Introduction to Bayesian Statistics

Part 3
Prior & Posterior Distributions



### This lecture

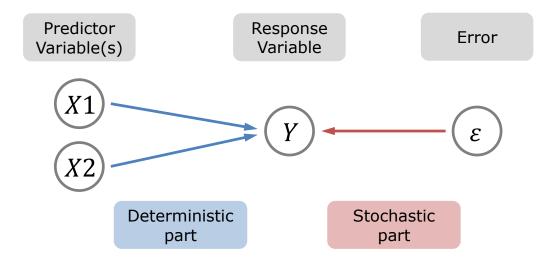
Short summary of last lecture

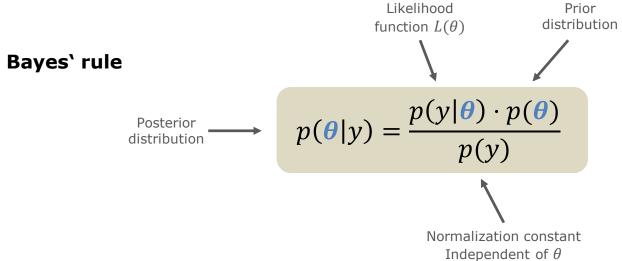
Some useful distributions

The prior distribution

The posterior distribution

Posterior predictions and model evaluation





Update beliefs (prior) by gaining new information (data & likelihood)

Posterior distribution used for quantitative & direct statements on research questions

Don't have access to posterior distribution Approximate by MCMC sampling

- 1) Research question (hypotheses)
- 2) Data collection
- 3) Statistical model
- 4) Prior distribution choice
- 5) Model fitting (MCMC)
- 6) Evaluate model output
- 7) Quantitative statements on hypotheses

Revise model

- Example: number of individuals from a population
   of N = 10 that survive the winter
- y discrete and bounded variable with outcomes 0, 1, 2, ..., 10
- Average survival probability  $\theta = 0.6 (60\%)$
- Binomial distribution:  $y \sim \text{Binomial}(N, \theta)$  random variable "distributed as" parameters: size N probability  $\theta$

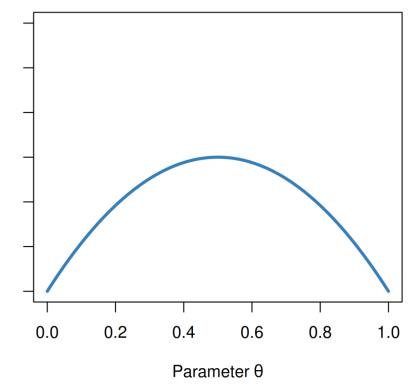


#### **Prior distribution**

Chosen by you

Density known over full parameter range

$$p(\theta) = \text{dbeta}(\theta \mid 2,2)$$

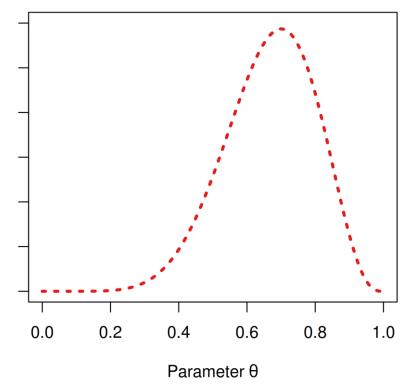


#### **Likelihood function**

Defined by **your** data and **your** statistical model (deterministic & stochastic part)

Can be computed for every single parameter value But values not known over full parameter range

$$L(\theta) = \prod_{i=1}^{n} p(y_i | \theta)$$
  
=  $\prod_{i=1}^{n} dBinom(survived_i, total_i | \theta)$ 



#### **Posterior distribution**

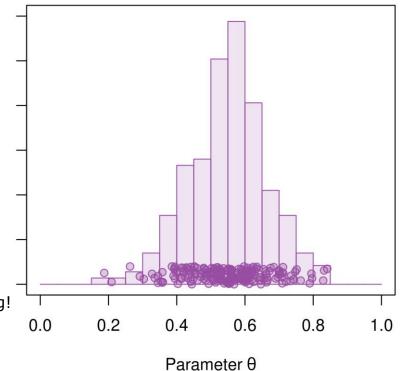
Software **output**: approximation by MCMC sampling

$$p(\theta|y) \sim p(\theta) \cdot L(\theta)$$

Represented by samples  $\theta_1, \theta_2, \theta_3, ..., \theta_{1000}$  only!

