



Hierarchical Models

Where We Are

- We now know how to carry out a Bayesian analysis for simple models.
 - t-tests
 - regression
 - use MCMC
- But most real problems are more complicated
- Now we find out how to deal with a lot of them!

A Problem

- How big are Swedish frogs?
 - and how does the size vary?
- Variation at several levels
 - between individuals
 - between populations (i.e. ponds)
 - between regions
- Firstly, look at the population and individual levels
 - sample several frogs from different ponds

How to Model

- We want to model the variation between individuals and between ponds
- Treat the pond mean as coming from a random distribution
 - e.g. Normal
 - Random effect
- Quantify the amount of variation

The Model

- Individual i from pond j
- x_{ij} – Size (“Snout Ventral Length”)

$$x_{ij} \sim N(\mu_j, \tau)$$

- Common variance
- Means differ between ponds
- Model this as a Normal distribution:

- $\mu_j \sim N(\mu_0, \tau_0)$

Something Interesting

- For the pond means, we have this:

$$\mu_j \sim N(\mu_0, \tau_0)$$

- If we knew the means, this would be a normal inference
 - treating the μ_j s as data
- We don't know them, but we estimate them:

$$x_{ij} \sim N(\mu_j, \tau)$$

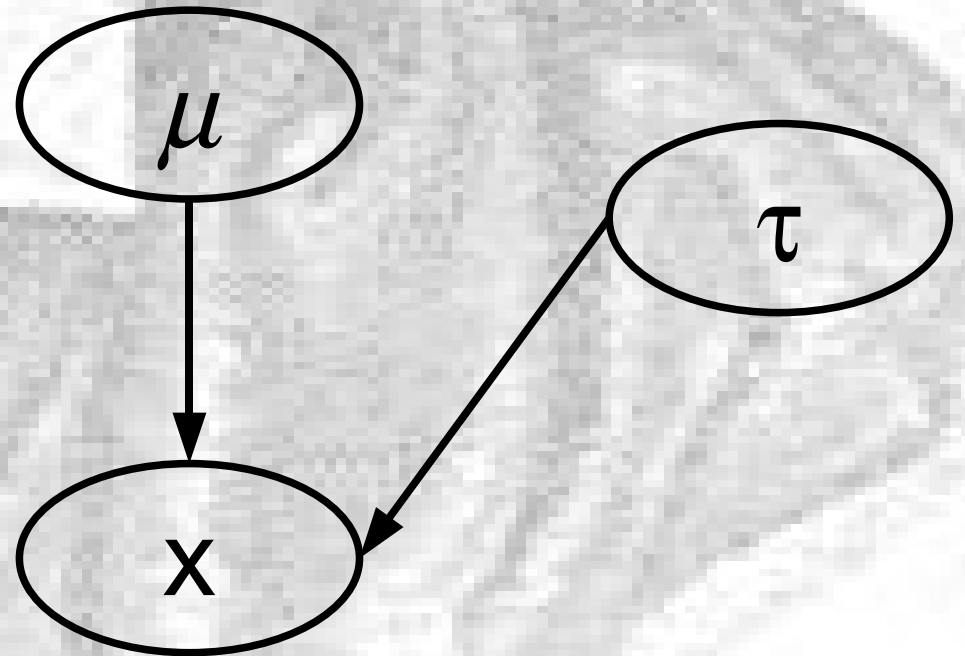
- The posterior for μ_0 and τ is then integrated over the uncertainty in the μ_i 's

DAGs

- DAGs are very convenient ways of drawing hierarchical models

$$x \sim N(\mu, \tau)$$

Parent of x



Child of μ and τ

Priors

- For the data (x_{ij}), we can view the distribution of μ_i as the prior for its mean
- So x_{ij} only depends on μ_0 and τ through μ_i
- This makes things easier
 - we can follow the dependencies more easily
- This is a simple hierarchical model

Hierarchical Models

- The essence of a hierarchical model is that the dependencies between variables can be defined easily
- Variables only depend on those below them
 - through the likelihood
- And those above them
 - through the prior
- This gives us a nice way of describing our models

