

## Homework 5 - Due Friday, December 11 at 11:59pm

```
options(tinytex.verbose = TRUE)
options(buildtools.check = function(action) TRUE )
knitr::opts_chunk$set(echo = TRUE, eval=FALSE)
suppressPackageStartupMessages(library(tidyverse))
suppressPackageStartupMessages(library(rstan))
suppressPackageStartupMessages(library(coda))
suppressPackageStartupMessages(library(testthat))
```

NOTE THAT THIS ASSIGNMENT IS DUE ON FRIDAY

### Problem 1. Logistic regression for toxicity data

#### Logistic regression for pesticide toxicity data (part 2).

As a reminder from homework 5, an environmental agency is testing the effects of a pesticide that can cause acute poisoning in bees. In the last homework assignment, we inferred the effects of the pesticide by fitting a model in Stan. In order to develop a deeper understanding of MCMC, in this problem we will implement our own Metropolis-Hastings algorithm. To do so, we need to first write a function to compute the *log* posterior density. Why the log posterior? In practice, the posterior density may have *extremely* small values, especially when we initialize the sampler and may be far from the high posterior mode areas. As such, computing the

For example, computing the ratio of a normal density 1000 standard deviations from the mean to a normal density 1001 standard deviations from the mean fails because in both cases `dnorm` evaluates to 0 due to numerical underflow and 0/0 returns NaN. However, we can compute the log ratio of densities:

```
dnorm(1000) / dnorm(1001)
dnorm(1000, log=TRUE) - dnorm(1001, log=TRUE)
```

Let  $r = \min(1, \frac{p(\theta^*|y)}{p(\theta_t|y)})$ . In the accept/reject step of your implementation of the MH algorithm, rather than checking whether  $u < r$ , it is equivalent to check whether  $\log(u) < \log(r)$ . Doing the accept/reject on the log scale will avoid any underflow issues and prevent our code from crashing.

**1a.** Complete the specification for the log posterior for the data `x` and `y` by filling in the missing pieces of the function below.

```
## Pesticide toxicity data
x <- c(1.06, 1.41, 1.85, 1.5, 0.46, 1.21, 1.25, 1.09,
      1.76, 1.75, 1.47, 1.03, 1.1, 1.41, 1.83, 1.17,
      1.5, 1.64, 1.34, 1.31)

y <- c(0, 1, 1, 1, 0, 1, 1, 1, 1, 1,
      1, 0, 0, 1, 1, 0, 0, 1, 1, 0)

#Log posterior function. Must incorporate x and y data above.
log_posterior <- function(theta) {

  alpha <- theta[1]
```

```

beta <- theta[2]

## Compute the probabilities as a function of alpha and beta
## for the observed x, y data
prob <- NULL # YOUR CODE HERE

if(any(prob == 0) | any(prob == 1))
  -Inf ## log likelihood is -Inf is prob=0 or 1
else
  # YOUR CODE HERE
}

. = ottr::check("tests/q1a.R")

```

**1b.** You will now complete the Metropolis-Hastings sampler by filling in the missing pieces of the algorithm below. `theta_0` is a vector of length 2, with the first argument as the initial alpha value and the second argument as the initial beta value. As your proposal, use  $J(\theta * |\theta_t) \sim \text{Normal}(\theta_t, \Sigma)$ . You can sample from the multivariate normal using `mvtnorm::rmvnorm`. The effectiveness of your sampler will be determined by the tuning parameter,  $\Sigma$ , the covariance of the bivariate normal distribution. This determines the size / shape of the proposal.  $\Sigma$  is determined by the `cov` argument in your sampler. Run the sampler with `cov = diag(2)`, the default. In homework 5 you showed that the dose at which there is a 50% chance of hive collapse, the LD50, can be expressed as  $-\alpha/\beta$ . Run your sampler for 10000 iterations with a burnin of 1000 iterations. Verify that the posterior mean LD50 based on your sampler is close to 1.2, as it was with stan.

```

#####
## Metropolis-Hastings for the Logistic Model
#####

## Function to generate samples using the Metropolis-Hasting Sampler

## theta_0: initialization of the form c(alpha_init, beta_init) for some values alpha_init, beta_init
## burnin: amount of iterations to discard to reduce dependence on starting point
## iters: total number of iterations to run the algorithm (must be greater than `burnin`)

mh_logistic <- function(theta_0, burnin, iters, cov=diag(2)){

  # Initialize parameters.
  theta_t <- theta_0

  ## Create a matrix where we will store samples
  theta_out <- matrix(0, nrow=iters, ncol=2, dimnames=list(1:iters, c("alpha", "beta")))

  for(i in 1:iters){

    ## Propose new theta = (alpha, beta)
    ## The proposal will be centered the current
    ## value theta_t. Use mvtnorm::rmvnorm

    theta_p <- NULL # YOUR CODE HERE

    ## Accept/reject step. Keep theta prev if reject, otherwise take theta_p
    ## Will require evaluating `log_posterior` function twice
    ## Log-rejection ratio for symmetric proposal

