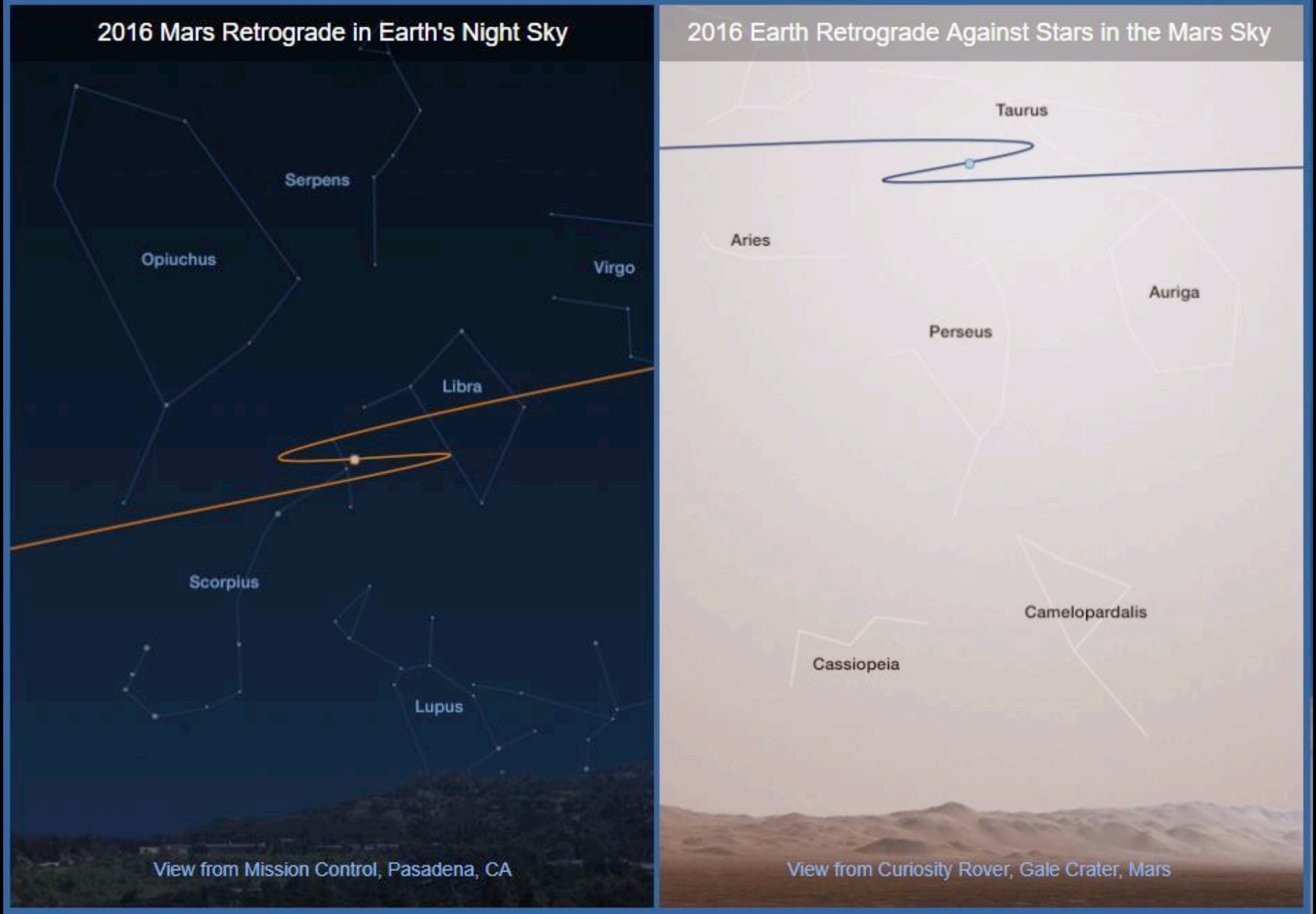
Statistical Rethinking

2022

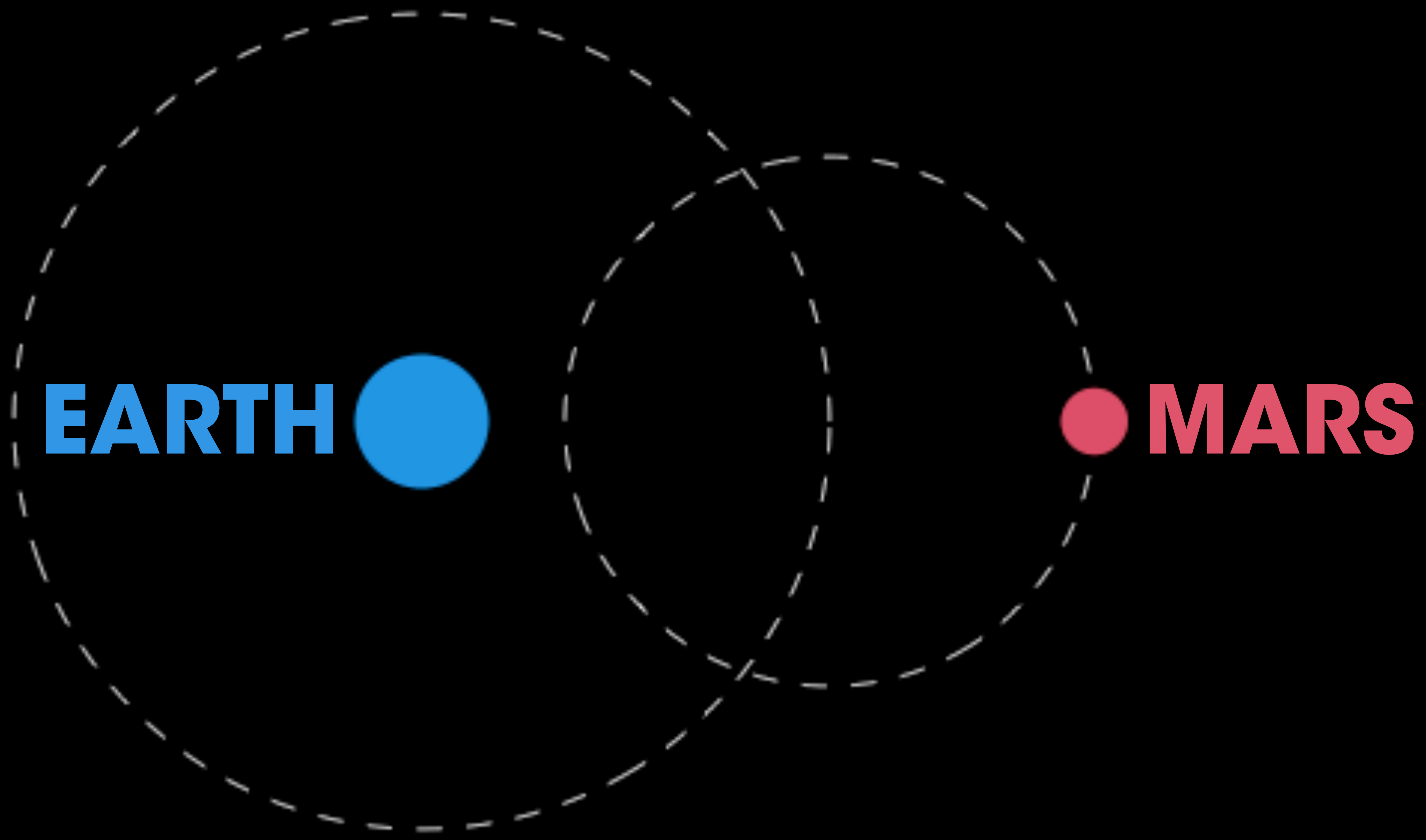
03: Geocentric Models

Mars: June 2020 until Feb 2021 — Tunç Tezel — https://vimeo.com/user48630149


2016 Mars Retrograde in Earth's Night Sky
Serpens
Opiuchus
Virgo
Libra
Scorpius
Lupus
View from Mission Control, Pasadena, CA
2016 Earth Retrograde Against Stars in the Mars Sky
Taurus
Aries
Auriga
Perseus
Camelopardalis
Cassiopeia
View from Curiosity Rover, Gale Crater, Mars

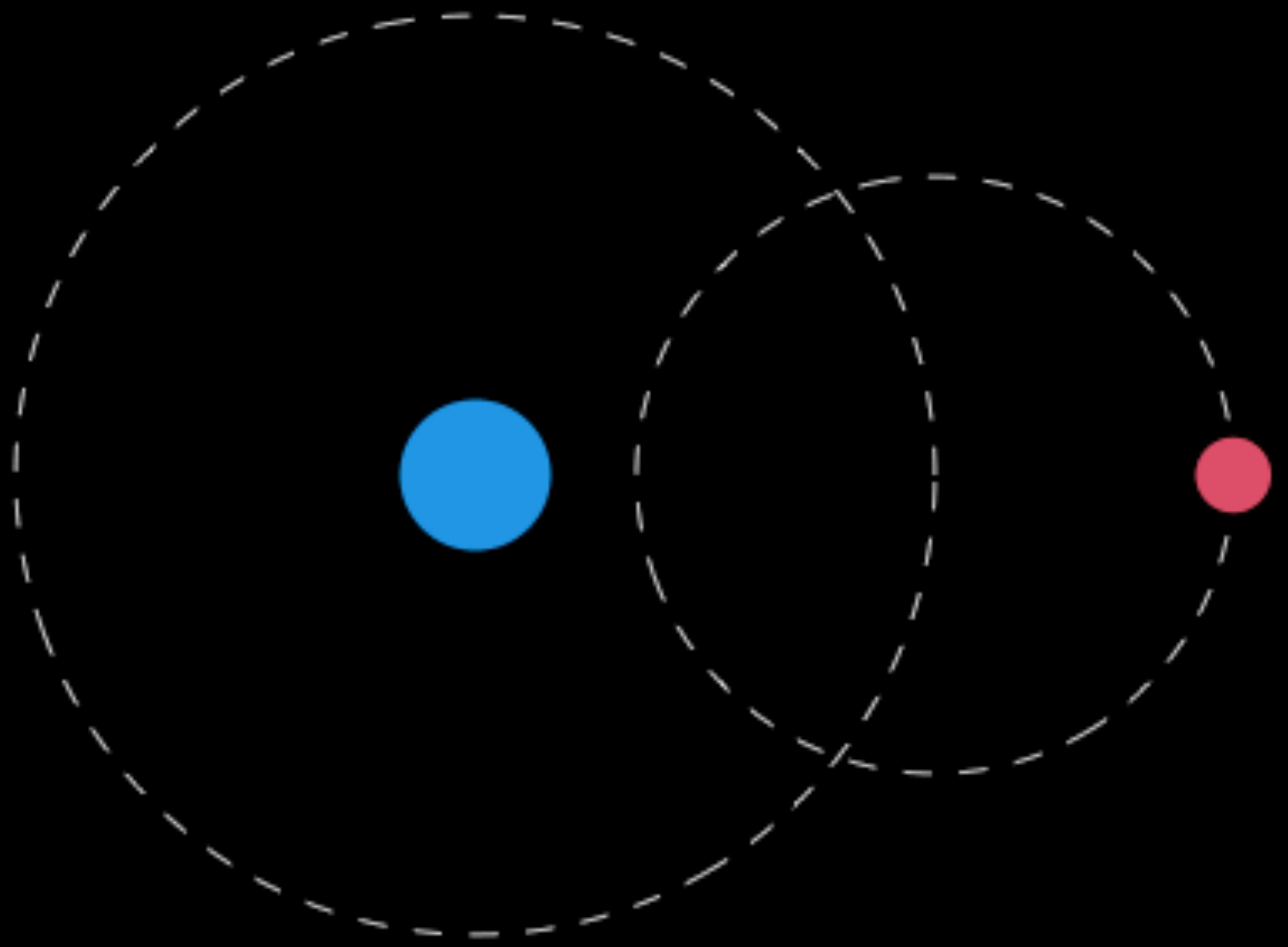

MARS
EARTH

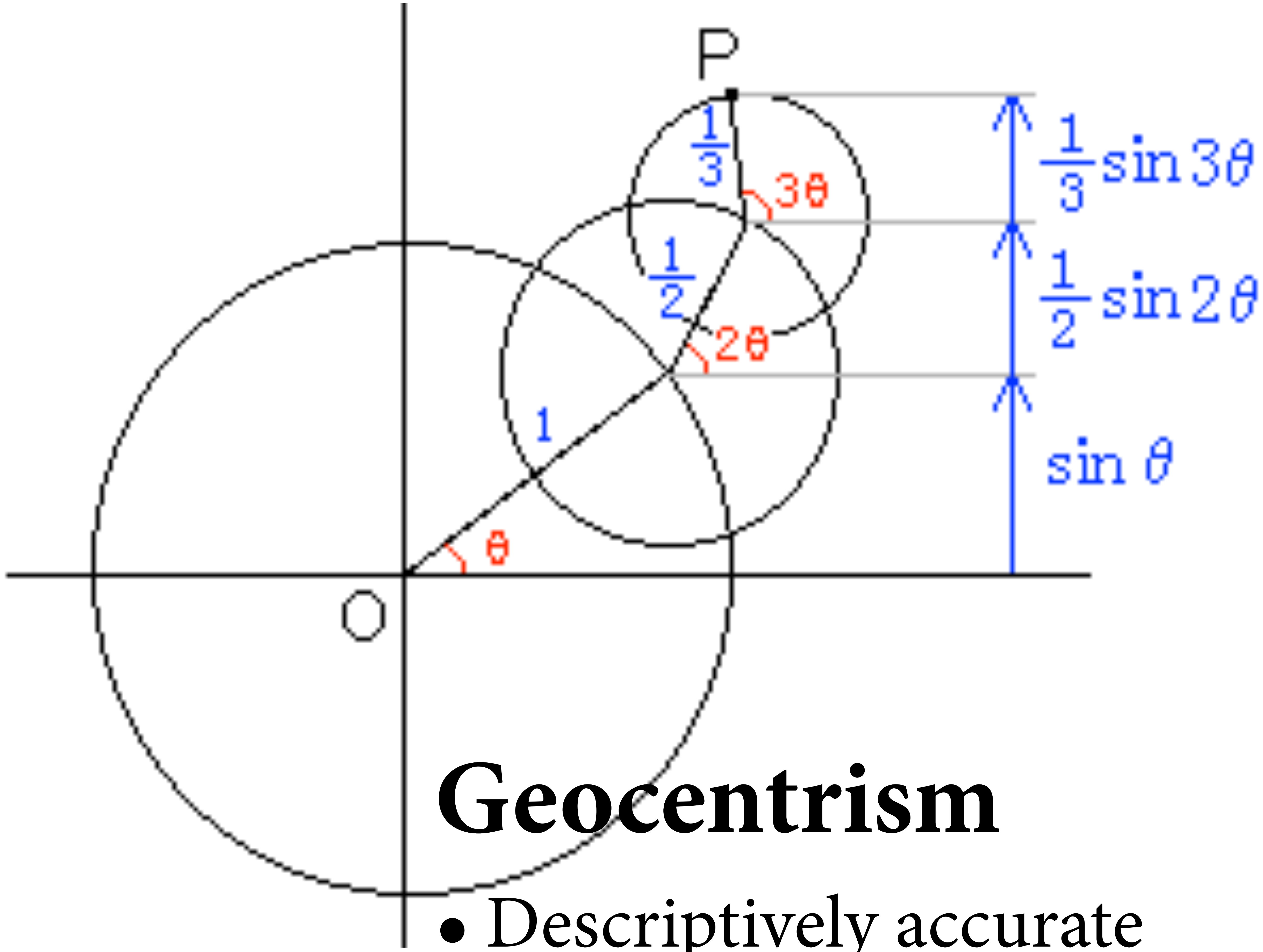
Geocentric Model



Geocentric Model

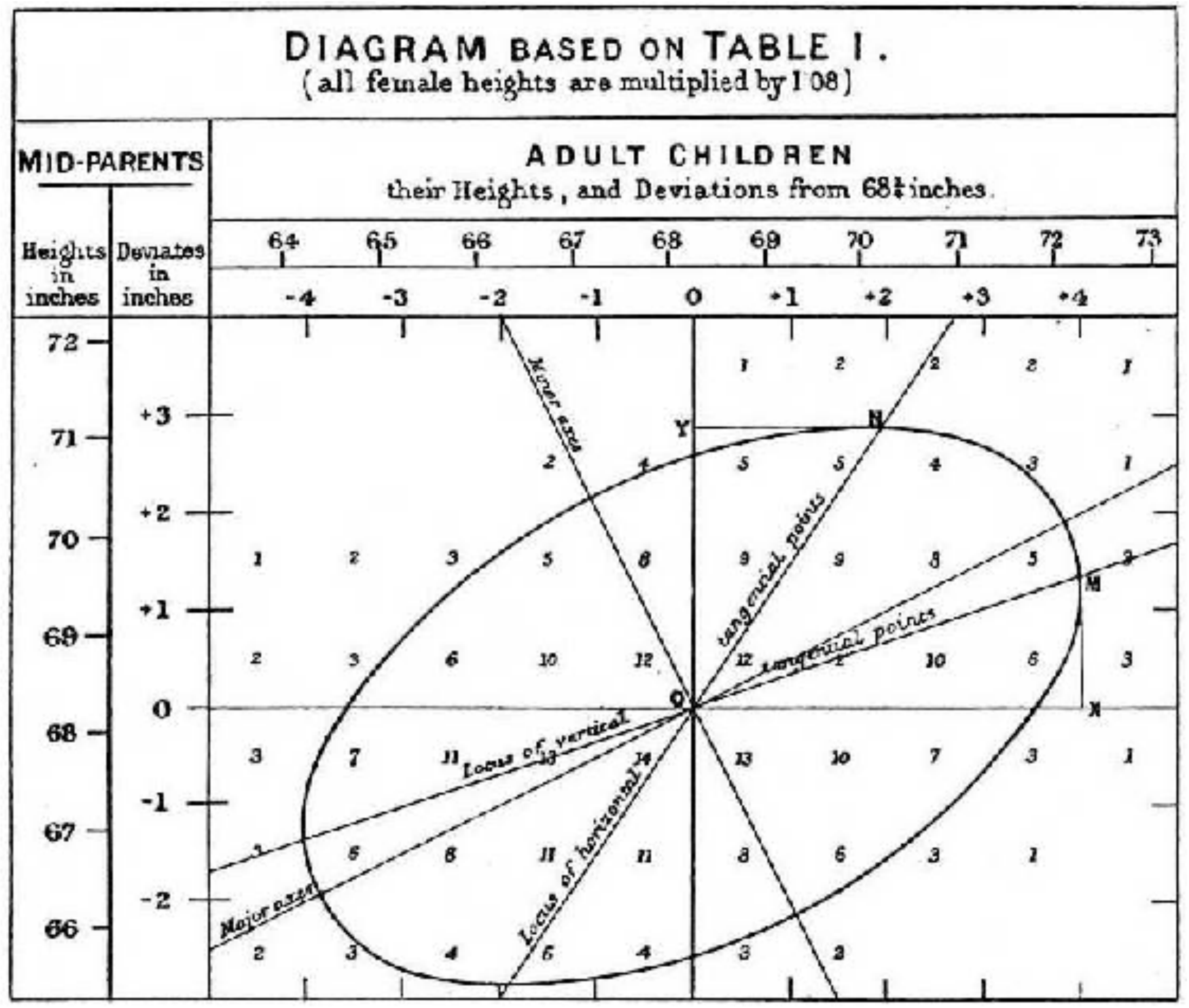
Prediction
Without
Explanation





Geocentrism

- Descriptively accurate
- Mechanistically wrong
- General method of approximation
- Known to be wrong



Linear Regression

- Descriptively accurate
- Mechanistically wrong
- General method of approximation
- Taken too seriously

Linear Regression

Simple statistical golems

Model of **mean** and **variance** of variable

Mean as **weighted sum** of other variables

Many special cases: ANOVA, ANCOVA, t-test, MANOVA

Can also be generative models

From *Breath of Bones: A Tale of the Golem*

1809 Bayesian argument for normal error and least-squares estimation

Positions

Distribution

Why Normal?

