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Suggested solutions for MSA100 / MVE186 Computer Intensive Statistical Methods Re-exam 5 June 2017

1. The first statement is used within frequentist statistics. Its interpretation is as follows: There are statistics L_1 and L_2 defined in terms of a sample x'_1, \ldots, x'_n from a normal distribution with expectation θ and variance 1, such that the stochastic interval $[L_1, L_2]$ contains θ with 95% probability; the values of these statistics computed on the given data is $L_1 = 2.3$ and $L_2 = 2.5$.

The second statement is used within Bayesian statistics. Its interpretation is as follows: With some prior on θ (not specified in the question), the posterior probability that θ is in the interval [2.3, 2.5] is 95%.

2. (a) If $p \sim \text{Beta}(\alpha, \beta)$ and $x \mid p \sim \text{Neg-Bin}(r, p)$, then

$$\pi(p \mid x) \propto_p \pi(x \mid p) \pi(p) \propto_p (1-p)^r p^x p^{\alpha-1} (1-p)^{\beta-1} = p^{\alpha+x-1} (1-p)^{\beta+r-1}.$$

Thus $p \mid x \sim \text{Beta}(\alpha + x, \beta + r)$, and the Beta family of distributions is conjugate to to the Negative Binomial distribution for the *p* parameter.

(b) We get

$$\pi(x) = \frac{\pi(x \mid p)\pi(p)}{\pi(p \mid x)} = \frac{\binom{x+r-1}{x}(1-p)^r p^x \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)} p^{\alpha-1}(1-p)^{\beta-1}}{\frac{\Gamma(\alpha+x+\beta+r)}{\Gamma(\alpha+x)\Gamma(\beta+r)} p^{\alpha+x-1}(1-p)^{\beta+r-1}}$$
$$= \binom{x+r-1}{x} \frac{\Gamma(\alpha+\beta)\Gamma(\alpha+x)\Gamma(\beta+r)}{\Gamma(\alpha)\Gamma(\beta)\Gamma(\alpha+x+\beta+r)}$$

(c) The posterrior predictive is the same as the prior predictive using the posterior given x as the prior when predicting x_{NEW} . Using (a), we get in our case that

$$p \mid x \sim \text{Beta}(\alpha + x, \beta + r) = \text{Beta}(2 + 1, 1 + 2) = \text{Beta}(3, 3)$$

and using (b) we then get

$$\pi(x_{NEW} \mid x) = {\binom{x_{NEW} + 2 - 1}{x_{NEW}}} \frac{\Gamma(3+3)\Gamma(3+x_{NEW})\Gamma(3+2)}{\Gamma(3)\Gamma(3)\Gamma(3+x_{NEW}+3+2)}$$

= $720 \frac{x_{NEW} + 1}{(x_{NEW} + 3)(x_{NEW} + 4)(x_{NEW} + 5)(x_{NEW} + 6)(x_{NEW} + 7)}$

(d) Let *C* be a variable such that C = 1 means model 1 is used and C = 2 means model 2 is used. The Bayes factor *B* is equal to the likelihood ratio $\pi(x | C = 1)/\pi(x | C = 2)$. Thus it is equal to the ratio of the corresponding prior predictive distributions:

$$B = \frac{\begin{pmatrix} x+r-1\\ x \end{pmatrix} \frac{\Gamma(\alpha_1+\beta_1)\Gamma(\alpha_1+x)\Gamma(\beta_1+r)}{\Gamma(\alpha_1)\Gamma(\beta_1)\Gamma(\alpha_1+x+\beta_1+r)}}{\begin{pmatrix} x+r-1\\ x \end{pmatrix} \frac{\Gamma(\alpha_2+\beta_2)\Gamma(\alpha_2+x)\Gamma(\beta_2+r)}{\Gamma(\alpha_2)\Gamma(\beta_2)\Gamma(\alpha_2+x+\beta_2+r)}}} = \frac{\Gamma(\alpha_1+\beta_1)\Gamma(\alpha_1+x)\Gamma(\beta_1+r)\Gamma(\alpha_2)\Gamma(\beta_2)\Gamma(\alpha_2+x+\beta_2+r)}{\Gamma(\alpha_1)\Gamma(\beta_1)\Gamma(\alpha_1+x+\beta_1+r)\Gamma(\alpha_2+\beta_2)\Gamma(\alpha_2+x)\Gamma(\beta_2+r)}$$

