Bayesian Hierarchical Modeling

1: Hierarchical Models for Meta-Analysis

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Hierarchical Models for Combining Information

Formulating hierarchical models for quantitative outcomes from scientific context

Case Study: *Meta-analysis of effects of* **aspirin** *on heart attacks*. Table 5.1 (Draper et al., 1993a) gives the number of patients and **mortality rate** from all causes, for six **randomized controlled experiments** comparing the use of aspirin and placebo by patients following a heart attack.

Table 5.1. Aspirin meta-analysis data.

	Aspirin		Placebo	
Study (i)	# of Patients	Mortality Rate (%)	# of Patients	Mortality Rate (%)
UK-1	615	7.97	624	10.74
CDPA	758	5.80	771	8.30
GAMS	317	8.52	309	10.36
UK-2	832	12.26	850	14.82
PARIS	810	10.49	406	12.81
AMIS	2267	10.85	2257	9.70
Total	5599	9.88	5217	10.73

	Comparison			
Study (i)	$y_i =$ Diff (%)	$\sqrt{V_i} =$ SE of Diff (%)	$Z_i^{\ddagger}$	$p_i^{\S}$
UK-1	2.77	1.65	1.68	.047
CDPA	2.50	1.31	1.91	.028
GAMS	1.84	2.34	0.79	.216
UK-2	2.56	1.67	1.54	.062
PARIS	2.31	1.98	1.17	.129
AMIS	−1.15	0.90	−1.27	.898
Total	0.86	0.59	1.47	.072

$^{\ddagger}Z_i$ denotes the ratio of the difference in mortality rates over its standard error, assuming a binomial distribution. $^{\S}p_i$ is the one-sided p value associated with Z_i, using the normal approximation.

Meta-Analysis

The first five trials are reasonably consistent in showing a (weighted average) **mortality decline** for aspirin patients of 2.3 percentage points, a **20% drop** from the (weighted average) placebo mortality of 11.5% (this difference is **highly clinically significant**).

However, the sixth and largest trial, AMIS, went the other way: an **increase** of 1.2 percentage points in aspirin mortality (a 12% rise from the placebo baseline of 9.7%).

Some **relevant questions** (Draper, 1995):

$\boxed{\mathbf{Q}_1}$ Why did AMIS get such **different results**?

$\boxed{\mathbf{Q}_2}$ What should be done next to **reduce the uncertainty** about Q_1?

$\boxed{\mathbf{Q}_3}$ If you were a doctor treating a patient like those eligible for the trials in Table 5.1, **what therapy should you employ** while answers to Q_1 and Q_2 are sought?

One possible **paraphrase** of Q_3: $\boxed{\mathbf{Q}_4}$ How should the information from these six experiments be **combined** to produce a **more informative summary** than those obtained from each experiment by itself?

The discipline of **meta-analysis** is devoted to answering questions like Q_4.

One leading school of **frequentist meta-analysis** (e.g., Hedges and Olkin, 1985) looks for methods for combining the Z and p values in Table 5.1, an approach that often leads only to an overall p value.

A Gaussian HM

A **more satisfying** form of meta-analysis (which has both frequentist and Bayesian versions) builds a **hierarchical model (HM)** that indicates how to combine information from the mortality differences in the table.

A **Gaussian meta-analysis model** for the aspirin data, for example (Draper et al., 1993a), might look like

$$\begin{array}{rcll} (\mu, \sigma^2) & \sim & p(\mu, \sigma^2) & \text{(prior)} \\ (\theta_i | \mu, \sigma^2) & \overset{\text{IID}}{\sim} & N(\mu, \sigma^2) & \text{(underlying effects)} \\ (y_i | \theta_i) & \overset{\text{indep}}{\sim} & N(\theta_i, V_i) & \text{(data)} \ . \end{array} \qquad (1)$$

The bottom level of (1), the **data** level of the HM, says that—because of relevant differences in patient cohorts and treatment protocols—each study has its own **underlying treatment effect** θ_i, and the observed mortality differences y_i are like random draws from a normal distribution with mean θ_i and variance V_i (the normality is reasonable because of the **Central Limit Theorem**, given the large numbers of patients).

In meta-analyses of data like those in Table 5.1 the V_i are typically taken to be **known** (again because the patient sample sizes are so big), $V_i = SE_i^2$, where SE_i is the standard error of the mortality difference for study i in Table 5.1.

The middle level of the HM is where you would bring in the **study-level covariates**, if you have any, to try to explain why the studies differ in their underlying effects.

Here there are no study-level covariates, so the middle level of (1) is equivalent to a **Gaussian regression with no predictor variables**.

A Gaussian HM (continued)

Why the "error" distribution should be **Gaussian** at this level of the HM is not clear—it's a **conventional** option, not a choice that's automatically scientifically reasonable (in fact I'll challenge it later).

σ^2 in this model represents **study-level heterogeneity**.

The top level of (1) is where the **prior** distribution on the regression parameters from the middle level is specified.

Here, with only an intercept term in the regression model, a popular **conventional choice** is the normal/scaled-inverse-χ^2 prior we looked at earlier in our first Gaussian case study.

Fixed effects and random effects. If σ^2 were known somehow to be 0, all of the θ_i would have to be equal **deterministically** to a common value μ, yielding a simpler model: $(y_i|\mu) \overset{\text{indep}}{\sim} N(\mu, V_i)\,, \mu \sim p(\mu)$.

Meta-analysts call this a **fixed-effects** model, and refer to model (1) as a **random-effects** model.

When σ^2 is not assumed to be 0, with this terminology the θ_i are called **random effects** (this parallels the use of this term in the **random-effects Poisson regression** case study).

Approximate Fitting of Gaussian Hierarchical Models: Maximum Likelihood and Empirical Bayes

Fitting HM (1). Some algebra based on model (1) yields that the conditional distributions of the study-level effects θ_i given the data and the parameters (μ, σ^2), have a **simple and revealing form** (I'll show this later):

$$\left(\theta_i | y_i, \mu, \sigma^2\right) \overset{\text{indep}}{\sim} N[\theta_i^*, V_i(1 - B_i)], \tag{2}$$

$$\text{with} \quad \theta_i^* = (1 - B_i)\, y_i + B_i\, \mu \quad \text{and} \quad B_i = \frac{V_i}{V_i + \sigma^2}. \tag{3}$$

In other words, the conditional mean of the effect for study i given y_i, μ, and σ^2 is a **weighted average** of the sample mean for that study, y_i, and the overall mean μ.

The weights are given by the so-called **shrinkage factors** B_i (e.g., Draper et al., 1993a), which in turn depend on how the variability V_i **within study** i compares to the **between-study** variability σ^2: the more accurately y_i estimates θ_i, the more weight the "local" estimate y_i gets in the weighted average.

The term **shrinkage** refers to the fact that, with this approach, unusually high or low individual studies are **drawn back** or "shrunken" toward the overall mean μ when making the calculation $(1 - B_i)\, y_i + B_i\, \mu$.

Note that θ_i^* uses data from all the studies to estimate the effect for study i—this is referred to as **borrowing strength** in the estimation process.

Closed-form expressions for $p(\mu|y)$ and $p(\theta_i|y)$ with $y = (y_1, \ldots, y_k), k = 6$ are not available even with a normal-χ^{-2} prior for (μ, σ^2); **MCMC** is needed (see below).

Maximum Likelihood and Empirical Bayes

In the meantime **maximum likelihood** calculations provide some idea of what to expect: the likelihood function based on model (1) is

$$l\left(\mu, \sigma^2 | y\right) = c \left[\prod_{i=1}^{k} \frac{1}{\sqrt{V_i + \sigma^2}}\right] \exp\left[-\frac{1}{2}\sum_{i=1}^{k} \frac{(y_i - \mu)^2}{V_i + \sigma^2}\right]. \qquad (4)$$

The maximum likelihood estimates (MLEs) $\left(\widehat{\mu}, \widehat{\sigma}^2\right)$ then turn out to be the **iterative** solutions to the following equations:

$$\widehat{\mu} = \frac{\sum_{i=1}^{k} \widehat{W}_i \, y_i}{\sum_{i=1}^{k} \widehat{W}_i} \quad \text{and} \quad \widehat{\sigma}^2 = \frac{\sum_{i=1}^{k} \widehat{W}_i^2 \left[(y_i - \widehat{\mu})^2 - V_i\right]}{\sum_{i=1}^{k} \widehat{W}_i^2}, \qquad (5)$$

$$\text{where} \quad \widehat{W}_i = \frac{1}{V_i + \widehat{\sigma}^2}. \qquad (6)$$

Start with $\widehat{\sigma}^2 = 0$ and **iterate (5–6) to convergence** (if $\widehat{\sigma}^2$ converges to a negative value, $\widehat{\sigma}^2 = 0$ is the MLE); the MLEs of the θ_i are then given by

$$\widehat{\theta}_i = \left(1 - \widehat{B}_i\right) y_i + \widehat{B}_i \, \widehat{\mu} \quad \text{where} \quad \widehat{B}_i = \frac{V_i}{V_i + \widehat{\sigma}^2}. \qquad (7)$$

These are called **empirical Bayes** (EB) estimates of the study-level effects, because it turns out that this analysis approximates a fully Bayesian solution by (in effect) using the data to **estimate** the prior specifications for μ and σ^2.

Large-sample (mainly meaning large k) approximations to the (frequentist) distributions of the MLEs are given by

$$\widehat{\mu} \sim N\left(\mu, \left[\sum_{i=1}^{k} \frac{1}{V_i + \widehat{\sigma}^2}\right]^{-1}\right) \quad \text{and} \quad \widehat{\theta}_i \sim N\left[\theta_i, V_i\left(1 - \widehat{B}_i\right)\right]. \qquad (8)$$

MLEB (continued)

NB The variances in (8) **don't account fully for the uncertainty in** σ^2 and therefore underestimate the actual sampling variances for small k (adjustments are available; see, e.g., Morris (1983, 1988)).

MLEB estimation can be **implemented** simply in about 15 lines of `R` code (Table 5.2).

Table 5.2. `R` program to perform MLEB calculations.

```
mleb <- function( y, V, m ) {
  sigma2 <- 0.0
  for ( i in 1:m ) {
    W <- 1.0 / ( V + sigma2 )
    theta <- sum( W * y ) / sum( W )
    sigma2 <- sum( W^2 * ( ( y - theta )^2 - V ) ) / sum( W^2 )
    B <- V / ( V + sigma2 )
    effects <- ( 1 - B ) * y + B * theta
    se.theta <- 1.0 / sqrt( sum( 1.0 / ( V + sigma2 ) ) )
    se.effects <- sqrt( V * ( 1.0 - B ) )
    print( c( i, theta, se.theta, sigma2 ) )
    print( cbind( W, ( W / sum( W ) ), B, y, effects, se.effects ) )
  }
}
```

With the aspirin data it takes **18 iterations** (less than 0.1 second on a 400MHz `UltraSPARC` Unix machine) to get convergence to **4-digit accuracy**, leading to the summaries in Table 5.3 and the following estimates (standard errors in parentheses):

$$\widehat{\mu} = 1.45 \ (0.809), \quad \widehat{\sigma}^2 = 1.53.$$

Table 5.3. Maximum likelihood empirical Bayes meta-analysis of the aspirin data.

study(i)	$\widehat{W}_i$	normalized $\widehat{W}_i$	$\widehat{B}_i$	y_i	$\widehat{\theta}_i$	$\widehat{SE}\left(\widehat{\theta}_i\right)$
1	0.235	0.154	0.640	2.77	1.92	0.990
2	0.308	0.202	0.529	2.50	1.94	0.899
3	0.143	0.0934	0.782	1.84	1.53	1.09
4	0.232	0.151	0.646	2.56	1.84	0.994
5	0.183	0.120	0.719	2.31	1.69	1.05
6	0.427	0.280	0.346	−1.15	−0.252	0.728

Aspirin Meta-Analysis: Conclusions

Note that (1) AMIS gets **much less weight** (normalized $\widehat{W}_i$) than would have been expected given its small V_i; (2) the **shrinkage factors** ($\widehat{B}_i$) are considerable, with AMIS shrunk almost all the way into positive territory (see Figure 5.1); (3) there is **considerable study-level heterogeneity** ($\widehat{\sigma} \doteq 1.24$ percentage points of mortality); and (4) the standard errors of the effects are by and large smaller than the $\sqrt{V_i}$ (from the **borrowing of strength**) but are still considerable.

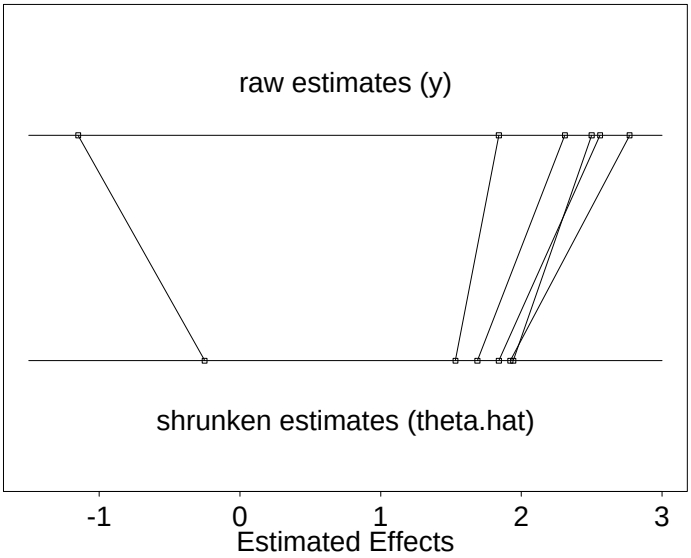


Figure 5.1. **Shrinkage plot** for the aspirin MLEB meta-analysis.

The **95% interval estimate** of μ, the overall underlying effect of aspirin on mortality, from this approach comes out

$$\widehat{\mu} \pm 1.96 \cdot \widehat{SE}(\widehat{\mu}) \doteq (-0.140, 3.03),$$

which if **interpreted Bayesianly** gives

$$\boxed{P(\text{aspirin reduces mortality}|\text{data}) \doteq 1 - \Phi\left(\tfrac{0-1.45}{0.809}\right) = \mathbf{0.96}},$$

where Φ is the **standard normal CDF**.

Thus although the interval includes 0, so that in a frequentist sense the effect is not statistically significant, **in fact from a Bayesian point of view the evidence is running strongly in favor of aspirin's usefulness**.

MCMC Details

In many cases (as with this example) empirical Bayes methods have the advantage of yielding **closed-form solutions**, but I view them at best as approximations to fully Bayesian analyses—which can in any case be carried out with MCMC—so I won't have any more to say about EB methods here (see Carlin and Louis, 1996, for more on this topic).

MCMC details. First let's derive that **likelihood function** I mentioned on page 7: the **model**, once again, is

$$\begin{array}{rcll} (\mu, \sigma^2) & \sim & p(\mu, \sigma^2) & \text{(prior)} \\ (\theta_i|\mu, \sigma^2) & \overset{\text{IID}}{\sim} & N(\mu, \sigma^2) & \text{(underlying effects)} \\ (y_i|\theta_i) & \overset{\text{indep}}{\sim} & N(\theta_i, V_i) & \text{(data)} \ . \end{array} \tag{9}$$

The **parameters** we're interested in here are (μ, σ^2); **Bayes's Theorem** gives (as usual)

$$p(\mu, \sigma^2|y) = c\, p(\mu, \sigma^2)\, p(y|\mu, \sigma^2), \tag{10}$$

so let's look at the **sampling distribution** for a single y_i:

$$\begin{aligned} p(y_i|\mu, \sigma^2) &= \int_{-\infty}^{\infty} p(y_i, \theta_i|\mu, \sigma^2)\, d\theta_i \\ &= \int_{-\infty}^{\infty} p(y_i|\theta_i, \mu, \sigma^2)\, p(\theta_i|\mu, \sigma^2)\, d\theta_i \qquad (11) \\ &= \int_{-\infty}^{\infty} p(y_i|\theta_i)\, p(\theta_i|\mu, \sigma^2)\, d\theta_i \end{aligned}$$

(what we're doing here is **integrating out** the **random effect** θ_i).

Now $p(y_i|\theta_i)$ is **normal** in this model, and $p(\theta_i|\mu, \sigma^2)$ is **also normal**; you could put in the **normal densities** and **grind away** at the **algebra** and **integration**, but there's a **better way**: the last line of (11) is a **mixture representation**, and a **normal mixture of normals is normal**, so I know that $p(y_i|\mu, \sigma^2)$ is **normal**, and the only questions are, what are its **mean** and **variance**?

