HW 13

Problem 1

A novel test has:

- An α chance of detecting the cancer if the tumor is malignant,

- A .02 chance of falsely finding cancer if the tumor is benign.

Using the Bayes rule the updated $\pi(\theta = \text{cancer}|T)$ is

$$\frac{0.9\alpha}{0.9\alpha + 0.1 \times 0.02}, \text{ if } T \text{ is positive,}$$

$$\frac{0.9(1-\alpha)}{0.9(1-\alpha) + 0.1 \times 0.98}, \text{ if } T \text{ is negative.}$$

The quality-adjusted life expectancy given that T is positive is:

$$\begin{aligned}
u(a_1) &= 15.7\pi(\theta = \text{cancer}|T = 1) + 33.8(1 - \pi(\theta = \text{cancer}|T = 1)) \\
&= 33.8 - 18.1\pi(\theta = \text{cancer}|T = 1), \\
u(a_2) &= 12.195\pi(\theta = \text{cancer}|T = 1) + 21.62(1 - \pi(\theta = \text{cancer}|T = 1)) \\
&= 21.62 - 9.425\pi(\theta = \text{cancer}|T = 1), \\
u(a_3) &= 5.6\pi(\theta = \text{cancer}|T = 1) + 34.8(1 - \pi(\theta = \text{cancer}|T = 1)) \\
&= 34.8 - 29.2\pi(\theta = \text{cancer}|T = 1).
\end{aligned}$$

Similarly the quality-adjusted life expectancy given that T is negative is:

$$\begin{aligned}
u(a_1) &= 33.8 - 18.1\pi(\theta = \text{cancer}|T = 0), \\
u(a_2) &= 21.62 - 9.425\pi(\theta = \text{cancer}|T = 0), \\
u(a_3) &= 34.8 - 29.2\pi(\theta = \text{cancer}|T = 0).
\end{aligned}$$

First we notice that under our current assumption the life expectancy of a_2 the surgery way is always less than that of a_1 the radiotherapy way regardless of any medical test procedure. So it remains to compare a_1 and a_3. Solving the equation we know that when $\pi = 10/111$ the life expectancy of a_1 and a_3 are equal. This tells us that we need an α such that

$$\begin{aligned}
\frac{0.9\alpha}{0.9\alpha + 0.1 \times 0.02} &\geq 10/111 \\
\frac{0.9(1-\alpha)}{0.9(1-\alpha) + 0.1 \times 0.98} &< 10/111,
\end{aligned}$$

or the other way around to make sure that the test can affect the decision. Thus we have $\alpha \leq \frac{1}{4545}$ or $\alpha \geq \frac{4496}{4545}$.

If $\alpha \leq \frac{1}{4545}$, which means the test is stably bad at detecting real malignant tumor, in fact it is more likely that a malignant tumor is there if the test shows negative, then if the test is positive it 's better to do nothing and if the test is negative it is better to choose radiotherapy. On the other hand, if $\alpha \geq \frac{4496}{4545}$, which means the test is pretty solid, then if the test is positive then it's better to choose radiotherapy and if the test is negative it is better to do nothing. In both cases the test result can not be ignored and will affect the decision.

Problem 2

(1)

```
y0 <- c(rep(1, 557+38+4+3), rep(2, 427+27+1), rep(3, 87+1))
x <- c(rep(1, 557), rep(2, 38), rep(3, 4), rep(4, 3),
       rep(1, 427), rep(2, 27), rep(3, 1),
       rep(1, 87), rep(2, 1))

y<- cbind(y0, y0, y0)
y[, 1][y[, 1] != 1] <- 0
y[, 2][y[, 2] != 2] <- 0
y[, 3][y[, 3] != 3] <- 0
```

We are trying to study the population preference on their vote for the election. The data is collected by random calling phone lines and ask the person who picked the phone two questions: 1) Your preference 2) How many phone lines do you have in your house. The second question is necessary because if the household has several phone lines then the probability of getting sampled is multiplied by the number of phone lines. If we do not account this in our model then our survey is in favor of people who own more phone lines so the result is not fair. The following are technical details.