Posterior density values  $p(\theta_1|y), p(\theta_2|y), ..., p(\theta_{1000}|y)$  not required, don't need to be saved

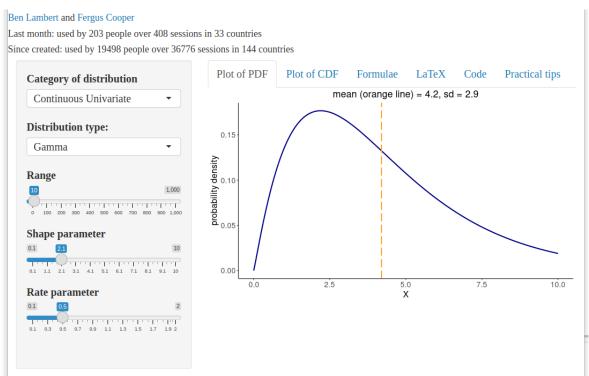
**Counting instead of integrating** for hypotheses testing!



Super easy once you have a posterior sample

### **Distribution zoo app**

#### https://ben18785.shinyapps.io/distribution-zoo/



## **Probability playground app**

#### https://www.acsu.buffalo.edu/~adamcunn/probability/probability.html

The gamma distribution is a "waiting time" distribution. Suppose events occur independently and randomly with an average time between events of  $\beta$ . The waiting time until  $\alpha$  events have occurred is a gamma( $\alpha$ ,  $\beta$ ) random variable.

The parameter  $\alpha$  is known as the shape parameter, and the parameter  $\beta$  is called the scale parameter. Increasing  $\alpha$  leads to a more "peaked" distribution, while increasing  $\beta$  increases the "spread" of the distribution.

The function  $\Gamma(s)$  in the denominator of the pdf and cdf denotes the <u>gamma function</u>, while the function  $\gamma(s,x)$  in the cdf denotes the <u>lower incomplete</u> gamma function.

Parameter	Range	Description
α	a > 0	Shape parameter
β	β > 0	Scale parameter

Probability Density Function	Support
$f(x; \alpha, \beta) = \frac{1}{\Gamma(\alpha)\beta^{\alpha}} x^{\alpha - 1} e^{-x/\beta}$	$0 \le x < \infty$

Mean	Variance	
αβ	$\alpha \beta^2$	

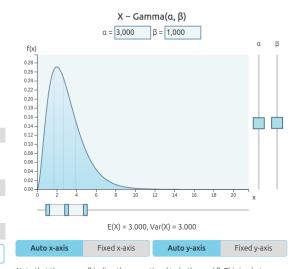
A radioactive substance emits two alpha particles every second on		
average. Let $X$ be the waiting time for three particles to be	3.000	0.5000
emitted.		

Cars arrive at an intersection at an average rate of one every two minutes. Let  $\it X$  be the waiting time until five cars have arrived. 5.000 2.000

6.000 5.000

Garage door lightbulbs last five years on average and are replaced when they fail. Let  $\it X$  be the time that a box of six bulbs lasts.

Example



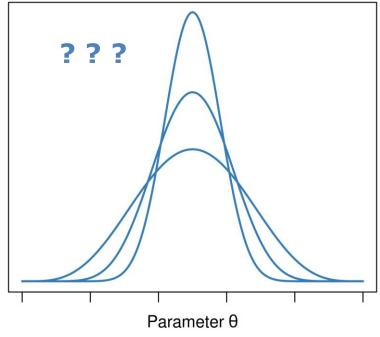
Note that the mean  $\alpha\beta$  is directly proportional to both  $\alpha$  and  $\beta$ . This is what we would intuitively expect - the mean time spent waiting for  $\alpha$  events to occur increases in proportion to both the number of events  $\alpha$  and the average time  $\beta$  between events.

