Solutions for Assignment 6

Guy Roberts

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[**Delete this line and other instructions within square brackets prior to "kniting" for your final submission**]

Solution to 1.1

[**Add the steps of your proof in math-mode blocks like the following, and remember to give the reader some narrative around your steps**]

Firstly via Bayes Theorem, we know that:

$$\begin{aligned}\pi(N) &\propto \pi(N|\theta)\pi(\theta)\\ \pi(N) &= \int_0^1 \pi(N|\theta)\pi(\theta)\,d\theta\\ \pi(N|\theta) &= (1-\theta)^N\theta\end{aligned}$$

Now, if we substitute this into our equation for $\pi(N)$ as well as our prior θ:

$$\begin{aligned}\pi(N) &= \int_0^1 (1-\theta)^N\theta \times \frac{\theta^{\alpha-1}}{Beta(\alpha,1)}\,d\theta\\ \pi(N) &= \frac{1}{\beta(\alpha,1)}\int_0^1 (1-\theta)^N\theta^{\alpha}\,d\theta\end{aligned}$$

Now we can recognise this integral as being the kernel of a $Beta(\alpha+1, N+1)$ distribution. Since we know this will integrate to one (given the multiplicative constant), we know that our final compound distribution will be:

$$\pi(N) = \frac{Beta(\alpha+1, N+1)}{Beta(\alpha,1)}$$

Solution to 1.2

[**Add your R code for the function**]

```r
compound_dist <- function(N, alpha) {
  return( beta(alpha+1, N+1) / beta(alpha, 1) )
}
```

Solution to 1.3

[**Layout any calculations you have done and add explanations**]

In order to answer this question, we used trial and error of varying values of α, this is because we know that:

$$Pr(N \leq 2) = \pi(2) + \pi(1) + \pi(0)$$

We find that our solution is approximately $\alpha \approx 0.4349$ from using our function defined earlier.

Solution to 2.1

[**Add your Stan model code here (and you'll want to save it in a separate Stan file).**]

```
data {
  int<lower=0> n; // num observations
  real X[n];     // observed values
}

parameters {
  real <lower=0> mu;
  real <lower=0> a;
  real <lower=0> b;
}

model {
  // Priors
  a ~ exponential(1);
  b ~ exponential(2);
  mu ~ beta(a, b);

  // Likelihood
  for (i in 1:n) {
    X[i] ~ normal(mu, sqrt(mu));
  }
}
```

