



BAYESIAN MODELING WITH RJAGS

The Normal-Normal Model

Alicia Johnson

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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.



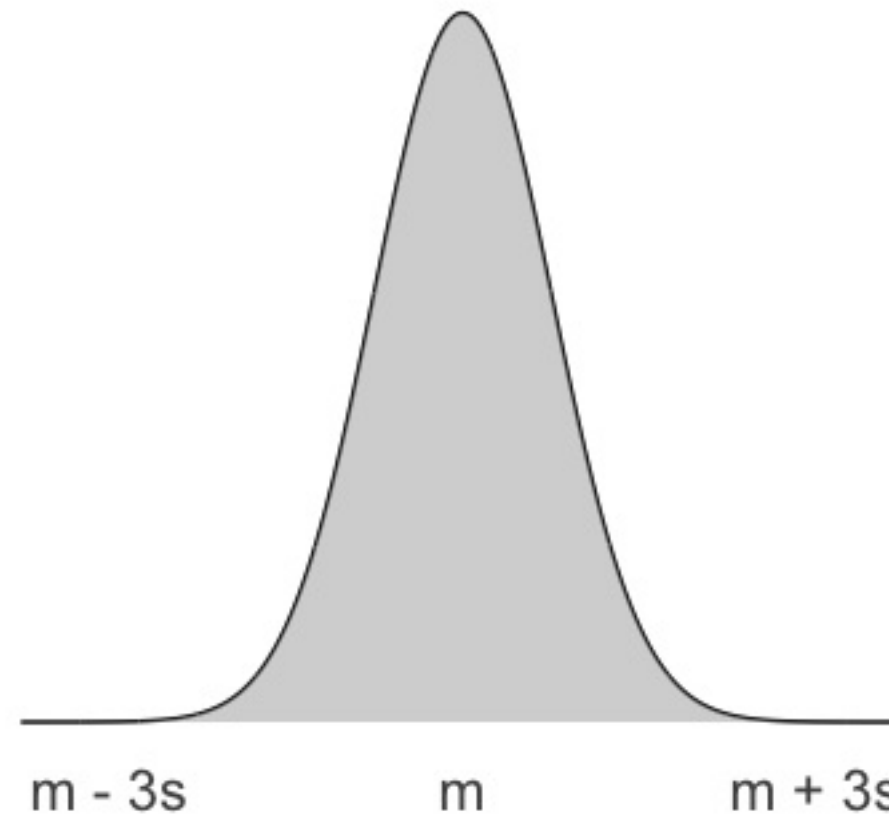
Modeling change in reaction time

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

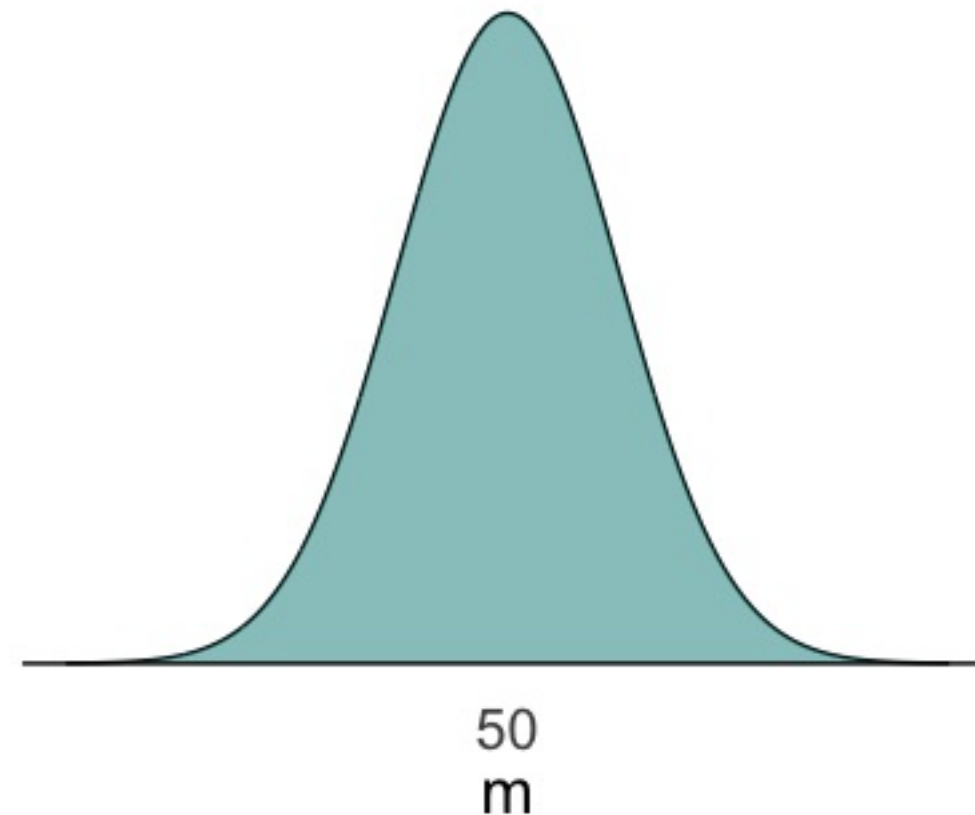
Y_i = change in reaction time (ms)

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

m = average Y_i

Prior information:

- with *normal* sleep, average reaction time is ~ 250 ms
- expect average to \nearrow by ~ 50 ms



Prior model for parameter m

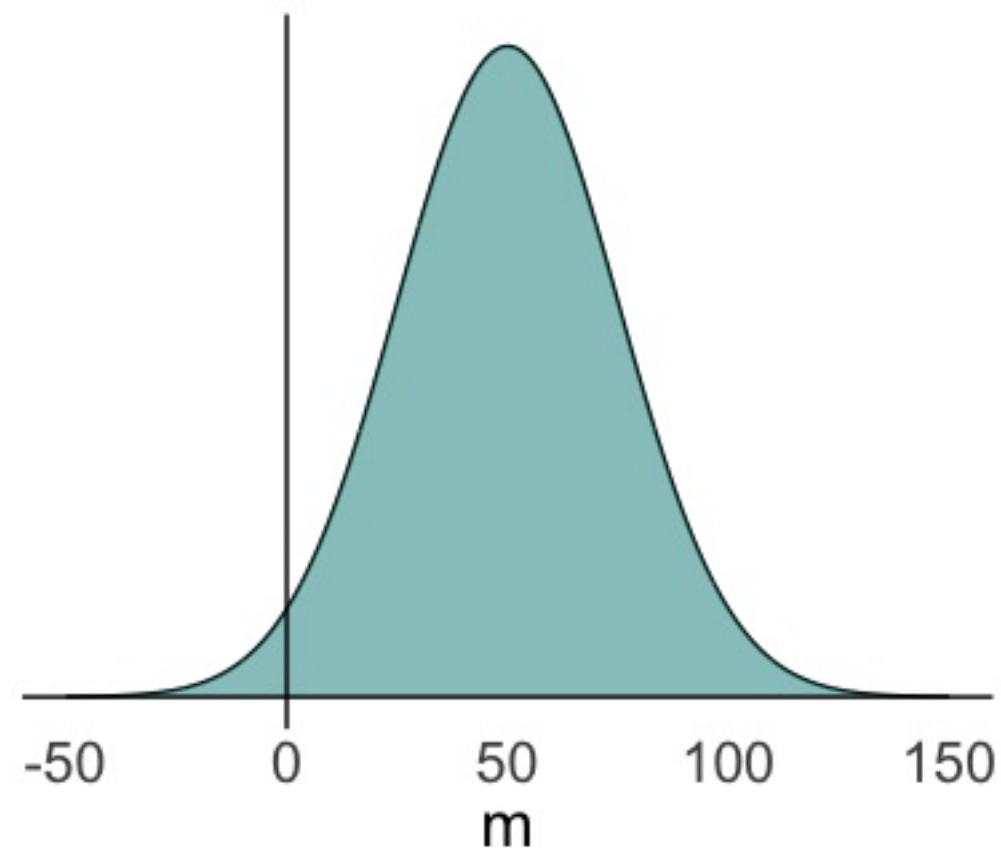
Y_i = change in reaction time (ms)

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

m = average Y_i

Prior information:

- with *normal* sleep, average reaction time is ~ 250 ms
- expect average to \nearrow by ~ 50 ms
- average is unlikely to \searrow & unlikely to \nearrow by more than ~ 150 ms



Prior model for parameter m

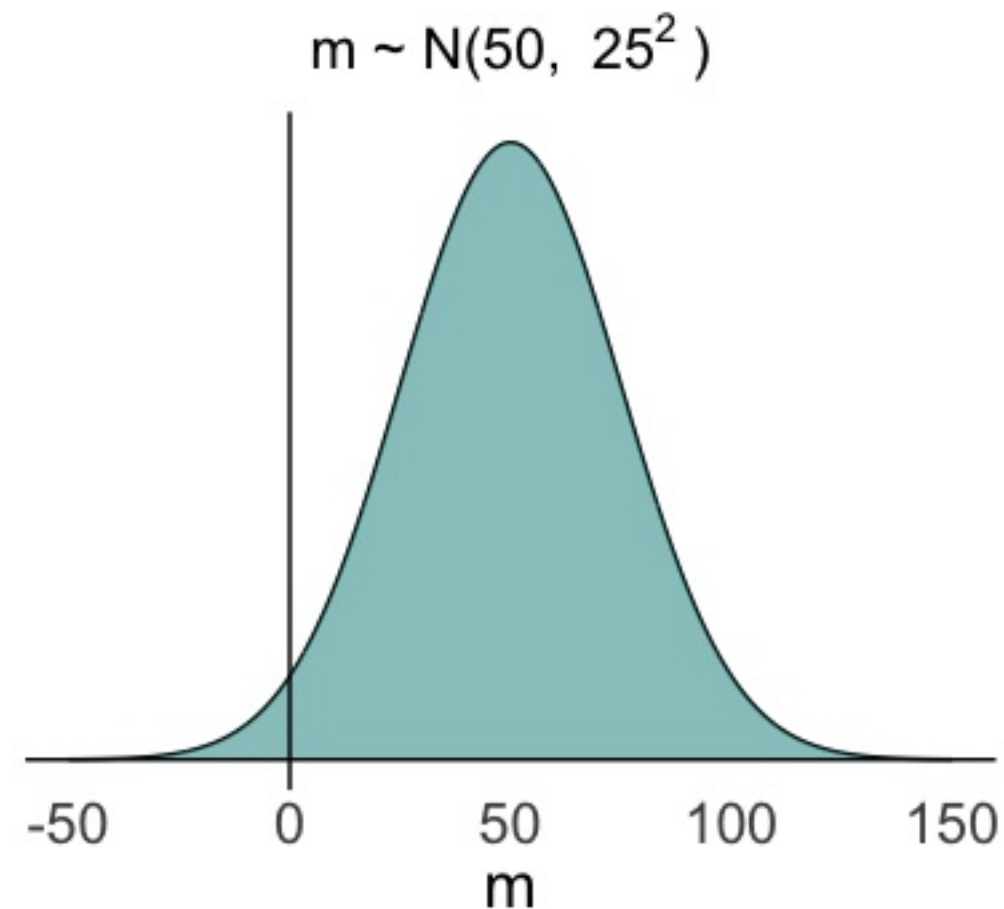
Y_i = change in reaction time (ms)

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

m = average Y_i

Prior information:

- with *normal* sleep, average reaction time is ~ 250 ms
- expect average to \nearrow by ~ 50 ms
- average is unlikely to \searrow & unlikely to \nearrow by more than ~ 150 ms



Prior model for parameter s

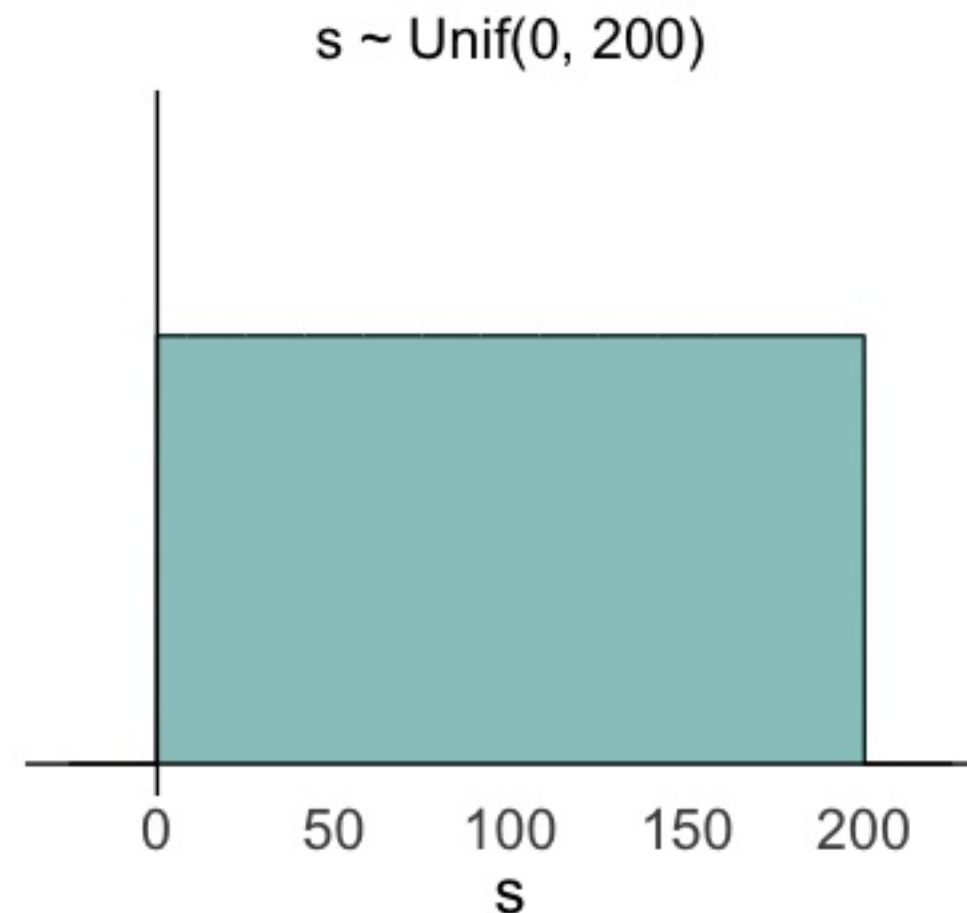
Y_i = change in reaction time (ms)

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

s = standard deviation of Y_i

Prior information:

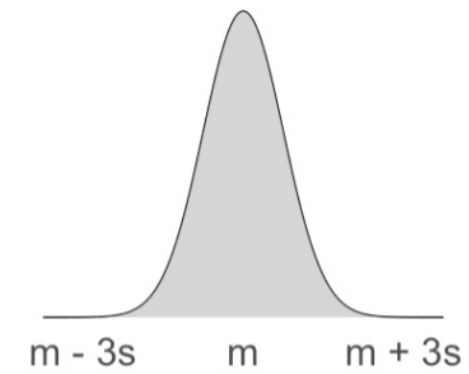
- $s > 0$
- with *normal* sleep, s.d. in reaction times is ~ 30 ms
- s is equally likely to be anywhere from 0 to 200 ms



The Normal-Normal Model

Likelihood:

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





The Normal-Normal Model

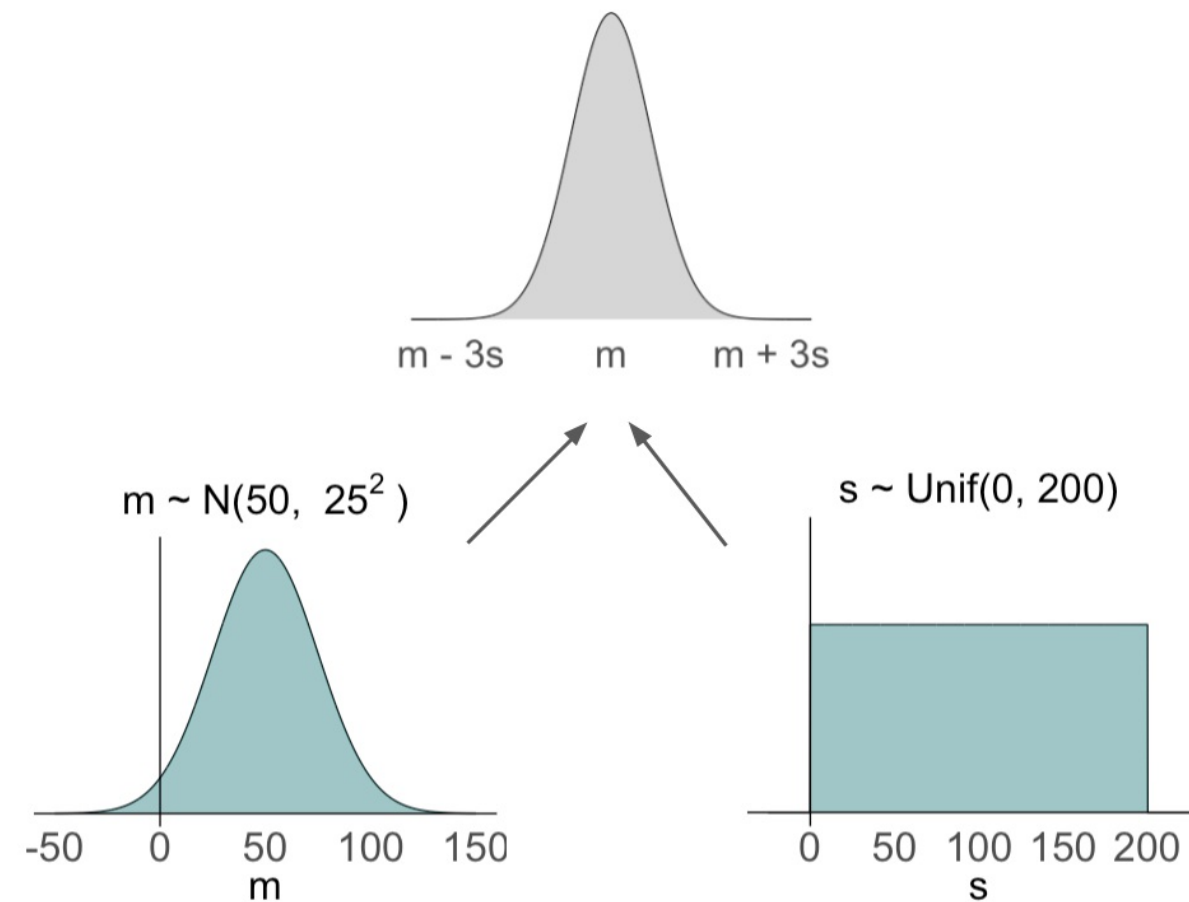
Likelihood:

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

Priors:

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

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





BAYESIAN MODELING WITH RJAGS

Let's practice!



BAYESIAN MODELING WITH RJAGS

Simulating the Normal-Normal in RJAGS

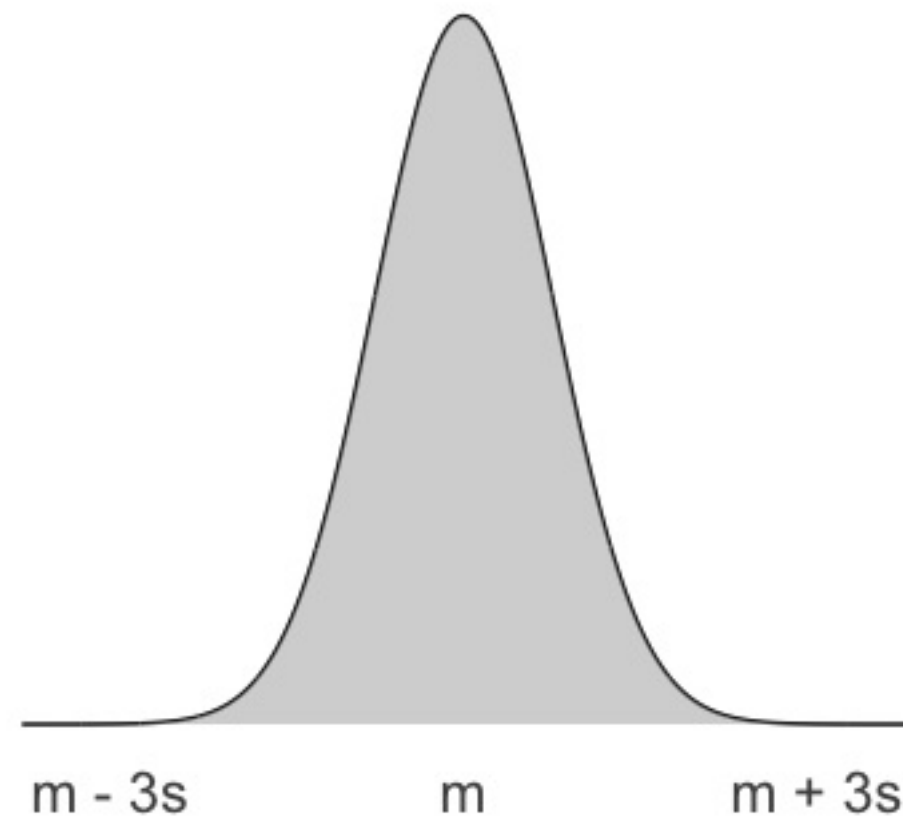
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Sleep study

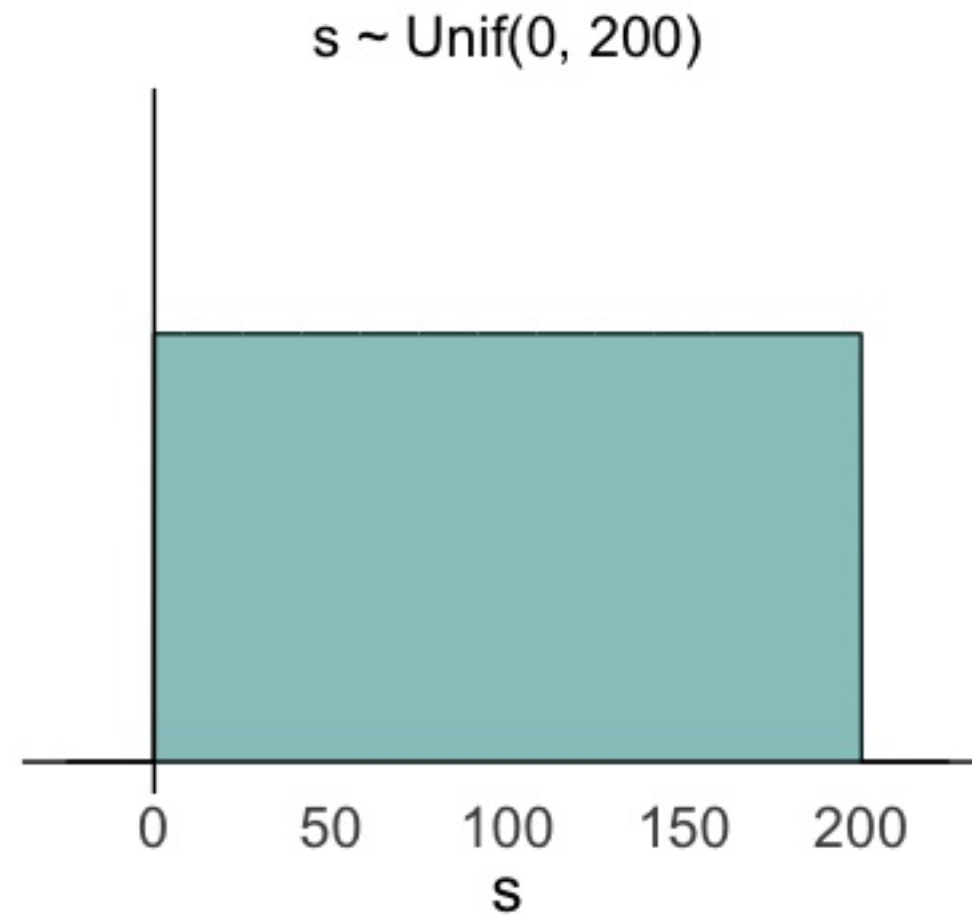
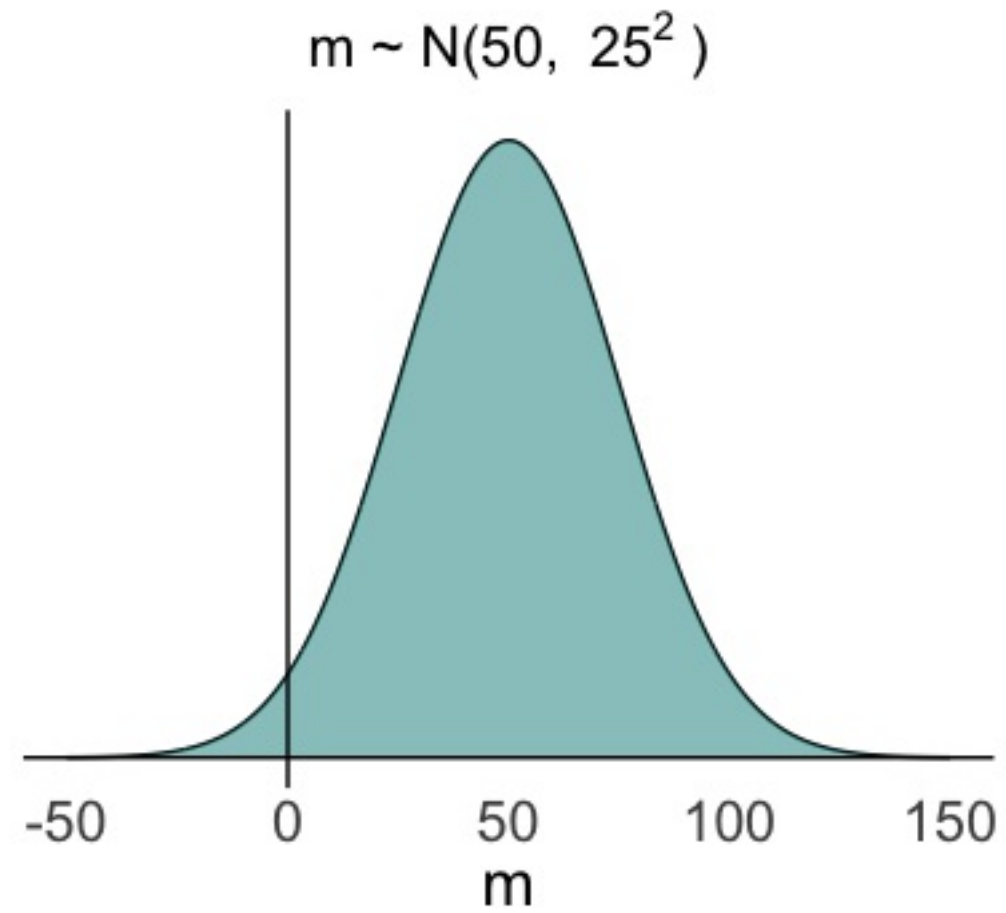
Y_i = change in reaction time (ms) after 3 days of sleep deprivation

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

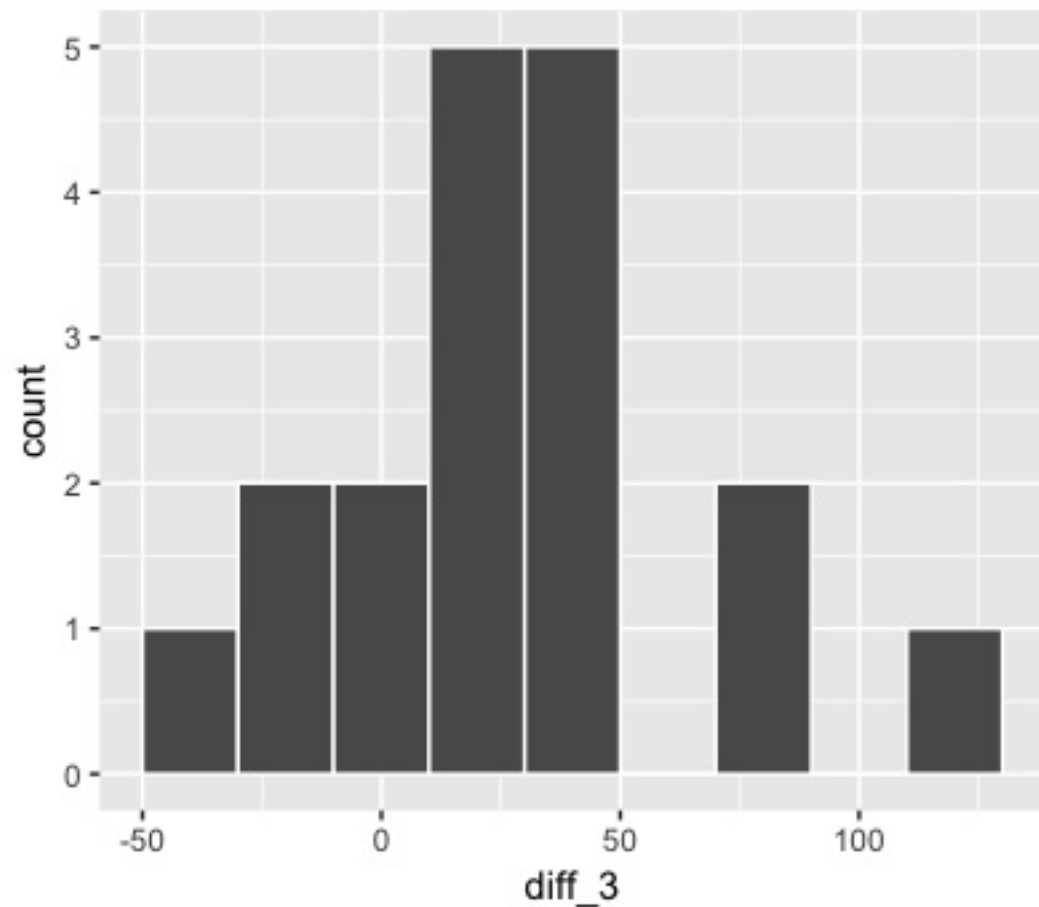




Insights from the priors



Insights from the data (& likelihood)



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

```
> mean(sleep_study$diff_3)
[1] 26.34021
> sd(sleep_study$diff_3)
[1] 37.20764
```



Posterior insights

A diagram illustrating the Bayesian posterior equation. It consists of three colored rectangular boxes arranged horizontally. The first box on the left is teal and contains the word "POSTERIOR" in bold black capital letters. To its right is a yellow box containing the word "LIKELIHOOD" in bold black capital letters. To the right of the yellow box is a blue box containing the word "PRIOR" in bold black capital letters. Between the teal and yellow boxes is a black proportional symbol (\propto). Between the yellow and blue boxes is a black multiplication dot (\cdot).

$$\text{POSTERIOR} \propto \text{LIKELIHOOD} \cdot \text{PRIOR}$$



DEFINE the Normal-Normal

```
sleep_model <- "model{  
  # Likelihood model for Y[i]  
  
  # Prior models for m and s  
  
}"
```



DEFINE the Normal-Normal

```
sleep_model <- "model{  
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```

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



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 $1, 2, \dots, 18$



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 $1, 2, \dots, 18$

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 $1, 2, \dots, 18$

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)) {  
    Y[i] ~ dnorm(m, s^(-2))  
  }  
  
  # 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 $1, 2, \dots, 18$

NOTE: precision = variance⁻¹ =
 s^{-2}

- $m \sim N(50, 25^2)$
- $s \sim Unif(0, 200)$

COMPILE the Normal-Normal