The shape of the pdf depends on the parameter  $\alpha$ . For values of  $\alpha \le 1$ , the pdf is strictly decreasing. For values of  $\alpha > 1$ , the pdf is unimodal.

Prior distributions

### **Prior information**

- Priors represent belief about model parameters (for example effect size of an x-y association)
- Traditional viewpoint: before we see the data y
   Data information is already contained in the likelihood!
- Use information from
  - General expectation / reasonable range
  - Previous experiments
  - Related studies in the literature
- *Modern* viewpoint:
  - Priors used for regularization
  - Prior predictive checks:Are predictions from the prior in the same range / magnitude as observed data?
- Priors are problem-specific



### **Types of priors**

#### Flat / uninformative prior

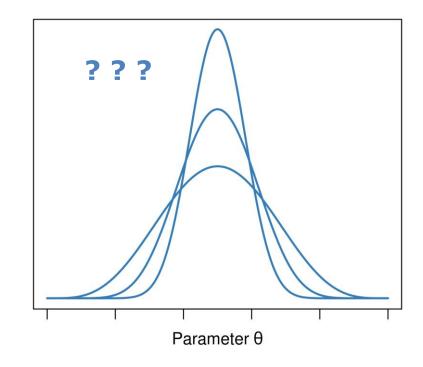
- You know absolutely nothing about the parameter
- This is rarely the case

#### Vague / weakly informative prior

- You have a vague idea
- For example about the order of magnitude, or sign

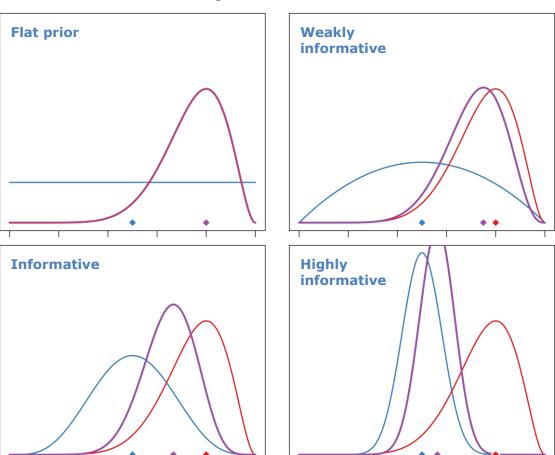
#### **Informative prior**

• You have some idea about the parameter



→ There is no formal definition of these terms!

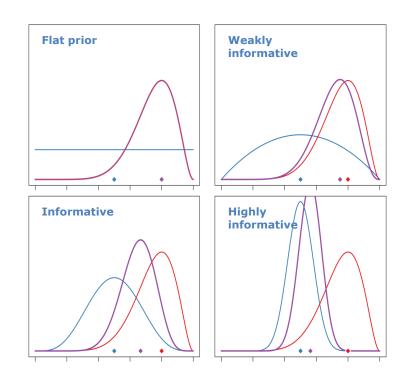
### **Prior affects the posterior**



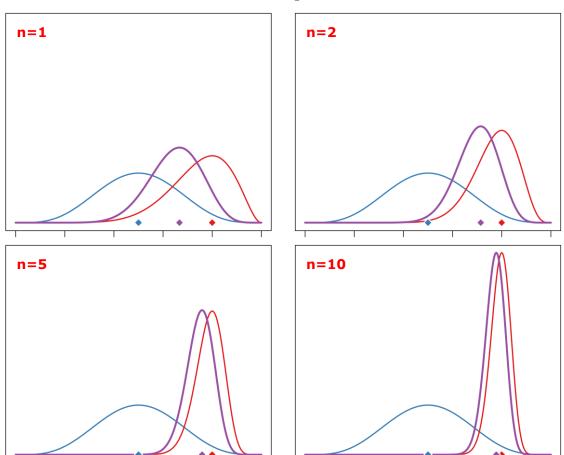
- Example: survival rate  $\theta \in [0,1]$
- 1 Observation: 8/10 survived
- Binomial likelihood function
- Priors all beta distributions with mean = 0.5
- but different standard deviations
   (concentration around mean)