It will be too complicated to model the missing mechanism for x, the phone line number response, so we assume that it is missing completely at random. As a result it does not affect the inference of θ and we will not include it in the model. Also, we do not model the preference of households that do not have a phone line by assuming that not having phone line has nothing to do with their voting preference. This is also a missing completely at random assumption.

In general, the above assumptions mean that those households who did not respond to the "number of phone lines" question or do not own a phone share no different voting preference comparing to the population. As a result it is okay to model and estimate desired parameter ignoring those missing data.

Suppose the missing mechanism for y is known, that is, there is no parameter to be estimated for the missing mechanism. The complete model is

$$p(y, x, I|\theta, \phi) = p(y|\theta, x)p(I|x, y)p(x|\phi).$$

We've assume that y is missing completely at random so we have $p(I|x, y) = p(I|x)$. Then the complete model becomes

$$p(y, x, I|\theta, \phi) = p(y|\theta, x)p(I|x)p(x|\phi).$$

And thanks to this assumption the likelihood for observed data is just

$$p(y_{\text{obs}}, x, I | \theta, \phi) = \int p(I|x)p(x|\phi)p(y_{\text{obs}}, y_{\text{mis}}|\theta, x)dy_{\text{mis}}$$
$$= p(I|x)p(x|\phi)p(y_{\text{obs}}|\theta, x),$$

where we set the probability of being sampled to be proportional to the number of phone lines

$$p(I_i = 1|x_i) \propto x_i$$

assuming that the total number of sampling candidate is finite. For the model of population number of phone lines we use Geometric distribution: for any $x_i \in 1, 2, 3, \ldots$

$$p(x_i|\phi) \propto (1 - \phi)^{x_i - 1}\phi.$$

For the preference model, we set

$$y_i|x_i, \theta \sim y_i|\theta \sim \text{Multinomial}(1, \theta),$$

where $\theta = (\theta_1, \theta_2, \theta_3)$. To better construct the model we set

$$\alpha_1 = \frac{\theta_1}{\theta_1 + \theta_2}$$
$$\alpha_2 = 1 - \theta_3.$$

In above parameterization α_1 is the probability of preferring Bush given that a preference is expressed and $alpha_2$ is the probability of expressing a preference. Then we relax these parameters to the logit scale in the following way

$$\beta_1 = \text{logit}(\alpha_1) \text{ and } \beta_2 = \text{logit}(\alpha_2),$$

where we assign a bivariate normal prior to β

$$\beta|\mu_1, \mu_2, \tau_1, \tau_2, \rho = \text{N}\left(\begin{pmatrix} \mu_1 \\ \mu2 \end{pmatrix}, \begin{pmatrix} \tau_1^2 & \rho\tau_1\tau_2 \\ \rho\tau_1\tau_2 & \tau_2^2 \end{pmatrix}\right).$$

Priors for hyperparameters $(\mu_1, \mu_2, \tau_1, \tau_2, \rho)$ will be assigned later.

Under the above hierarchical model, the posterior for (β, ϕ) is

$$p(\beta, \phi, \mu_1, \mu_2, \tau_1, \tau_2, \rho | x, y_{\text{obs}}, I) \propto p(\mu_1, \mu_2, \tau_1, \tau_2, \rho)p(\beta|\mu_1, \mu_2, \tau_1, \tau_2, \rho)p(\phi)\prod_{i=1}^{n} p(I_i|x_i)p(x_i|\phi)p(y_{\text{obs},i}|\beta, x_i).$$

Please note that we are using the β parameterization and β it is deterministically determined by θ. We will use a uniform prior for $\mu_1, \mu_2, \tau_1, \tau_2, \rho$ and ϕ on feasible region and the resulting posterior is proper.

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library(mvtnorm)
library(mc2d)


