The Normal-Normal model

BAYESIAN MODELING WITH RJAGS

Alicia Johnson
Associate Professor, Macalester College

Chapter 2 goals

- Engineer the two-parameter Normal-Normal model
- Define, compile, and simulate the Normal-Normal in RJAGS
- Explore Markov chains, the mechanics of an RJAGS simulation

Sleep deprivation

Research Question

How does sleep deprivation impact reaction time?

The Study

- Measure reaction time on Day 0
- Restrict sleep to 3 hours per night
- Measure reaction time on Day 3
- Measure the change in reaction time

[1] Belenky, G. et al (2003). Journal of Sleep Research, 12:1–12. [2] Data provided in the lme4 package.

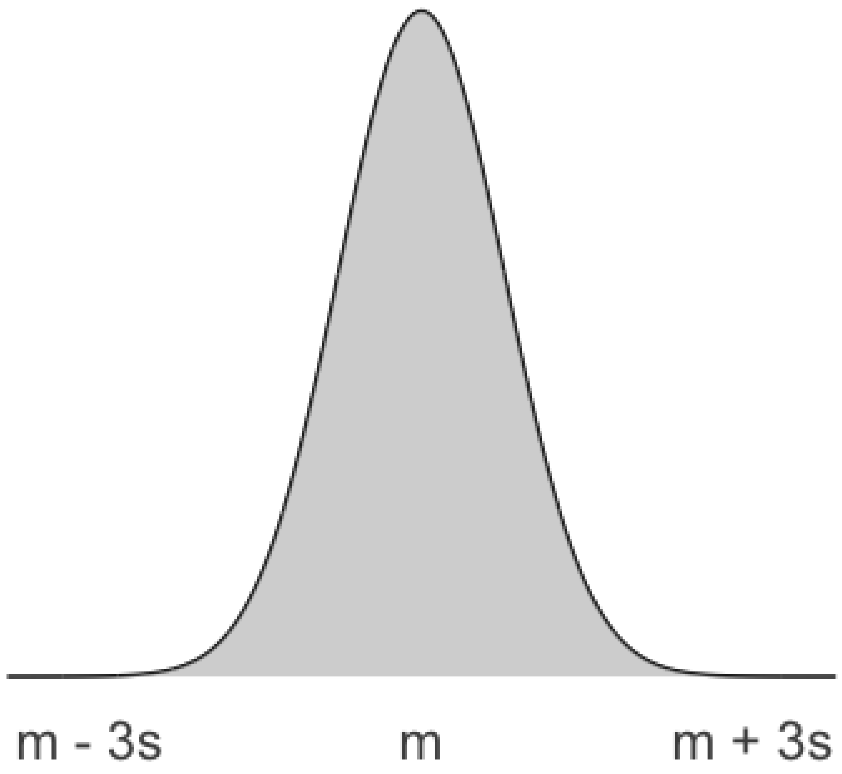
Modeling change in reaction time

Y_i = change in reaction time (ms)

Assume

Y_i are *Normally* distributed around some *average* change in reaction time m with *standard deviation* s.

$$Y_i \sim N(m, s^2)$$



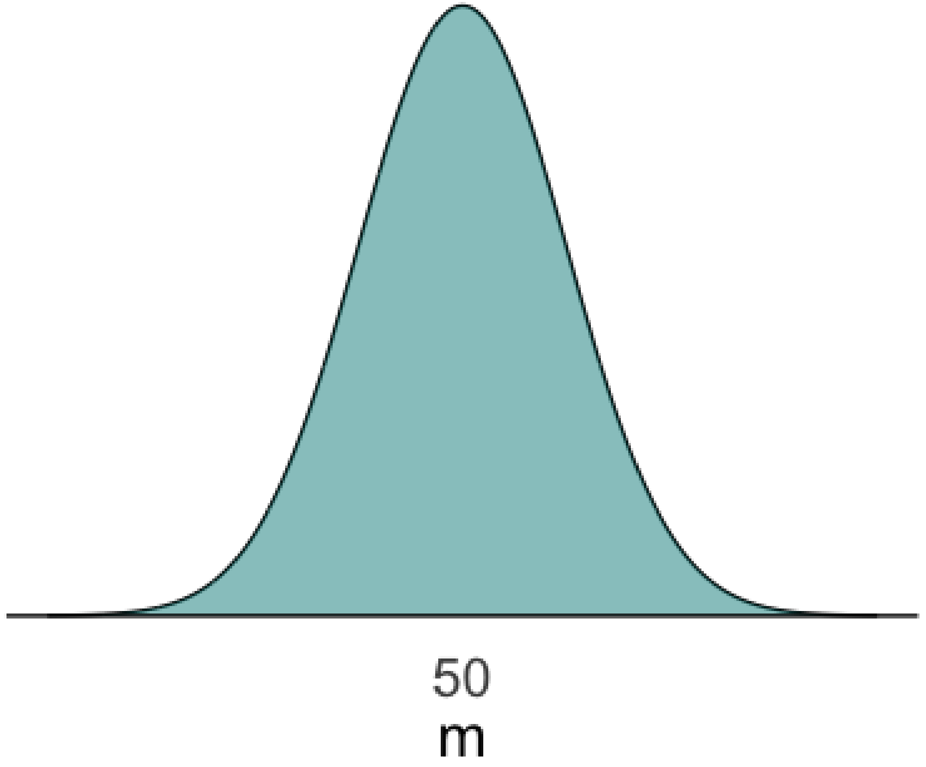
Prior model for parameter m

Y_i = change in reaction time (ms) $Y_i \sim N(m, s^2)$

m = average Y_i

Prior information:

- With *normal* sleep, average reaction time is ~250 ms
- Expect average to ↗ by ~50 ms



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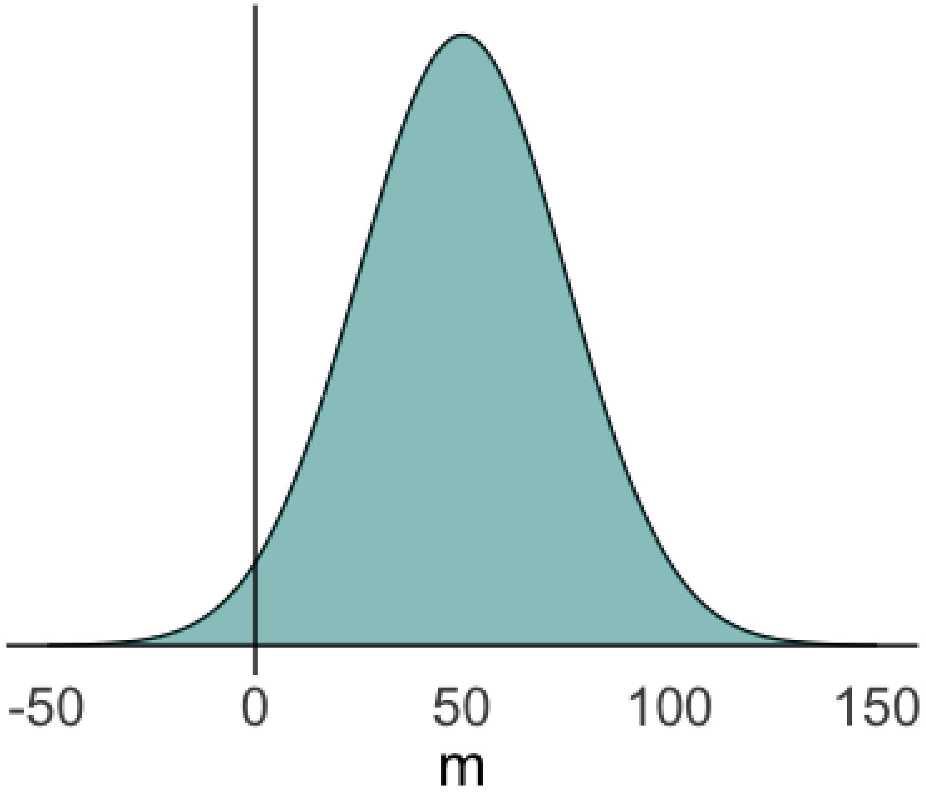
m = average Y_i

Prior information:

- With *normal* sleep, average reaction time is ~250 ms
- Expect average to $\nearrow$ by ~50 ms
- Average is unlikely to $\searrow$ & unlikely to $\nearrow$ by > ~150 ms



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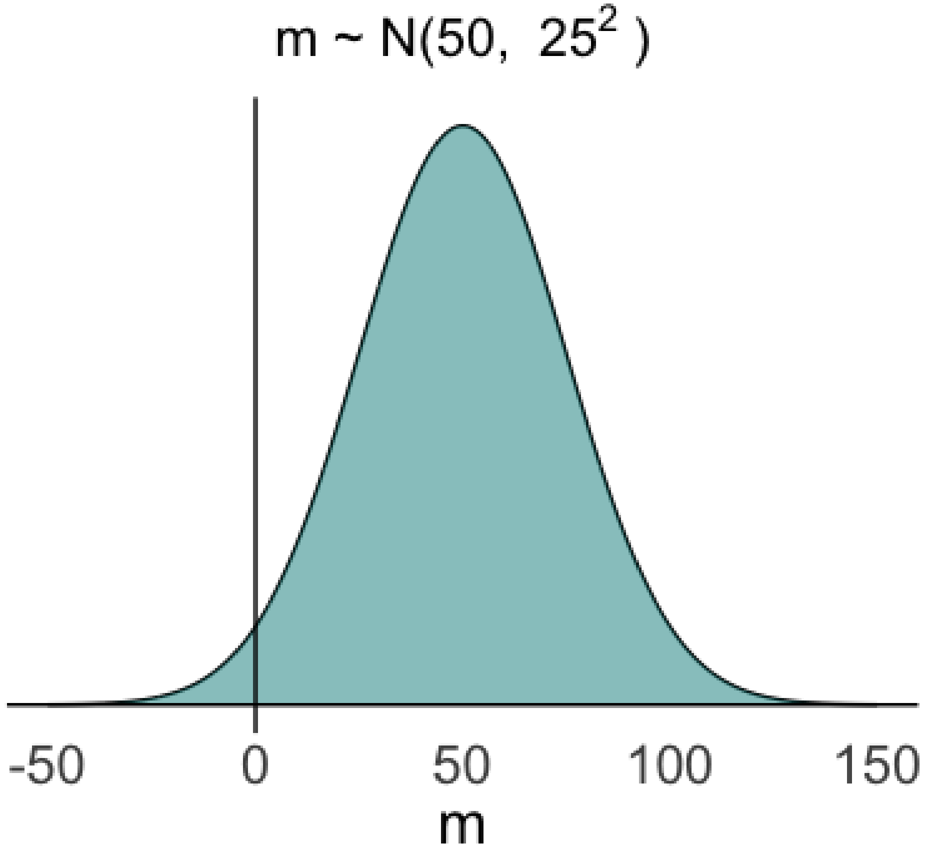
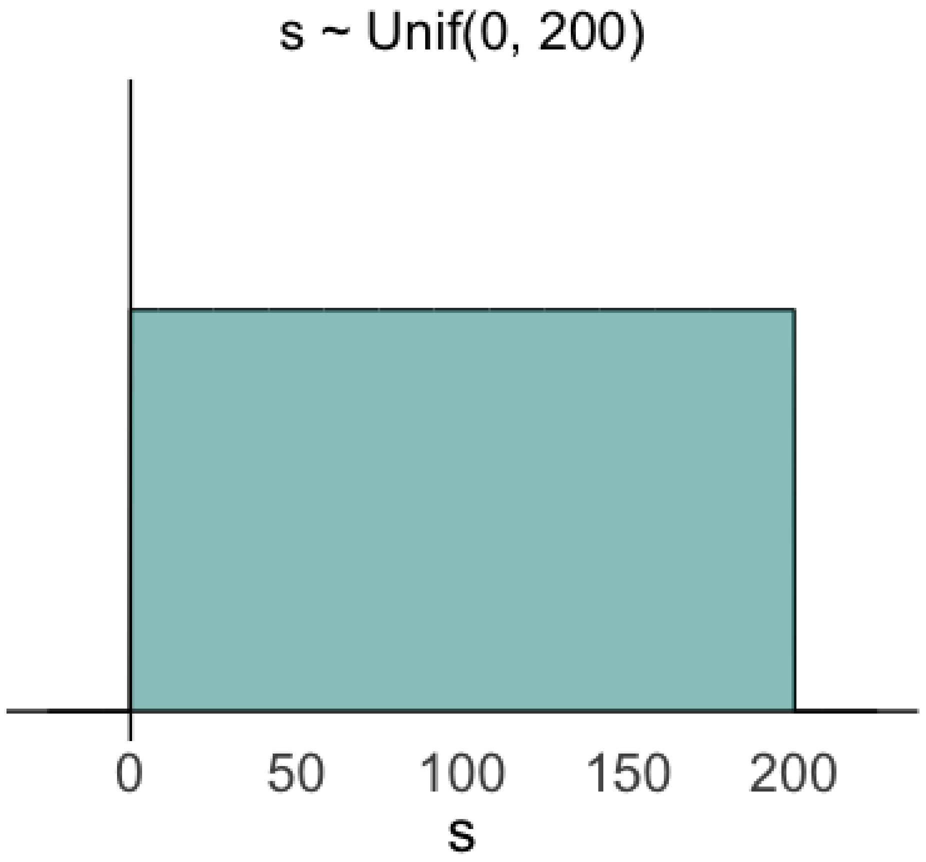


Prior model for parameter s

Y_i = change in reaction time (ms) $Y_i \sim N(m, s^2)$
s = standard deviation of Y_i