### **Prior affects the posterior**

- For flat priors, posterior is proportial to likelihood
- For any other prior, posterior is a compromise between prior and likelihood
- For weakly informative priors, even little data dominates the posterior
- More informative priors (lower sdev)
   draw the posterior mean further away from
   the maximum likelihood estimate (MLE)
   towards the prior mean



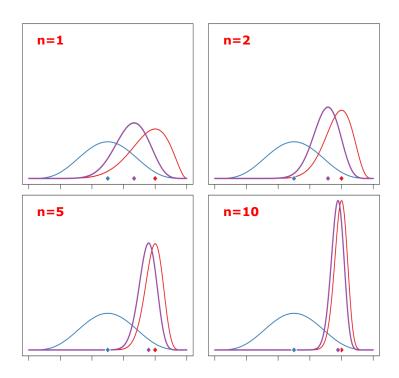
## **Likelihood affects the posterior**



- Example: survival rate  $\theta \in [0,1]$
- "informative prior" from last slide
- Different numbers of obs. *n*
- Width of likelihood function decreases with n (higher certainty)

## Likelihood affects the posterior

- For small datasets (little experimental evidence),
   the prior can dominate the posterior
- In large datasets, likelihood can dominate the posterior
- Number of observations decreases the width of the likelihood and therefore also posterior uncertainty (stronger experimental evidence)
- Number of observations draws posterior mean towards maximum likelihood estimate (MLE)

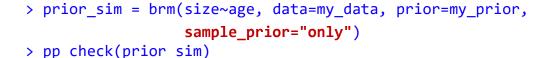


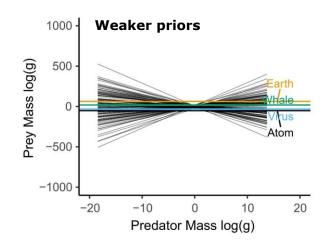
# **Are priors subjective?**

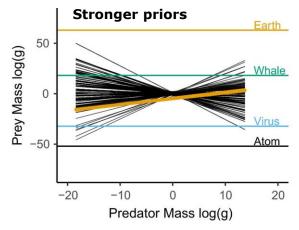


## **Prior predictive checks**

- Test if priors make sense
- Generate predictions with samples from prior distribution
- Compare them to the range of observed data
- Helpful when using data transformations
   (GLMs use nonlinear link-functions, like log or logit)
- Traditional viewpoint (old school):
   Priors should be chosen before even looking at the data
- Modern viewpoint: Prior predictive simulations are useful!
   E.g. McElreath: Statistical Rethinking (2020, 2nd ed.)







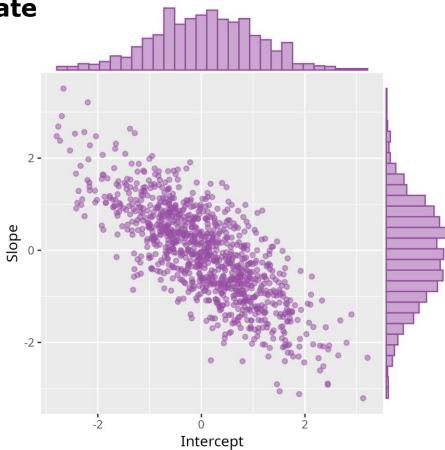
## brms default priors

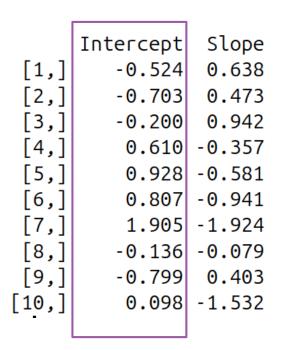
- brms automatically chooses priors for intercepts and standard deviations
- Based on the observed data
- Overriding intercept default prior must be handled carefully:
   brms internally uses mean-centered predictors, which changes intercept
- → My advice: leave them unless you want to include specific information on these parameters
- brms default priors for effect sizes / regression **slopes** are flat priors!
- → Choose your own priors for them!

