# STA 6352, Report 7.6

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### Problem

### Introduction

The rat growth data set, originally analyzed by Gelfand et al. (1990), consists of weight measurements of 30 rats over a five-week period. The goal is to model each rat's weight as a linear function of time while accounting for individual differences among rats. A hierarchical Bayesian model is suitable for this analysis as it allows for partial pooling of information across rats while estimating individual growth trajectories.

### Model Specification

Let $y_{ij}$ denote the weight of rat $i$ at week $j$, and let $x_j$ represent the week index. We consider the hierarchical model:

$$
\begin{aligned}
y_{ij} &\sim \mathcal{N}(\alpha_i + \beta_i x_j, \sigma^2), \\
\alpha_i &\sim \mathcal{N}(\beta_0, \sigma_\alpha^2), \\
\beta_i &\sim \mathcal{N}(\beta_1, \sigma_\beta^2), \\
\sigma, \sigma_\alpha, \sigma_\beta &\sim \text{Uniform}(0, 200), \\
\beta_0, \beta_1 &\sim \mathcal{N}(0, 1000).
\end{aligned}
$$

This formulation captures individual differences in both intercepts and slopes while sharing information through the hyperparameters. The Stan model was fit using the following file:

```
model_string <- "
  data {
    int<lower=0> N;
    int<lower=0> J;
    int<lower=0> K;
    int<lower=1, upper=J> rat[N];
    vector[N] x;
    vector[N] y;
  }
  parameters {
    real beta_0;
    real beta_1;
    vector[J] alpha;
    vector[J] beta;
    real<lower=0> sigma;
```

```
    real<lower=0> sigma_alpha;
    real<lower=0> sigma_beta;
  }
  model {
    beta_0 ~ normal(0, 1000);
    beta_1 ~ normal(0, 1000);
    alpha ~ normal(beta_0, sigma_alpha);
    beta ~ normal(beta_1, sigma_beta);
    sigma_alpha ~ uniform(0, 200);
    sigma_beta ~ uniform(0, 200);
    sigma ~ uniform(0, 200);
    for (n in 1:N)
      y[n] ~ normal(alpha[rat[n]] + beta[rat[n]] * x[n], sigma);
  }
"
writeLines(model_string, "rat_model.stan")
```

**Analysis**

We fit this model using Stan in two ways:

- extbfWithout centering: Using the raw week indices $x_j = \{1, 2, 3, 4, 5\}$.
- extbfWith centering: Transforming the week indices to $x_j - 3 = \{-2, -1, 0, 1, 2\}$, which helps with parameter estimation stability.

**Results and Diagnostics**

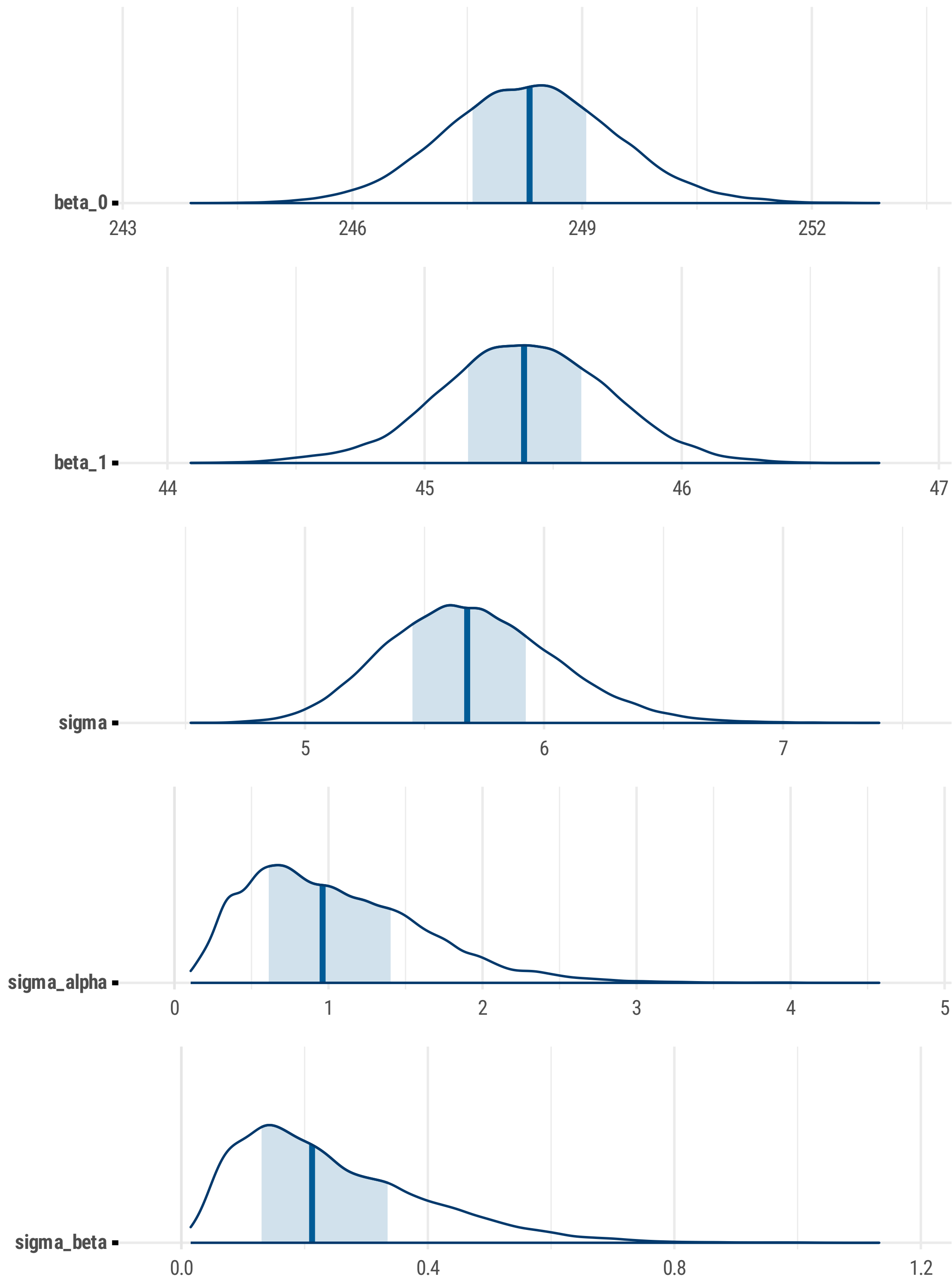
We examine posterior summaries, posterior density plots, and convergence diagnostics for key parameters $(\beta_0, \beta_1, \sigma, \sigma_\alpha, \sigma_\beta)$. The centering approach improves sampling efficiency, as evidenced by better chain mixing and reduced autocorrelation.