Prior information:

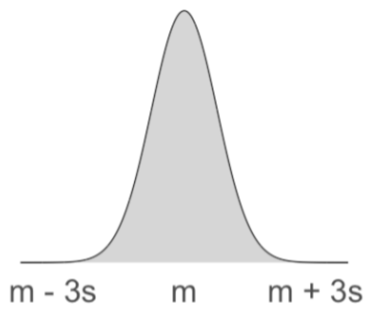
- $s > 0$
- With *normal* sleep, s.d. in reaction times is ~30 ms
- s is equally likely to be anywhere from 0 to 200 ms



The Normal-Normal Model

Likelihood:

$Y_i \sim N(m, s^2)$



The Normal-Normal Model

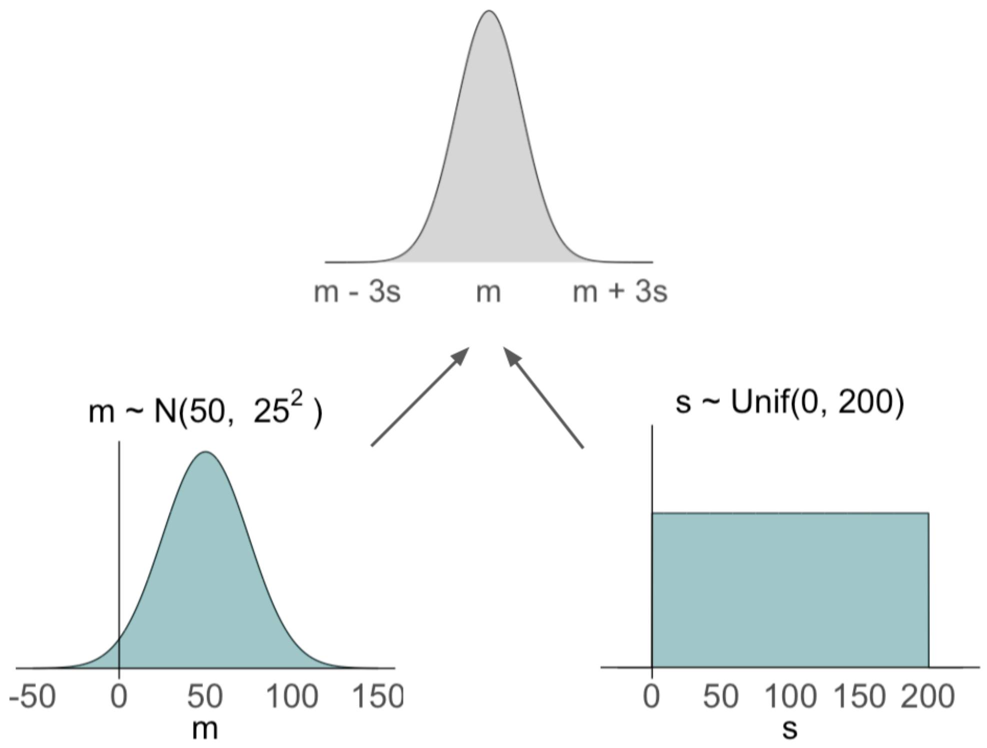
Likelihood:

$Y_i \sim N(m, s^2)$

Priors:

$m \sim N(50, 25^2)$

$s \sim \text{Unif}(0, 200)$



Let's practice!

BAYESIAN MODELING WITH RJAGS

Simulating the Normal-Normal in RJAGS

BAYESIAN MODELING WITH RJAGS

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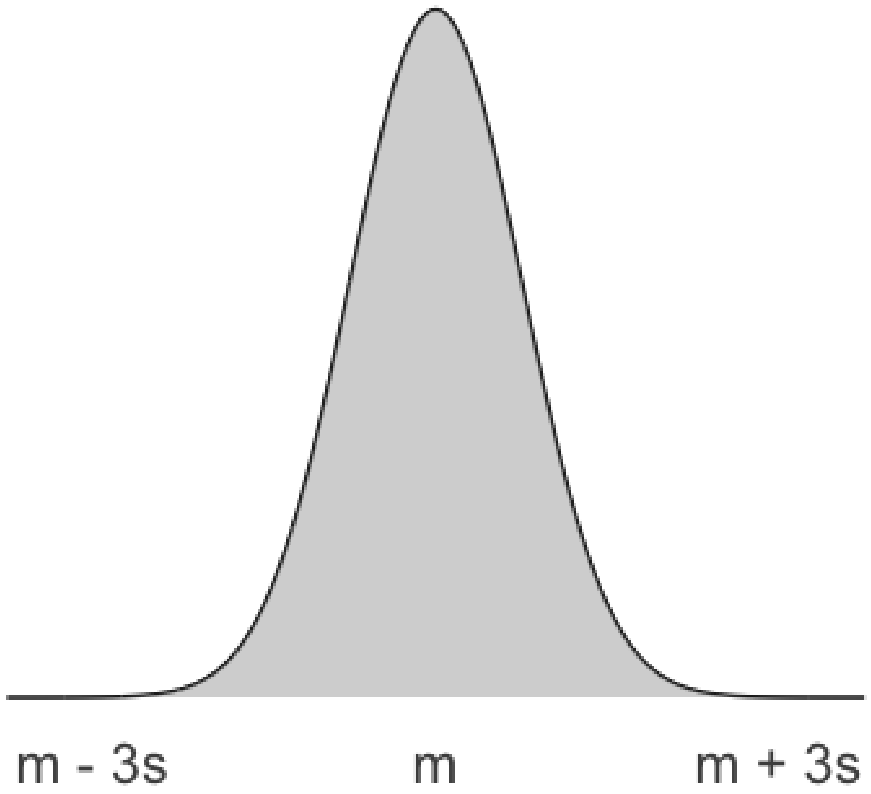
Associate Professor, Macalester College

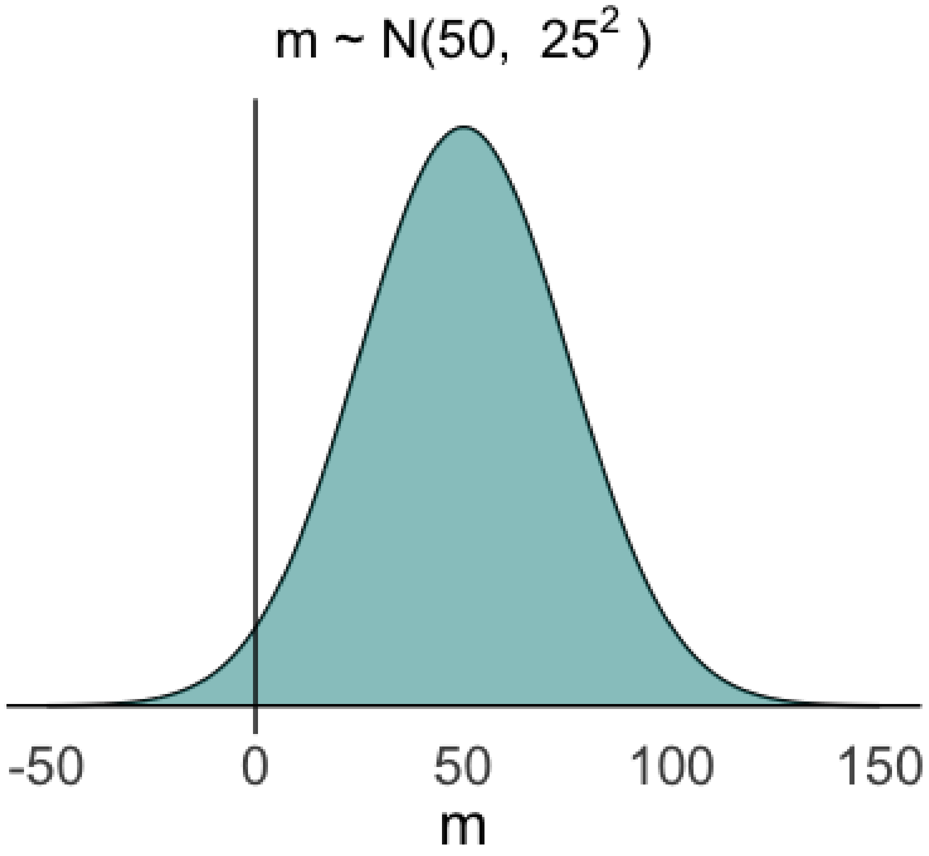
Sleep study

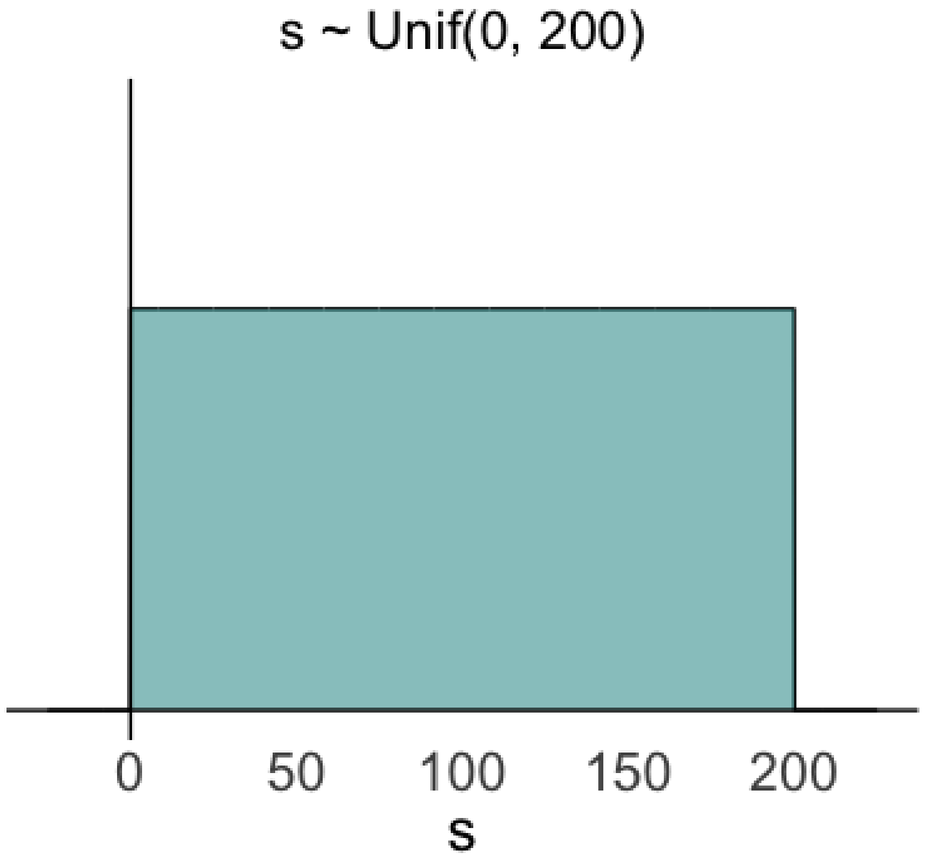
Y_i = change in reaction time (ms) after 3 days of sleep deprivation

$$Y_i \sim N(m, s^2)$$

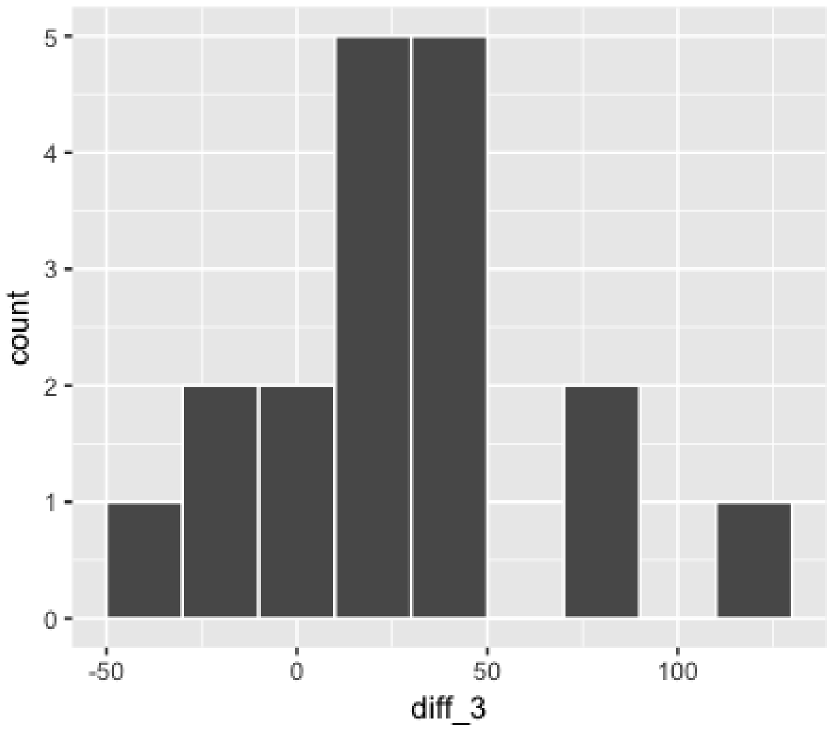


Insights from the priors


$m \sim N(50, 25^2)$


$s \sim Unif(0, 200)$

Insights from the data (& likelihood)



```
mean(sleep_study$diff_3)
sd(sleep_study$diff_3)
```

```
26.34021
37.20764
```

Assuming these data are generated from $Y_i \sim N(m, s^2)$, they are most likely to have occurred if...