Posterior distribution

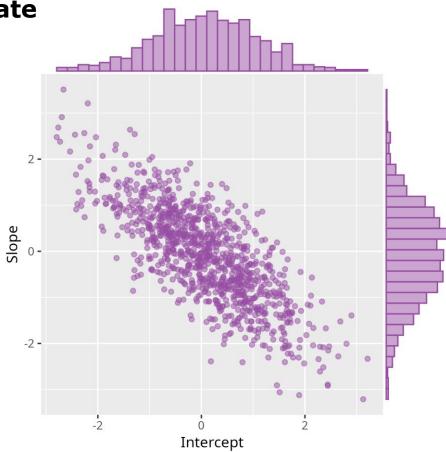
	Intercept	Slope
[1,]	-0.524	0.638
[2,]	-0.703	0.473
[3,]	-0.200	0.942
[4,]	0.610	-0.357
[5,]	0.928	-0.581
[6,]	0.807	-0.941
[7,]	1.905	-1.924
[8,]	-0.136	-0.079
[9,]	-0.799	0.403
[10,]	0.098	-1.532

MCMC output is a matrix / dataframe !



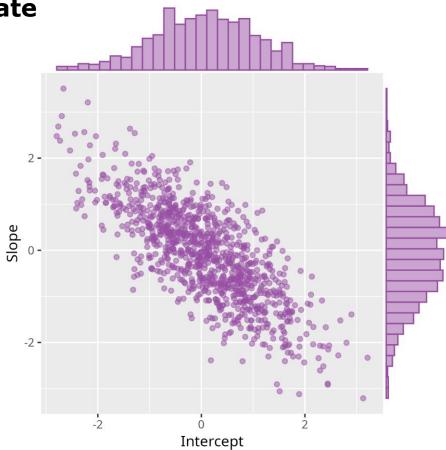


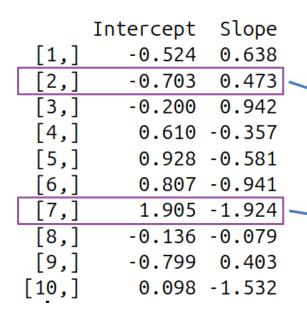
Each **column** contains all samples of 1 parameter



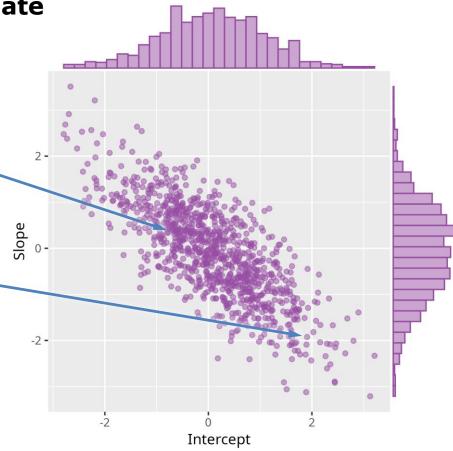
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Each **row** contains 1 sample of all parameters

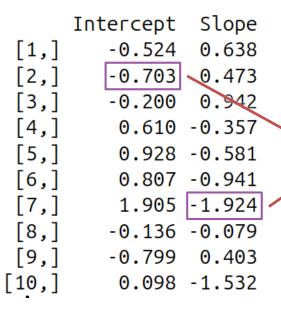




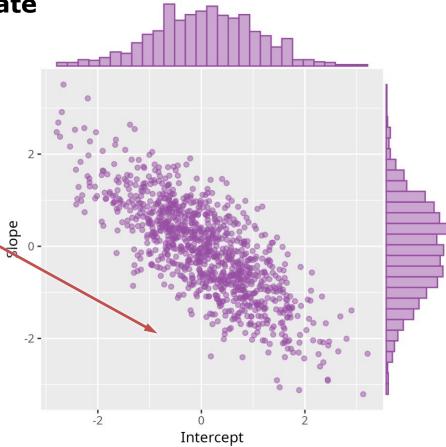
A random row is part of the posterior sample



