Bayesian Statistics

Analysis of Hierarchical Models

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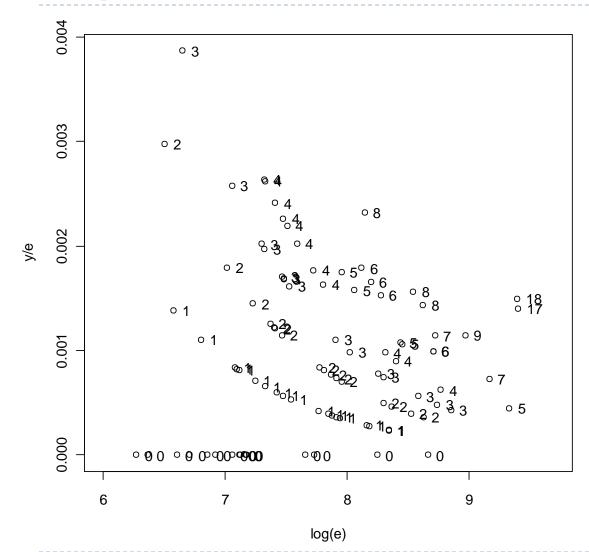
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Hierarchical Modeling

- Heart transplant mortality rates (section 7.3)
 - Goal: learn about the rate of success of heart transplant surgery of a particular hospital in the United States
 - ▶ Prior: $\lambda \sim gamma(\alpha, \beta)$
 - ▶ Based on pilot data from 10 hospitals: $(\alpha, \beta) = (16,15174)$
 - ▶ Data: $y_i \sim Poisson(e_i \lambda_i)$, i = 1, ..., 94
 - e_i : exposure
 - λ_i : mortality rate per unit exposure
 - Separate estimates, pooled estimate, or combined?

Death rates vs log(exposure) for all hospitals

Each point is labeled by the number of observed deaths.



- Death rate = y_i/e_i
- The estimated rates are highly variable, especially for programs with small exposures.
- The programs experiencing no deaths (a plotting label of 0) also are primarily associated with small exposures.

Pooled estimate (section 7.4)

- Assume equal mortality rates at all hospitals
- Use a noninformative prior

$$g(\lambda) \propto \frac{1}{\lambda}$$
.

▶ Posterior: $gamma(\sum_j y_j, \sum_j e_j)$

$$g(\lambda|\text{data}) \propto \frac{1}{\lambda} \prod_{j=1}^{94} \left[\lambda^{y_j} \exp(-e_j \lambda) \right]$$
$$= \lambda^{\sum_{j=1}^{94} y_j - 1} \exp\left(-\sum_{j=1}^{94} e_j \lambda \right)$$