The Maths

- The full probability model can be worked out from the graph:
- If v is a stochastic node
 - i.e. an oval
- and V is the set of all nodes
 - i.e. all stochastic parts of the model
- Then $P(V)$ is the probability density for the model, and:

$$Pr(V) = \prod_{V \in V} P(v | Parents[v])$$

The Bayesian Bit

$$Pr(V) = \prod_{V \in \mathcal{V}} P(v | Parents[v])$$

- For Bayesian analysis, v is a parameter, so $P(v)$ is the posterior distribution

- As we all know:

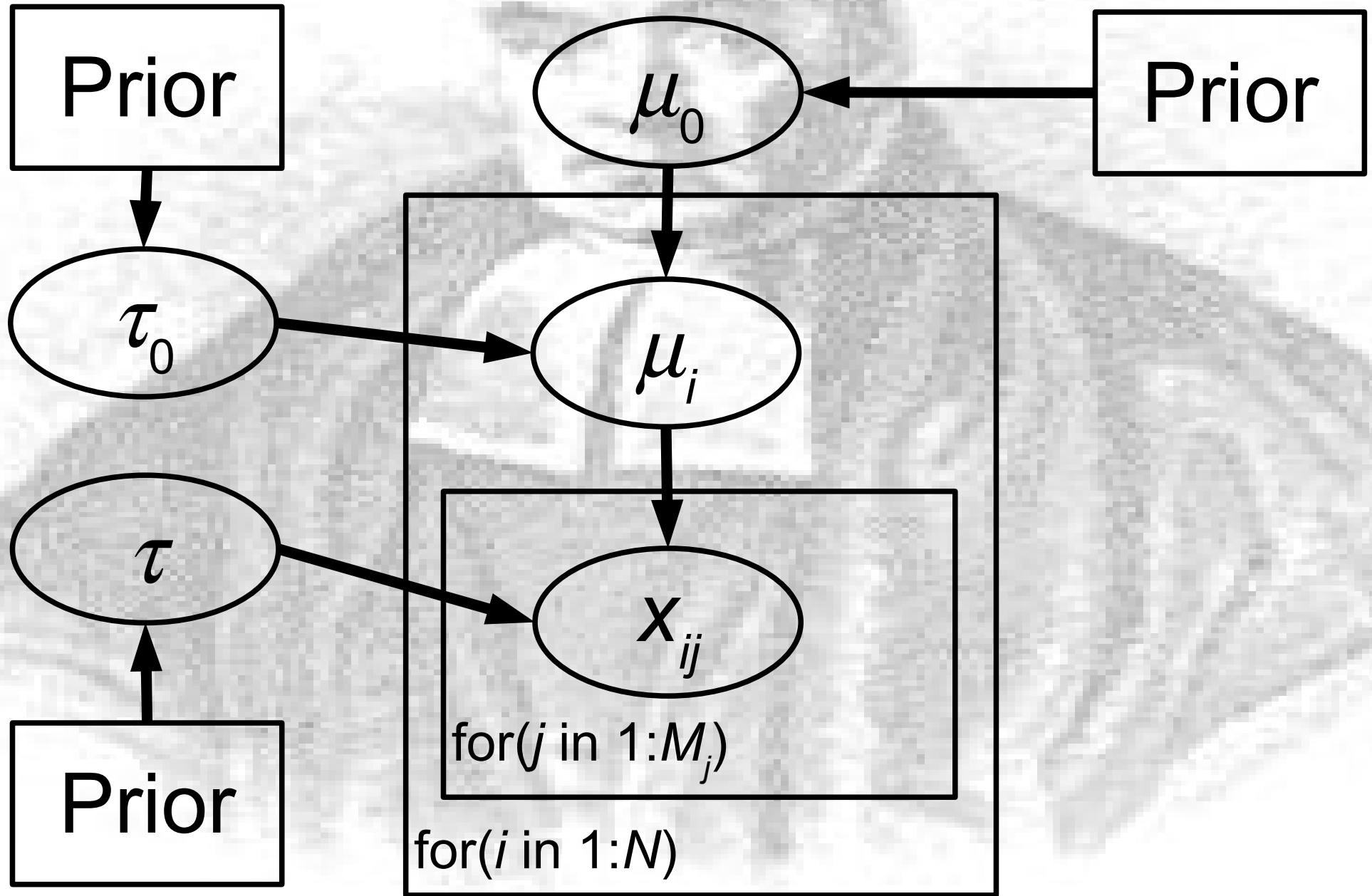
$$P(\theta | X) \propto P(X | \theta) P(\theta)$$

