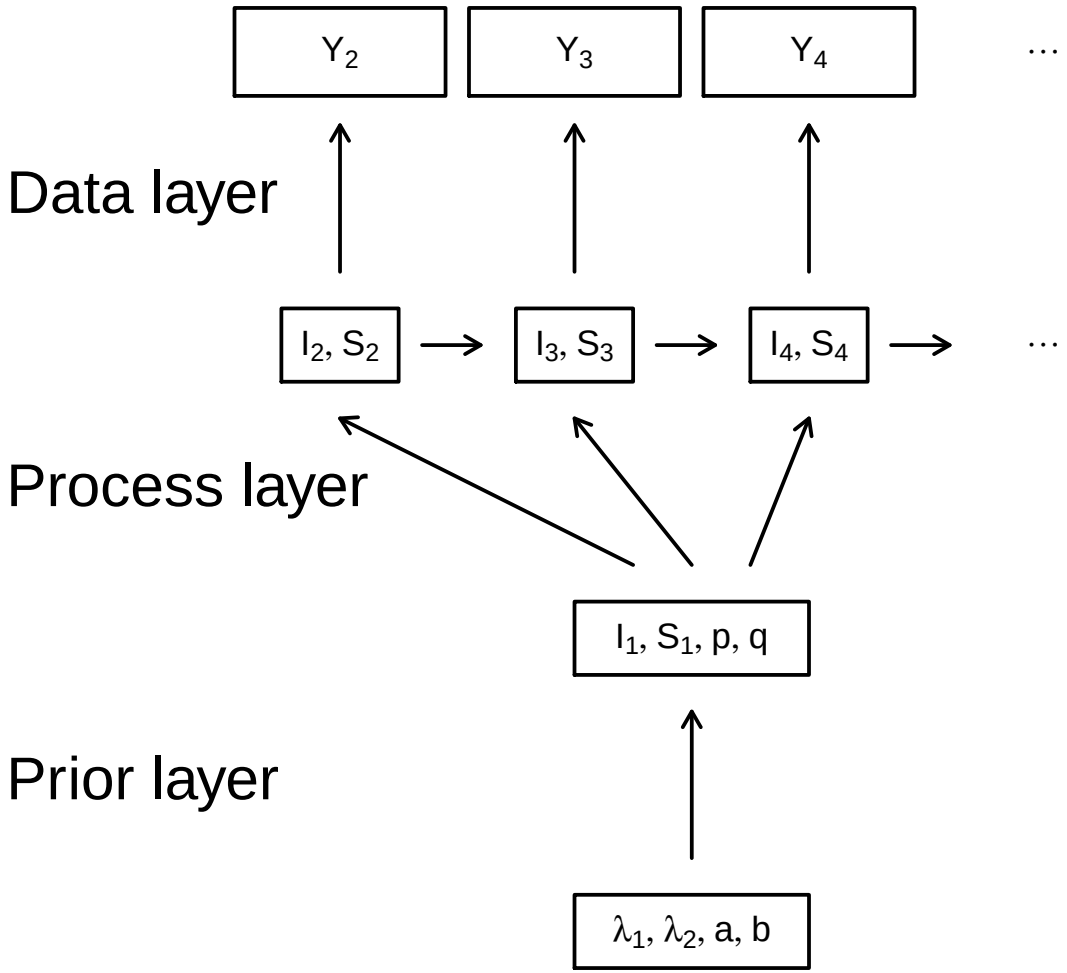
- In the previous example $a$, $b$, $\lambda_1$ and $\lambda_2$ are fixed
- But we will have uncertainty about the correct value
- Maybe replace a fixed value with another layer, say $a \sim \text{Uniform}(0, \theta)$?
- Then maybe $\theta \sim \text{Exponential}(\xi)$, $\xi \sim \text{Uniform}(0, \eta)$, etc.
- Rule of thumb: Be careful assigning priors to parameters in layers without replication.
- For example, even if we knew $p$ exactly this would be just one value and we couldn't hope to estimate the parameters of its beta distribution.

