Gene Expression Analysis

A specific example of Gibbs sampling - canonical Markov chain Monte Carlo method for calculations in Bayesian statistical models, as well as a key applied model class.

♠ Simulation of Posteriors

- For any statistical model, simulated values of posterior distributions are nowadays the standard in statistical computation: summarise large samples of parameter values from a posterior distribution to easily understand the information contained in that posterior about the parameters
- MCMC methods, such as Gibbs sampling, generate simulations sequentially using Markov chains
- Gibbs sampling represents an approach in which sets of coupled conditional posteriors derived from the model are used for these simulations
- Here's a key example

A Probit Model

- Expression level vector \mathbf{x}_j on array (tumor sample, etc) $j = 1, \ldots, n$
- Binary outcome: $z_j = 0$ or 1
- Probit probability model: $\pi_j = Pr(z_j = 1)$ (conditional on chosen predictor variables and model parameters: in full, $\pi_j = Pr(z_j = 1 | \mathbf{x}_j, \boldsymbol{\beta})$)
- Linear regression model based on regression function $\mu_j = \mathbf{x}'_j \boldsymbol{\beta}$ (perhaps \mathbf{x}_j is extended with a leading 1 to include an intercept term β_0)
- Probit regression:

$$\pi_i = \Phi(\mu_i)$$

where Φ is standard normal cumulative distribution function

Prior and Posterior

- Example: $\beta \sim N(0, \mathbf{C}^{-1})$ and we'll take the precision as diagonal
- Posterior for regression parameters

$$p(\boldsymbol{\beta}|\mathbf{z}) \propto \exp(-\boldsymbol{\beta}' \mathbf{C} \boldsymbol{\beta}) \prod_{j=1}^{n} \Phi(\mu_j)^{z_j} (1 - \Phi(\mu_j))^{1-z_j}$$

which can be evaluated, numerically optimized (it is unimodal) using standard NR routines,

- Exercise: Write code (in C/C++ or other) to implement a Newton-Raphson search for the mode of the posterior density. As ALWAYS in such problems, work with the log-posterior, i.e., maximise the log of the target function for numerical stability
- Under vague reference prior $(\mathbf{C} \to 0)$ the posterior is the normalised likelihood function. The MLE and related information can be computer using R/Splus glm functions, Matlab glmfit function, or (quite easily) by user-written code as a special case

♠ Latent Variables and Data Augmentation

- For each sample, recognise an underlying latent variable \mathbf{y}_i
- $\pi_j = Pr(y_j > 0)$ when $y_j \sim N(\mu_j, 1) = N(\mathbf{x}'_j \boldsymbol{\beta}, 1)$
- $z_j = 1$ if and only if $y_j > 0$
 - e.g., latent variable is positive for ER+ cases, negative for ER- cases

- could precisely classify cases if we could observe the latent y_j , but we do not; result is the binary probability model
- MCMC calculations impute these "missing" values along with values of the parameters $oldsymbol{eta}$

♠ Conditional Posteriors

• $p(\boldsymbol{\beta}|\mathbf{y}, \mathbf{z})$

If **y** were known, we have a linear regression of the y_j with regression variables \mathbf{x}_j , parameter $\boldsymbol{\beta}$ and error variance 1. The actual value of **z** is at this point irrelevant – the information they contain is already there in the (current, imputed or candidate) values of **y**: Formally, $\boldsymbol{\beta}$ is conditionally independent of **z** given **y**. The posterior (see earlier notes) is multivariate normal

$$\boldsymbol{\beta} | \mathbf{y}, \mathbf{z} \sim N(\mathbf{b}, \mathbf{B}^{-1})$$

with $\mathbf{B} = \mathbf{C} + \mathbf{H}'\mathbf{H}$ and $\mathbf{b} = \mathbf{B}^{-1}\mathbf{H}'\mathbf{y}$ where $\mathbf{H} = \mathbf{X}'$ is the $n \times p$ design matrix. For multivariate normals, use programmed functions (multivariate normal simulation is very standard - e.g., rMNorm.m or similar) or use direct Cholesky decomposition: e.g., by hand in matlab

 $\mathbf{b} + chol(inv(\mathbf{B})) * randn(p, 1)$

for a single draw

• $p(\mathbf{y}|\boldsymbol{\beta}, \mathbf{z})$

If β were known, then the y_j are independent normals but subject to the information provided by the z_j - in each case, we just condition the initial normal on the information that y_j must be positive (if $z_j = 1$) or negative (if $z_j = 0$). The result may be written simply in terms of the posterior cumulative distribution function, as

$$P(y_j|z_j = 1) = [\Phi(y_j - \mu_j) - (1 - \pi_j)]/\pi_j, \quad \text{for } y_j > 0,$$

and

$$P(y_j|z_j = 0) = \Phi(y_j - \mu_j)/(1 - \pi_j),$$
 for $y_j < 0$

(check that you can derive this). Or, for any value of $z_j = 0, 1$,

$$P(y_j|z_j) = [\Phi(y_j - \mu_j) - z_j(1 - \pi_j)] / [z_j \pi_j + (1 - z_j)(1 - \pi_j)].$$

Simulated values of the y_j are then drawn, independently, via the inverse CDF approach: generate $u_j \sim U(0,1)$ and solve for y_j in $P(y_j|z_j) = u_j$. It can be written trivially as

 $y_j = \mu_j + \Phi^{-1} \{ z_j (1 - \pi_j) + u_j (z_j + (1 - \pi_j)(1 - 2z_j)) \}$

with Φ^{-1} being the normal quantile function (inverse CDF - qnorm function).

♠ Including Additional Parameters

MCMC neatly extends to include other parameters. Here's a key example.

• Suppose $\mathbf{C} = \operatorname{diag}(\gamma_0, \gamma_1, \dots, \gamma_p)$ with prior variances $\tau_i^2 = \gamma_i^{-1}$ defining element-wise shrinkage parameters for the individual predictor variables. The above discussion all applied now explicitly conditional on values of \mathbf{C} , so that the simulation iterations can run with simulations of \mathbf{C} coupled in too. That requires priors on elements of \mathbf{C} ; if these are independent gamma priors, $\gamma_j \sim Ga(k/2, h/2)$ for each j, say, then the relevant conditional posteriors are also independent gammas, namely

$$\gamma_j \sim Ga((k+1)/2, (h+\beta_j^2)/2)$$

This allows for learning on differential shrinkage parameters across variables.

- Exercise: Develop the MCMC with these priors.
- Think about choices of prior parameters: One general way to think about ranges of relevant parameter values in binary regression models is to consider how variation in μ_j translates through to the probability scale π_j . Absolute values of μ_j bigger than 2 or so lead to probabilities that are already very extreme.

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