HW5 Solutions
STAT431 Spr19

February 2019

Contents

1 Exchangeability

$$Z \sim \mathcal{N}(0,1) \tag{1}$$
$$\epsilon_1 \sim \mathcal{N}\left(0,\sigma_1^2\right) \tag{2}$$
$$\epsilon_2 \sim \mathcal{N}\left(0,\sigma_2^2\right) \tag{3}$$
$$Y_1 = Z + \epsilon_1 \tag{4}$$
$$Y_2 = Z + \epsilon_2 \tag{5}$$

and $Z, \epsilon_1, \epsilon_2$ are all mutually independent.

1.1 Exchangeable priors

Y_1 and Y_2 are exchangeable if the joint distribution for (Y_1, Y_2) is the same as for (Y_2, Y_1).

$$P(Y_1, Y_2) = P(Z + \epsilon_1, Z + \epsilon_2) \tag{6}$$

This is equal to $P(Z + \epsilon_2, Z + \epsilon_1)$ if and only if the distributions for ϵ_1 and ϵ_2 are identical, i.e. if $\sigma_1^2 = \sigma_2^2$. In other words, if the σ^2's are equal, Y_1 and Y_2 will be conditionally iid given Z, hence exchangeable.

1.2 Independence of Y_1 and Y_2

$$\begin{aligned} \mathrm{Cov}(Y_1, Y_2) &= \mathrm{Cov}(Z + \epsilon_1, Z + \epsilon_2) && (7)\\ &= \mathrm{Cov}(Z, Z) + \mathrm{Cov}(Z, \epsilon_2) + \mathrm{Cov}(\epsilon_1, Z) + \mathrm{Cov}(\epsilon_1, \epsilon_2) && (8)\\ &= \mathrm{Cov}(Z, Z) && (9)\\ &= 1 && (10) \end{aligned}$$

Under no conditions are Y_1 and Y_2 independent, as their covariance is never nonzero due to the fact that they are both constructed from the same random variable Z.

2 Heart attack biomarker analysis

2.1 Directed Acyclic Graph

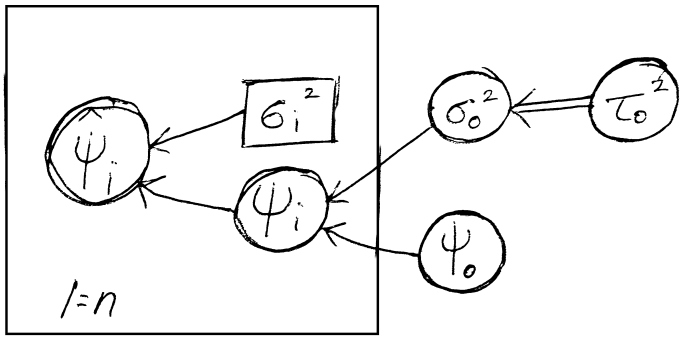

Figure 1: Directed acyclic graph of our model. Squares represent constant nodes, while circles represent random variables. Double arrows represent a deterministic assignment, while single arrows represent a stochastic relationship.

2.2 JAGS model

```
model {
```

```
  for (i in 1:length(psihat)) {
    psihat[i] ~ dnorm(psi[i], tausq[i])
    psi[i] ~ dnorm(psi0, tausq0)
    tausq[i] <- 1 / sigma[i]^2
  }

  psi0 ~ dnorm(0, 0.001)

  tausq0 ~ dgamma(0.001, 0.001)

  sigmasq0 <- 1 / tausq0
}
```

2.3 Amount of burn-in needed for convergence

We ran a preliminary run of the algorithm to assess how many burn-in samples we require to reach an equilibrium state. We ran three separate chains, with initial values

```
inits = list( list('psi' = rep(0, n), 'psi0' = 0, 'tausq0' = 1),
              list('psi' = rep(10, n), 'psi0' = 10, 'tausq0' = 0.01),
              list('psi' = rep(-10, n), 'psi0' = -10, 'tausq0' = 100))
```

We used the Gelman-Rubin statistic for assessing convergence, where the Gelman-Rubin statistic is a ratio of the across-chain variance against the within-chain variance. Values below 1.05 can be considered as converged. See Figure 2 for Gelman-Rubin statistics evaluated for a preliminary run of 5,000 iterations. Based on these diagnostic plots, we recommend at least 3,000 iterations for burn-in.

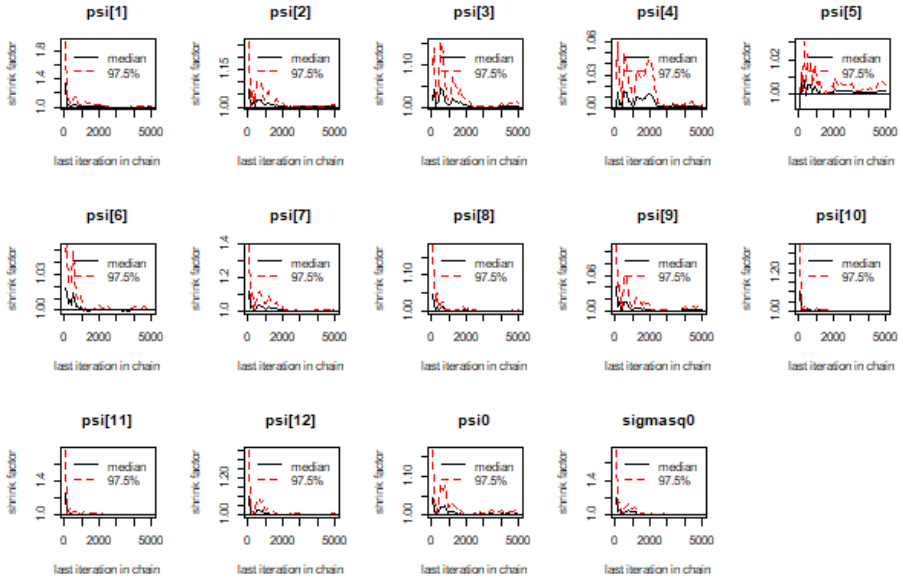

Figure 2: Gelman-Rubin statistic for assessing convergence.