# Directed acyclic graphs (DAGs)

- A DAG is a graphical representation of a hierarchical model
- DAGS sometimes go by the name Bayesian networks
- Each observation and parameter is a node
- An arrow for $X$ to $Y$ means that the conditional distribution of $Y$ depends on $X$
- "Directed" means that arrows only go one way
- Acyclic means there are no cycles, e.g.,

$$X \to Y \to Z \to X$$

# Epidemiology example - DAG



# Directed acyclic graphs (DAGs)

- Building models this way ensures we will always have a valid joint distribution
- For example, say we need to specify the joint distribution of $(X, Y, Z)$
- Any joint distribution can be written as

$$f(X, Y, Z) = f(X)f(Y|X)f(Z|X, Y)$$

- This is a fully-connected DAG
- Ad-hoc constructions like

$$f(X, Y, Z) = f(X|Z)f(Y|X)f(Z|X, Y)$$

may or may not give a valid joint PDF

# Hierarchical models and MCMC

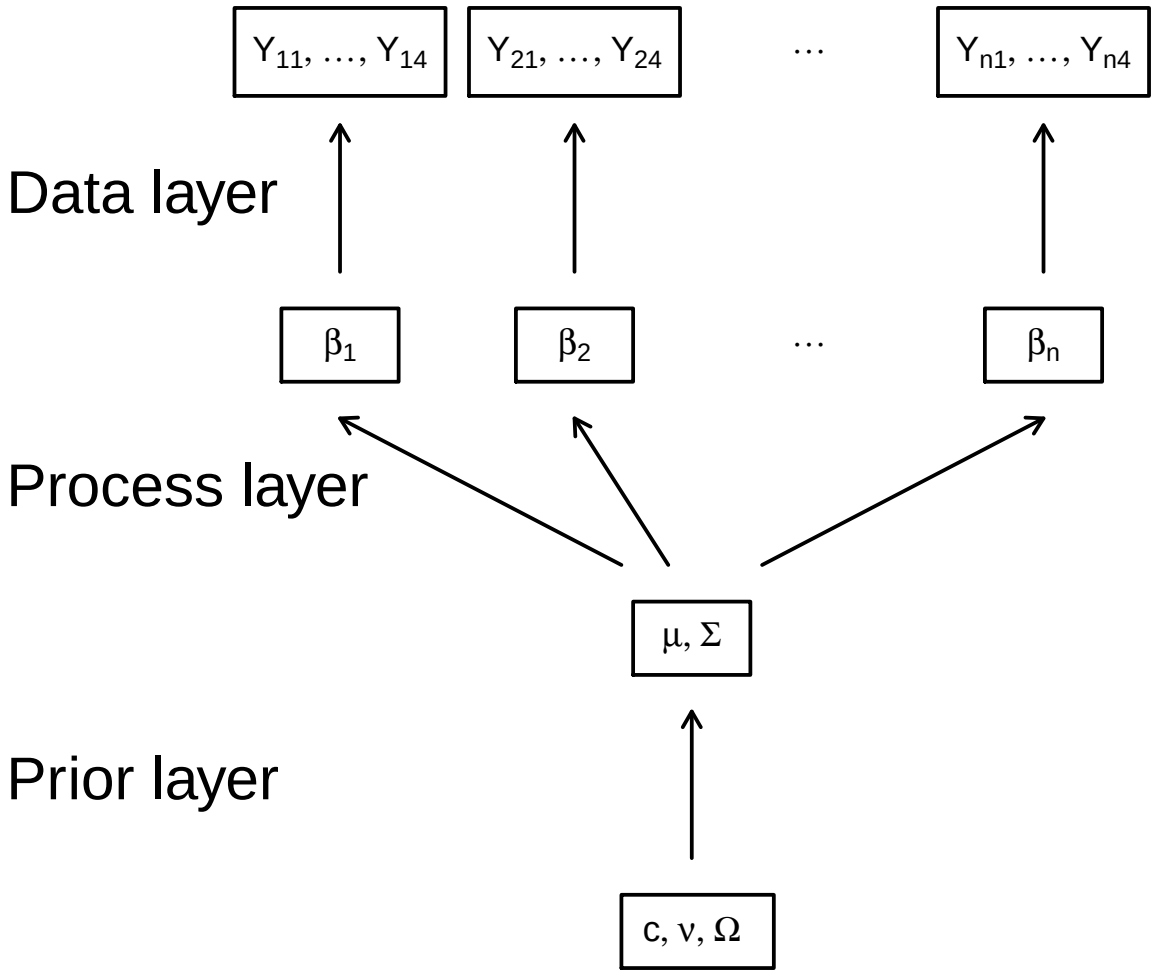
- Consider the classic one-way random effects model:

$$Y_{ij} \sim \mathrm{N}(\theta_i, \sigma^2) \quad \text{and} \quad \theta_i \sim N(\mu, \tau^2)$$

  where $Y_{ij}$ is the $j^{th}$ replicate for unit $i$ and $\boldsymbol{\alpha} = (\mu, \sigma^2, \tau^2)$ has an uninformative prior