- $m \approx 26$ ms
- $s \approx 37$ ms

Posterior insights

POSTERIOR ∝ LIKELIHOOD • PRIOR

DEFINE the Normal-Normal

```
sleep_model <- "model{
    # Likelihood model for Y[i]





    # Prior models for m and s


}"
```

DEFINE the Normal-Normal

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sleep_model <- "model{
    # Likelihood model for Y[i]




    # Prior models for m and s


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```

- $Y_i \sim N(m, s^2)$ for i in $1, 2, \ldots, 18$

DEFINE the Normal-Normal

```
sleep_model <- "model{
    # Likelihood model for Y[i]
    for(i in 1:length(Y)) {

    }

    # Prior models for m and s


}"
```

- $Y_i \sim N(m, s^2)$ for i in $1, 2, \ldots, 18$

DEFINE the Normal-Normal

```
sleep_model <- "model{
    # Likelihood model for Y[i]
    for(i in 1:length(Y)) {
        Y[i] ~ dnorm(m, s^(-2))
    }

    # Prior models for m and s


}"
```

- $Y_i \sim N(m, s^2)$ for i in $1, 2, \ldots, 18$
  - NOTE: precision = variance^{-1} = s^{-2}

DEFINE the Normal-Normal

```
sleep_model <- "model{
    # Likelihood model for Y[i]
    for(i in 1:length(Y)) {
        Y[i] ~ dnorm(m, s^(-2))
    }

    # Prior models for m and s
    m ~ dnorm(50, 25^(-2))

}"
```

- $Y_i \sim N(m, s^2)$ for i in $1, 2, \ldots, 18$
    - NOTE: precision = variance^{-1} = s^{-2}
- $m \sim N(50, 25^2)$

DEFINE the Normal-Normal

```
sleep_model <- "model{
    # Likelihood model for Y[i]
    for(i in 1:length(Y)) {
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    }

    # Prior models for m and s
    m ~ dnorm(50, 25^(-2))
    s ~ dunif(0, 200)
}"
```

- $Y_i \sim N(m, s^2)$ for i in $1, 2, \ldots, 18$
    - NOTE: precision = variance^{-1} = s^{-2}
- $m \sim N(50, 25^2)$
- $s \sim \text{Unif}(0, 200)$

COMPILE the Normal-Normal

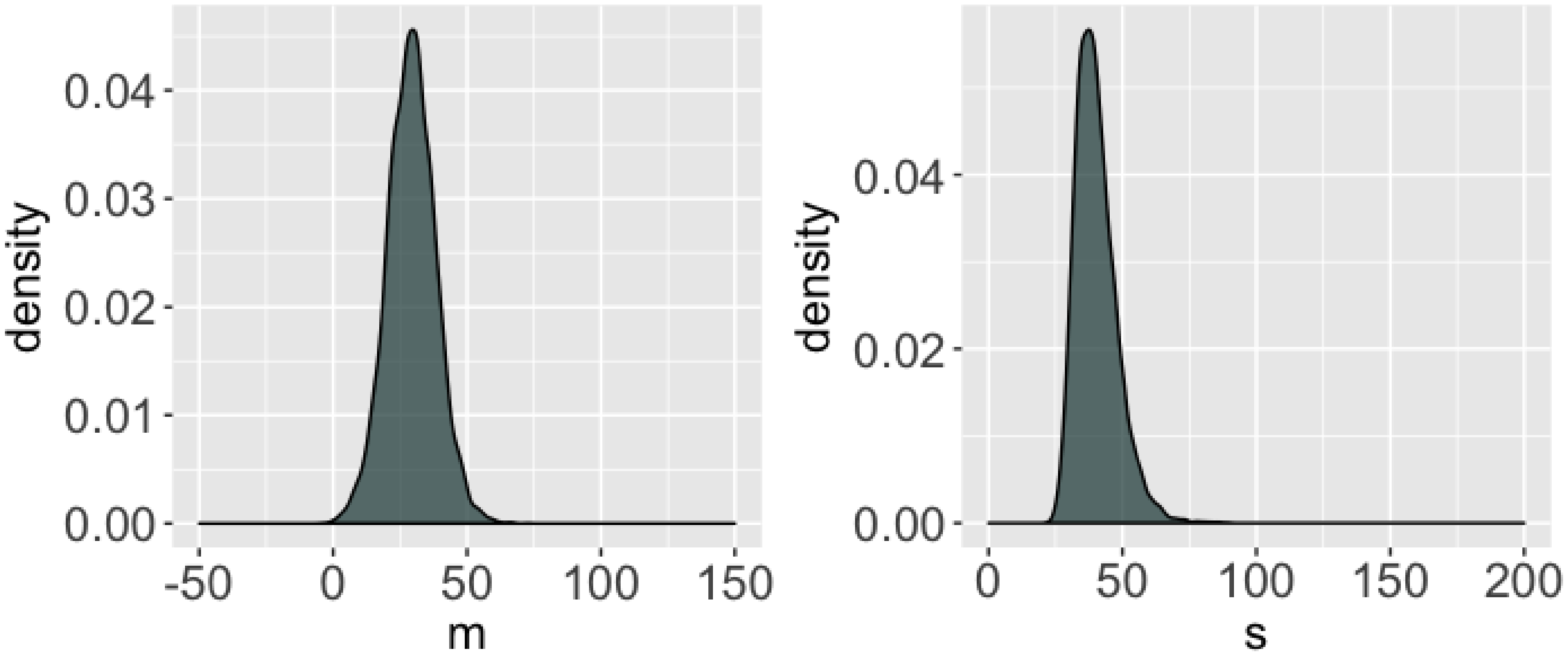
```r
# COMPILE the model
sleep_jags <- jags.model(textConnection(sleep_model),
    data = list(Y = sleep_study$diff_3),
    inits = list(.RNG.name = "base::Wichmann-Hill",
                 .RNG.seed = 1989))
    sleep_study$diff_3
```

```
 [1]  71.8798 -18.0269  33.7877 -36.4096  32.5074  74.9082
 [7]  15.9673 -10.8008  29.1938  33.7556  18.8188  -0.7697
[13]  30.0626 125.1784   5.7331  15.2090  11.9091  41.2199
```

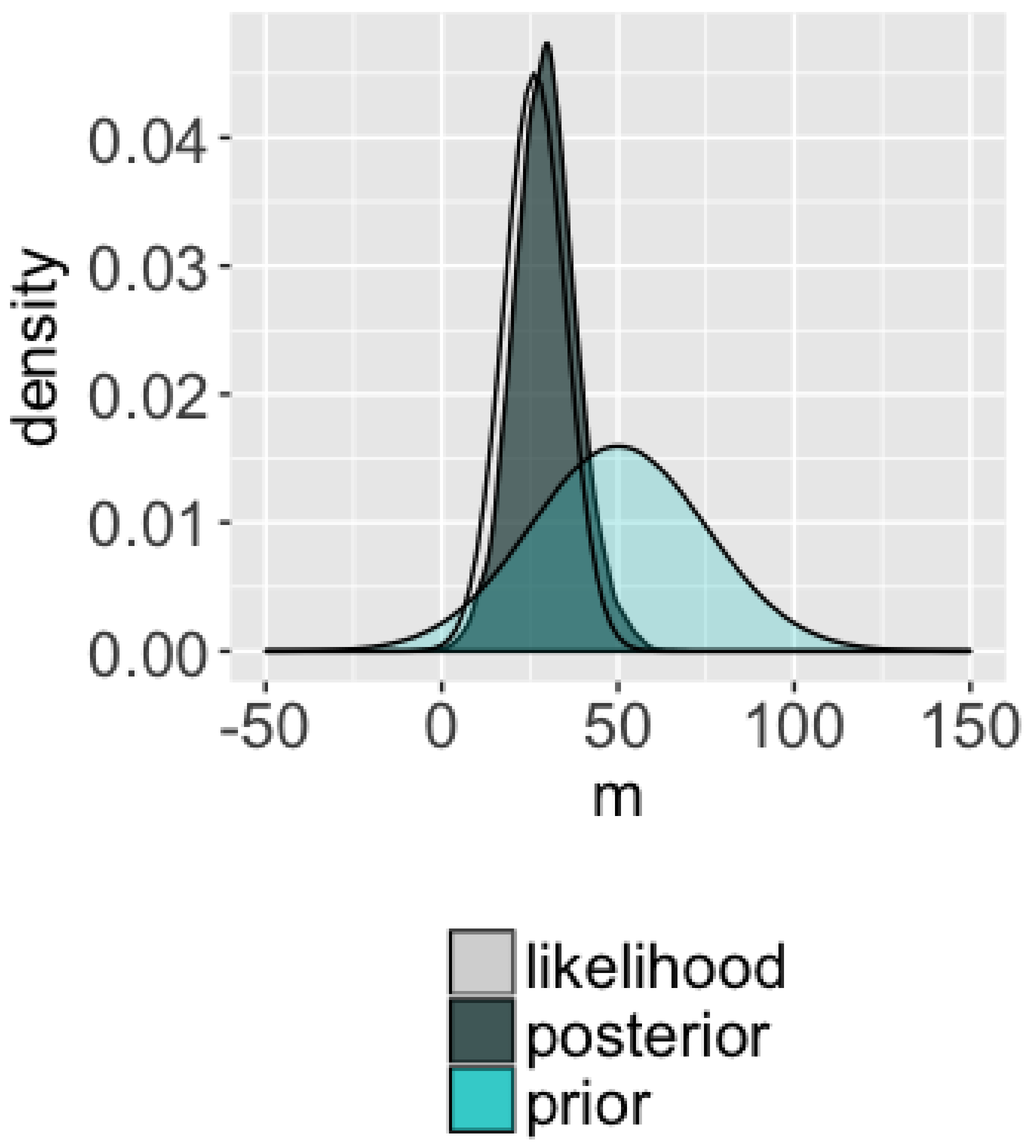
SIMULATE the Normal-Normal

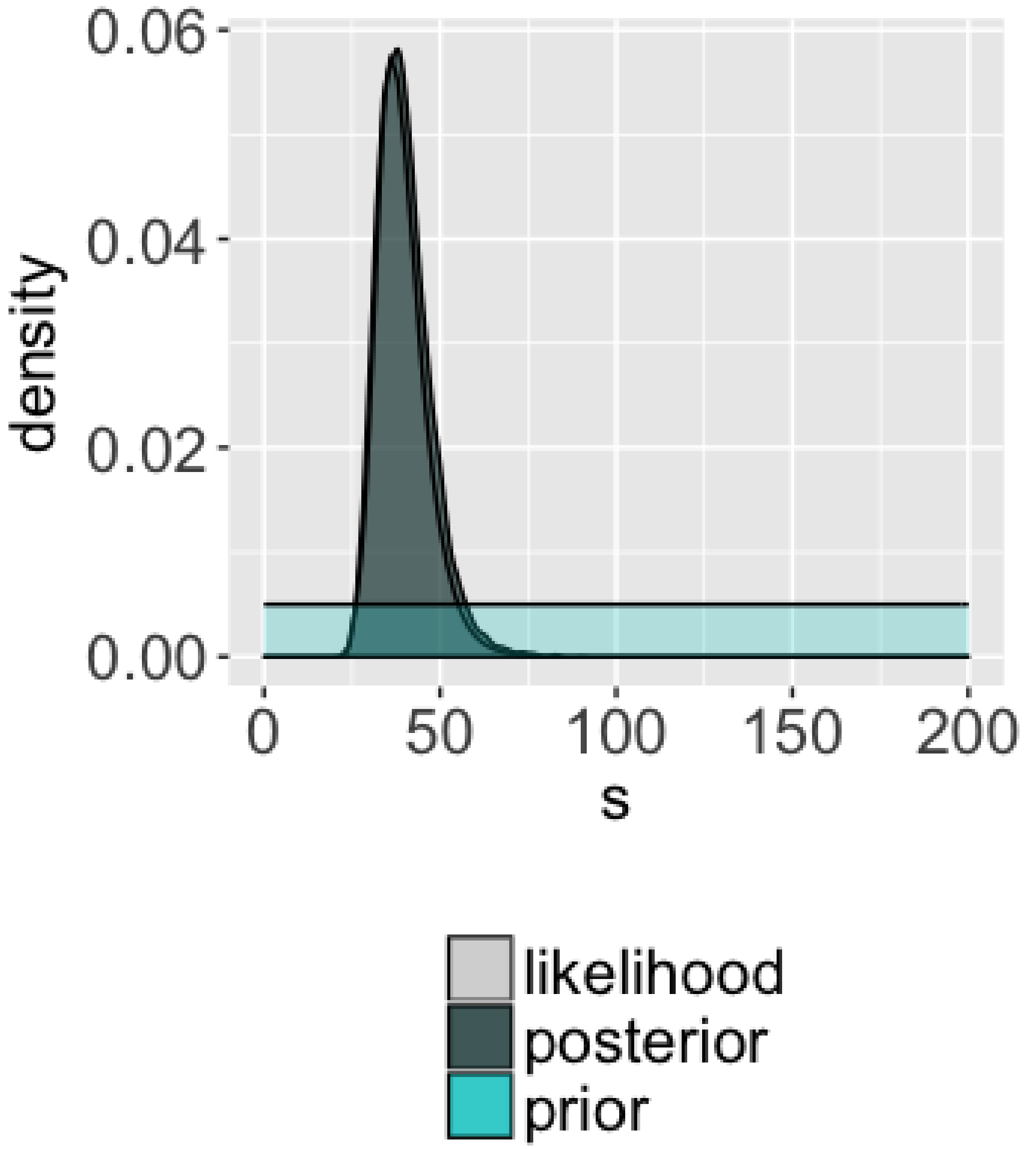
```r
# COMPILE the model
sleep_jags <- jags.model(textConnection(sleep_model),
    data = list(Y = sleep_study$diff_3),
    inits = list(.RNG.name = "base::Wichmann-Hill",
                 .RNG.seed = 1989))

# SIMULATE the posterior
sleep_sim <- coda.samples(model = sleep_jags,
    variable.names = c("m", "s"),
    n.iter = 10000)
```

SIMULATE the Normal-Normal



SIMULATE the Normal-Normal





Let's practice!