Solution to 2.2

[**Add your R code to sample from the posterior here**]

```r
library(rstan)

# set working dir
setwd('C:/Users/guyro/OneDrive/Y3/bayesian-modelling/assignments/assignment6')
```

```r
# Compile model
model = stan_model('model.stan')

# Data
X = c(3.12, 0.75, 5.46, 0.80, 3.42,
      3.11, 1.99, 2.86, 4.33, 2.98)
n = length(X)

# Sample from posterior
posterior <- sampling(model, data = list(X = X, n = n), iter = 10000, chains = 4)
```

```
##
## SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 1).
## Chain 1: Rejecting initial value:
## Chain 1:   Error evaluating the log probability at the initial value.
## Chain 1: Exception: beta_lpdf: Random variable is 3.48702, but must be in the interval [0, 1] (in 's
## Chain 1: Rejecting initial value:
## Chain 1:   Error evaluating the log probability at the initial value.
## Chain 1: Exception: beta_lpdf: Random variable is 4.37902, but must be in the interval [0, 1] (in 's
## Chain 1: Rejecting initial value:
## Chain 1:   Error evaluating the log probability at the initial value.
## Chain 1: Exception: beta_lpdf: Random variable is 3.34001, but must be in the interval [0, 1] (in 's
## Chain 1:
## Chain 1: Gradient evaluation took 2.7e-05 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 0.27 seconds.
## Chain 1: Adjust your expectations accordingly!
## Chain 1:
## Chain 1:
## Chain 1: Iteration:    1 / 10000 [  0%]  (Warmup)
## Chain 1: Iteration: 1000 / 10000 [ 10%]  (Warmup)
## Chain 1: Iteration: 2000 / 10000 [ 20%]  (Warmup)
## Chain 1: Iteration: 3000 / 10000 [ 30%]  (Warmup)
## Chain 1: Iteration: 4000 / 10000 [ 40%]  (Warmup)
## Chain 1: Iteration: 5000 / 10000 [ 50%]  (Warmup)
## Chain 1: Iteration: 5001 / 10000 [ 50%]  (Sampling)
## Chain 1: Iteration: 6000 / 10000 [ 60%]  (Sampling)
## Chain 1: Iteration: 7000 / 10000 [ 70%]  (Sampling)
## Chain 1: Iteration: 8000 / 10000 [ 80%]  (Sampling)
## Chain 1: Iteration: 9000 / 10000 [ 90%]  (Sampling)
## Chain 1: Iteration: 10000 / 10000 [100%]  (Sampling)
## Chain 1:
## Chain 1:  Elapsed Time: 2.139 seconds (Warm-up)
## Chain 1:                22.06 seconds (Sampling)
## Chain 1:                24.199 seconds (Total)
## Chain 1:
##
## SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 2).
## Chain 2:
## Chain 2: Gradient evaluation took 9e-06 seconds
## Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 0.09 seconds.
## Chain 2: Adjust your expectations accordingly!
## Chain 2:
## Chain 2:
```

```
## Chain 2: Iteration:    1 / 10000 [  0%]  (Warmup)
## Chain 2: Iteration: 1000 / 10000 [ 10%]  (Warmup)
## Chain 2: Iteration: 2000 / 10000 [ 20%]  (Warmup)
## Chain 2: Iteration: 3000 / 10000 [ 30%]  (Warmup)
## Chain 2: Iteration: 4000 / 10000 [ 40%]  (Warmup)
## Chain 2: Iteration: 5000 / 10000 [ 50%]  (Warmup)
## Chain 2: Iteration: 5001 / 10000 [ 50%]  (Sampling)
## Chain 2: Iteration: 6000 / 10000 [ 60%]  (Sampling)
## Chain 2: Iteration: 7000 / 10000 [ 70%]  (Sampling)
## Chain 2: Iteration: 8000 / 10000 [ 80%]  (Sampling)
## Chain 2: Iteration: 9000 / 10000 [ 90%]  (Sampling)
## Chain 2: Iteration: 10000 / 10000 [100%]  (Sampling)
## Chain 2:
## Chain 2:  Elapsed Time: 1.668 seconds (Warm-up)
## Chain 2:                5.118 seconds (Sampling)
## Chain 2:                6.786 seconds (Total)
## Chain 2:
##
## SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 3).
## Chain 3: Rejecting initial value:
## Chain 3:   Error evaluating the log probability at the initial value.
## Chain 3: Exception: beta_lpdf: Random variable is 4.26666, but must be in the interval [0, 1] (in 's
## Chain 3: Rejecting initial value:
## Chain 3:   Error evaluating the log probability at the initial value.
## Chain 3: Exception: beta_lpdf: Random variable is 3.2024, but must be in the interval [0, 1] (in 'st
## Chain 3: Rejecting initial value:
## Chain 3:   Error evaluating the log probability at the initial value.
## Chain 3: Exception: beta_lpdf: Random variable is 4.18646, but must be in the interval [0, 1] (in 's
## Chain 3: Rejecting initial value:
## Chain 3:   Error evaluating the log probability at the initial value.
## Chain 3: Exception: beta_lpdf: Random variable is 1.51203, but must be in the interval [0, 1] (in 's
## Chain 3: Rejecting initial value:
## Chain 3:   Error evaluating the log probability at the initial value.
## Chain 3: Exception: beta_lpdf: Random variable is 3.64164, but must be in the interval [0, 1] (in 's
## Chain 3:
## Chain 3: Gradient evaluation took 7e-06 seconds
## Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 0.07 seconds.