Adam and Eve

These questions can be answered with **little difficulty** via the **Double Expectation Theorem**, which has **two parts** that are so **central** to **Bayesian calculations** that **Carl Morris** refers to them as **Adam** and **Eve**: for any two random variables X and Y,

$$\begin{array}{rcll} E(Y) & = & E_X\left[E(Y|X)\right] & \text{(Adam)} \\ V(Y) & = & E_X\left[V(Y|X)\right] + V_X\left[E(Y|X)\right] & \text{(Eve),} \end{array} \tag{12}$$

in which E_X and V_X refer to **expectation** and **variance** with respect to the **distribution** of X.

If there's **additional conditioning** going on, you just need to remember to **include it** in all the **relevant places**: for any three random variables X, Y and Z,

$$\begin{array}{rcl} E(Y|Z) & = & E_{(X|Z)}\left[E(Y|X,Z)\right] \\ V(Y|Z) & = & E_{(X|Z)}\left[V(Y|X,Z)\right] + V_{(X|Z)}\left[E(Y|X,Z)\right], \end{array} \tag{13}$$

and **so on**.

The application here is in **two parts** (Adam and Eve):

$$\begin{array}{rcl} E(y_i|\mu,\sigma^2) & = & E_{(\theta_i|\mu,\sigma^2)}\left[E(y_i|\mu,\sigma^2,\theta_i)\right] \\ & = & E_{(\theta_i|\mu,\sigma^2)}\left[E(y_i|\theta_i)\right] \\ & = & E_{(\theta_i|\mu,\sigma^2)}\left[\theta_i\right] \\ & = & \mu, \quad \text{and} \end{array}$$

$$\begin{array}{rcl} V(y_i|\mu,\sigma^2) & = & E_{(\theta_i|\mu,\sigma^2)}\left[V(y_i|\mu,\sigma^2,\theta_i)\right] + V_{(\theta_i|\mu,\sigma^2)}\left[E(y_i|\mu,\sigma^2,\theta_i)\right] \\ & = & E_{(\theta_i|\mu,\sigma^2)}\left[V(y_i|\theta_i)\right] + V_{(\theta_i|\mu,\sigma^2)}\left[E(y_i|\theta_i)\right] \\ & = & E_{(\theta_i|\mu,\sigma^2)}\left[V_i\right] + V_{(\theta_i|\mu,\sigma^2)}\left[\theta_i\right] \\ & = & V_i + \sigma^2. \end{array} \tag{14}$$

Direct Use of Gibbs Sampling

So (a) $(y_i|\mu,\sigma^2) \sim N(\mu, V_i+\sigma^2)$, (b) by **inspection** of the **form** of the **model**, the y_i are **independent** given (μ,σ^2), so

$$\begin{aligned} l(\mu,\sigma^2|y) &= c\,p(y|\mu,\sigma^2) = c\prod_{i=1}^{k} p(y_i|\mu,\sigma^2) \qquad (15)\\ &= c\left[\prod_{i=1}^{k}\frac{1}{\sqrt{V_i+\sigma^2}}\right]\exp\left[-\frac{1}{2}\sum_{i=1}^{k}\frac{(y_i-\mu)^2}{V_i+\sigma^2}\right], \end{aligned}$$

as **desired**.

MCMC: how best to sample from the posterior?

All **MCMC** (with a **parameter space** of **fixed dimension**) is one **special case** or another of the **Metropolis-Hastings** algorithm, but (as usual) we have a **number of possibilities**: **generic** (e.g., **random-walk**) **Metropolis?** Metropolis mixed with **Gibbs** steps? **All Gibbs?** With or without **auxiliary** (e.g., **latent**) **variables**? ...

First let's try **direct Gibbs**, for which we would need the **full conditionals**:

$$\begin{aligned} p(\mu|\sigma^2,y) &= c\,p(\mu,\sigma^2,y) \qquad (16)\\ &= c\,p(\mu,\sigma^2)\,p(y|\mu,\sigma^2). \end{aligned}$$

By virtue of **integrating out** the **random effects** above, we have $p(y|\mu,\sigma^2)$ as a **product** of **independent univariate Gaussians**; what shall we take for the **prior** $p(\mu,\sigma^2)$, given that there's no **conjugate choice**?

Even with **somewhat informative priors** on a **vector of parameters**, for **simplicity** people often assume **independence** of the **components** — in this case, $p(\mu,\sigma^2) = p(\mu)\,p(\sigma^2)$ — on the ground that whatever **correlation** the parameters should have in the **posterior** will be learned via the **likelihood function**; let's make this **simplifying assumption**; then

$$p(\mu|\sigma^2,y) = c\,p(\mu)\,p(\sigma^2)\,p(y|\mu,\sigma^2) = c\,p(\mu)\,p(y|\mu,\sigma^2). \qquad (17)$$

Direct Gibbs; Latent Gibbs

Now the **product of two Gaussians is Gaussian**, so if we take the **prior** for μ to be **Gaussian** we'll have a **Gaussian full conditional** for μ that'll be **easy to sample from**; what about σ^2?

$$\begin{aligned} p(\sigma^2|\mu, y) &= c\, p(\mu, \sigma^2, y) \\ &= c\, p(\mu, \sigma^2)\, p(y|\mu, \sigma^2) \\ &= c\, p(\mu)\, p(\sigma^2)\, p(y|\mu, \sigma^2) \\ &= c\, p(\sigma^2)\, p(y|\mu, \sigma^2). \end{aligned} \tag{18}$$

Here we run into **trouble**: when considered as a **function** of σ^2 for fixed μ and y, $p(y|\mu, \sigma^2)$ is **not recognizable** as a member of a **standard parametric family** (because the y_i (given μ and σ^2) are **independent** but **not identically distributed**); we could choose, e.g., a χ^{-2} prior on σ^2 and use **rejection sampling** to sample from the resulting **non-standard full conditional**, but that would not be especially **pleasant**.

So instead let's use a **trick** that's generally helpful in **random-effects** models: treat the **(latent) random effects** as **auxiliary variables** to be sampled along with (μ, σ^2).

In other words, letting $\theta = (\theta_1, \ldots, \theta_k)$, we're going to sample from the **augmented posterior** $p(\mu, \sigma^2, \theta|y)$; the hope is that this will have **completely tractable full conditionals**; let's see.

$$\begin{aligned} p(\mu|\sigma^2, \theta, y) &= c\, p(\mu, \sigma^2, \theta, y) \\ &= c\, p(\mu, \sigma^2)\, p(\theta|\mu, \sigma^2)\, p(y|\theta, \mu, \sigma^2) \end{aligned} \tag{19}$$

Notice how naturally this **factorization** matches the **hierarchical character** of (9), which starts at the **top** with a model for (μ, σ^2), and then builds a **model** for $(\theta|\mu, \sigma^2)$, and then at the **bottom** there's a model for $p(y|\theta, \mu, \sigma^2)$, which — by virtue of the **hierarchical** structure — can be **simplified** to $p(y|\theta)$.

Latent Gibbs (continued)

Since (a) we're **assuming** that $p(\mu, \sigma^2) = p(\mu)\, p(\sigma^2)$ and (b) $p(y|\theta)$ **doesn't involve** μ, the **full conditional** for μ becomes

$$p(\mu|\sigma^2, \theta, y) = c\, p(\mu)\, p(\theta|\mu, \sigma^2)\,; \tag{20}$$

with a **Gaussian** prior on μ this will be **Gaussian**; how about σ^2?

$$\begin{aligned} p(\sigma^2|\mu, \theta, y) &= c\, p(\mu, \sigma^2, \theta, y) \\ &= c\, p(\mu, \sigma^2)\, p(\theta|\mu, \sigma^2)\, p(y|\theta, \mu, \sigma^2) \\ &= c\, p(\mu)\, p(\sigma^2)\, p(\theta|\mu, \sigma^2)\, p(y|\theta) \\ &= c\, p(\sigma^2)\, p(\theta|\mu, \sigma^2). \end{aligned} \tag{21}$$

Here's another **trick**: instead of **slogging** through the **details**, try to **recognize** situations in which you already know the **conjugate updating**, and just use what you **already know**.

For example, in this calculation $(\theta|\mu, \sigma^2)$ is **Gaussian** with **known** μ and **unknown** σ^2, and we know the **conjugate prior** for σ^2 in that model — χ^{-2} — so with that **prior choice** the **full conditional** for σ^2 will also be χ^{-2}; how about θ?

$$\begin{aligned} p(\theta|\mu, \sigma^2, y) &= c\, p(\mu, \sigma^2, \theta, y) \\ &= c\, p(\mu, \sigma^2)\, p(\theta|\mu, \sigma^2)\, p(y|\theta, \mu, \sigma^2) \\ &= c\, p(\theta|\mu, \sigma^2)\, p(y|\theta). \end{aligned} \tag{22}$$

Here $p(\theta|\mu, \sigma^2)$ and $p(y|\theta)$ are both **Gaussian**, so the **full conditional** for θ — the **product** — will also be **Gaussian**.

Thus using the **latent Gibbs** approach in this **random-effects** model, all of the **full conditionals** have familiar forms; this approach will **work smoothly**; we just need to work out the **details**.

(I recommend this as a **basic Gibbs strategy**: in the first step make a **sketchy pass** through the **full conditionals** without working out all of the details, to ensure that everything **works fine**, and then go back and **fill in the details**.)

Details

(1) **Full conditional** for μ:

$$p(\mu|\sigma^2, \theta, y) = c\, p(\mu)\, p(\theta|\mu, \sigma^2). \tag{23}$$

In this **calculation** (a) σ^2 is known and (b) the **latent vector** $\theta = (\theta_1, \ldots, \theta_k)$ acts like the **data vector** $y = (y_1, \ldots, y_n)$ in the model $\mu \sim N(\mu_0, \sigma^2_{\mu 0}), (y_i|\mu) \overset{\text{IID}}{\sim} N(\mu, \sigma^2)$ $(i = 1, \ldots, n)$, so we already know the **answer**: $(\mu|\sigma^2, \theta, y) \sim N(\mu_k, \sigma^2_k)$, where

$$\mu_k = \frac{k_0 \mu_0 + k\bar{\theta}}{k_0 + k} \quad \text{and} \quad \sigma^2_k = \frac{\sigma^2}{k_0 + k}, \tag{24}$$

and in which the **prior sample size** is $k_0 = \frac{\sigma^2}{\sigma^2_{\mu 0}}$ and $\bar{\theta} = \frac{1}{k} \sum_{i=1}^{k} \theta_i$.

(2) **Full conditional** for σ^2:

$$p(\sigma^2|\mu, \theta, y) = c\, p(\sigma^2)\, p(\theta|\mu, \sigma^2). \tag{25}$$

In **parallel** with the situation with μ, in this **calculation** (a) μ is known and (b) the **latent vector** $\theta = (\theta_1, \ldots, \theta_k)$ acts like the **data vector** $y = (y_1, \ldots, y_n)$ in the model $\sigma^2 \sim \chi^{-2}(\nu_0, \sigma^2_{\sigma 0}), (y_i|\sigma^2) \overset{\text{IID}}{\sim} N(\mu, \sigma^2)$ $(i = 1, \ldots, n)$, so we already know the **answer**: $(\sigma^2|\mu, \theta, y) \sim \chi^{-2}(\nu_k, \sigma^2_k)$, where

$$\nu_k = \nu_0 + k \quad \text{and} \quad \sigma^2_k = \frac{\nu_0\, \sigma^2_{\sigma 0} + k\, v}{\nu_0 + k}, \tag{26}$$

in which $v = \frac{1}{k} \sum_{i=1}^{k} (\theta_i - \mu)^2$.

Details (continued)

(3) **Full conditional** for θ:

$$\begin{aligned} p(\theta|\mu,\sigma^2,y) &= c\,p(\theta|\mu,\sigma^2)\,p(y|\theta) \\ &= c\prod_{i=1}^{k} p(\theta_i|\mu,\sigma^2)\,p(y_i|\theta_i). \end{aligned} \tag{27}$$

Now $(\theta_i|\mu,\sigma^2) \sim N(\mu,\sigma^2)$ and $(y_i|\theta_i) \sim N(\theta_i, V_i)$ (with V_i known), so this is just our **old friend**

{**Gaussian likelihood** (for y_i) with **unknown mean** θ_i and **known variance** V_i + **Gaussian prior** for θ_i with **hyper-parameters** μ and σ^2};

the **(un-normalized) product** $p(\theta_i|\mu,\sigma^2)\,p(y_i|\theta_i)$ is just the **posterior** for θ_i, and the **answer** is therefore the **same** as it was in the **full conditional** for μ:
$(\theta_i|\mu,\sigma^2,y) \sim N(\theta_i^*,\sigma_i^2)$, with

$$\begin{aligned} \theta_i^* &= \frac{\frac{1}{\sigma^2}\mu + \frac{1}{V_i}y_i}{\frac{1}{\sigma^2}+\frac{1}{V_i}} = \frac{V_i\mu+\sigma^2 y_i}{V_i+\sigma^2} = B_i\mu + (1-B_i)y_i \quad \text{and} \\ \sigma_i^2 &= \frac{1}{\frac{1}{\sigma^2}+\frac{1}{V_i}} = \frac{V_i\sigma^2}{V_i+\sigma^2} = V_i(1-B_i), \end{aligned} \tag{28}$$

in which $B_i = \frac{V_i}{V_i+\sigma^2}$ is the **shrinkage factor** for study i (this is the **demonstration** of equations (2) and (3) earlier).

Thus $(\theta|\mu,\sigma^2,y) \sim N_k(\theta^*,\Sigma)$ with $\theta^* = (\theta_1^*,\ldots,\theta_k^*)$ and $\Sigma = \text{diag}(\sigma_i^2)$, and **one scan** of the **Gibbs sampler** can be described as follows:

(a) **draw** μ from $p(\mu|\sigma^2,\theta,y)$, **obtaining** μ_*;

(b) **draw** σ^2 from $p(\sigma^2|\mu_*,\theta,y)$, **obtaining** σ_*^2; and

(c) **draw** θ from $p(\theta|\mu_*,\sigma_*^2,y)$, either **univariately** on the θ_i (one by one) or **multivariately** on θ all at once.

