ECON 3640–001

Problem Set 3 – Solutions

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Problem 1

(a) Simulate 1,000 values drawn from a **Poisson**-distributed random variable, with rate parameter 16. Do not forget to set a **seed** for reproducibility.

ANSWER:

```r
set.seed(123)
x_a <- rpois(n = 1000, lambda = 16)
```

(b) Generate 10,000 values drawn from a **Beta**-distributed random variable, with shape parameters 10 and 15. Do not forget to set a **seed** for reproducibility.

ANSWER:

```r
set.seed(123)
x_b <- rbeta(n = 10000, shape1 = 10, shape2 = 15)
```

(c) Generate 1,000 values drawn from a **uniformly**-distributed random variable, ranging from 0 to 20. Do not forget to set a **seed** for reproducibility.

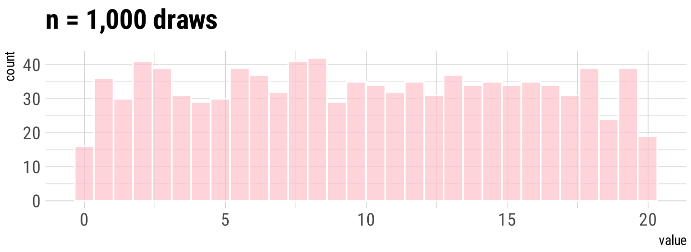
ANSWER:

See part (d).

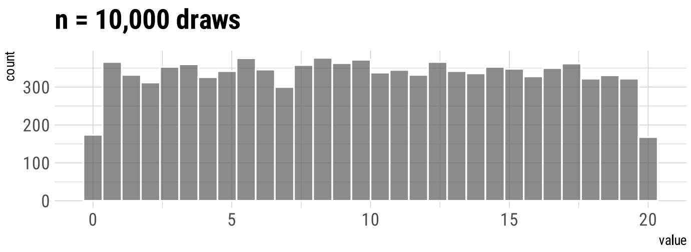
(d) Repeat part (c), now simulating 10,000 values. Produce a histogram for both parts, and compare your results.

ANSWER:

```
set.seed(123)
x_c <- runif(n = 1000, min = 0, max = 20)

x_c %>%
  as_tibble() %>%
  ggplot(aes(x = value)) +
  geom_histogram(color = "white", alpha = 0.7, fill = "pink") +
  labs(title = "n = 10,000 draws") +
  labs(title = "n = 1,000 draws")
```



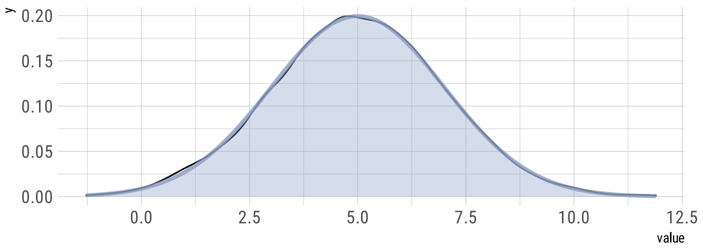
```
# Notice the difference on the vertical axis!

set.seed(123)
x_d <- runif(n = 10000, min = 0, max = 20)

x_d %>%
  as_tibble() %>%
  ggplot(aes(x = value)) +
  geom_histogram(color = "white", alpha = 0.7) +
  labs(title = "n = 10,000 draws")
```



(e) Generate 5,000 draws from a Normal distribution, with mean 5 and standard deviation 2. Generate these simulated data's density curve, and put, on the same plot, its long-run probability density function (PDF) curve. Compare your results. Do not forget to set a **seed** for reproducibility.

ANSWER:

```
set.seed(123)
x_e ← rnorm(n = 5000, mean = 5, sd = 2)


x_e %>%
  as_tibble() %>%
  ggplot(aes(x = value)) +
  geom_density() +
  stat_function(fun = dnorm, args = list(mean = 5, sd = 2),
                size = 1.2, alpha = 0.8, color = "#8b9dc3") +
  stat_function(fun = dnorm, args = list(mean = 5, sd = 2),
                geom = "area", fill = "#8b9dc3", alpha = 0.35)
```



Problem 2

Consider the following model:

$$\begin{aligned} Y|\theta &\sim \text{Binomial}(n, \theta) \\ \theta &\sim \text{Beta}(3, 8) \end{aligned}$$

Approximate the posterior distribution, $\theta|Y$, using **grid approximation**. How "thin" the grid will be is up to you, but make sure to play around with different values.