### Conclusion

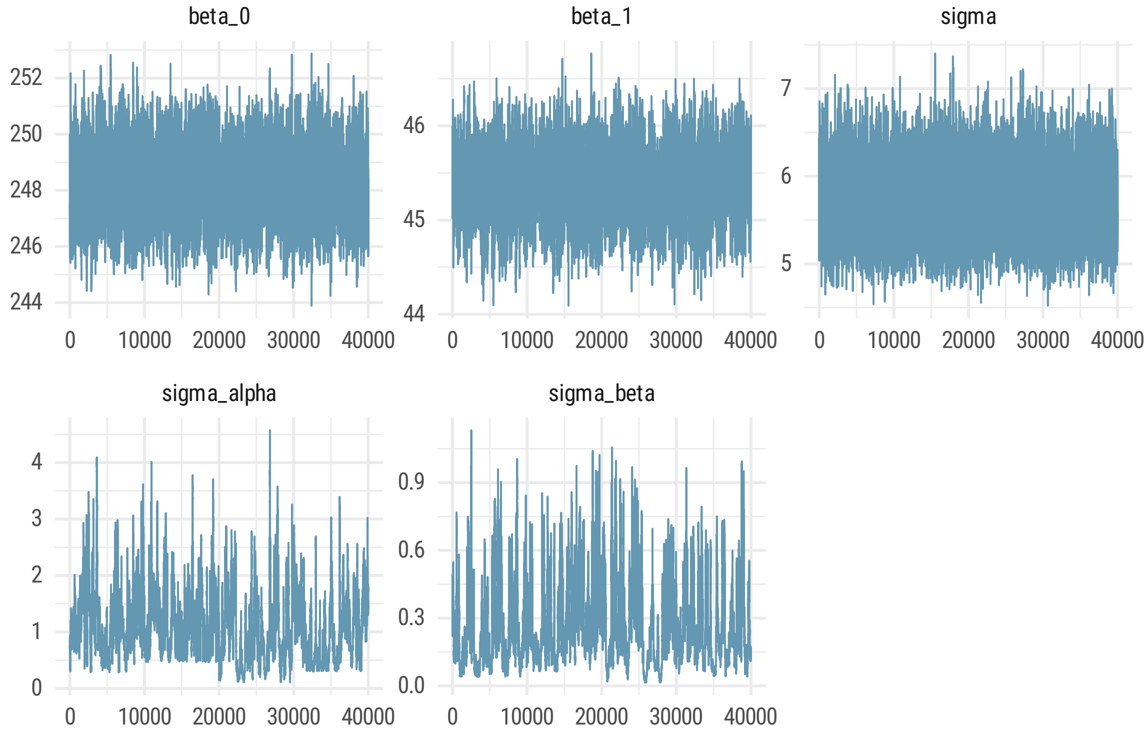
The hierarchical Bayesian approach effectively models rat growth while allowing individual variation. Centering the predictor enhances inference stability, making it the preferred approach.