R Code

```
meta.analysis.gibbs <- function( mu.0, sigma2.mu.0, nu.0, sigma2.sigma.0,
  mu.initial, sigma2.initial, theta.initial, y, V, M, B ) {

  k <- length( y )

  mu <- rep( 0, M + B + 1 )

  sigma2 <- rep( 0, M + B + 1 )

  theta <- matrix( 0, M + B + 1, k )

  mu[ 1 ] <- mu.initial

  sigma2[ 1 ] <- sigma2.initial

  theta[ 1, ] <- theta.initial

  for ( m in 2:( M + B + 1 ) ) {

    mu[ m ] <- mu.full.conditional( mu.0, sigma2.mu.0, sigma2[ m - 1 ],
      theta[ m - 1, ], y )

    sigma2[ m ] <- sigma2.full.conditional( nu.0, sigma2.sigma.0,
      mu[ m ], theta[ m - 1, ], y )

    theta[ m, ] <- theta.full.conditional( mu[ m ], sigma2[ m ], y, V )

    if ( m %% 1000 == 0 ) print( m )

  }

  return( cbind( mu, sigma2, theta ) )

}

mu.full.conditional <- function( mu.0, sigma2.mu.0, sigma2.current,
  theta.current, y ) {

  k <- length( y )

  k.0 <- sigma2.current / sigma2.mu.0

  theta.bar <- mean( theta.current )
```

R Code (continued)

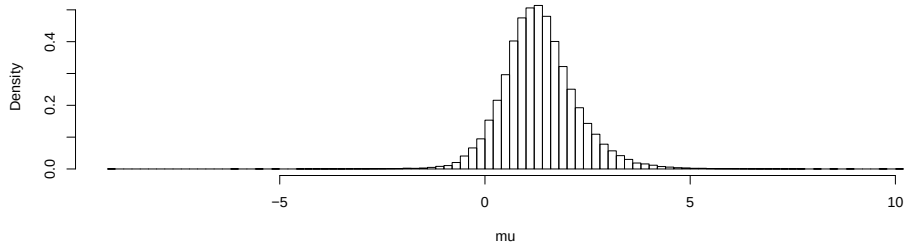
```
  mu.k <- ( k.0 * mu.0 + k * theta.bar ) / ( k.0 + k )

  sigma2.k <- sigma2.current / ( k.0 + k )

  mu.star <- rnorm( n = 1, mean = mu.k, sd = sqrt( sigma2.k ) )

  return( mu.star )

}

sigma2.full.conditional <- function( nu.0, sigma2.sigma.0,
  mu.current, theta.current, y ) {

  k <- length( y )

  nu.k <- nu.0 + k

  v <- mean( ( theta.current - mu.current )^2 )

  sigma2.k <- ( nu.0 * sigma2.sigma.0 + k * v ) / ( nu.0 + k )

  sigma2.star <- rsichi2( 1, nu.k, sigma2.k )

  return( sigma2.star )

}

rsichi2 <- function( n, nu, sigma2 ) {

  sigma2.star <- 1 / rgamma( n, shape = nu / 2,
    rate = nu * sigma2 / 2 )

  return( sigma2.star )

}

theta.full.conditional <- function( mu.current, sigma2.current, y, V ) {

  k <- length( y )

  theta.star <- ( V * mu.current + sigma2.current * y ) /
    ( V + sigma2.current )
```

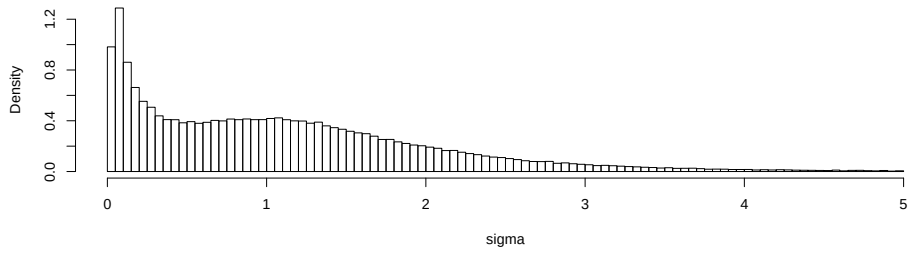
R Code (continued)

```
  sigma2.star <- V * sigma2.current / ( V + sigma2.current )

  theta.sim <- rnorm( n = k, mean = theta.star,
    sd = sqrt( sigma2.star ) )

  return( theta.sim )

}

mu.0 <- 0.0

sigma2.mu.0 <- 100^2

nu.0 <- 0.001

sigma2.sigma.0 <- 1.53

mu.initial <- 1.45

sigma2.initial <- 1.53

theta.initial <- c( 1.92, 1.94, 1.53, 1.84, 1.69, -0.252 )

y <- c( 2.77, 2.50, 1.84, 2.56, 2.32, -1.15 )

V <- c( 1.65, 1.31, 2.34, 1.67, 1.98, 0.90 )^2

M <- 100000

B <- 1000

mcmc.data.set <- meta.analysis.gibbs( mu.0, sigma2.mu.0, nu.0,
  sigma2.sigma.0, mu.initial, sigma2.initial, theta.initial,
  y, V, M, B )

% took 47 seconds

mcmc.data.set <- cbind( mcmc.data.set[ , 1:2 ],
  sqrt( mcmc.data.set[ , 2 ] ), mcmc.data.set[ , 3:8 ] )
```

R Code (continued)

```
apply( mcmc.data.set[ 1001:101001, ], 2, mean )

        mu     sigma2
1.33013835 2.24106295 1.12196766 1.68639681 1.67526967 1.38514567 1.62389213
1.51615795 0.09356775

apply( mcmc.data.set[ 1001:101001, ], 2, sd )

       mu    sigma2
0.9042468 4.4707971 0.9910910 1.1576621 1.0311309 1.2381000 1.1391841
1.1917662 0.9944885

mu.star <- mcmc.data.set[ 1001:101001, 1 ]

sum( mu.star > 0 ) / length( mu.star )

[1] 0.9484605

sigma.star <- mcmc.data.set[ 1001:101001, 3 ]

par( mfrow = c( 2, 1 ) )

hist( mu.star, nclass = 100, main = '', probability = T,
  xlab = 'mu' )

hist( sigma.star[ sigma.star < 5 ], nclass = 100, main = '',
  probability = T, xlab = 'sigma' )
```





WinBUGS Analysis of Aspirin Data

Aspirin meta-analysis revisited. I create three files for WinBUGS: a **model** file, a **data** file, and an **initial values** file (I'm using the most recent release, 1.4.1, of WinBUGS).

The (first) **model** file for the aspirin data:

```
{

  mu ~ dnorm( 0.0, 1.0E-6 )
  tau.theta ~ dgamma( 1.0E-3, 1.0E-3 )

  for ( i in 1:k ) {

    theta[ i ] ~ dnorm( mu, tau.theta )
    y[ i ] ~ dnorm( theta[ i ], tau.y[ i ] )

  }

  sigma.theta <- 1.0 / sqrt( tau.theta )

}
```

WinBUGS Analysis of Aspirin Data

Here μ plays the role of θ in model (10) above to avoid using the name `theta` twice for two different purposes in the `WinBUGS` program.

In specifying a normal distribution `WinBUGS` works not with a **standard deviation** (SD) or a **variance** but with a **precision**—the **reciprocal** of the variance—so that the $N(\mu, \sigma^2)$ distribution is specified by `dnorm( mu, tau )` with $\tau = \frac{1}{\sigma^2}$.

Then the **SD** has to be computed as a derived quantity ($\sigma = \frac{1}{\sqrt{\tau}}$) which is written above as

```
sigma.theta <- 1.0 / sqrt( tau.theta )
```

If—before the aspirin experiments were performed—I'm relatively **ignorant** about the quantities θ (μ) and σ in model (10), or equivalently μ and $\tau = \frac{1}{\sigma^2}$, I can build a **diffuse** or `flat` prior for both quantities that expresses this relative ignorance.

Since μ lives on $(-\infty, \infty)$ a convenient choice for a flat prior for it is a **normal** distribution with mean (say) 0 and very small precision: `mu` $\sim$ `dnorm( 0.0, 1.0E-6 )`

For `tau.theta`, which lives on $(0, \infty)$, I want something that's flat throughout (almost) all of that range; a convenient choice (to get an **initial idea** of where the posterior distribution for `sigma.theta` is **concentrated**) is a **gamma** distribution with small positive values of both of its parameters.

This is the $\boxed{\Gamma(\epsilon, \epsilon)}$ distribution for some **small** $\epsilon > 0$ like 0.001: `tau.theta` $\sim$ `dgamma( 1.0E-3, 1.0E-3 )`

WinBUGS **Aspirin Analysis (continued)**

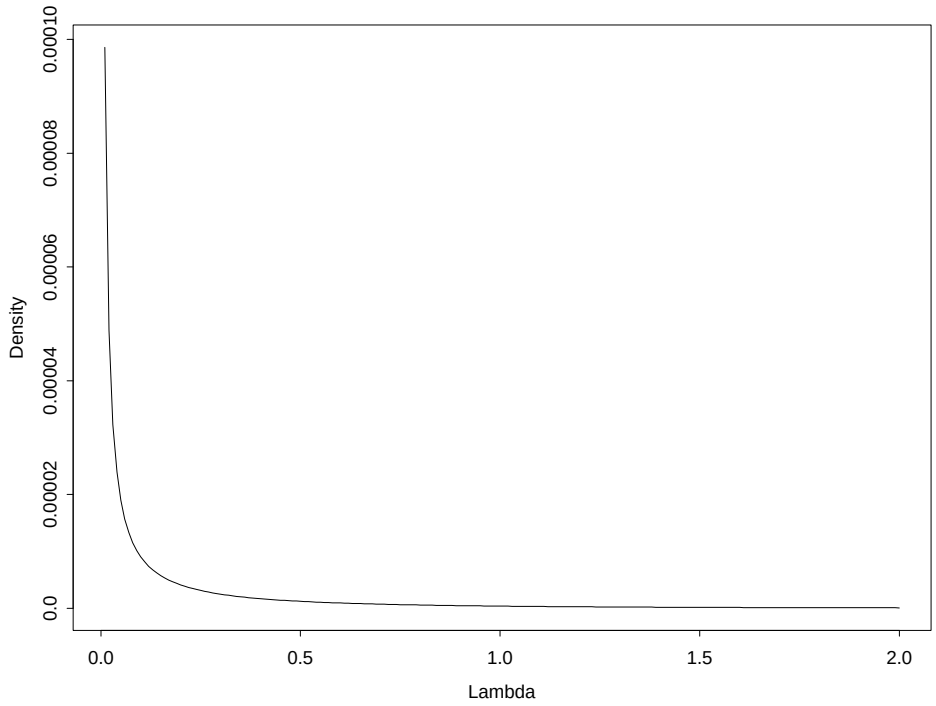


Figure 3.1. The $\Gamma(0.001, 0.001)$ distribution.

The **data** file in the aspirin meta-analysis is

```
list( k = 6, y = c( 2.77, 2.50, 1.84, 2.56, 2.31, -1.15 ),
  tau.y = c( 0.3673, 0.5827, 0.1826, 0.3586, 0.2551, 1.235 ) )
```

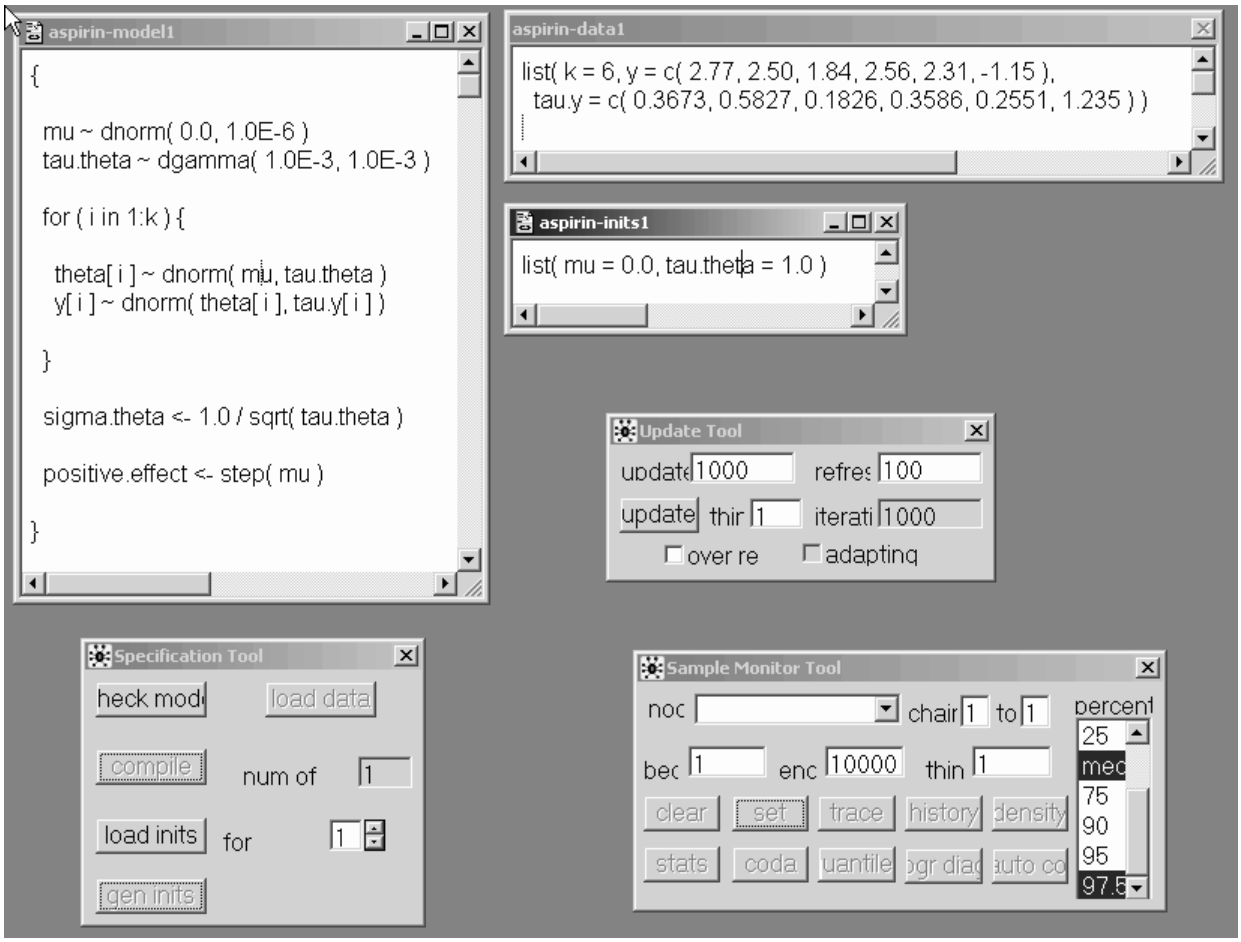
Here, e.g., `tau.y[ 1 ]` $= \frac{1}{1.65^2} \doteq 0.3673$, where 1.65 is the **standard error** of the difference `y[ 1 ]` for experiment 1 in Table 2.1 on p. 20.

Finally, the **initial values** file in the aspirin meta-analysis is

```
list( mu = 0.0, tau.theta = 1.0 )
```

In a simple example like this there's no harm in starting the Markov chain off in a **generic** location: since μ and τ_θ live on $(-\infty, \infty)$ and $(0, \infty)$, convenient generic choices for their starting values are 0 and 1, respectively (more care may be required in models with **more complex random-effects structure**).

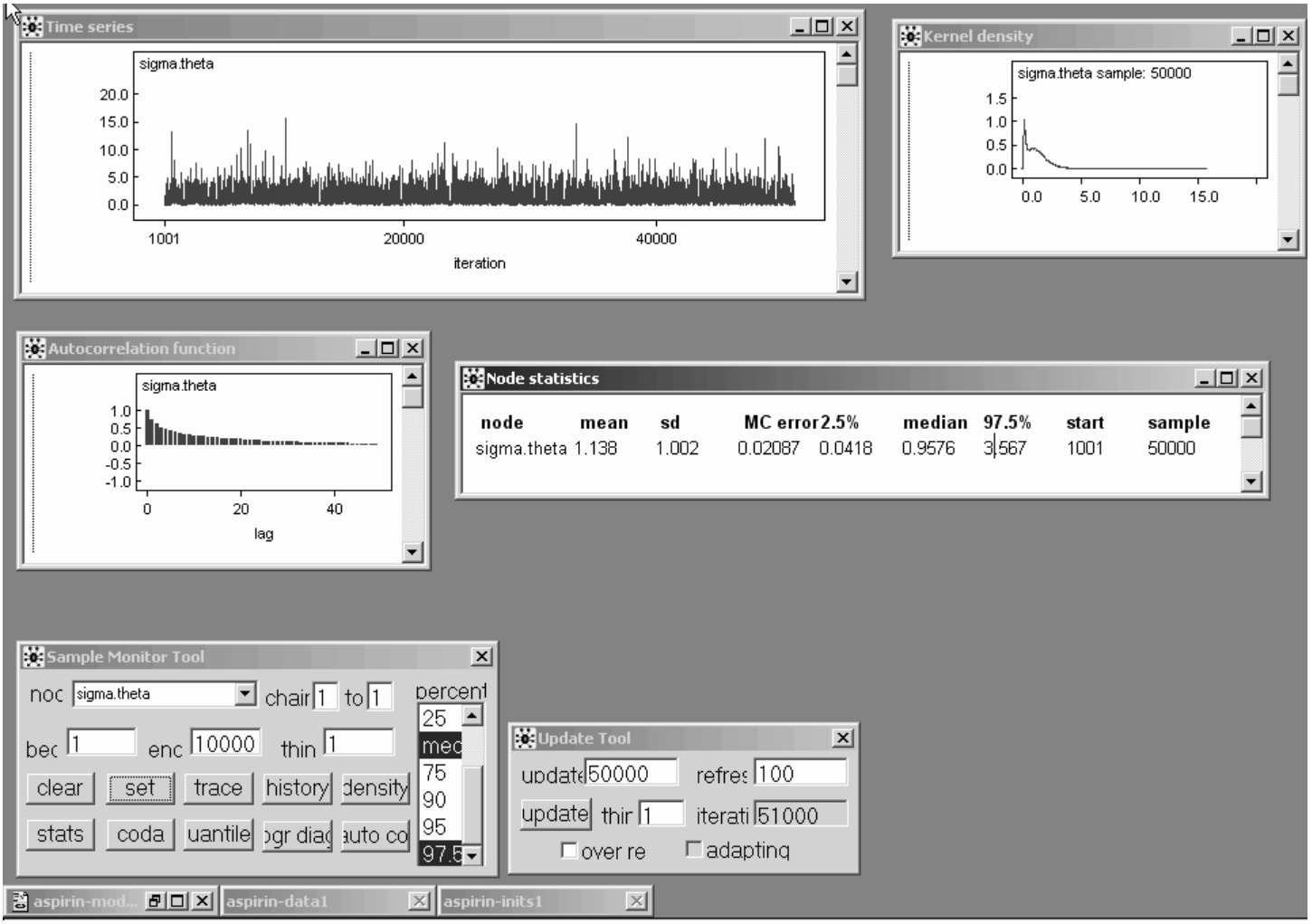
WinBUGS **Aspirin Analysis (continued)**



I (1) get a `Specification Tool` from the `Model` menu, (2) click on the **model** window and click `check model`, (3) click on the **data** window and click `load data` and `compile`, (4) click on the **initial values** window and click `load inits`, and (5) click `gen inits` (because the random effects θ_i were uninitialized in the inits file); I'm now ready to do some MCMC sampling.