```
# 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
```



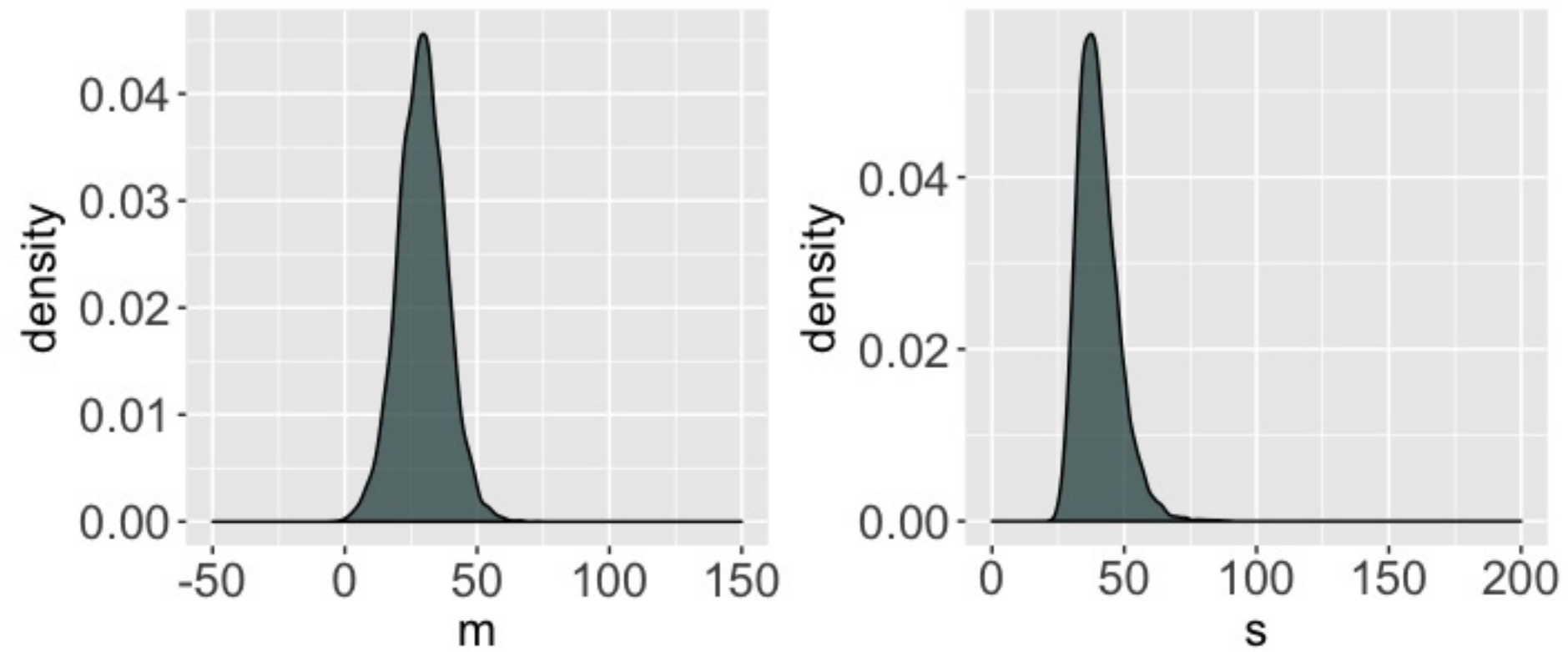
SIMULATE the Normal-Normal

```
# 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)
```

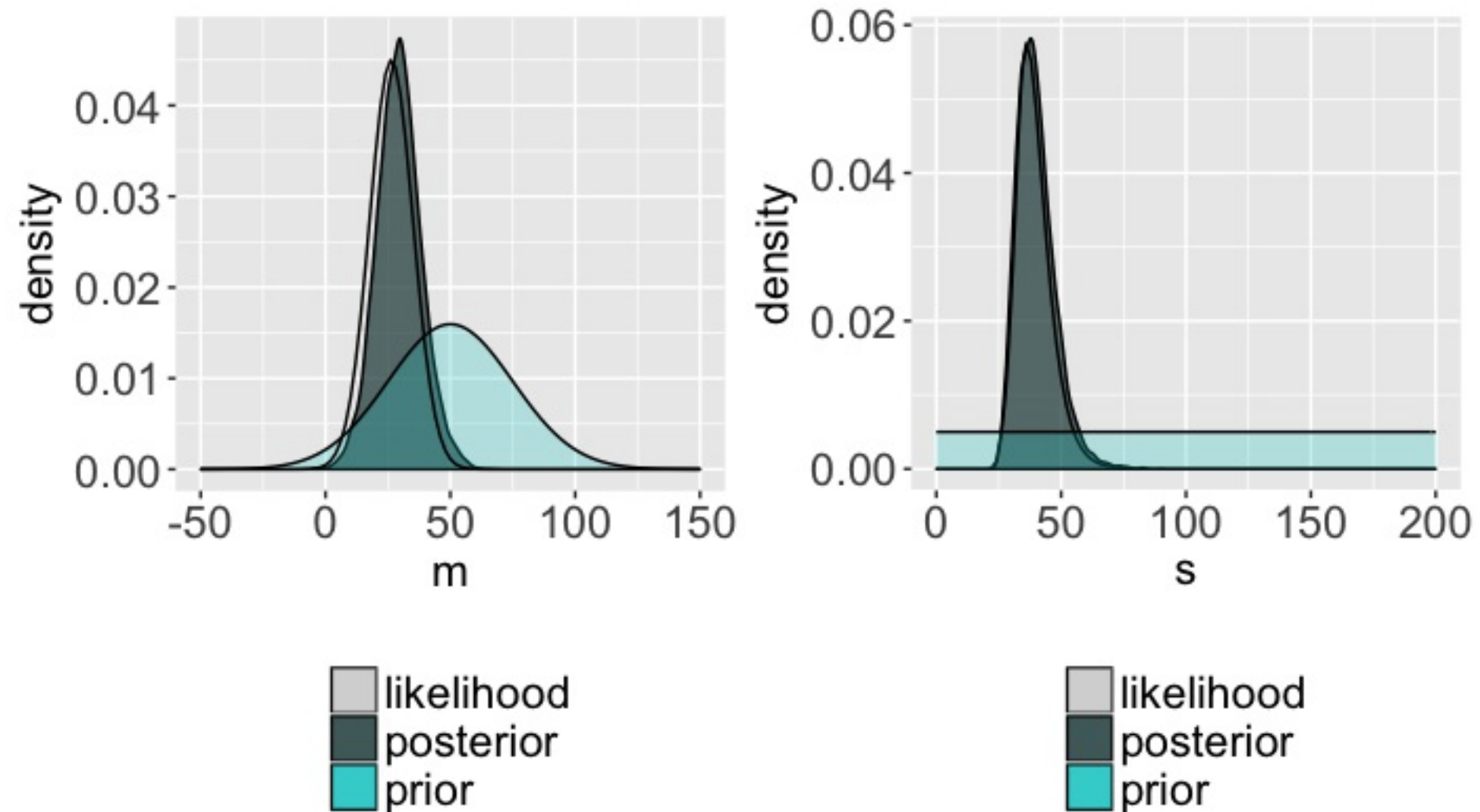



SIMULATE the Normal-Normal





SIMULATE the Normal-Normal





BAYESIAN MODELING WITH RJAGS

Let's practice!



BAYESIAN MODELING WITH RJAGS

Markov chains

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Posterior Simulation

Normal-Normal model:

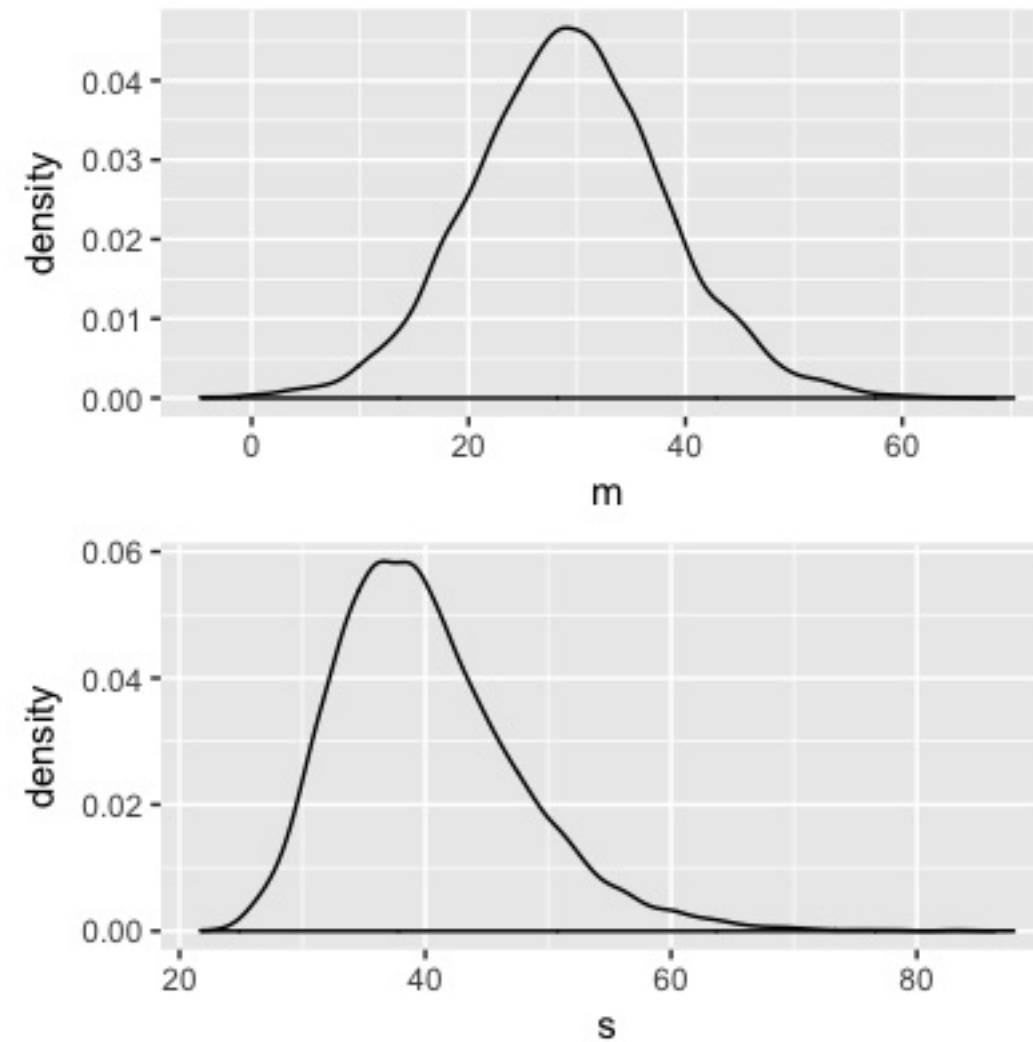
Y_i = change in reaction time (ms)

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

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

$$s \sim Unif(0, 200)$$

Approximate posteriors:





Markov chains

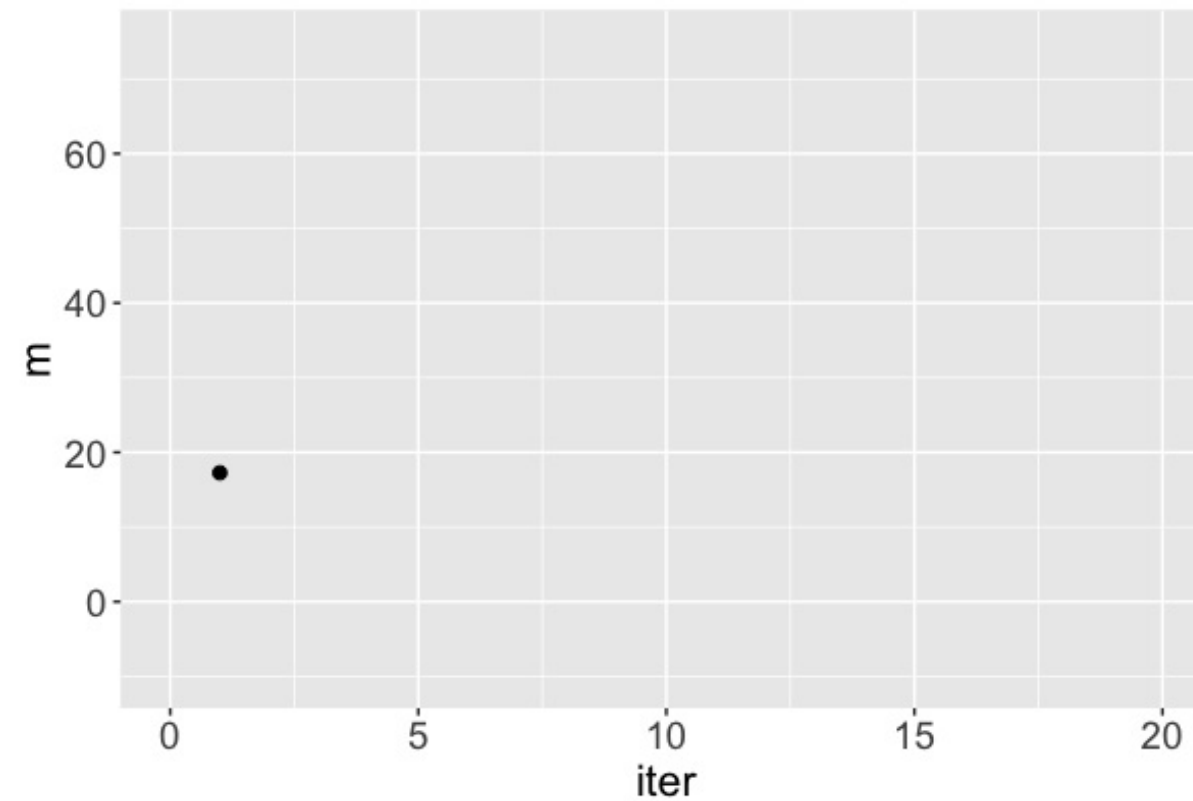
```
> head(sleep_chains, 20)
      m      s iter
1 17.25796 31.46256   1
2 34.58469 37.88655   2
3 36.45480 39.58056   3
4 25.00971 39.69494   4
5 29.95475 35.90001   5
6 28.43894 37.46466   6
7 38.32427 35.44081   7
8 27.90956 42.07951   8
9 28.09270 52.36360   9
10 29.70648 28.30665  10
11 32.10350 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
```

- 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



Markov chain dependence

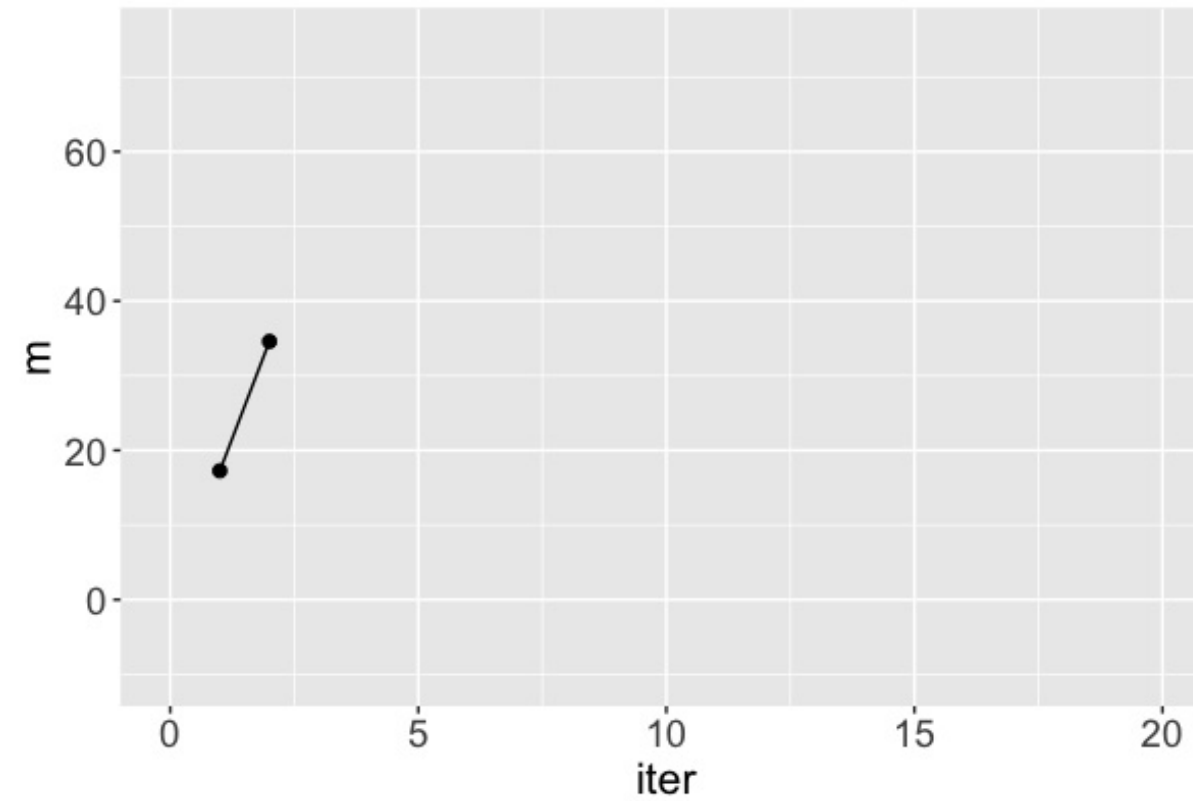
```
> head(sleep_chains, 20)
      m      s iter
1 17.25796 31.46256   1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
```





Markov chain dependence

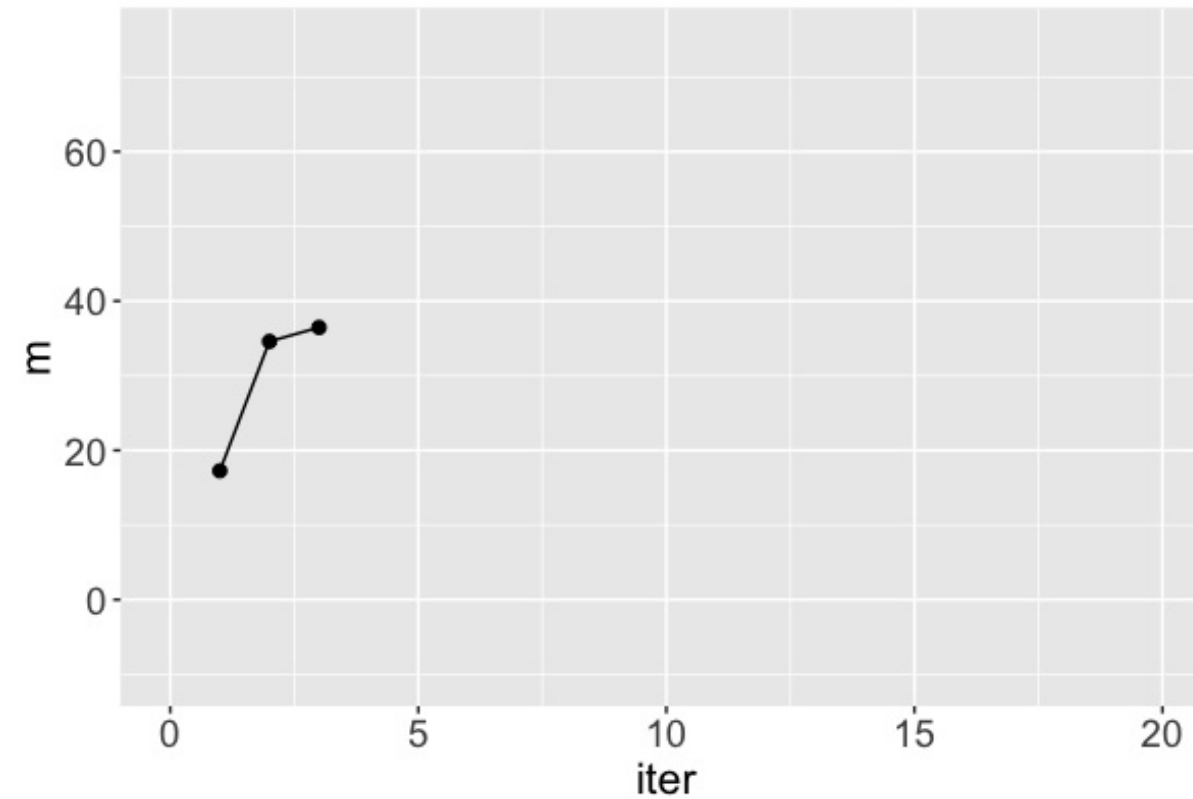
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> head(sleep_chains, 20)
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1 17.25796 31.46256   1
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3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
```