Two arguments

(1) Generative: Summed fluctuations tend towards normal distribution

(2) Statistical: For estimating mean and variance, normal distribution is least informative distribution (maxent)

Variable does not have to be normally distributed for normal model to be useful

Making Normal Models

Goals:

(1) Language for representing models

(2) How to calculate bigger posterior distributions

(3) Constructing & understanding linear models


FLOW

Language for modeling

Revisit globe tossing model:

$$W \sim \text{Binomial}(N, p)$$
$$p \sim \text{Uniform}(0, 1)$$

Language for modeling

Revisit globe tossing model:

outcome

$$W \sim \text{Binomial}(N, p)$$

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Language for modeling

Revisit globe tossing model:

"is distributed"

outcome

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Language for modeling

Revisit globe tossing model:

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data distribution (likelihood)

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parameter to estimate

Language for modeling

Revisit globe tossing model:

"is distributed"

outcome

data distribution (likelihood)

$$W \sim \text{Binomial}(N, p)$$

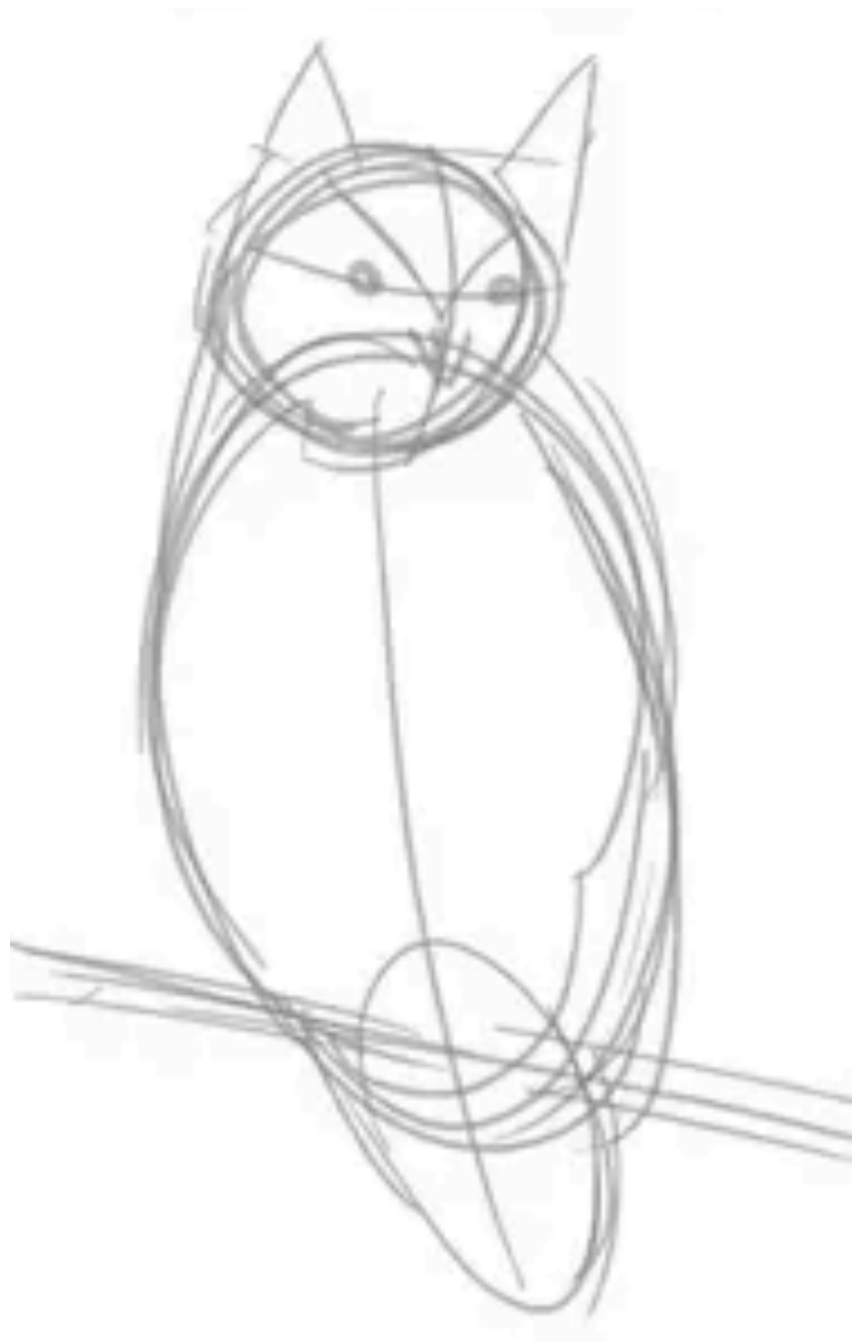
$$p \sim \text{Uniform}(0, 1)$$

parameter to estimate

prior distribution

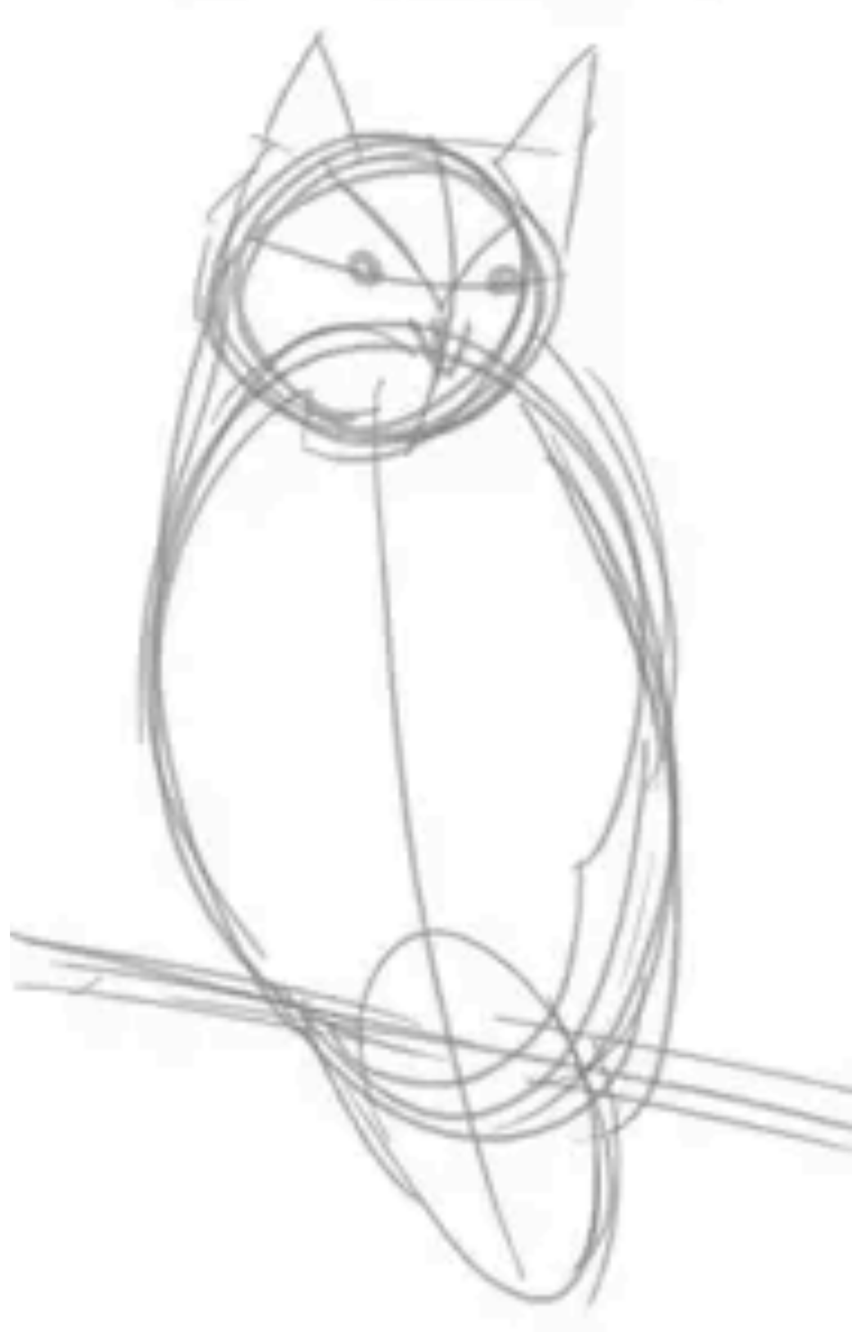
Now make it compute — arrange as probability statements

$$W \sim \text{Binomial}(N, p)$$
$$p \sim \text{Uniform}(0, 1)$$



Now make it compute — arrange as probability statements

$$\Pr(W|N,p) = \text{Binomial}(W|N,p)$$
$$\Pr(p) = \text{Uniform}(p|0,1)$$



Now make it compute — arrange as probability statements

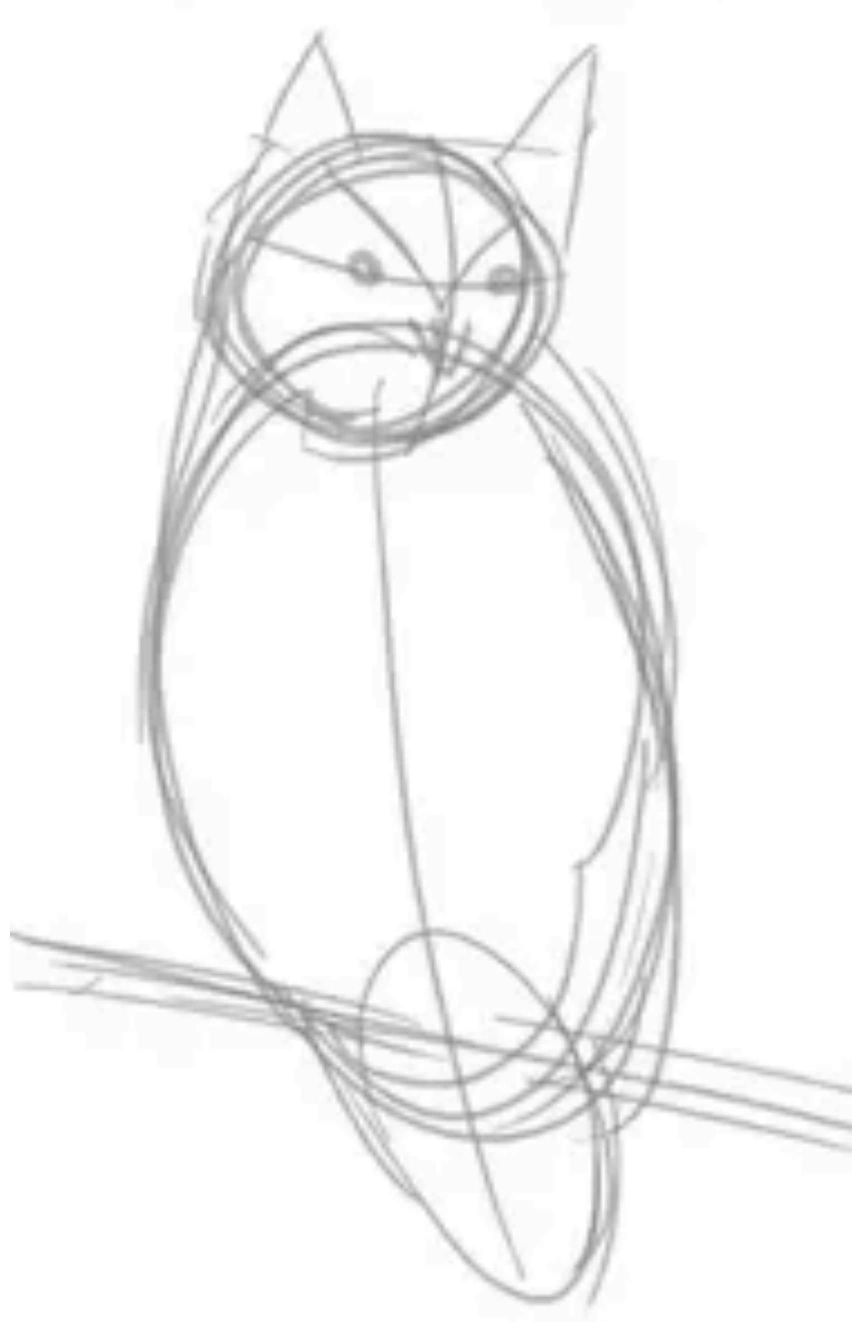
$$\Pr(W|N,p) = \text{Binomial}(W|N,p)$$

$$\Pr(p) = \text{Uniform}(p|0,1)$$

Posterior distribution

$$\Pr(p|W,N) \propto \text{Binomial}(W|N,p)\,\text{Uniform}(p|0,1)$$

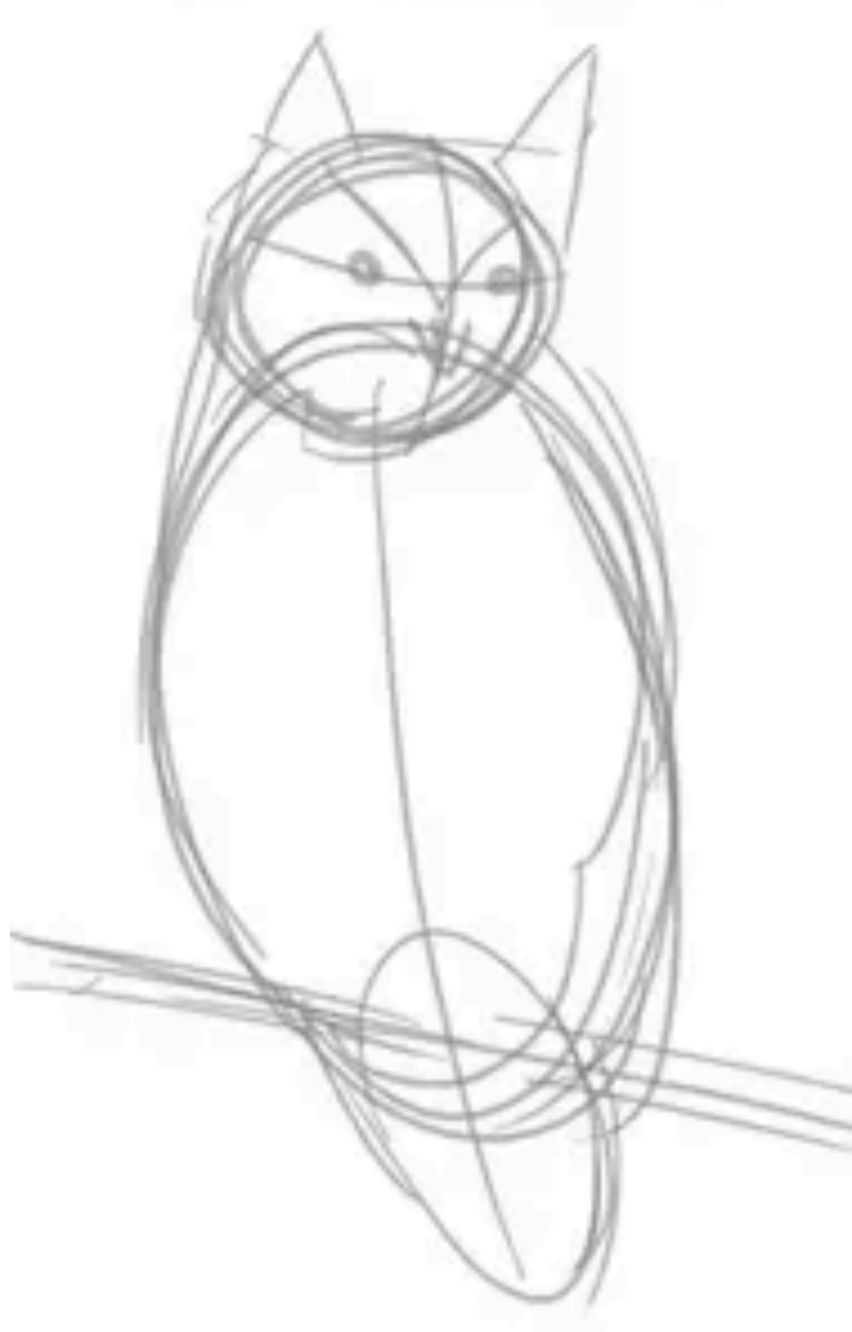
"proportional to"



Now make it compute — using code

$$\Pr(p|W, N) \propto \text{Binomial}(W|N, p)\ \text{Uniform}(p|0,1)$$

```
W <- 6
N <- 9
p <- seq(from=0,to=1,len=1000)
PrW <- dbinom(W,N,p)
Prp <- dunif(p,0,1)
posterior <- PrW * Prp
```



Linear Regression

Drawing the Owl

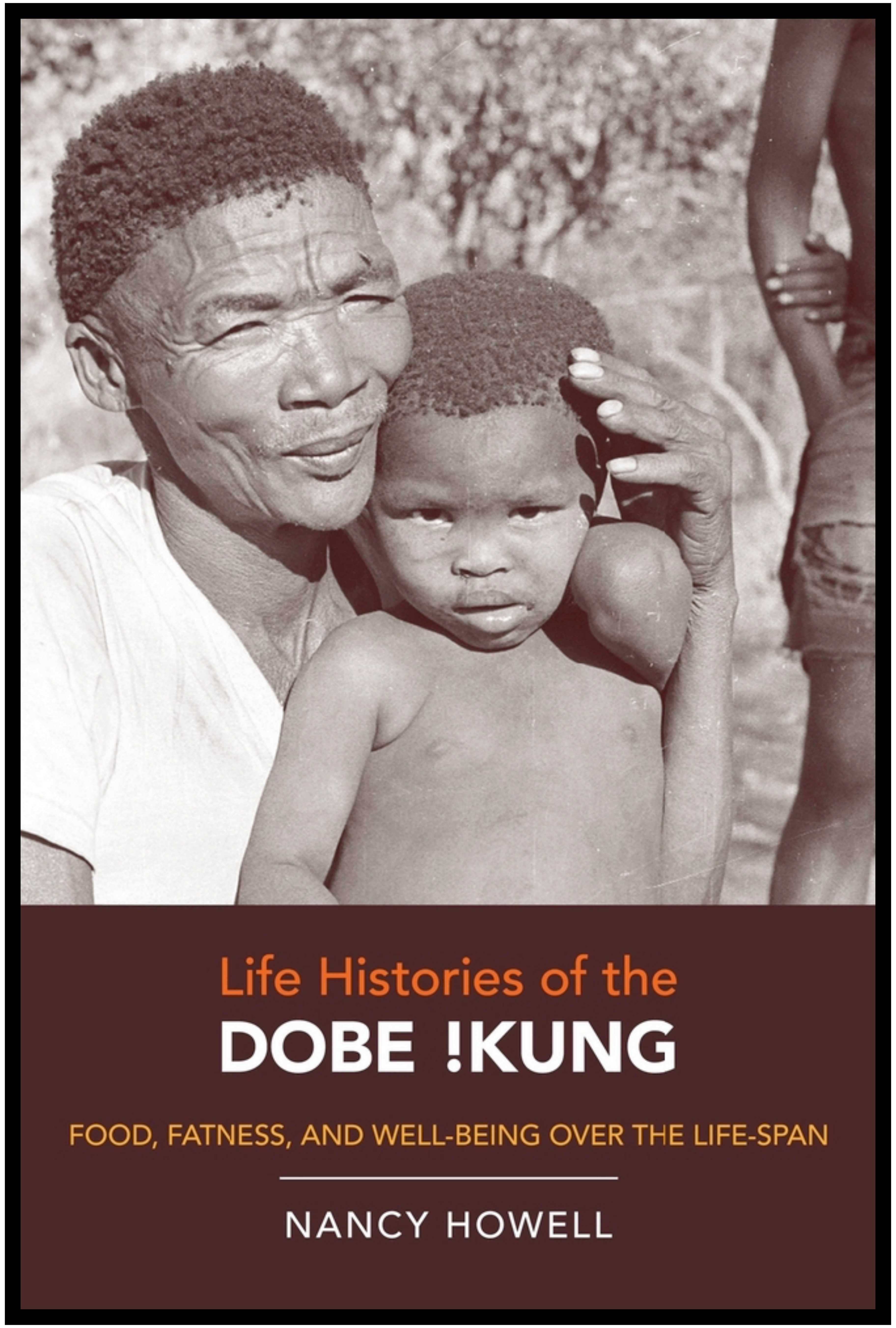
(1) Question/goal/estimand

(2) Scientific model

(3) Statistical model(s)

(4) Validate model

(5) Analyze data



Linear Regression

```
library(rethinking)
data(Howell1)
```

Drawing the Owl

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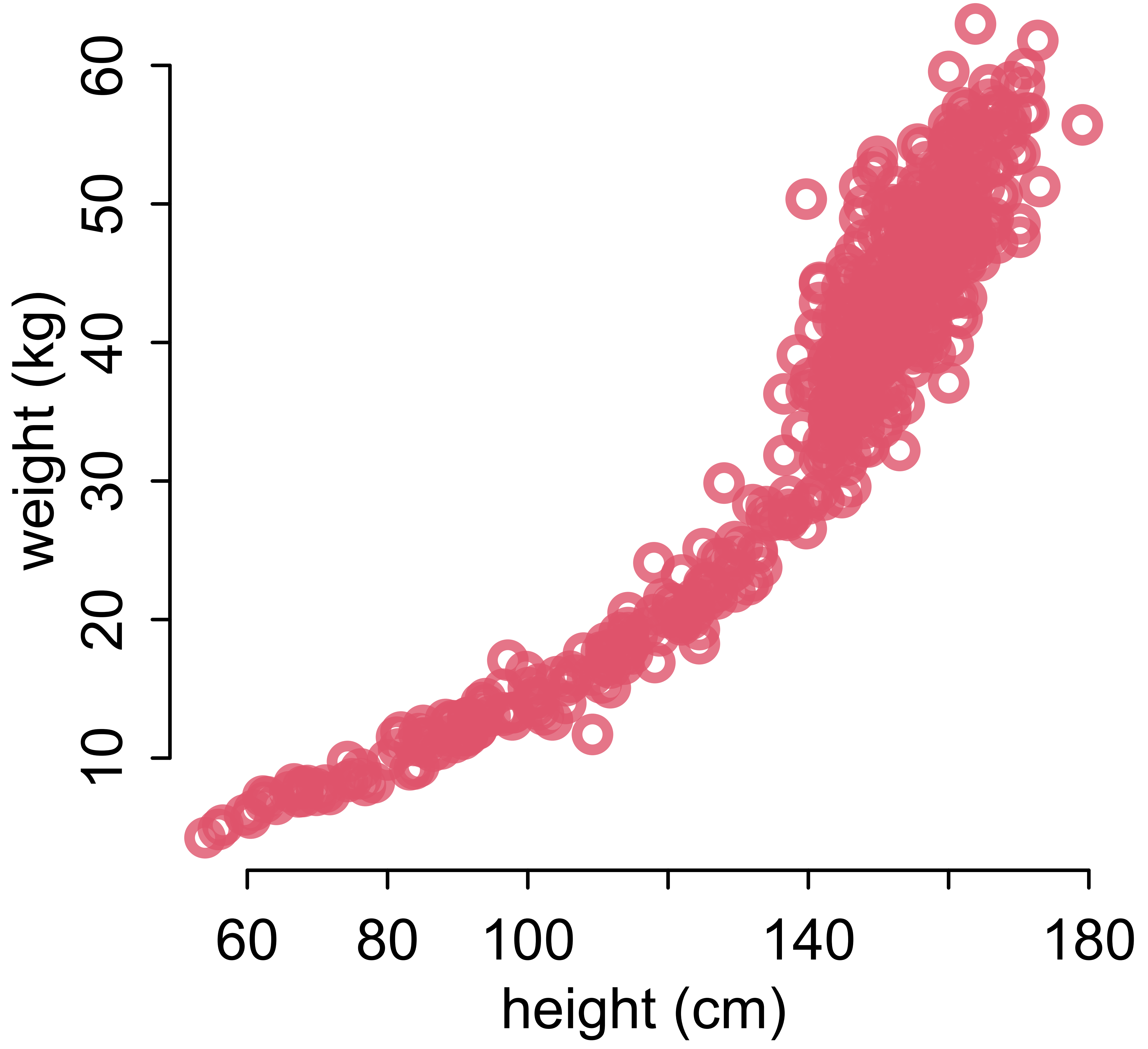