I (6) get an `Update Tool` from the `Model` menu, and click `update` to perform a **burn-in** of 1,000 iterations (the default), which takes **0s** at 1.6 Pentium GHz; (7) I then get a `Sample Monitoring Tool` from the `Inference` menu, and type `sigma.theta` and click `set`.

WinBUGS **Aspirin Analysis (continued)**



(8) I type `50000` in the `updates` window in the `Update Tool` and click `update` to get a **monitoring** run of **50,000** iterations (this took **15s**).

Then (9) selecting `sigma.theta` in the node window, all 10 buttons from `clear` through `autoC` are active, and I click on `history` (to get a `Time Series` window), `density` (to get a `Kernel density` window), `autoC` to get an `Autocorrelation function` window, and `stats` (to get a `Node statistics` window), **yielding the screen above**.

The output of an MCMC sampler, when considered as a **time series**, often exhibits **positive autocorrelation**; in fact it often looks like a realization of an **autoregressive** AR_p model of order $p = \mathbf{1}$ ($\theta_t = \alpha + \beta\theta_{t-1} + e_t$) with **positive first-order autocorrelation** ρ.

WinBUGS Aspirin Analysis (continued)

This does not affect the **validity** of Monte Carlo inferences about the unknowns (e.g., the mean of any **stationary stochastic process** is a **consistent** estimator of the underlying process mean), but it does affect the **efficiency** of these inferences: for example, the Monte Carlo variance of the sample mean $\bar{\theta}$ based on M draws from an AR_1 time series is

$$V(\bar{\theta}) = \frac{\sigma_\theta^2}{M}\left(\frac{1+\rho}{1-\rho}\right), \tag{29}$$

and the **sample size inflation factor** $\frac{1+\rho}{1-\rho} \to \infty$ as $\rho \to +1$.

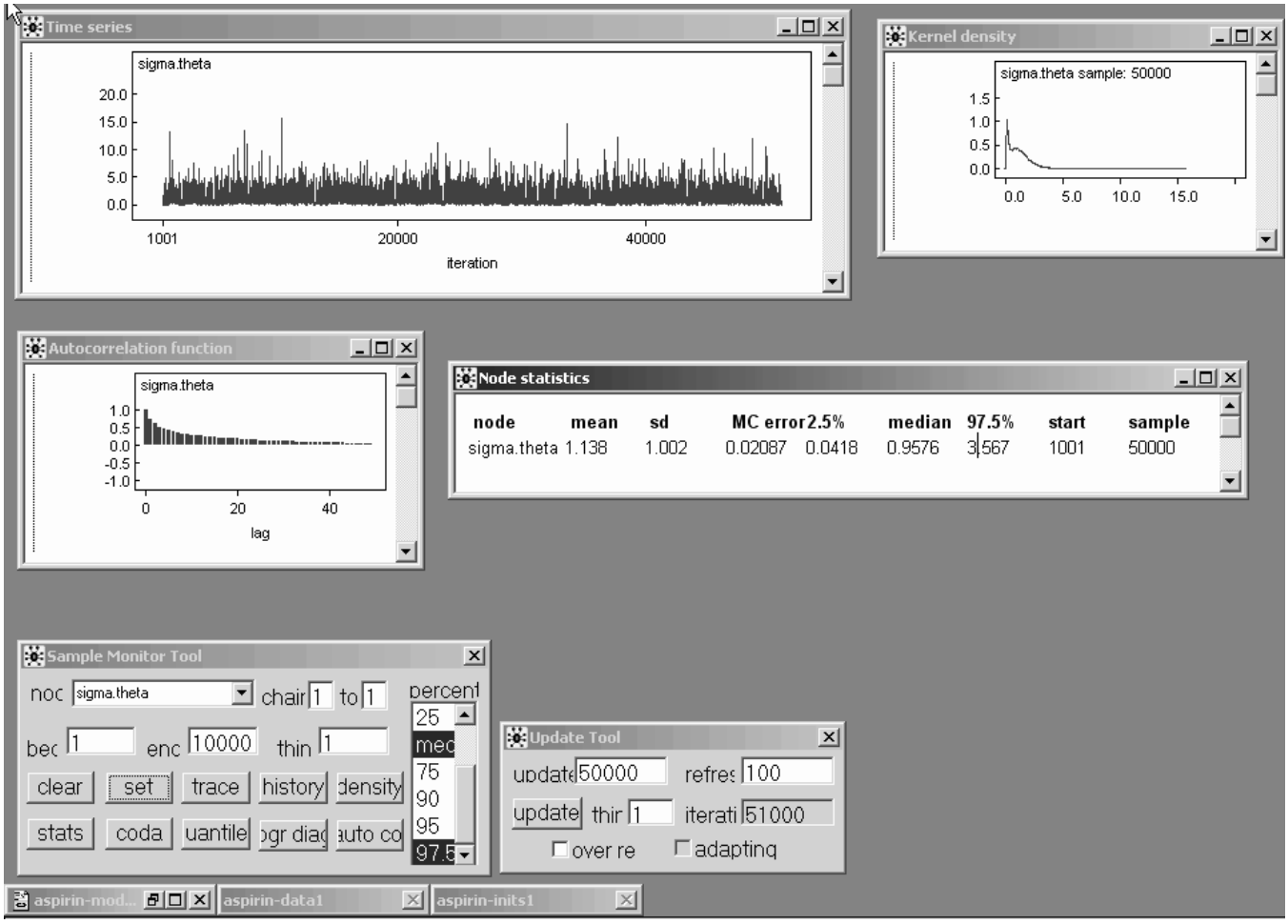
An MCMC sampler which produces output for any given unknown θ with ρ near 0 (if $\rho = 0$ the output is white noise, i.e., equivalent to IID draws from the posterior) is said to be **mixing well** in that unknown.

The time series trace for σ_θ above is only mixing **moderately well**: the autocorrelation function has the familiar ski-slope shape of an AR_1 series with $\rho \doteq 0.7$ (the height of the bar at lag 1).

The **marginal posterior distribution** for σ_θ (from the `Kernel density` window) looks heavily skewed to the right, which makes sense for a scale parameter.

The **posterior mean** and **SD** of σ_θ (using the $\Gamma(\epsilon, \epsilon)$ prior for τ_θ) are estimated to be 1.14 and 1.00, respectively; the **Monte Carlo standard error** of the posterior mean estimate is 0.021 (so that with 50,000 monitoring iterations I don't yet have **3 significant figures** of accuracy for the posterior mean); the **posterior median** is estimated to be 0.96; and a **95% central interval** for σ_θ with this prior is estimated to run from 0.042 to 3.57.

WinBUGS **Aspirin Analysis (continued)**



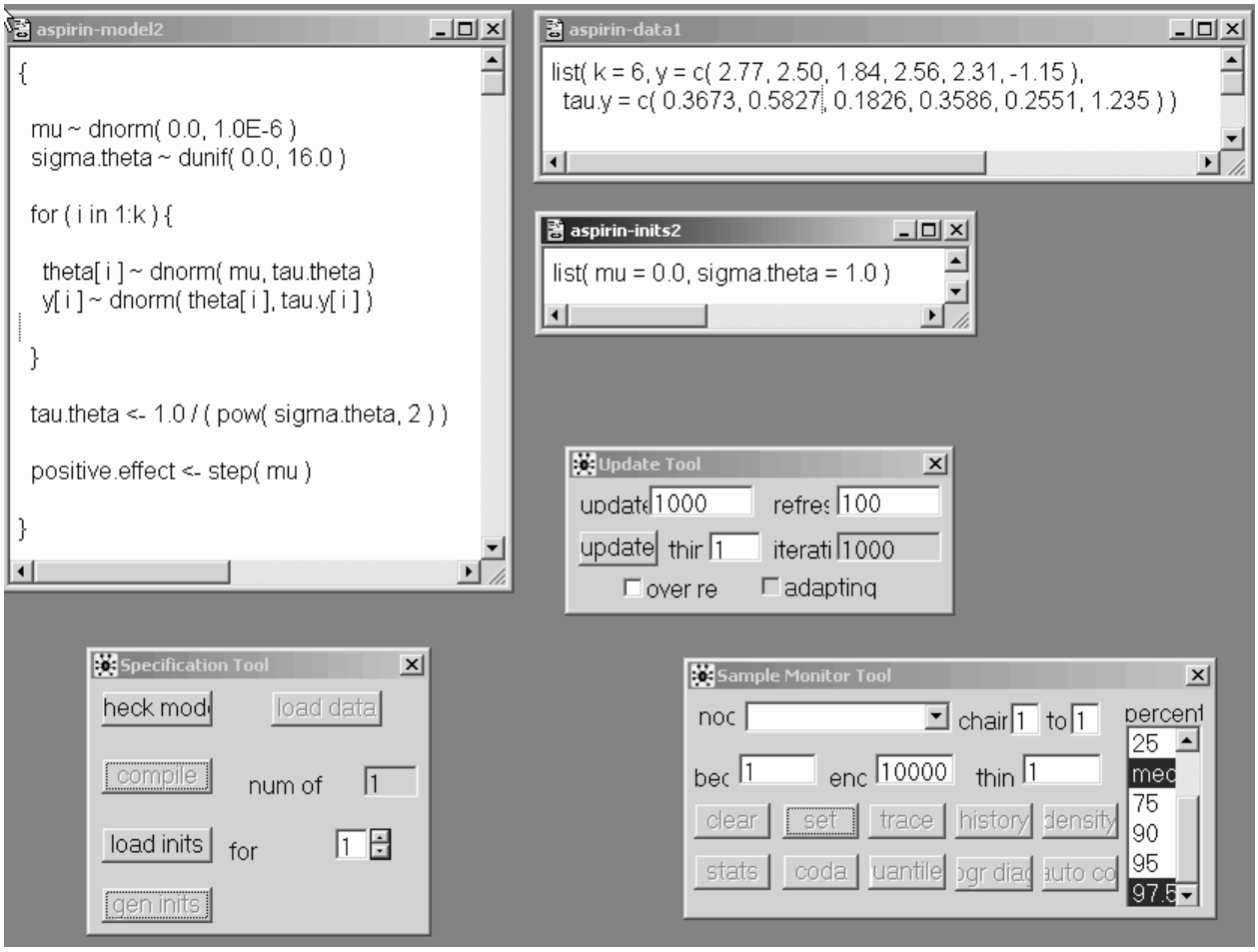
The main thing to notice, however, is that the **range of plausible values** for `sigma.theta` in its posterior is approximately from **0 to 16**.

It has recently been shown that the **simplest diffuse prior** on σ_θ that has **good calibration properties** (i.e., such that 95% **nominal** Bayesian interval estimates for all of the parameters in model (10) do in fact have **actual coverage close to 95%**) is

$$\sigma_\theta \sim U(0, c), \tag{30}$$

where c is chosen to be (roughly) the **smallest value that doesn't truncate the likelihood function** for σ_θ; here it's evident that $c \doteq 16$ will **work well**.

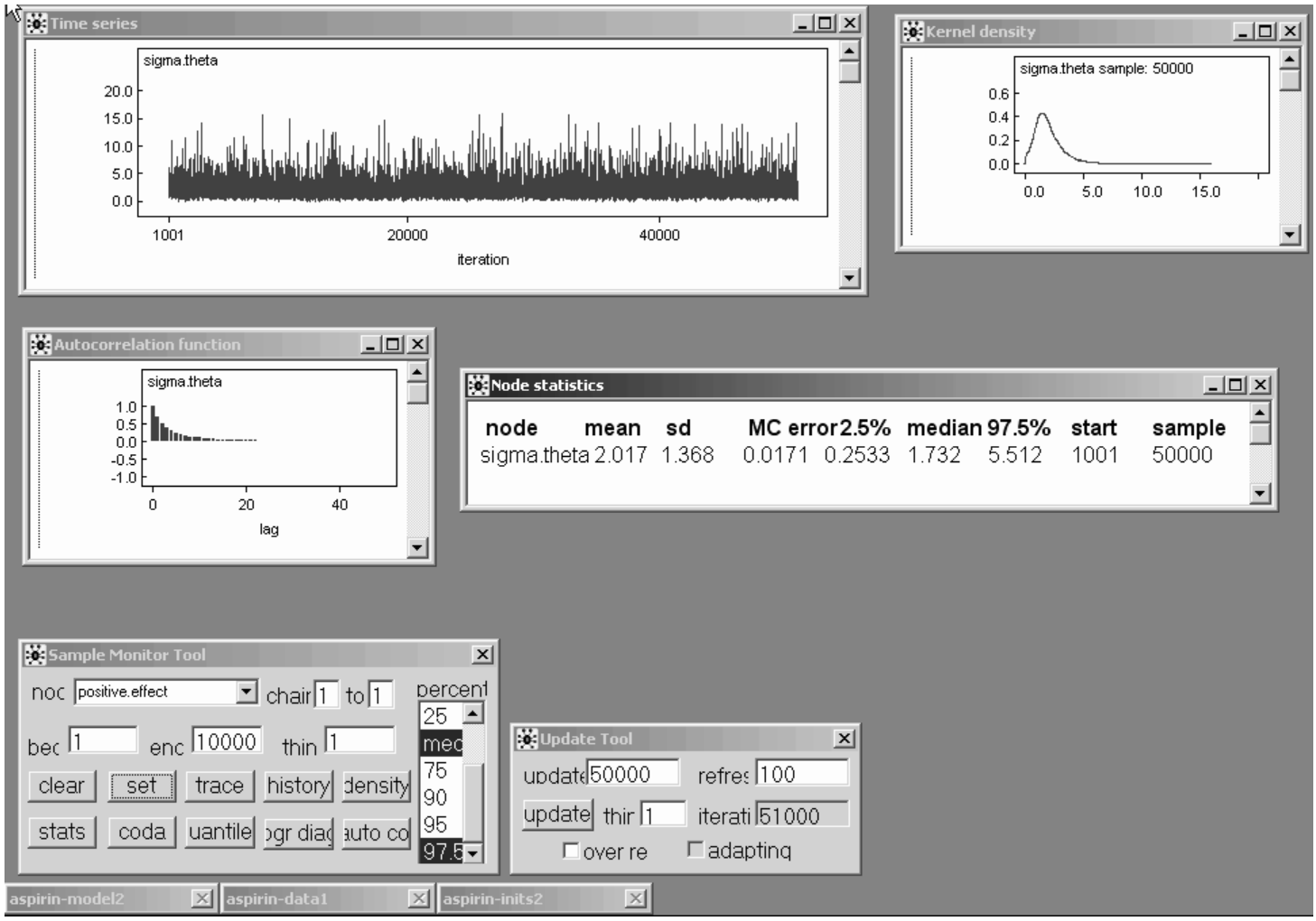
WinBUGS **Aspirin Analysis (continued)**



So I estimate a **second model** placing a Uniform$(0, c)$ prior on σ_θ (this model also requires a **new initial values file** that initializes `sigma.theta` instead of `tau.theta`).

This time in the `Sample Monitor Tool` I `set` all of the **interesting** quantities: `mu`, `sigma.theta`, `theta`, and `positive.effect`, and I use the same MCMC strategy as before (a **burn-in of 1,000** followed by a **monitoring run of 50,000**).