- This hierarchy can be written using a directed acyclic graph

# Random effects example - DAG



# Hierarchical models and MCMC

- MCMC is efficient in this case even if the number of parameter or levels of the hierarchy is large
- You only need to consider "connected nodes" when you update each parameter
- 1. $[\theta_i|\cdot]$
  2. $[\mu|\cdot]$
  3. $[\sigma^2|\cdot]$
  4. $[\tau^2|\cdot]$
- Each of these updates is a draw from a standard one-dimensional normal or inverse gamma

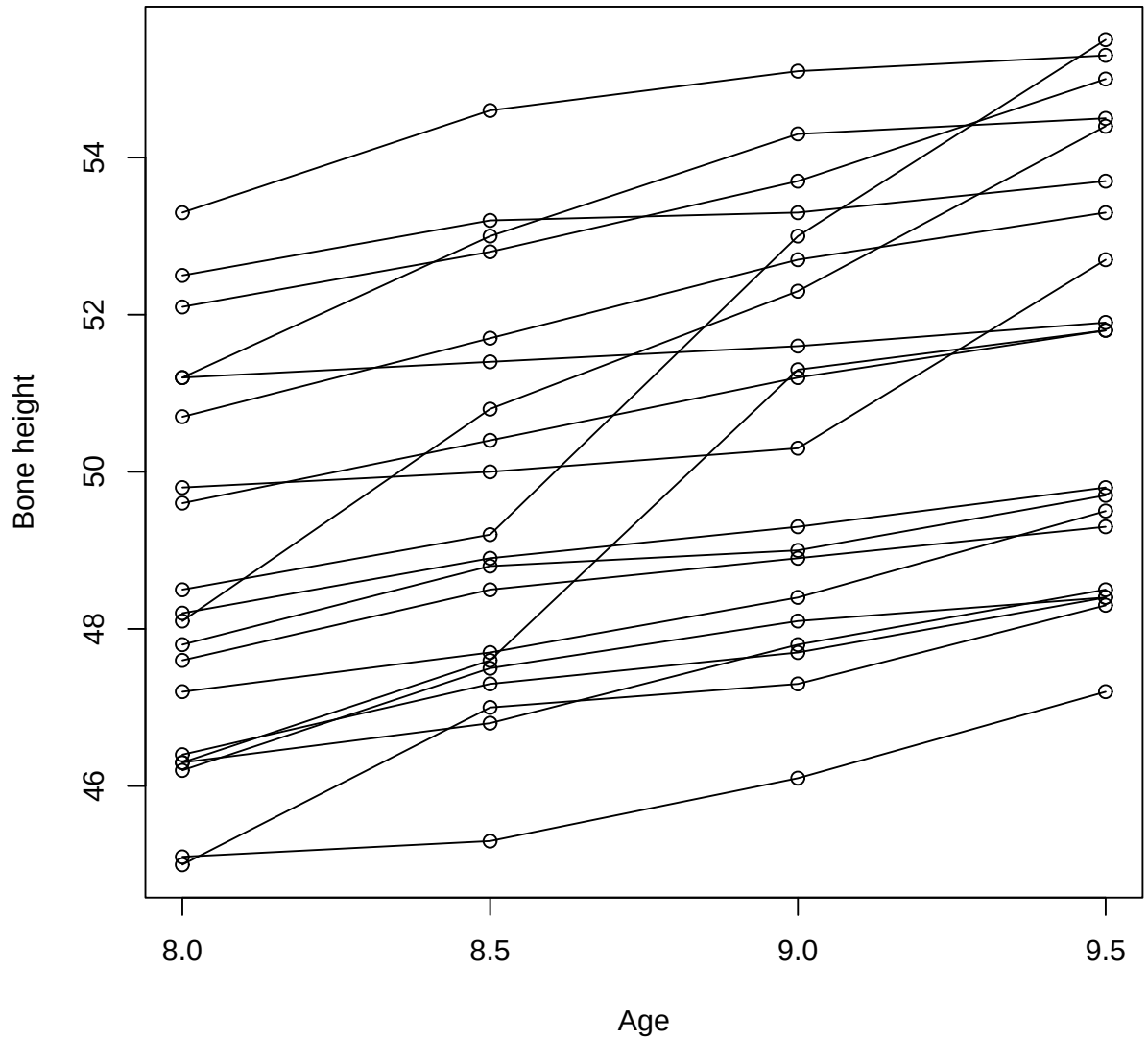
# Random slopes model

- Let $Y_{ij}$ be the $j^{th}$ observation for subject $i$
- As an example, consider the data plotted on the next slide were $Y_{ij}$ is the bone density for child $i$ at age $X_j$.
- Here we might specify a different regression for each child to capture variability over the population of children:

$$Y_{ij} \sim \text{Normal}(\gamma_{0i} + X_i\gamma_{1i}, \sigma^2)$$

- $\gamma_i = (\gamma_{i0}, \gamma_{i1})^T$ controls the growth curve for child $i$
- These separate regression are tied together in the prior, $\gamma_i \sim \text{Normal}(\beta, \Sigma)$, which borrows strength across children
- This is a linear mixed model: $\gamma_i$ are random effects specific to one child and $\beta$ are fixed effects common to all children

# Bone height data



# Draw a DAG and work out the full conditional for $\gamma_1$

# Missing data models

- We will deal with missing data in the linear regression context, but the ideas apply to all models

- The model is

$$Y_i \sim \text{Normal}(\beta_0 + \beta_1 X_{i1} + ... + \beta_p X_{ip}, \sigma^2)$$

- Often either $Y_i$ or elements $X_{ij}$ are missing

- We will study separately the case of missing responses and missing covariates

# Missing responses

- If the response is missing this is essentially a prediction problem
- We have seen how to handle this in JAGS
- We obtain samples from the PPD of $Y_i$
- At each MCMC iteration we simply draw

$$Y_i \sim \text{Normal}(\beta_0 + \beta_1 X_{i1} + ... + \beta_p X_{ip}, \sigma^2)$$

- This distribution accounts for random error as well as uncertainty in the model parameters
- For the other updates the data are essentially complete