Markov chains

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Associate Professor, Macalester College

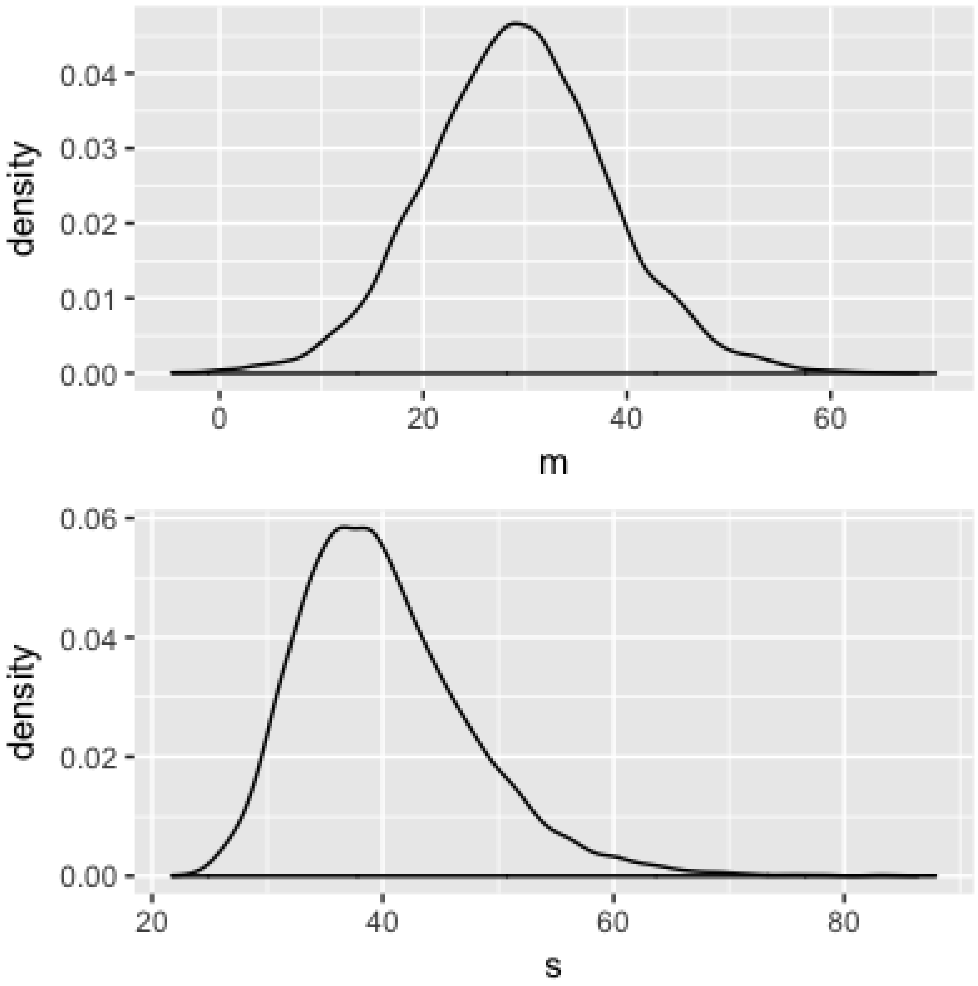
Posterior simulation

Normal-Normal model:

Y_i = change in reaction time (ms)

$$Y_i \sim N(m, s^2)$$
$$m \sim N(50, 25^2)$$
$$s \sim \text{Unif}(0, 200)$$

Approximate posteriors:



Markov chains

```r
head(sleep_chains, 20)
```

- `m` is a **Markov chain**, NOT a random sample from the posterior
- `RJAGS` **goal:** Utilize Markov chains to *approximate* posteriors that are otherwise too complicated to define or sample

```
          m        s iter
1  17.25796 31.46256    1
2  34.58469 37.88655    2
3  36.45480 39.58056    3
4  25.00971 39.69494    4
5  29.95475 35.90001    5
6  28.43894 37.46466    6
7  38.32427 35.44081    7
8  27.90956 42.07951    8
9  28.09270 52.36360    9
10 29.70648 28.30665   10
11 32.10350 46.64174   11
12 34.41397 28.86993   12
13 23.33649 37.46498   13
14 39.26587 32.91031   14
15 27.95317 43.13887   15
16 18.91718 44.64376   16
17 28.63141 43.49800   17
18 41.22929 47.42336   18
19 33.12585 42.81980   19
20 35.86270 30.47737   20
```

Markov chain dependence

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head(sleep_chains, 20)
```

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          m         s iter
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...
```

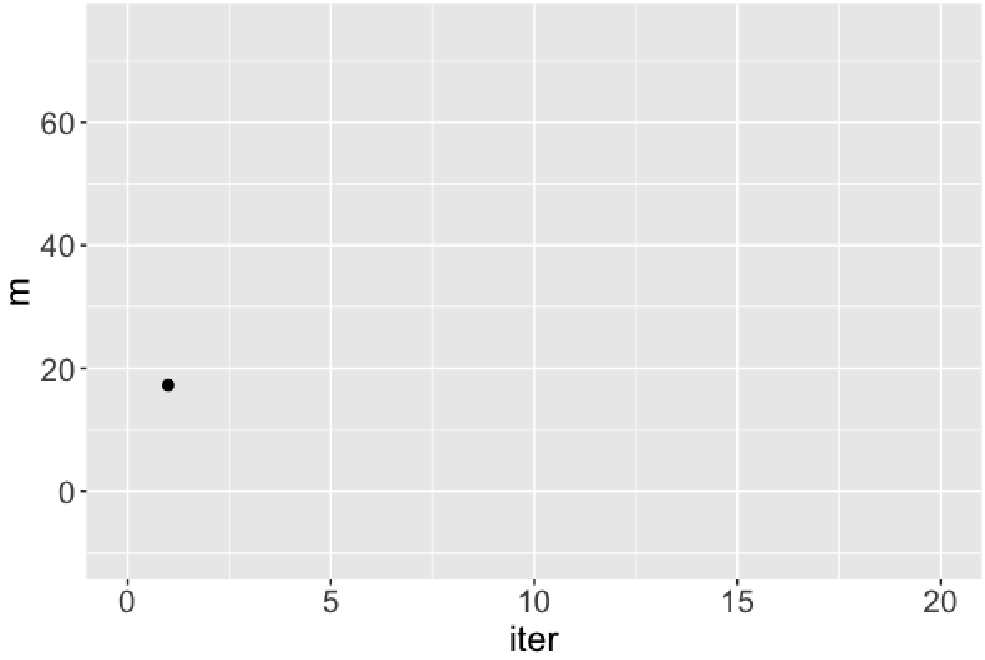

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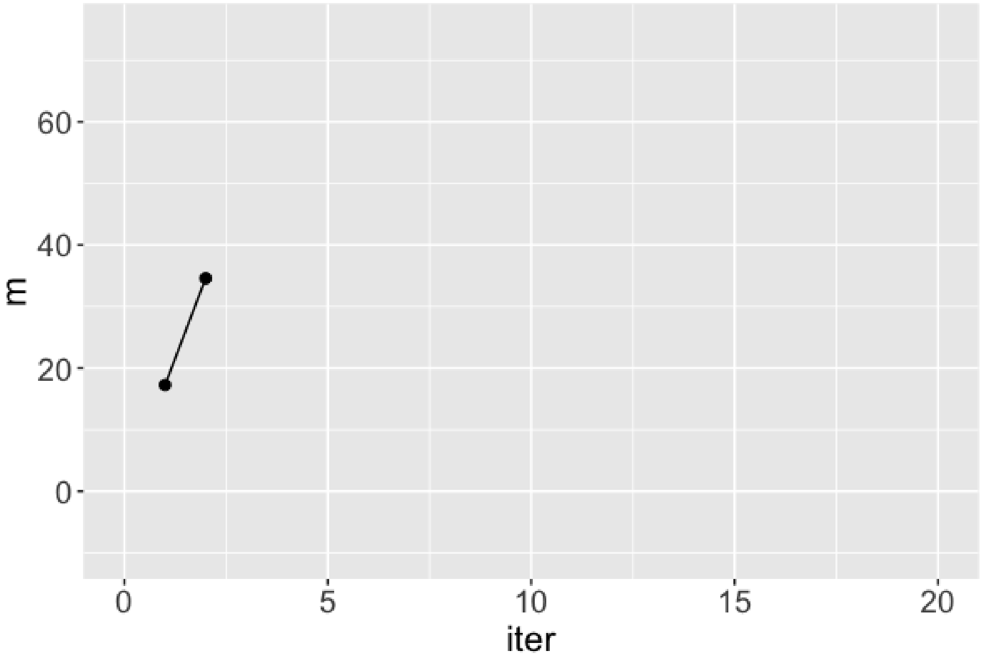

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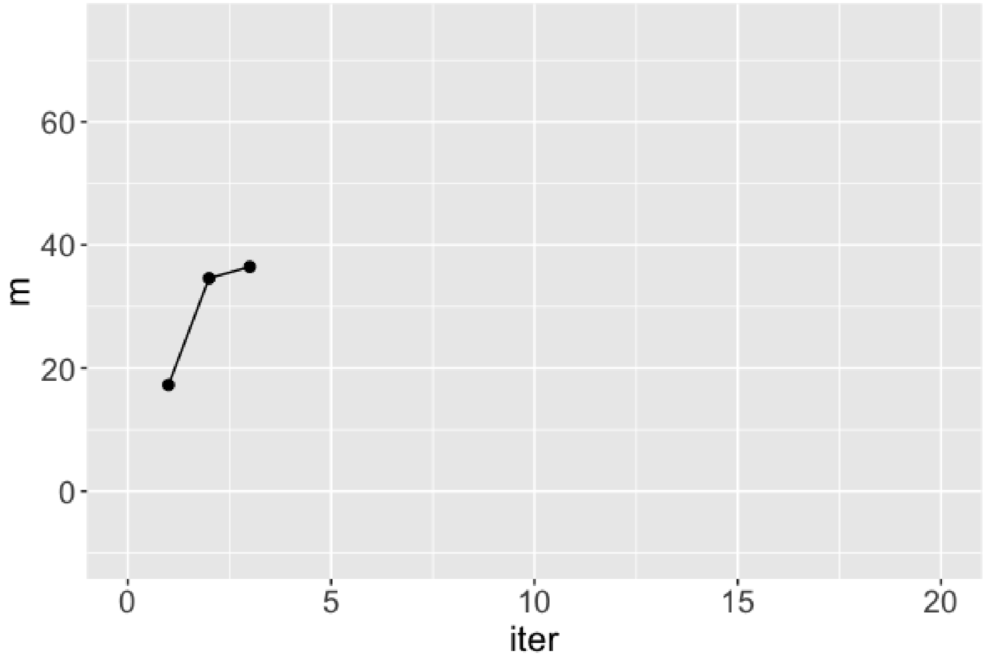