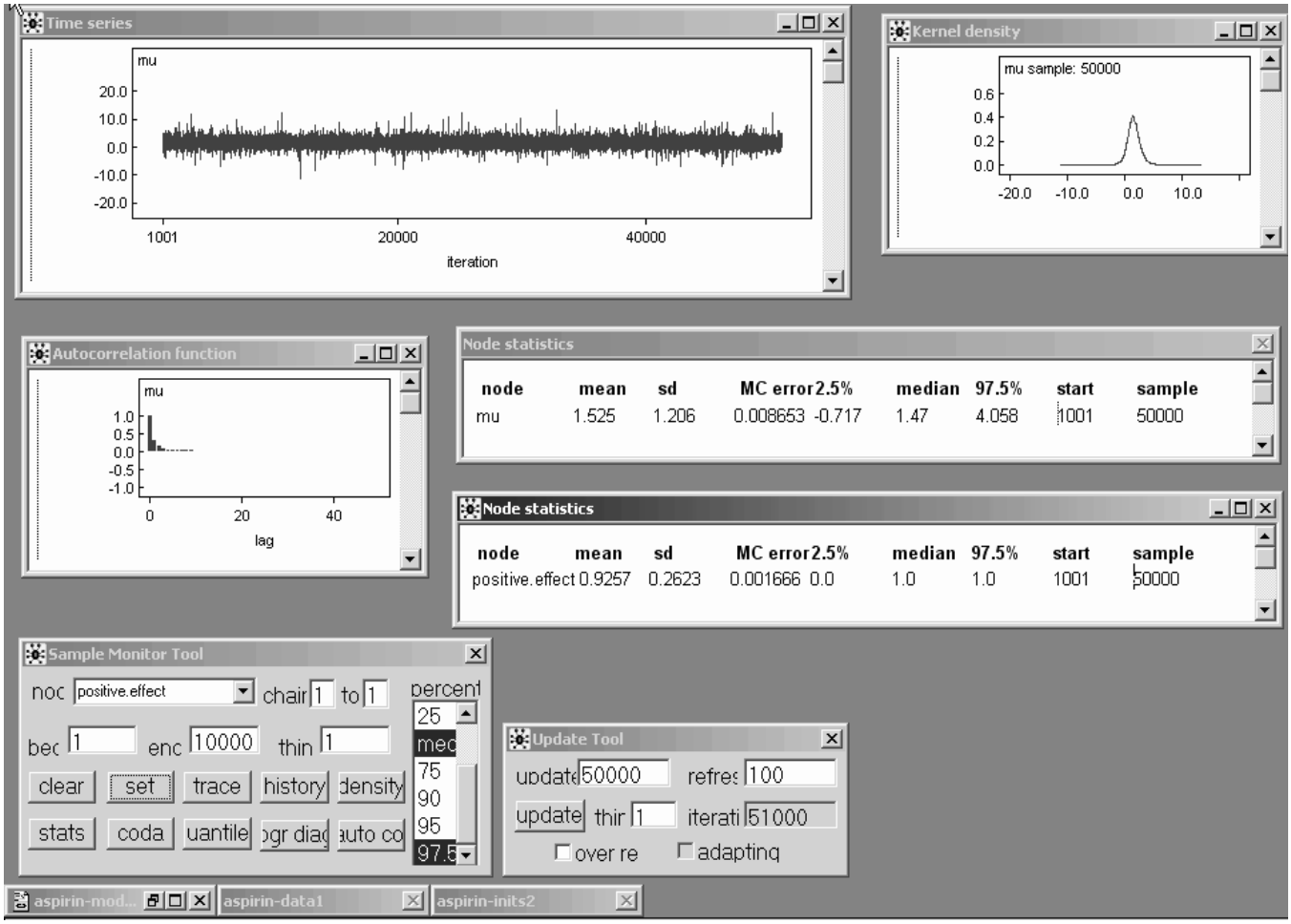
WinBUGS **Aspirin Analysis (continued)**



With the Uniform$(0, c)$ prior on σ_θ the posterior mean of σ_θ is now **sharply higher** than before (**2.02** versus the **1.14** value I got with the initial $\Gamma(\epsilon, \epsilon)$ prior (this sort of **discrepancy** will only arise when the number of studies k is **small**; when it does arise I **trust** the results from the Uniform$(0, c)$ prior).

Note that the posterior mean of σ_θ is also **quite a bit bigger** than the value (**1.24**) obtained from **MLEB** back on page 25—this is a reflection of the **tendency of MLEB to understate the between-study heterogeneity** in model (10) with small k.

WinBUGS **Aspirin Analysis (continued)**



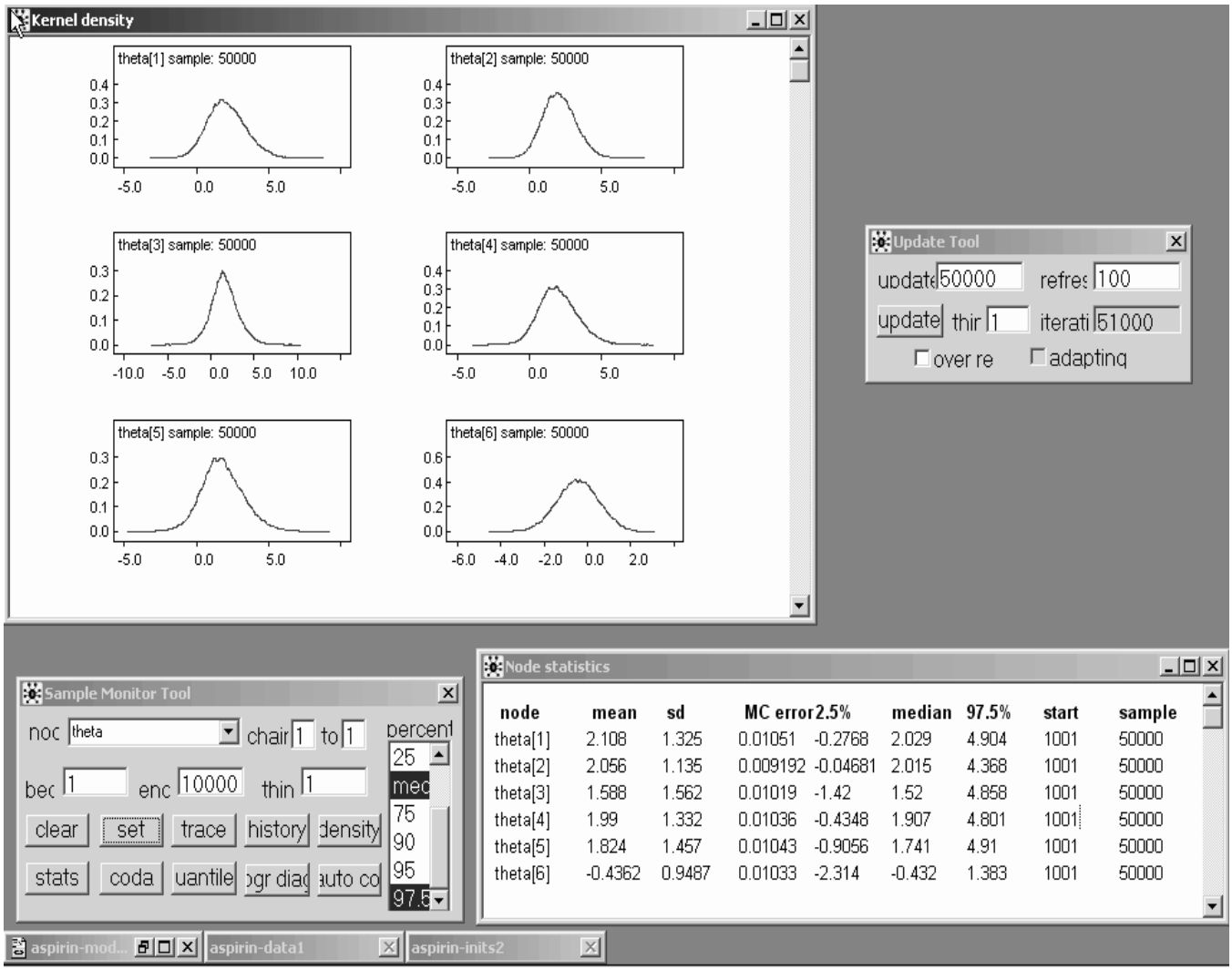
On pp. 25–26 above we saw that the MLEB estimate of μ was **1.45** with an approximate standard error of **0.809**, and an approximate 95% confidence interval for μ ran from -0.14 to $+3.03$.

The corresponding **Bayesian** results are: posterior **mean 1.52**, posterior **SD 1.21**, 95% **interval (−0.72, 4.06)**.

As is often true, the simple MLEB approximations leading to these estimates have **underestimated the actual uncertainty** about μ: the Bayesian 95% interval with the Uniform prior is **50% wider**.

It's easy to monitor the **posterior probability that aspirin is beneficial**, with the built-in `step` function applied to `mu`: $P(\mu > 0|\text{data, diffuse prior information}) \doteq$ **0.93**, i.e., posterior betting odds of about **12.5 to 1 that aspirin reduces mortality**.

WinBUGS **Aspirin Analysis (continued)**



The marginal density plots of the θ_i values show **interesting departures from normality**, and the Bayesian estimates (a) exhibit **rather less shrinkage** and (b) have **27–43% larger** uncertainty estimates.

Table 3.1. MLEB and Bayesian (posterior mean) estimates of the θ_i.

	Maximum Likelihood		Bayesian Posterior	
study(i)	$\hat{\theta}_i$	$\widehat{SE}(\hat{\theta}_i)$	mean	SD
1	1.92	0.990	2.11	1.33
2	1.94	0.899	2.06	1.14
3	1.53	1.09	1.59	1.56
4	1.84	0.994	1.99	1.33
5	1.69	1.05	1.82	1.46
6	−0.252	0.728	−0.44	0.95

Hierarchical Model Expansion

Looking at the **shrinkage plot** on p. 26 or the **raw data values** themselves, it's evident that a **Gaussian** model for the θ_i may not be appropriate: study 6 is so different than the other 5 that a **heavier-tailed distribution** may be a better choice.

This suggests **expanding** the HM (10), by embedding it in a **richer model class** of which it's a **special case** (this is the main Bayesian approach in practice to **dealing with model inadequacies**).

A **natural choice** would be a t model for the θ_i with **unknown degrees of freedom** ν:

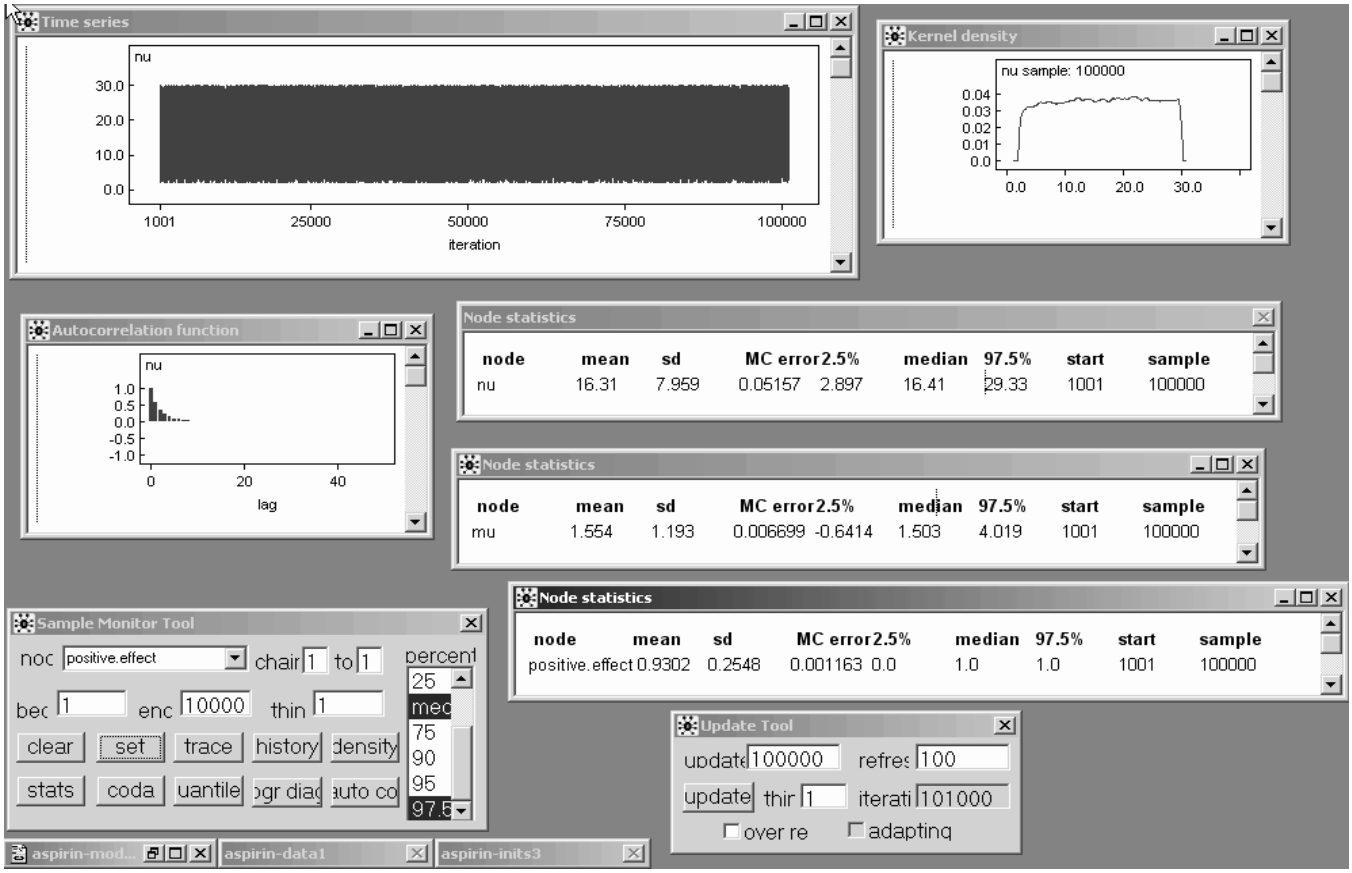
$$\begin{array}{rcll} (\theta, \sigma^2, \nu) & \sim & p(\theta, \sigma^2, \nu) & \text{(prior)} \\ (\theta_i | \theta, \sigma^2, \nu) & \overset{\text{IID}}{\sim} & t\big(\theta, \sigma^2, \nu\big) & \text{(underlying effects)} \\ (y_i | \theta_i) & \overset{\text{indep}}{\sim} & N(\theta_i, V_i) & \text{(data)} \ . \end{array} \tag{31}$$

Here $\eta \sim t\big(\theta, \sigma^2, \nu\big)$ just means that $\left(\frac{\eta - \theta}{\sigma}\right)$ follows a **standard** t **distribution** with ν degrees of freedom. This is **amazingly easy** to implement in `WinBUGS` (it is considerably more difficult to carry out an **analogous ML analysis**).

The new model file is

```
{

  mu ~ dnorm( 0.0, 1.0E-6 )
  sigma.theta ~ dunif( 0.0, 16.0 )
  nu ~ dunif( 3.0, 30.0 )

  for ( i in 1:k ) {

    theta[ i ] ~ dt( mu, tau.theta, nu )
    y[ i ] ~ dnorm( theta[ i ], tau.y[ i ] )

  }

  tau.theta <- 1.0 / pow( sigma.theta, 2 )

}
```

Model Expansion (continued)



To express comparative prior ignorance about ν I use a **uniform** prior on the interval from 2.0 to 30.0 (below $\nu = 2$ the t distribution has **infinite variance**, and above about 30 it starts to be **indistinguishable** in practice from the Gaussian).

A **burn-in** of 1,000 and a **monitoring run** of 100,000 iterations takes **about twice as long as with 50,000 iterations in the Gaussian model** (i.e., about the **same speed per iteration**) and yields the **posterior summaries** above.

It's clear that there's **little information in the likelihood function** about ν: the prior and posterior for this parameter **virtually coincide**.

The results for μ and the θ_i are **almost unchanged**; this would not necessarily be the case if study 6 had been **more extreme**.

Educational Meta-Analysis

Incorporating Study-Level Covariates

Case Study: *Meta-analysis of the effect of teacher expectancy on student IQ* (Bryk and Raudenbush, 1992).
Do **teachers' expectations** influence students' intellectual development,
as measured by IQ scores?