(e) We have, apriori, that $\pi(C = 1) = \pi(C = 2) = 0.5$. The posterior probabilities for the two models can be computed using Bayes formula on odds form, i.e.,

$$\frac{\pi(C=1 \mid x)}{1 - \pi(C=1 \mid x)} = B \cdot \frac{\pi(C=1)}{\pi(C=2)} = B \cdot 1$$

which solves to $\pi(C = 1 | x) = B/(1 + B)$. Using the posterior for each model computed in (a), the posterior probability density for p given x is

$$\frac{B}{1+B} \cdot \frac{\Gamma(\alpha_1 + x + \beta_1 + r)}{\Gamma(\alpha_1 + x)\Gamma(\beta_1 + r)} p^{\alpha_1 + x - 1} (1-p)^{\beta_1 + r - 1} + \frac{1}{1+B} \cdot \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\beta_2 + r)} p^{\alpha_2 + x - 1} (1-p)^{\beta_2 + r - 1} + \frac{1}{1+B} \cdot \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\beta_2 + r)} p^{\alpha_2 + x - 1} (1-p)^{\beta_2 + r - 1} + \frac{1}{1+B} \cdot \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\beta_2 + r)} p^{\alpha_2 + x - 1} (1-p)^{\beta_2 + r - 1} + \frac{1}{1+B} \cdot \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\beta_2 + r)} p^{\alpha_2 + x - 1} (1-p)^{\beta_2 + r - 1} + \frac{1}{1+B} \cdot \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\beta_2 + r)} p^{\alpha_2 + x - 1} (1-p)^{\beta_2 + r - 1} + \frac{1}{1+B} \cdot \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\beta_2 + r)} p^{\alpha_2 + x - 1} (1-p)^{\beta_2 + r - 1} + \frac{1}{1+B} \cdot \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\beta_2 + r)} p^{\alpha_2 + x - 1} (1-p)^{\beta_2 + r - 1} + \frac{1}{1+B} \cdot \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\beta_2 + r)} p^{\alpha_2 + x - 1} (1-p)^{\beta_2 + r - 1} + \frac{1}{1+B} \cdot \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\beta_2 + r)} p^{\alpha_2 + x - 1} (1-p)^{\beta_2 + r - 1} + \frac{1}{1+B} \cdot \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\beta_2 + r)} p^{\alpha_2 + x - 1} (1-p)^{\beta_2 + r - 1} + \frac{1}{1+B} \cdot \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\beta_2 + r)} p^{\alpha_2 + x - 1} + \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\beta_2 + r)} p^{\alpha_2 + x - 1} + \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\beta_2 + r)} p^{\alpha_2 + x - 1} + \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\beta_2 + r)} p^{\alpha_2 + x - 1} + \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\beta_2 + r)} p^{\alpha_2 + x - 1} + \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\alpha_2 + r)} p^{\alpha_2 + x - 1} + \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\alpha_2 + r)} p^{\alpha_2 + x - 1} + \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\alpha_2 + r)} p^{\alpha_2 + x - 1} + \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\alpha_2 + r)} p^{\alpha_2 + x - 1} + \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\alpha_2 + r)} p^{\alpha_2 + x - 1} + \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\alpha_2 + r)} p^{\alpha_2 + x - 1} + \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\alpha_2 + r)} p^{\alpha_2 + x - 1} + \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\alpha_2 + r)} p^{\alpha_2 + x - 1} + \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\alpha_2 + r)} p^{\alpha_2 + x - 1} + \frac{\Gamma(\alpha_2 + x + \beta_2 + r)}{\Gamma(\alpha_2 + x)\Gamma(\alpha_2 + r)} p^{\alpha_2 + x - 1} + \frac{\Gamma(\alpha_2 + x + \beta_$$

3. (a) The cumulative density for an Exponential distribution with parameter 2.7 is, for $x \ge 0$,

$$F(x) = 1 - \exp(-2.7x).$$

Writing U = F(x), we get $x = -\log(1 - U)/2.7$. Thus, we may simulate from the distribution by first simulating U' uniformly on the interval [0, 1], and then computing $x = -\log(U')/2.7$.