Markov chain dependence

```
> head(sleep_chains, 20)
      m      s iter
1 17.25796 31.46256   1
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3 36.45480 39.58056   3
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9
10
11
12
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15
16
17
18
19
20
```

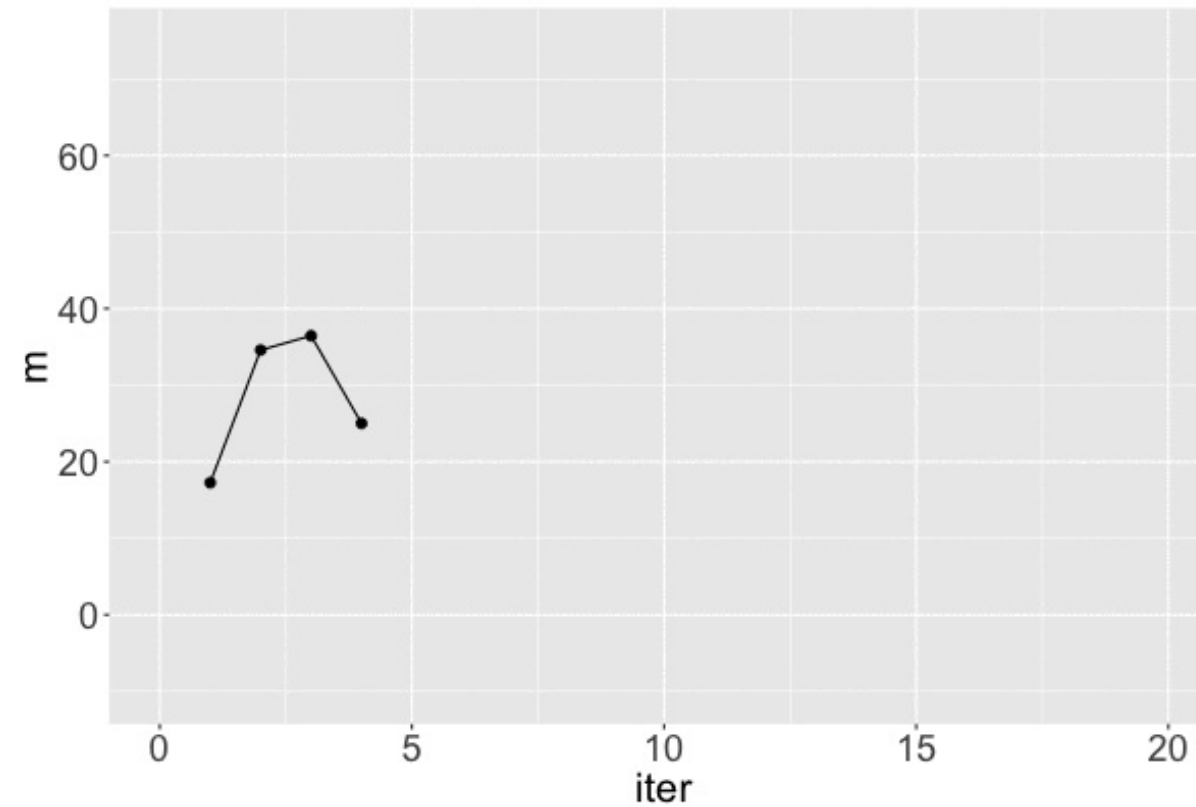




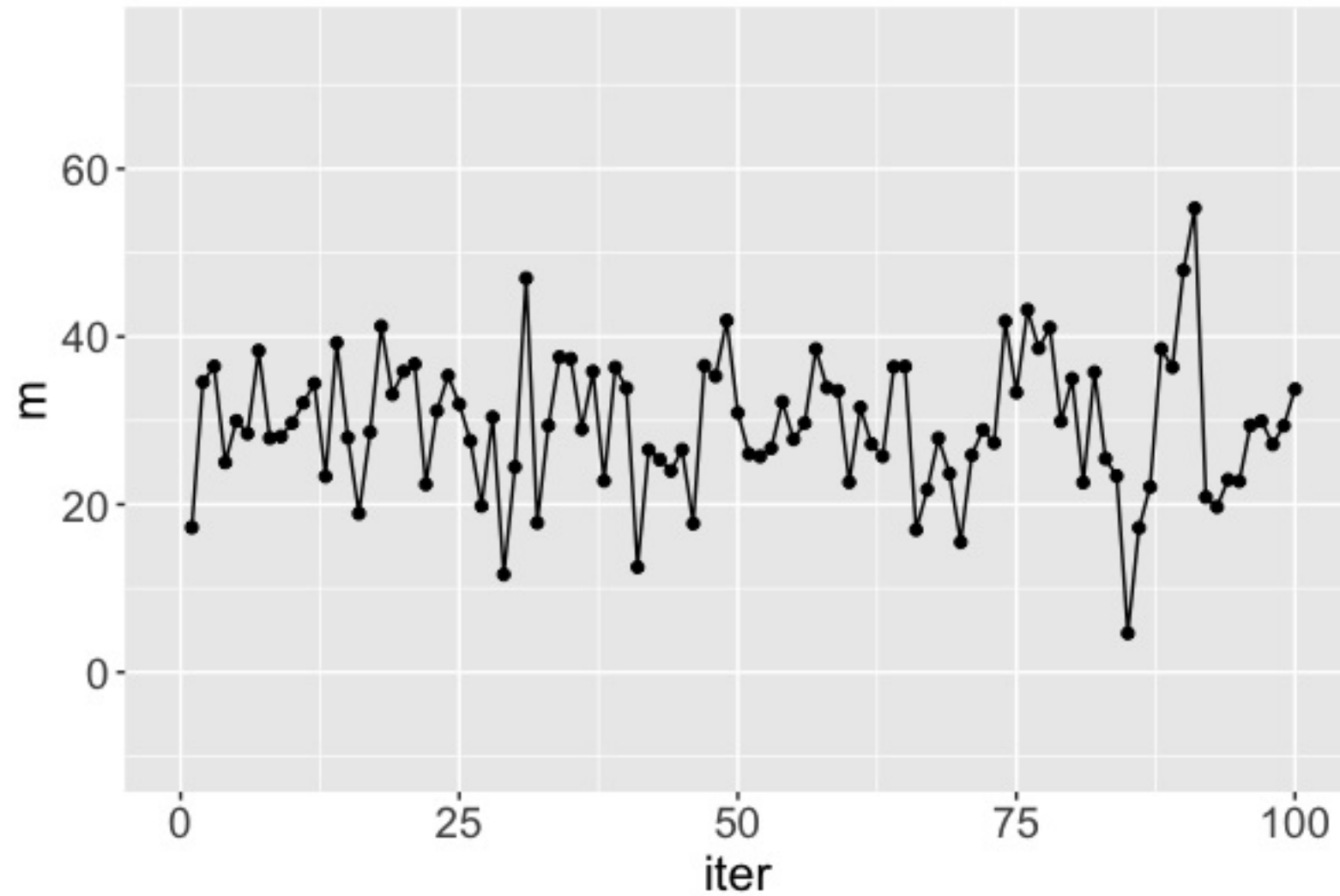
Markov chain dependence

```
> head(sleep_chains, 20)
```

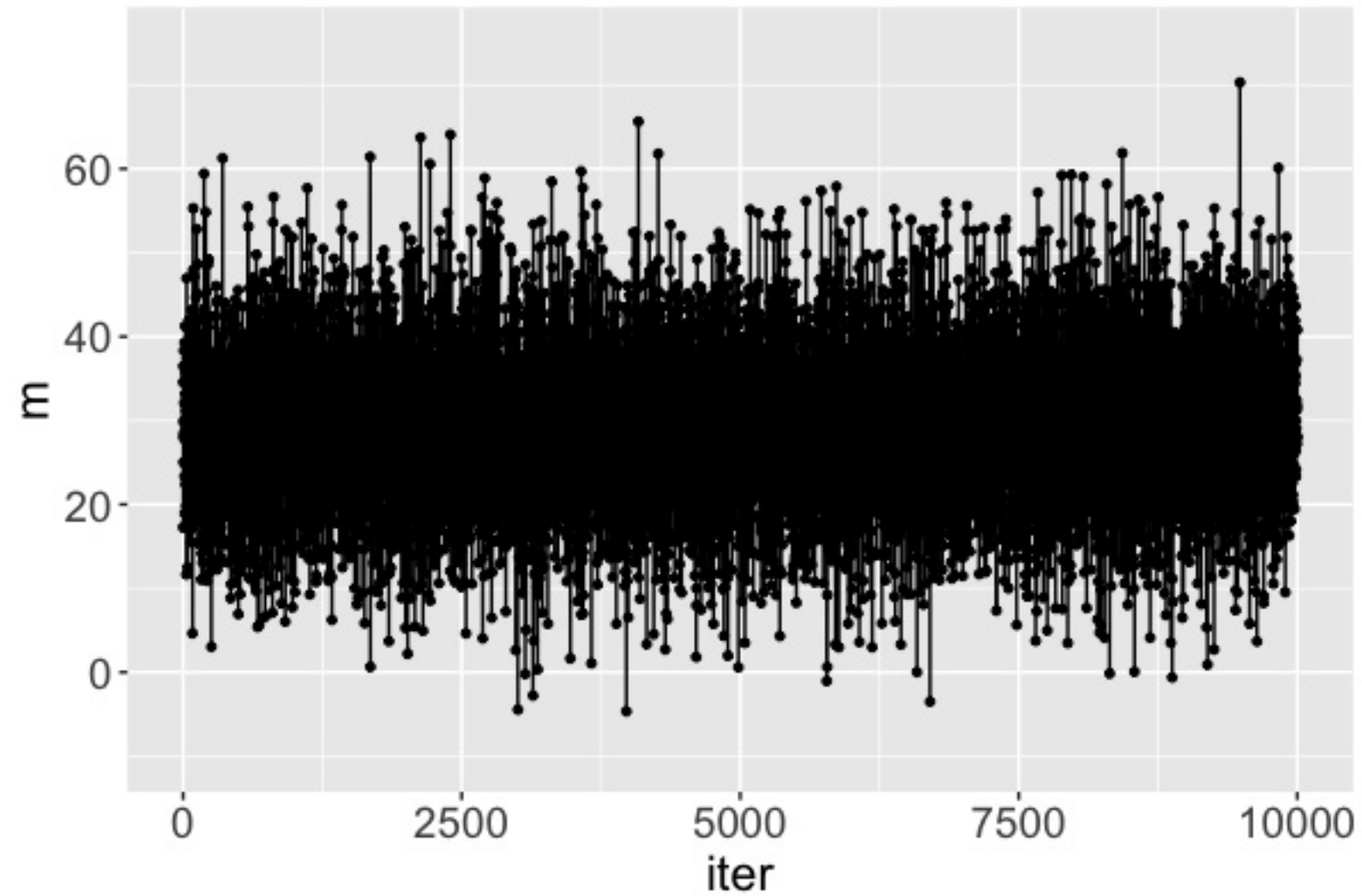
	m	s	iter
1	17.25796	31.46256	1
2	34.58469	37.88655	2
3	36.45480	39.58056	3
4	25.00971	39.69494	4
5	29.95475	35.90001	5
6	28.43894	37.46466	6
7	38.32427	35.44081	7
8	27.90956	42.07951	8
9	28.09270	52.36360	9
10	29.70648	28.30665	10
11	32.10350	46.64174	11
12	34.41397	28.86993	12
13	23.33649	37.46498	13
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