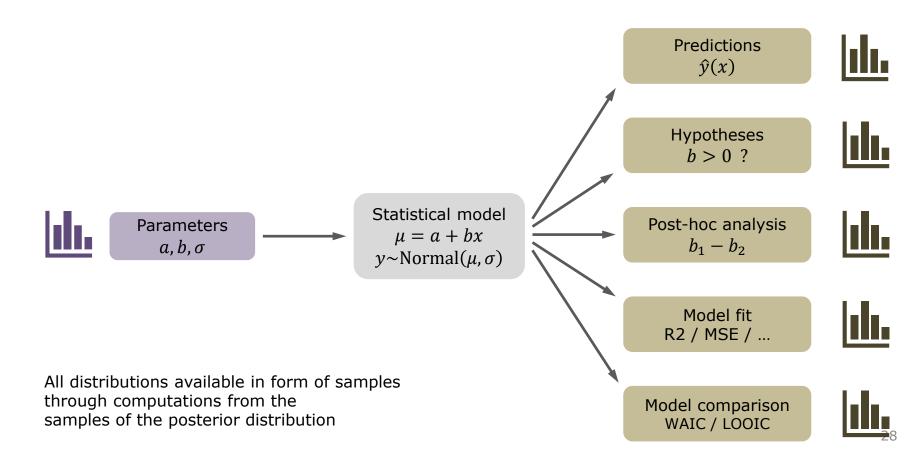




Random entries of each column (mixed) are **not** part of the posterior sample



## **Everything is a distribution!**



Posterior predictions

## **Example:**

Example: linear relationship between age x and body mass y of sea turtles

Deterministic part:  $\mu(x) = a + b \cdot x$ 

Stochastic part:  $y \sim \text{Normal}(\mu, \sigma)$ 

Parameters: a intercept

b slope

 $\sigma$  standard deviation



### **Model output**

```
> fit1 = brm(weight ~ age, data=data)
> summary(fit1)

Family: gaussian
Links: mu = identity: sigma = identity
```

```
Links: mu = identity; sigma = identity

Formula: weight ~ age

Data: data (Number of observations: 8)

Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;

total post-warmup draws = 4000
```

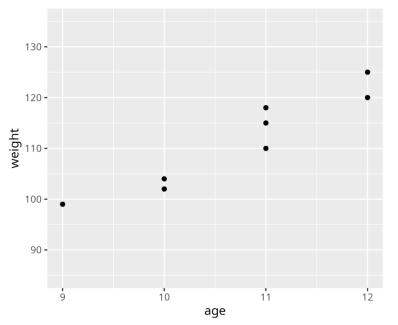
Regression Coefficients:

Regression Coerrectenes.							
		Est.Error					
Intercept	19.99	16.24	-13.79	53.23	1.00	2848	1916
age	8.53	1.50	5.46	11.59	1.00	2817	1838

Further Distributional Parameters:

```
Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS sigma 4.01 1.43 2.19 7.73 1.00 1606 1766
```

Draws were sampled using sampling(NUTS). For each parameter, Bulk\_ESS and Tail\_ESS are effective sample size measures, and Rhat is the potential scale reduction factor on split chains (at convergence, Rhat = 1).



**mean** and **sdev** of parameters' posterior distribution

### How to predict?

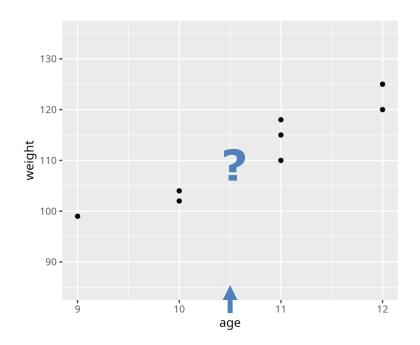
What is the predicted weight at age x = 10.5 ?

Deterministic part:  $\mu(x) = a + b \cdot x$ 

We have mean values for intercept a=19.99 and slope b=8.53

However, in Bayesian statistics, we **don't** use mean parameter values to make prediction.

We use the **whole posterior distribution** to quantify prediction uncertainty correctly!