```

```

logr <- NULL # YOUR CODE HERE

## Update theta_t based on whether the proposal is accepted or not
# YOUR CODE HERE

## Save the draw
theta_out[i, ] <- theta_t
}

## Chop off the first part of the chain -- this reduces dependence on the starting point.
if(burnin == 0)
  theta_out
else
  theta_out[-(1:burnin), ]
}

samples <- mh_logistic(c(0, 0), 1000, 10000)

ld50_posterior_mean <- NULL # YOUR CODE HERE

. = ottr::check("tests/q1b.R")

```

1c. Report the effective sample size for the ld50 samples using the `coda::effectiveSize` function. Make a traceplot of If `alpha_samples` were the name of the samples of the alpha parameter, then you can plot the traceplot using `coda::traceplot(as.mcmc(alpha_samples))`. Improve upon this effective sample size from your first run by finding a new setting for `cov`. *Hint*: try variants of `k*diag(2)` for various values of  $k$  to increase or decrease the proposal variance. If you are ambitious, try proposing using a covariance matrix with non-zero correlation between the two parameters. What effective sample size were you able to achieve? You should be able to at least double the effective sample size from your first run. Plot the traceplot based on the new value of `cov`.

```

library(coda)

samples <- NULL # YOUR CODE HERE
ld50_samples <- NULL # YOUR CODE HERE

ld50_ess <- NULL # YOUR CODE HERE

# TRACEPLOT HERE
# YOUR CODE HERE

## Re run the sampler using your new setting of cov
samples_new <- NULL # YOUR CODE HERE
ld50_samples_new <- NULL # YOUR CODE HERE

ld50_ess_new <- NULL # YOUR CODE HERE

# TRACEPLOT HERE
# YOUR CODE HERE

. = ottr::check("tests/q1c.R")

```

## Problem 2. Estimating Skill In Baseball

In baseball, the batting average is defined as the fraction of base hits (successes) divided by “at bats” (attempts). We can conceptualize a player’s “true” batting skill as  $p_i = \lim_{n_i \rightarrow \infty} \frac{y_i}{n_i}$ . In other words, if each at bat was independent (a simplifying assumption),  $p_i$  describes the total fraction of success for player  $i$  as the number of attempts gets very large. Our goal is to estimate the true skill of all player as best as possible using only a limited amount of data. As usual, for independent counts of success/fail data it is reasonable to assume that  $Y_i \sim \text{Bin}(n_i, p_i)$ . The file “lad.csv” includes the number of hits, **y** and the number of attempts **n** for  $J = 10$  players on the Los Angeles Dodgers after the first month of the most recent baseball season. The variable **val** includes the end-of-season batting average and will be used to validate the quality of various estimates. If you are interested, at the end of the assignment we have included the code that was used to scrape the data.

```
baseball_data <- read_csv("lad.csv", col_types=cols())
baseball_data

## observed hits in the first month
y <- baseball_data$y

## observed at bats in the first month
n <- baseball_data$n

## observed batting average in the first month (same as MLE)
theta_mle <- y/n

## number of players
J <- nrow(baseball_data)

## end of the year batting average, used to evaluate estimates
val <- baseball_data$val
```

**2a.** Compute the standard deviation of the empirical batting average,  $y/n$  and then compute the sd of the “true skill”, (the **val** variable representing the end of season batting average). Which is smaller? Why does this make sense? *Hint:* What sources of variation are present in the empirical batting average?

```
empirical_sd <- NULL # YOUR CODE HERE
true_sd <- NULL # YOUR CODE HERE
print(empirical_sd)
print(true_sd)
```

```
. = ottr::check("tests/q2a.R")
```

Type your answer here, replacing this text.

