In many situations, there will be data from several/many subpopulations or groups.

Rather than performing separate analyses for each group, it may make good sense to assume that there is some relationship between the parameters of different groups. That is, introduce a higher level of randomness on the parameters.

This is a meta-analysis approach, and is a particularly effective approach when the information from each sub-population is limited.

Hierarchical modeling also includes mixed-effects models, variance component models and continuous mixture models.

The frequentist application of meta-analysis is often mis-called empirical Bayes modeling.
Meta-analysis Example 1


They fitted the Ricker stock-recruit curve

\[ R_t = \alpha S_t e^{-\beta S_t} \]

In the case of a semelparous species, \( \alpha \) is the maximum population reproductive rate.

Lognormal error on \( R_t \) was assumed. That is

\[ y_t = \log\left(\frac{R_t}{S_t}\right) = \log(\alpha) - \beta S_t + \epsilon_t \]

where \( \epsilon_t \) are iid \( N(0,\sigma^2) \).

Letting \( i \) index the sub-populations, our notation is

\[ y_{i,t} = \log\left(\frac{R_{i,t}}{S_{i,t}}\right) = \log(\alpha_i) - \beta_i S_{i,t} + \epsilon_{i,t} \]

where \( \epsilon_{i,t} \) are iid \( N(0,\sigma_i^2) \).
Meta-analysis Example 1, ctd...

Myers et al. assumed that $\alpha_i$’s were log-normally distributed across the different sub-populations of each species.

That is, for sub-population $i$

$$\log \alpha_i \sim N(\mu, \tau^2)$$

No relationship between $\beta_i$’s was assumed.

The hierarchical model requires hyper-priors on parameters $\mu$ and $\tau^2$.

What would be a good choice for the hyper-priors?

The reference hyper-priors for hierarchical models (Gelman, 2005) are

$$\mu \sim \text{Unif}(-\infty, \infty)$$
$$\tau \sim \text{Unif}(0, \infty)$$

That is, the prior $\pi(\mu, \tau)$ is flat.

Previously, the prior $\pi(\tau) = 1/\tau$ had been used extensively in hierarchical models. However, Gelman (2005) showed this to have undesirable properties.

The WinBUGS 1.4.1 patch modified the hierarchical model examples to use Gelman’s hyper-priors.
Meta-analysis Example 1, ctd...

We will fit a Bayesian version of this model to Chinook salmon data, using WinBUGS.

Note that the model also requires priors for each of the $\beta_i$ and $\sigma_i$ parameters.

The full prior specification used is:

$$
\mu \sim \text{Unif} (-\infty, \infty)
$$

$$
\tau \sim \text{Unif} (0, \infty)
$$

$$
\beta_i \sim \text{Unif} (-\infty, \infty)
$$

$$
\log(\sigma_i) \sim \text{Unif} (-\infty, \infty)
$$

Meta-analysis Example 2

Millar and Methot (2002) implemented a hierarchical model for the bulk catchability, $Q$, of U.S. West Coast rockfish ($Sebastes$ spp.)

$$
q_i = \log(Q_i) \sim N(\mu_q, \sigma_q^2)
$$

where vaguely informative hyper-priors were placed on $\mu_q$ and $\sigma_q^2$.

The model was fitted using Automatic Differentiation Model Builder (ADMB).
In the previous two examples, the meta-analysis was applied to “raw” data from each of the sub-populations:
- Chinook stock-recruit data in Example 1
- Rockfish CPUE in Example 2

In this third example (Gelman et al. 2003), the sub-population data have already been (individually) analyzed, resulting in a table of point estimates and associated std errors.
**Meta-analysis Example 3**

The estimate, $y_i$, is a measure of the effectiveness of special coaching programs on SAT test scores.

The question of interest is whether the coaching programs increase SAT score.

<table>
<thead>
<tr>
<th>school</th>
<th>estimate</th>
<th>sd</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>A</td>
<td>28.39</td>
</tr>
<tr>
<td>2</td>
<td>B</td>
<td>7.94</td>
</tr>
<tr>
<td>3</td>
<td>C</td>
<td>-2.75</td>
</tr>
<tr>
<td>4</td>
<td>D</td>
<td>6.82</td>
</tr>
<tr>
<td>5</td>
<td>E</td>
<td>-0.64</td>
</tr>
<tr>
<td>6</td>
<td>F</td>
<td>0.63</td>
</tr>
<tr>
<td>7</td>
<td>G</td>
<td>18.01</td>
</tr>
<tr>
<td>8</td>
<td>H</td>
<td>12.16</td>
</tr>
</tbody>
</table>

To keep things simple, it will be assumed that the estimated std errors are the true std deviations of the estimates. (We could try relaxing this assumption later.)

So, we have 

$$y_i \sim N(\mu_i, \sigma_i^2)$$

where $\sigma_i$ are assumed known.

The hierarchical bit is 

$$\mu_i \sim N(\nu, \tau^2)$$

with flat priors on $\nu$ and $\tau$. 
Exchangeability

Exchangeability is the assumption that (a subset of) the subpopulation parameters can be assumed to be a random sample from a higher-level distribution.

Care must be taken to ensure that exchangeability is a reasonable assumption. E.g.,

- In the stock-recruit meta-analysis, it may be reasonable to assume that the $\alpha_i$ (the maximum population reproductive rates) are exchangeable for a common species.

- However, would it be reasonable to assume that the $\beta_i$ were exchangeable?