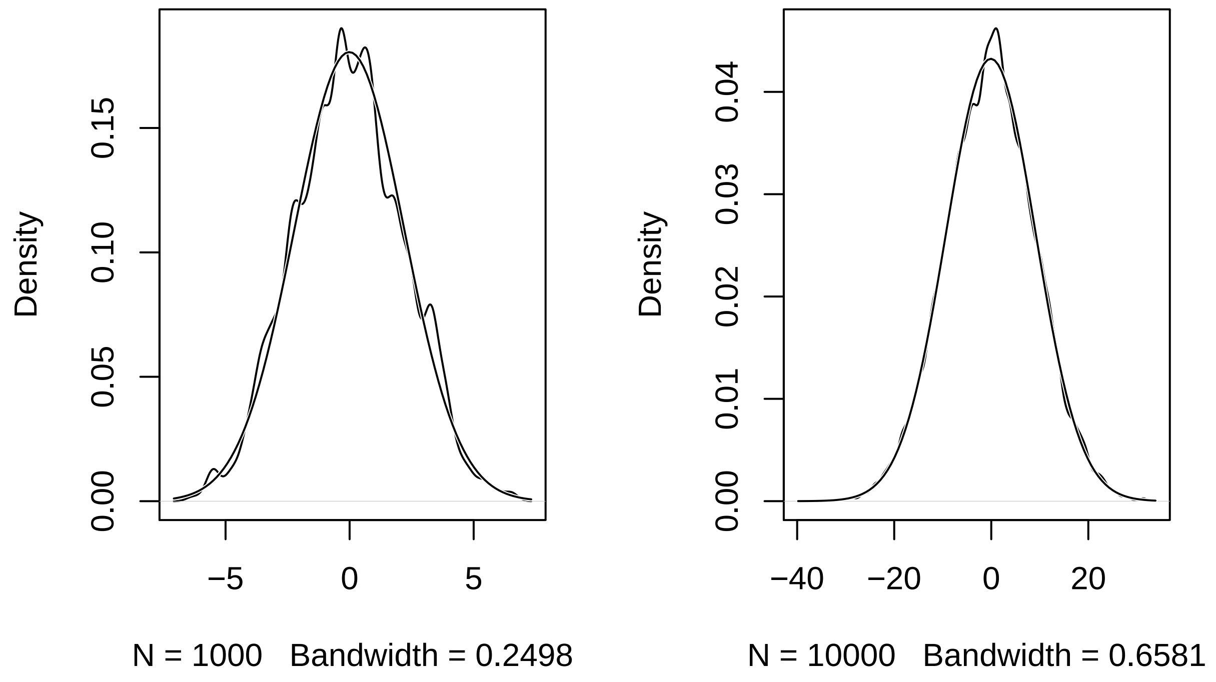
4 - Linear Models

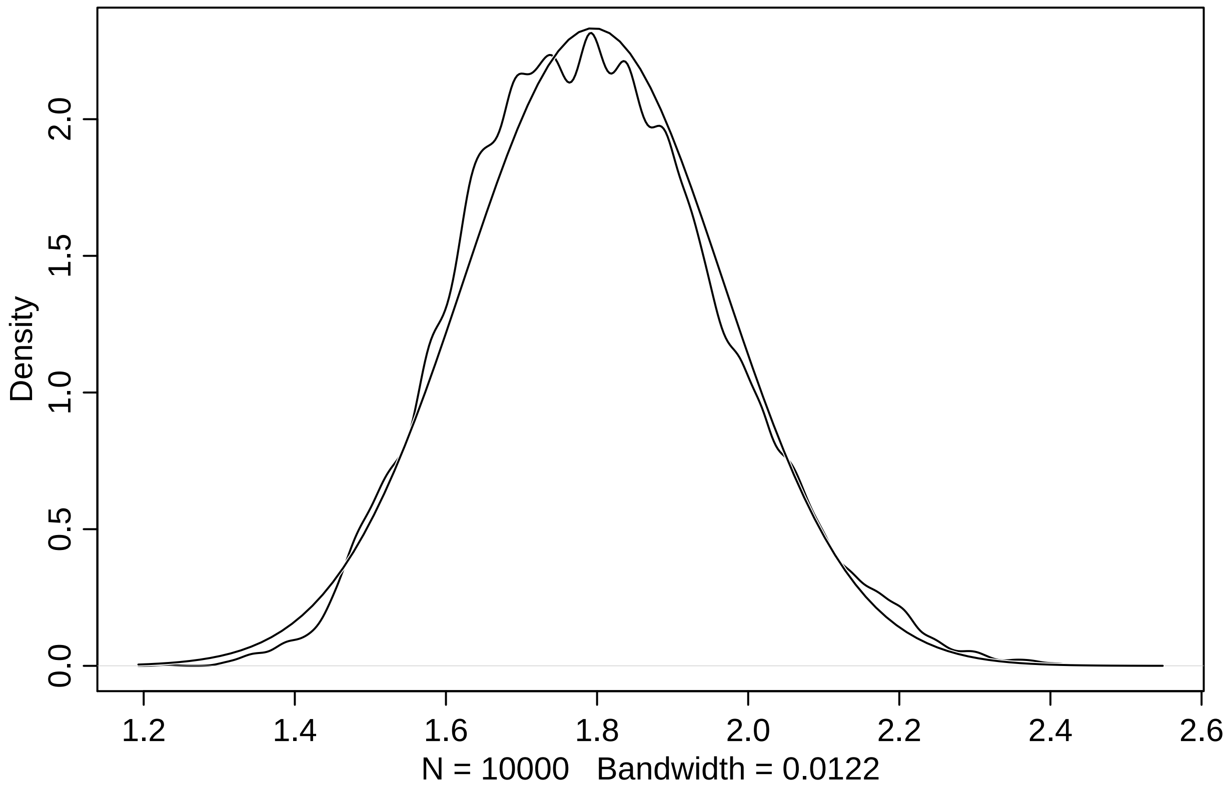
4.1.1. Normal by addition

```r
# 4.1
pos <- replicate(1000, sum(runif(16, -1, 1)))
par(mfrow=c(1, 2))
dens(pos, norm.comp = T)
dens(replicate(10000, sum(runif(256, -1, 1))), norm.comp = T)
```