- So, $P(v)$ depends on its parents...
 - through $P(\theta)$
- ... and its children
 - through $P(X | \theta)$

Fitting the Model

- We can calculate $P(v)$ [= $P(\theta|X)$] conditionally on its parents and children
- Given these, it is independent of the rest of the model
- Therefore, we can use a Gibbs sampler to estimate the parameters
 - Gibbs sample = cunning MCMC method

Frogs: The Model



Summarising the Results

- We can summarise the amount of variation that is regional by the proportion of total variation due to the region = ρ :

$$\rho = \frac{1/\tau}{1/\tau + 1/\tau_0}$$

– “intra-class correlation”

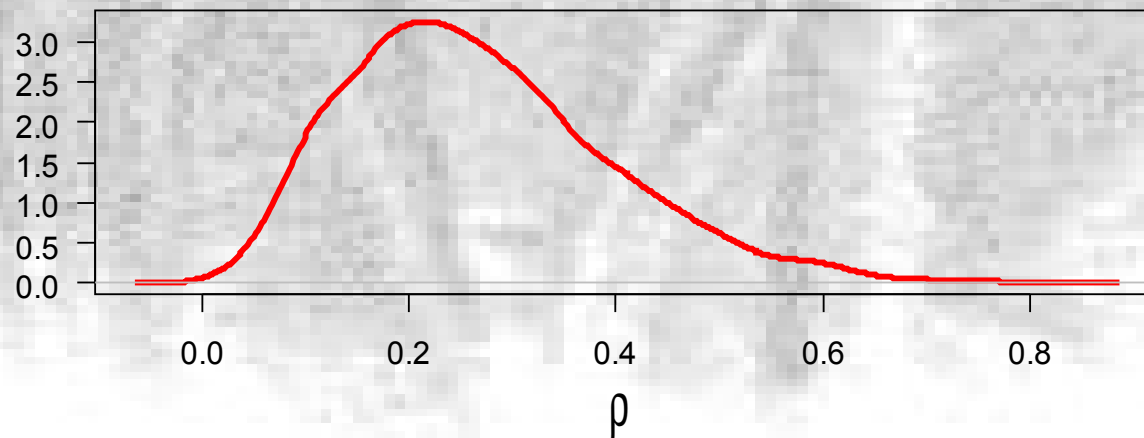
- To calculate this we use each draw from the posterior for τ and τ_0 and calculate it from this...

The Estimation

- If we have τ and τ_0 , we calculate ρ :

τ	τ_0	ρ
1.380	4.347	0.241
1.748	3.421	0.338
1.842	1.939	0.487
1.598	3.429	0.318
1.947	3.084	0.387

- And this gives the correct posterior:



More Models

- The response does not have to be normally distributed
- Some alternatives:
 - Binomial
 - Poisson
 - Negative Binomial
 - Gamma
- Likelihood different, but use same approach
 - extend generalised linear models

