Problem2_14.12 c

```
## Loading required package: StanHeaders
```

```
## Loading required package: ggplot2
```

```
## rstan (Version 2.19.2, GitRev: 2e1f913d3ca3)
```

```
## For execution on a local, multicore CPU with excess RAM we recommend calling
## options(mc.cores = parallel::detectCores()).
## To avoid recompilation of unchanged Stan programs, we recommend calling
## rstan_options(auto_write = TRUE)
```

```
## This is bayesplot version 1.7.0
```

```
## - Online documentation and vignettes at mc-stan.org/bayesplot
```

```
## - bayesplot theme set to bayesplot::theme_default()
```

```
##    * Does _not_ affect other ggplot2 plots
```

```
##    * See ?bayesplot_theme_set for details on theme setting
```

```
## Loading required package: Rcpp
```

```
## Registered S3 method overwritten by 'xts':
##   method     from
##   as.zoo.xts zoo
```

```
## rstanarm (Version 2.19.2, packaged: 2019-10-01 20:20:33 UTC)
```

```
## - Do not expect the default priors to remain the same in future rstanarm versions.
```

```
## Thus, R scripts should specify priors explicitly, even if they are just the defaults.
```

```
## - For execution on a local, multicore CPU with excess RAM we recommend calling
```

```
## options(mc.cores = parallel::detectCores())
```

```
## - bayesplot theme set to bayesplot::theme_default()
```

```
##    * Does _not_ affect other ggplot2 plots
```

```
##    * See ?bayesplot_theme_set for details on theme setting
```

```
##
## Attaching package: 'rstanarm'
```

```
## The following object is masked from 'package:rstan':
##
##     loo
```

Baysian Linear Regression

1. Data

```
X <- log(c(31.2, 24.0, 19.8, 18.2, 9.6, 6.5, 3.2)) #Body Mass
Y <- log(c(1113, 982, 908, 842, 626, 430, 281)) #Metabolic Rate
stan_data <- list(x = X, N = length(Y), y = Y)
```