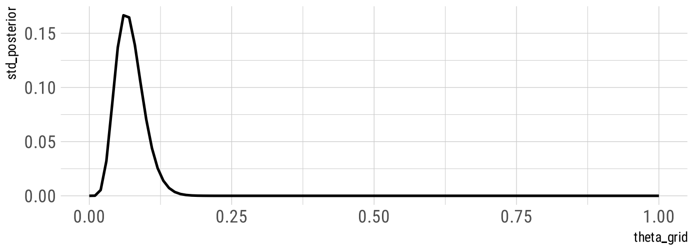
Lastly, assume that you observe $n = 100$ trials, with $Y = 5$ successes.

ANSWER:

```
# Setting up the grid, prior, and likelihood:

data_grid <- tibble(

  theta_grid = seq(from = 0, to = 1, by = 0.01),

  prior = dbeta(theta_grid, shape1 = 3, shape2 = 8),

  likelihood = dbinom(x = 5, size = 100, prob = theta_grid)
)
```

```
# Calculating the unstandardized and standardized posteriors:

data_grid <- data_grid %>%
  mutate(unstd_posterior = prior * likelihood,
         std_posterior = unstd_posterior/sum(unstd_posterior))
```

```
# Plotting the posterior:

data_grid %>%
  ggplot(aes(x = theta_grid, y = std_posterior)) +
  geom_line(size = .8)
```



Problem 3

Use **grid approximation** to estimate the posterior distribution for a Gamma-Poisson model, where you observe $n = 3$ independent data points $(Y_1, Y_2, Y_3) = (0, 1, 0)$. The likelihood and prior are the following:

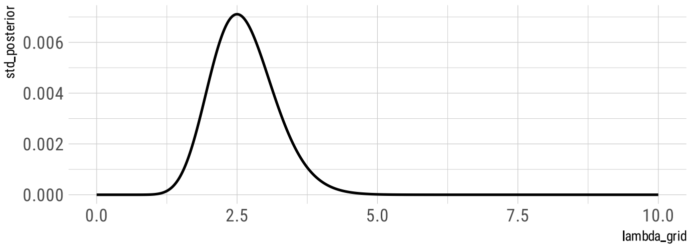
$$Y_i|\lambda \sim \text{Poisson}(\lambda)$$
$$\lambda \sim \text{Gamma}(20, 5)$$

ANSWER:

```r
# Setting up the grid, prior, and likelihood:

data_grid_gp <- tibble(

  lambda_grid = seq(from = 0, to = 10, by = 0.01),

  prior = dgamma(x = lambda_grid, shape = 20, rate = 5),

  likelihood = dpois(x = 0, lambda = lambda_grid) *
    dpois(x = 1, lambda = lambda_grid) *
    dpois(x = 0, lambda = lambda_grid)  ## recall that we have 3 independent observations.
)
```

```r
# Calculating the unstandardized and standardized posteriors:

data_grid_gp <- data_grid_gp %>%
  mutate(unstd_posterior = prior * likelihood,
         std_posterior = unstd_posterior/sum(unstd_posterior))
```

```r
# Plotting the posterior:

data_grid_gp %>%
  ggplot(aes(x = lambda_grid, y = std_posterior)) +
  geom_line(size = .8)
```



Problem 4

Using `stan` syntax, set up the `model{}` block of a model string for an MCMC simulation for the following priors and likelihood functions:

(a) $Y|\theta \sim \text{Binomial}(20, \theta)$ and $\theta \sim \text{Beta}(1, 1)$;

ANSWER:

```
model_a <- "
  data {

  int<lower=0, upper=20> Y;

  }

  parameters {

  real<lower=0, upper=1> theta;

  }

  model {

  Y ~ binomial(20, theta);
  theta ~ beta(1, 1);

  }
"
```

(b) $Y|\lambda \sim \text{Poisson}(\lambda)$ and $\lambda \sim \text{Gamma}(4, 2)$;

ANSWER:

```
model_b <- "
  data {

  int<lower=0> n;
  int<lower=0, upper=n> Y;

  }

  parameters {

  real<lower=0> lambda;

  }

  model {

  Y ~ poisson(lambda);
  lambda ~ gamma(4, 2);

  }
"
```

(c) $Y|\mu \sim \mathcal{N}(\mu, 1)$ and $\mu \sim \mathcal{N}(0, 10)$;

ANSWER:

```
model_c <- "

  data {

real Y;


  }

  parameters {

real mu;


  }

  model {

Y ~ normal(mu, 1);   // Here, sigma is known.
mu ~ normal(0, 10);

  }

"
```

(d) $Y|\mu \sim \mathcal{N}(\mu, \sigma)$, with $\mu \sim \mathcal{N}(0, 10)$ and $\sigma \sim \text{Uniform}(0, 100)$.