Frog Survival

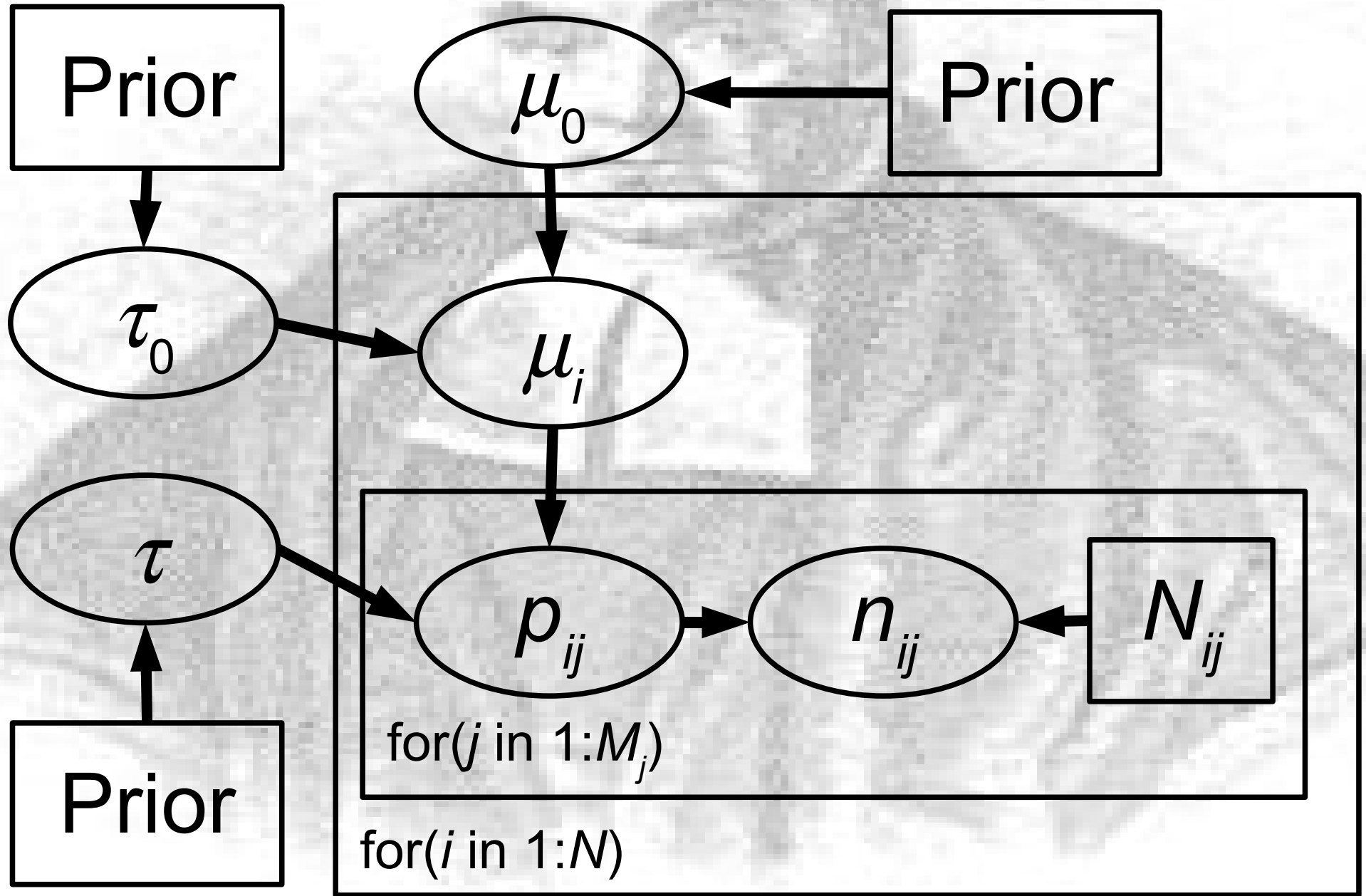
- Rather than look at size, we can look at survival of offspring
- Treat this as a trait, like size
 - each offspring has a probability p of surviving
- Of N_{ij} offspring from individual i , from population j , n_{ij} survive

$$n_{ij} \sim \text{Bin}(N_{ij}, p_{ij})$$

- Then model logit p_{ij} :