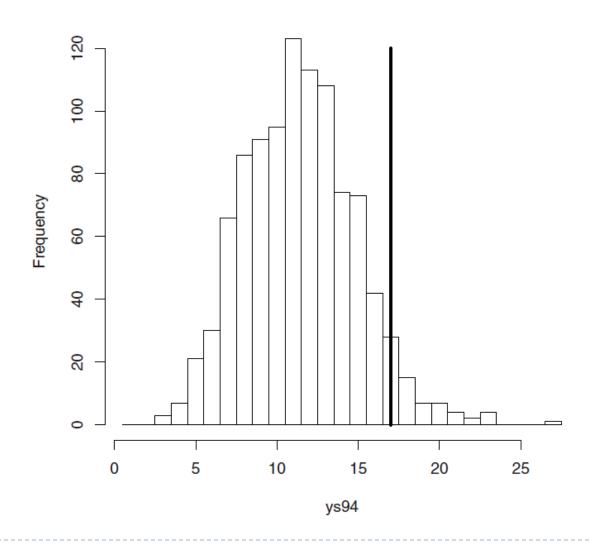
Pooled estimate

Check model fit using predictive distribution

$$f(y_i^*|e_i, y) = \int f_P(y_i^*|e_i\lambda)g(\lambda|y)d\lambda,$$

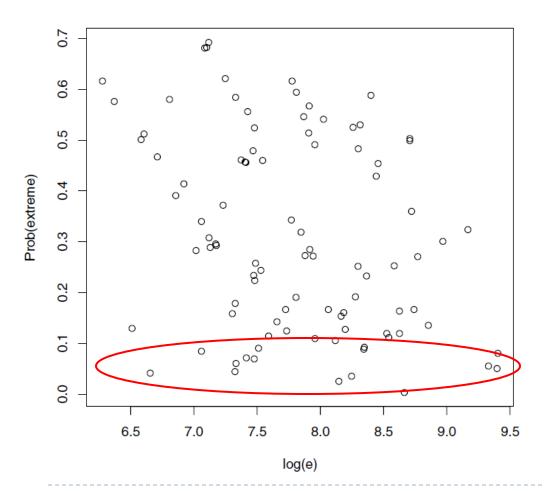
- If the actual number of observed deaths y_i is in the middle of this predictive distribution, then we can say that our observation is consistent with our model fit.
- On the other hand, if the observed y_i is in the extreme tails of the distribution $f(y_i^*|e_i,y)$, then this observation indicates that the model is inadequate in fitting this observation.

Hospital 94, $y_{94} = 17$



Probability that the future observation y_i^* is at least as extreme as y_i for all hospitals

$$\min\{P(y_i^* \le y_i), P(y_i^* \ge y_i)\}.$$



Note that a number of these tail probabilities appear small (15 are smaller than 0.10), which means that the "equalrates" model is inadequate for explaining the distribution of mortality rates for the group of 94 hospitals.

Hierarchical model (section 7.5)

- $y_i \sim Poisson(e_i \lambda_i), i = 1, ..., 94$
- Exchangeability $\rightarrow \lambda_1, \dots, \lambda_{94} \sim gamma\left(\alpha, \frac{\alpha}{\mu}\right)$

$$f(\lambda | \alpha, \mu) = \frac{\left(\frac{\alpha}{\mu}\right)^{\alpha} \lambda^{\alpha - 1} \exp(-\alpha \lambda / \mu)}{\Gamma(\alpha)}$$

- Prior mean: μ
- Prior variance: $\frac{\mu^2}{\alpha}$
- Hyper-prior:
 - $\mu \sim Inv gamma(a, b)$
 - $\alpha \sim g(\alpha)$
 - \triangleright μ and α are independent
- This model induces positive correlation between λ_i
 - See Albert (2009)

Practical setup

Noninformative prior

$$g(\mu) \propto rac{1}{\mu}, \mu > 0.$$
 This is a relatively flat distribution. $g(\alpha) = rac{z_0}{(\alpha + z_0)^2}, \alpha > 0.$

 $ightharpoonup z_0$ is the prior median of α . We set $z_0 = 0.53$.

Posterior

- $\lambda_i | \mu, \alpha, y \sim gamma(y_i + \alpha, e_i + \frac{\alpha}{\mu})$
- By integrating the joint posterior $f(\alpha, \mu, \lambda_1, ..., \lambda_{94}|y)$ w.r.t. λ_i

$$p(\alpha, \mu | \text{data}) = K \frac{1}{\Gamma^{94}(\alpha)} \prod_{j=1}^{94} \left[\frac{(\alpha/\mu)^{\alpha} \Gamma(\alpha + y_i)}{(\alpha/\mu + e_i)^{(\alpha + y_i)}} \right] \frac{z_0}{(\alpha + z_0)^2} \frac{1}{\mu},$$

Simulating from the posterior distribution (section 7.7)