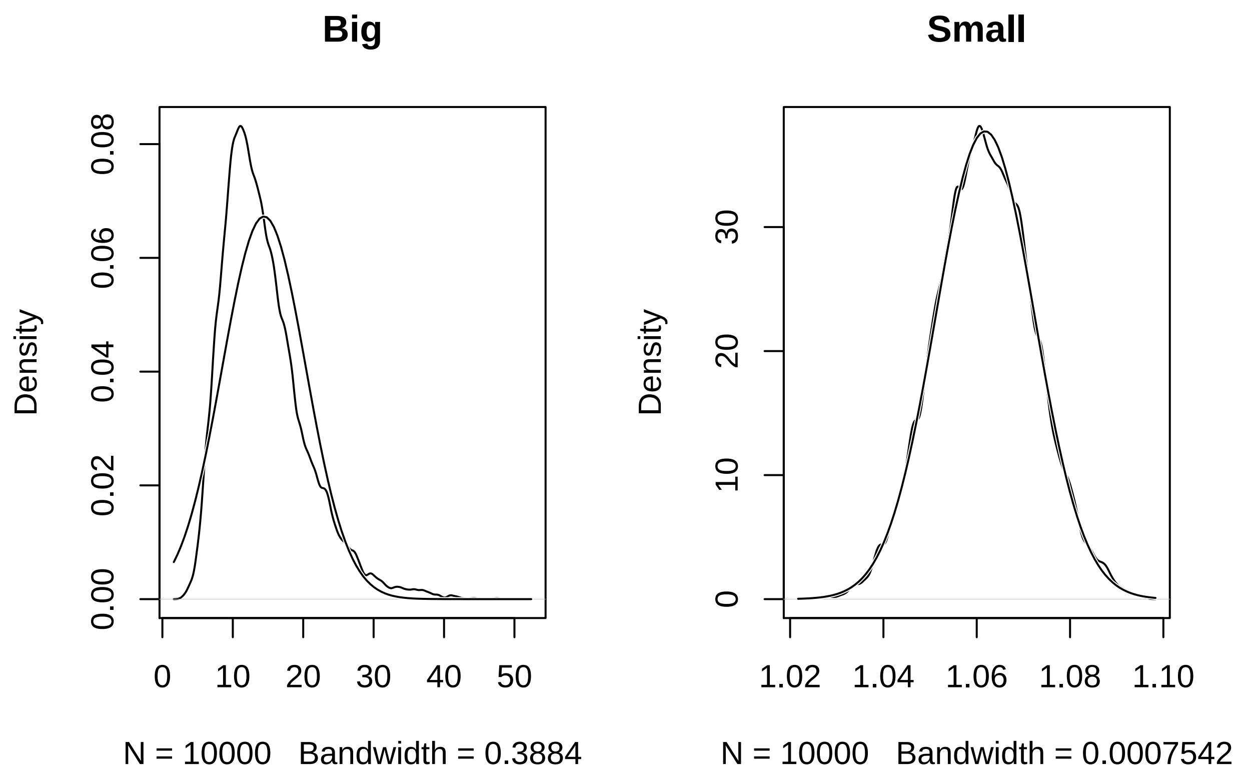


4.1.2. Normal by multiplication

```r
# 4.2
dens(replicate(1e4, prod(1 + runif(12, 0, 0.1))), norm.comp = T)
```

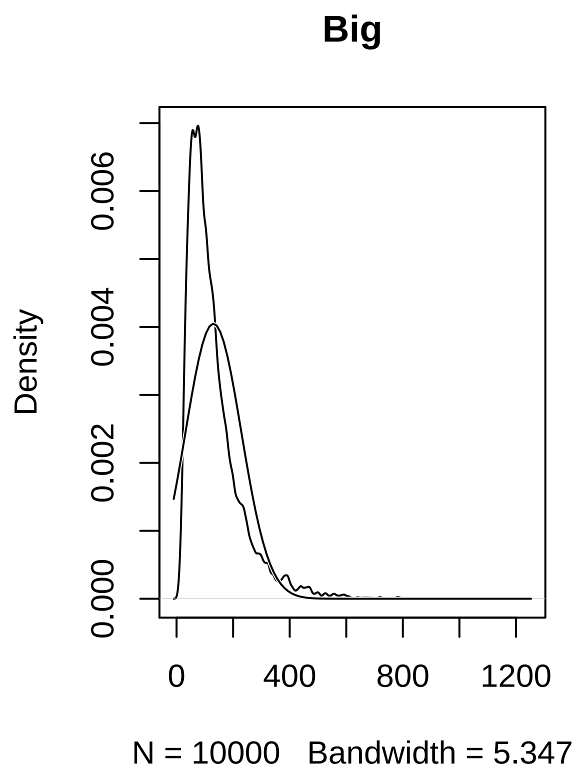


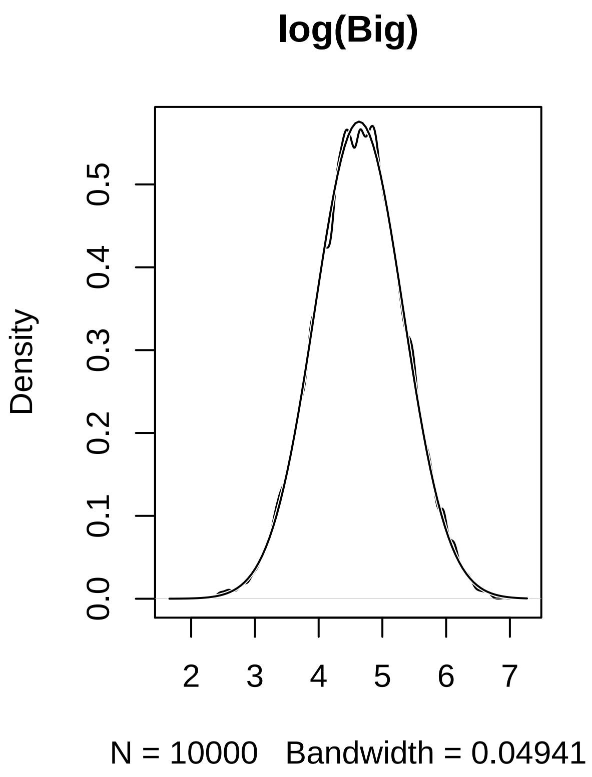
```r
# 4.4
big <- replicate(1e4, prod(1 + runif(12, 0, 0.5)))
small <- replicate(1e4, prod(1 + runif(12, 0, 0.01)))
par(mfrow=c(1, 2))
dens(big, norm.comp = T, main = "Big")
dens(small, norm.comp = T, main = "Small")
```



Normal by log-multiplication

```
# 4.5
big <- replicate(1e4, prod(1 + runif(12, 0, 1)))
log_big <- log(big)
par(mfrow=c(1, 2))
dens(big, norm.comp = T, main = "Big")
dens(log_big, norm.comp = T, main = "log(Big)")
```





4.3 A Gaussian model of height

```
# 4.7
library(rethinking)
data(Howell1)
d <- Howell1
```

```
# 4.8
str(d)
```

```
## 'data.frame':    544 obs. of  4 variables:
##  $ height: num  152 140 137 157 145 ...
##  $ weight: num  47.8 36.5 31.9 53 41.3 ...
##  $ age   : num  63 63 65 41 51 35 32 27 19 54 ...
##  $ male  : int  1 0 0 1 0 1 0 1 0 1 ...
```

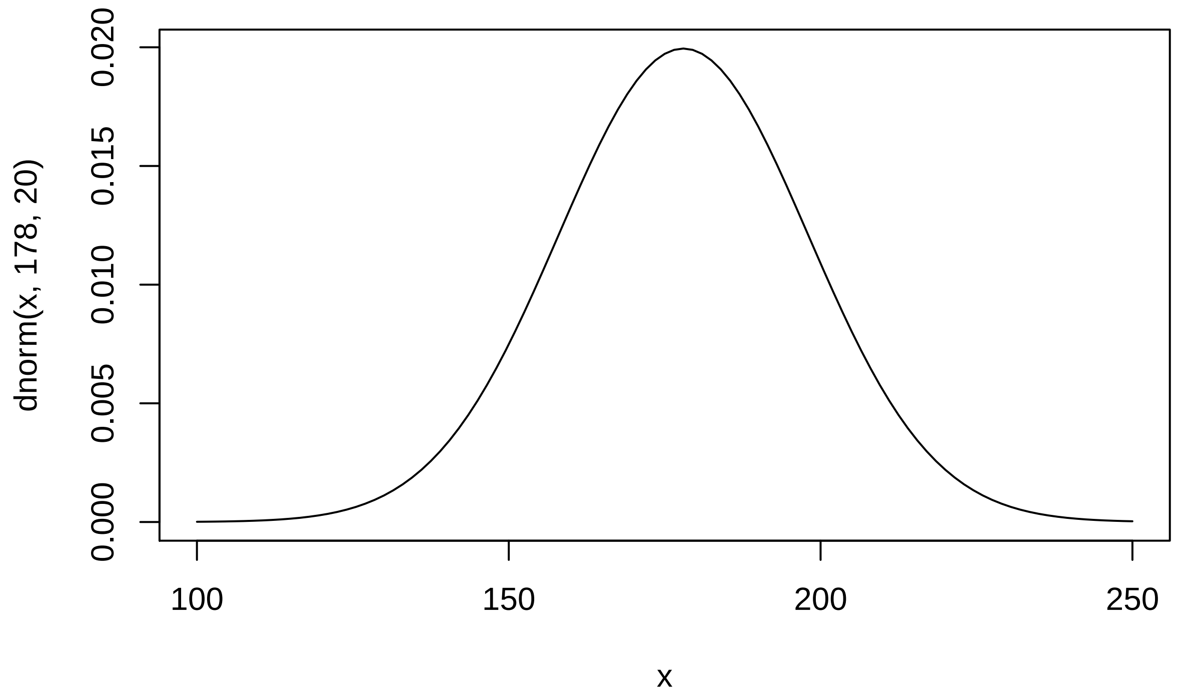
We want heights of adults only (352 rows):

```
# 4.10
d2 <- d[d$age >= 18, ]
```

4.3.2 The model

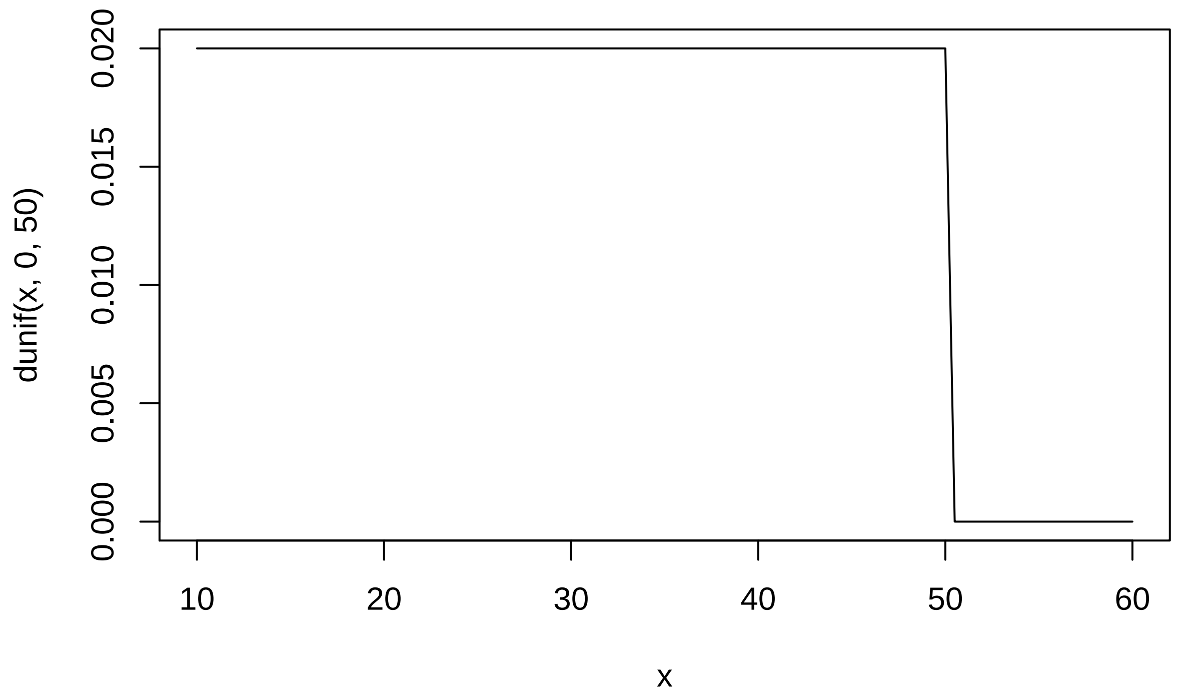
Height mean:

```r
# 4.11
curve(dnorm(x, 178, 20), from=100, to=250)
```