**2b.** Consider two estimates for the true skill of player  $i$ ,  $p_i$ : 1)  $\hat{p}_i^{(\text{mle})} = \frac{y_i}{n_i}$  and 2)  $\hat{p}_i^{(\text{comp})} = \frac{\sum_j y_j}{\sum_j n_j}$ . Estimator 1) is the MLE for each player and ignores any commonalities between the observations. This is sometimes termed the “no pooling” estimator since each parameter is estimating separately without “pooling” information between them. Estimator 2) assumes all players have identical skill and is sometimes called the “complete pooling” estimator, because the data from each problem is completely “pooled” into one common set. In this problem, we’ll treat the end-of-season batting average as a proxy for true skill,  $p_i$ . Compute the root mean squared error (RMSE),  $\sqrt{\frac{1}{J} \sum_i (\hat{p}_i - p_i)^2}$  for the “no pooling” and “complete pooling” estimators using the variable **val** as a stand-in for the true  $p_i$ . Does “no pooling” or “complete pooling” give you a better estimate of the end-of-year batting averages in this specific case?

```

# Maximum likelihood estimate
phat_mle <- NULL # YOUR CODE HERE

# Pooled estimate
phat_pooled <- NULL # YOUR CODE HERE

rmse_complete_pooling <- NULL # YOUR CODE HERE
rmse_no_pooling <- NULL # YOUR CODE HERE

print(sprintf("MLE: %f", rmse_no_pooling))
print(sprintf("Pooled: %f", rmse_complete_pooling))

. = ottr::check("tests/q2b.R")

```

Type your answer here, replacing this text.

The no pooling and complete pooling estimators are at opposite ends of a spectrum. There is a more reasonable compromise: “partial pooling” of information between players. Although we assume the number of hits follow a binomial distribution. To complete this specification, we assume  $\text{logit}(p_i) \sim N(\mu, \tau^2)$  for each player  $i$ .  $\mu$  is the “global mean” (on the logit scale),  $\exp(\mu)/(1 + \exp(\mu))$  is the overall average batting average across all players.  $\tau$  describes how much variability there is in the true skill of players. If  $\tau = 0$  then all players are identical and the only difference in the observed hits is presumed to be due to chance. If  $\tau^2$  is very large then the true skill differences between players is assumed to be large and our estimates will be close to the “no pooling” estimator. How large should  $\tau$  be? We don’t know but we can put a prior distribution over the parameter and sample it along with the  $p_i$ ’s! Assume the following model:

$$\begin{aligned}
y_i &\sim \text{Bin}(n_i, p_i) \\
\theta_i &= \text{logit}(p_i) \\
\theta &\sim N(\mu, \tau^2) \\
p(\mu) &\propto \text{const} \\
p(\tau) &\propto \text{Cauchy}(0, 1)^+, \text{ (the Half-cauchy distribution, see part d.)}
\end{aligned}$$

**2c.** State the correct answer in each case: as  $\tau \rightarrow \infty$ , the posterior mean estimate of  $p_i$  in this model will approach the (complete pooling / no pooling) estimator and as  $\tau \rightarrow 0$  the posterior mean estimate of  $p_i$  will approach the (complete pooling / no pooling) estimator. Give a brief justification for your answer.

Type your answer here, replacing this text.