Linear Regression

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library(rethinking)
data(Howell1)
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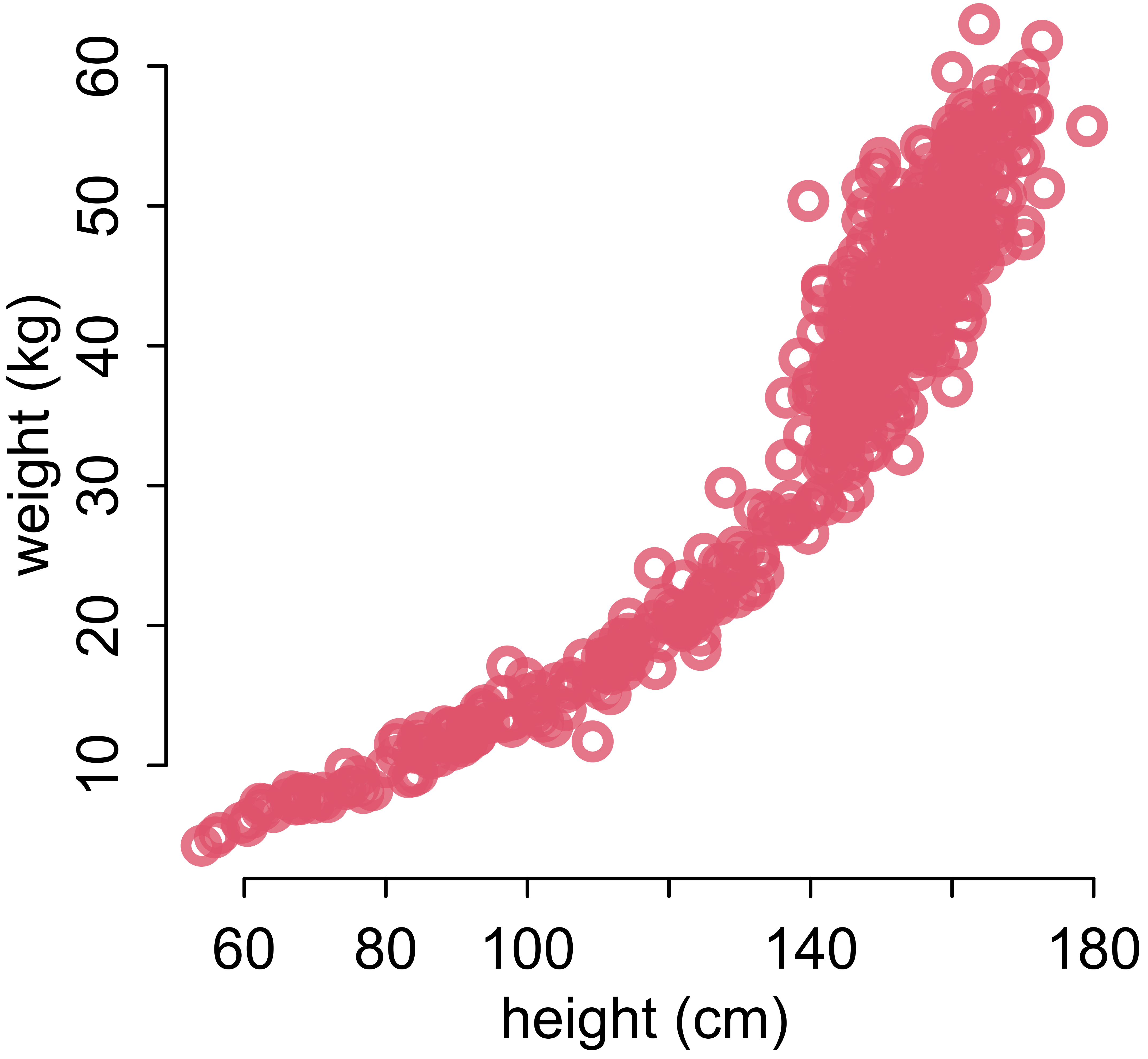
Drawing the Owl

(1) Question/goal/estimand

Describe association between **weight** and **height**



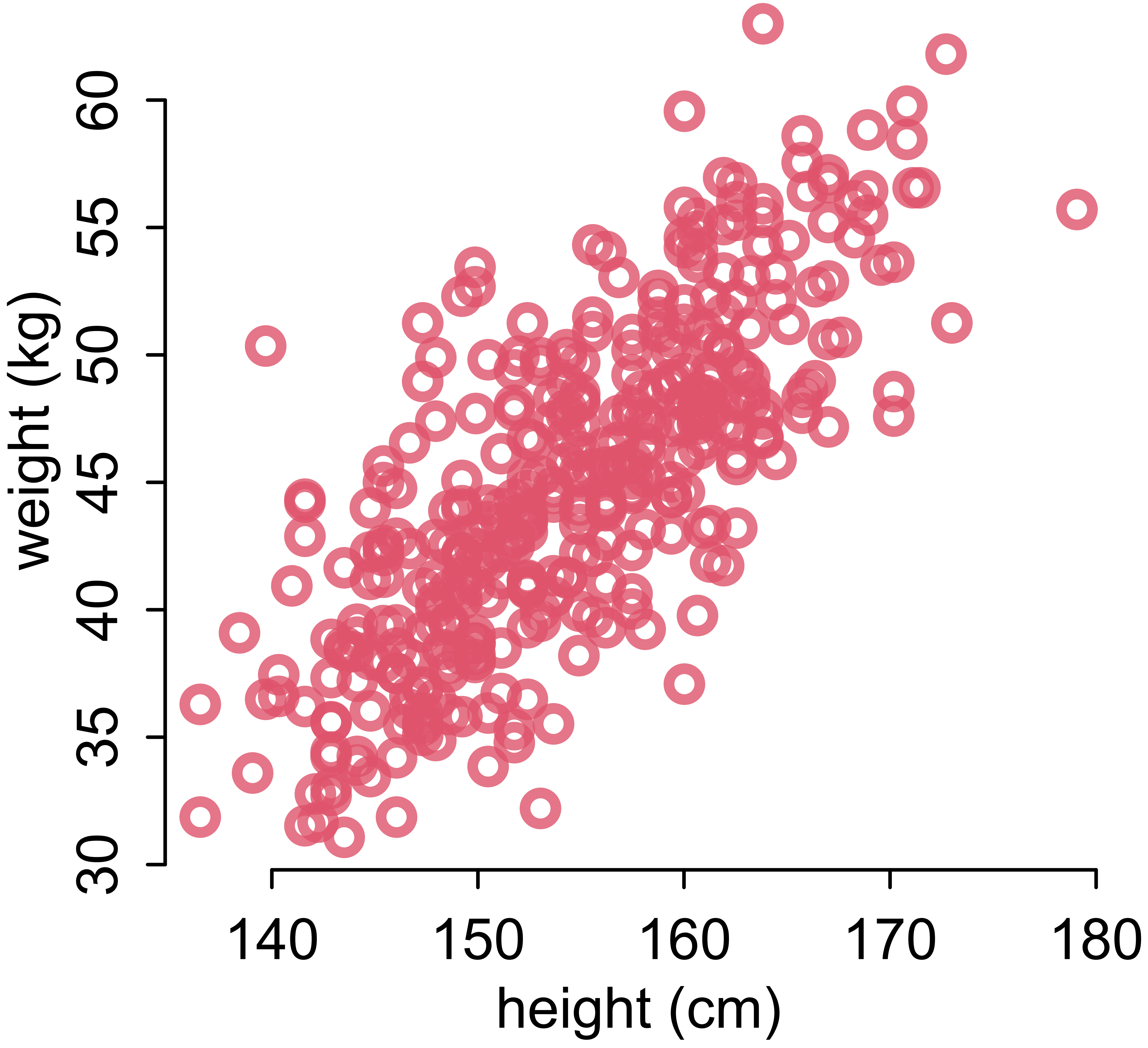
Linear Regression

```
data(Howell1)
d <- Howell1[Howell1$age>=18,]
```

Drawing the Owl

(1) Question/goal/estimand

Describe association between ADULT **weight** and **height**



Linear Regression

```
data(Howell1)
d <- Howell1[Howell1$age>=18,]
```

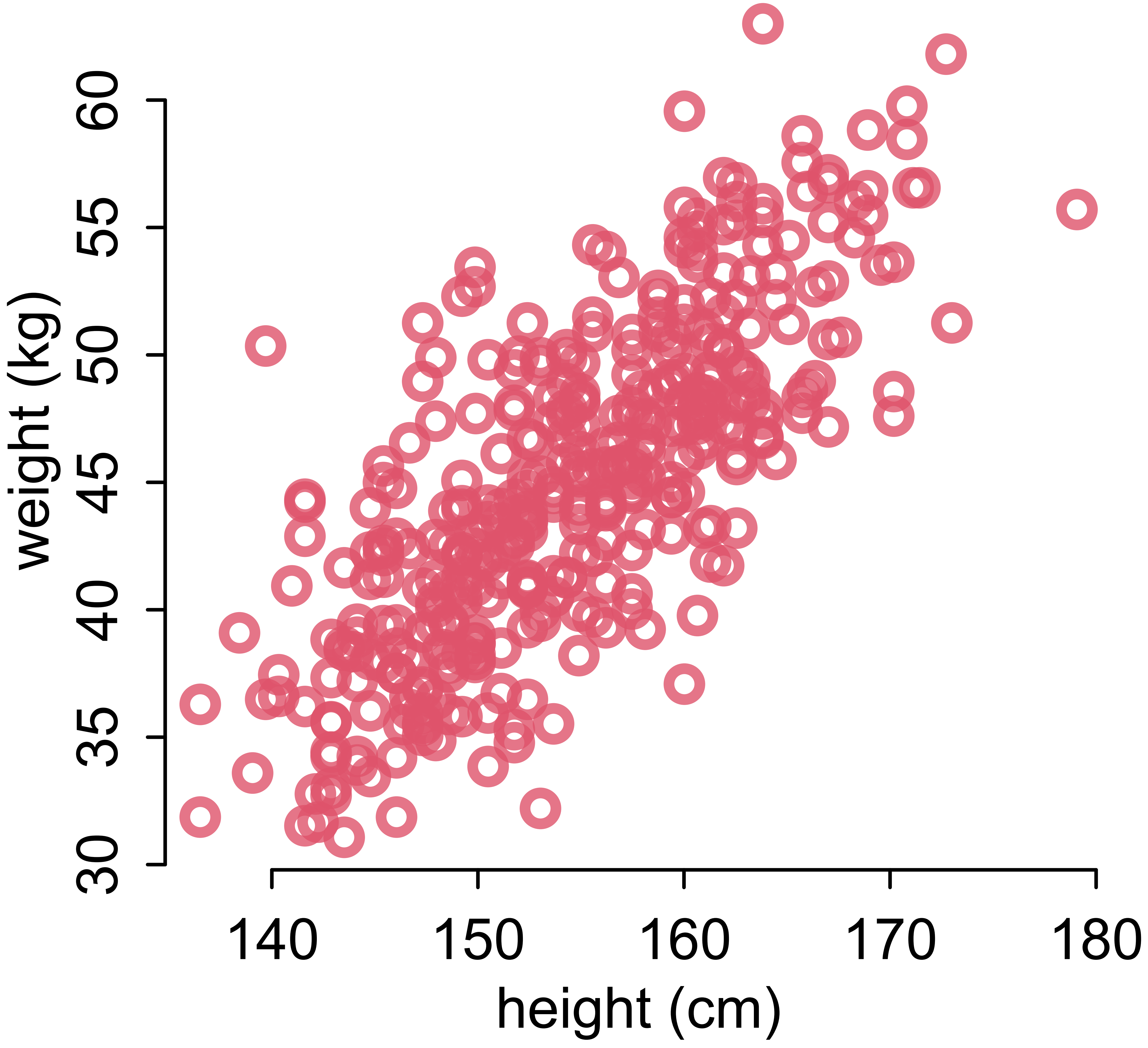
(2) Scientific model

How does **height** influence **weight**?

$$H \longrightarrow W$$

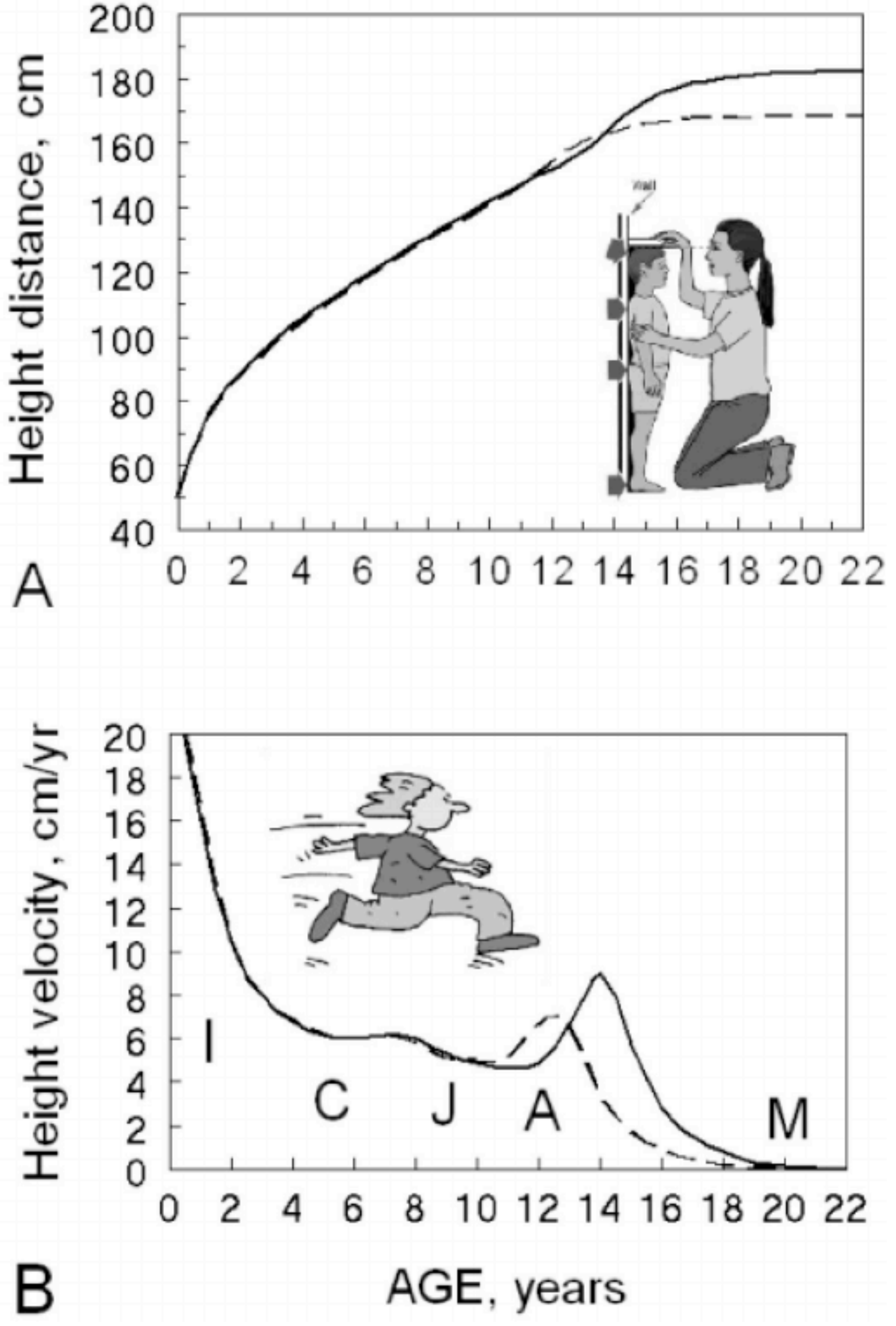
$$W = f(H)$$

"Weight is some function of height"



Generative models

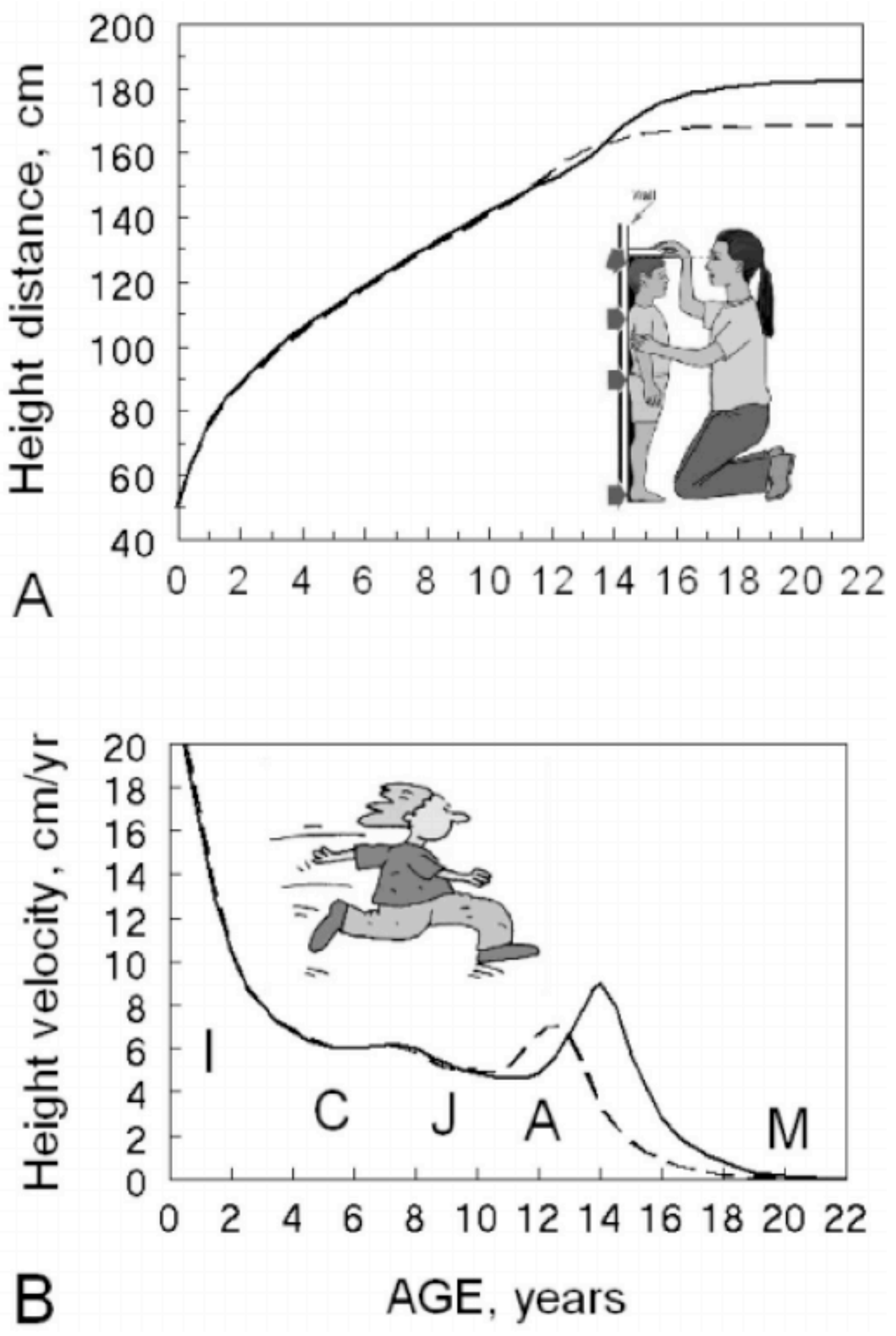
Options



Generative models

Options

(1) **Dynamic**: Incremental growth of organism; both mass and height (length) derive from growth pattern; Gaussian variation result of summed fluctuations

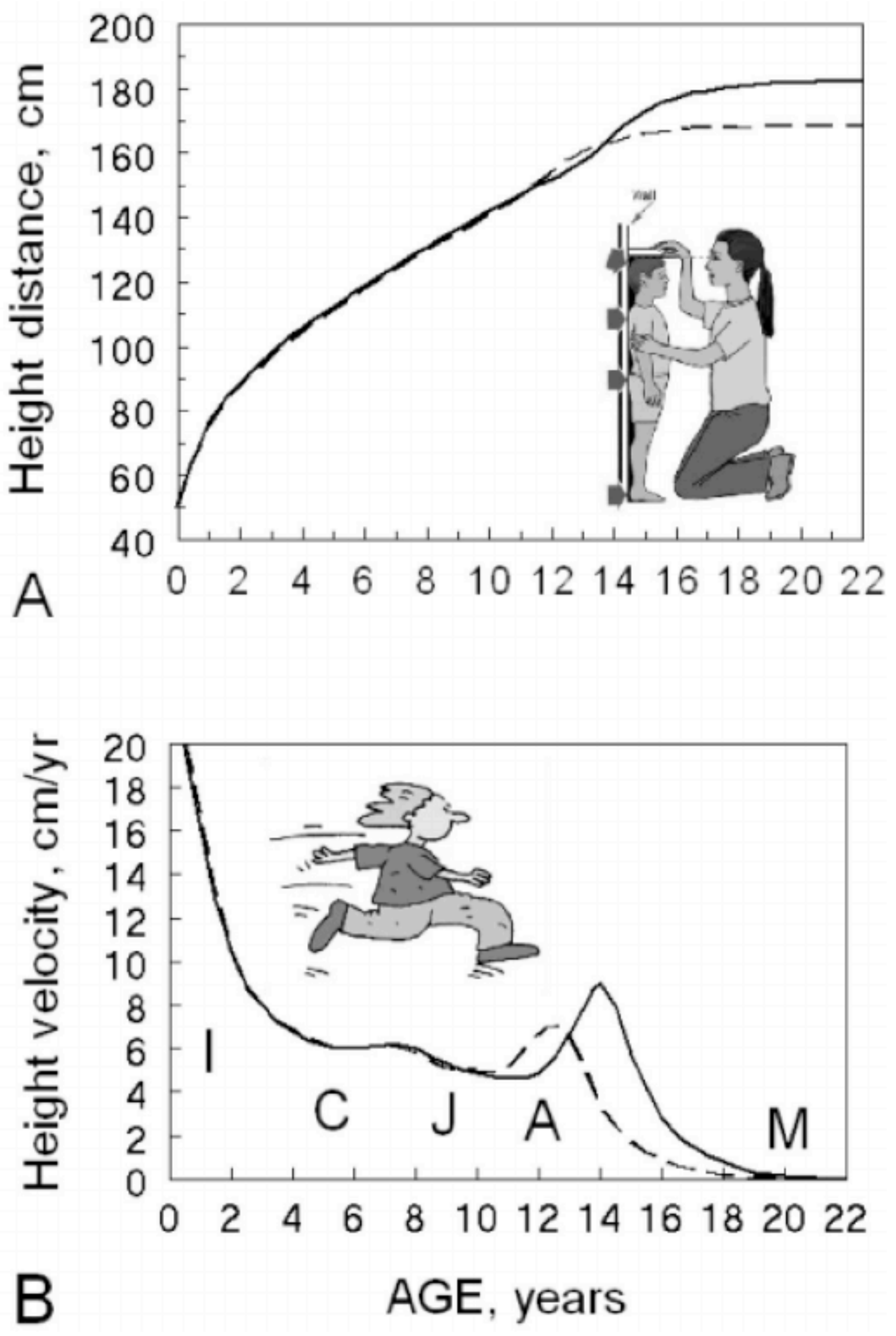


Generative models

Options

(1) **Dynamic**: Incremental growth of organism; both mass and height (length) derive from growth pattern; Gaussian variation result of summed fluctuations