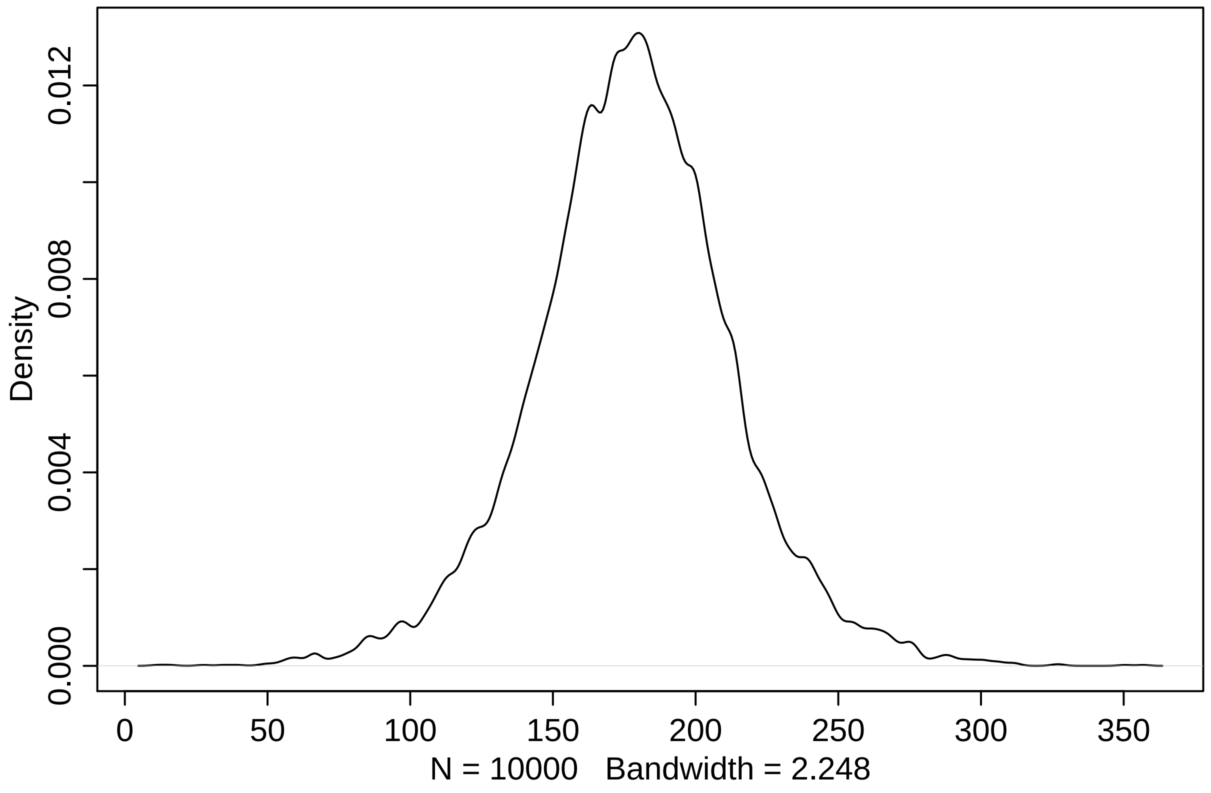


Height standard deviation:

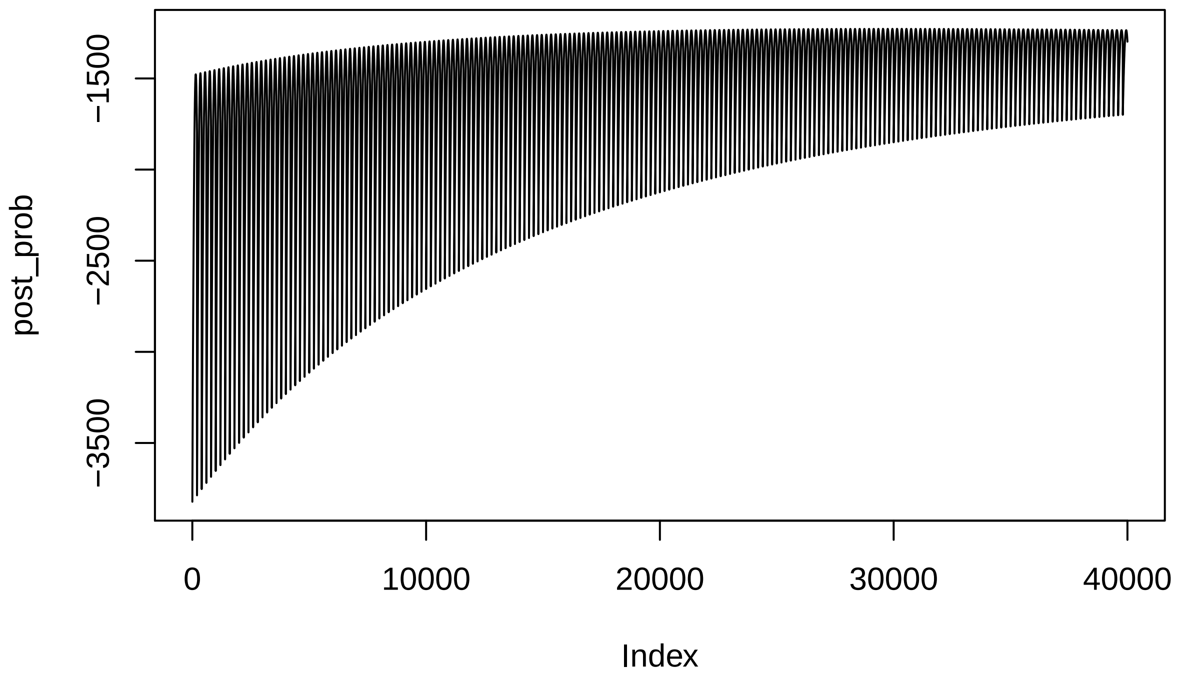
```r
# 4.12
curve(dunif(x, 0, 50), from=10, to=60)
```



```
# 4.13
sample_mu <- rnorm(1e4, 178, 20)
sample_sigma <- runif(1e4, 0, 50)
prior_h <- rnorm(1e4, sample_mu, sample_sigma)
dens(prior_h)
```

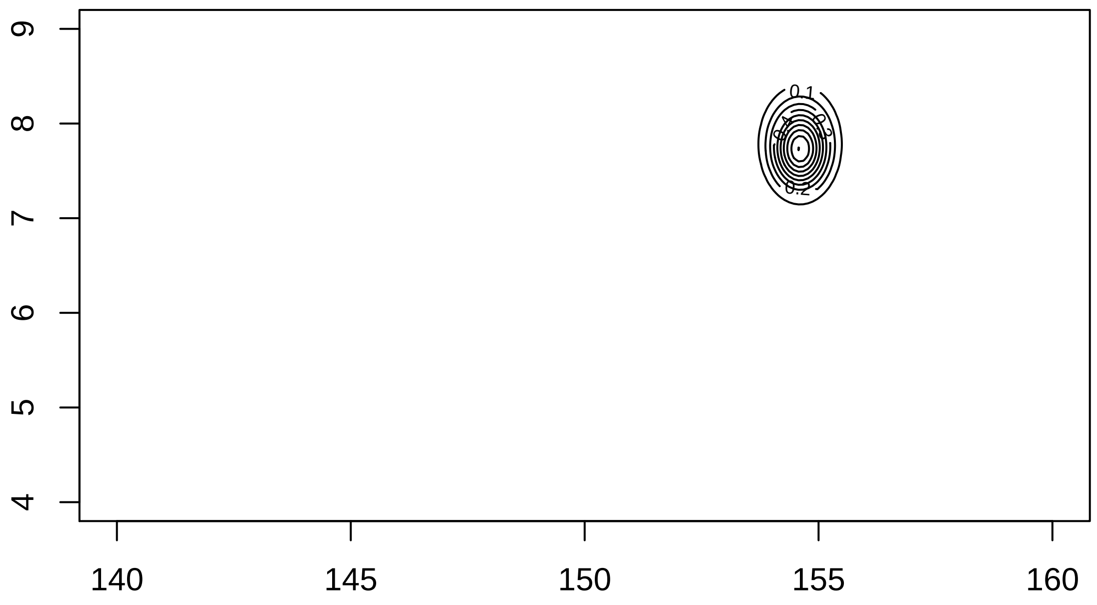


```
# 4.14
mu_list <- seq(from=140, to=160, length.out=200)
sigma_list <- seq(from=4, to=9, length.out=200)
post <- expand.grid(mu=mu_list, sigma=sigma_list)
post_ll <- sapply(1:nrow(post), function(i) sum(dnorm(
  d2$height,
  mean=post$mu[i],
  sd=post$sigma[i],
  log=T
)))
post_prob <- post_ll + dnorm(post$mu, 178, 20, T) + dunif(post$sigma, 0, 50, T)
plot(post_prob, type="l")
```

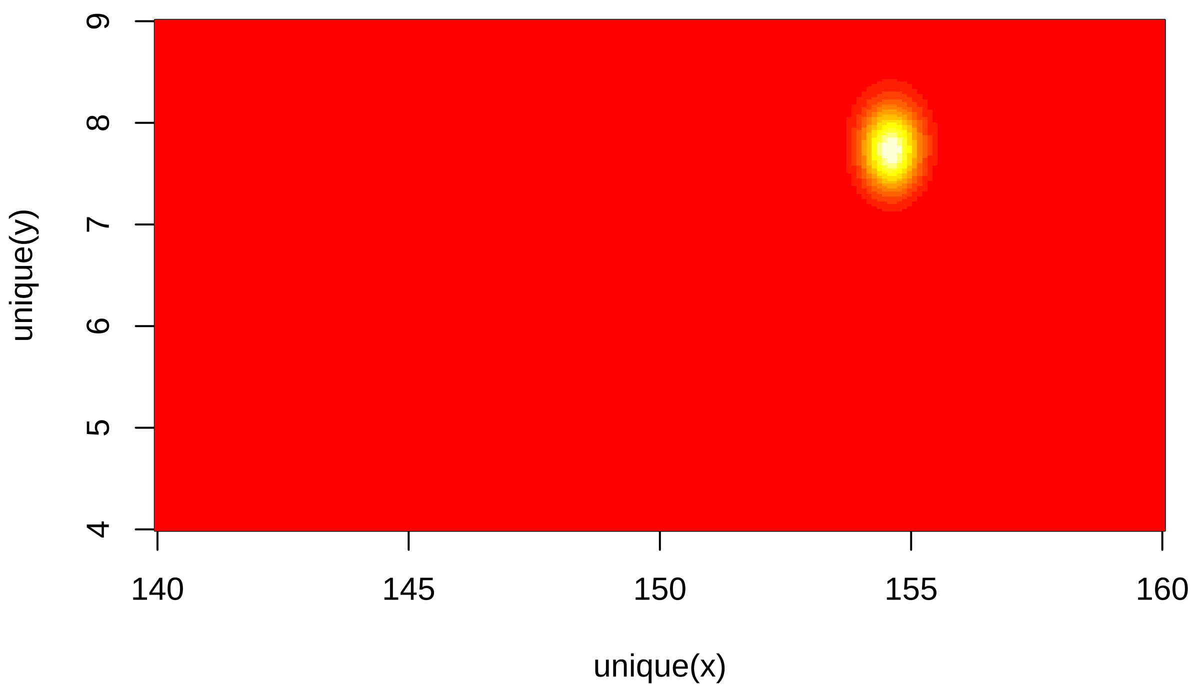


```
post_prob <- exp(post_prob - max(post_prob))
```

```
# 4.15
contour_xyz(post$mu, post$sigma, post_prob)
```