### Model Fit for Noncentered Data

```
## Inference for Stan model: anon_model.
## 4 chains, each with iter=20000; warmup=10000; thin=1;
## post-warmup draws per chain=10000, total post-warmup draws=40000.
##
##               mean se_mean   sd   2.5%    25%    50%    75%  97.5% n_eff Rh
## beta_0      248.32    0.03 1.11 246.16 247.57 248.31 249.05 250.52  1756 1
## beta_1       45.39    0.01 0.33  44.71  45.17  45.39  45.61  46.03  1526 1
## sigma         5.70    0.00 0.35   5.06   5.45   5.68   5.92   6.43  5898 1
## sigma_alpha   1.05    0.05 0.57   0.24   0.61   0.96   1.40   2.36   118 1
## sigma_beta    0.25    0.01 0.15   0.04   0.13   0.21   0.33   0.60   159 1
##
## Samples were drawn using NUTS(diag_e) at Wed Feb 12 10:53:55 2025.
## 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).
```

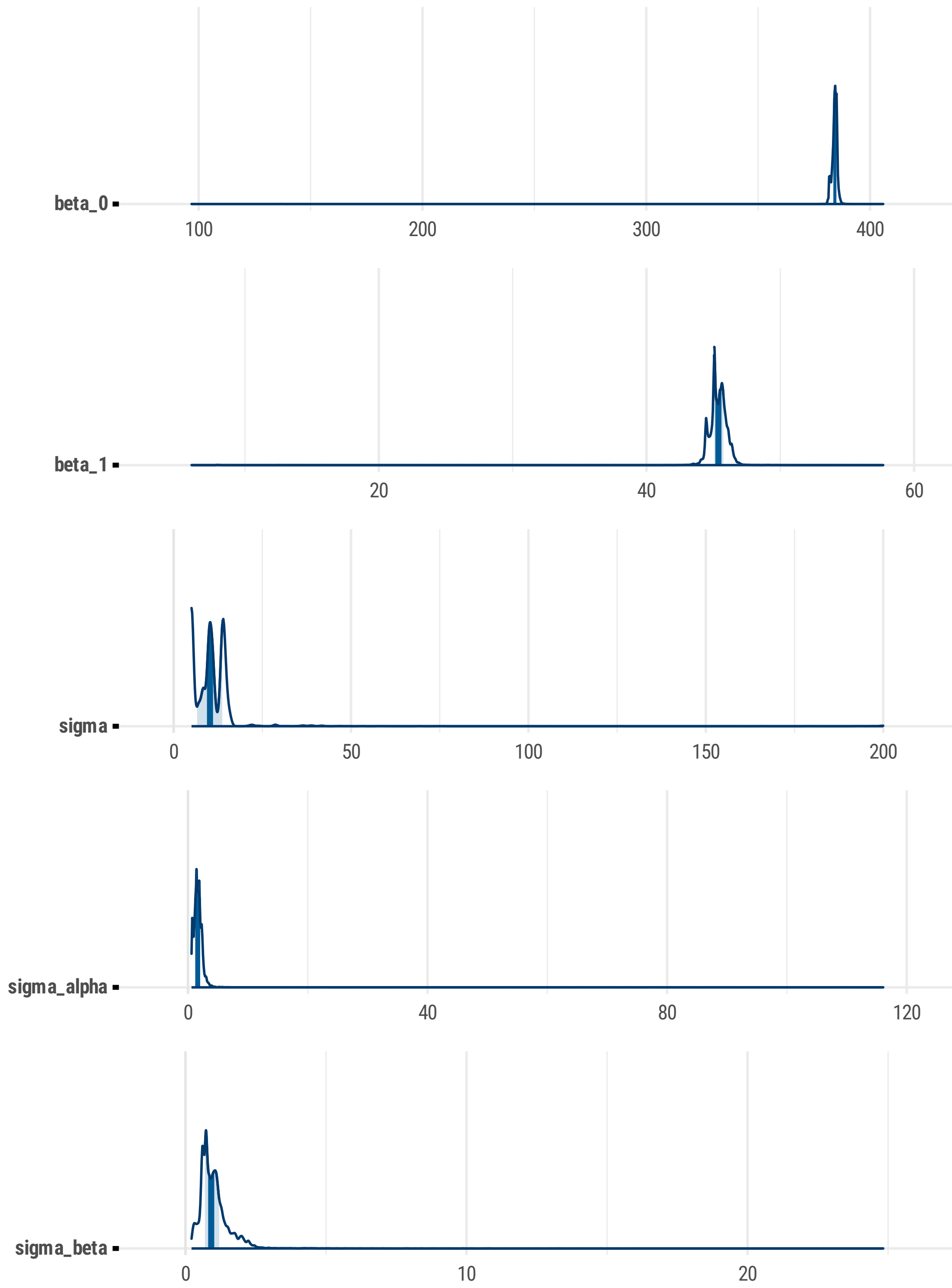


beta_0
243
246
249
252
beta_1
44
45
46
47
sigma
5
6
7
sigma_alpha
0
1
2
3
4
5
sigma_beta
0.0
0.4
0.8
1.2