(2) **Static**: Changes in height result in changes in weight, but no mechanism; Gaussian variation result of growth history



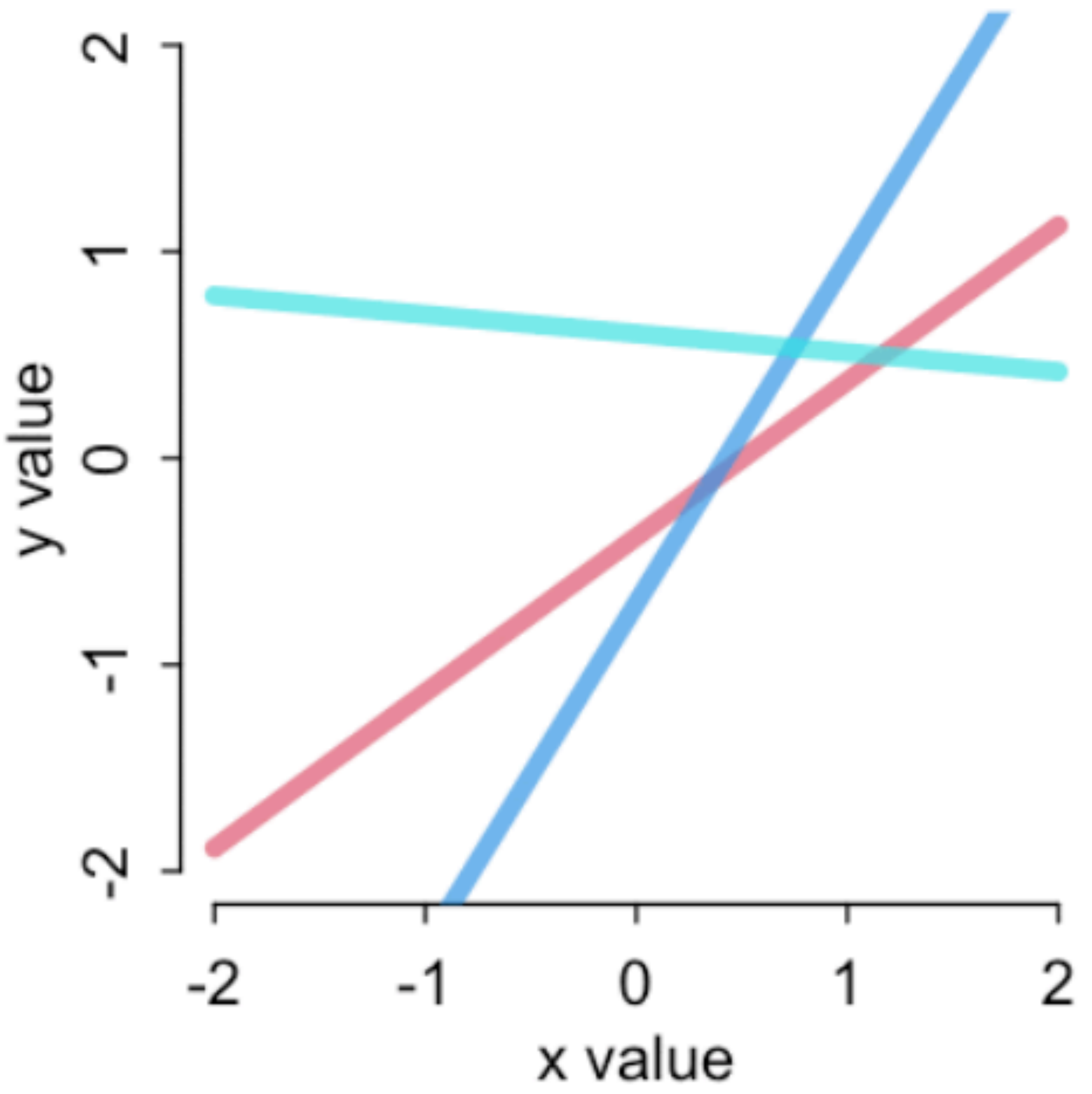
Anatomy of a linear model

$$y_i = \alpha + \beta x_i$$

index

intercept

slope



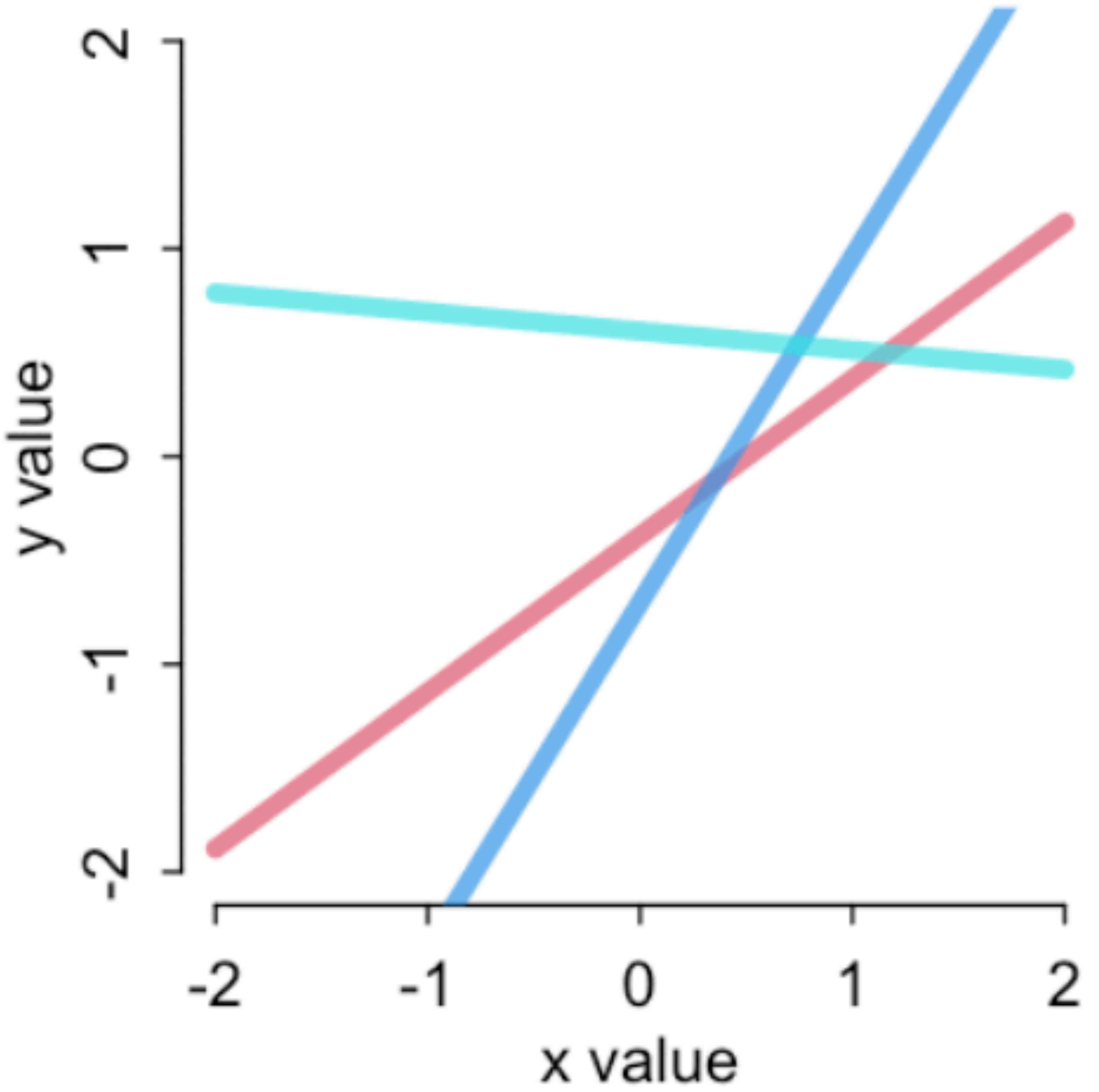
Anatomy of a linear model

standard deviation

expectation

$$y_i \sim \text{Normal}(\mu_i, \sigma)$$
$$\mu_i = \alpha + \beta x_i$$

"Each x value has a different expectation, $E(y|x) = \mu$"



Generative model: H → W

$$W_i \sim \text{Normal}(\mu_i, \sigma)$$
$$\mu_i = \alpha + \beta H_i$$

```
alpha <- 0
beta <- 0.5
sigma <- 5
n_individuals <- 100

H <- runif(n_individuals,130,170)

mu <- alpha + beta*H
W <- rnorm(n_individuals,mu,sigma)
```

Generative model: H → W

$$W_i \sim \text{Normal}(\mu_i, \sigma)$$
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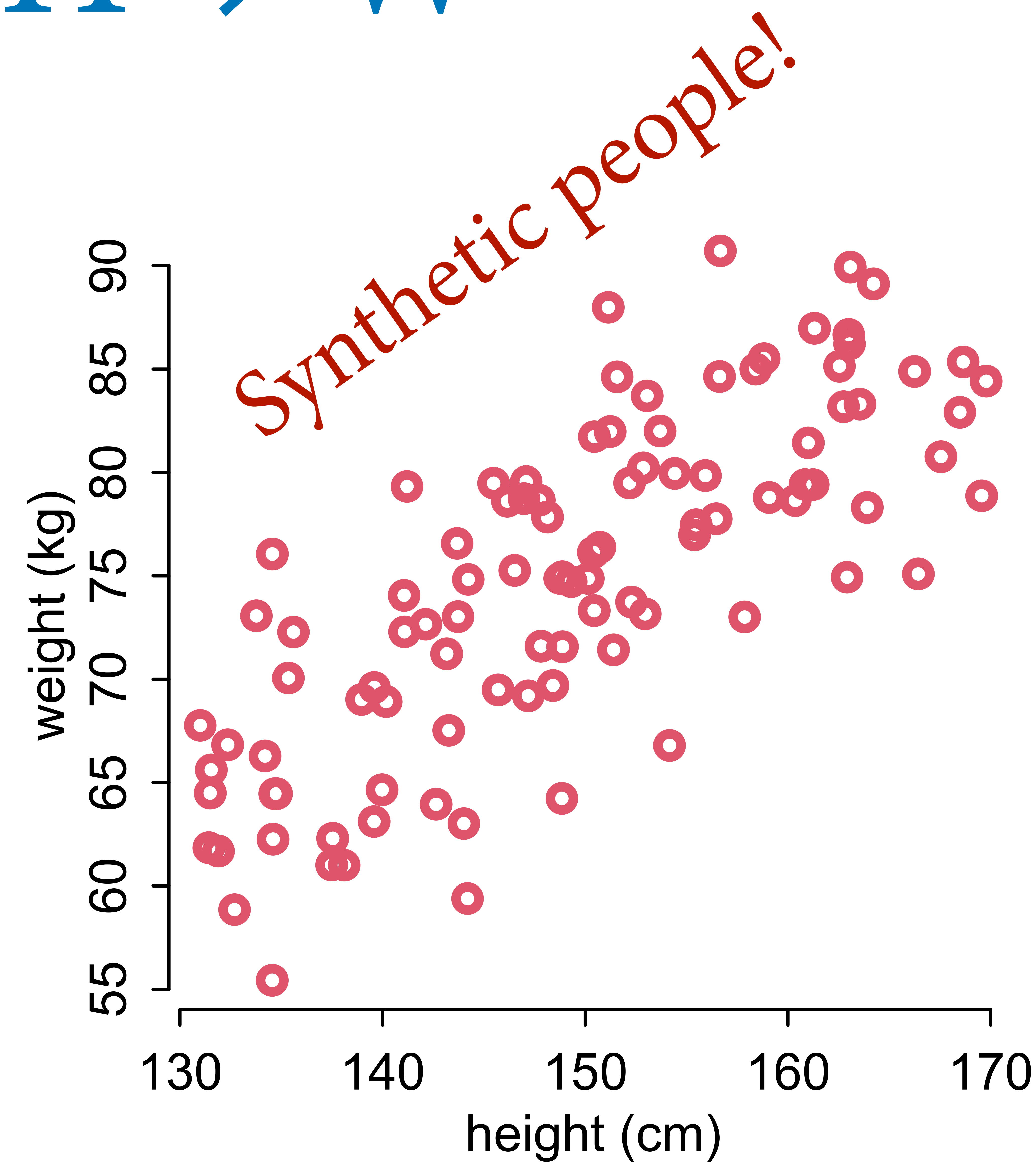


PAUSE

Linear Regression

```r
data(Howell1)
d <- Howell1[Howell1$age>=18,]
```

Drawing the Owl

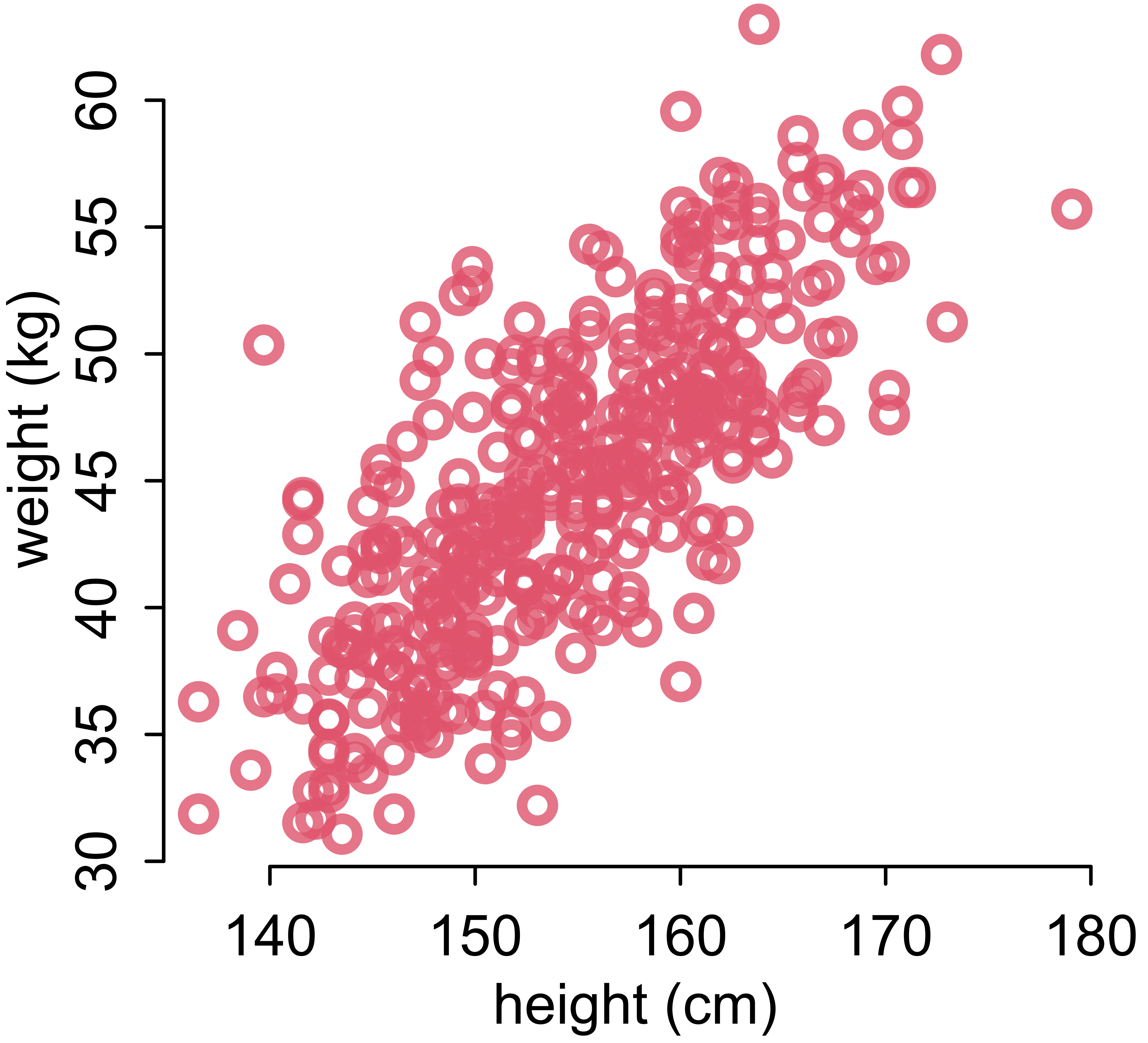
(1) Question/goal/estimand

(2) Scientific model

(3) Statistical model(s)

(4) Validate model

(5) Analyze data



Anatomy of a linear model

$$y_i \sim \text{Normal}(\mu_i, \sigma)$$
$$\mu_i = \alpha + \beta x_i$$
$$\alpha \sim \text{Normal}(0,1)$$
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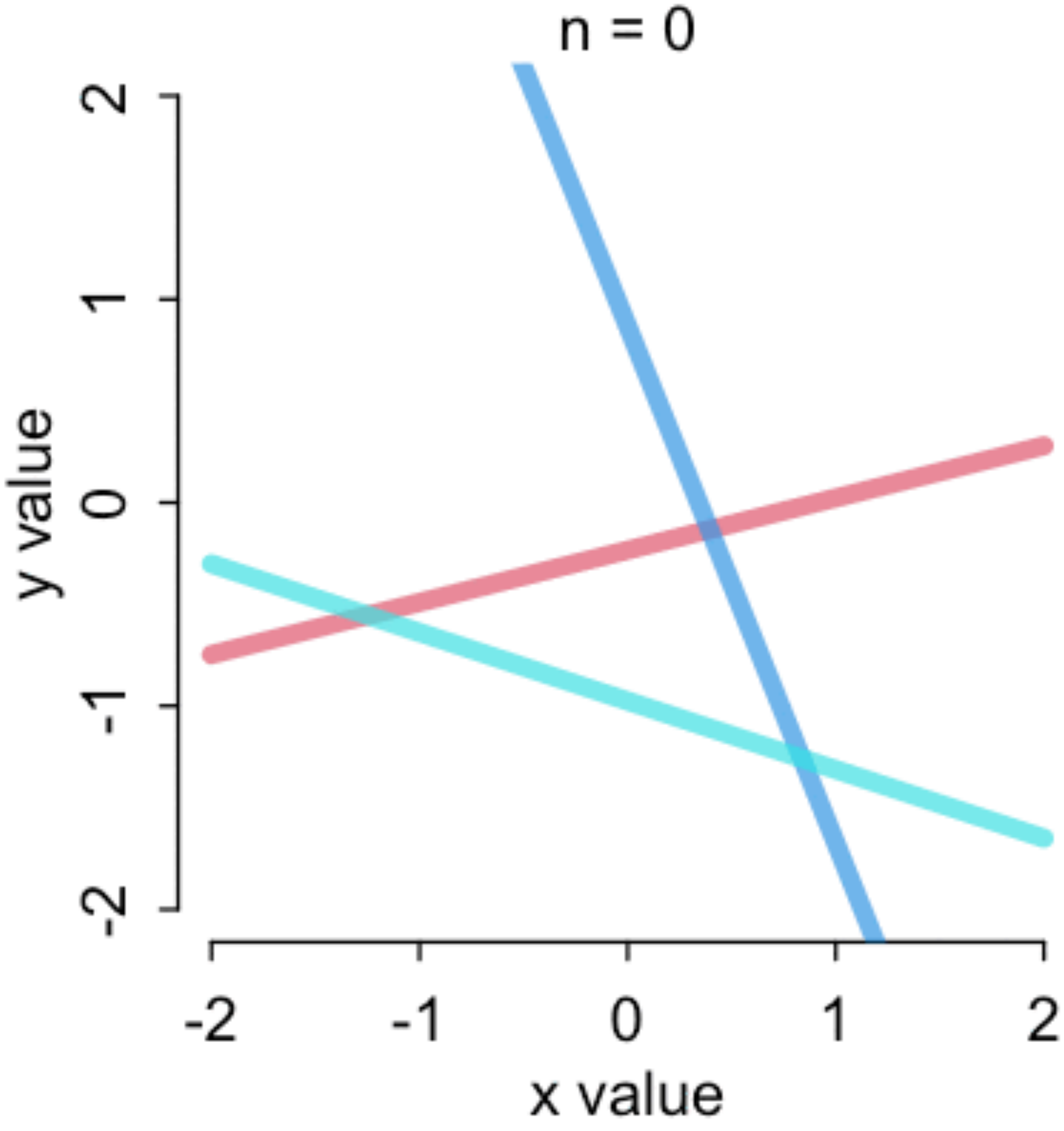
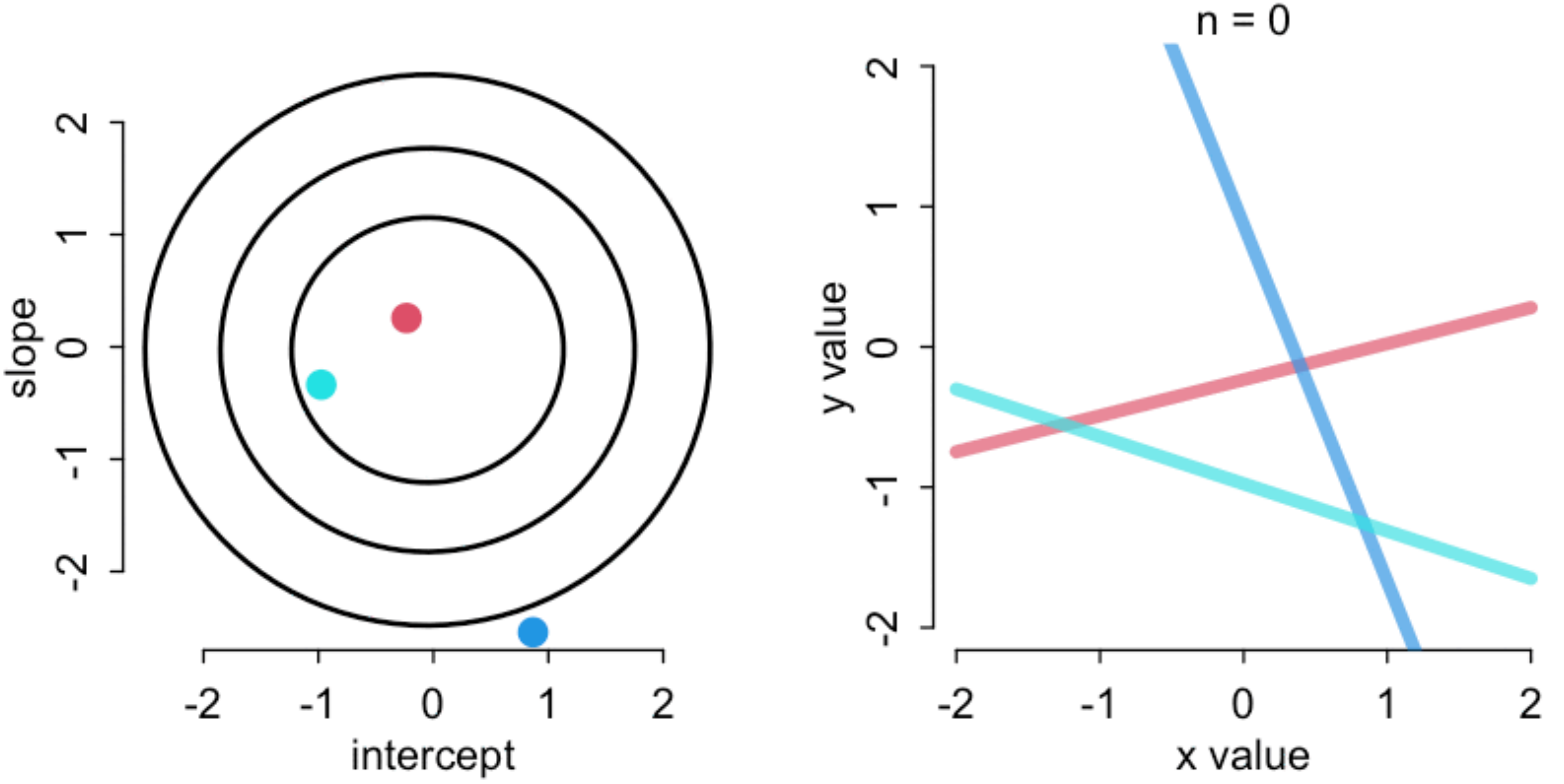