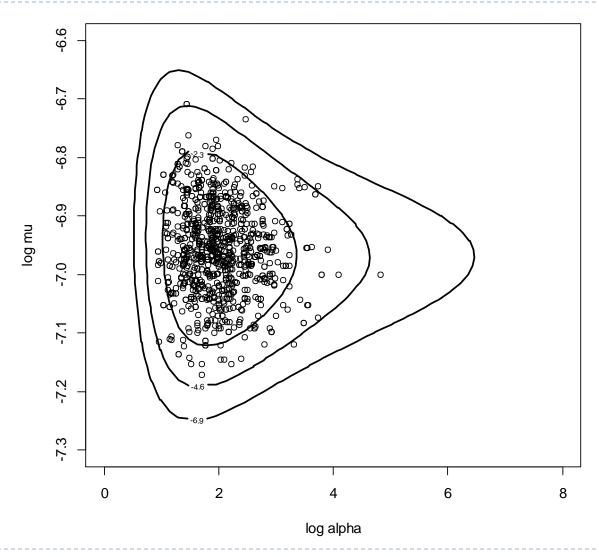
Simulation

- Simulate from $p(\mu, \alpha | \text{data})$
- Simulate from $\lambda_i | \mu, \alpha, y \sim gamma(y_i + \alpha, e_i + \frac{\alpha}{\mu})$
- Since both μ and α are positive, consider parameter transformation: Let $\theta_1 = \log(\alpha)$, $\theta_2 = \log(\mu)$

$$p(\theta_1, \theta_2 | \text{data}) = K \frac{1}{\Gamma^{94}(\alpha)} \prod_{i=1}^{94} \left[\frac{\left(\frac{\alpha}{\mu}\right)^{\alpha} \Gamma(\alpha + y_i)}{\left(\frac{\alpha}{\mu} + e_i\right)^{\alpha + y_i}} \right] \frac{z_0 \alpha}{(\alpha + z_0)^2}$$

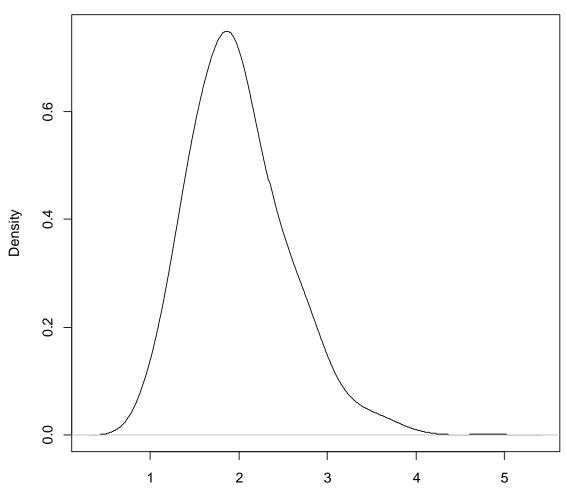
- $\log p(\theta_1, \theta_2 | \text{data})$ is defined by R function poissgamexch in the package LearnBayes
- A Metropolis-within-Gibbs algorithm is used to sample from this distribution using the function gibbs

Contour plot of the posterior density of $(\log \alpha, \log \mu)$ with simulate values imposed



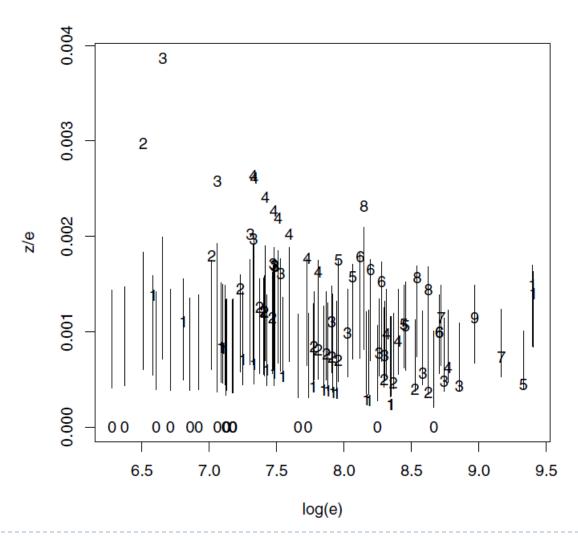
Marginal posterior density of $log\alpha$

density.default(x = fitgibbs\$par[, 1], bw = 0.2)



Math459: Bayesian Statistics

Plot of observed death rates against log(exposure) together with intervals representing 90% posterior probability bands for the true rates $\{\lambda_i\}$.