$$\text{logit}(p_{ij}) \sim \text{N}(\mu_i, \tau)$$

Frog Survival



Quantitative Genetics

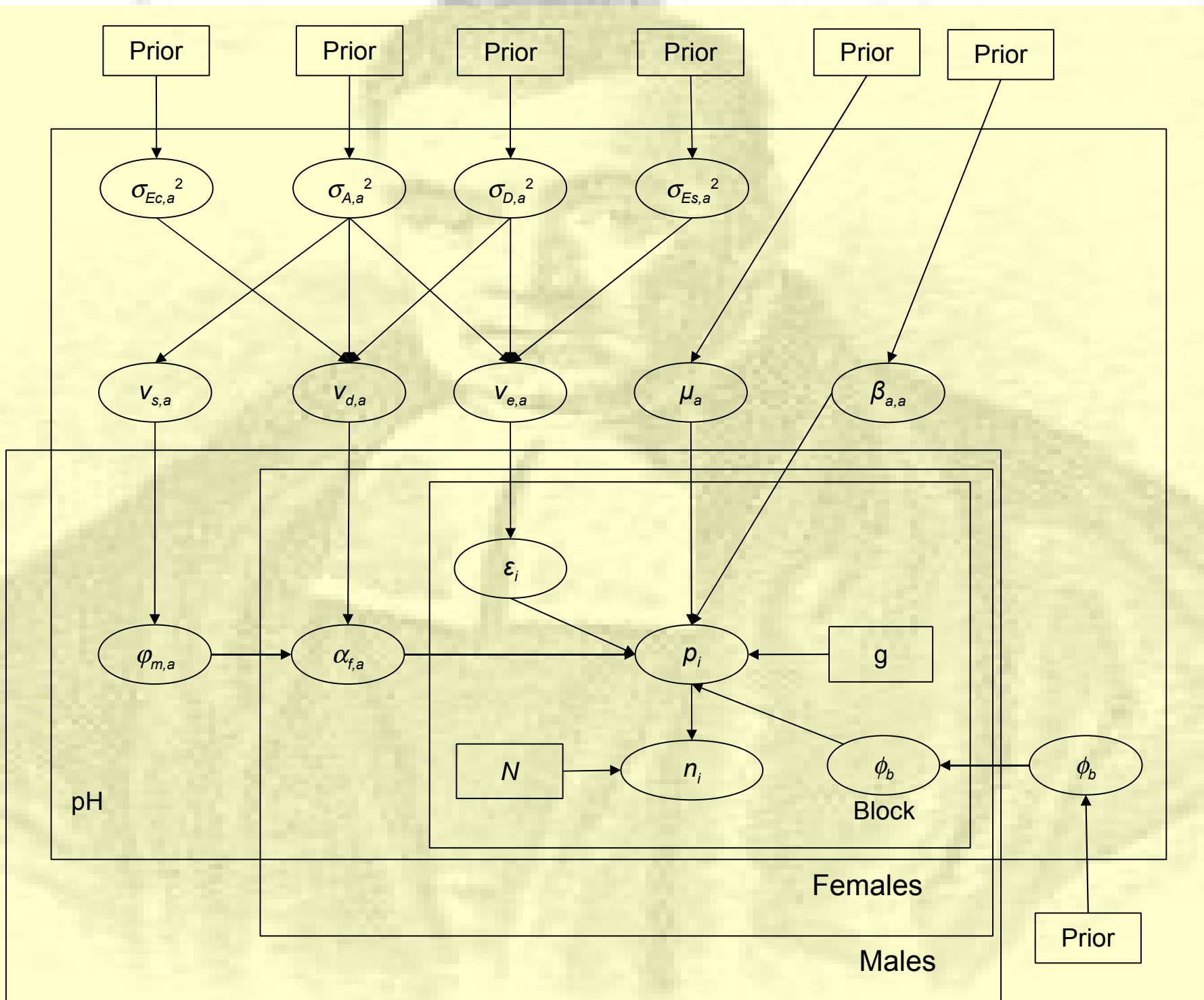
- Interested in genetics of variation in traits
- Set up crosses, look at offspring
- Partition variation into different components
 - Genetic (additive, dominance)
 - Maternal
 - Environmental
- Traditionally calculate by subtraction
- Bayesian approach: use all the information

The Model

- The trait has a value η_i for individual i
 - trait either measured, e.g. size
 - or latent, e.g. probability of surviving
- Look at variation between crosses
- Partition the total variation into variation
 - between female parents
 - between male parents
 - between full sibs

Genetics Variances

- Each component of experimental variation is a sum of causal components
 - e.g. Sire = Additive/4
 - Dam = Additive/4 + Dominance/4 + Maternal
- We then put priors on Additive etc.
- Use all of the information
 - variation in posterior correct
- And now – the full model



The Message

- Hierarchical models can get complicated
- We can keep control with the DAG
 - still able to fit them to the data
- Great flexibility available
- When do we stop adding to the model?
 - when we can no longer interpret the results
 - when the data is not rich enough
 - e.g. too few values