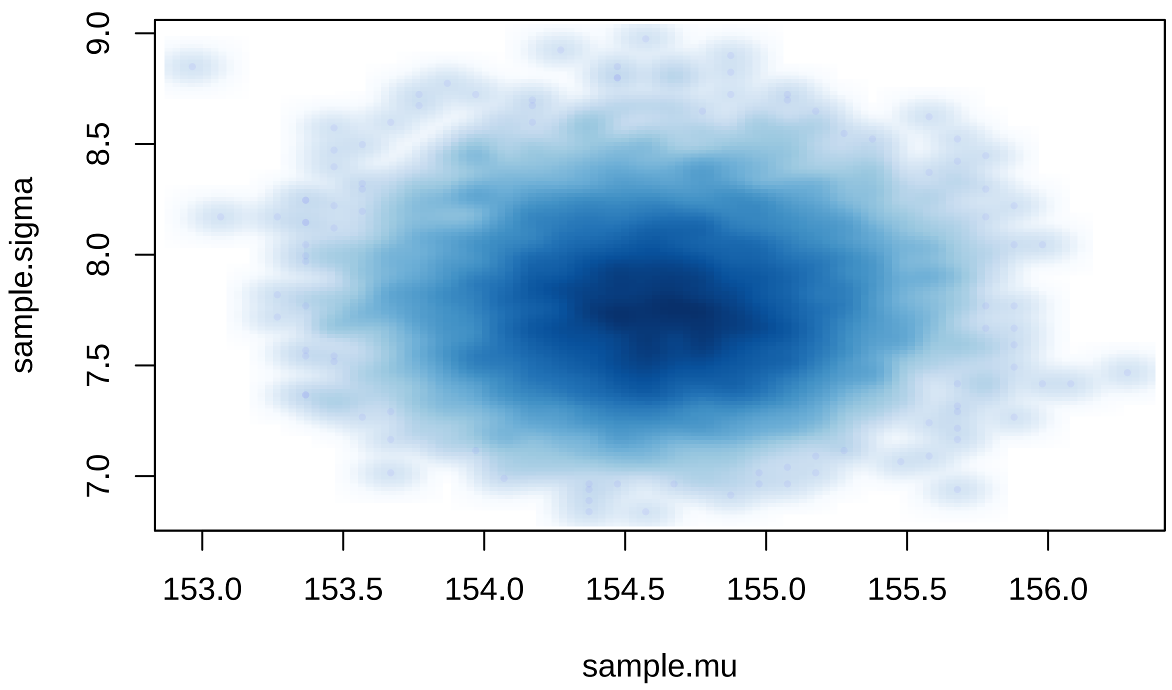
```r
# 4.16
image_xyz(post$mu, post$sigma, post_prob)
```



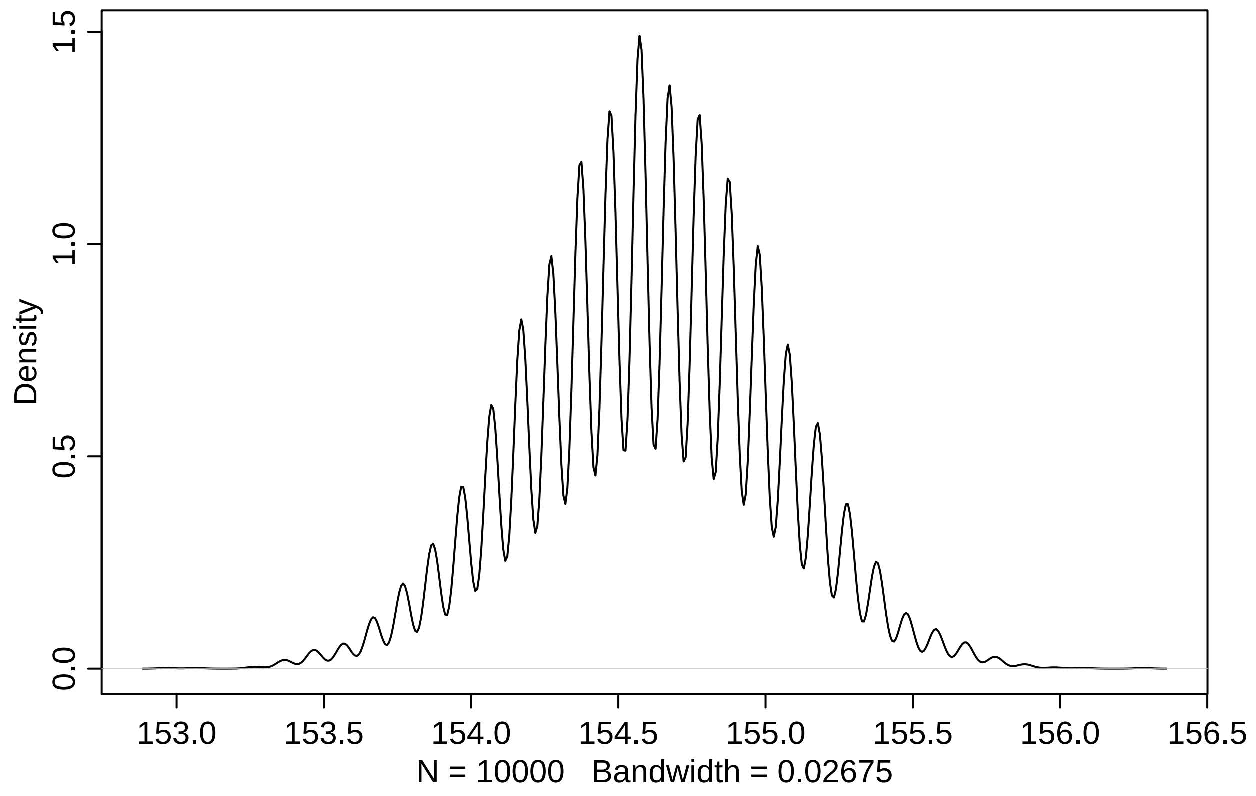
4.3.4 Sampling from the posterior

```
# 4.17
sample.rows <- sample(1:nrow(post), size=1e4, replace = T, prob = post_prob)
sample.mu <- post$mu[sample.rows]
sample.sigma <- post$sigma[sample.rows]
```

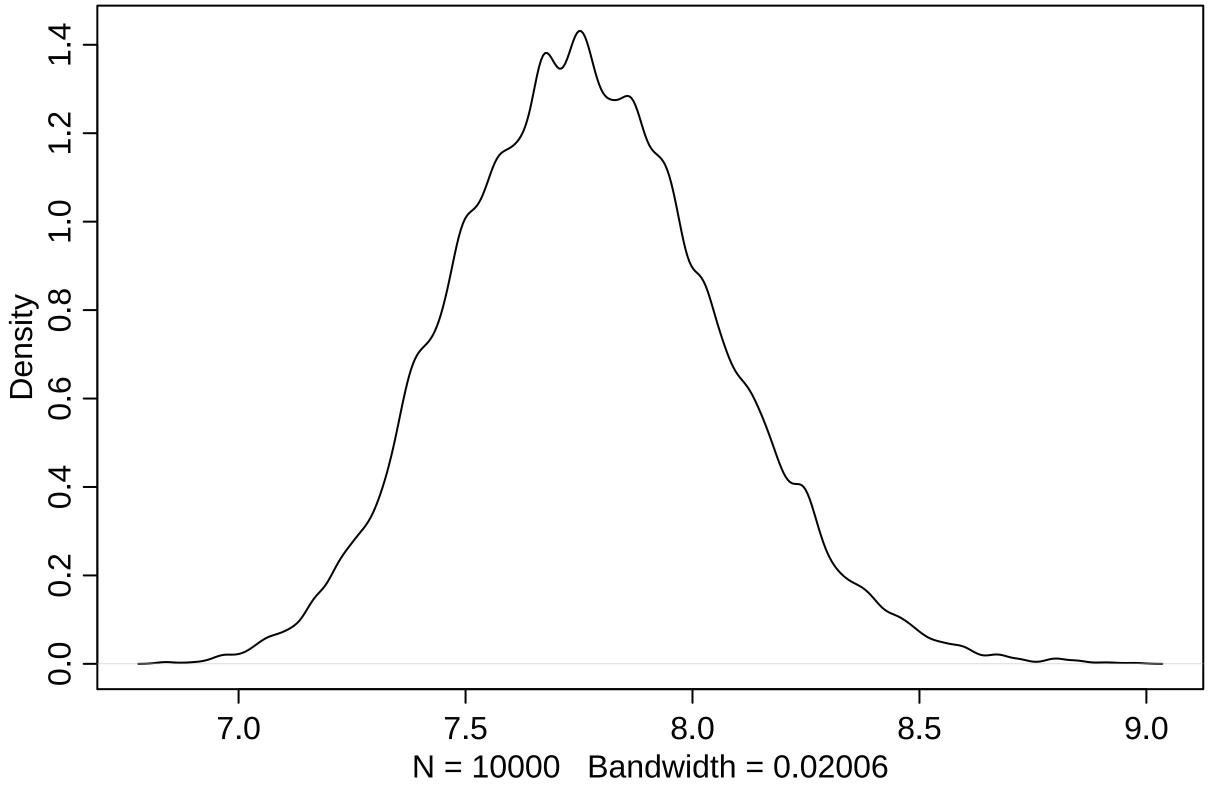
```
# 4.18
smoothScatter(sample.mu, sample.sigma, cex=0.5, pch=16, col=col.alpha(rangi2, 0.1))
```



```
# 4.19
dens(sample.mu)
```



```
dens(sample.sigma)
```



```
# 4.20
HPDI(sample.mu)
```

```
##     |0.89    0.89|
## 153.8693 155.1759
```

```
HPDI(sample.sigma)
```