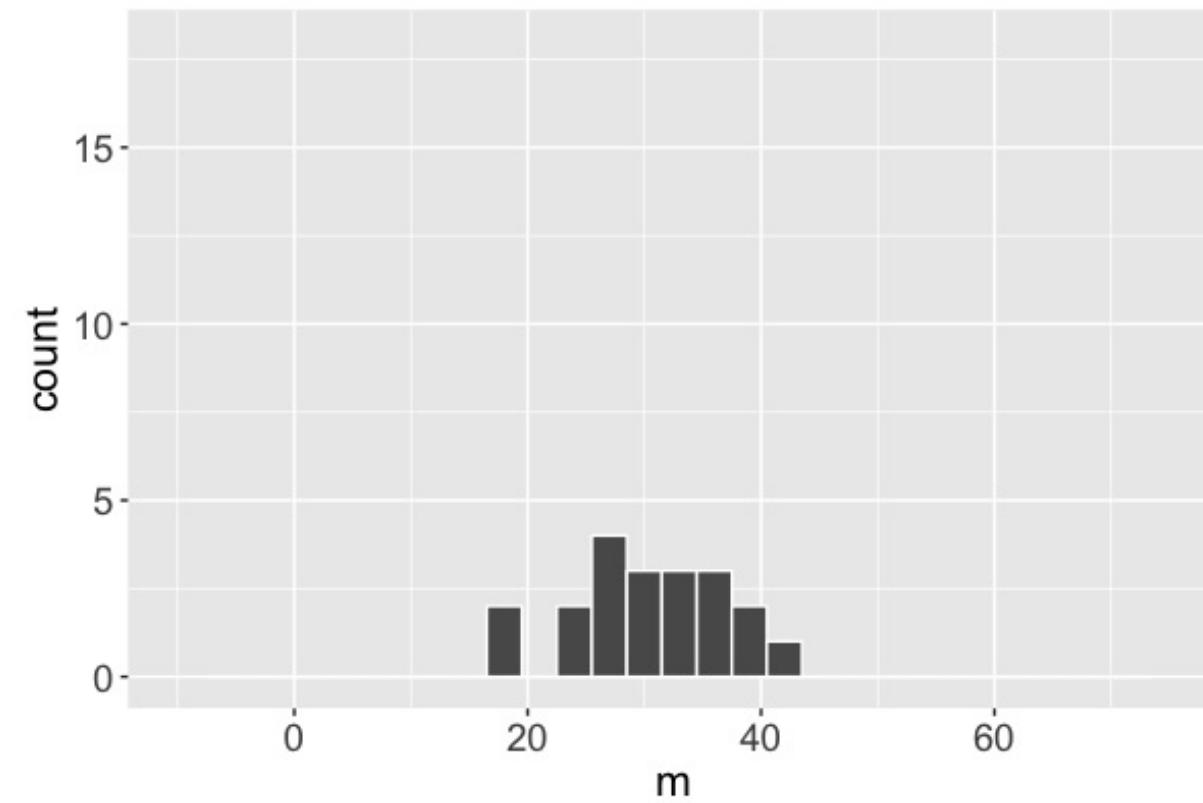
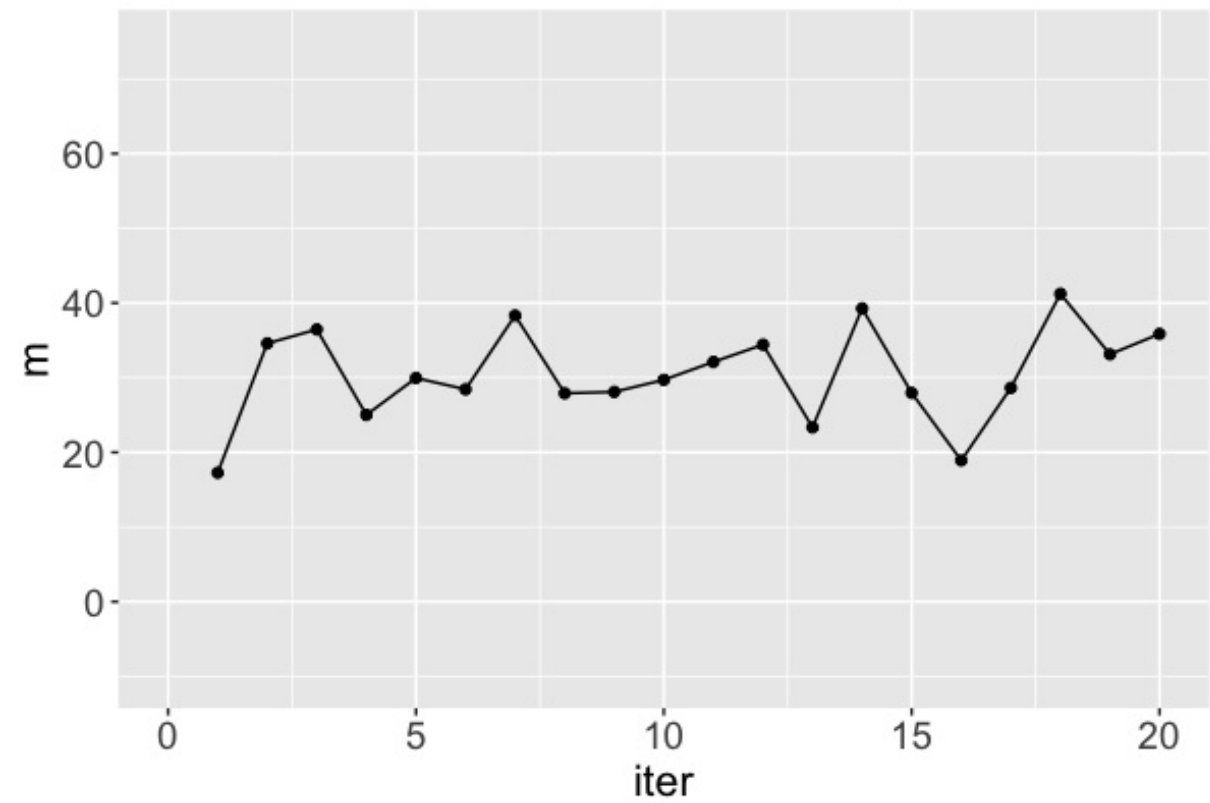


Markov chain trace plot



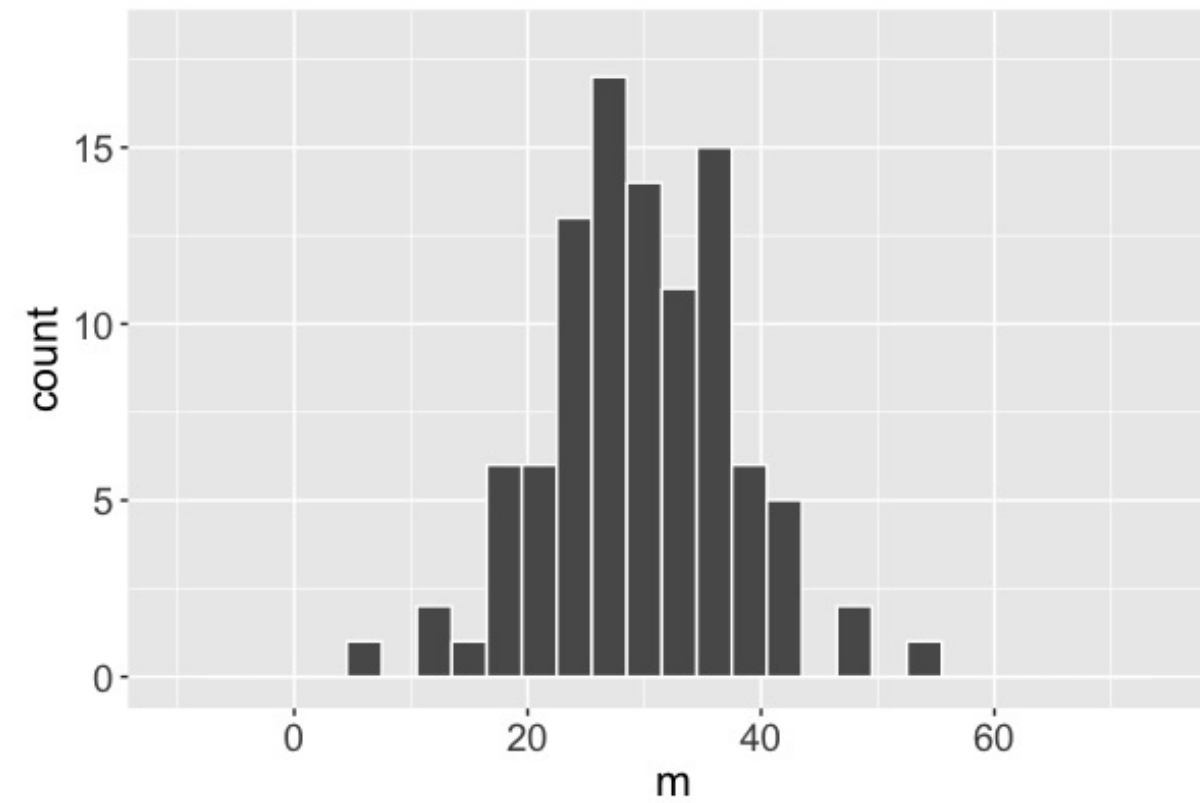
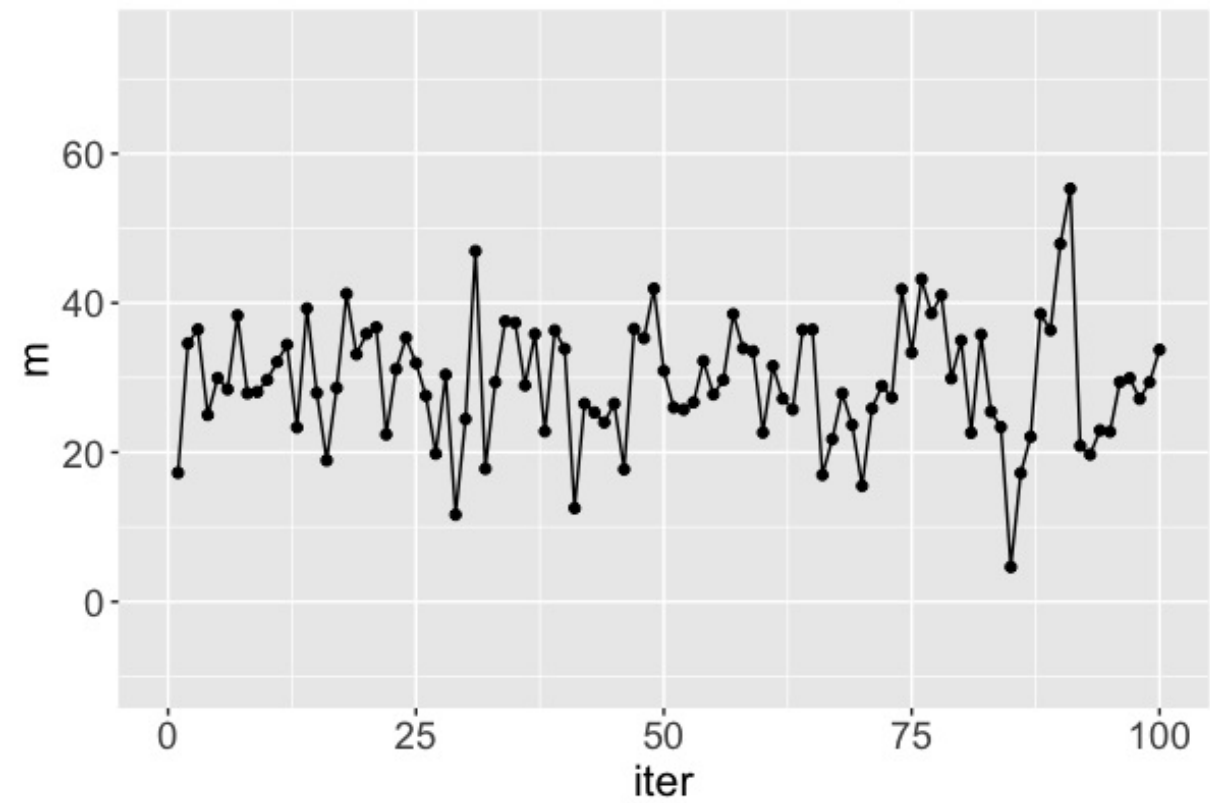