(b) Simulation may be done in several ways; one option is to simulate x from a Gamma distribution with parameters $\alpha = 2.7$ and $\beta = 9.1$ and output 1/x. The Gamma distribution has density

$$\pi(x) = \frac{\beta^{\alpha}}{\Gamma(\alpha)} x^{\alpha - 1} \exp(-\beta x)$$

and it is possible to simulate from it using rejection sampling. Differentiation shows that this density has its maximum at $(\alpha - 1)/\beta = 1.7/9.1 = 0.1868132$, where the density is then 2.652551. But we can also use the identity $\log(x) \le x - 1$ to show that

$$\pi(x) = \frac{\beta^{\alpha}}{\Gamma(\alpha)} \exp(-\beta x + (\alpha - 1)\log(x)) \le \frac{\beta^{\alpha}}{\Gamma(\alpha)} \exp(-\beta x + (\alpha - 1)(x - 1)) \\ = 45.94846 \cdot \exp(-7.4x) < 6.21 \cdot 7.4 \exp(-7.4x)$$

when we use that $\alpha = 2.7$ and $\beta = 9.1$. Thus a simple solution is to use rejection sampling with an exponential distribution with parameter 7.4 as a proposal distribution, and M = 6.21. (More efficient simulation solutions exist, for example by using a different proposal density for small x).

(c) We can recognize this density as a mixture of normal densities:

$$\pi(x) = \sum_{i=1}^{7} w_i \operatorname{Normal}(x; u_i, 1)$$

where Normal($x; u_i, 1$) denotes the value in x of the normal density with expectation u_i and variance 1. To simulate from this density, simulate first an index i according to the probabilities w_1, \ldots, w_7 . This can be done by simulating U uniformly on [0, 1] and finding the smallest i such that $w_1 + \cdots + w_i \ge U$. Then, if ϕ^{-1} is the inverse of the cumulative distribution function for the standard normal distribution, we may output

$$\phi^{-1}(V) + u_i$$

where V is uniformly simulated on [0, 1].

- 4. (a) A Bayesian Network is a Directed Acyclic Graph (DAG), for each node *i* in the network a variable x_i, and for each such node a conditional probability density π(x_i | x_{j1},..., x_{jk}), where j₁,..., j_k are the indices of the parents of node *i* in the DAG. The product of these conditional probability densities represents the joint probability density for the network.
 - (b) A Markov Network is an undirected graph, for each node *i* in the network a variable x_i , and for each set of nodes with indices j_1, \ldots, j_k such that all nodes in the set are connected in the graph a nonnegative function $\phi(x_{j_1}, \ldots, x_{j_k})$. The product of all the factors represents the (unnormalized) probability density of the network.
 - (c) If the value x_i of a node *i* is observed in a Bayesian network, the probability density for the remaining nodes is obtained as the conditional density given x_i . If the value of node *i* is set by *intervention* in a causal network with the same structure, the probability density for the remaining nodes is obtained by first removing the conditional density $\pi(x_i | x_{j_1}, \ldots, x_{j_i})$ in the product of conditional densities representing the Bayesian network, before conditioning on the value x_i in the remaining product.
 - (d) Two nodes *i* and *j* are connected in the Markov graph if and only if $\tau_{ij} \neq 0$, where τ_{ij} is the value in the *i*'th row and *j*'th column of the precision matrix.
- 5. If an integral is written as $I = \int f(x)g(x) dx$ with g(x) being a probability density, then Monte Carlo integration means making the approximation

$$I = E_g[f(x)] = \int f(x)g(x) \, dx \approx \frac{1}{n} \sum_{i=1}^n f(x_i) = \hat{I}$$

where x_1, \ldots, x_n is a sample from the density g(x). As long as f(x) has finite variance σ^2 when x is distributed according to g(x), the Central Limit Theorem tells us that, for large *n*, and assuming the sample is a random sample, we have approximately

$$\hat{I} \sim \operatorname{Normal}\left(E_g\left[f(x)\right], \sigma^2/n\right)$$

and this can be used to obtain approximate estimates for $\hat{I} - I$.