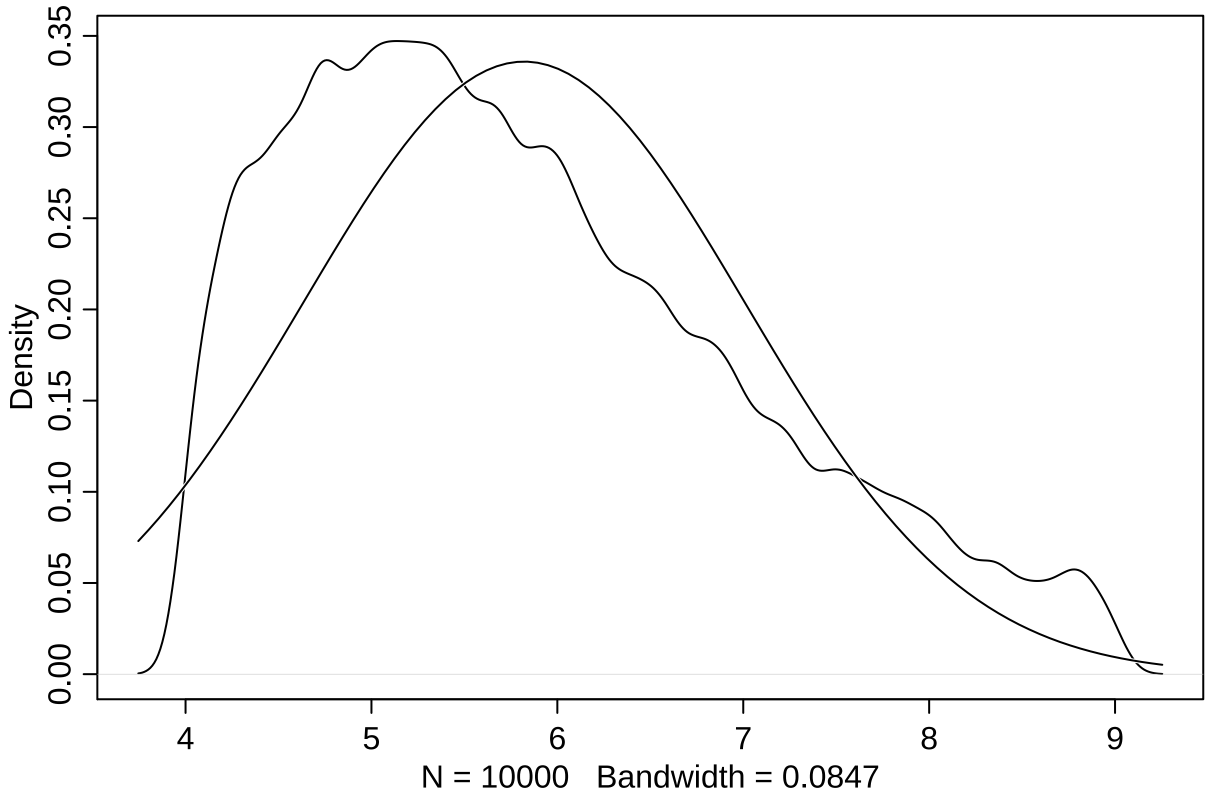
```
##     |0.89    0.89|
## 7.341709 8.246231
```

Smaller Sample

To illustrate the posterior is not always Guassian in shape.

```
# 4.22
d3 <- sample(d2$height, size=10)

small.post_ll <- sapply(1:nrow(post), function(i) sum(dnorm(d3, mean=post$mu[i], sd=post$sigma[i], log='

small.post_product <- small.post_ll + dnorm(post$mu, 178, 20, T) + dunif(post$sigma, 0, 50, T)

small.post_proba <- exp(small.post_product - max(small.post_product))

small.sample.rows <- sample(1:nrow(post), size=1e4, replace = T, prob=small.post_proba)

small.sample.mu <- post$mu[small.sample.rows]
small.sample.sigma <- post$sigma[small.sample.rows]
```

```
# 4.23
dens(small.sample.sigma, norm.comp = T)
```



4.3.5. Fitting the model with *map*

map finds the values of μ and σ that maximize the posterior probability.

```
# 4.25
model.list <- alist(
  height ~ dnorm(mu, sigma),
  mu ~ dnorm(178, 20),
  sigma ~ dunif(0, 50)
)
```

```
# 4.26
model.solved <- map(model.list, data=d2)
```

```
# 4.27
precis(model.solved)
```

```
##         Mean StdDev   5.5%  94.5%
## mu    154.61   0.41 153.95 155.27
## sigma   7.73   0.29   7.27   8.20
```

Compare to HPDI intervals from above.

```
HPDI(sample.mu)
```

```
##    |0.89    0.89|
## 153.8693 155.1759
```

```
HPDI(sample.sigma)
```

```
##    |0.89    0.89|
## 7.341709 8.246231
```

We've calculated the HPDI intervals using the grid approximation. The model is solved via a quadratic approximation. The quadratic approximation does a very good in identifying the 89% intervals.

It works because the posterior is approximately Gaussian.

The priors we used so far are very weak. We'll splice in a more informative prior for μ.

```
#4.29
model.solved_narrow_mu <- map (
  alist(
    height ~ dnorm(mu, sigma),
    mu ~ dnorm(178, 0.1),
    sigma ~ dunif(0, 50)
  ),
  data=d2)
precis(model.solved_narrow_mu)
```

```
##         Mean StdDev   5.5%  94.5%
## mu    177.86   0.10 177.70 178.02
## sigma  24.52   0.93  23.03  26.00
```

The estimate for μ has hardly moved off the prior. The estimate for σ has changed a lot, even though we didn't change the prior at all. Our machine had to make μ and σ fit out data. Since μ is very concerntrated around 178, the machine had to change σ to accomodate the data.

4.3.6. Sampling from a *map* fit.

Variance-covariance matrix:

```
# 4.30
vcov(model.solved)
```

```
##                  mu        sigma
## mu    0.1697396732 0.0002180523
## sigma 0.0002180523 0.0849058990
```

We can split it into (1) vector of variances, and (2) the correlation matrix:

```
# 4.31
diag(vcov(model.solved))
```

```
##        mu     sigma
## 0.1697397 0.0849059
```

```
cov2cor(vcov(model.solved))
```

```
##                 mu       sigma
## mu    1.000000000 0.001816352
## sigma 0.001816352 1.000000000
```

Sampling from the posterior:

```
# 4.34
coef(model.solved)
```

```
##         mu      sigma
## 154.607025   7.731334
```

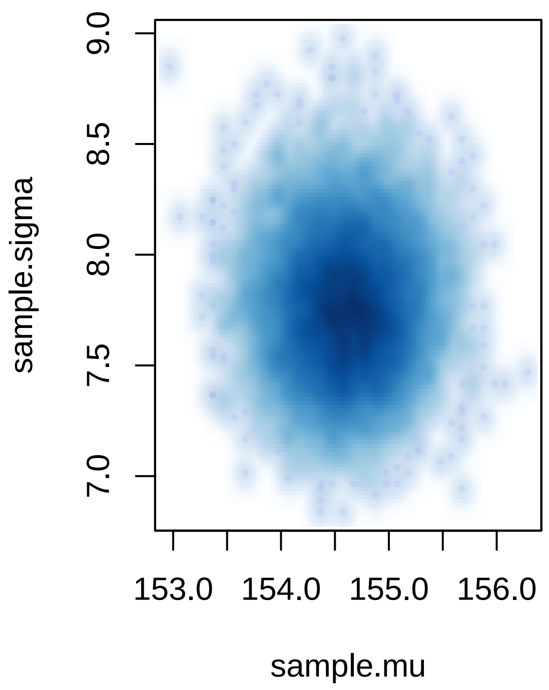
```
library(MASS)
post <- mvrnorm(n=1e4, mu=coef(model.solved), Sigma=vcov(model.solved))
post = data.frame(post)
head(post)
```

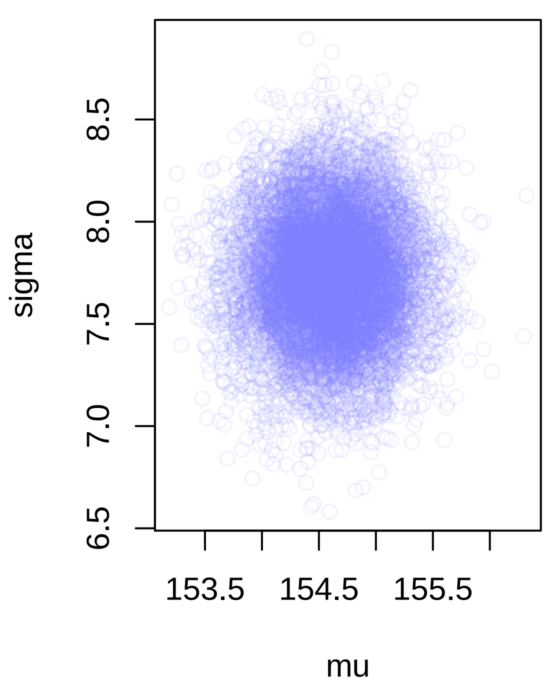
```
##         mu    sigma
## 1 154.1712 7.565005
## 2 153.9953 7.766587
## 3 155.4626 7.465068
## 4 153.7310 7.409712
## 5 154.0156 7.667090
## 6 154.8036 7.617207
```

```
# 4.33
precis(post)
```

```
##         Mean StdDev  |0.89  0.89|
## mu    154.60   0.41 153.97 155.26
## sigma   7.73   0.29   7.28   8.21
```

```
par(mfrow=c(1, 2))
smoothScatter(sample.mu, sample.sigma, cex=0.5, pch=16, col=col.alpha(rangi2, 0.1))
plot(post, col=col.alpha(rangi2, 0.1))
```