Markov chain distribution



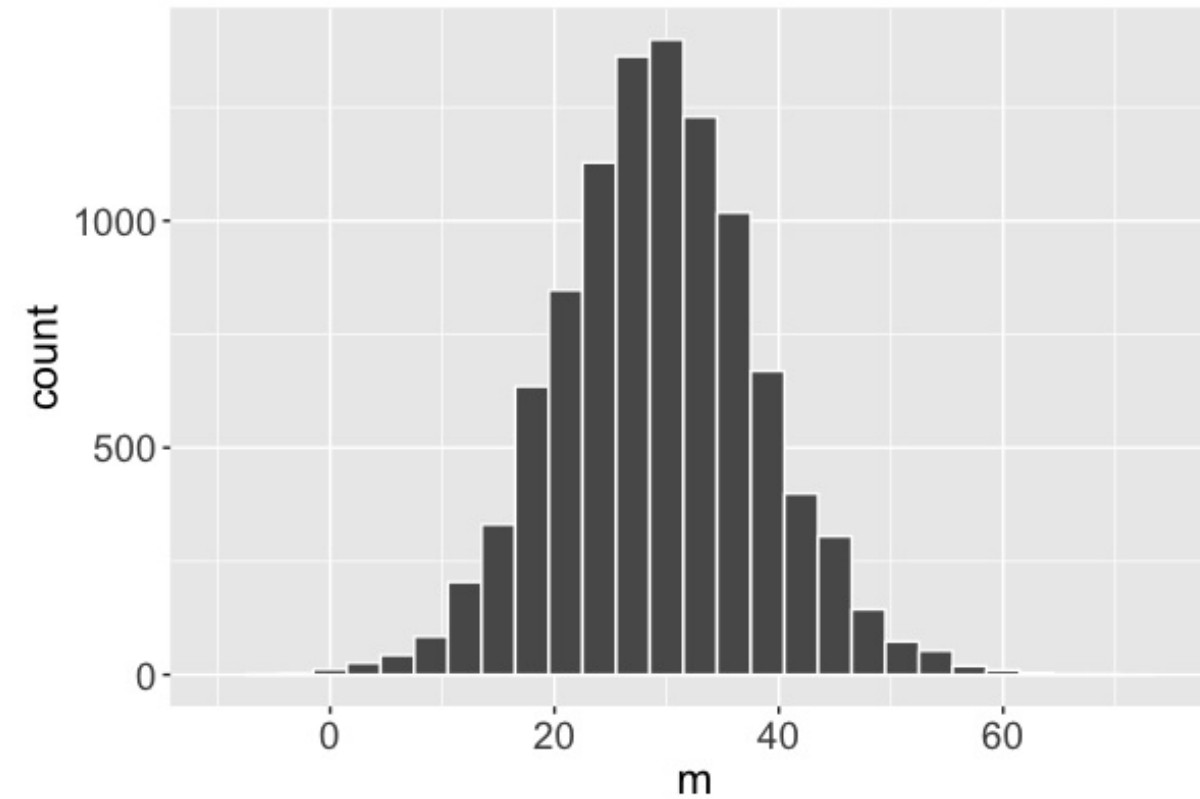
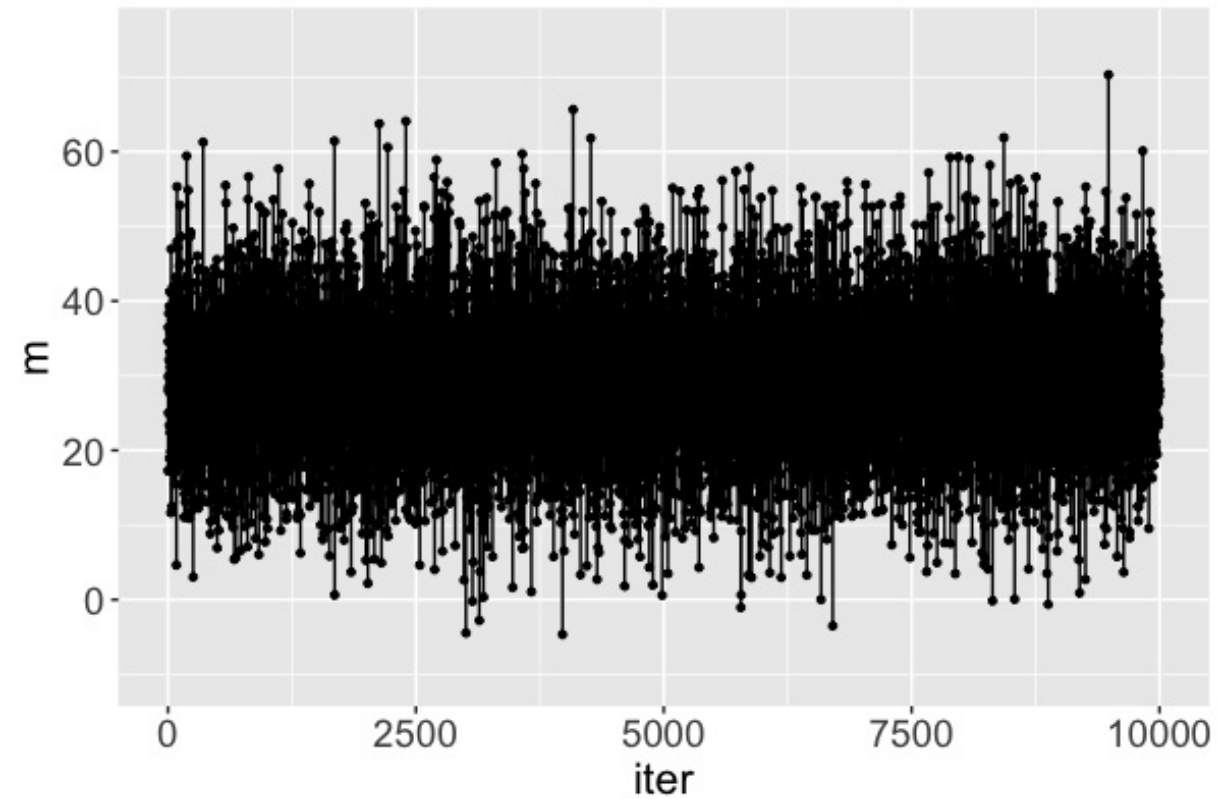


Markov chain distribution



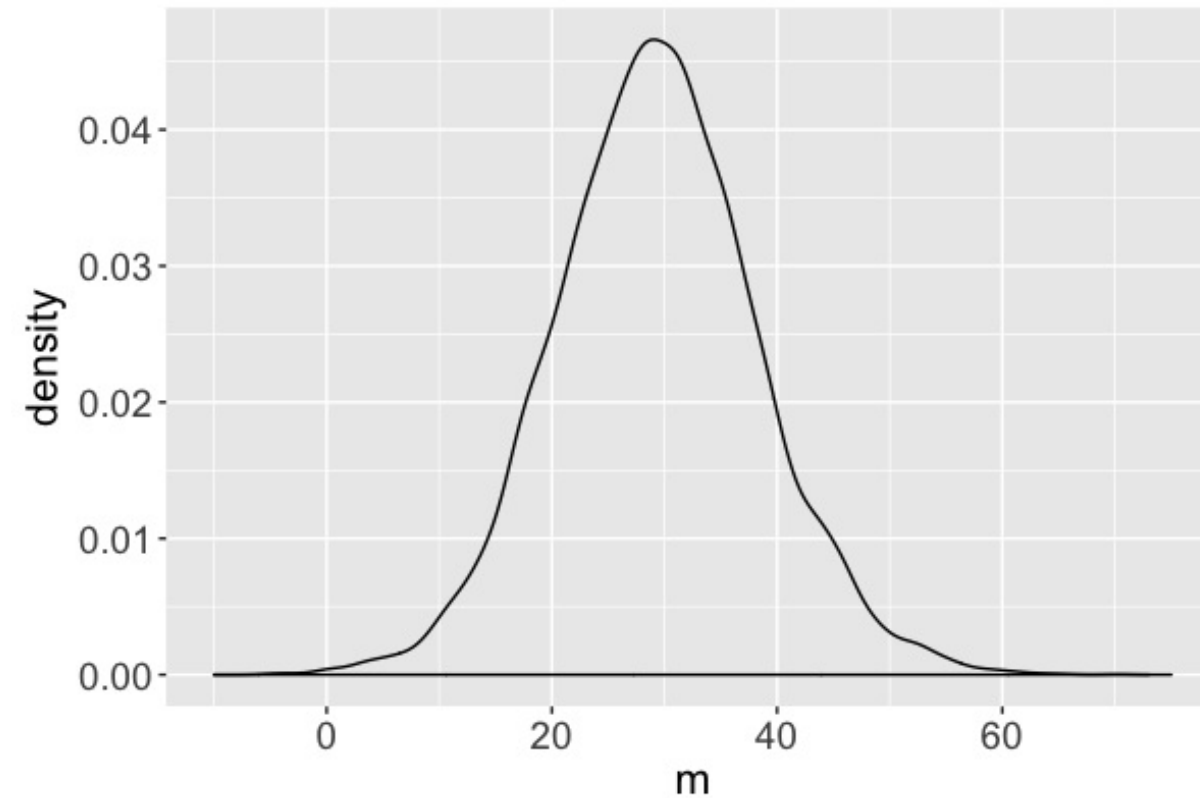
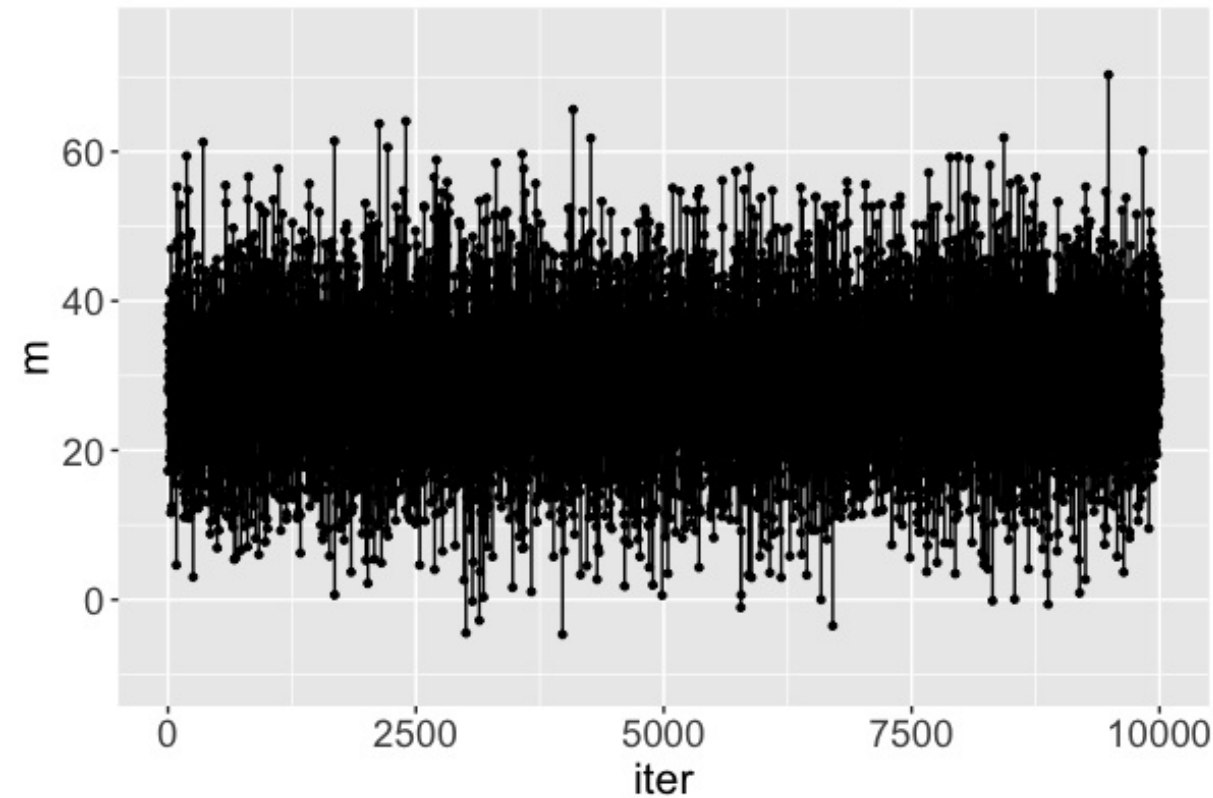


Markov chain distribution





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.



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Let's practice!



BAYESIAN MODELING WITH RJAGS

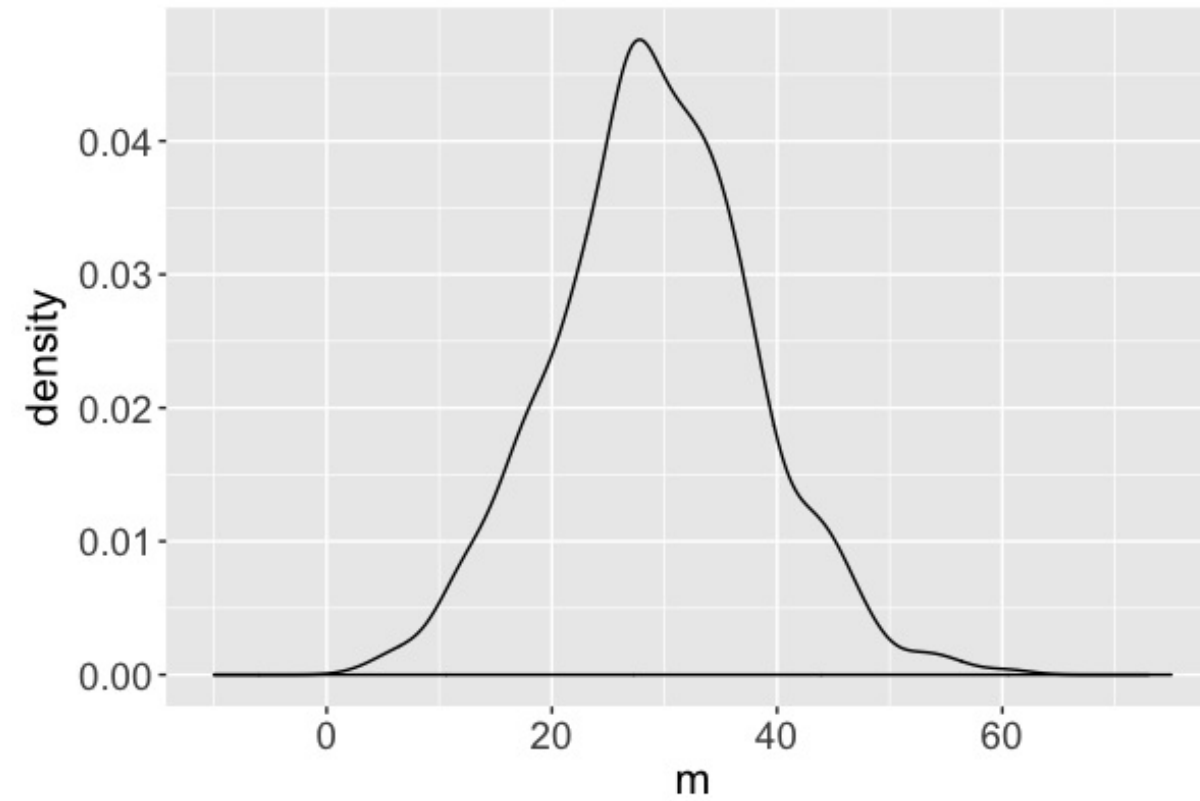
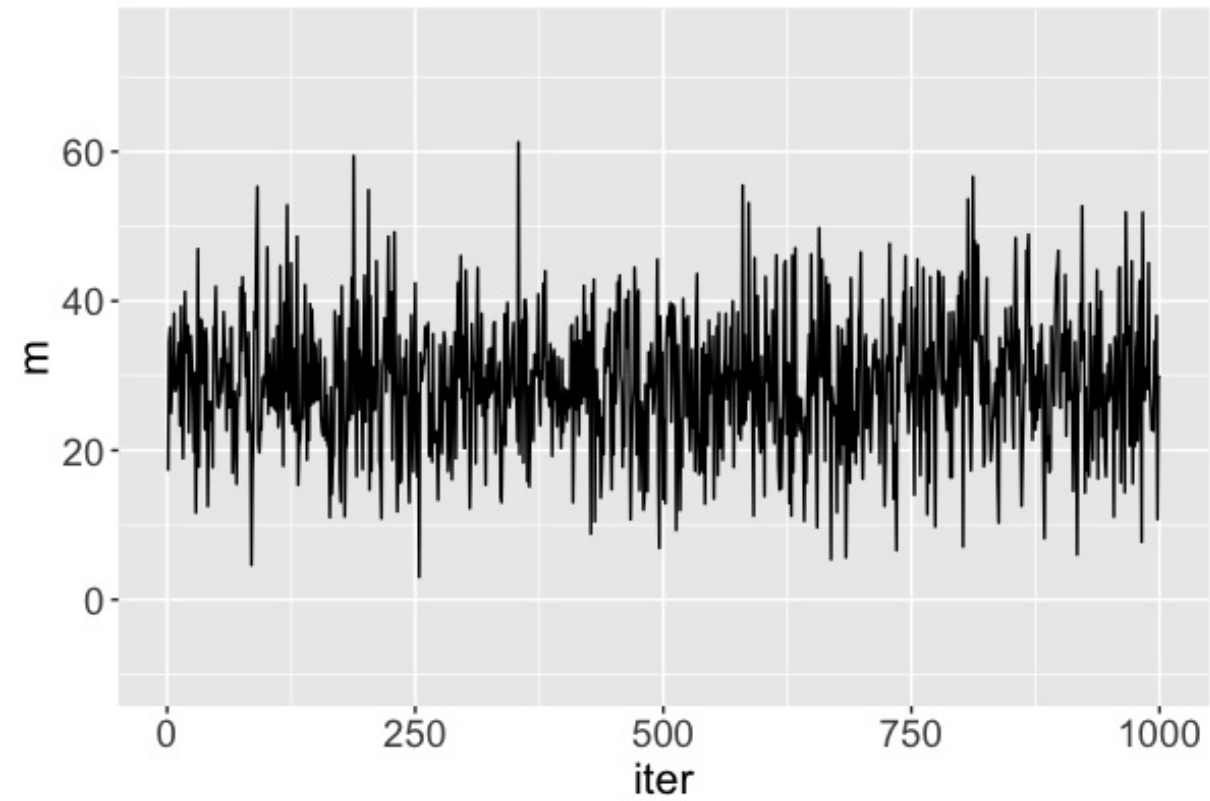
Markov chain diagnostics & reproducibility