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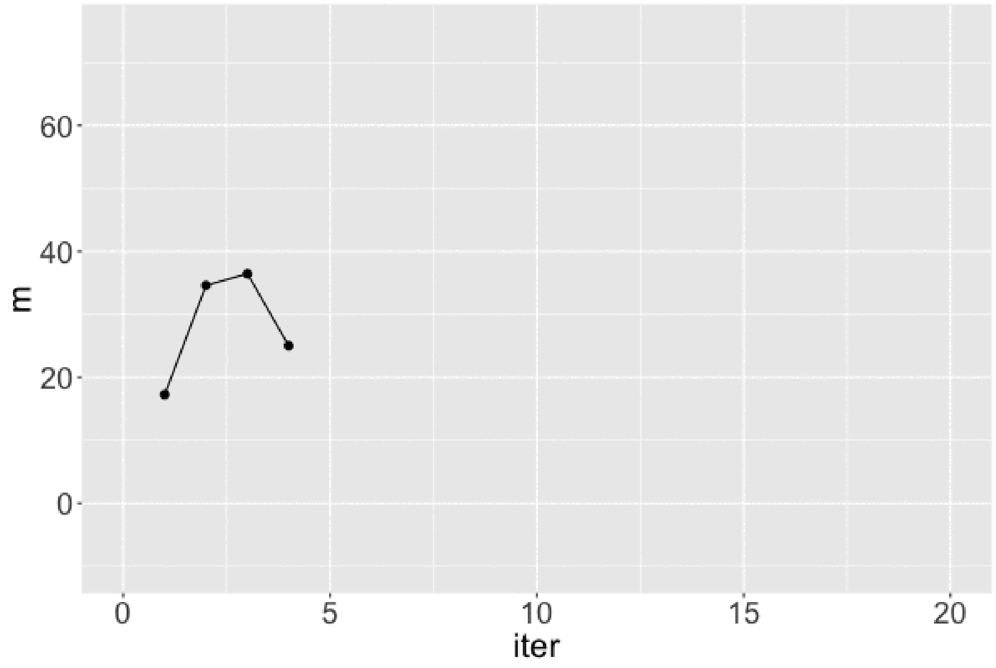
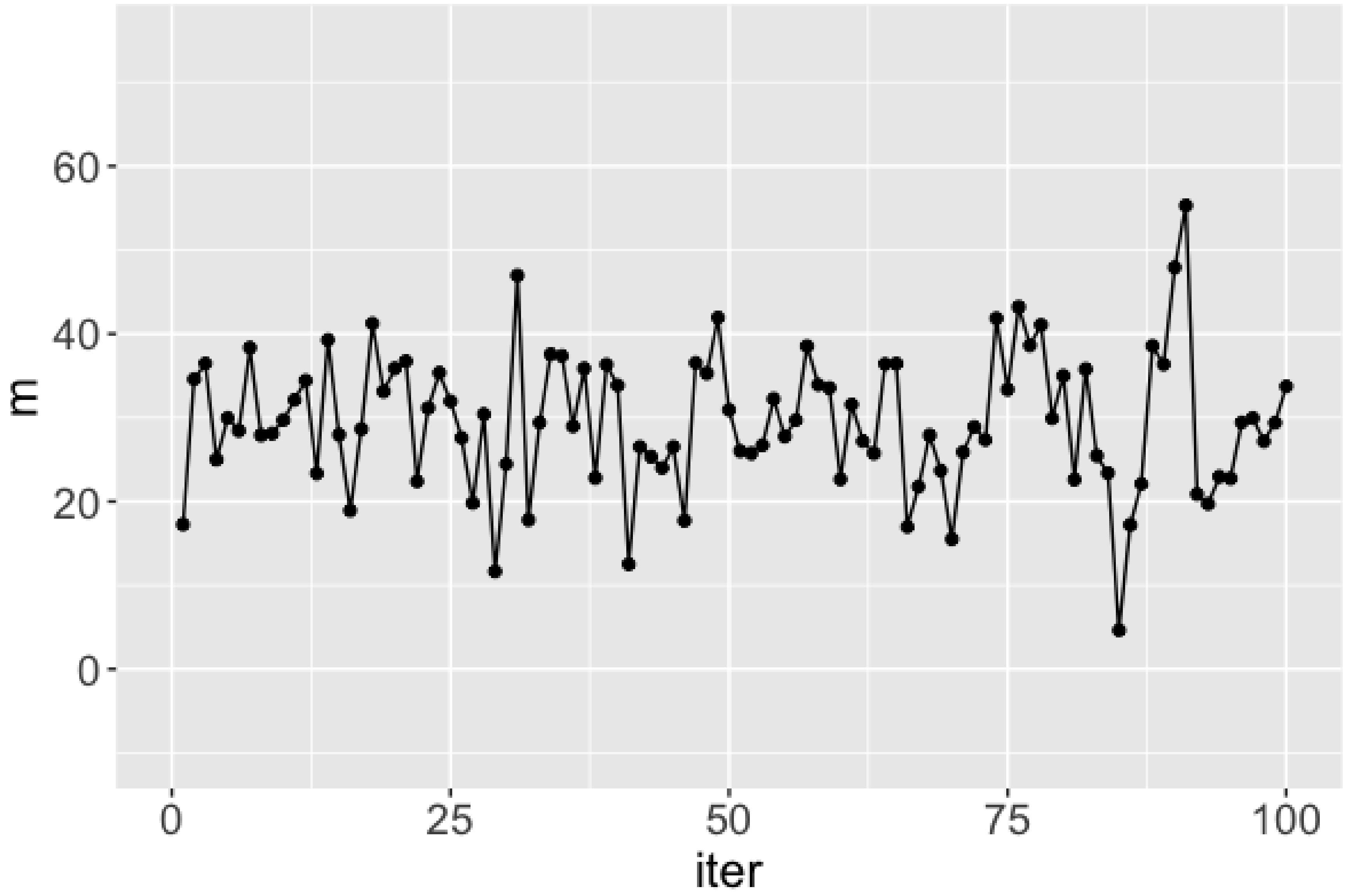
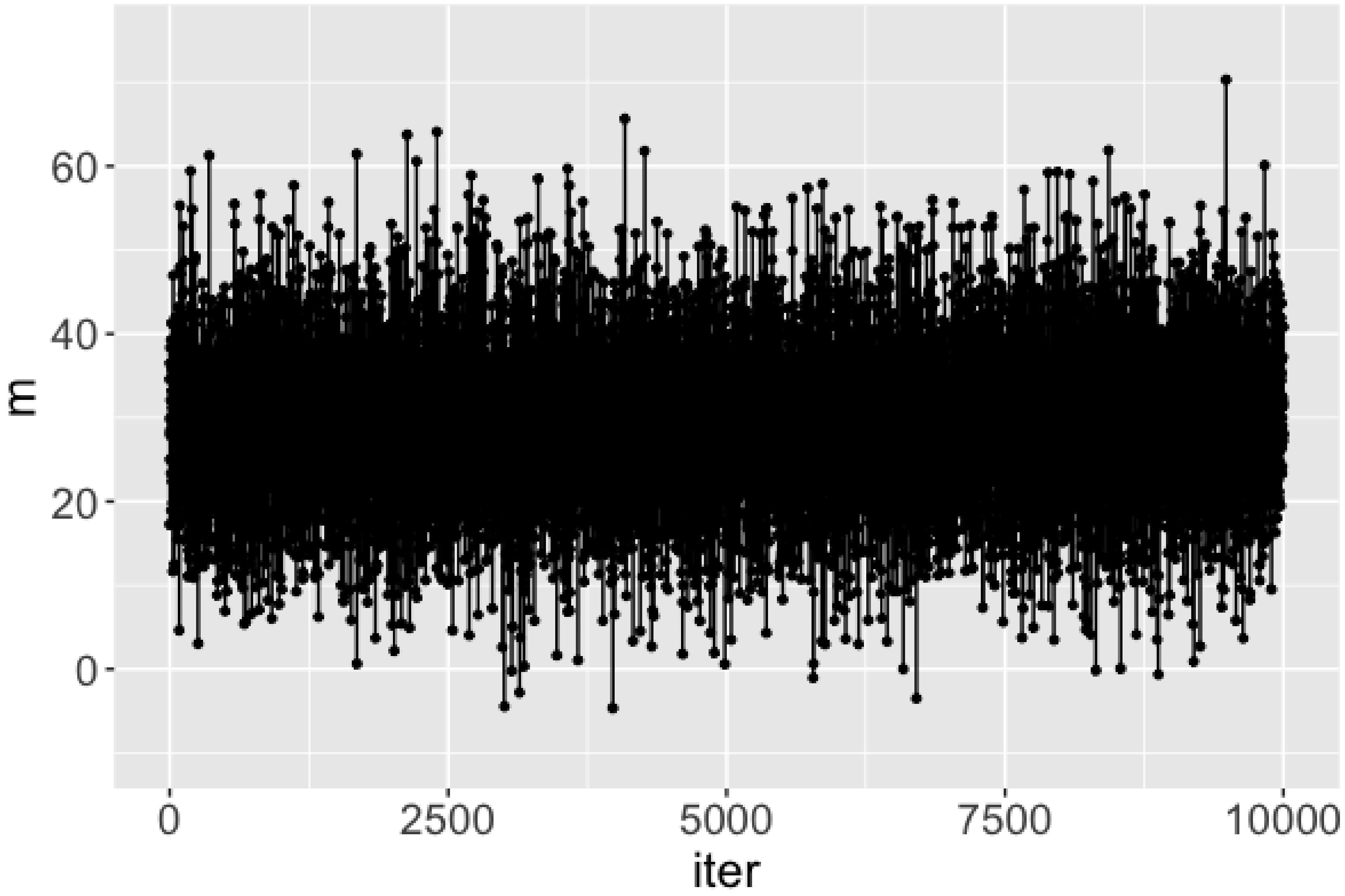