ANSWER:

```
model_d <- "

  data {

real Y;


  }

  parameters {

real mu;
real <lower=0> sigma;   // the standard deviation cannot be negative.

  }

  model {

Y ~ normal(mu, sigma);   // now, sigma is unknown.
mu ~ normal(0, 10);
sigma ~ uniform(0, 100);

  }

"
```

Problem 5

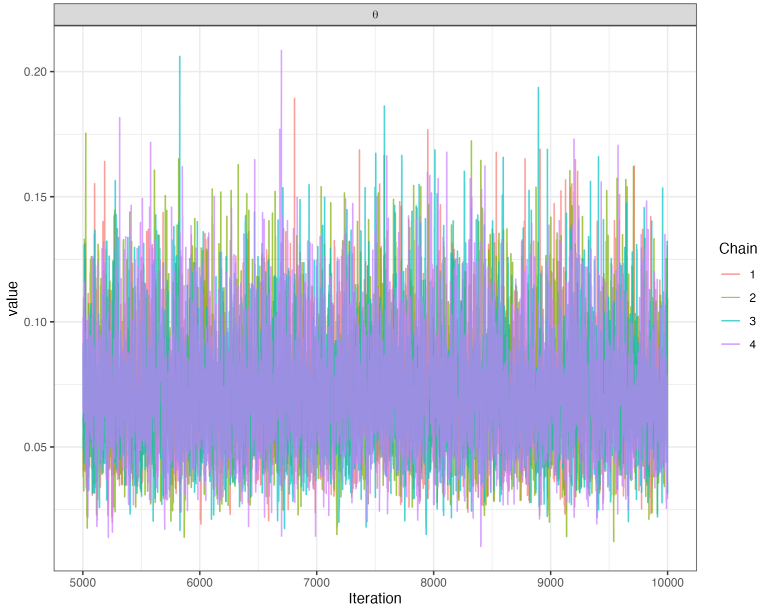
Using the information from **Problem 2**, set up an **MCMC** simulation using `rstan` with 4 chains and 10,000 iterations. Then, do the following:

```
model_5 <- "

  data {

  int<lower=0> n;
  int<lower=0, upper=n> Y;

  }

  parameters {

  real<lower=0, upper=1> theta;

  }

  model {

  Y ~ binomial(100, theta);
  theta ~ beta(3, 8);

  }
"
```

```
library(rstan)

set.seed(123)    ## don't forget to set a seed!

model_5_mcmc <- stan(
  model_code = model_5,            ## the model from before.
  data = list(Y = 5, n = 100),     ## hyperparameters were defined above.
  chains = 4, iter = 5000 * 2      ## run 4 parallel Markov chains, with 10,000 simulations.
)
```

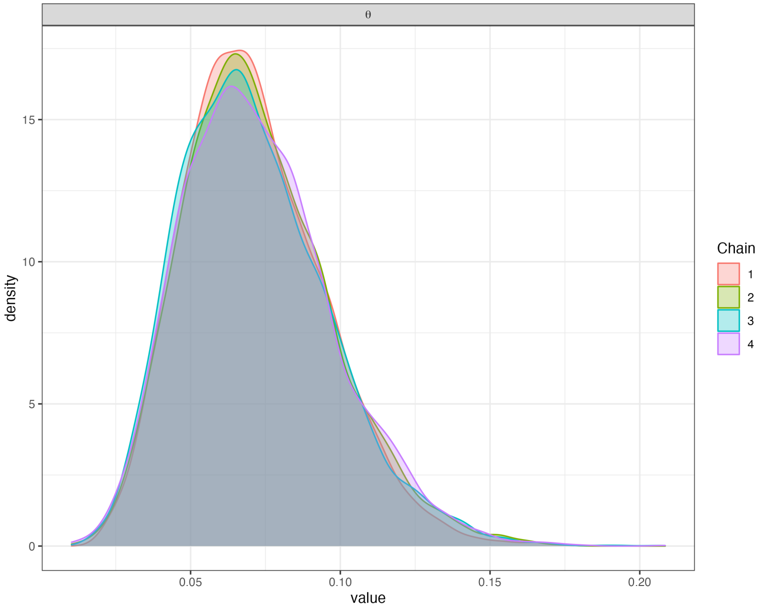
(a) Generate trace plots for your Markov chains. Did they converge?