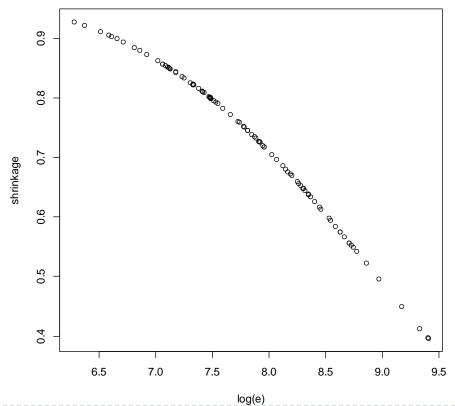


Shrinkage effect

plot of posterior shrinkage vs log(exposure)

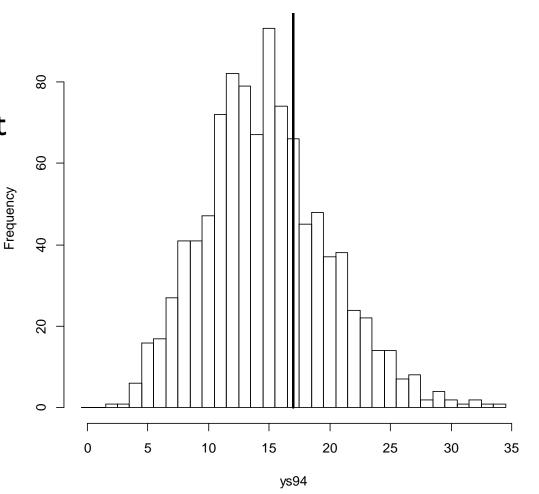
$$E(\lambda_i|data) \approx \left(1 - E(B_i|data)\right) \frac{y_i}{e_i} + E(B_i|data) \frac{\sum_{j=1}^{94} y_j}{\sum_{j=1}^{94} e_j}$$

Size of shrinkage: $B_i = \alpha/(\alpha + e_i \mu)$



Posterior Predictive Model Checking (section 7.10)

- $p(y_{94}^*|y)$
- The observed value of $y_{94} = 17$ is in the middle, which indicates agreement of this observation with the fitted model.

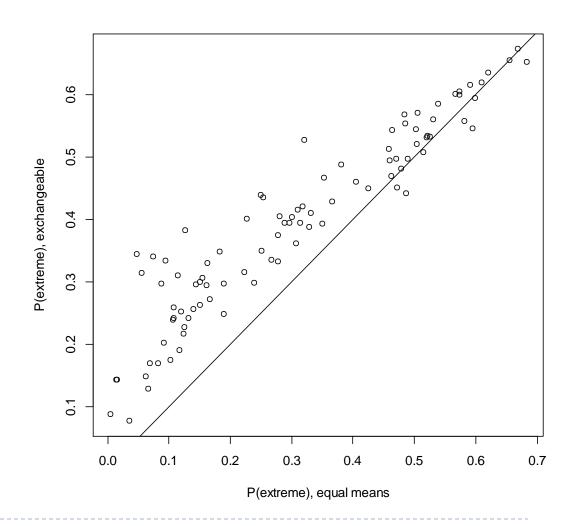


Posterior Predictive Model Checking

Perform this for all y_i , i = 1, ..., 94 and in each case calculate the posterior predictive pvalue (ppp)

$$\min\{P(y_i^* \le y_i), P(y_i^* \ge y_i)\}.$$

The plot on the right shows a comparison between the ppp from the hierarchical model and the simple equalrate model



Basic analysis of MCMC output (section 6.8)

- ▶ R package coda
- ▶ To use various diagnostic and summary tools in coda, one first needs to convert the MCMC output using the function mcmc
 - You may perform thinning when using mcmc()
 - It is usually necessary to discard a burn-in period

Graphics

- Trace plot (can use any plotting function in R)
- Autocorrelation (autocorr.plot)
- Basic numeric summary
 - summary.mcmc()

Exercise

• Recall that we used a Metropolis-within-Gibbs algorithm to simulate from $p(\theta_1, \theta_2 | \text{data})$ in the hospital example

```
library(LearnBayes)
data(hearttransplants)
attach(hearttransplants)

datapar = list(data = hearttransplants, z0 = 0.53)
start = c(4, -7)
fitgibbs = gibbs(poissgamexch, start, 1000, c(1,.15), datapar)
```

Perform a basic analysis to the MCMC output

```
xyplot(mcmc(fitgibbs$par))
autocorr.plot(mcmc(fitgibbs$par))
summary(mcmc(fitgibbs$par))
batchSE(mcmc(fitgibbs$par))
```