2. Bayesian Linear Model

fit stan model with iteration 1000 times and 4 chains.

```
stan_model <- "~/Documents/BU_2019_Fall/HW6/linear_model.stan"
fit <- stan(file = stan_model, data = stan_data, iter = 1000, chains = 4, control=list(a
dapt_delta=0.99,max_treedepth = 12))
```

```
## DIAGNOSTIC(S) FROM PARSER:
## Info: Comments beginning with # are deprecated.  Please use // in place of # for line
comments.
##
##
## SAMPLING FOR MODEL 'linear_model' NOW (CHAIN 1).
## Chain 1:
## Chain 1: Gradient evaluation took 4e-05 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 0.4 secon
ds.
## Chain 1: Adjust your expectations accordingly!
## Chain 1:
## Chain 1:
## Chain 1: Iteration:   1 / 1000 [  0%]  (Warmup)
## Chain 1: Iteration: 100 / 1000 [ 10%]  (Warmup)
## Chain 1: Iteration: 200 / 1000 [ 20%]  (Warmup)
## Chain 1: Iteration: 300 / 1000 [ 30%]  (Warmup)
## Chain 1: Iteration: 400 / 1000 [ 40%]  (Warmup)
## Chain 1: Iteration: 500 / 1000 [ 50%]  (Warmup)
## Chain 1: Iteration: 501 / 1000 [ 50%]  (Sampling)
## Chain 1: Iteration: 600 / 1000 [ 60%]  (Sampling)
## Chain 1: Iteration: 700 / 1000 [ 70%]  (Sampling)
## Chain 1: Iteration: 800 / 1000 [ 80%]  (Sampling)
## Chain 1: Iteration: 900 / 1000 [ 90%]  (Sampling)
## Chain 1: Iteration: 1000 / 1000 [100%]  (Sampling)
## Chain 1:
## Chain 1:  Elapsed Time: 0.300824 seconds (Warm-up)
## Chain 1:                0.343986 seconds (Sampling)
## Chain 1:                0.64481 seconds (Total)
## Chain 1:
##
## SAMPLING FOR MODEL 'linear_model' NOW (CHAIN 2).
## Chain 2:
## Chain 2: Gradient evaluation took 6e-06 seconds
## Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 0.06 seco
nds.
## Chain 2: Adjust your expectations accordingly!
## Chain 2:
## Chain 2:
## Chain 2: Iteration:   1 / 1000 [  0%]  (Warmup)
## Chain 2: Iteration: 100 / 1000 [ 10%]  (Warmup)
## Chain 2: Iteration: 200 / 1000 [ 20%]  (Warmup)
## Chain 2: Iteration: 300 / 1000 [ 30%]  (Warmup)
## Chain 2: Iteration: 400 / 1000 [ 40%]  (Warmup)
## Chain 2: Iteration: 500 / 1000 [ 50%]  (Warmup)
## Chain 2: Iteration: 501 / 1000 [ 50%]  (Sampling)
## Chain 2: Iteration: 600 / 1000 [ 60%]  (Sampling)
## Chain 2: Iteration: 700 / 1000 [ 70%]  (Sampling)
## Chain 2: Iteration: 800 / 1000 [ 80%]  (Sampling)
## Chain 2: Iteration: 900 / 1000 [ 90%]  (Sampling)
## Chain 2: Iteration: 1000 / 1000 [100%]  (Sampling)
## Chain 2:
## Chain 2:  Elapsed Time: 0.377937 seconds (Warm-up)
```

```
## Chain 2:                0.338954 seconds (Sampling)
## Chain 2:                0.716891 seconds (Total)
## Chain 2:
##
## SAMPLING FOR MODEL 'linear_model' NOW (CHAIN 3).
## Chain 3:
## Chain 3: Gradient evaluation took 6e-06 seconds
## Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 0.06 seco
nds.
## Chain 3: Adjust your expectations accordingly!
## Chain 3:
## Chain 3:
## Chain 3: Iteration:   1 / 1000 [  0%]  (Warmup)
## Chain 3: Iteration: 100 / 1000 [ 10%]  (Warmup)
## Chain 3: Iteration: 200 / 1000 [ 20%]  (Warmup)
## Chain 3: Iteration: 300 / 1000 [ 30%]  (Warmup)
## Chain 3: Iteration: 400 / 1000 [ 40%]  (Warmup)
## Chain 3: Iteration: 500 / 1000 [ 50%]  (Warmup)
## Chain 3: Iteration: 501 / 1000 [ 50%]  (Sampling)
## Chain 3: Iteration: 600 / 1000 [ 60%]  (Sampling)
## Chain 3: Iteration: 700 / 1000 [ 70%]  (Sampling)
## Chain 3: Iteration: 800 / 1000 [ 80%]  (Sampling)
## Chain 3: Iteration: 900 / 1000 [ 90%]  (Sampling)
## Chain 3: Iteration: 1000 / 1000 [100%]  (Sampling)
## Chain 3:
## Chain 3:  Elapsed Time: 0.325662 seconds (Warm-up)
## Chain 3:                0.285376 seconds (Sampling)
## Chain 3:                0.611038 seconds (Total)
## Chain 3:
##
## SAMPLING FOR MODEL 'linear_model' NOW (CHAIN 4).
## Chain 4:
## Chain 4: Gradient evaluation took 6e-06 seconds
## Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 0.06 seco
nds.
## Chain 4: Adjust your expectations accordingly!
## Chain 4:
## Chain 4:
## Chain 4: Iteration:   1 / 1000 [  0%]  (Warmup)
## Chain 4: Iteration: 100 / 1000 [ 10%]  (Warmup)
## Chain 4: Iteration: 200 / 1000 [ 20%]  (Warmup)
## Chain 4: Iteration: 300 / 1000 [ 30%]  (Warmup)
## Chain 4: Iteration: 400 / 1000 [ 40%]  (Warmup)
## Chain 4: Iteration: 500 / 1000 [ 50%]  (Warmup)
## Chain 4: Iteration: 501 / 1000 [ 50%]  (Sampling)
## Chain 4: Iteration: 600 / 1000 [ 60%]  (Sampling)
## Chain 4: Iteration: 700 / 1000 [ 70%]  (Sampling)
## Chain 4: Iteration: 800 / 1000 [ 80%]  (Sampling)
## Chain 4: Iteration: 900 / 1000 [ 90%]  (Sampling)
## Chain 4: Iteration: 1000 / 1000 [100%]  (Sampling)
## Chain 4:
## Chain 4:  Elapsed Time: 0.35916 seconds (Warm-up)
## Chain 4:                0.358412 seconds (Sampling)
```

```
## Chain 4:                0.717572 seconds (Total)
## Chain 4:
```