ANSWER:



(b) Generate the density plots of your parameter. Are these densities similar to each other?

ANSWER:



(c) What is the posterior mean of your parameter?

ANSWER:

```
model_5_mcmc
```

```
# Inference for Stan model: fab6b48f5279803ac7a47101cf196f51.
# 4 chains, each with iter=10000; warmup=5000; thin=1;
# post-warmup draws per chain=5000, total post-warmup draws=20000.

#          mean se_mean   sd   2.5%    25%    50%    75%  97.5% n_eff Rhat
# theta    0.07    0.00 0.02   0.03   0.05   0.07   0.09   0.13  6769    1
# lp__   -29.26    0.01 0.72 -31.29 -29.43 -28.98 -28.80 -28.75  6043    1
```

The posterior mean for θ is 0.07, given our data and prior model.

(d) Interpret the 95% credibility interval you've obtained from your simulation.

ANSWER:

From the summary above, we can conclude that, given our data and prior, about 95% of our posterior observations lie between 0.03 and 0.13.

Problem 6

Using the `howell.csv` data set (available on Canvas), run an MCMC simulation to approximate the posterior distribution for the average *height*, but only for adults (i.e., individuals older than 18 years old). In other words, make sure to apply the `filter()` function to your data set first.

You may assume, for simplicity, that the standard deviation parameter, σ, is constant and known. You may use any value you want, as long as it makes sense. Recall that, if your data are normally distributed, approximately 95% of the observations lie within 2 standard deviations of the mean, or $\mu \pm 2 \cdot \sigma$. Take this detail into account when setting up your Bayesian model.

Answer the same questions from Problem 5.

ANSWER:

```r
howell <- read_csv("howell.csv")

howell_adults <- howell %>%
  filter(age > 18)   ## just the adult individuals here.
```

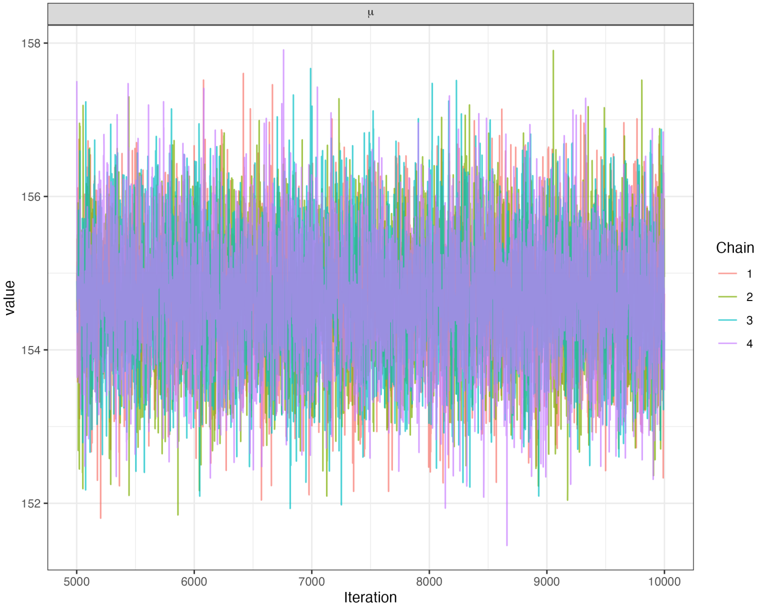
If we assume that the average height of 170 cm for an adult population is normally distributed with a standard deviation on 15 cm, approximately 95% of the individuals will have a height between 140 and 200 cm.

Let's use these as our priors.