6. (a) The posterior density for the model can be written as

$$\pi(\alpha)\pi(\beta)\prod_{i=1}^{k}\left[\left[\prod_{j=1}^{s}\pi(c_{ij}\mid\lambda_i)\right]\pi(\lambda_i\mid\alpha,\beta)\right]$$
$$\propto \beta^{5-1}\exp(-2\beta)\prod_{i=1}^{k}\left[\left[\prod_{j=1}^{s}\exp(-\lambda_i)\frac{\lambda_i^{c_{ij}}}{c_{ij}!}\right]\frac{\beta^{\alpha}}{\Gamma(\alpha)}\lambda_i^{\alpha-1}\exp(-\beta\lambda_i)\right]$$

Taking the logarithm and removing additive terms not depending on α , β , or $\lambda_1, \ldots, \lambda_k$, we get the log posterior

$$4\log(\beta) - 2\beta + \sum_{i=1}^{k} \left[\left[\sum_{j=1}^{s} -\lambda_i + c_{ij}\log(\lambda_i) \right] + \alpha\log(\beta) - \log(\Gamma(\alpha)) + (\alpha - 1)\log(\lambda_i) - \beta\lambda_i \right]$$
$$= (4 + k\alpha)\log(\beta) - 2\beta - k\log(\Gamma(\alpha)) - (s + \beta)\sum_{i=1}^{k}\lambda_i + \sum_{i=1}^{k} \left(\alpha + \sum_{j=1}^{s} c_{ij} - 1\right)\log(\lambda_i)$$

- (b) Given a function $f(\theta_1, \ldots, \theta_n)$ proportional to a joint density for the parameters $\theta = (\theta_1, \ldots, \theta_n)$, assume you can derive and simulate from each of the conditional distributions $\pi(x_i | x_1, \ldots, x_{i-1}, x_{i+1}, \ldots, x_n)$, for $i = 1, \ldots, n$. Then Gibbs sampling entails first simulating a vector of parameters $\theta^{(0)}$ from some distribution, followed by, for each *t*, updating $\theta^{(t)}$ to $\theta^{(t+1)}$ by sequentially simulating from the conditional distributions mentioned above, using updated values for the remaining parameters each time. This can be seen as a version of the Metropolis Hastings algorithm, and thus, under general conditions, the distribution of $\theta^{(t)}$ will approach the original joint density when $t \to \infty$.
- (c) In the model above, we see from the loglikelihood of question (a) that, for i = 1, ..., k,

$$\lambda_i \mid \alpha, \beta, c_{i1}, \dots, c_{is} \sim \text{Gamma}\left(\alpha + \sum_{j=1}^s c_{ij}, \beta + s\right)$$

while

$$\beta \mid \alpha \lambda_1, \dots, \lambda_k \sim \text{Gamma}\left(5 + k\alpha, 2 + \sum_{i=1}^k \lambda_i\right)$$

For α we get

$$\pi(\alpha \mid \beta, \lambda_1, \dots, \lambda_k) \propto \exp\left(\left(k \log(\beta) + \sum_{i=1}^k \log(\lambda_i)\right) \alpha - k \log(\Gamma(\alpha))\right)$$

This can be simulated from using for example rejection sampling.

7. (a) The simplest (but not by a long shot the most efficient) alternative would be to use as proposal density g a uniform distribution on the interval [-15, 35]. Its density on this

interval would be 1/50 = 0.02, and so we can see from the figure that choosing for example M = 7, we get $Mg(x) \ge f(x)$, where f(x) is the target density. For each iteration, the algorithm would simulate $x \sim \text{Uniform}[-15, 35]$ and $U \sim \text{Uniform}[0, 0.14]$, and would then reject x unless $U \le f(x)$.

- (b) The simplest possibility would again be to use a uniform distribution on [-15, 35] as proposal function. The main difference with (a) would be that the chain would contain a number of repeated values; it would "get stuck" for a while at values corresponding to the peaks in the figure. However, one may also use a more tailored proposal function, for example a mixture of three normals, with expectations -6, 6, and 11, respectively, and with respective standard deviations 1, 1, and 4, for example.
- (c) With a random walk Metropolis Hastings, you would like the Markov chain to be able to jump from one area of high density to another, i.e., occationally it should jump a length around 8. Thus a normal distribution with standard deviation 4 could be suitable.
- (d) If you rescale the proposal function to a much smaller variance, there is a danger that the Markov chain would get stuck in one of the areas of high density for a very long time, as a chain passing the areas of low density would be unlikely. If ou rescale to a much larger variance, one would get the problem that the proposed values would very rarely be accepted, and the chain would be stuck at a single value for that reason.