Table 5.4. Results from 19 experiments estimating the effects of teacher expectancy on pupil IQ.

Study (i)	Weeks of Prior Contact (x_i)	Estimated Effect Size (y_i)	Standard Error of $y_i = \sqrt{V_i}$
1. Rosenthal et al. (1974)	2	0.03	0.125
2. Conn et al. (1968)	3	0.12	0.147
3. Jose & Cody (1971)	3	-0.14	0.167
4. Pellegrini & Hicks (1972)	0	1.18	0.373
5. Pellegrini & Hicks (1972)	0	0.26	0.369
6. Evans & Rosenthal (1969)	3	-0.06	0.103
7. Fielder et al. (1971)	3	-0.02	0.103
8. Claiborn (1969)	3	-0.32	0.220
9. Kester & Letchworth (1972)	0	0.27	0.164
10. Maxwell (1970)	1	0.80	0.251
11. Carter (1970)	0	0.54	0.302
12. Flowers (1966)	0	0.18	0.223
13. Keshock (1970)	1	-0.02	0.289
14. Henrickson (1970)	2	0.23	0.290
15. Fine (1972)	3	-0.18	0.159
16. Greiger (1970)	3	-0.06	0.167
17. Rosenthal & Jacobson (1968)	1	0.30	0.139
18. Fleming & Anttonen (1971)	2	0.07	0.094
19. Ginsburg (1970)	3	-0.07	0.174

Teacher Expectancy

Raudenbush (1984) found $k = 19$ experiments, published between 1966 and 1974, estimating **the effect of teacher expectancy on student IQ** (Table 5.4).

In each case the experimental group was made up of children for whom teachers were (**deceptively**) encouraged to have high expectations (e.g., experimenters gave treatment teachers lists of students, **actually chosen at random**, who allegedly displayed dramatic potential for intellectual growth), and the controls were students about whom no particular expectations were encouraged.

The estimated **effect sizes** $y_i = \frac{\bar{T}_i - \bar{C}_i}{\text{SD}_{i:\text{pooled}}}$ (column 3 in Table 5.4) ranged from $-.32$ to $+1.18$; why?

One good reason: the studies differed in **how well the experimental teachers knew their students** at the time they were given the deceptive information—this time period x_i (column 2 in Table 5.4) ranged from 0 to 3 weeks.

Figure 5.2 plots y_i against x_i—you can see that **the studies with bigger x_i had smaller IQ effects on average**.

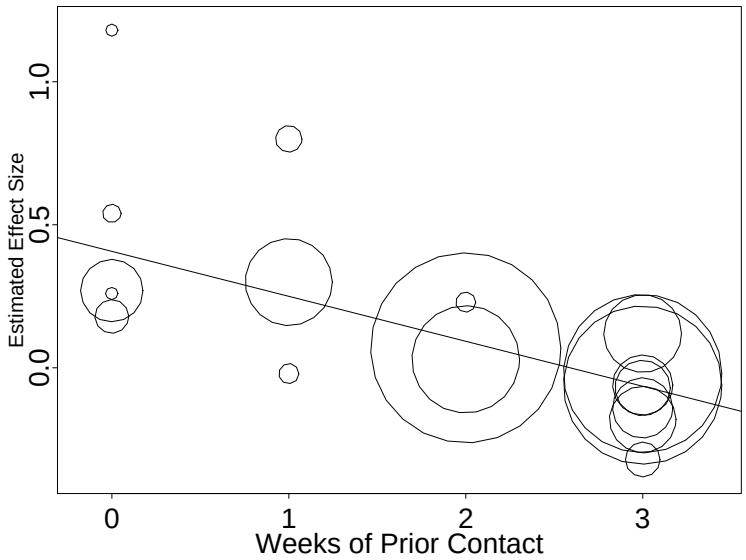


Figure 5.2. Scatterplot of estimated effect size against weeks of prior contact in the IQ meta-analysis. Radii of circles are proportional to $w_i = V_i^{-1}$ (see column 4 in Table 5.4); fitted line is from weighted regression of y_i on x_i with weights w_i.

Conditional Exchangeability

Evidently model (1) will not do here — it says that your predictive uncertainty about all the studies is **exchangeable** (similar, i.e., according to (1) the underlying study-level effects θ_i are like IID draws from a normal distribution), whereas Figure 5.2 **clearly shows** that the x_i are useful in predicting the y_i.

This is another way to say that your uncertainty about the studies is **not unconditionally exchangeable** but

conditionally exchangeable given x

(Draper et al., 1993b).

In fact Figure 5.2 suggests that the y_i (and therefore the θ_i) are related **linearly** to the x_i.

Bryk and Raudenbush, working in the **frequentist** paradigm, fit the following HM to these data:

$$\begin{aligned} (\theta_i|\alpha,\beta,\sigma_\theta^2) &\overset{\text{indep}}{\sim} N\left(\alpha+\beta\, x_i, \sigma_\theta^2\right) \quad \text{(underlying effects)} \\ (y_i|\theta_i) &\overset{\text{indep}}{\sim} N(\theta_i, V_i) \quad \text{(data).} \end{aligned} \tag{32}$$

According to this model the estimated effect sizes y_i are like **draws from a Gaussian** with mean θ_i and variance V_i, the squared standard errors from column 4 of Table 5.4—here as in model (1) the V_i are taken to be known—and the θ_i themselves are like **draws from a Gaussian** with mean $\alpha+\beta x_i$ and variance σ_θ^2.

The top level of this HM in effect assumes, e.g., that the 5 studies with $x=0$ are sampled **representatively** from {all possible studies with $x=0$}, and similarly for the other values of x.

This (and the Gaussian choice on the top level) are **conventional assumptions, not automatically scientifically reasonable**—for example, if you know of some way in which (say) two of the studies with $x=3$ differ from each other that's **relevant** to the outcome of interest, then you should **include** this in the model as a study-level covariate along with x.

An MLEB Drawback

Bryk and Raudenbush used MLEB methods, based on the **EM algorithm**, to fit this model.

As in Section 5.2, this estimation method combines the two levels of model (9) to construct a **single likelihood** for the y_i, and then **maximizes** this likelihood as usual in the ML approach.

They obtained $(\widehat{\alpha}, \widehat{\beta}) = (.407 \pm .087, -.157 \pm .036)$ and $\widehat{\sigma_\theta}^2 = 0$, naively indicating that **all of the study-level variability** has been "explained" by the covariate x.

However, from a **Bayesian** point of view, this model is **missing a third layer**:

$$\begin{array}{rcl} (\alpha, \beta, \sigma_\theta^2) & \sim & p(\alpha, \beta, \sigma_\theta^2) \\ (\theta_i | \alpha, \beta, \sigma_\theta^2) & \overset{\text{indep}}{\sim} & N\big(\alpha + \beta(x_i - \bar{x}), \sigma_\theta^2\big) \\ (y_i | \theta_i) & \overset{\text{indep}}{\sim} & N(\theta_i, V_i)\,. \end{array} \tag{33}$$

(it will help **convergence** of the sampling-based MCMC methods to make α and β uncorrelated by **centering** the x_i at 0 rather than at $\bar{x}$).

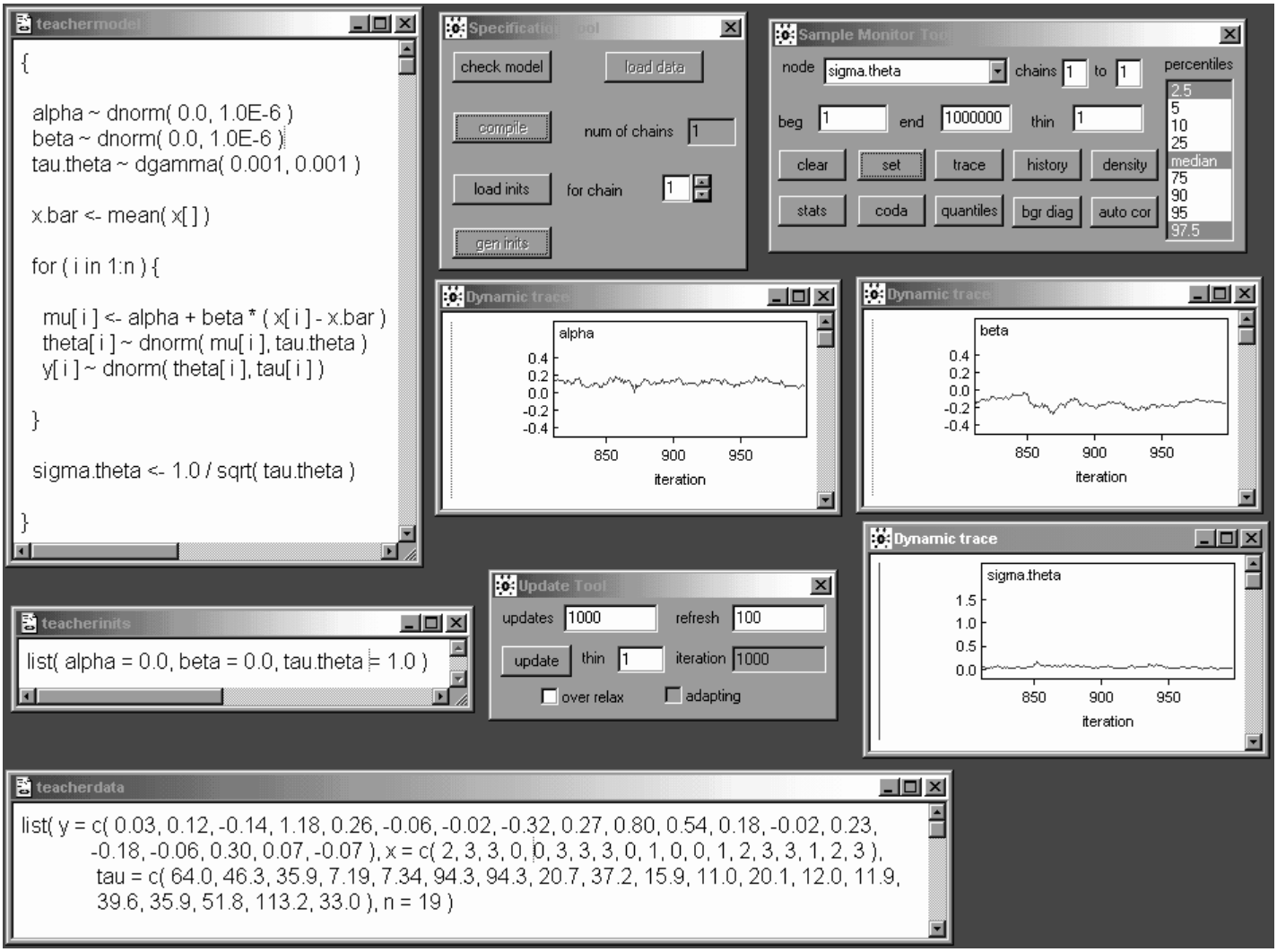
As will subsequently become clear, the trouble with MLEB is that in Bayesian language **it assumes in effect that the posterior for σ_θ^2 is point-mass on the MLE**. This is bad (e.g., Morris, 1983) for two reasons:

- If the posterior for σ_θ^2 is highly **skewed**, the mode will be a **poor summary**; and

- Whatever point-summary you use, pretending the posterior SD for σ^2 is zero **fails to propagate uncertainty** about σ_θ^2 through to uncertainty about α, β, and the θ_i.

The best way to carry out a fully Bayesian analysis of model (10) is with **MCMC** methods.

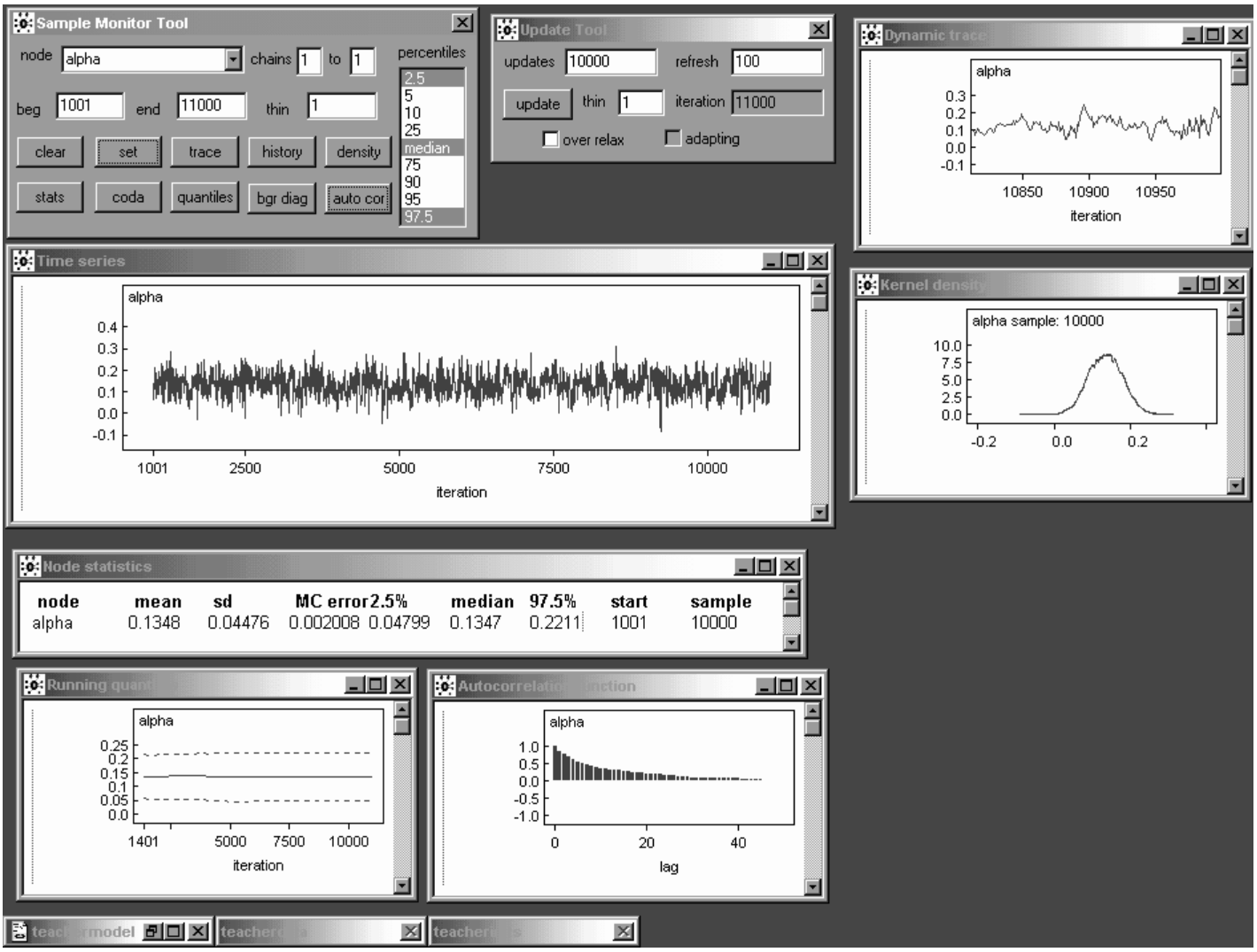
WinBUGS Implementation



For $p(\alpha, \beta, \sigma_\theta^2)$ in model (10) I've chosen the **usual** WinBUGS **diffuse prior** $p(\alpha)p(\beta)p(\sigma_\theta^2)$: since α and β live on the whole real line I've taken marginal Gaussian priors for them with mean 0 and precision 10^{-6}, and since $\tau_\theta = \frac{1}{\sigma^2}$ is positive I use a $\Gamma(0.001, 0.001)$ prior for it.

Model (10) treats the variances V_i of the y_i as **known** (and equal to the squares of column 4 in Table 5.4); I've **converted these into precisions** in the data file (e.g., $\tau_1 = \frac{1}{0.125^2} = 64.0$).