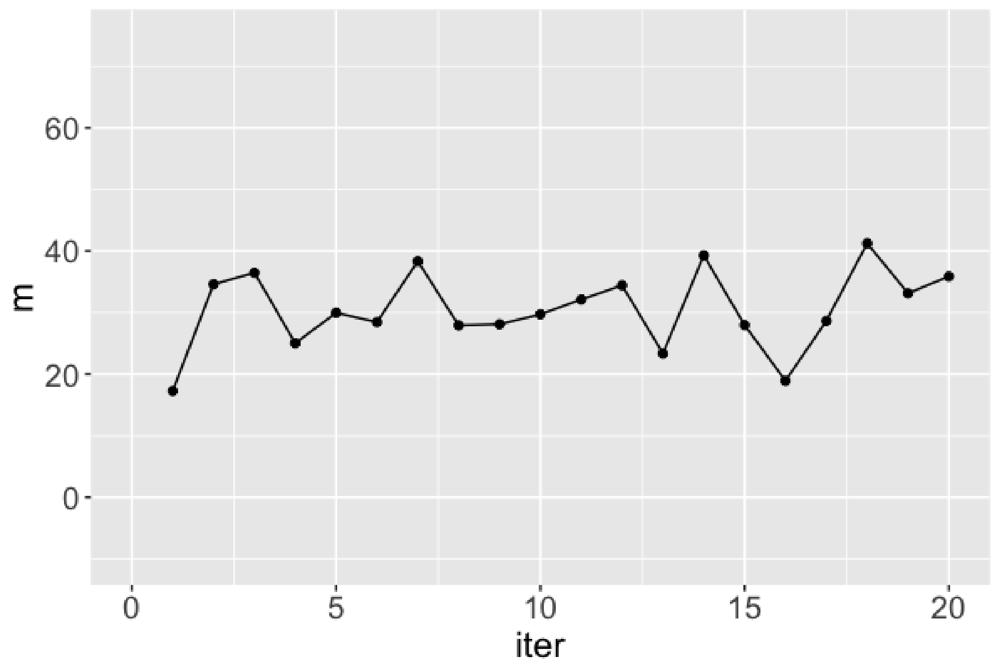
Markov chain dependence

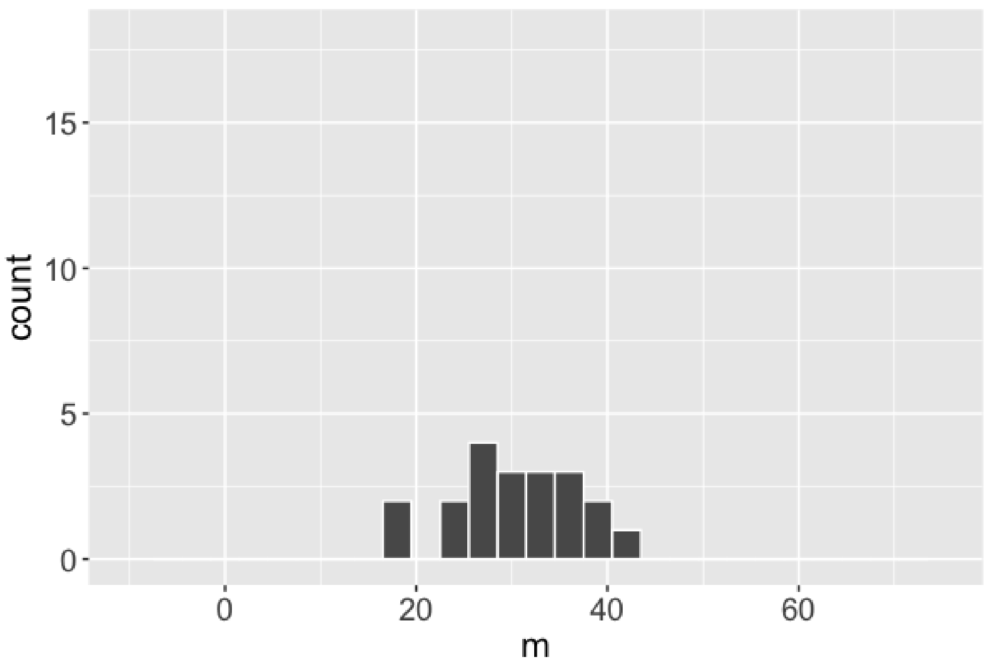


Markov chain trace plot

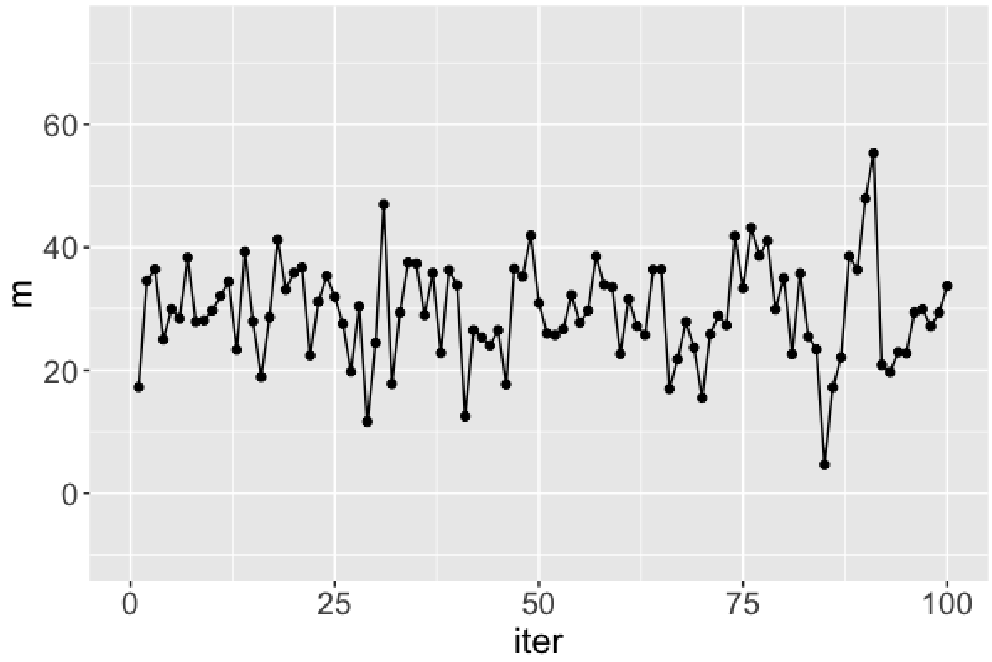


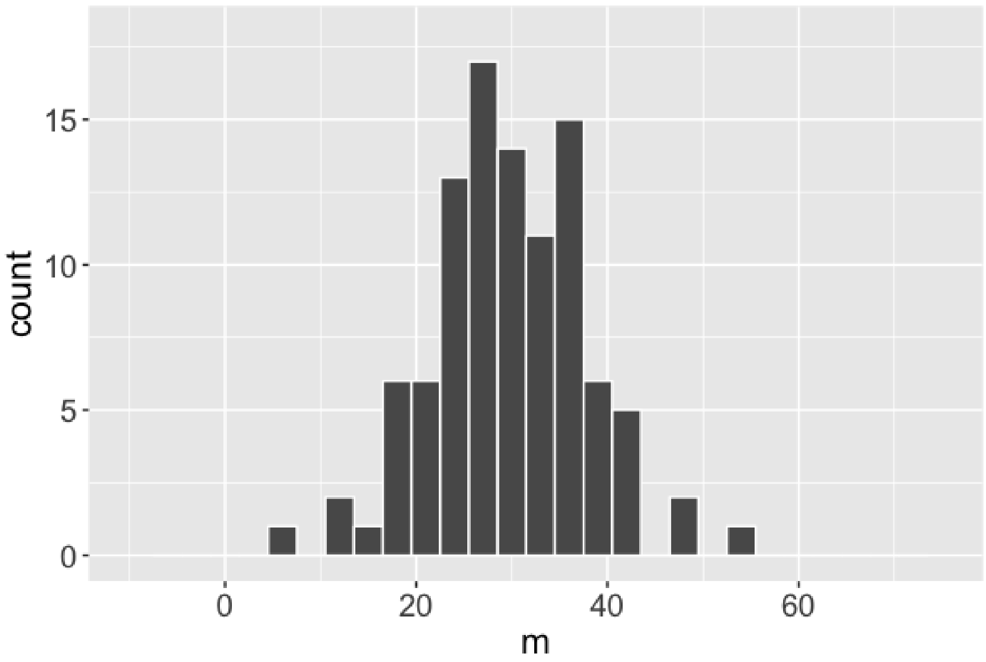
Markov chain distribution



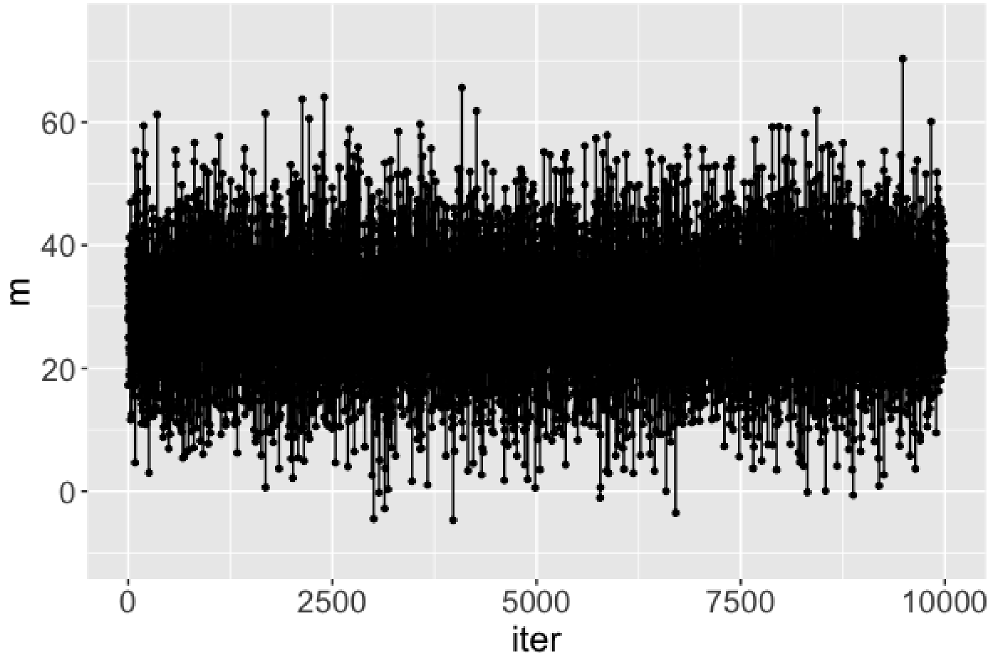


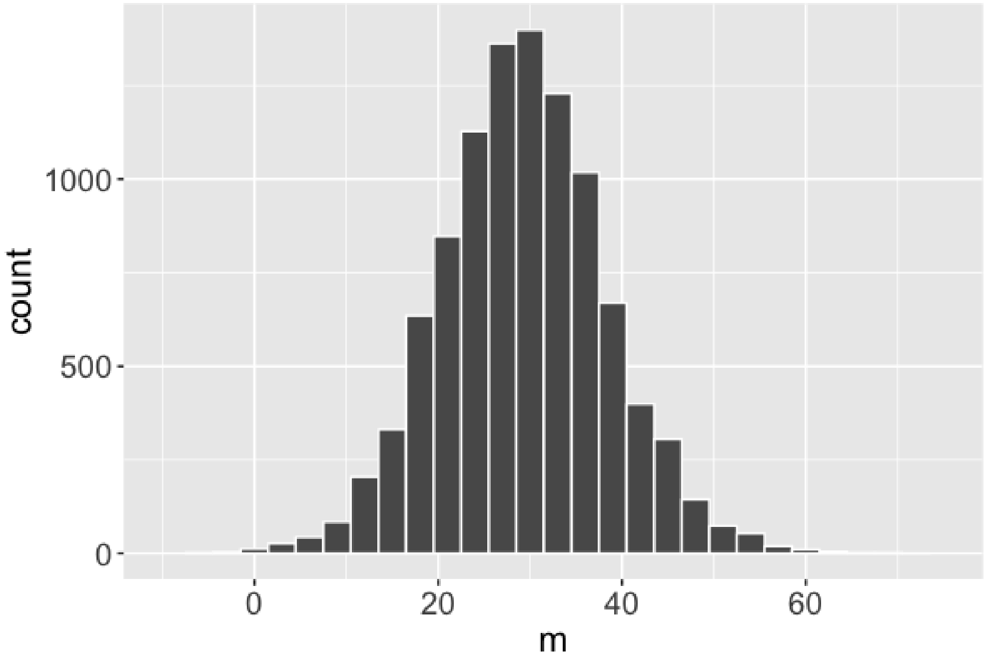
Markov chain distribution



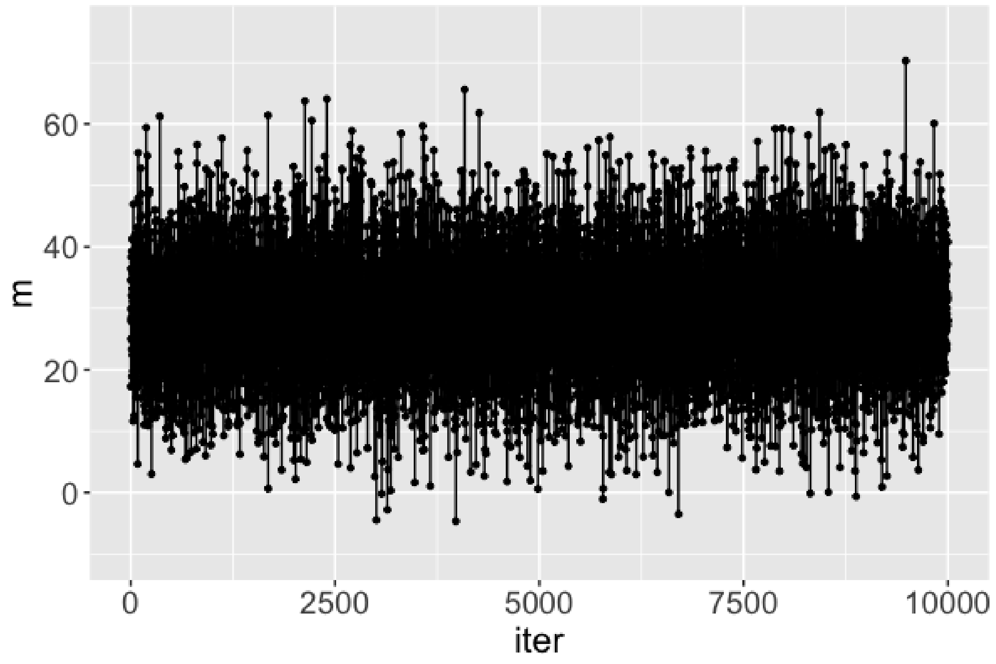


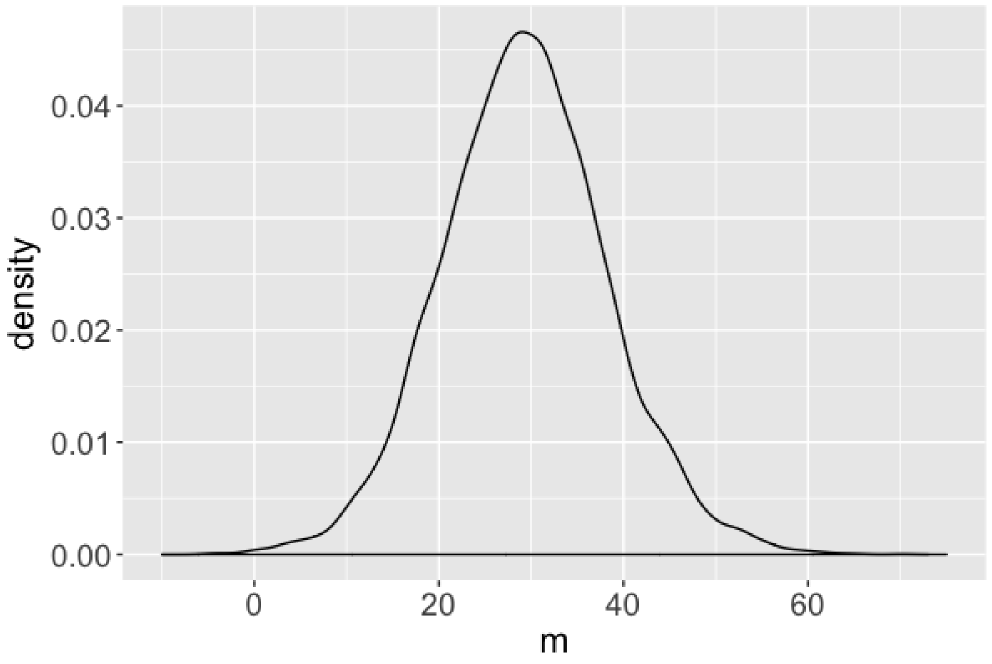
Markov chain distribution





Markov chain distribution: an approximation of the posterior!





The m Markov chain...

traverses the sample space of m,

mimics a random sample, and

converges to the posterior.

Let's practice!

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Markov chain diagnostics & reproducibility