Sampling the prior distribution

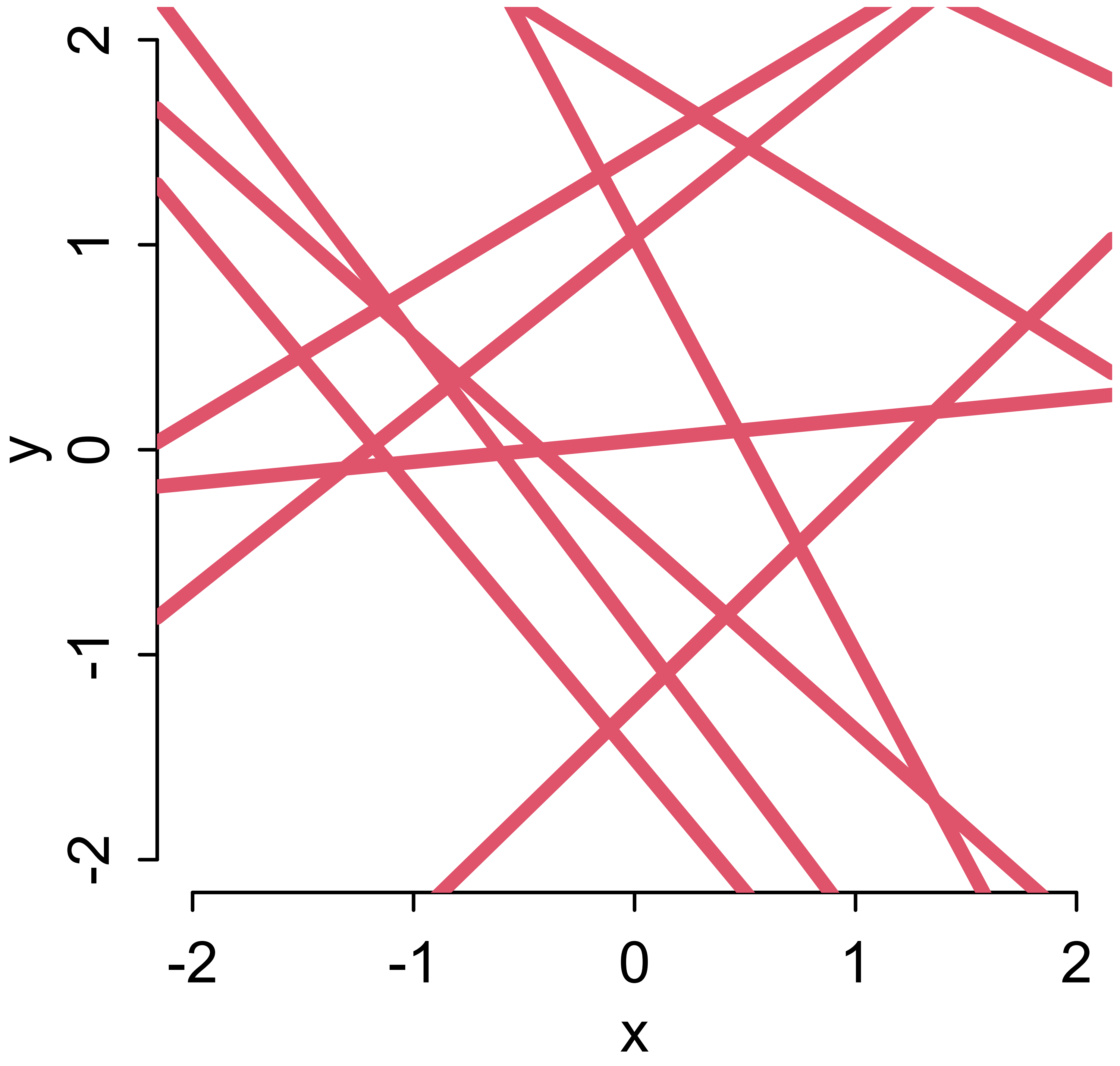


Sampling the prior distribution

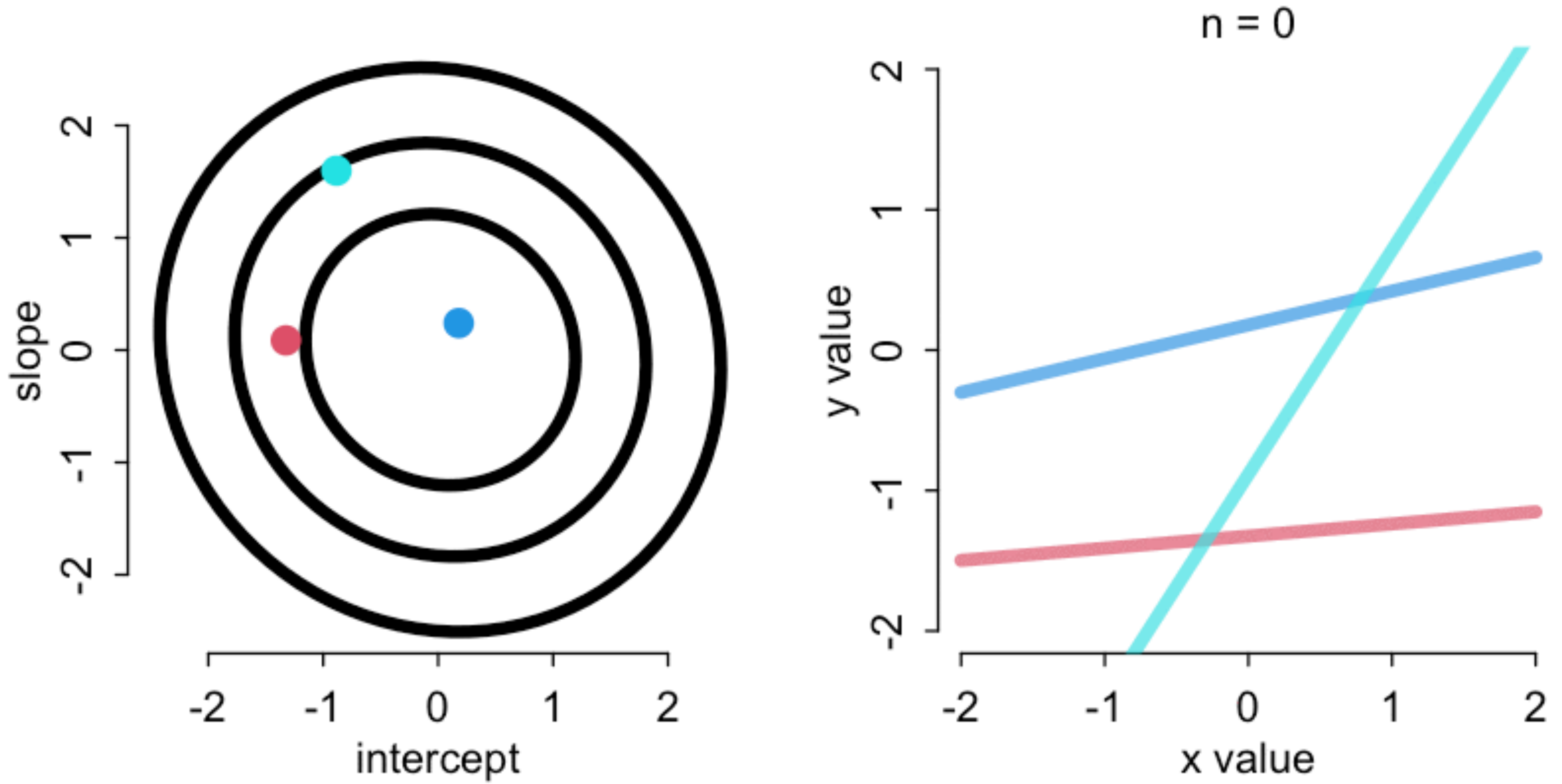
```
n_samples <- 10

alpha <- rnorm(n_samples,0,1)
beta <- rnorm(n_samples,0,1)

plot(NULL,xlim=c(-2,2),ylim=c(-2,2),
    xlab="x",ylab="y")
for ( i in 1:n_samples )
    abline(alpha[i],beta[i],lwd=4,col=2)
```



Updating the posterior



Statistical model for H → W

Structure of statistical model similar to generative model, BUT

(1) Useful to re-scale variables

(2) Must think about priors

These two things go together

$$W_i \sim \text{Normal}(\mu_i, \sigma)$$
$$\mu_i = \alpha + \beta(H_i - \bar{H})$$
$$\alpha \sim \text{Normal}(?, ?)$$
$$\beta \sim \text{Normal}(?, ?)$$
$$\sigma \sim \text{Uniform}(0, ?)$$

Statistical model for H → W

Re-scaling **height** so that the **intercept** makes sense

$$W_i \sim \text{Normal}(\mu_i, \sigma)$$
$$\mu_i = \alpha + \beta(H_i - \bar{H})$$

value of μ when $H_i - \bar{H} = 0$

mean value of H_i

Statistical model for H → W

Now what are scientifically reasonable priors?

α: average adult weight

β: kilograms per centimeter

Region	Adult population (millions)	Average weight
Africa	535	60.7 kg (133.8 lb)
Asia	2,815	57.7 kg (127.2 lb)

$$W_i \sim \text{Normal}(\mu_i, \sigma)$$

$$\mu_i = \alpha + \beta(H_i - \bar{H})$$

$$\alpha \sim \text{Normal}(60, 10)$$

$$\beta \sim \text{Normal}(0, 10)$$

$$\sigma \sim \text{Uniform}(0, 10)$$

Sampled regression lines

```
n <- 10
alpha <- rnorm(n,60,10)
beta <- rnorm(n,0,10)

Hbar <- 150
Hseq <- seq(from=130,to=170,len=30)
plot(NULL,xlim=c(130,170),ylim=c(10,100),
    xlab="height (cm)",ylab="weight (kg)")
for ( i in 1:n )
    lines( Hseq , alpha[i] + beta[i]*(Hseq-Hbar) ,
    lwd=3 , col=2 )
```

Sampled regression lines

```
n <- 10
alpha <- rnorm(n,60,10)
beta <- rnorm(n,0,10)

Hbar <- 150
Hseq <- seq(from=130,to=170,len=30)
plot(NULL,xlim=c(130,170),ylim=c(10,100),
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for ( i in 1:n )
    lines( Hseq , alpha[i] + beta[i]*(Hseq-Hbar) ,
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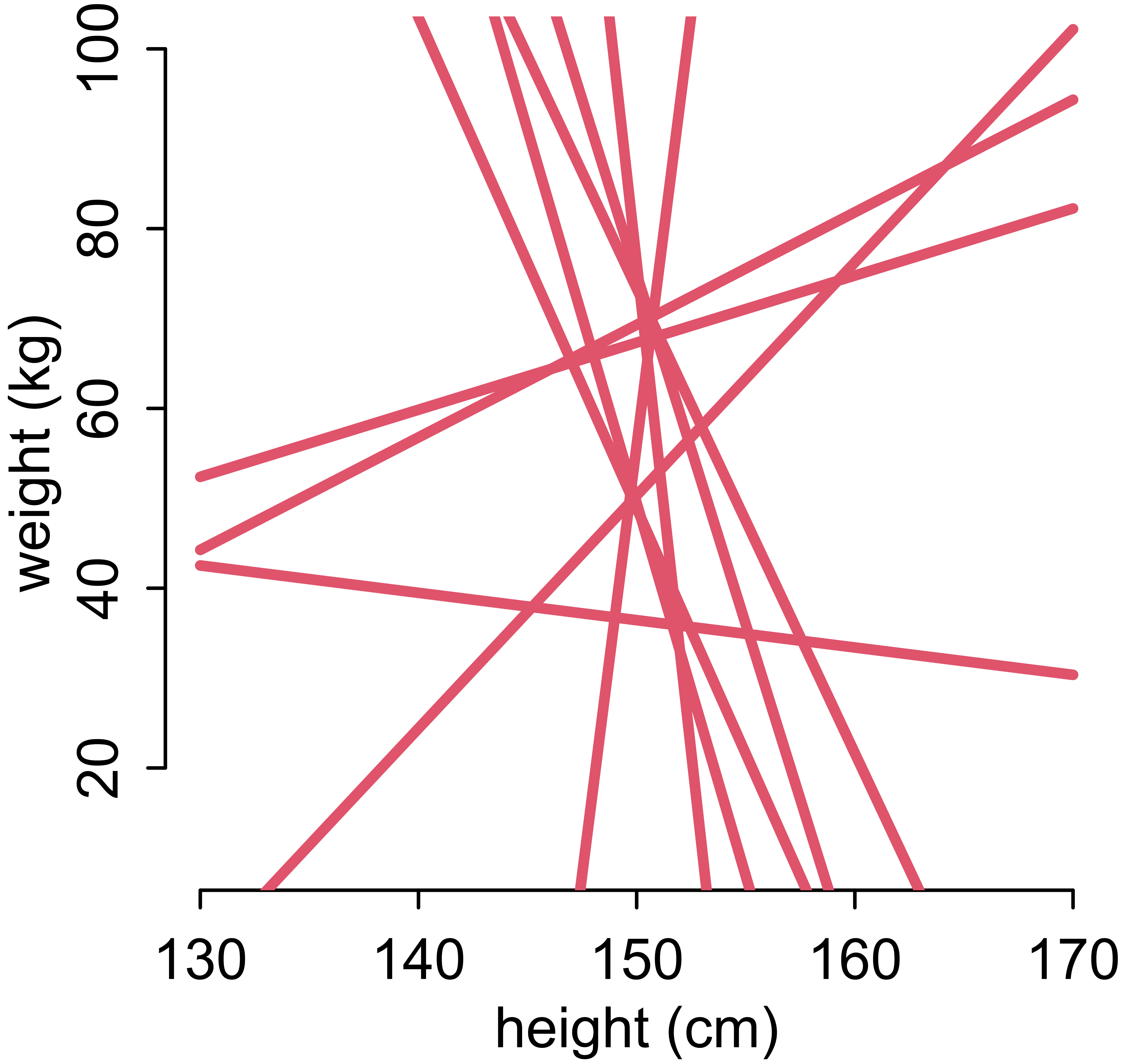
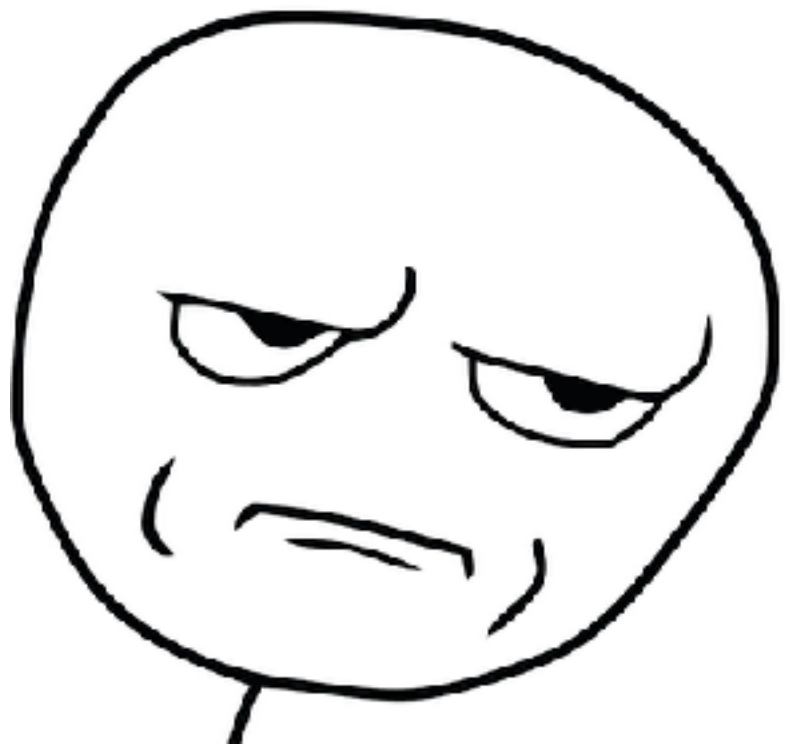
Sampled regression lines

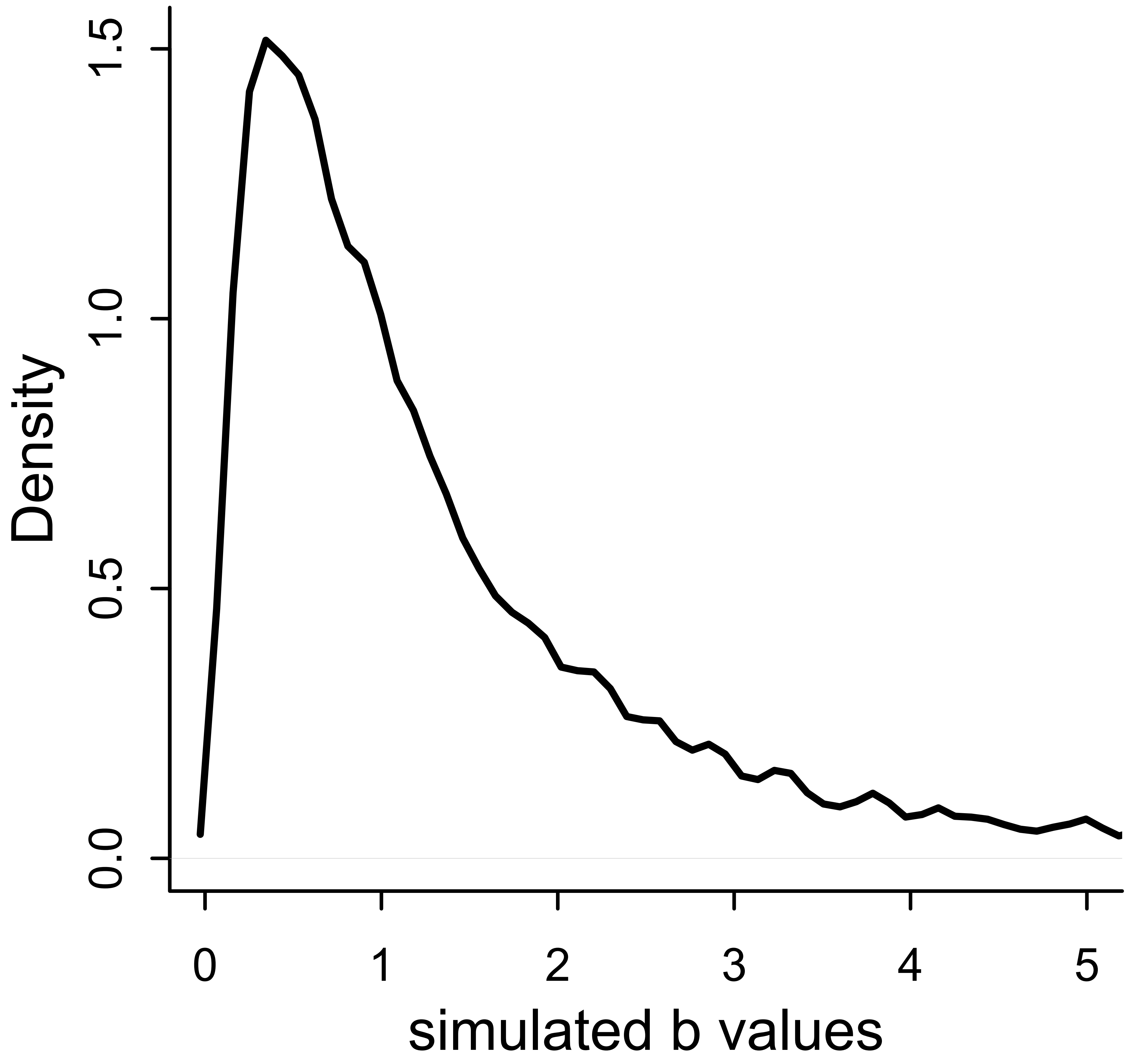
```r
n <- 10
alpha <- rnorm(n,60,10)
beta <- rnorm(n,0,10)