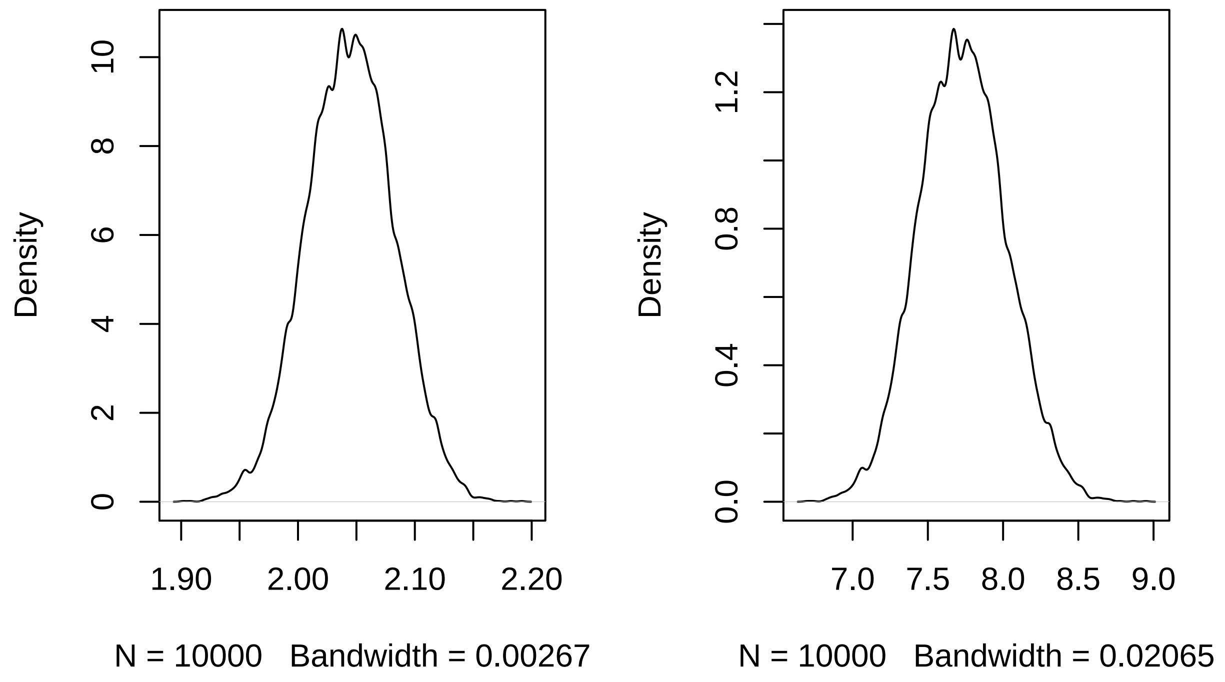


#### Getting sigma right

The quadratic assumption for σ may be not correct. In this case it's better to estimate $\log(\sigma)$ instead, because the distriubtion of *log* will be much closer to Guassian.

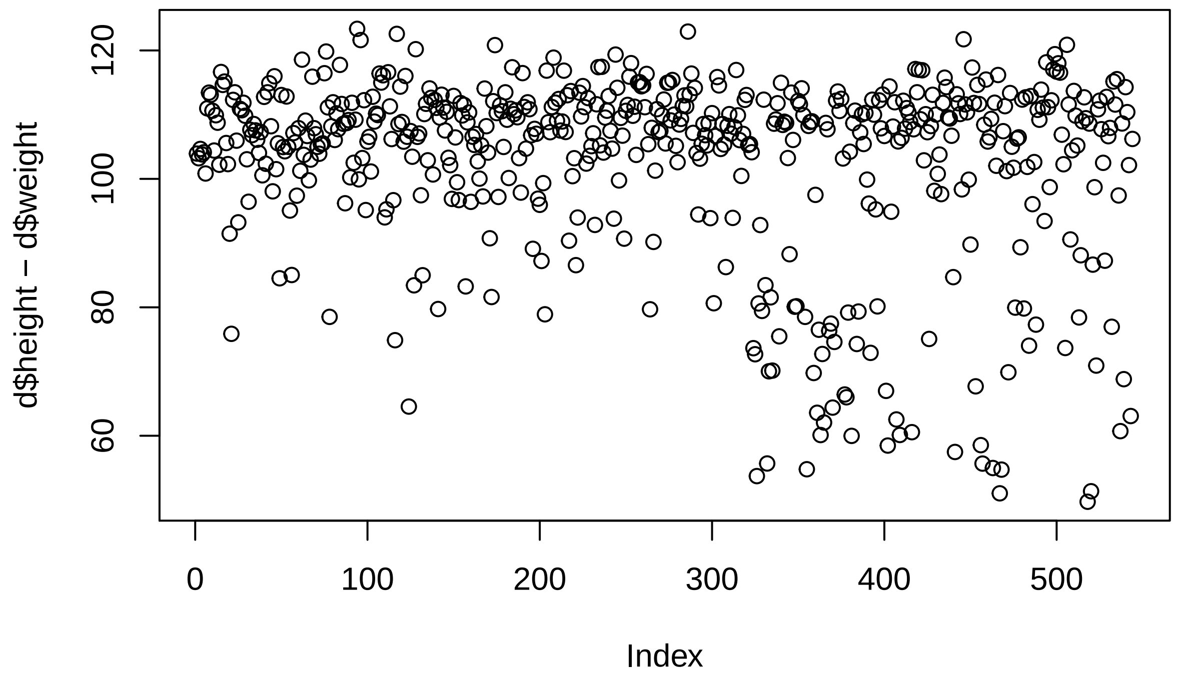
```
# 4.35
model.solved_log_sigma <- map(
  alist(
    height ~ dnorm(mu, exp(log_sigma)),
    mu ~ dnorm(178, 20),
    log_sigma ~ dnorm(2, 10)
  ),
  data = d2
)
```

```
# 4.36
post <- mvrnorm(n=1e4, mu=coef(model.solved_log_sigma), Sigma=vcov(model.solved_log_sigma))
post <- data.frame(post)
par(mfrow=c(1, 2))
dens(post$log_sigma)
dens(exp(post$log_sigma))
```



4.4. Adding a predictor

```
#4.37
plot(d$height - d$weight)
```



4.4.2. Fitting the model

```
# 4.38
model.linear_m43 <- map(
  alist(
    height ~ dnorm(mu, sigma),
    mu <- a + b * weight,
    a ~ dnorm(178, 100),
    b ~ dnorm (0, 10),
    sigma ~ dunif(0, 50)
  ),
  data=d2
)
```

```
# 4.40
precis(model.linear_m43, corr=T)
```

```
##         Mean StdDev   5.5%  94.5%     a     b sigma
## a     113.90   1.91 110.86 116.95  1.00 -0.99     0
## b       0.90   0.04   0.84   0.97 -0.99  1.00     0
## sigma   5.07   0.19   4.77   5.38  0.00  0.00     1
```

Centering

```
# 4.42
d2$weight_centered <- d2$weight - mean(d2$weight)
```

```
# 4.43
model.linear_m44 <- map(
  alist(
    height ~ dnorm(a + b * weight_centered, sigma),
    a ~ dnorm(178, 100),
    b ~ dnorm(0, 10),
    sigma ~ dunif(0, 50)
  )
  , data=d2
)
```

```
# 4.44
precis(model.linear_m44, corr=T)
```

```
##         Mean StdDev   5.5%  94.5% a b sigma
## a     154.60   0.27 154.17 155.03 1 0     0
## b       0.91   0.04   0.84   0.97 0 1     0
## sigma   5.07   0.19   4.77   5.38 0 0     1
```

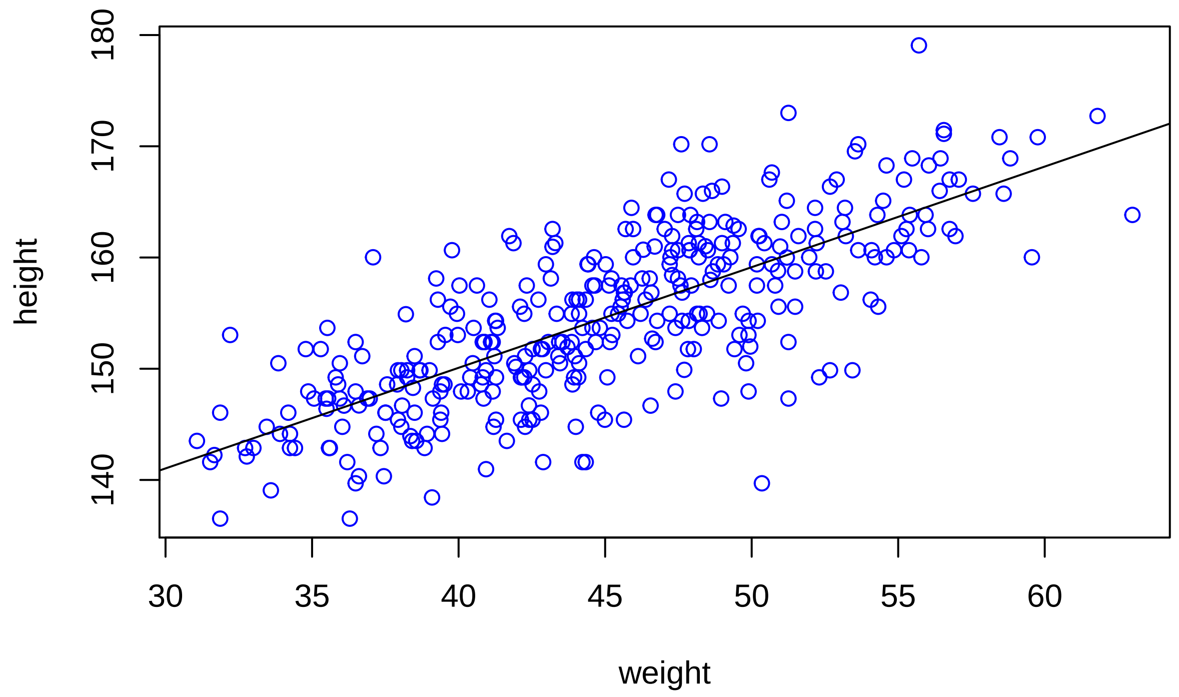
The new estimate for α is now the same as mean:

```
mean(d2$height)
```

```
## [1] 154.5971
```

Let's plot the posterior against the data:

```
# 4.45
plot(height ~ weight, data=d2, col="blue")
abline(a=coef(model.linear_m43)["a"], b = coef(model.linear_m43)["b"])
```



This line is just the posterior mean, the most plausible line. There are infinite regression lines from the posterior.