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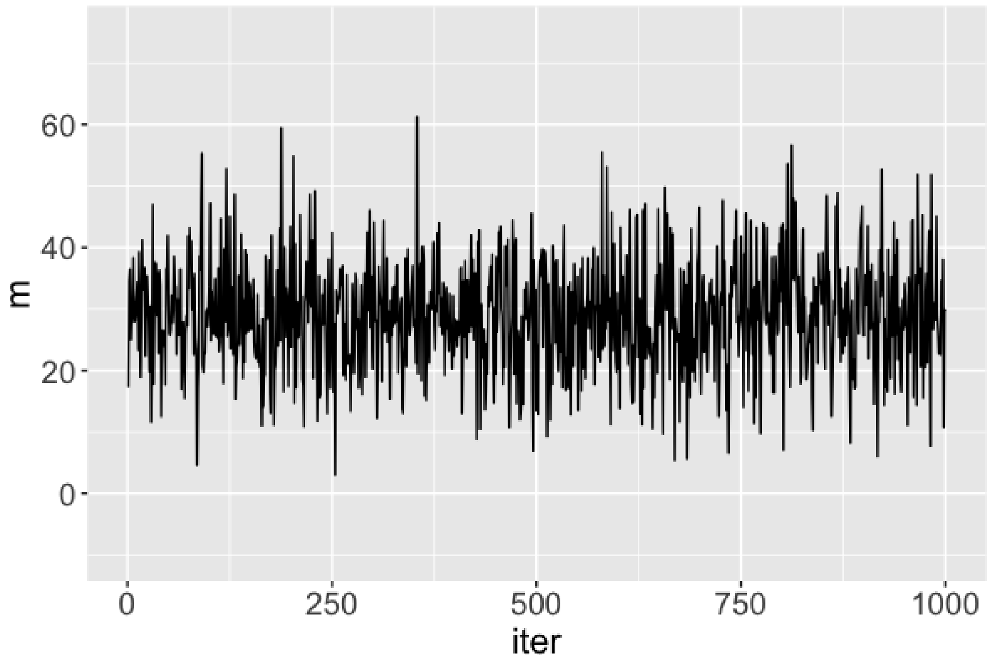
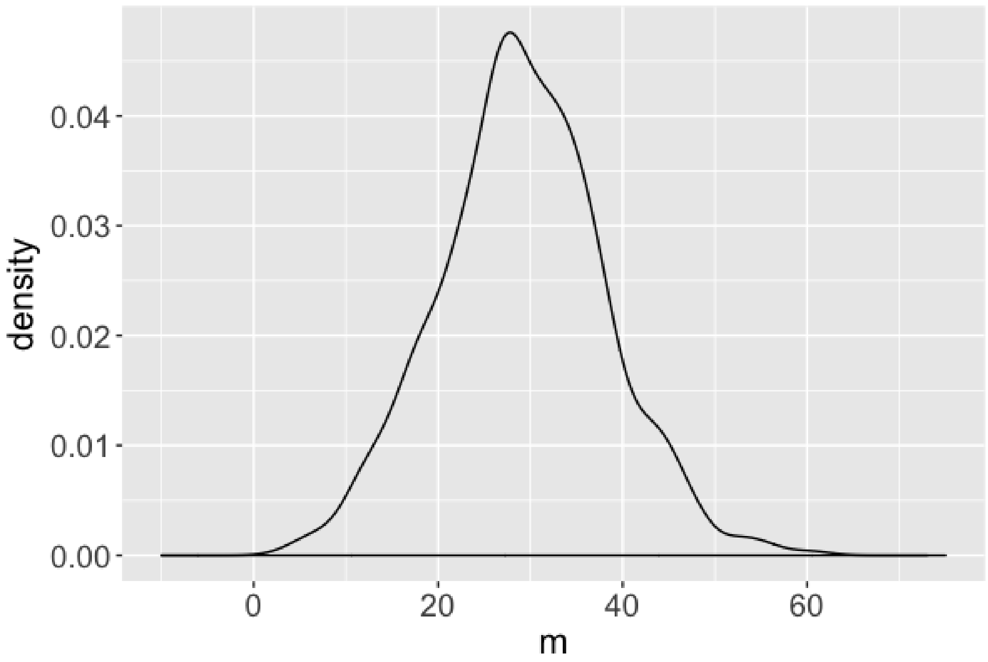
Markov chain output

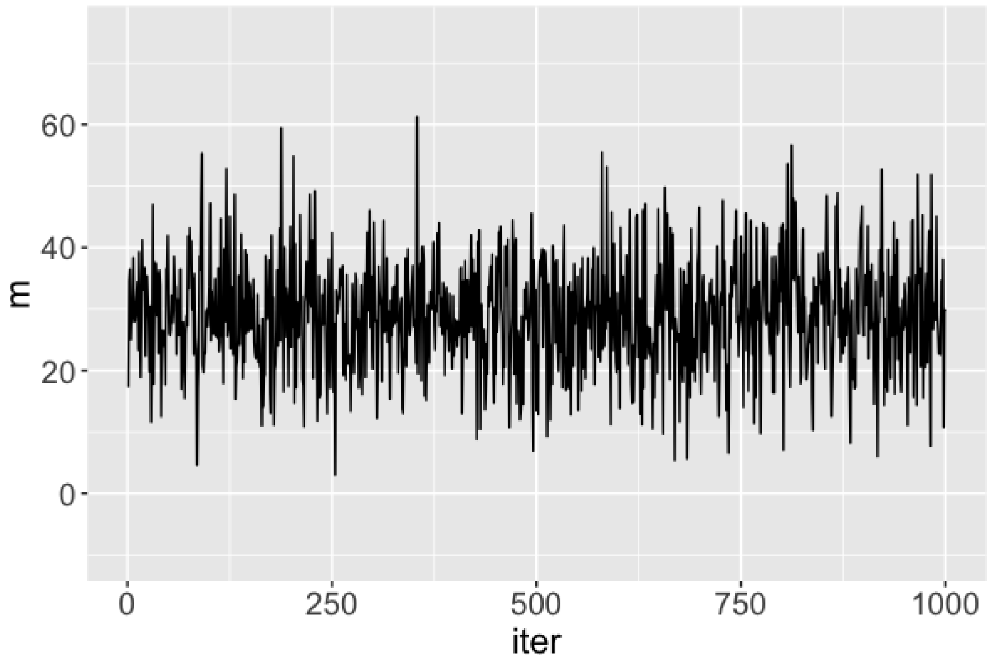




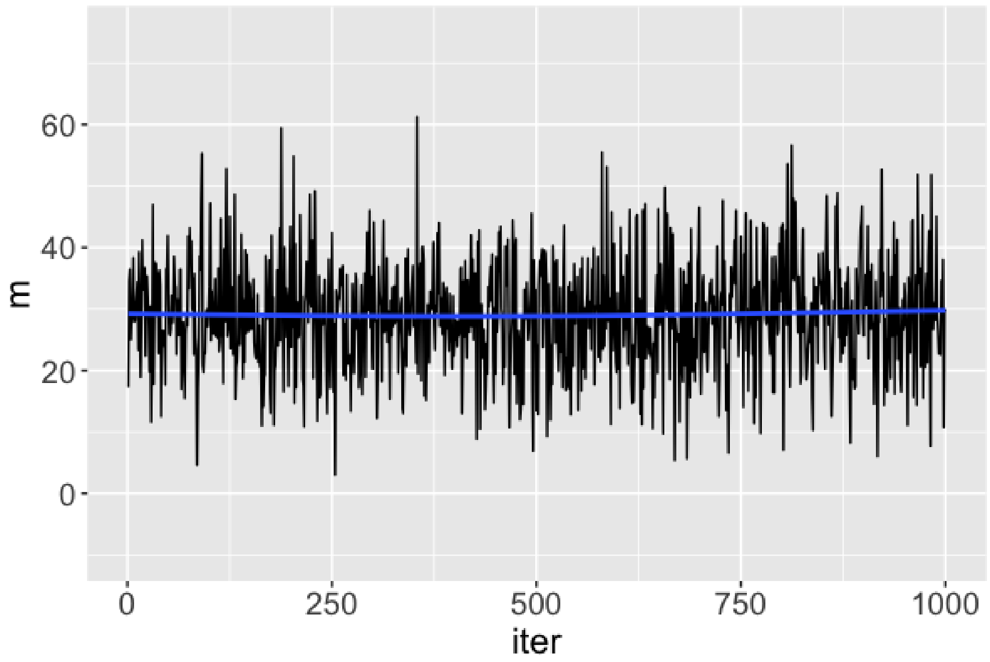
Questions to consider

- What does a "good" Markov chain look like?
- How accurate is the Markov chain approximation of the posterior?
- For how many iterations should we run the Markov chain?

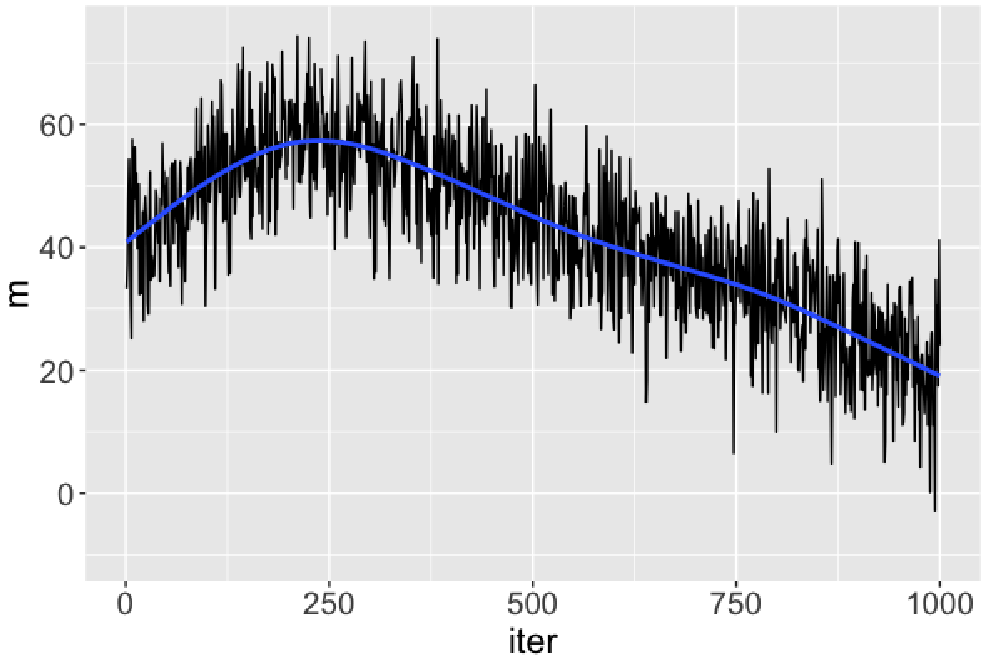
Diagnostic: trace plots



Diagnostic: trace plots



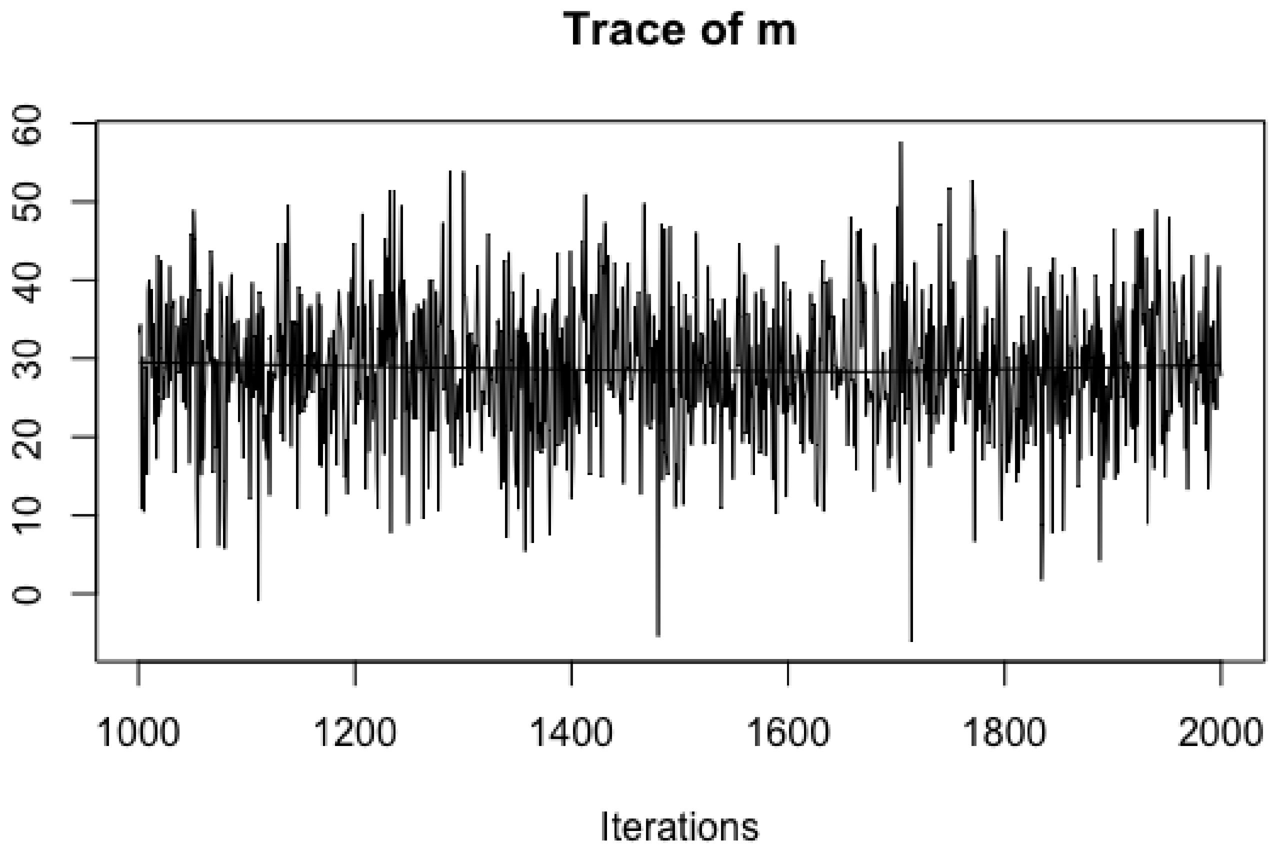
Good: stability!