Hbar <- 150
Hseq <- seq(from=130,to=170,len=30)
plot(NULL,xlim=c(130,170),ylim=c(10,100),
    xlab="height (cm)",ylab="weight (kg)")
for ( i in 1:n )
    lines( Hseq , alpha[i] + beta[i]*(Hseq-Hbar) ,
    lwd=3 , col=2 )
```





Statistical model for H → W

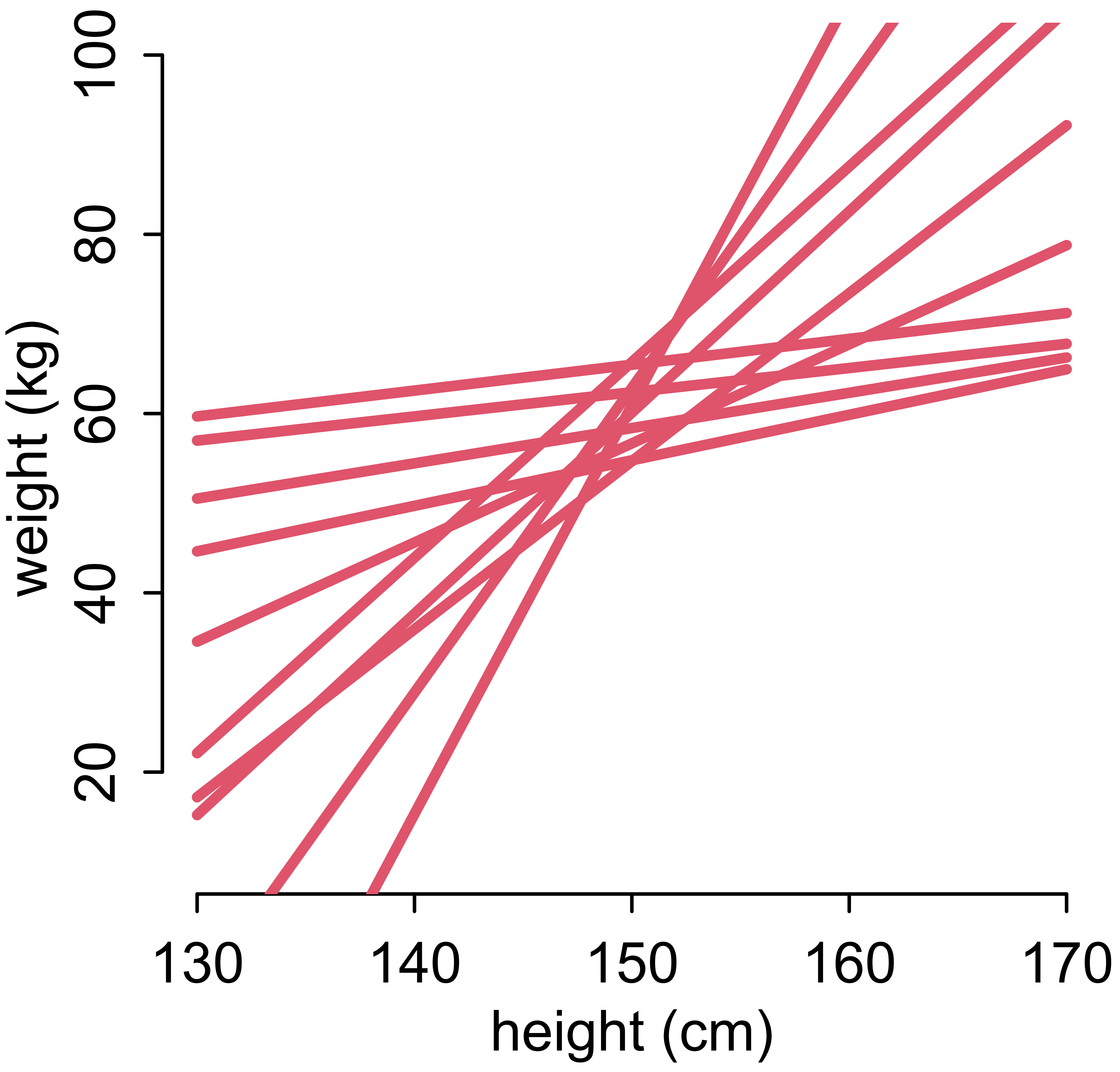


$$W_i \sim \text{Normal}(\mu_i, \sigma)$$
$$\mu_i = \alpha + \beta(H_i - \bar{H})$$
$$\alpha \sim \text{Normal}(60,10)$$
$$\beta \sim \text{LogNormal}(0,1)$$
$$\sigma \sim \text{Uniform}(0,10)$$

Sampled regression lines

```
n <- 10
alpha <- rnorm(n,60,10)
beta <- rlnorm(n,0,1)

Hbar <- 150
Hseq <- seq(from=130,to=170,len=30)
plot(NULL,xlim=c(130,170),ylim=c(10,100),
    xlab="height (cm)",ylab="weight (kg)")
for ( i in 1:n )
    lines( Hseq , alpha[i] + beta[i]*(Hseq-Hbar) ,
    lwd=3 , col=2 )
```



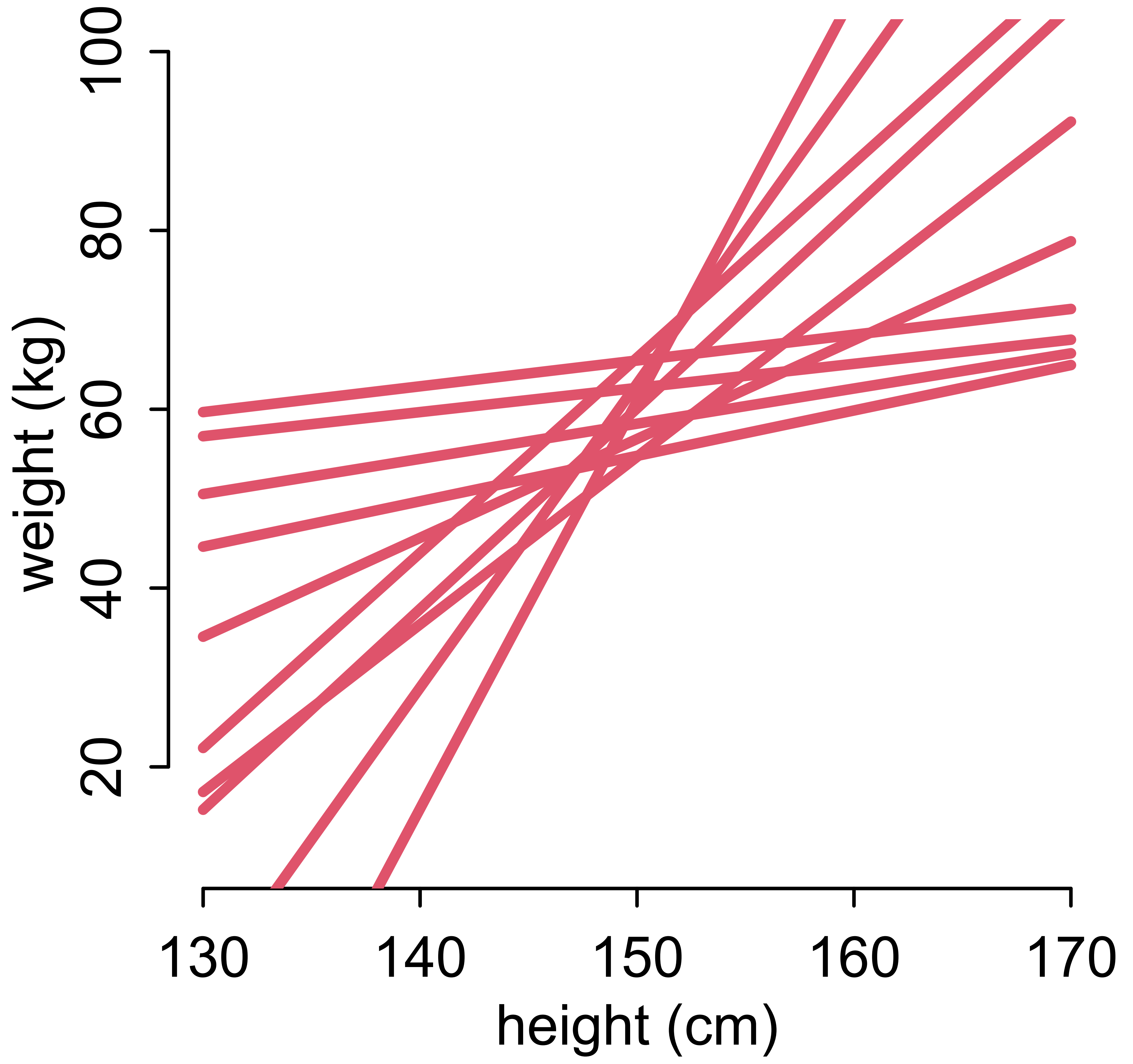
Sermon on Priors

There are no correct priors, only scientifically justifiable priors

Justify with information outside the data — **like rest of model**

Priors not so important in simple linear models

But need to practice now: simulate, understand, expand



Fitting the model

$$W_i \sim \text{Normal}(\mu_i, \sigma) \qquad \Pr(W_i \mid \mu_i, \sigma)$$

$$\mu_i = \alpha + \beta(H_i - \bar{H})$$

$$\alpha \sim \text{Normal}(60, 10) \qquad \Pr(\alpha)$$

$$\beta \sim \text{LogNormal}(0, 1) \qquad \Pr(\beta)$$

$$\sigma \sim \text{Uniform}(0, 10) \qquad \Pr(\sigma)$$

Posterior is $\Pr(\alpha, \beta, \sigma \mid W, H)$

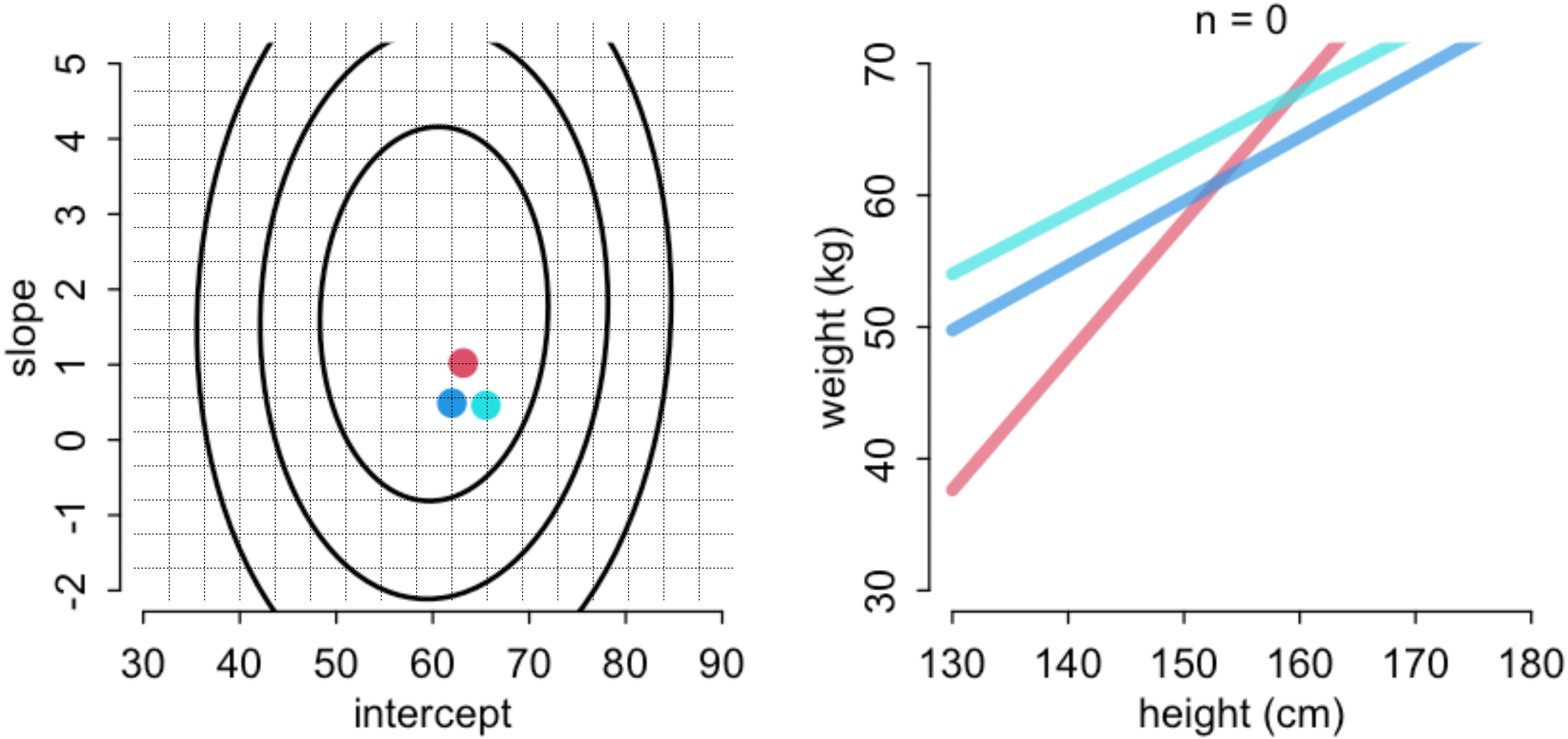
Fitting the model

$$\Pr(\alpha, \beta, \sigma \mid W, H) \propto \text{Normal}(W \mid \mu, \sigma)$$
$$\times \text{Normal}(\alpha \mid 60, 10)$$
$$\times \text{LogNormal}(\beta \mid 0, 1)$$
$$\times \text{Uniform}(\sigma \mid 0, 10)$$

Grid approximation expensive:
100 values of each parameter => 1 million calculations

See page 85 in book for coded example

30 adults from Howell1



Approximate posterior

Many posterior distributions are approximately Gaussian

Instead of grid approximation, Gaussian approximation

Sometimes called **quadratic** or **Laplace approximation**

See page 41 in book for more detail

Linear Regression

```
data(Howell1)
d <- Howell1[Howell1$age>=18,]
```

Drawing the Owl

(1) Question/goal/estimand

(2) Scientific model

(3) Statistical model(s)

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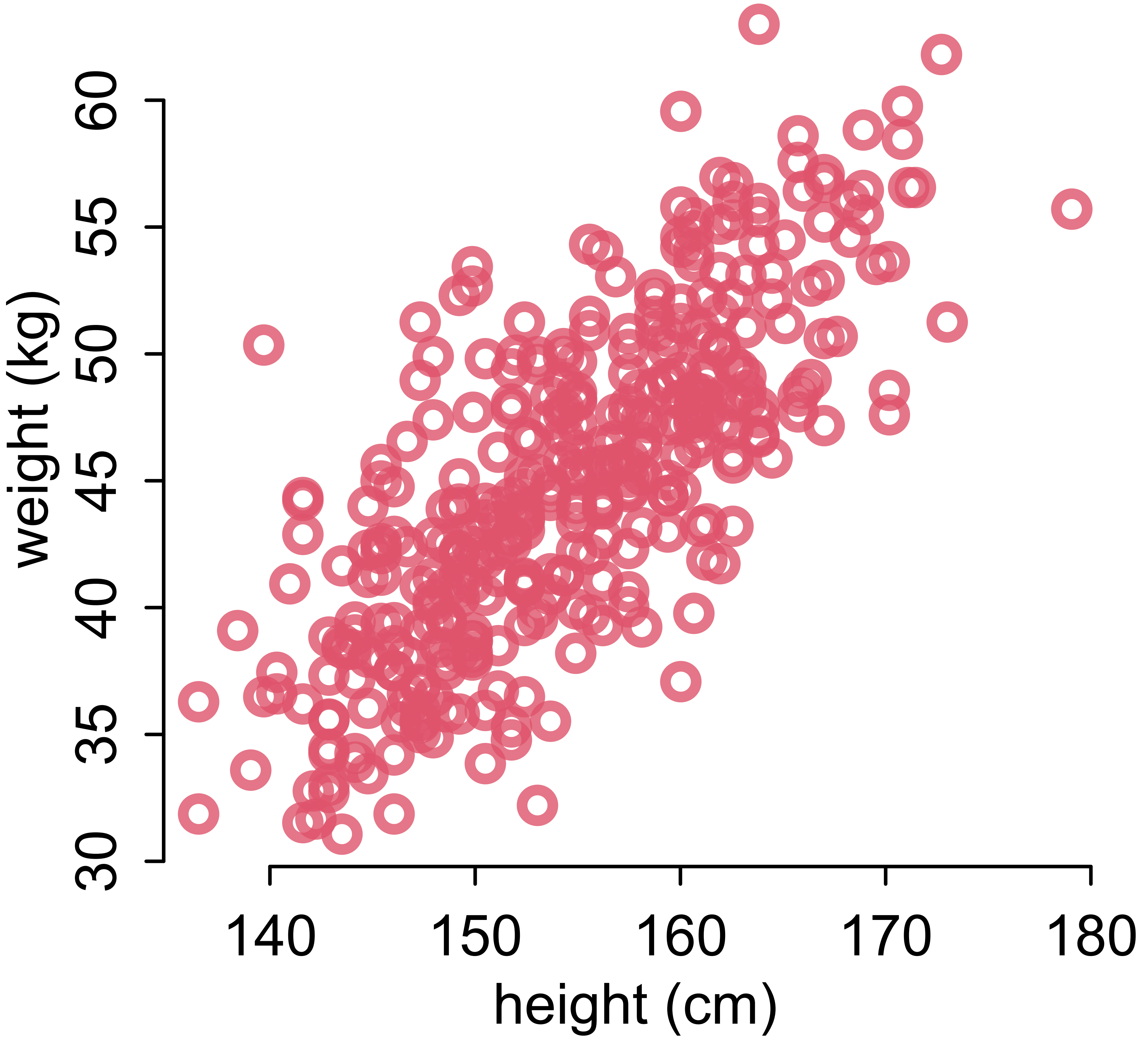


Simulation-Based Validation

Bare minimum: Test statistical model with simulated observations from scientific model

Golem might be broken

Even working golems might not deliver what you hoped

Strong test: Simulation-Based Calibration

Fahrvergnügen

Model formula

```
W ~ dnorm(mu,sigma),
mu <- a + b*(H-Hbar),
a ~ dnorm(60,10),
b ~ dlnorm(0,1),
sigma ~ dunif(0,10)
```

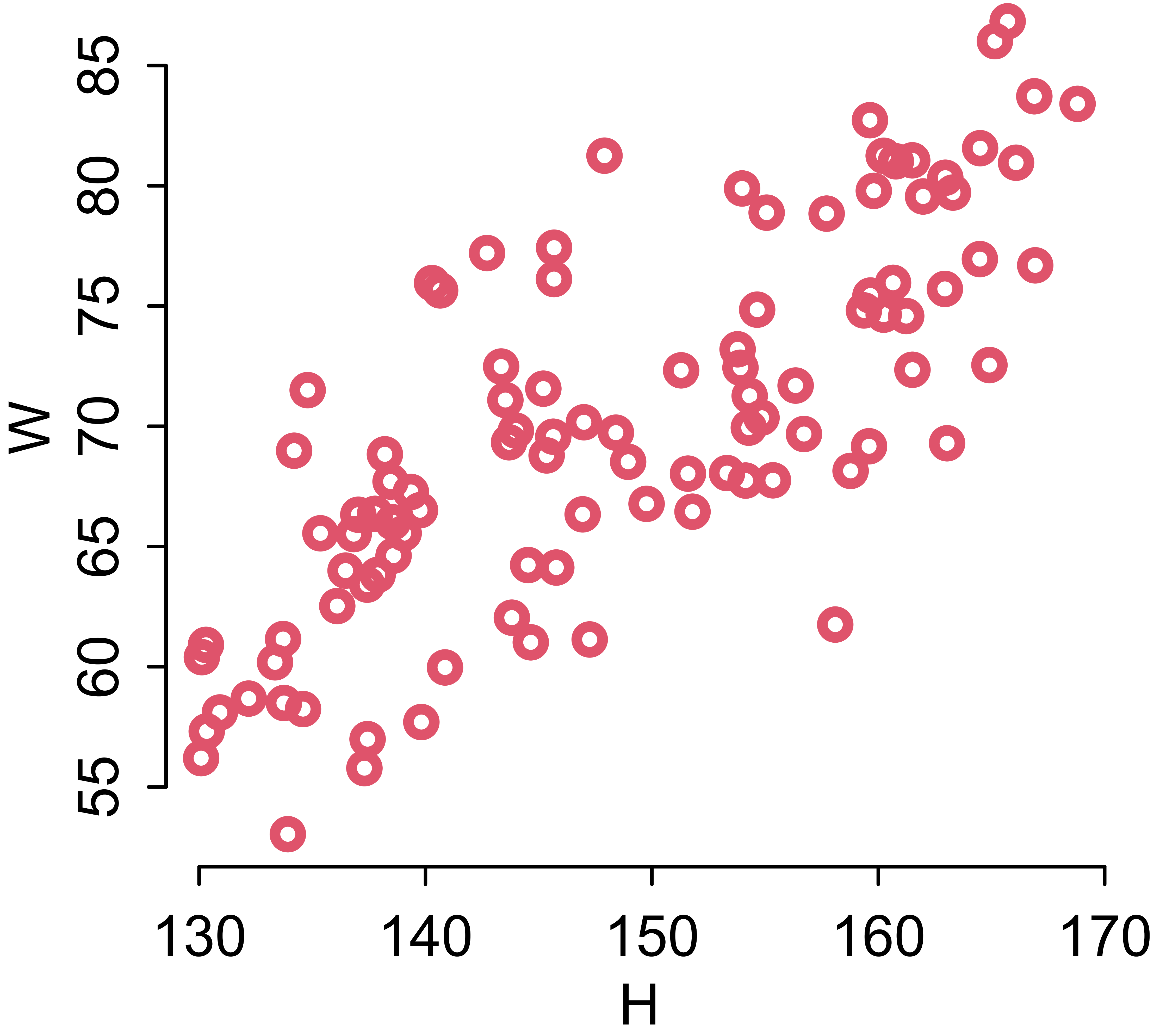
$$
\begin{aligned}
W_i &\sim \text{Normal}(\mu_i, \sigma) \\
\mu_i &= \alpha + \beta(H_i - \bar{H}) \\
\alpha &\sim \text{Normal}(60,10) \\
\beta &\sim \text{LogNormal}(0,1) \\
\sigma &\sim \text{Uniform}(0,10)
\end{aligned}
$$

First validate with simulation