##
## Attaching package: 'mc2d'

## The following objects are masked from 'package:base':
##
##     pmax, pmin
```

```r
log_post <- function(beta, phi, mu, tau, rho) {
  if (phi >0 & phi <=1 & prod(tau >= 0) == 1 & rho <= 1 & rho >=-1) {
    sigma <- diag(tau^2)
    sigma[1, 2] <- prod(tau)*rho
    sigma[2, 1] <- sigma[1, 2]
    theta <- c(plogis(beta[1])*plogis(beta[2]),
               1-(1-plogis(beta[2]))-plogis(beta[1])*plogis(beta[2]),
               1-plogis(beta[2]))
    dmvnorm(beta, mean=mu, sigma=sigma, log=T) + sum(log(x)) + sum(dgeom(x-1, phi, log=T)) +
      sum(dmultinomial(y, prob=theta))
  } else {
    -Inf
  }
}

init <- c(0, 0, 0.8, 0, 0, 1, 1, 0)
iter <- 1e3

Param <- matrix(0, nrow=iter+1, ncol=length(init))
Param[1, ] <- init

for (i in 1:iter) {
  cand_beta <- rnorm(2, mean=Param[i, 1:2])
  log_u <- log(runif(1))
  obj <- log_post(cand_beta, Param[i, 3], Param[i, 4:5],
                  Param[i, 6:7], Param[i, 8]) -
         log_post(Param[i, 1:2], Param[i, 3], Param[i, 4:5],
                  Param[i, 6:7], Param[i, 8])
  if (log_u <= obj) {
    Param[i+1, 1:2] <- cand_beta
  } else {
    Param[i+1, 1:2] <- Param[i, 1:2]
  }

  cand_phi <- runif(1, min=max(0, Param[i, 3]-.2), max=min(1, Param[i, 3] + .2))
  log_u <- log(runif(1))
  obj <- log_post(Param[i+1, 1:2], cand_phi, Param[i, 4:5],
                  Param[i, 6:7], Param[i, 8]) -
         log_post(Param[i+1, 1:2], Param[i, 3], Param[i, 4:5],
                  Param[i, 6:7], Param[i, 8]) +
         dunif(Param[i, 3], min=max(0, cand_phi-.2),
               max=min(1, cand_phi + .2), log=T) -
         dunif(cand_phi, min=max(0, Param[i, 3]-.2),
               max=min(1, Param[i, 3] + .2), log=T)
   if (log_u <= obj) {
    Param[i+1, 3] <- cand_phi
  } else {
    Param[i+1, 3] <- Param[i, 3]
  }

  cand_mu <- rnorm(2, mean=Param[i, 4:5])
  log_u <- log(runif(1))
  obj <- log_post(Param[i+1, 1:2], Param[i+1, 3], cand_mu,
```

```
                Param[i, 6:7], Param[i, 8]) -
        log_post(Param[i+1, 1:2], Param[i+1, 3], Param[i, 4:5],
                Param[i, 6:7], Param[i, 8])
  if (log_u <= obj) {
    Param[i+1, 4:5] <- cand_mu
  } else {
    Param[i+1, 4:5] <- Param[i, 4:5]
  }

  cand_tau <- runif(2, min=c(0,0), max=Param[i, 6:7]+5)
  log_u <- log(runif(1))
  obj <- log_post(Param[i+1, 1:2], Param[i+1, 3], Param[i+1, 4:5],
                cand_tau, Param[i, 8]) -
        log_post(Param[i+1, 1:2], Param[i+1, 3], Param[i+1, 4:5],
                Param[i, 6:7], Param[i, 8]) +
        sum(dunif(Param[i, 6:7], min=c(0,0), max=cand_tau+5, log=T)) -
        sum(dunif(cand_tau, min=c(0,0), max=Param[i, 6:7]+5, log=T))
  if (log_u <= obj) {
    Param[i+1, 6:7] <- cand_tau
  } else {
    Param[i+1, 6:7] <- Param[i, 6:7]
  }

  cand_rho <- runif(1)
  log_u <- log(runif(1))
  obj <- log_post(Param[i+1, 1:2], Param[i+1, 3], Param[i+1, 4:5],
                Param[i+1, 6:7], cand_rho) -
        log_post(Param[i+1, 1:2], Param[i+1, 3], Param[i+1, 4:5],
                Param[i+1, 6:7], Param[i, 8])
  if (log_u <= obj) {
    Param[i+1, 8] <- cand_rho
  } else {
    Param[i+1, 8] <- Param[i, 8]
  }
  print(i)
}
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The posterior mean of parameters are

```
colMeans(Param[round(.3*iter):iter+1, ])
```

```
## [1]   16.1265688   28.7309447    0.9323629 -27.5724732    5.2214894   25.9383065
## [7]   16.3367036    0.6081912
```