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Markov chain output

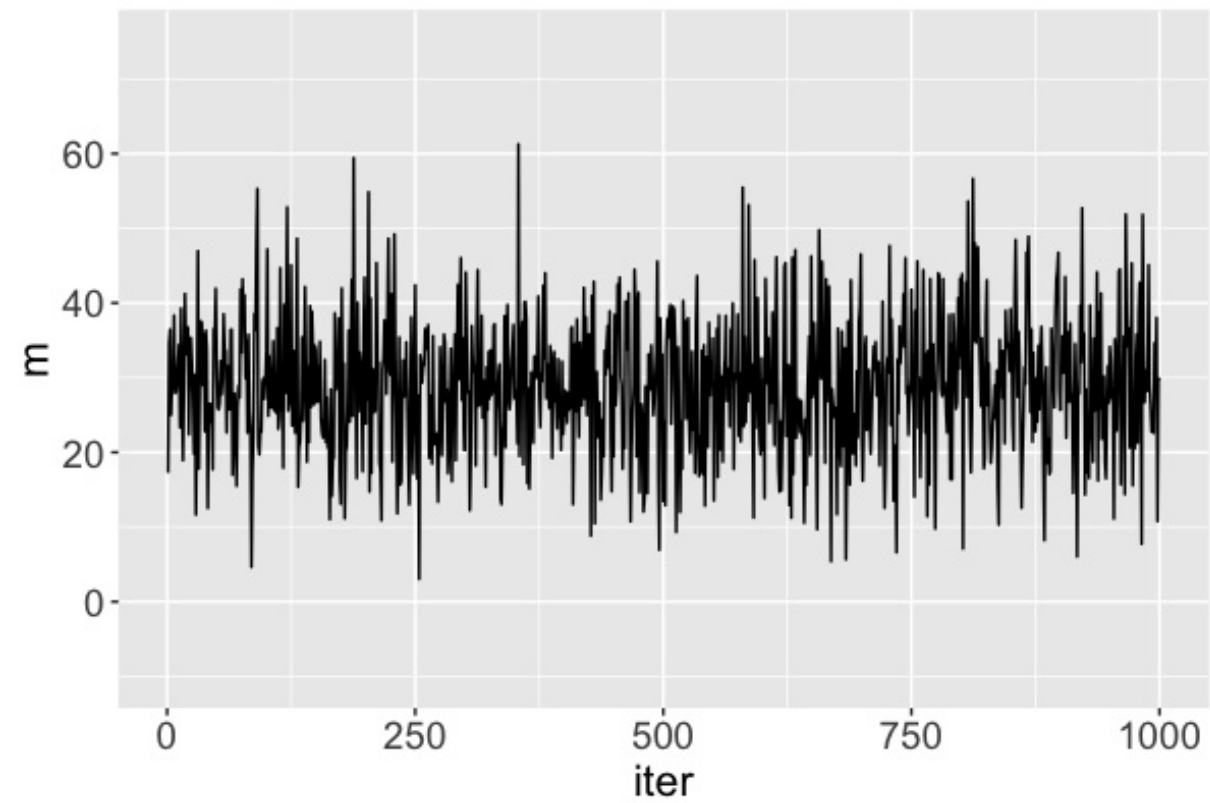




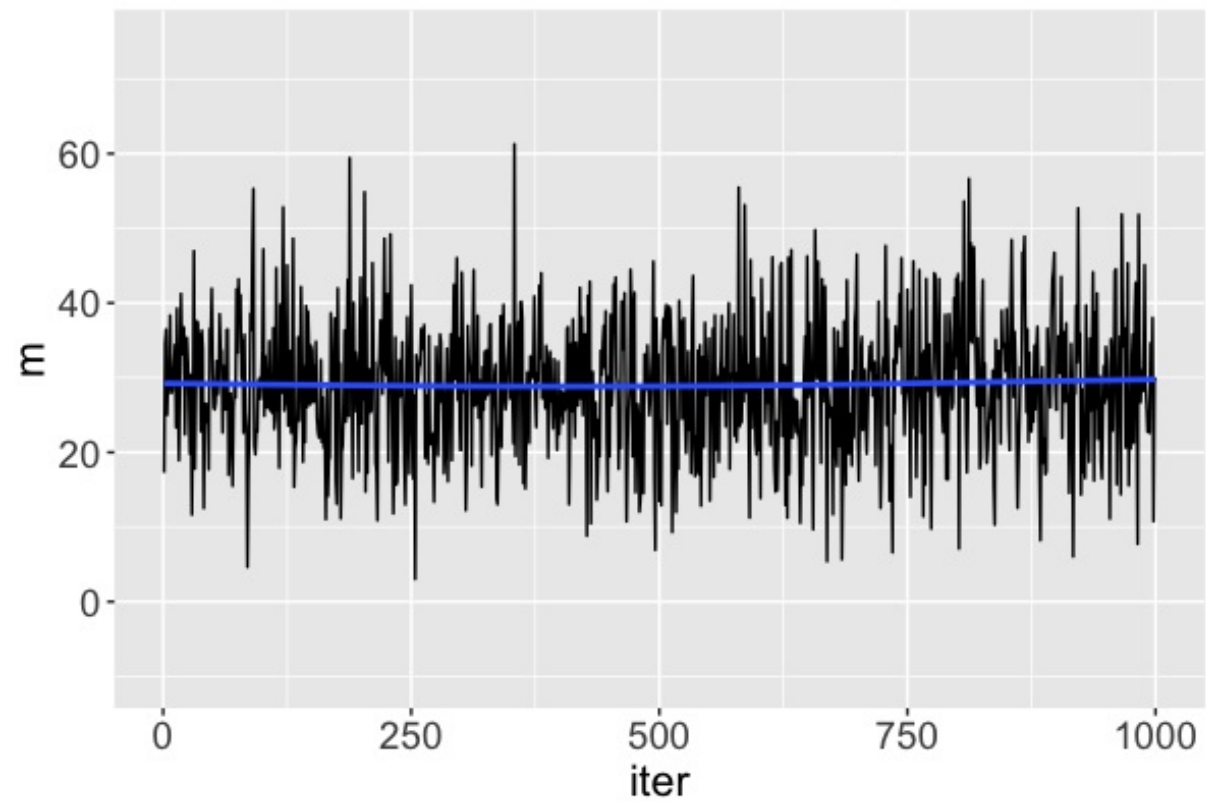
Questions to consider

- 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?

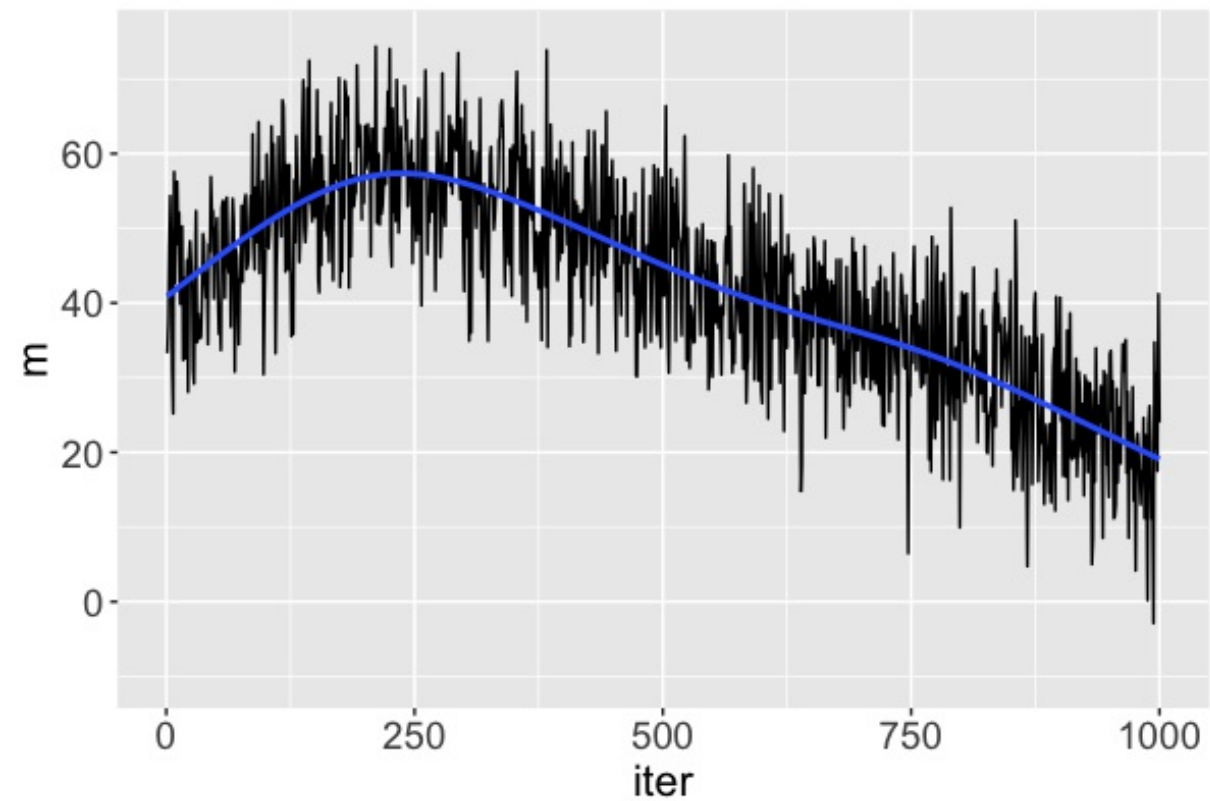
Diagnostic: trace plots



Diagnostic: trace plots



good: stability!