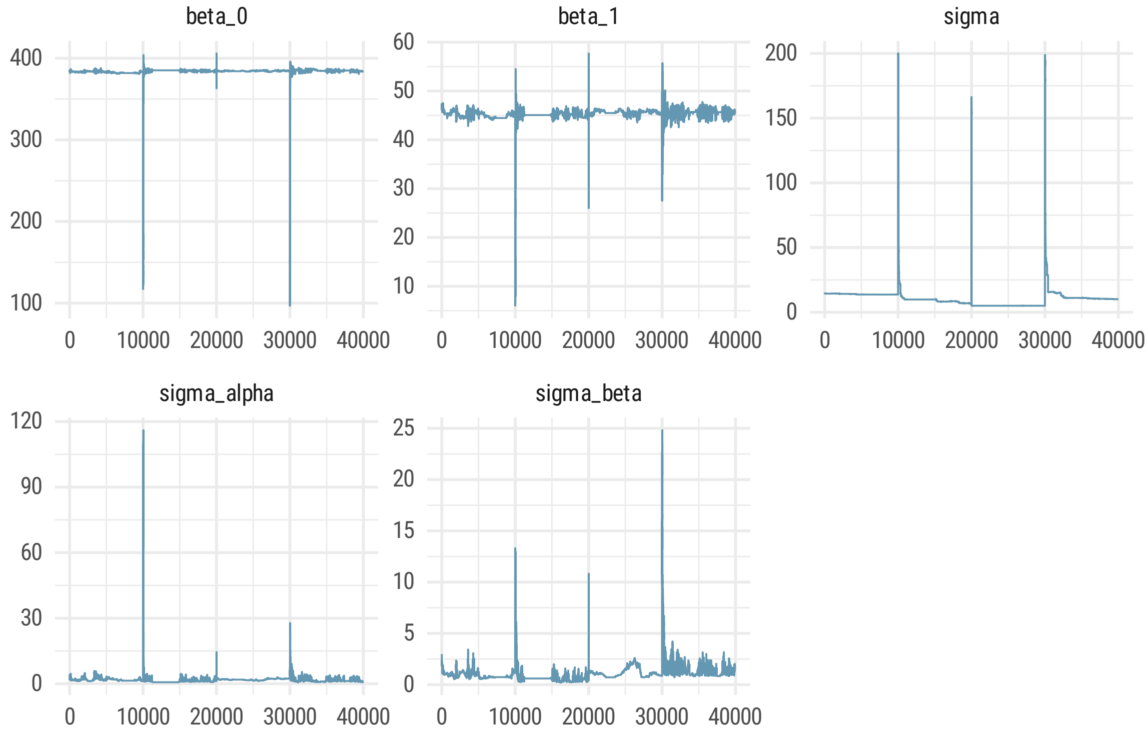



**Model Fit for Centered Data**

```
## Inference for Stan model: anon_model.
## 4 chains, each with iter=20000; warmup=10000; thin=1;
## post-warmup draws per chain=10000, total post-warmup draws=40000.
##
##                mean se_mean    sd   2.5%    25%    50%    75%  97.5% n_eff
## beta_0       383.68    0.37 10.48 381.85 383.59 384.31 384.95 386.13   823
## beta_1        45.32    0.11  1.45  44.27  45.07  45.38  45.75  46.49   185
## sigma         10.80    2.42 10.68   5.05   6.60  10.24  13.69  15.78    19
## sigma_alpha    1.81    0.16  3.28   0.71   1.22   1.60   2.03   3.22   422
## sigma_beta     1.04    0.18  0.78   0.31   0.69   0.92   1.20   2.26    19
##
## Samples were drawn using NUTS(diag_e) at Wed Feb 12 10:54:07 2025.
## 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).
```



beta_0
100
200
300
400
beta_1
20
40
60
sigma
0
50
100
150
200
sigma_alpha
0
40
80
120
sigma_beta
0
10
20


beta_0
400
300
200
100
0
10000
20000
30000
40000
beta_1
60
50
40
30
20
10
sigma
200
150
100
50
sigma_alpha
120
90
60
30
sigma_beta
25
20
15
10
5