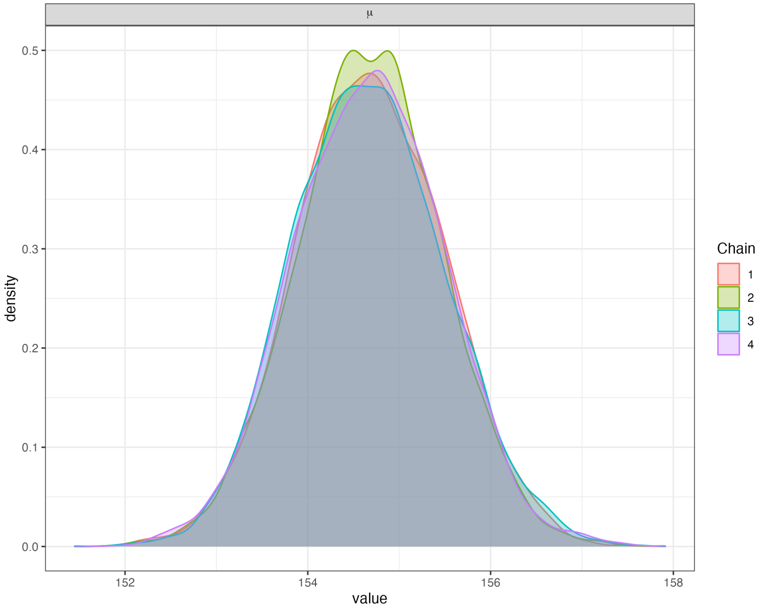
```
model_6 <- "

  data {

real<lower=0> Y[346];  // the filtered data set has 346 adults.


  }

  parameters {

real<lower=0> mu;   // we cannot have negative heights.


  }

  model {

Y ~ normal(mu, 15);   // sigma is assumed to be known here.
mu ~ normal(170, 15);

  }

"
```

```
# Running the MCMC sampler:

set.seed(123)

model_6_mcmc <- stan(
  model_code = model_6,
  data = list(Y = howell_adults$height), ## selecting the 'height' column.
  chains = 4,
  iter = 5000 * 2
)
```

(a) Trace plot:


μ
158
156
154
152
value
5000
6000
7000
8000
9000
10000
Iteration
Chain
1
2
3
4

(b) Density plot:



(c) The posterior mean for μ is 154.68 cm, given our data and prior model.

(d)

```
model_6_mcmc
```

```
# Inference for Stan model: 6043b9632a6b63cd5fdc40421532ba54.
# 4 chains, each with iter=10000; warmup=5000; thin=1;
# post-warmup draws per chain=5000, total post-warmup draws=20000.

#          mean se_mean   sd   2.5%    25%    50%    75%  97.5% n_eff Rhat
# mu     54.68     0.01 0.81 153.12 154.13 154.67 155.23 156.26  6862    1
# lp__  -42.31     0.01 0.71 -44.32 -42.48 -42.04 -41.86 -41.81  8806    1
```

From the summary above, we can conclude that, given our data and prior, about 95% of our posterior observations for the average height of adults (μ) lies between 153.12 cm and 156.26 cm.

Problem 7

Still using the `howell.csv` data set, now estimate a Bayesian model for the posterior distributions for *weights* (in kilograms). This time, you will have to set a prior for σ as well.

Here, make sure to play around with models including every individual in the sample, but also for adults only.

As a bonus, you may estimate models also based on `gender` since, these data are also available in this data set. With different research questions in mind, make sure to think about your priors and adjust your data accordingly.

ANSWER:

Let's assume that weights of individuals are normaly distributed, with mean and standard deviation parameters μ and σ, respectively.

Since we don't know σ, we need to set priors for both parameters.

Priors: $\mu \sim \mathcal{N}(\theta, \tau)$
$\sigma \sim \text{Uniform}(0, 20)$

Let's set up now the model string:

```
model_7 <- "

  data {


real<lower=0> Y[544];  // using the whole sample.


  }

  parameters {

real<lower=0> mu;      // we cannot have negative weights.
real <lower=0, upper=20> sigma;

  }

  model {

Y ~ normal(mu, sigma);
mu ~ normal(65, 10);      // assuming  ~ N(60,20) for the average weight.
sigma ~ uniform(0, 20);   // assuming the SD to be uniformly distributed between 0 and 20.

  }

"
```