### The fitted distribution

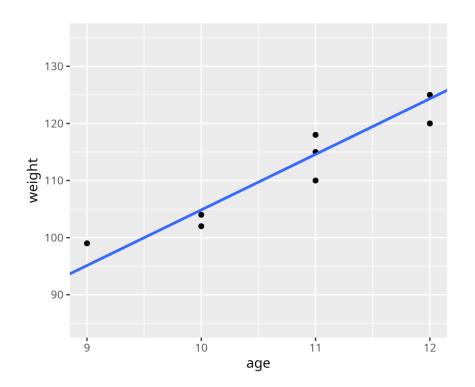
draw b	_Intercept	b_age	fitted(	age=10.5)	
1	7.473	9.738		109.720	
2	30.477	7.614		110.425	
3	22.153	8.273		109.022	
4	34.008	7.310		110.763	llh l
5	39.144	6.667	Deterministic part	109.147	
6	12.472	9.328	$\mu = a + b \cdot x$	110.415	
7	7.005	9.674		108.579	
8	-3.196	10.633		108.446	
9	23.362	8.309		110.602	100 110 120
10	23.745	8.247		110.342	$\mu(age = 10.5)$

Each sample from the posterior  $(a_i, b_i)$  generates 1 sample for,  $\mu_i(\text{age} = 10.5) = a_i + b_i \cdot 10.5$ 

> posterior\_epred(fit1, newdata=data.frame(age=10.5))

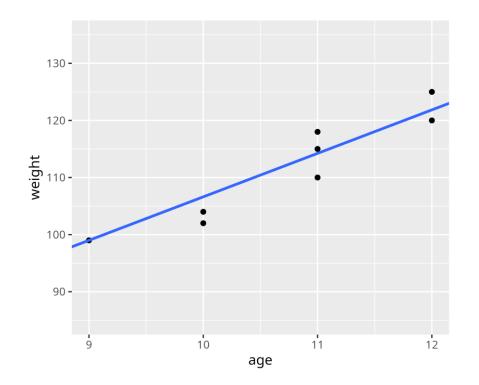
## Each posterior sample generates a regression line

<u>draw b</u>	_Intercept	b_age	sigma
1	7.473	9.738	4.128
2	30.477	7.614	3.456
3	22.153	8.273	3.474
4	34.008	7.310	4.200
5	39.144	6.667	4.456
6	12.472	9.328	3.671
7	7.005	9.674	4.045
8	-3.196	10.633	4.117
9	23.362	8.309	3.519
10	23.745	8.247	3.336
11	27.194	7.948	4.249
12	18.373	8.566	3.351
13	20.358	8.522	3.447
14	10.307	9.322	3.007
15	24.486	8.224	3.408



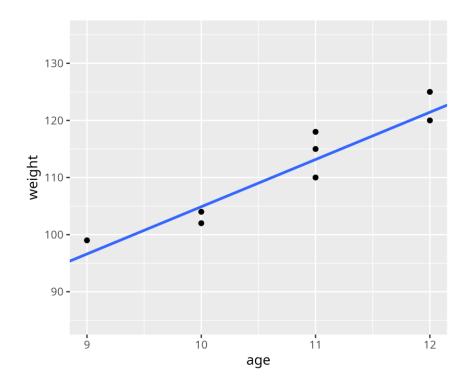
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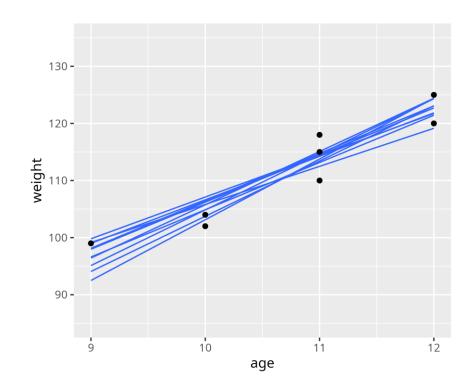
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#### **Credible intervals**

Distribution of fitted values / regression lines with **deterministic model part only** 