Bad: instability

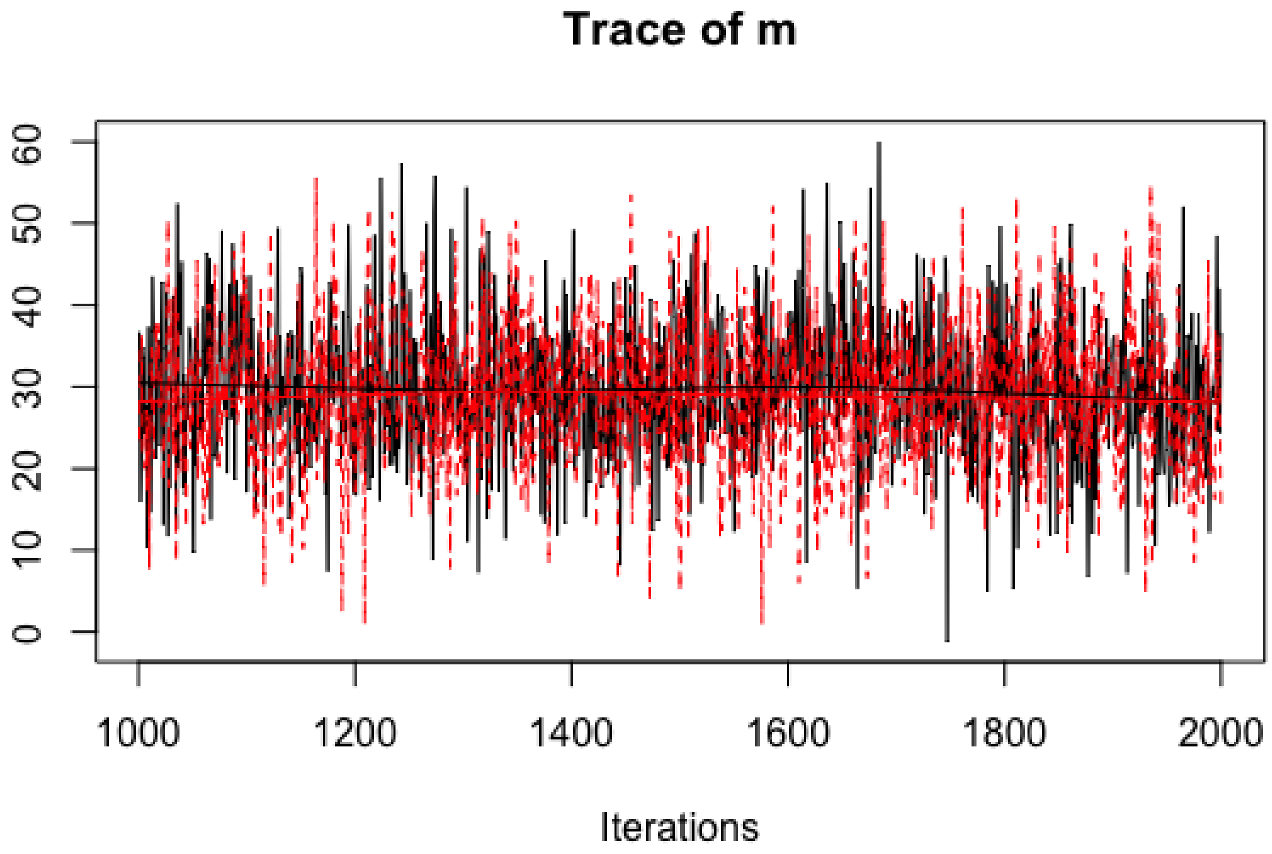
Diagnostic: multiple chains

```
# COMPILE the model
sleep_jags <- jags.model(..., n.chains = 1)
```



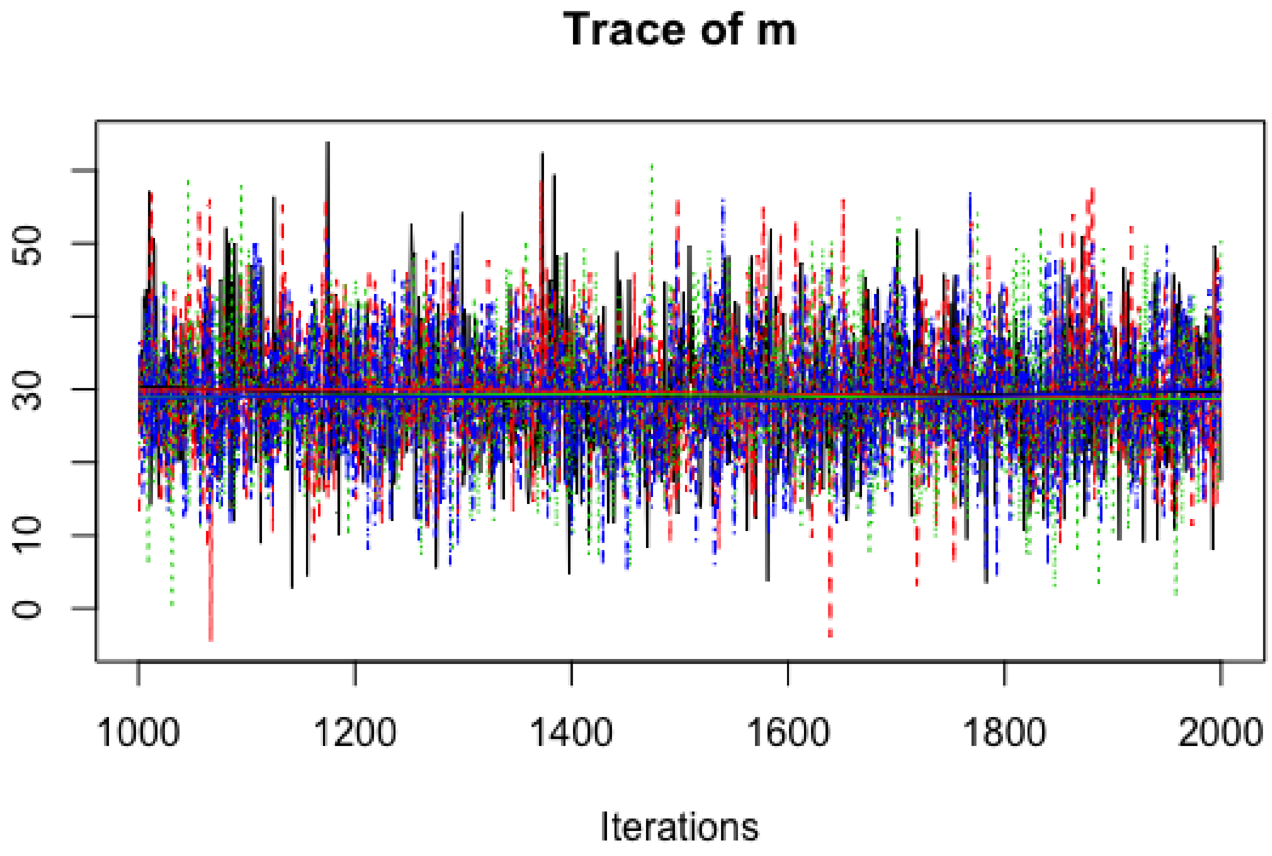
Diagnostic: multiple chains

```
# COMPILE the model
sleep_jags <- jags.model(..., n.chains = 2)
```



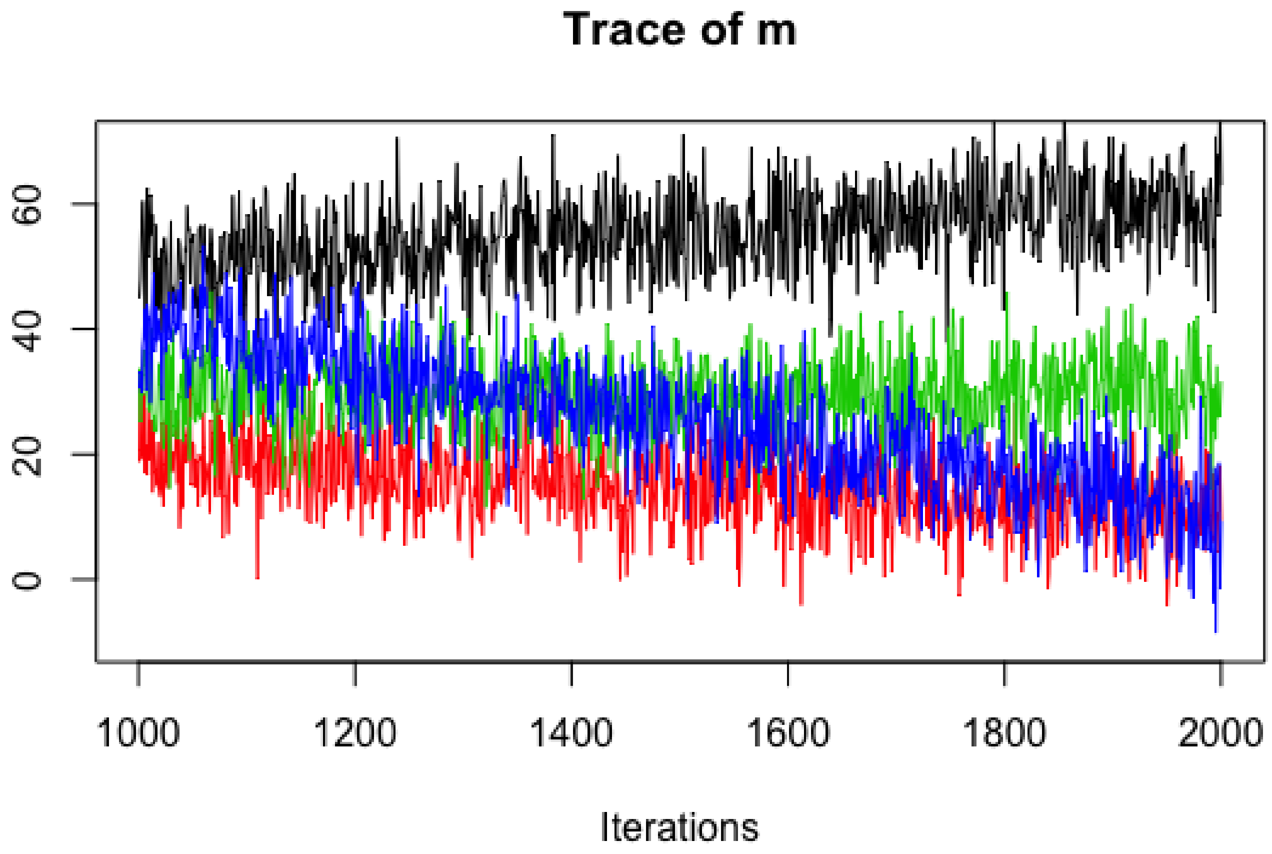
Diagnostic: multiple chains

```
# COMPILE the model
sleep_jags <- jags.model(..., n.chains = 4)
```



Diagnostic: multiple chains

```
# COMPILE the model
sleep_jags <- jags.model(..., n.chains = 4)
```



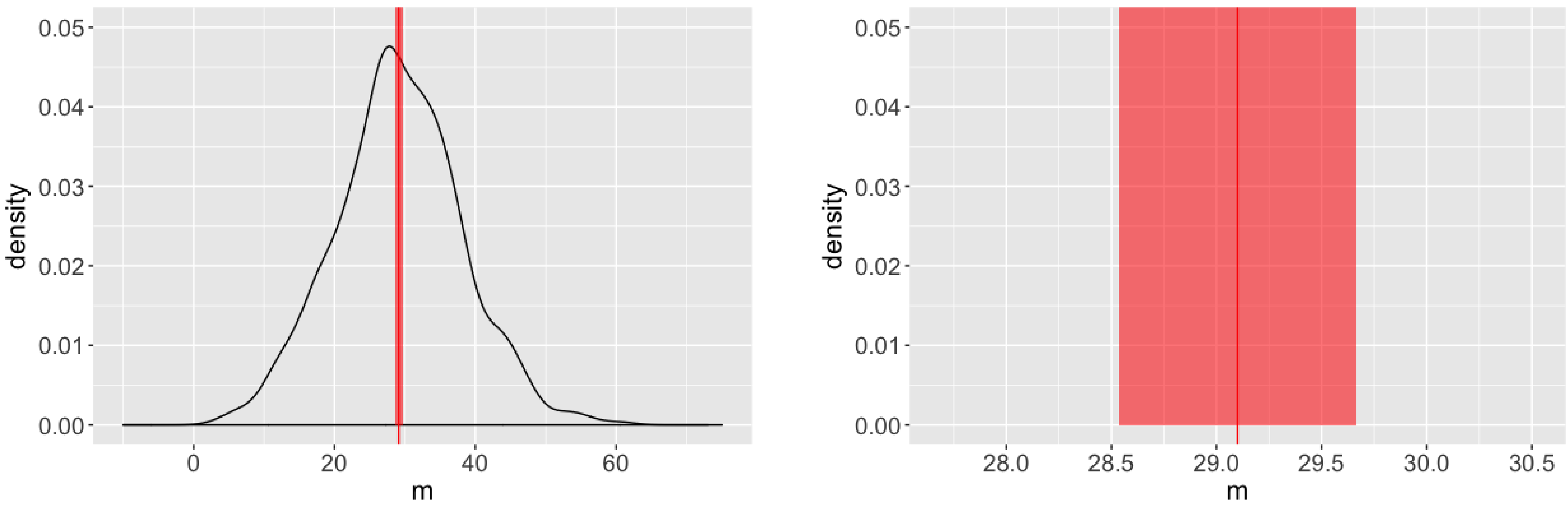
```
summary(sleep_sim)
```

```
1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

   Mean    SD Naive SE Time-series SE
m 29.10 8.968   0.2836         0.2820
s 40.07 7.887   0.2494         0.4227

2. Quantiles for each variable:

   2.5%   25%   50%   75% 97.5%
m 11.42 23.27 28.85 34.76 46.76
s 28.31 34.65 38.93 43.91 57.56
```

- **Estimate** of the posterior mean of m = 29.10 ms
- **(Naive) standard error** of this estimate = 0.2836 ms

  `SD` / $\sqrt{\text{number of iterations}}$

Diagnostic: standard error



- **Estimated** mean = 29.10 ms
- **(Naive) standard error =** 0.2836 ms
- $29.10 \pm 2 * 0.2836$

Markov chain work flow

- Define, compile, simulate the model
- Examine the following diagnostics:
  - Trace plots
  - Multiple chain output
  - Standard errors
- Finalize the simulation

Finalizing the Markov chain: Reproducibility

```
sleep_jags <- jags.model(textConnection(sleep_model),
    data = list(Y = sleep_study$diff_3),
    inits = list(.RNG.name = "base::Wichmann-Hill",
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```

Let's practice!

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