Let's extract some examples from the model:

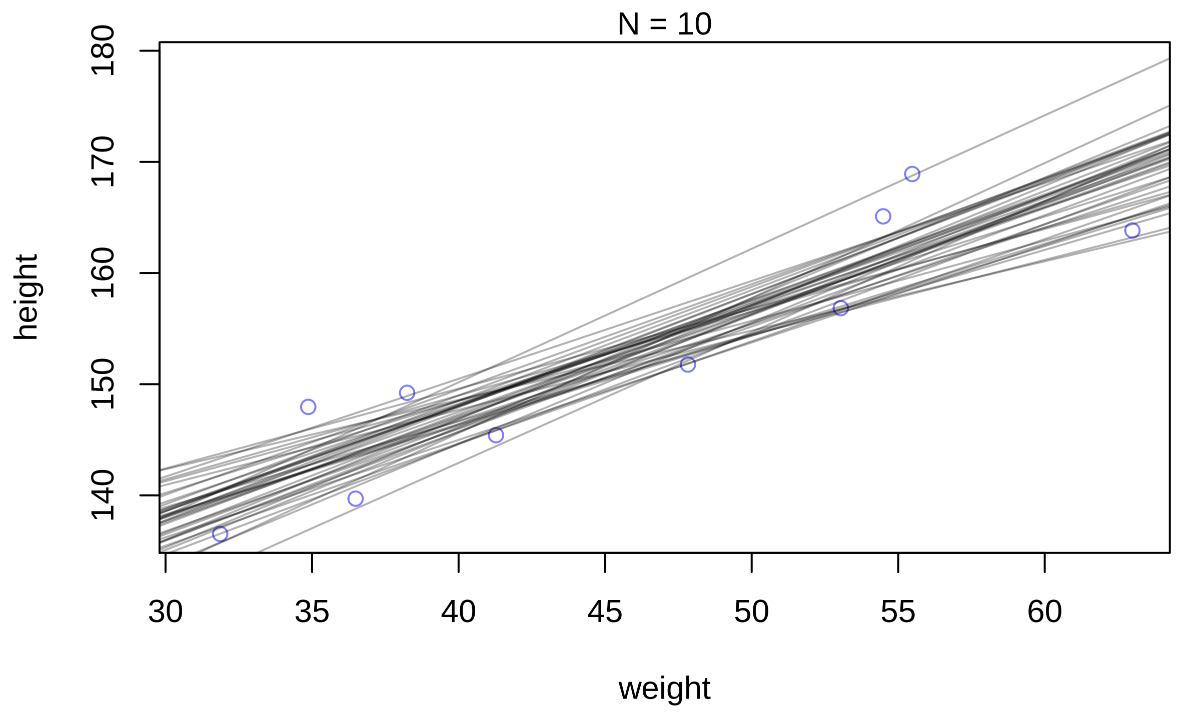
```
# 4.46
post <- mvrnorm(n=1e4, mu=coef(model.linear_m43), Sigma=vcov(model.linear_m43))
post <- data.frame(post)
post[1:6, ]
```

```
##          a         b    sigma
## 1 115.2913 0.8697019 5.132483
## 2 113.5741 0.9090416 5.242504
## 3 114.4479 0.9006979 4.827414
## 4 111.9728 0.9499098 5.375142
## 5 112.9567 0.9276711 4.818484
## 6 115.4724 0.8805881 5.046249
```

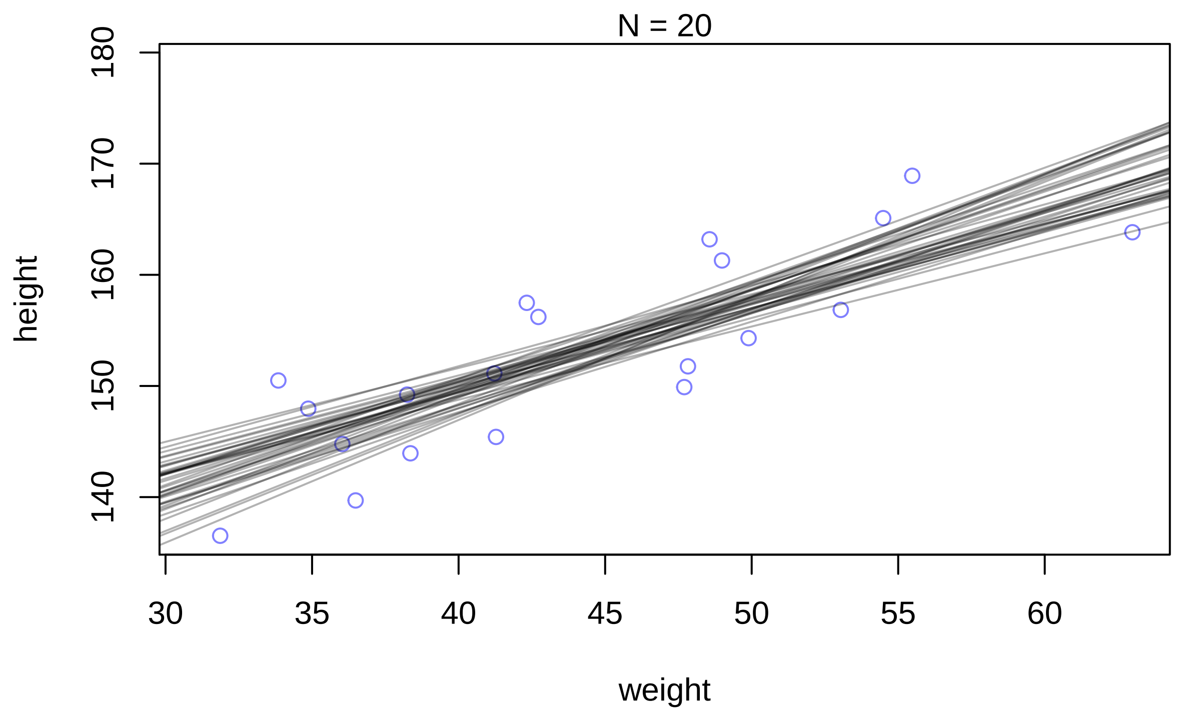
Let's try on the small data set first to see how the regression lines vary:

```
# 4.48

ablines_N = function (N_) {
  library(rethinking)
  data(Howell1)
  d <- Howell1
  d2 <- d[d$age >= 18, ]

  dN <- d2[1:N_,]
  mN <- map(
    alist(
      height ~ dnorm(a + b * weight, sigma),
      a ~ dnorm(178, 100),
      b ~ dnorm(0, 10),
      sigma ~ dunif(0, 50)
    ),
    data = dN
  )
  post <- mvrnorm(n=40, mu=coef(mN), Sigma=vcov(mN))
  post <- data.frame(post)

  plot(dN$weight, dN$height, xlim=range(d2$weight), ylim=range(d2$height),
       col=rangi2, xlab="weight", ylab="height")
  mtext(concat("N = ", N_))

  for (i in 1:nrow(post))
    abline(a=post$a[i], b=post$b[i], col=col.alpha("black", 0.3))
}
```