WinBUGS Implementation

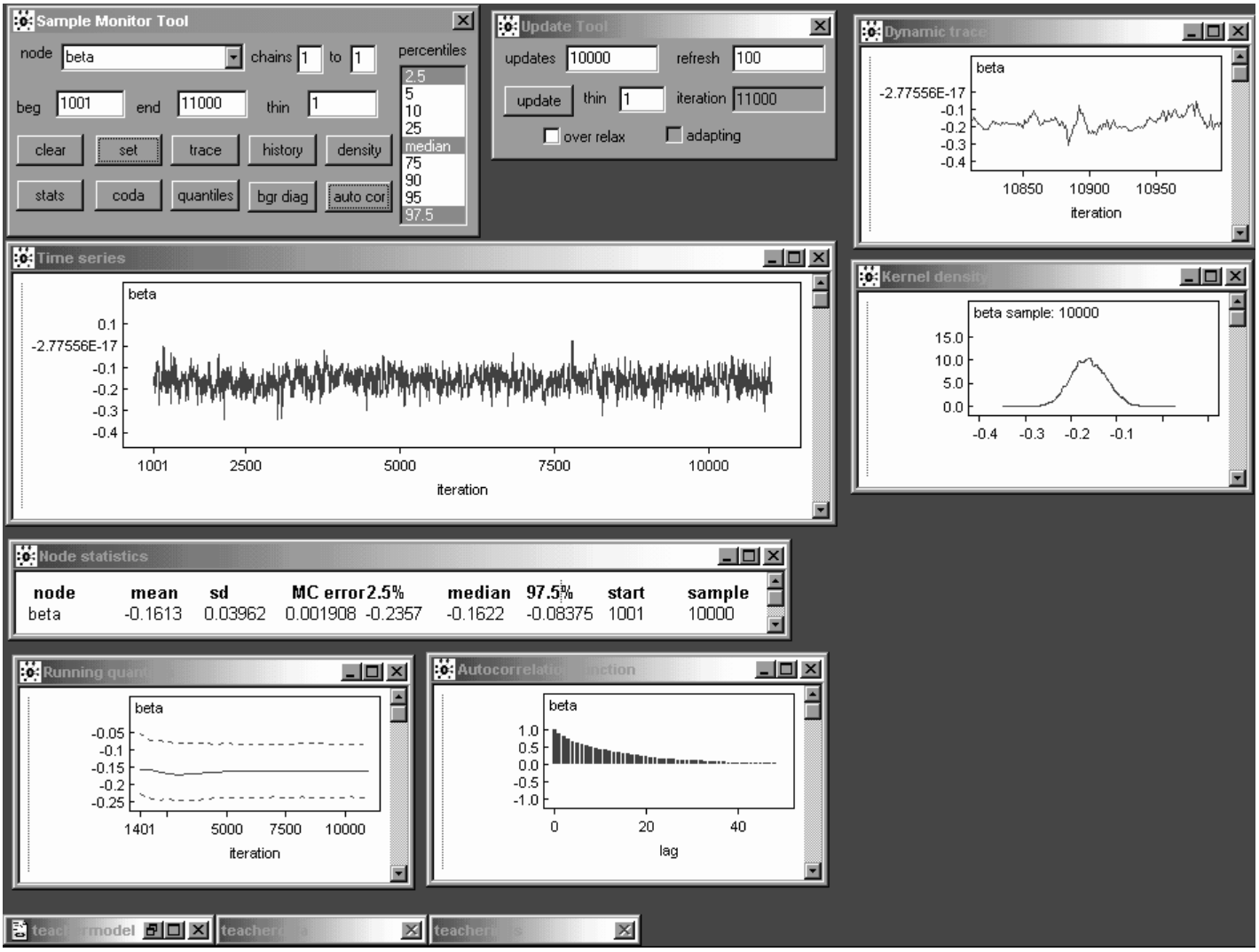


A burn-in of 1,000 (**certainly longer than necessary**) from **default** initial values $(\alpha, \beta, \tau_\theta) = (0.0, 0.0, 1.0)$ and a monitoring run of 10,000 yield the following **preliminary MCMC results**.

Because this is a **random-effects model** we don't expect anything like IID mixing: the output for α behaves like an AR_1 time series with $\widehat{\rho}_1 \doteq 0.86$.

The posterior mean for α, 0.135 (with an MCSE of 0.002), shows that α in model (10) and α in model (9) are **not comparable** because of the **recentering** of the predictor x in model (10): the MLE of α in (9) was 0.41 ± 0.09.

WinBUGS Implementation

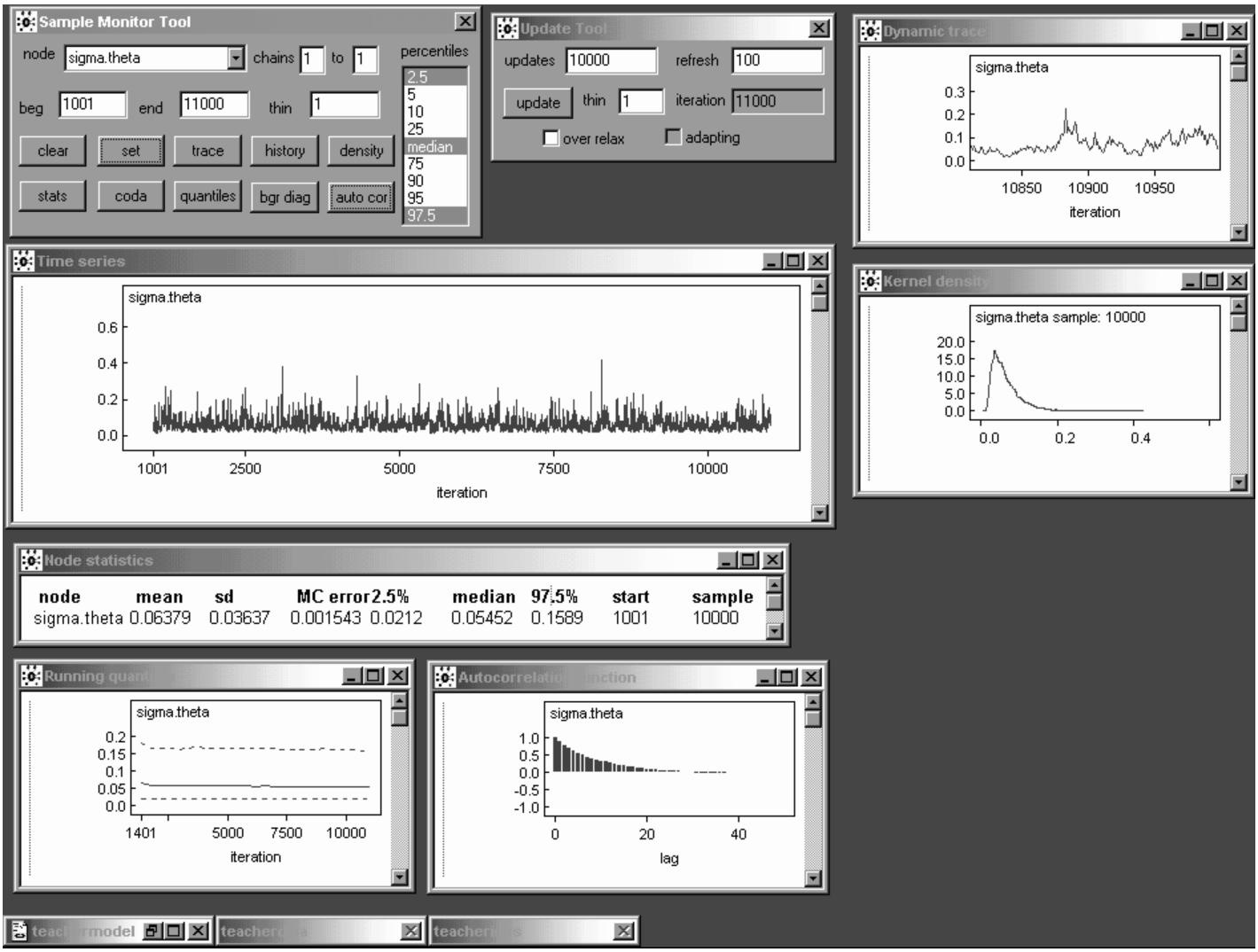


But β **means the same thing in both models** (9) and (10): its posterior mean in (10) is -0.161 ± 0.002, which is not far from the MLE -0.157.

Note, however, that the posterior SD for β, 0.0396, is **10% larger** than the standard error of the maximum likelihood estimate of β (0.036).

This is a reflection of the **underpropagation of uncertainty** about σ_θ in maximum likelihood mentioned on page 15.

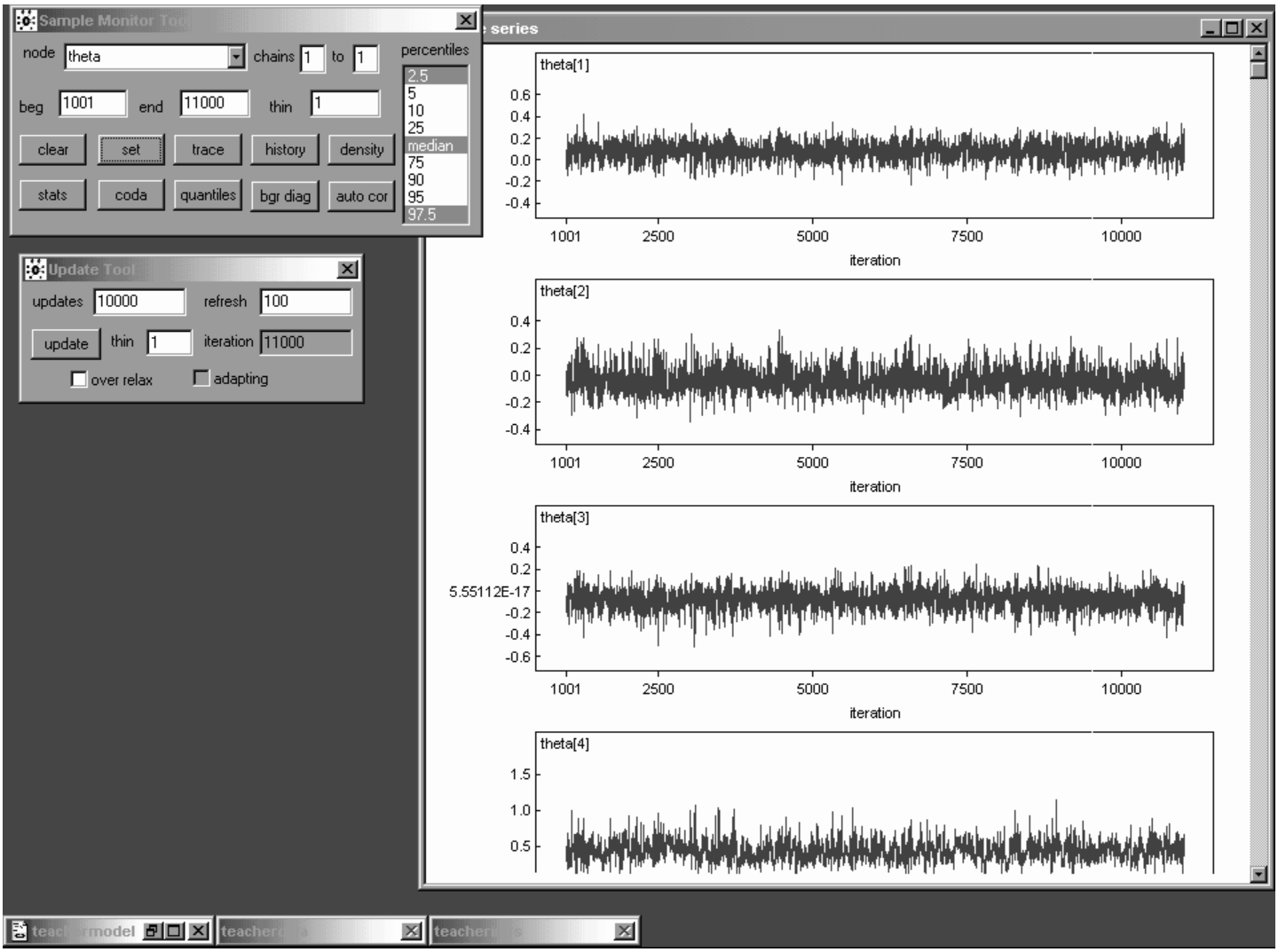
WinBUGS Implementation



In these preliminary results σ_θ has posterior mean 0.064 ± 0.002 and SD 0.036, providing **clear evidence** that the MLE $\hat{\sigma}_\theta = 0$ is a **poor summary**.

Note, however, that the likelihood for σ_θ may be **appreciable in the vicinity of 0** in this case, meaning that some **sensitivity analysis** with diffuse priors other than $\Gamma(0.001, 0.001)$—such as $U(0, c)$ for c around 0.5—would be in order.

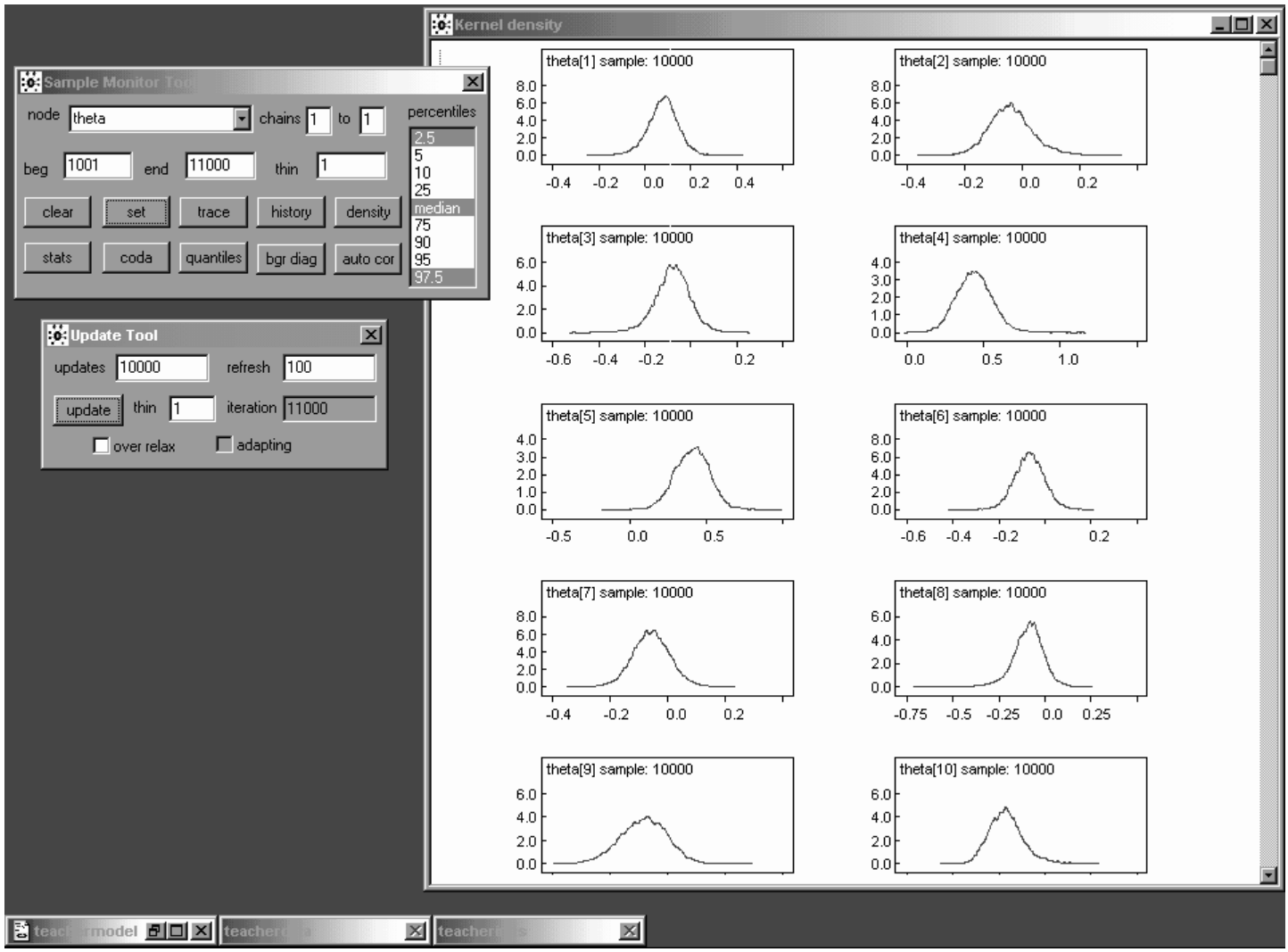
WinBUGS Implementation



When you specify node `theta` in the `Sample Monitor Tool` and then look at the results, you see that `WinBUGS` presents **parallel findings with a single click** for all elements of the vector θ.