```r
alpha <- 70
beta <- 0.5
sigma <- 5
n_individuals <- 100
H <- runif(n_individuals,130,170)
mu <- alpha + beta*(H-mean(H))
W <- rnorm(n_individuals,mu,sigma)

dat <- list( H=H , W=W , Hbar=mean(H) )

m_validate <- quap(
    alist(
        W ~ dnorm(mu,sigma),
        mu <- a + b*(H-Hbar),
        a ~ dnorm(60,10),
        b ~ dlnorm(0,1),
        sigma ~ dunif(0,10)
    ), data=dat )
```



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mu <- alpha + beta*(H-mean(H))
W <- rnorm(n_individuals,mu,sigma)

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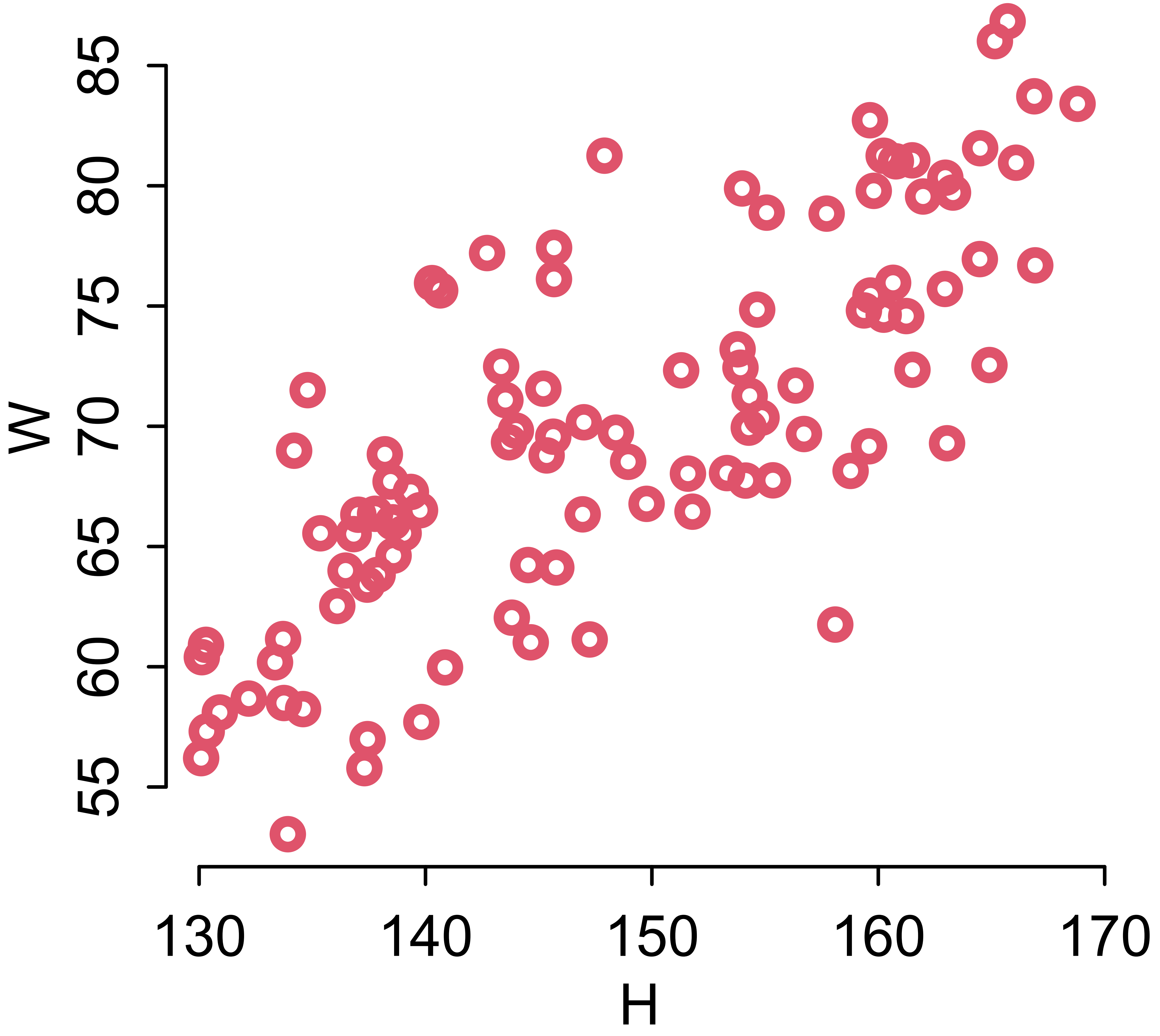
        mu <- a + b*(H-Hbar),
        a ~ dnorm(60,10),
        b ~ dlnorm(0,1),
        sigma ~ dunif(0,10)
    ), data=dat )
```

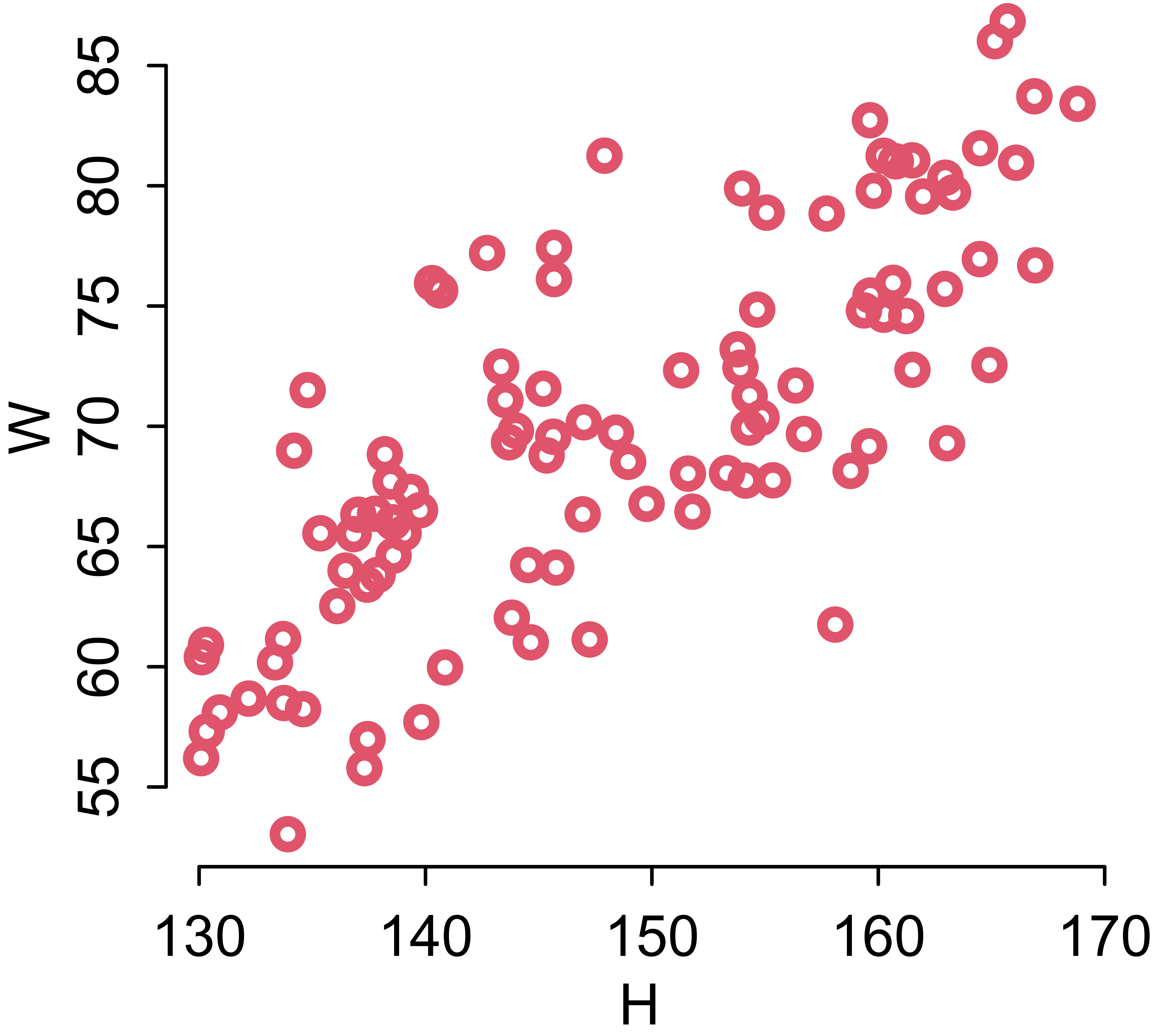


First validate with simulation

```
alpha <- 70
beta <- 0.5
sigma <- 5
n_individuals <- 100
H <- runif(n_individuals,130,170)
mu <- alpha + beta*(H-mean(H))
W <- rnorm(n_individuals,mu,sigma)

dat <- list( H=H , W=W , Hbar=mean(H) )

m_validate <- quap(
    alist(
        W ~ dnorm(mu,sigma),
        mu <- a + b*(H-Hbar),
        a ~ dnorm(60,10),
        b ~ dlnorm(0,1),
        sigma ~ dunif(0,10)
    ), data=dat )
```



First validate with simulation

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alpha <- 70
beta <- 0.5
sigma <- 5
n_individuals <
H <- runif(n_individuals,130,170)
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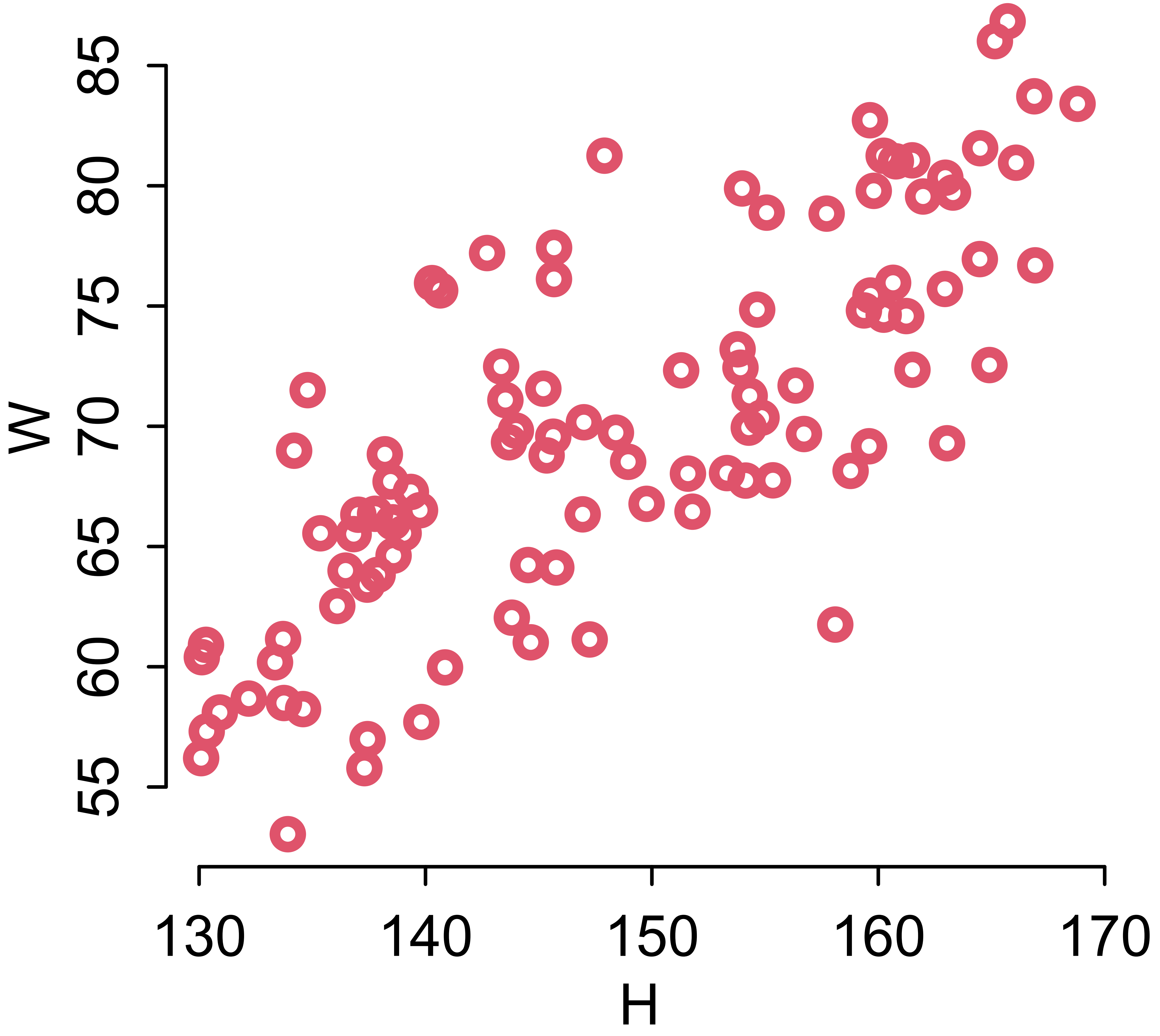
dat <- list( H=H , W=W , Hbar=mean(H) )

m_validate <- quap(
    alist(
        W ~ dnorm(mu,sigma),
        mu <- a + b*(H-Hbar),
        a ~ dnorm(60,10),
        b ~ dlnorm(0,1),
        sigma ~ dunif(0,10)
    ), data=dat )
```

```
> precis(m_validate)
       mean   sd  5.5% 94.5%
a     69.57 0.45 68.85 70.28
b      0.49 0.04  0.43  0.56
sigma  4.48 0.32  3.97  4.98
>
```



Now with the real data

```
data(Howell1)
d <- Howell1
d <- d[ d$age>=18 , ]

dat <- list(
    W = d$weight,
    H = d$height,
    Hbar = mean(d$height) )

m_adults <- quap(
    alist(
        W ~ dnorm(mu,sigma),
        mu <- a + b*(H-Hbar),
        a ~ dnorm(60,10),
        b ~ dlnorm(0,1),
        sigma ~ dunif(0,10)
    ), data=dat )
```

$$W_i \sim \text{Normal}(\mu_i, \sigma)$$
$$\mu_i = \alpha + \beta(H_i - \bar{H})$$
$$\alpha \sim \text{Normal}(60,10)$$
$$\beta \sim \text{LogNormal}(0,1)$$
$$\sigma \sim \text{Uniform}(0,10)$$

Obey The Law

First Law of Statistical Interpretation:

The **parameters are not independent** of one another and cannot always be independently interpreted

Instead:

Push out **posterior predictions** and describe/interpret those

```
> precis(m_adults)
       mean   sd  5.5% 94.5%
a     45.00 0.23 44.64 45.36
b      0.63 0.03  0.58  0.68
sigma  4.23 0.16  3.97  4.48
>
```