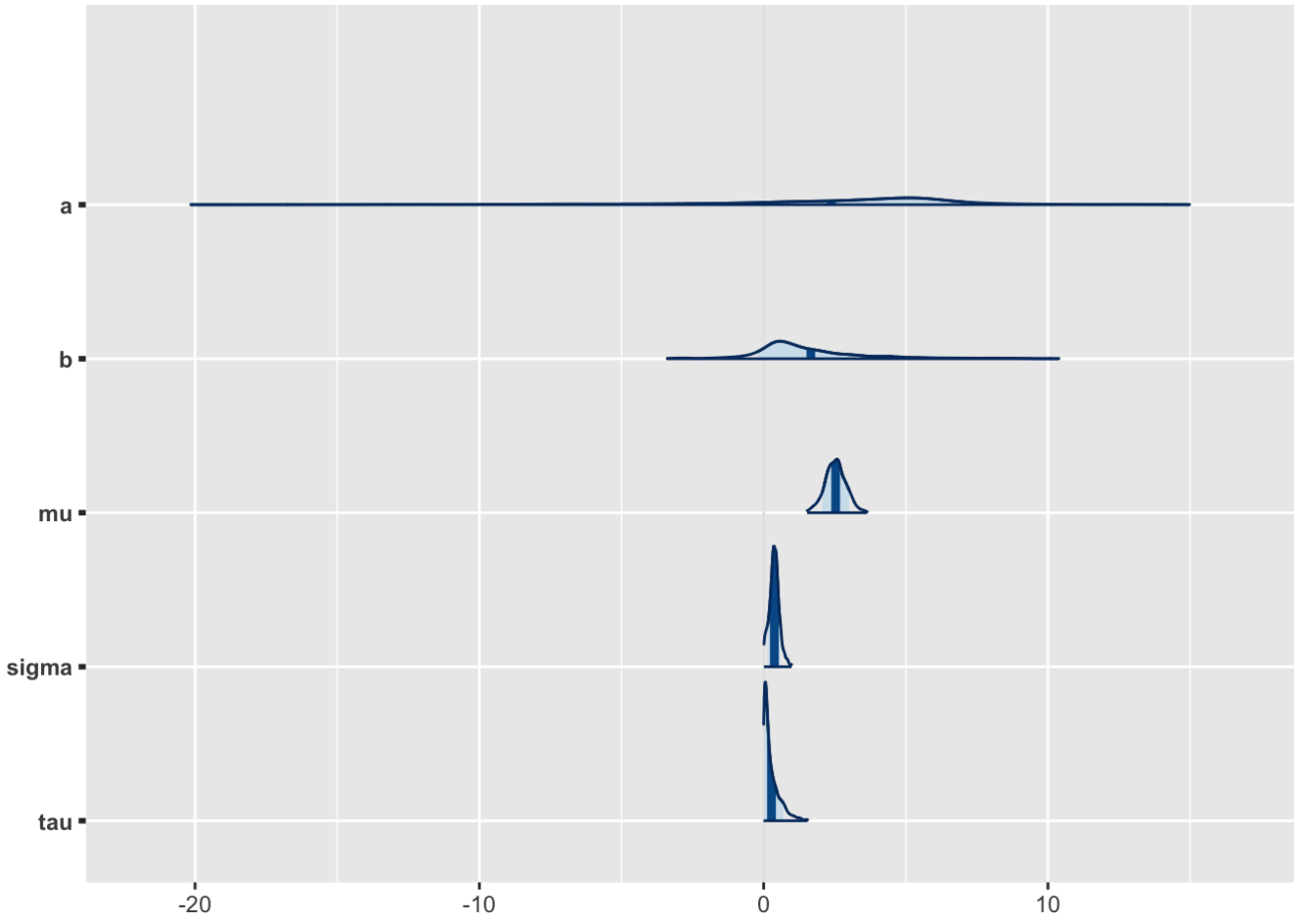
```
## Warning: Bulk Effective Samples Size (ESS) is too low, indicating posterior means and
medians may be unreliable.
## Running the chains for more iterations may help. See
## http://mc-stan.org/misc/warnings.html#bulk-ess
```

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

```
print(fit)
```

```
## Inference for Stan model: linear_model.
## 4 chains, each with iter=1000; warmup=500; thin=1;
## post-warmup draws per chain=500, total post-warmup draws=2000.
##
##        mean se_mean   sd   2.5%   25%   50%   75% 97.5% n_eff Rhat
## a      2.38    0.31 5.59 -12.73  0.61  3.73  5.51 11.18   321 1.01
## b      1.66    0.13 2.28  -1.77  0.40  1.07  2.38  8.07   322 1.00
## mu     2.53    0.02 0.38   1.76  2.28  2.53  2.78  3.31   615 1.00
## sigma  0.38    0.01 0.18   0.04  0.27  0.37  0.48  0.78   337 1.01
## tau    0.28    0.02 0.30   0.00  0.06  0.16  0.40  1.10   330 1.02
## lp__  -5.69    0.09 1.91 -10.40 -6.74 -5.35 -4.32 -2.96   410 1.01
##
## Samples were drawn using NUTS(diag_e) at Tue Nov 26 10:57:16 2019.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).
```

```
posterior <- extract(fit, permuted = FALSE)
mcmc_areas(
  posterior,
  pars = c("a","b","mu","sigma","tau"),
  prob = 0.8, # 80% intervals
  prob_outer = 0.99, # 99%
  point_est = "mean"
)
```


a
b
mu
sigma
tau
-20
-10
0
10