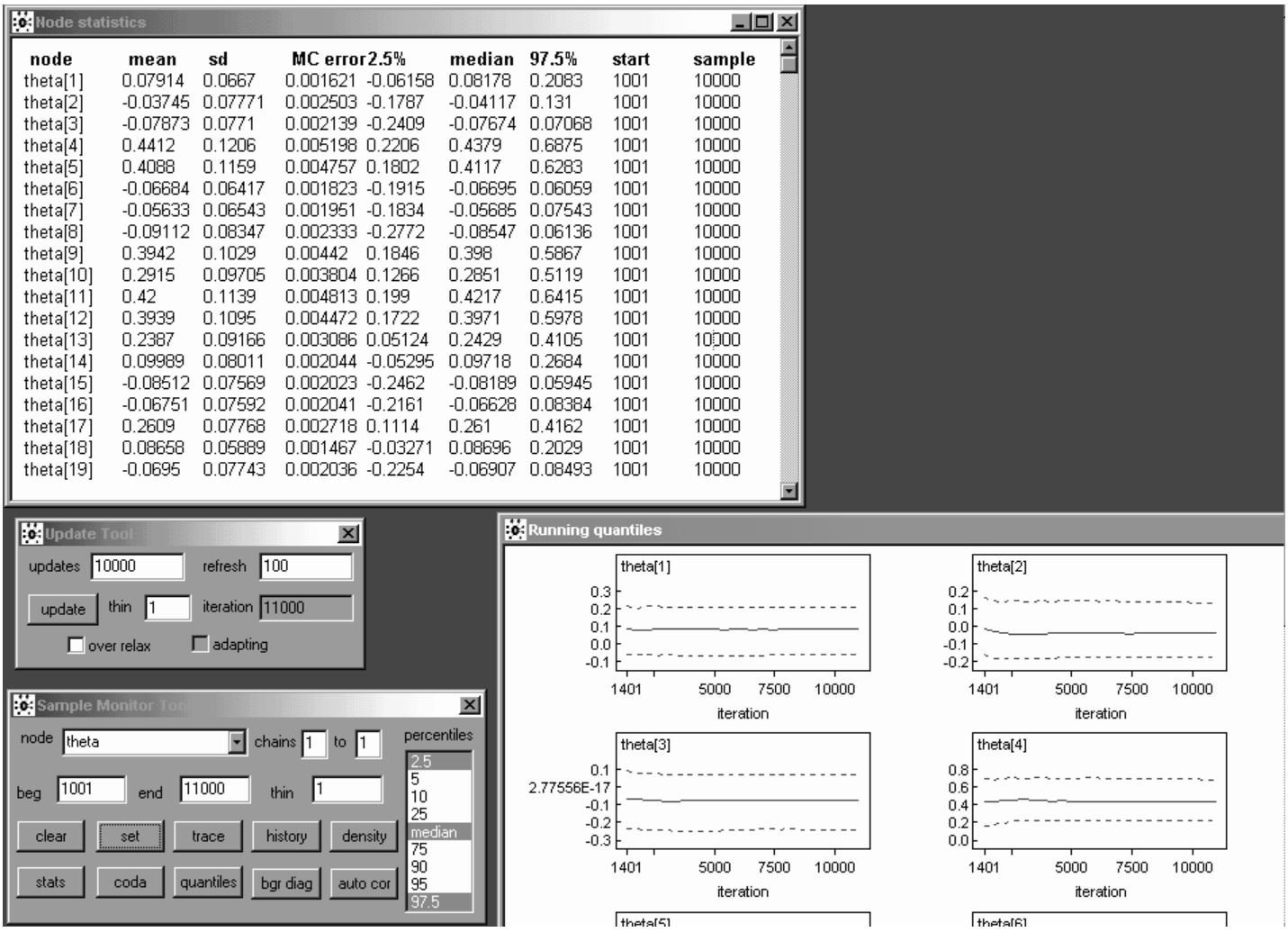
Some of the θ_i are evidently
mixing better than others.

WinBUGS Implementation



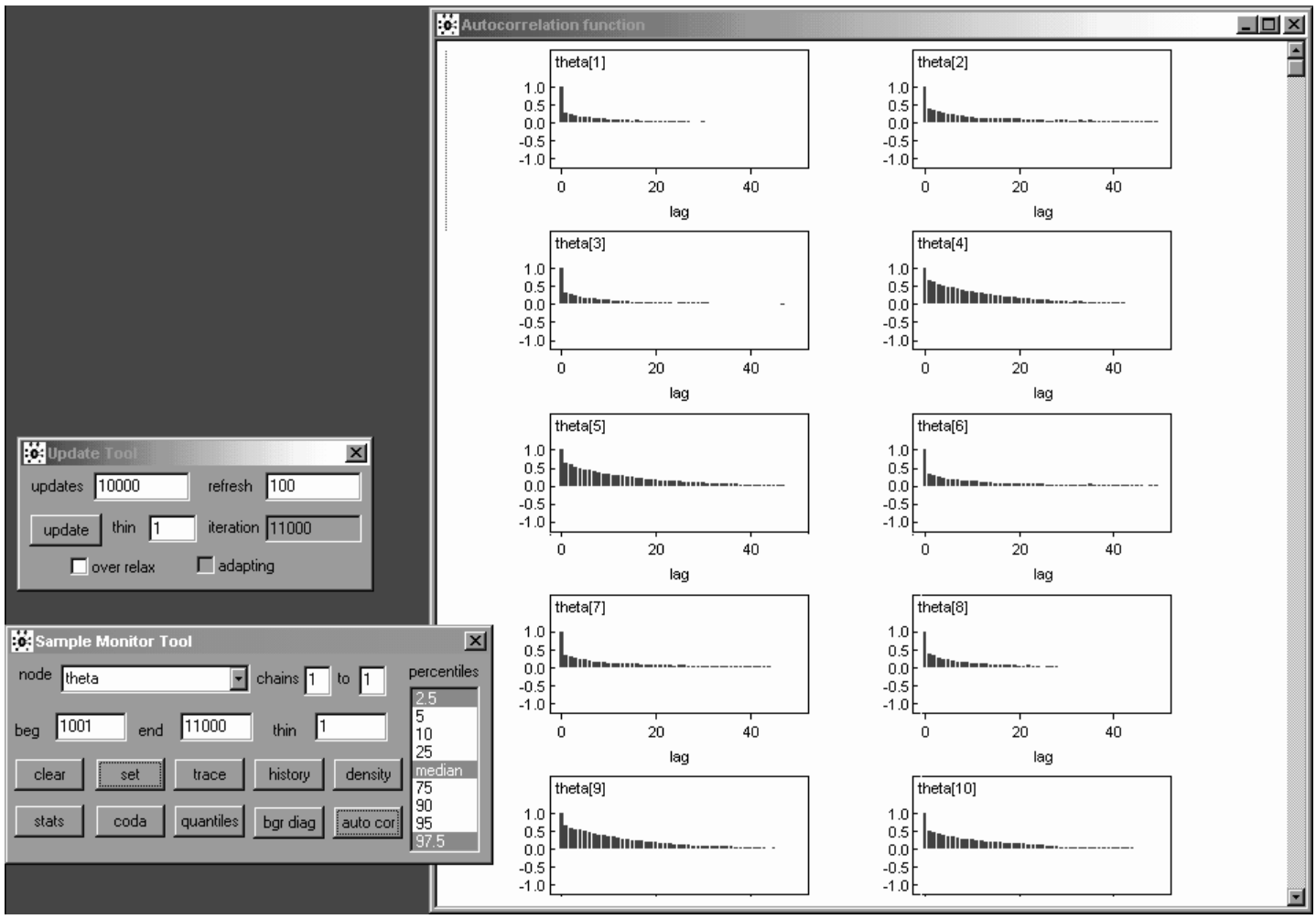
The **marginal density traces** of the θ_i look rather like t distributions with fairly low degrees of freedom (**fairly heavy tails**).

WinBUGS Implementation



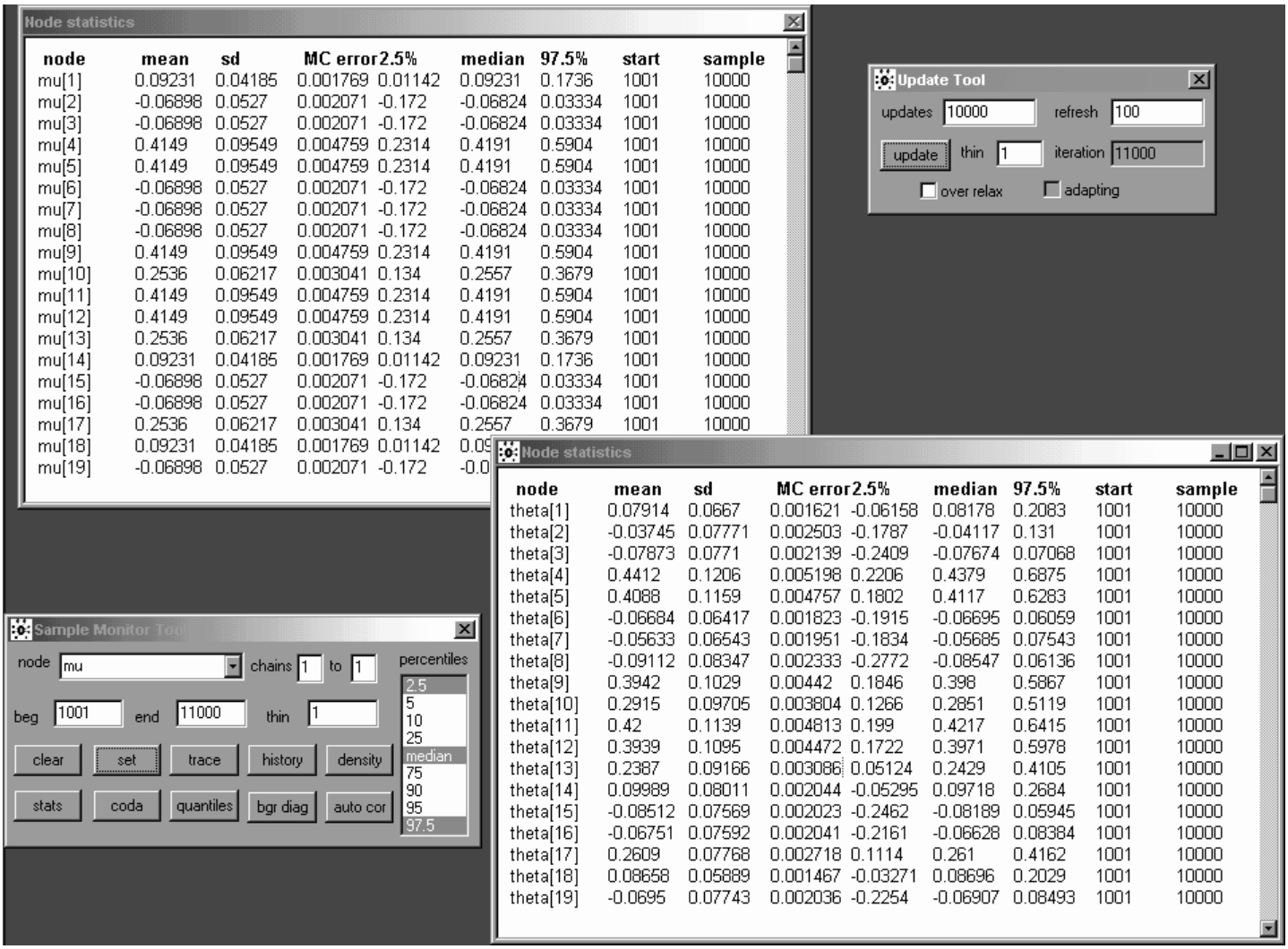
Many of the θ_i have **posterior probability concentrated near 0**, but not all; $\theta_4, \theta_5, \theta_9, \theta_{11}$, and θ_{12} are particularly large (looking back on page 12, what's **special** about the corresponding studies?).

WinBUGS Implementation



Some of the θ_i are **not far from white noise**; others are **mixing quite slowly**.

WinBUGS Implementation



It's also useful to monitor the $\mu_i = \alpha + \beta(x_i - \bar{x})$, because they represent an **important part of the shrinkage story** with model (10).

Shrinkage Estimation

In a manner parallel to the situation with the simpler model (1), the posterior means of the **underlying study effects** θ_i should be at least approximately related to the **raw effect sizes** y_i and the μ_i via the **shrinkage equation**

$$E(\theta_i|y) \doteq \left(1 - \widehat{B}_i\right) y_i + \widehat{B}_i E(\mu_i|y)\,; \qquad (34)$$

here $\widehat{B}_i = \frac{V_i}{V_i + \widehat{\sigma}^2_\theta}$ and $\widehat{\sigma}^2_\theta$ is the posterior mean of σ^2_θ.

This is **easy to check** in R:

```
> mu <- c( 0.09231, -0.06898, -0.06898, 0.4149, 0.4149, -0.06898, -0.06898,
    -0.06898, 0.4149, 0.2536, 0.4149, 0.4149, 0.2536, 0.09231, -0.06898,
    -0.06898, 0.2536, 0.09231, -0.06898 )

> y <- c( 0.03, 0.12, -0.14, 1.18, 0.26, -0.06, -0.02, -0.32, 0.27, 0.80,
    0.54, 0.18, -0.02, 0.23, -0.18, -0.06, 0.30, 0.07, -0.07 )

> theta <- c( 0.08144, -0.03455, -0.07456, 0.4377, 0.4076, -0.0628,
    -0.05262, -0.08468, 0.3934, 0.289, 0.4196, 0.3938, 0.2393, 0.1014,
    -0.08049, -0.06335, 0.2608, 0.08756, -0.06477 )

> V <- 1 / tau

> B.hat <- V / ( V + 0.064^2 )

> theta.approx <- ( 1 - B.hat ) * y + B.hat * mu
```

The Shrinkage Story (continued)

```
> cbind( y, theta, mu, sigma.2, B.hat, theta.approx )

          y    theta       mu        V     B.hat theta.approx
 [1,]  0.03  0.08144  0.09231 0.015625 0.7923026   0.07936838
 [2,]  0.12 -0.03455 -0.06898 0.021609 0.8406536  -0.03886671
 [3,] -0.14 -0.07456 -0.06898 0.027889 0.8719400  -0.07807482
 [4,]  1.18  0.43770  0.41490 0.139129 0.9714016   0.43678060
 [5,]  0.26  0.40760  0.41490 0.136161 0.9707965   0.41037637
 [6,] -0.06 -0.06280 -0.06898 0.010609 0.7214553  -0.06647867
 [7,] -0.02 -0.05262 -0.06898 0.010609 0.7214553  -0.05533688
 [8,] -0.32 -0.08468 -0.06898 0.048400 0.9219750  -0.08856583
 [9,]  0.27  0.39340  0.41490 0.026896 0.8678369   0.39574956
[10,]  0.80  0.28900  0.25360 0.063001 0.9389541   0.28695551
[11,]  0.54  0.41960  0.41490 0.091204 0.9570199   0.42027681
[12,]  0.18  0.39380  0.41490 0.049729 0.9239015   0.39702447
[13,] -0.02  0.23930  0.25360 0.083521 0.9532511   0.24080950
[14,]  0.23  0.10140  0.09231 0.084100 0.9535580   0.09870460
[15,] -0.18 -0.08049 -0.06898 0.025281 0.8605712  -0.08445939
[16,] -0.06 -0.06335 -0.06898 0.027889 0.8719400  -0.06783002
[17,]  0.30  0.26080  0.25360 0.019321 0.8250843   0.26171609
[18,]  0.07  0.08756  0.09231 0.008836 0.6832663   0.08524367
[19,] -0.07 -0.06477 -0.06898 0.030276 0.8808332  -0.06910155
```

You can see that equation (11) is indeed a **good approximation** to what's going on: the posterior means of the θ_i (column 3 of this table, counting the leftmost column of study indices) all fall between the y_i (column 2) and the posterior means of the μ_i (column 4), with the closeness to y_i or $E(\mu_i|y)$ expressed through the **shrinkage factor** $\widehat{B}_i$.

Since $\widehat{\sigma}^2_\theta$ is small (i.e., most—but not quite all—of the between-study variation has been explained by the covariate x), the raw y_i values are shrunken **almost all of the way toward the regression line** $\alpha + \beta(x_i - \overline{x})$.

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