```
> post <- extract.samples(m_adults)
> head(post)
         a         b    sigma
1 45.14733 0.7045790 4.380254
2 44.97759 0.6461353 4.372925
3 44.94856 0.6537192 4.111149
4 44.85016 0.6597310 4.379347
5 44.75898 0.6532690 4.200026
6 44.91711 0.6090434 4.105432
>
```

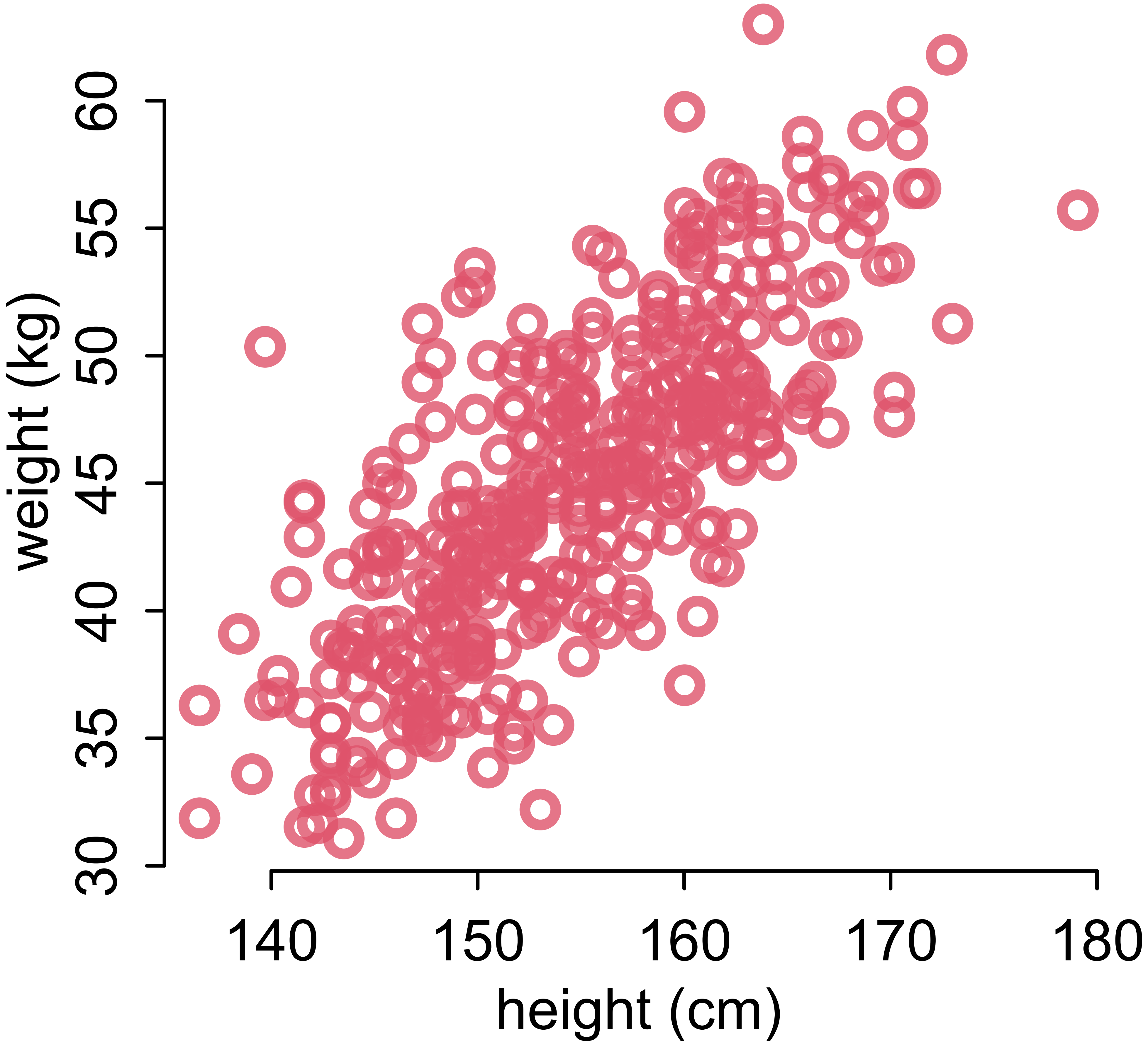
Posterior predictive distribution

(1) Plot the sample

(2) Plot the posterior mean

(3) Plot uncertainty of the mean

(4) Plot uncertainty of predictions



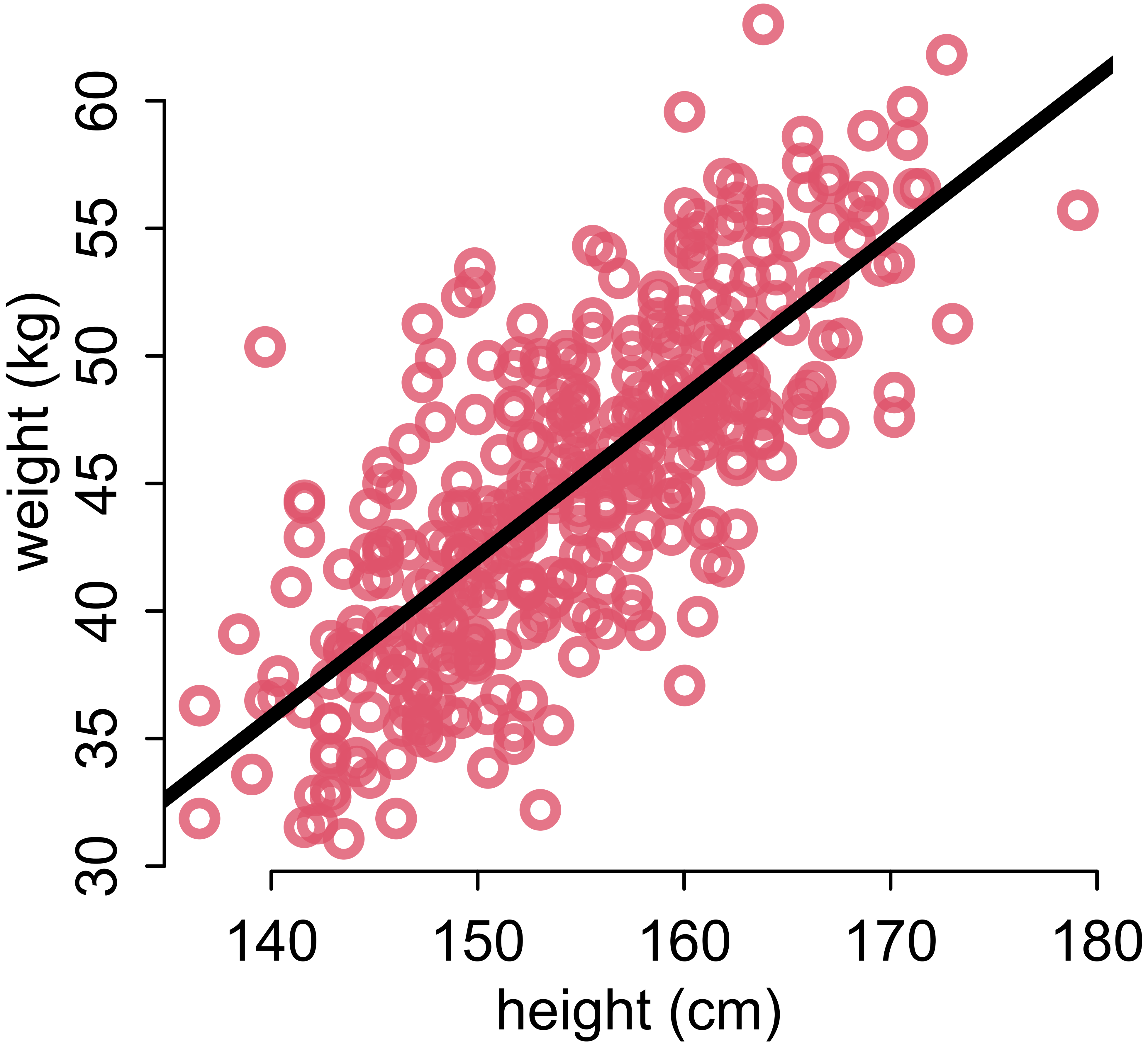
Posterior predictive distribution

(1) Plot the sample

(2) Plot the posterior mean

(3) Plot uncertainty of the mean

(4) Plot uncertainty of predictions



Posterior predictive distribution

(1) Plot the sample

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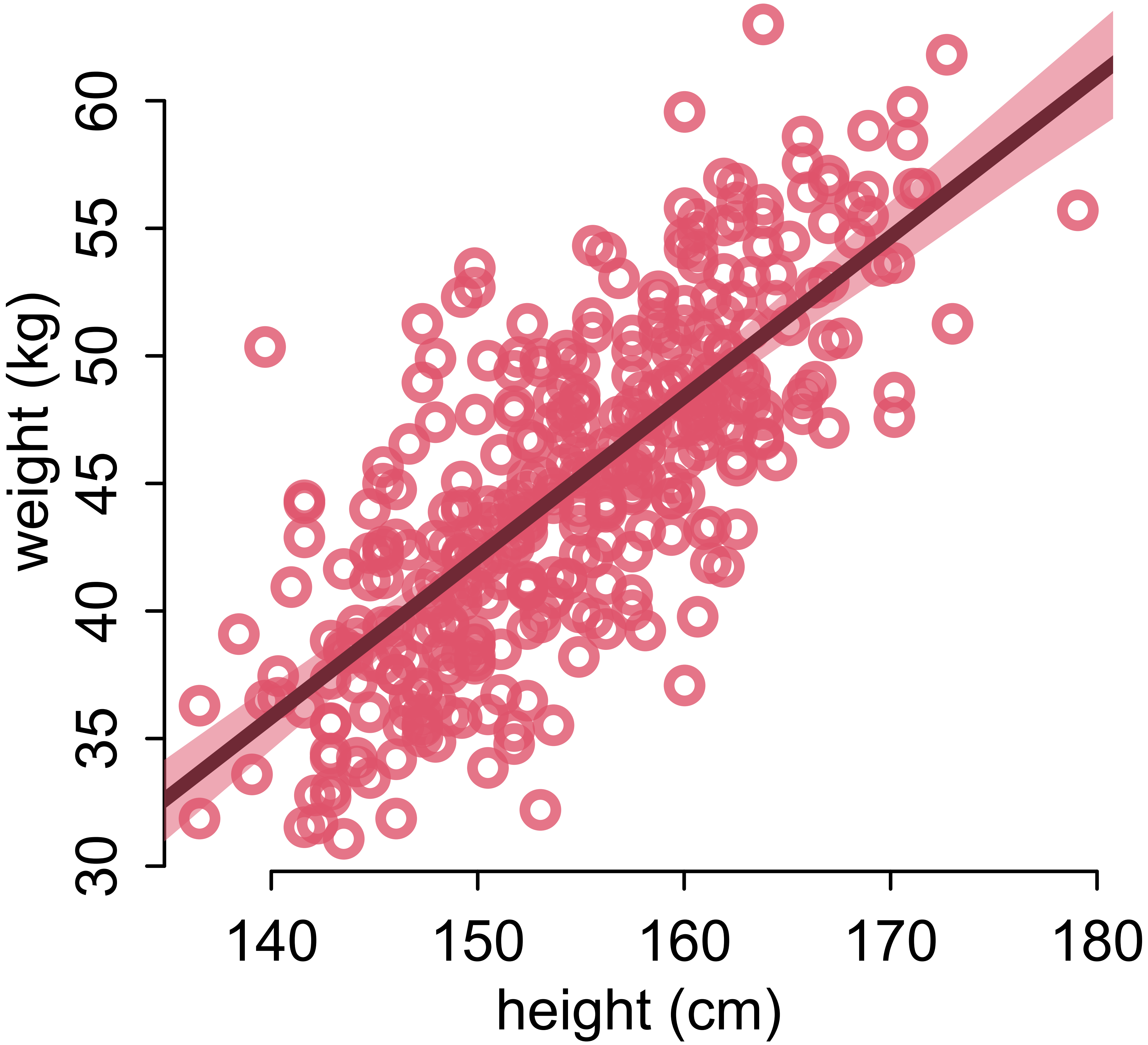

Posterior predictive distribution

(1) Plot the sample

(2) Plot the posterior mean

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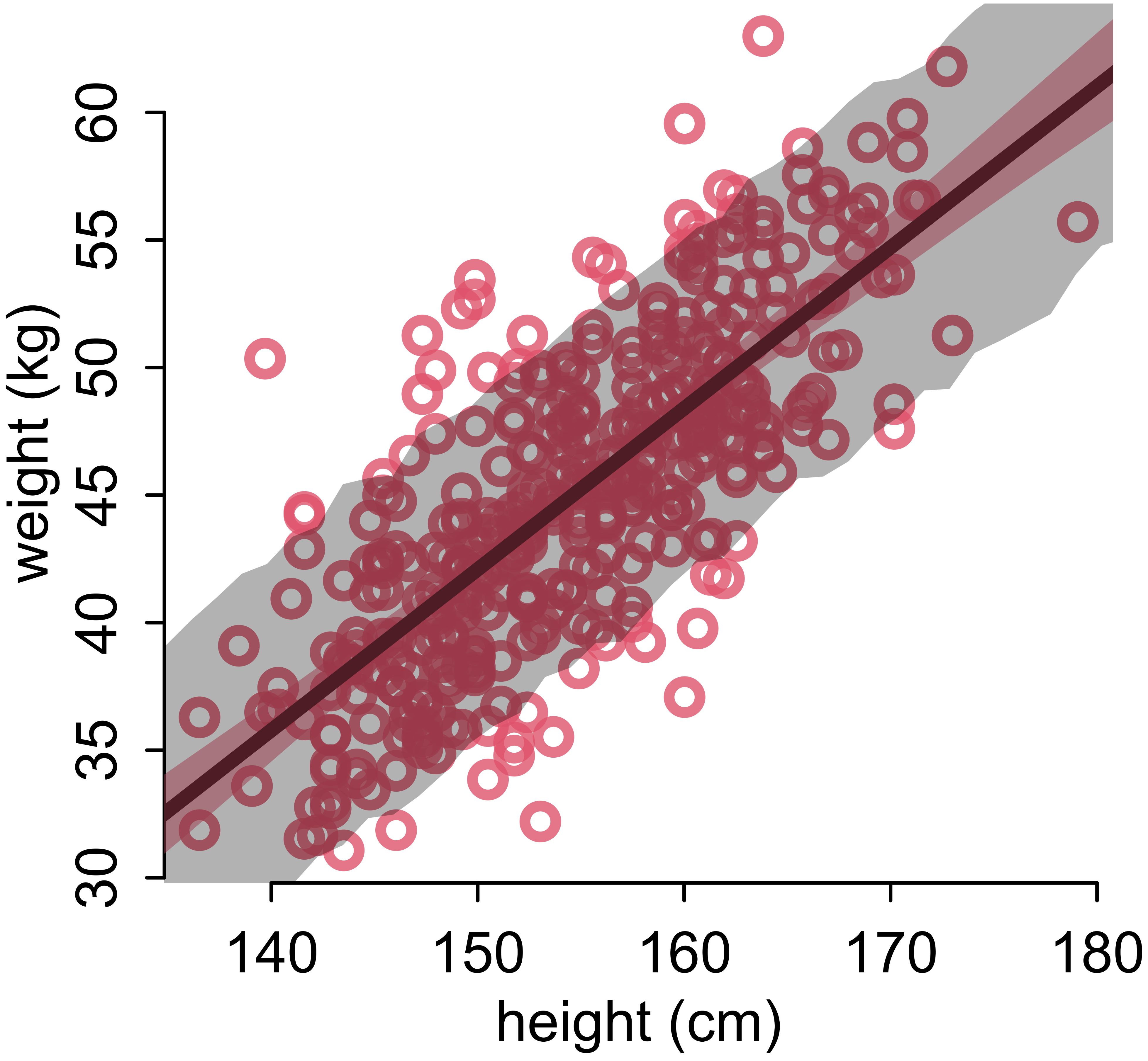
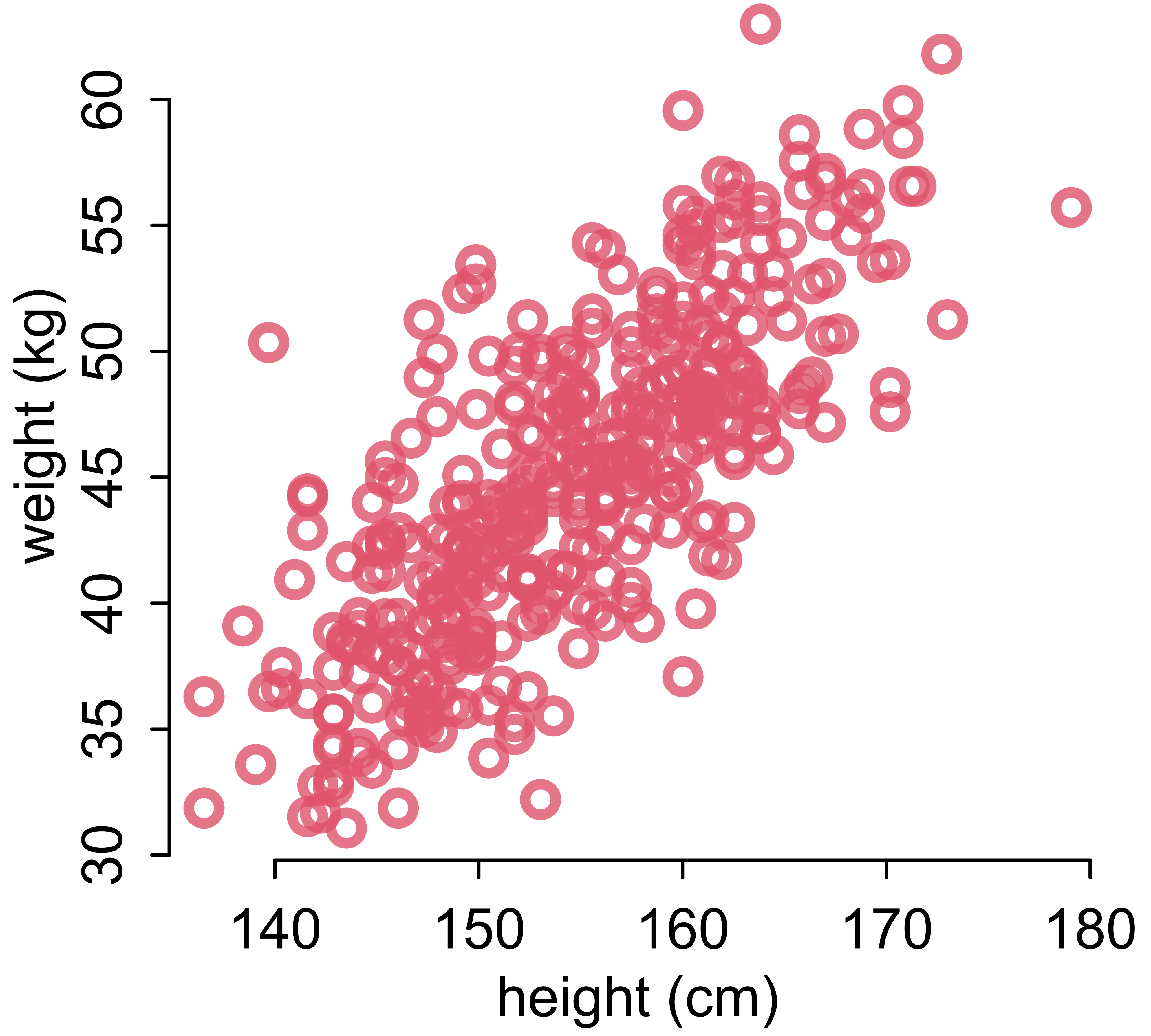


Posterior predictive distribution

```
# plot sample
col2 <- col.alpha(2,0.8)
plot( d$height , d$weight , col=col2 , lwd=3 ,
   cex=1.2 , xlab="height (cm)" , ylab="weight (kg)" )
```

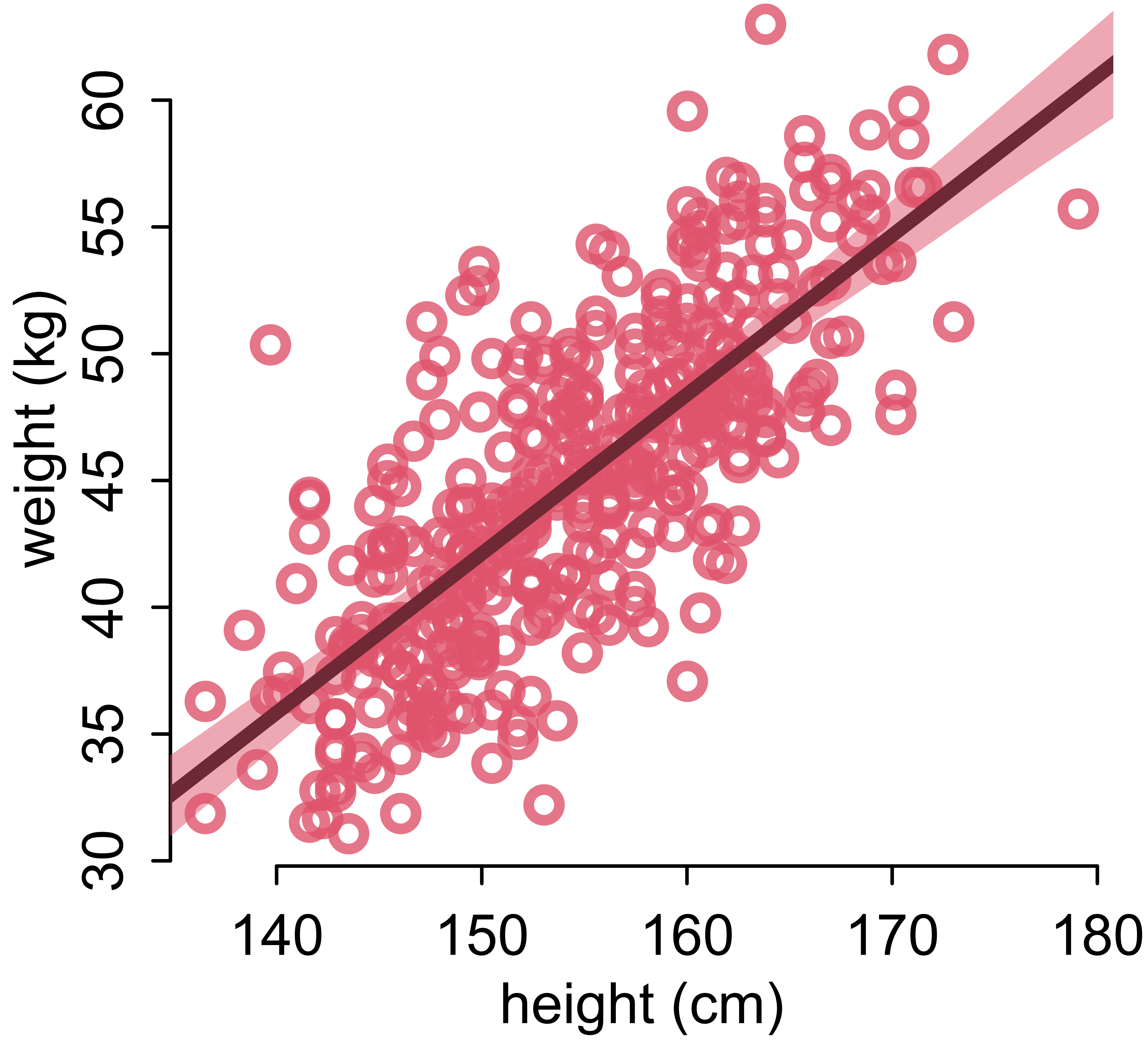


See 4.4.3 starting page 98 in book

Posterior predictive distribution

```
# plot sample
col2 <- col.alpha(2,0.8)
plot( d$height , d$weight , col=col2 , lwd=3 ,
   cex=1.2 , xlab="height (cm)" , ylab="weight (kg)" )

# expectation with 99% compatibility interval
xseq <- seq(from=130,to=190,len=50)
mu <- link(m0,data=list(H=xseq,Hbar=mean(d$height)))
lines( xseq , apply(mu,2,mean) , lwd=4 )
shade( apply(mu,2,PI,prob=0.99) , xseq ,
   col=col.alpha(2,0.5) )
```



See 4.4.3 starting page 98 in book

Posterior predictive distribution

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# plot sample
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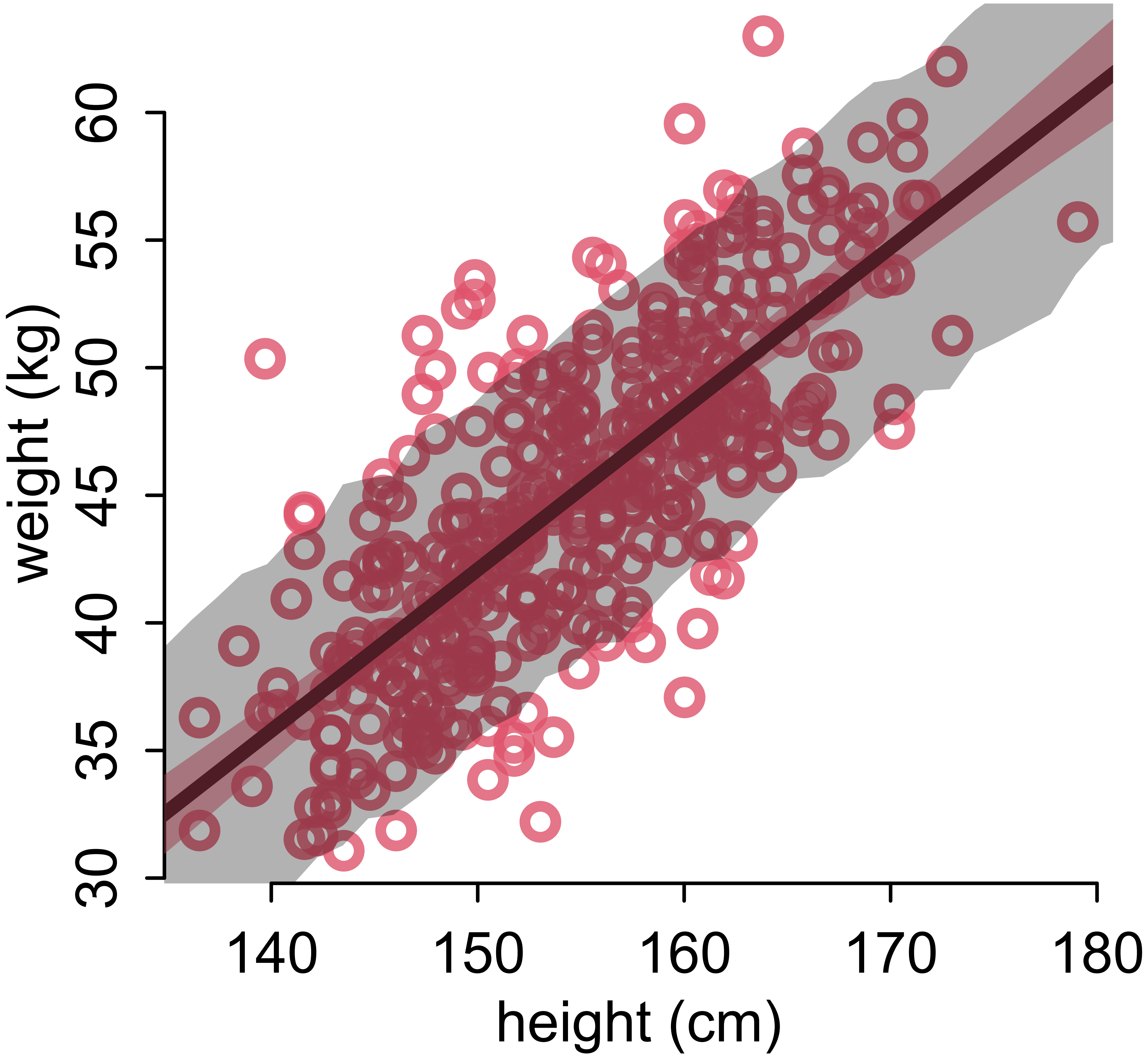
xseq <- seq(from=130,to=190,len=50)
mu <- link(m0,data=list(H=xseq,Hbar=mean(d$height)))
lines( xseq , apply(mu,2,mean) , lwd=4 )
shade( apply(mu,2,PI,prob=0.99) , xseq ,
   col=col.alpha(2,0.5) )

# 89% prediction interval
W_sim <- sim(m0,data=list(H=xseq,Hbar=mean(d$height)))
shade( apply(W_sim,2,PI,prob=0.89) , xseq ,
   col=col.alpha(1,0.3) )
```



See 4.4.3 starting page 98 in book


120
110
100
90
80
70
60
50
40
30
20
BLOOD HEAT

Flexible Linear Thermometers

(2) Scientific model

How does **height** influence **weight**?

$$H \longrightarrow W$$

$$W = f(H)$$

"Weight is some function of height"

$$
\begin{aligned}
W_i &\sim \text{Normal}(\mu_i, \sigma) \\
\mu_i &= \alpha + \beta(H_i - \bar{H}) \\
\alpha &\sim \text{Normal}(60, 10) \\
\beta &\sim \text{LogNormal}(0, 1) \\
\sigma &\sim \text{Uniform}(0, 10)
\end{aligned}
$$

Course Schedule

Week 1	Bayesian inference	Chapters 1, 2, 3
Week 2	Linear models & Causal Inference	Chapter 4
Week 3	Causes, Confounds & Colliders	Chapters 5 & 6
Week 4	Overfitting / Interactions	Chapters 7 & 8
Week 5	MCMC & Generalized Linear Models	Chapters 9, 10, 11
Week 6	Integers & Other Monsters	Chapters 11 & 12
Week 7	Multilevel models I	Chapter 13
Week 8	Multilevel models II	Chapter 14
Week 9	Measurement & Missingness	Chapter 15
Week 10	Generalized Linear Madness	Chapter 16

`https://github.com/rmcelreath/statrethinking_2022`