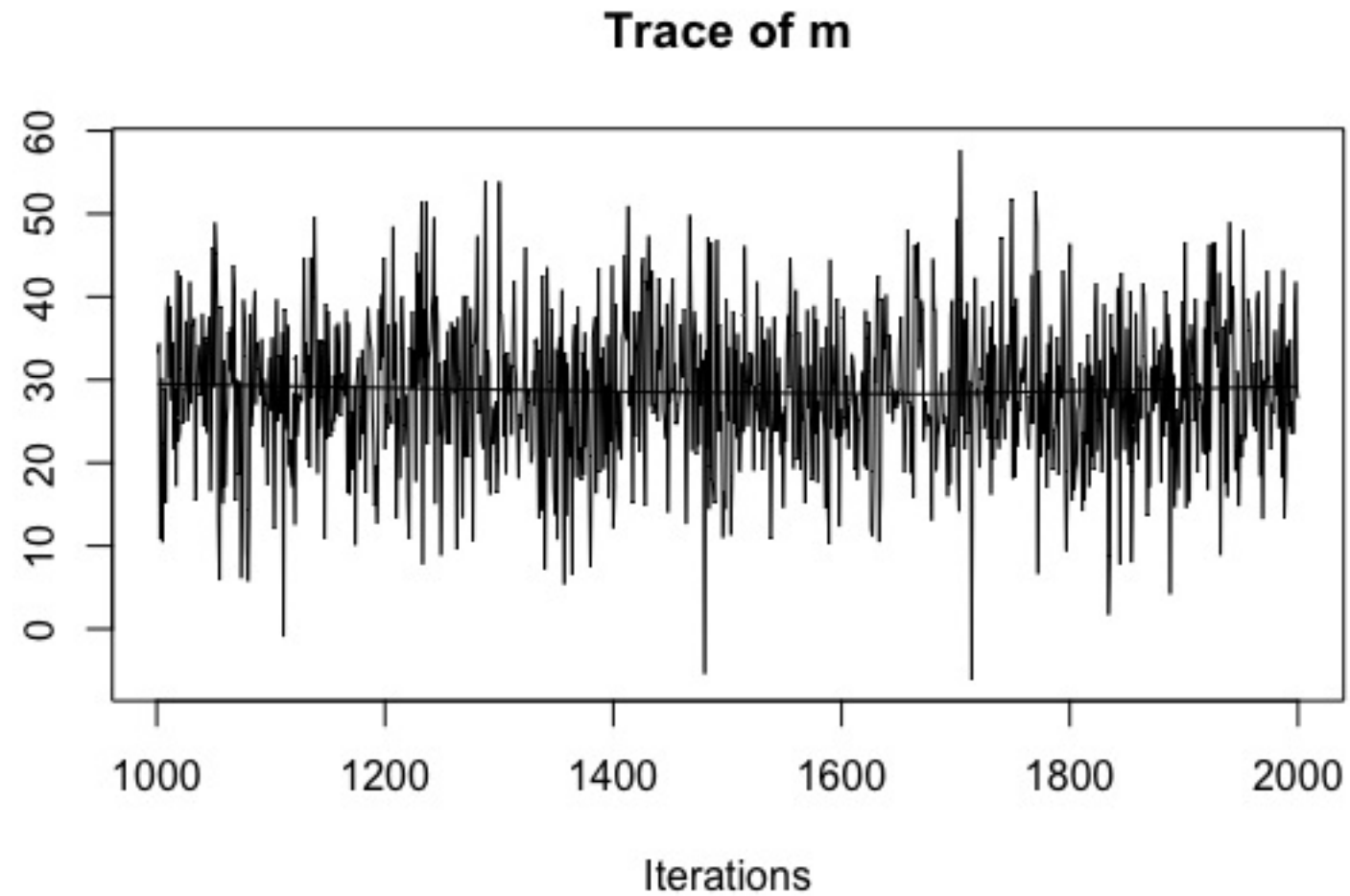


bad: instability



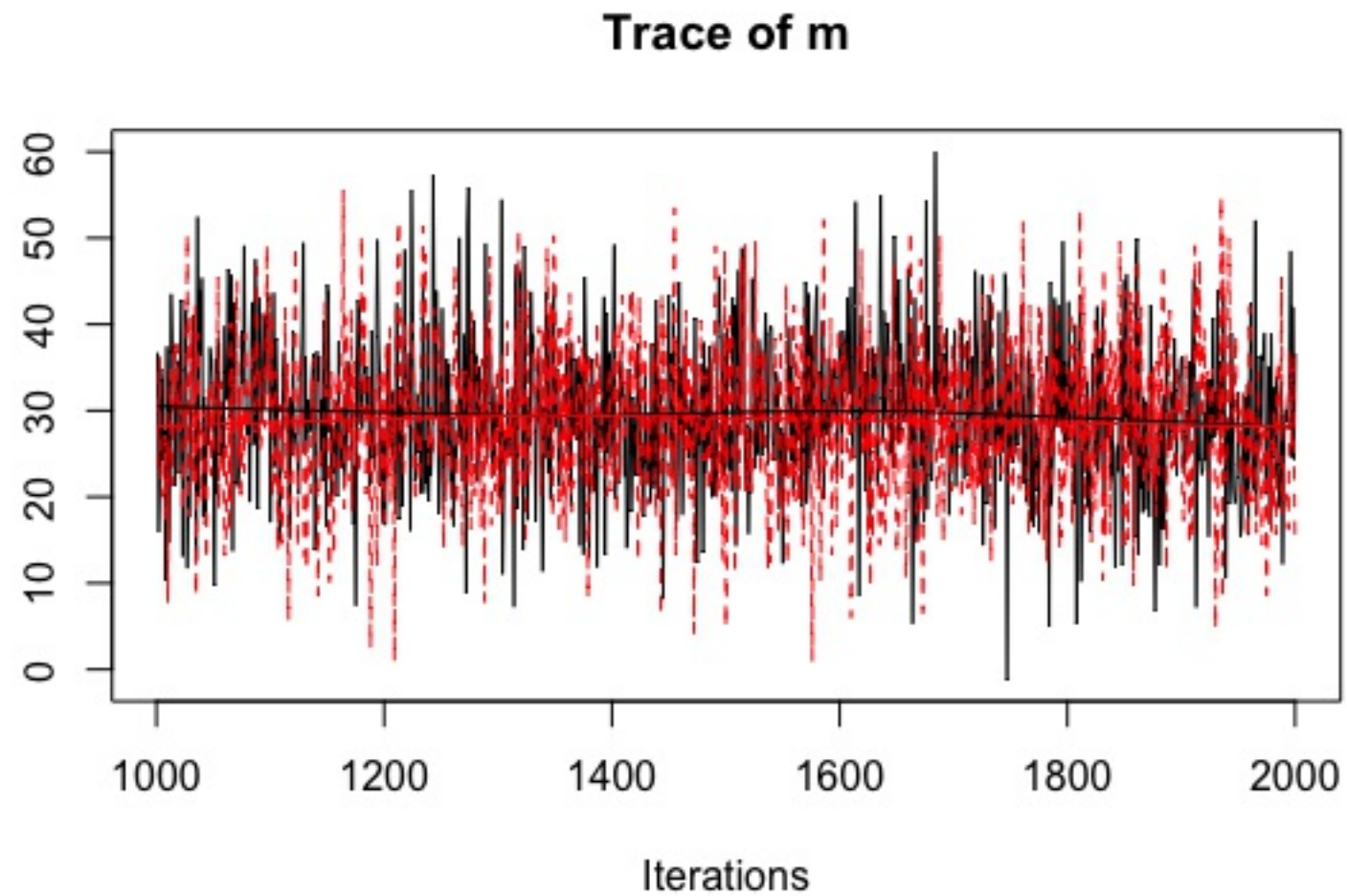
Diagnostic: multiple chains

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



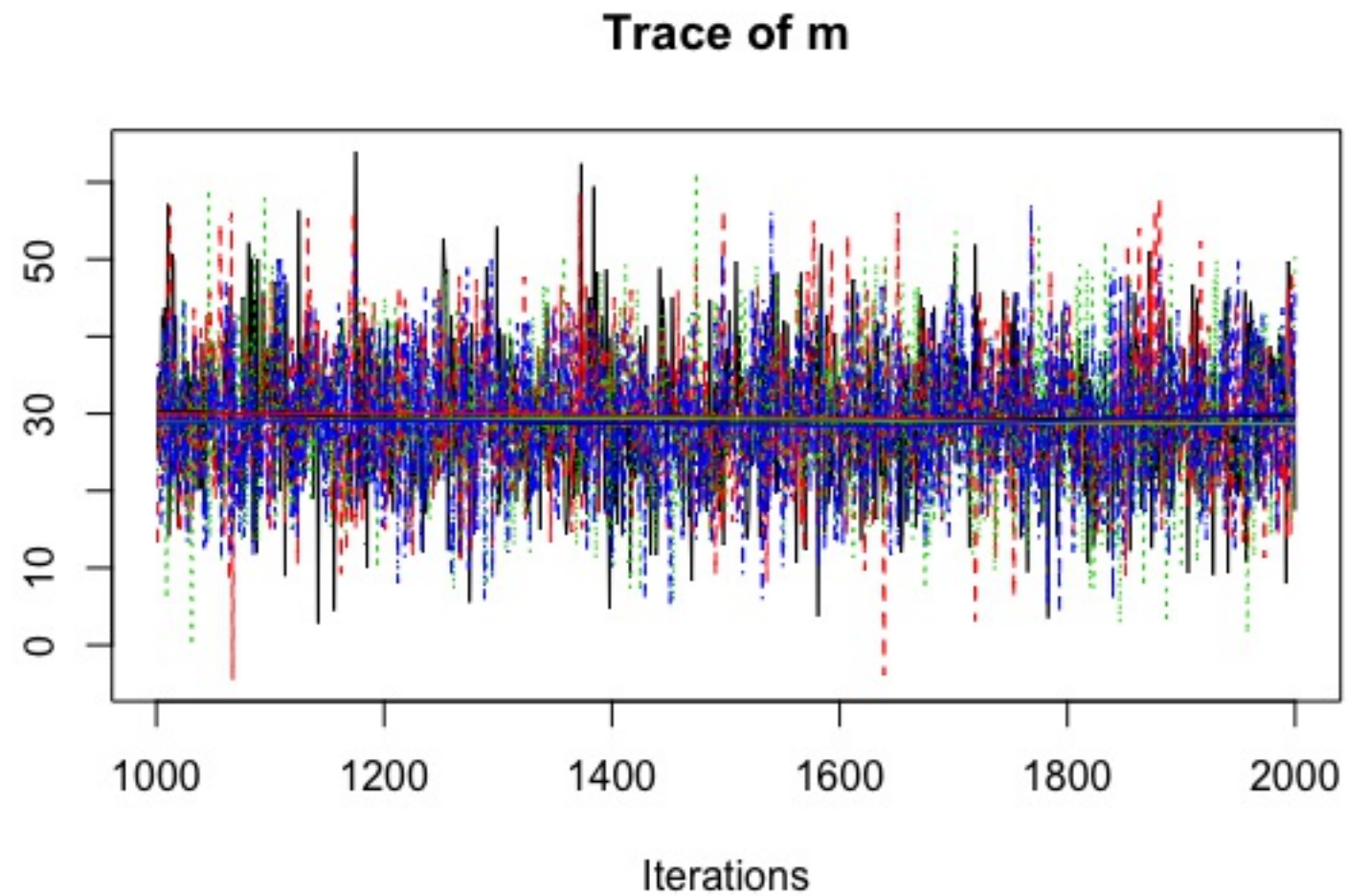
Diagnostic: multiple chains

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



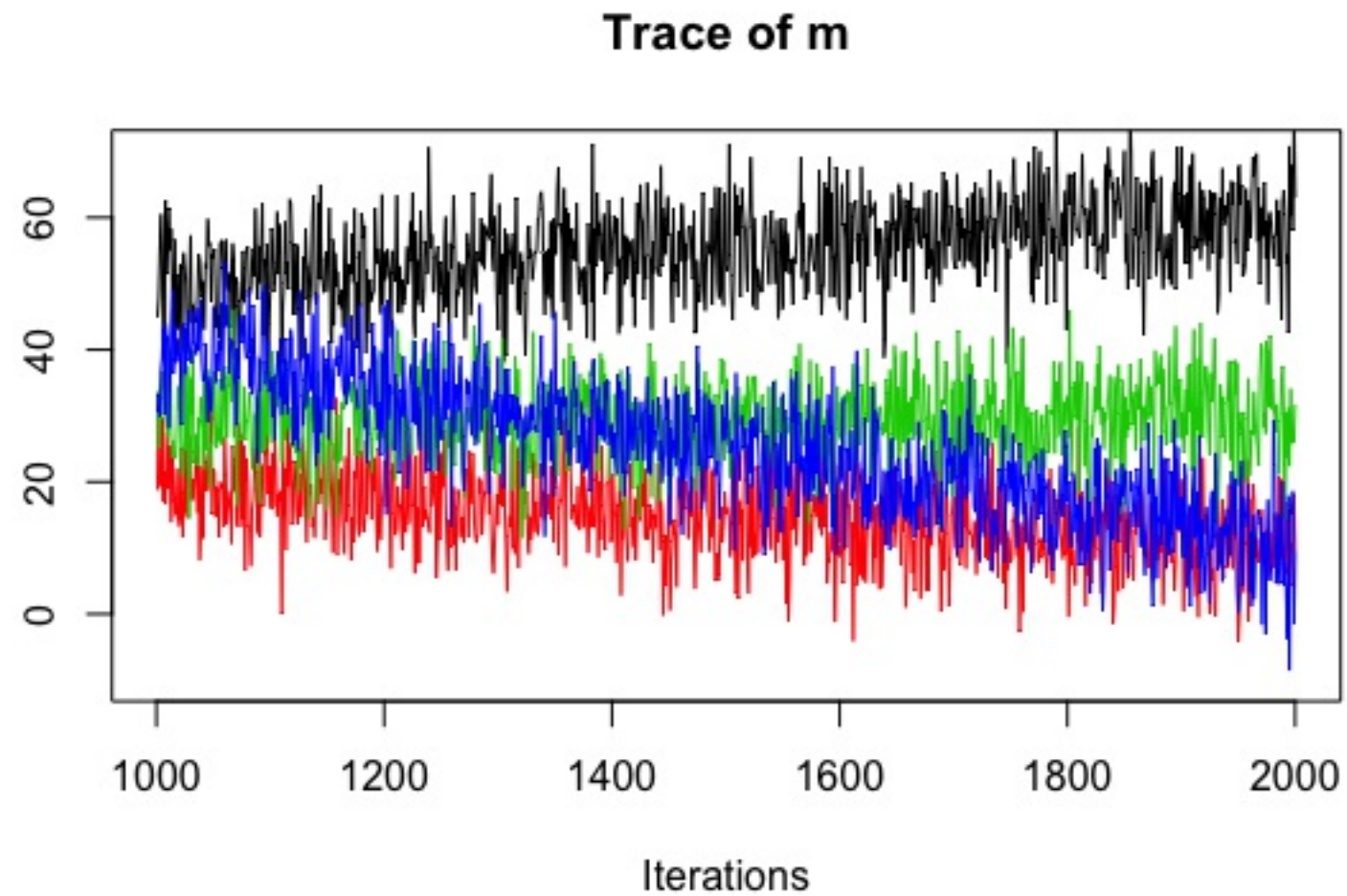
Diagnostic: multiple chains

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



Diagnostic: multiple chains

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



Diagnostic: standard error

```
> 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

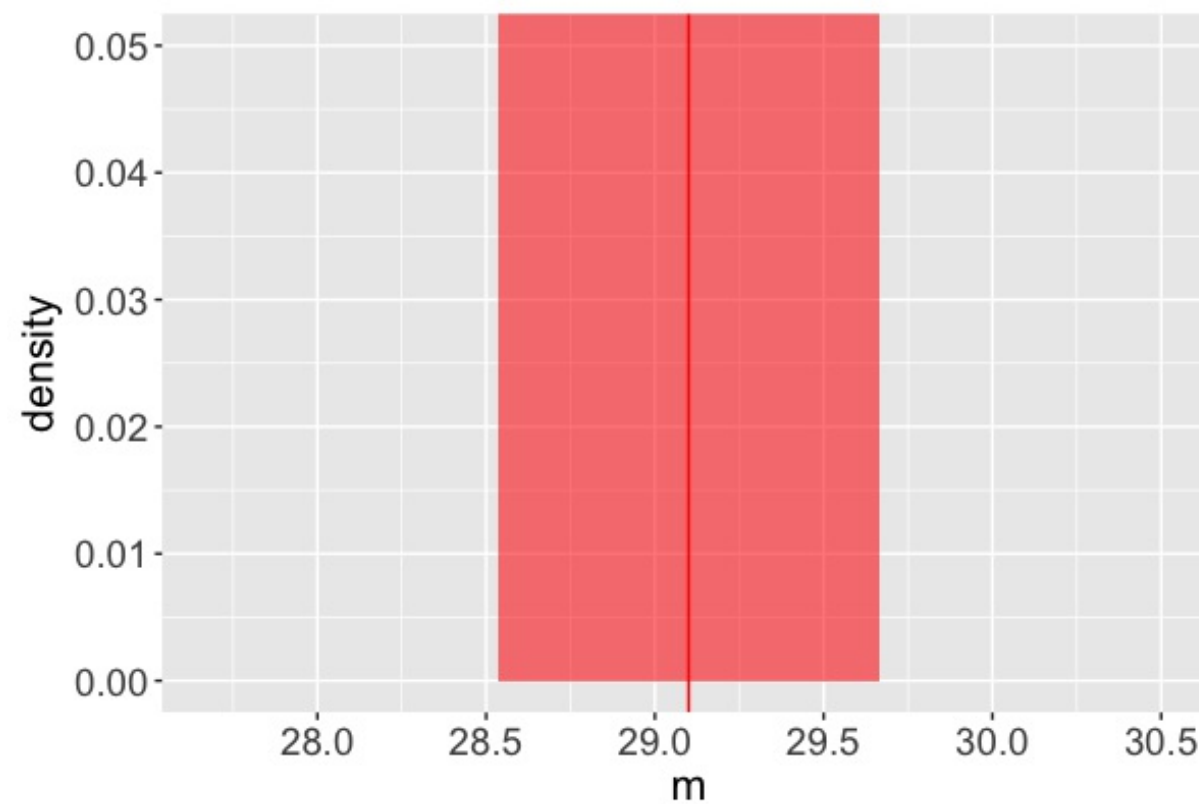
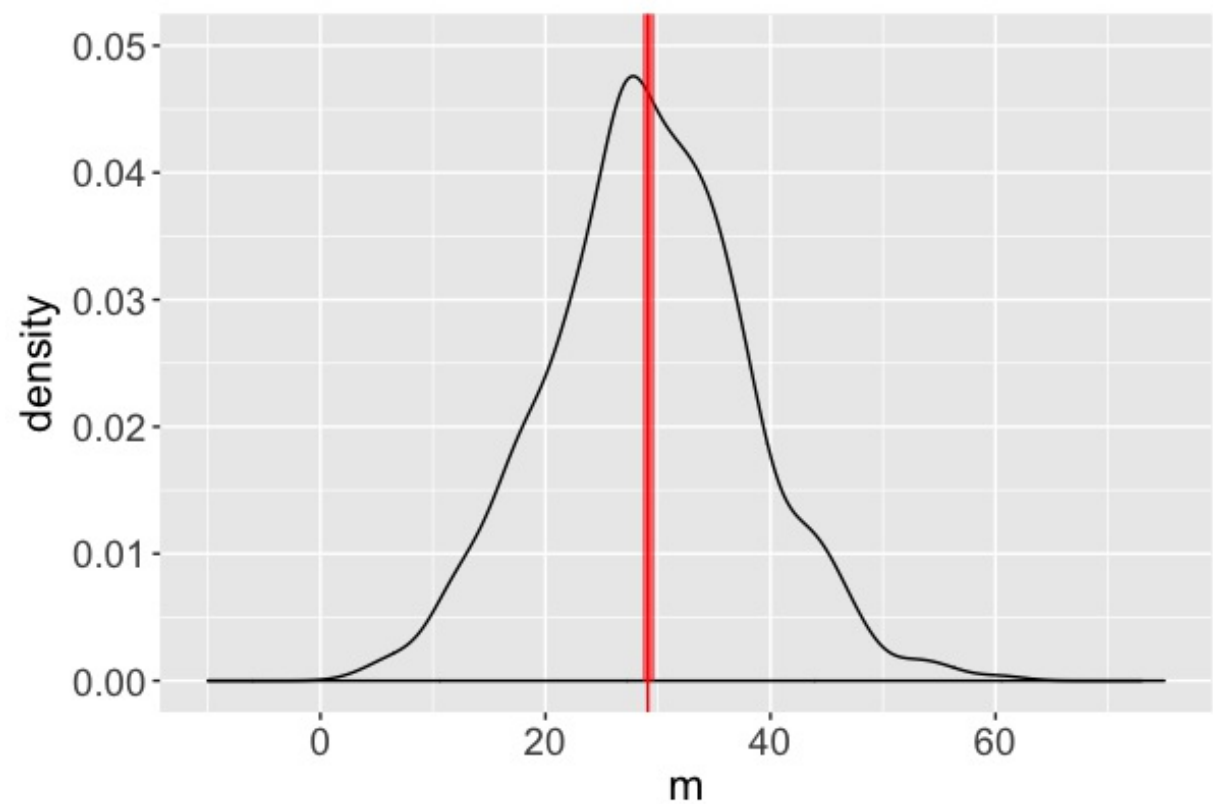
2. Quantiles **for** each variable:

	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

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

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", .RNG.seed = 1989))
```



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