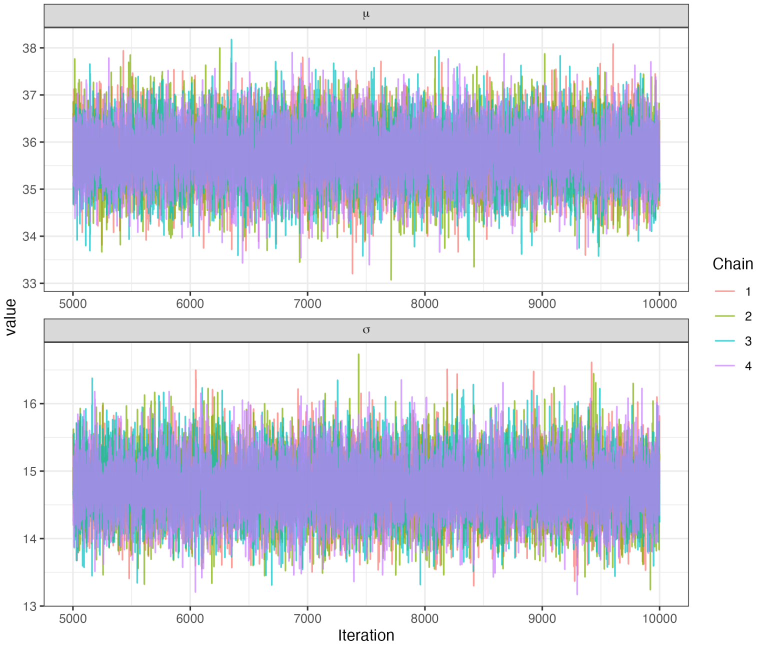
Then, we use `rstan` to run MCMC simulations.

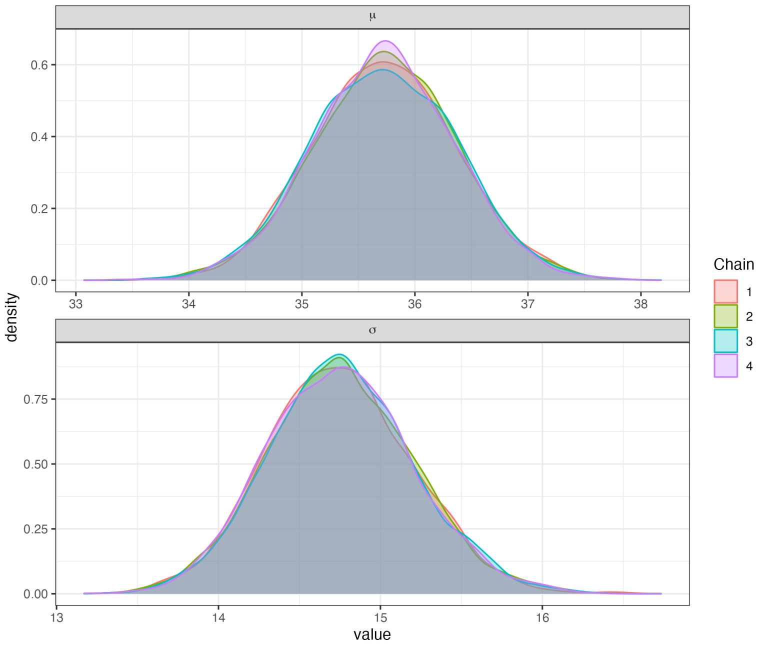
```r
set.seed(123)

model_7_mcmc <- stan(
  model_code = model_7,
  data = list(Y = howell$weight),
  chains = 4,
  iter = 5000 * 2
)
```

```
# Inference for Stan model: c80f0e81d8ee9675915a189dd491cfa7.
# 4 chains, each with iter=10000; warmup=5000; thin=1;
# post-warmup draws per chain=5000, total post-warmup draws=20000.

#            mean se_mean   sd     2.5%      25%      50%      75%    97.5% n_eff Rhat
# mu        35.73    0.00 0.64    34.47    35.30    35.73    36.17    36.99 16990    1
# sigma     14.75    0.00 0.45    13.90    14.45    14.74    15.05    15.68 17416    1
# lp__   -1734.80    0.01 1.05 -1737.64 -1735.20 -1734.47 -1734.06 -1733.79  8261    1
```

From this model, we see that, given our data and priors, the posterior average weight is of 35.73 kg, with a posterior mean standard deviation of 14.75 kg.

Let's have a look at trace and density plots:





The MCMC sampler has converged (as seen in the trace plots) and the density plots for all 4 chains are very similar, indicating a well-specified Bayesian posterior model.

Feel free to further customize and modify priors and the sample you will be investigating here, as suggested in the problem.