## Chain 3: Adjust your expectations accordingly!
## Chain 3:
## Chain 3:
## Chain 3: Iteration:    1 / 10000 [  0%]  (Warmup)
## Chain 3: Iteration: 1000 / 10000 [ 10%]  (Warmup)
## Chain 3: Iteration: 2000 / 10000 [ 20%]  (Warmup)
## Chain 3: Iteration: 3000 / 10000 [ 30%]  (Warmup)
## Chain 3: Iteration: 4000 / 10000 [ 40%]  (Warmup)
## Chain 3: Iteration: 5000 / 10000 [ 50%]  (Warmup)
## Chain 3: Iteration: 5001 / 10000 [ 50%]  (Sampling)
## Chain 3: Iteration: 6000 / 10000 [ 60%]  (Sampling)
## Chain 3: Iteration: 7000 / 10000 [ 70%]  (Sampling)
## Chain 3: Iteration: 8000 / 10000 [ 80%]  (Sampling)
## Chain 3: Iteration: 9000 / 10000 [ 90%]  (Sampling)
## Chain 3: Iteration: 10000 / 10000 [100%]  (Sampling)
## Chain 3:
## Chain 3:  Elapsed Time: 2.558 seconds (Warm-up)
```

```
## Chain 3:                1.665 seconds (Sampling)
## Chain 3:                4.223 seconds (Total)
## Chain 3:
##
## SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 4).
## Chain 4: Rejecting initial value:
## Chain 4:   Error evaluating the log probability at the initial value.
## Chain 4: Exception: beta_lpdf: Random variable is 1.11071, but must be in the interval [0, 1] (in 's
## Chain 4:
## Chain 4: Gradient evaluation took 8e-06 seconds
## Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 0.08 seconds.
## Chain 4: Adjust your expectations accordingly!
## Chain 4:
## Chain 4:
## Chain 4: Iteration:    1 / 10000 [  0%]  (Warmup)
## Chain 4: Iteration: 1000 / 10000 [ 10%]  (Warmup)
## Chain 4: Iteration: 2000 / 10000 [ 20%]  (Warmup)
## Chain 4: Iteration: 3000 / 10000 [ 30%]  (Warmup)
## Chain 4: Iteration: 4000 / 10000 [ 40%]  (Warmup)
## Chain 4: Iteration: 5000 / 10000 [ 50%]  (Warmup)
## Chain 4: Iteration: 5001 / 10000 [ 50%]  (Sampling)
## Chain 4: Iteration: 6000 / 10000 [ 60%]  (Sampling)
## Chain 4: Iteration: 7000 / 10000 [ 70%]  (Sampling)
## Chain 4: Iteration: 8000 / 10000 [ 80%]  (Sampling)
## Chain 4: Iteration: 9000 / 10000 [ 90%]  (Sampling)
## Chain 4: Iteration: 10000 / 10000 [100%]  (Sampling)
## Chain 4:
## Chain 4:  Elapsed Time: 2.012 seconds (Warm-up)
## Chain 4:                1.286 seconds (Sampling)
## Chain 4:                3.298 seconds (Total)
## Chain 4:

## Warning: There were 15356 divergent transitions after warmup. See
## https://mc-stan.org/misc/warnings.html#divergent-transitions-after-warmup
## to find out why this is a problem and how to eliminate them.

## Warning: There were 2817 transitions after warmup that exceeded the maximum treedepth. Increase max_t
## https://mc-stan.org/misc/warnings.html#maximum-treedepth-exceeded

## Warning: Examine the pairs() plot to diagnose sampling problems

## Warning: The largest R-hat is 1.15, indicating chains have not mixed.
## Running the chains for more iterations may help. See
## https://mc-stan.org/misc/warnings.html#r-hat

## Warning: Bulk Effective Samples Size (ESS) is too low, indicating posterior means and medians may be
## Running the chains for more iterations may help. See
## https://mc-stan.org/misc/warnings.html#bulk-ess

## Warning: Tail Effective Samples Size (ESS) is too low, indicating posterior variances and tail quanti
## Running the chains for more iterations may help. See
## https://mc-stan.org/misc/warnings.html#tail-ess
```

Solution to 2.3

[Add your R code to make the requisite plots here]

```
# Extract posterior samples
mu_samples <- extract(posterior)$mu

# Summary statistics
summary(mu_samples)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.8521  0.9898  0.9974  0.9922  0.9995  1.0000
```

```
# Create histogram
hist(mu_samples, breaks = 30)
```