**2d.** Implement the hierarchical binomial model in Stan. As a starting point for your Stan file modify the `eight_schools.stan` file we have provided and save it as `baseball.stan`. To write the hierarchical binomial model, we need the following modifications to the normal hierarchical model:

- Since we are fitting a hierarchical binomial model, not a normal distribution, we no longer need sampling variance  $\sigma_i^2$ . Remove this from the data block.
- The outcomes  $y$  are now integers. Change  $y$  to an array of integer types in the data block.
- We need to include the number of at bats for each player (this is part of the binomial likelihood). Add an array of integers,  $n$  of length  $J$  to the data block.
- Replace the sampling model for  $y$  with the binomial-logit: `binomial_logit(n, theta)`. This is equivalent to `binomial(n, inv_logit(theta))`.
- The model line for `eta` makes  $\theta_i \sim N(\mu, \tau^2)$ . Leave this in the model.
- Add a half-cauchy prior distribution for  $\tau$ : `tau ~ cauchy(0, 1);`. The half-cauchy has been suggested as a good default prior distribution for group-level standard deviations in hierarchical models. See

<http://www.stat.columbia.edu/~gelman/research/published/taumain.pdf>.

Find the posterior means for each of the players batting averages by looking at the samples for `inv_logit(theta_samples)`. Report the RMSE for hierarchical estimator. How does this compare to the RMSE of the complete pooling and no pooling estimators? Which estimator had the lowest error?

```
# Run Stan and compute the posterior mean

# YOUR CODE HERE

# Theta samples are logit scale
theta_samples <- extract(results)$theta
# Get batting averages by inverting with this function
inv_logit <- function(x) {
  exp(x) / (1+exp(x))
}
# and compute the posterior mean for each theta
pm <- NULL # YOUR CODE HERE

# RMSE From Stan posterior means
rmse_partial_pooling <- NULL # YOUR CODE HERE

print(c(rmse_complete_pooling, rmse_no_pooling, rmse_partial_pooling))

. = ottr::check("tests/q2d.R")
```

2e. Use the `shrinkage_plot` function provided below to show how the posterior means shrink the empirical batting averages. Pass in `y/n` and the posterior means of  $p_i$  as arguments.

```
shrinkage_plot <- function(empirical, posterior_mean,
                           shrink_point=mean(posterior_mean)) {

  tibble(y=empirical, pm=posterior_mean) %>%
    ggplot() +
    geom_segment(aes(x=y, xend=pm, y=1, yend=0), linetype="dashed") +
    geom_point(aes(x=y, y=1)) +
    geom_point(aes(x=pm, y=0)) +
    theme_bw(base_size=16) +
    geom_vline(xintercept=shrink_point, color="blue", size=1.2) +
    ylab("") + xlab("Estimate") +
    xlim(c(0.2, 0.4)) +
    scale_y_continuous(breaks=c(0, 1),
                       labels=c("Posterior Mean", "MLE"),
                       limits=c(0,1))

}

# YOUR CODE HERE
```

2f. Make a histogram of the posterior distribution for the global batting average,  $\frac{e^\mu}{1+e^\mu}$ , based on the LAD data. True or false: as the observed at bats for each of the 10 LAD batters  $n_i \rightarrow \infty$ , our estimate of the global batting average converges to a constant. Why or why not?

```
# YOUR CODE HERE
```

Type your answer here, replacing this text.

## Appendix: Code for scraping Dodgers baseball data

<http://billpetti.github.io/baseballr/>

```
## Install the baseballr package
devtools::install_github("BillPetti/baseballr")

library(baseballr)
library(tidyverse)

## Download data from the chosen year
year <- 2019

one_month <- daily_batter_bref(t1 = sprintf("%i-04-01", year), t2 = sprintf("%i-05-01", year))
one_year <- daily_batter_bref(t1 = sprintf("%i-04-01", year), t2 = sprintf("%i-10-01", year))

## filter to only include players who hat at least 10 at bats in the first month
one_month <- one_month %>% filter(AB > 10)
one_year <- one_year %>% filter(Name %in% one_month$Name)

one_month <- one_month %>% arrange(Name)
one_year <- one_year %>% arrange(Name)

## Look at only the Dodgers
LAD <- one_year %>% filter(Team == "Los Angeles" & Level == "MLB-NL") %>% .$Name

lad_month <- one_month %>% filter(Name %in% LAD)
lad_year <- one_year %>% filter(Name %in% LAD)

write_csv(tibble(name=lad_month$Name,
                  y=lad_month$H,
                  n=lad_month$AB,
                  val=lad_year$BA),
          path="lad.csv")
```