- If only responses are missing, can we delete them for the purpose of estimating $\beta$?

# Missing covariates

- Now say all responses are observed, but a some covariates are missing
- The simplest approach is imputation, e.g., just plug in the sample mean of the covariate for the missing values
- This doesn't account for uncertainty in the imputations
- Bayesian methods handle this well using MCMC

# Missing covariates

- The main idea is to treat the missing values as unknown parameters in the Bayesian model
- Unknown parameters need priors, so missing $\mathbf{X}_i = (X_{i1}, ..., X_{ip})^T$ must have priors such as

$$\mathbf{X}_i \sim \text{Normal}(\mu_X, \Sigma_X)$$

- Assumptions about missing data:
  - Missing status is independent of $Y$ and $\mathbf{X}$
  - Covariates are Gaussian
- There are ways to relax both assumptions, but it becomes complicated

# Missing covariates

- Of course if the prior is way off, the results will be invalid
- For example, if in reality the data are not missing at random the Bayesian model will likely give bad results
- Example of non-random missingness:
- If specified correctly, the model will lead to inference for $\beta$ that properly accounts for uncertainty about the missing data

# Hierarchical linear regression model with missing data

- $Y_i|\mathbf{X}_i, \beta, \sigma^2 \sim \text{Normal}(\mathbf{X}_i^T\beta, \sigma^2)$
- $\mathbf{X}_i|\mathbf{mu}, \Sigma \sim \text{Normal}(\mathbf{mu}, \Sigma)$
- $p(\beta) \propto 1$
- $\sigma^2 \sim \text{InvG}(0.01, 0.01)$
- $\mu \sim \text{Normal}(0, 100^2 I_p)$
- $\Sigma \sim \text{InvWishart}(0.01, 0.01 I_p)$

If some observations have missing $Y$ and some have missing $X$, can we delete those with missing $Y$? Can we delete those with missing $X$?

# Overview of the Gibbs sampling algorithm

- The full conditional of missing $Y_i$ is:
- The full conditional of missing $X_i$ is:
- In fact, all the full conditionals are conjugate

# Worked examples

The course website includes three complete data analyses of hierarchical models

- Missing data analysis of 2016 Boston marathon data
- Analysis of tyrannosaurid growth curves
- Species distribution mapping via data fusion