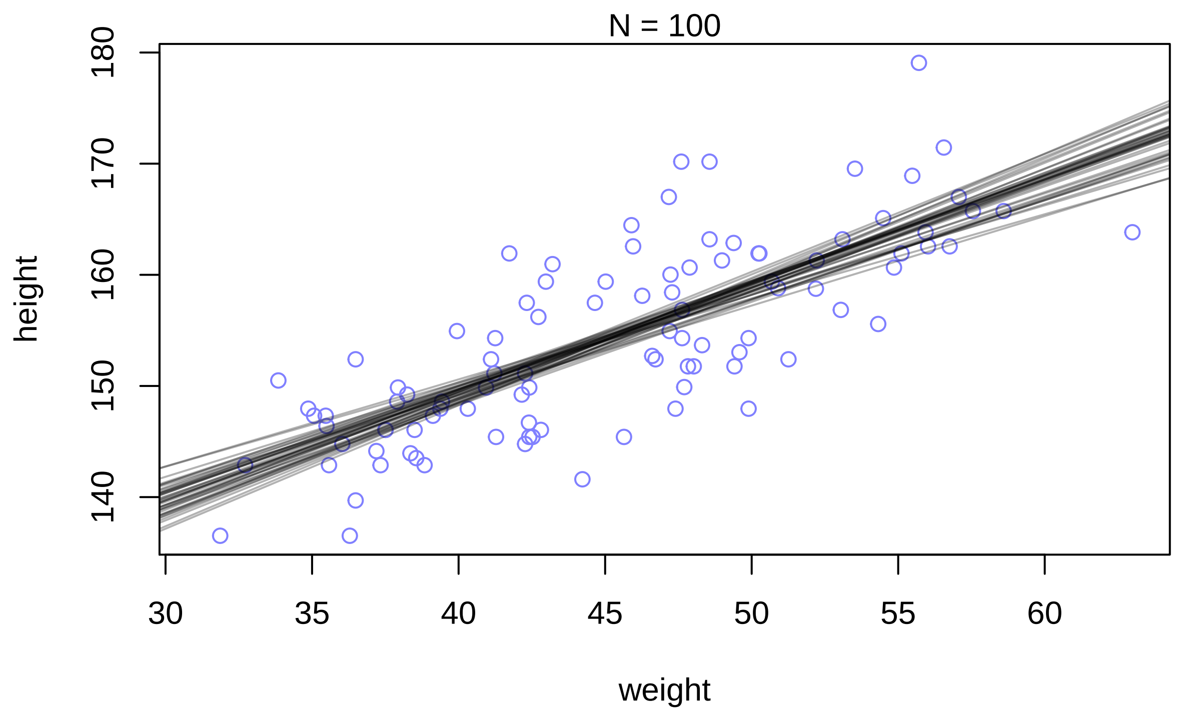
```
ablines_N(10)
```



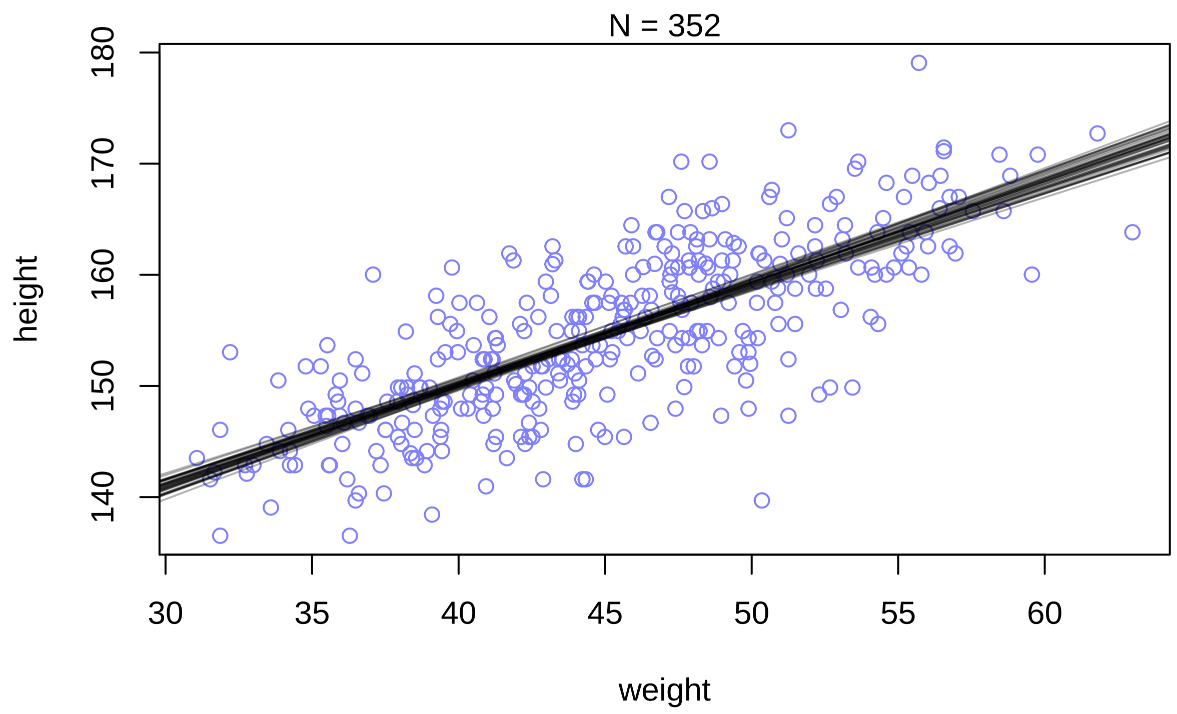
```
ablines_N(20)
```



```r
ablines_N(100)
```

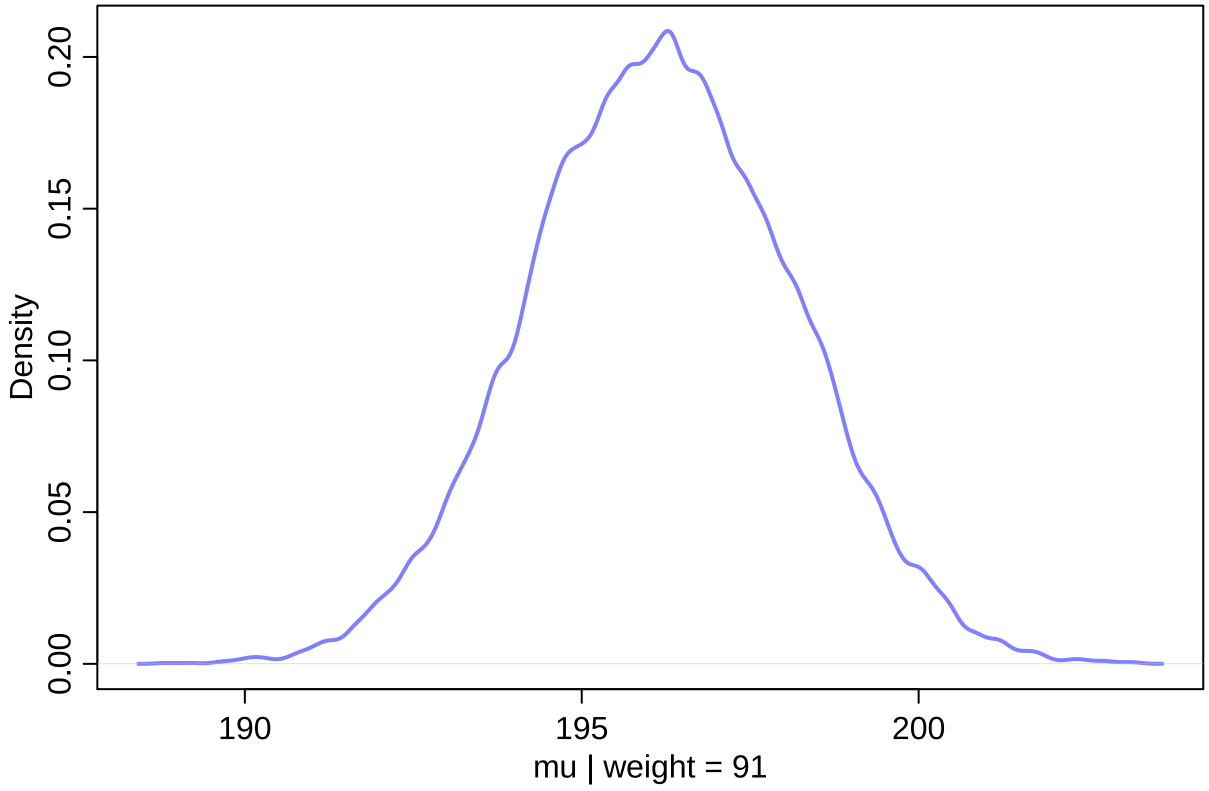


```r
ablines_N(352)
```



Let's predict value for individual who weighs 91 kg:

```
# 4.50
mu_at_50 <- post$a + post$b * 91
dens(mu_at_50, col=rangi2, lwd=2, xlab = "mu | weight = 91")
```



```
# 4.52
HPDI(mu_at_50, prob=0.89)
```

```
##    |0.89    0.89|
## 193.1921 199.3791
```

```
# 4.53
mu <- link(model.linear_m43)
```

```
## [ 100 / 1000 ]
[ 200 / 1000 ]
[ 300 / 1000 ]
[ 400 / 1000 ]
[ 500 / 1000 ]
[ 600 / 1000 ]
[ 700 / 1000 ]
[ 800 / 1000 ]
[ 900 / 1000 ]
[ 1000 / 1000 ]
```

```
str(mu)
```

```
##  num [1:1000, 1:352] 157 157 157 157 157 ...
```

Compute the distribution for each weight:

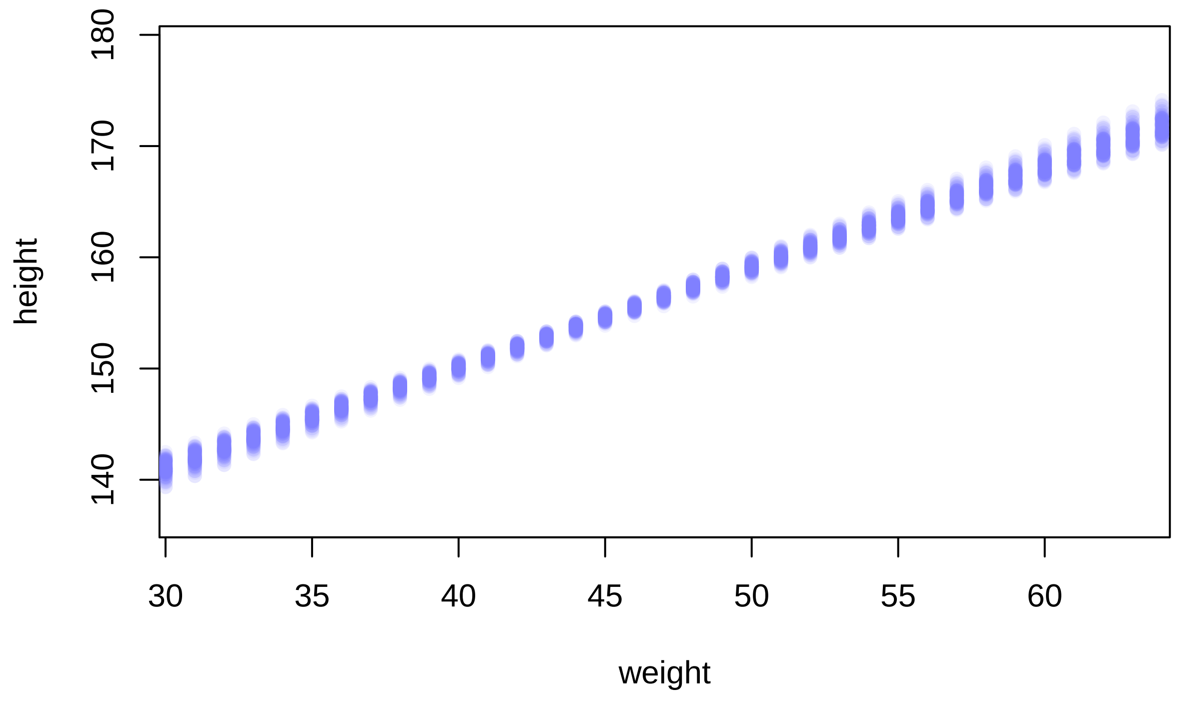
```
# 4.54
weight_seq <- seq(from=25, to=100, by=1)
mu <- link(model.linear_m43, data=data.frame(weight=weight_seq))
```

```
## [ 100 / 1000 ]
[ 200 / 1000 ]
[ 300 / 1000 ]
[ 400 / 1000 ]
[ 500 / 1000 ]
[ 600 / 1000 ]
[ 700 / 1000 ]
[ 800 / 1000 ]
[ 900 / 1000 ]
[ 1000 / 1000 ]
```

```
str(mu)
```

```
##  num [1:1000, 1:76] 137 136 137 137 135 ...
```

```
# 4.55
plot(height ~ weight, d2, type="n")
for (i in 1:100)
  points(weight_seq, mu[i,], pch=16, col=col.alpha(rangi2, 0.1))
```


height
weight