2.4 Results

After a burnin of 5,000 samples, we ran the algorithm for 100,000 iterations. Below is a summary of our posterior samples for ψ_0, σ_0^2.

```
Iterations = 5001:105000
Thinning interval = 1
Number of chains = 3
Sample size per chain = 1e+05

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

           Mean     SD  Naive SE Time-series SE
psi0     0.2022 0.1199 0.0002189      0.0003892
sigmasq0 0.1100 0.1002 0.0001830      0.0004309

2. Quantiles for each variable:

              2.5%     25%     50%    75%  97.5%
psi0     -0.015293 0.12340 0.19474 0.2737 0.4599
sigmasq0  0.007547 0.04647 0.08419 0.1418 0.3673
```

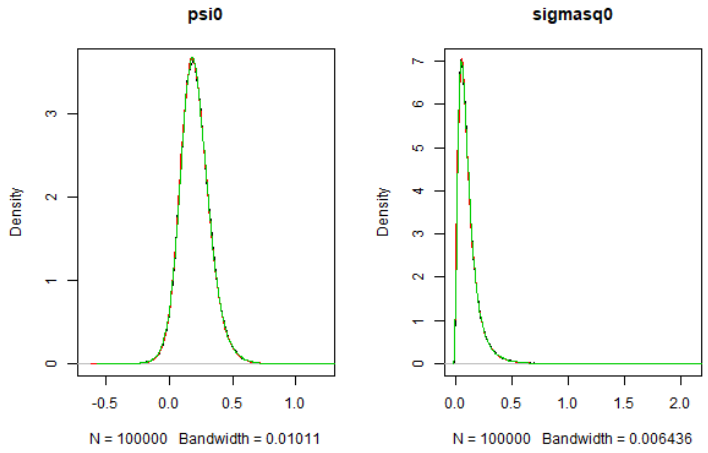

Figure 3: Posterior density plots

3 GRADUATE SECTION ONLY - predicting efficacy of a new study

Continuing with the set-up in Problem 2, we now assume that a new case-control study is to be conducted. We assume that the log-odds standard error σ_{new} is known to be 0.4. We will use the same data from the previous problem to predict $\hat{\psi}_{new}$ for the new study. Our model is slightly modified,

```
model {
  for (i in 1:length(psihat)) {
    psihat[i] ~ dnorm(psi[i], tausq[i])
    psi[i] ~ dnorm(psi0, tausq0)
    tausq[i] <- 1 / sigma[i]^2
  }

  psihat_new ~ dnorm(psi_new, tausq_new)
  psi_new ~ dnorm(psi0, tausq0)
  tausq_new <- 1 / 0.4^2

  psi0 ~ dnorm(0, 0.001)

  tausq0 ~ dgamma(0.001, 0.001)

  sigmasq0 <- 1 / tausq0

}
```

3.1 Results

```
Iterations = 5001:105000
Thinning interval = 1
Number of chains = 3
Sample size per chain = 1e+05

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

          Mean             SD       Naive SE Time-series SE
     0.2015109      0.5337977      0.0009746      0.0010067

2. Quantiles for each variable:

   2.5%     25%     50%     75%   97.5%
-0.8412 -0.1487  0.1967  0.5475  1.2646
```

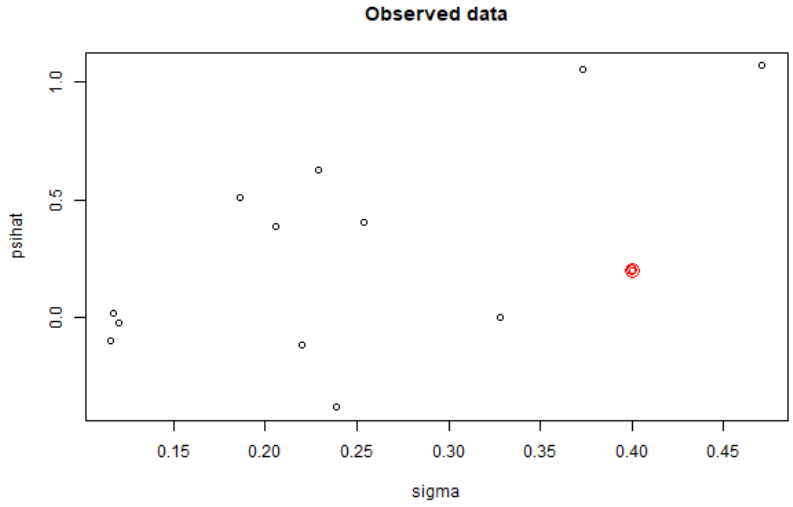

Figure 4: A scatter plot of the observed data, σ on the X-axis vs. $\hat{\psi}$ on the Y-axis. The point coloured in red represents our predicted $\hat{\psi}_{new}$ for a new study with standard deviation assumed to be $\sigma_{new} = 0.4$.

The 95% interval for $\hat{\psi}_{new}$ is very wide and covers 0.

3.2 Probability that a new study finds a significant results

```
mean((out %>% unlist()) > 2*0.4)
```

We estimate the probability that a new study finds a significant results, through the probability that the new estimated log-odds ratio $\hat{\psi}_{new}$ will be at least twice as large as its standard error σ_{new}, which is **0.12682**.