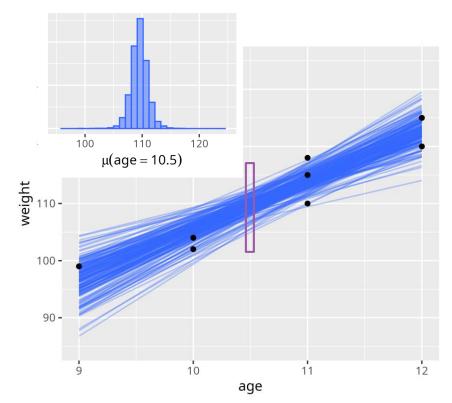
$$\mu_i(x) = a_i + b_i \cdot x$$
 (*i* = 1, ..., 1000)

Mean fitted value

$$\overline{\mu}(x) = \operatorname{mean}(\mu_1(x), \dots, \mu_{1000}(x))$$

95% intervals are called **credible intervals**. They quantify uncertainty of the regression line.

There is nothing magical about 95%, can also choose other intervals, e.g. 90%



> plot(conditional\_effects(fit1, spaghetti=TRUE, ndraws=200))

#### **Credible intervals**

Distribution of fitted values / regression lines with **deterministic model part only** 

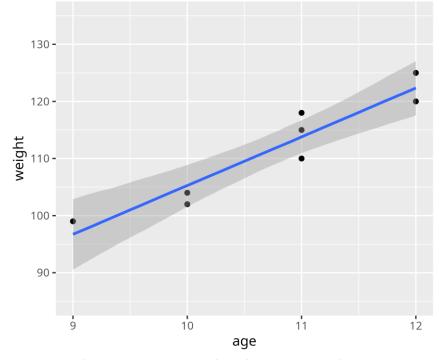
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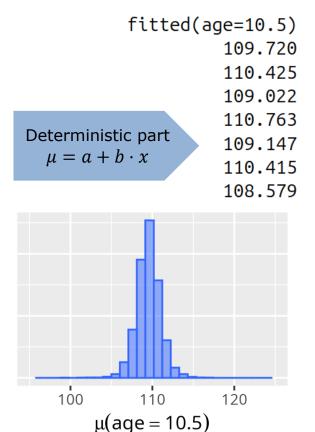
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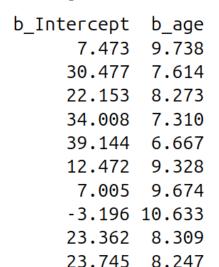
> plot(conditional\_effects(fit1), points=TRUE)

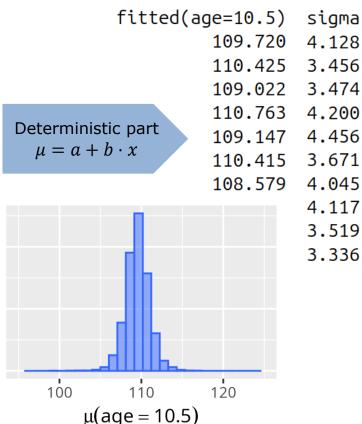
## The predictive distribution

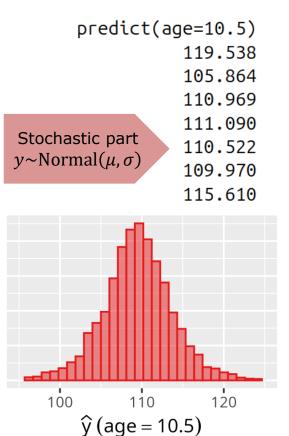
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### The predictive distribution







#### **Prediction intervals**

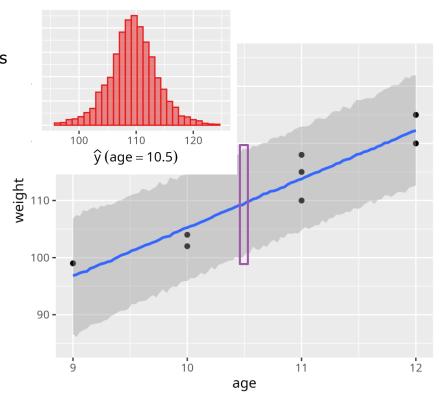
Predictions add random residual error to fitted values

Distribution of predicted values with **deterministic and stochastic model part** 

$$\widehat{y}_i(x) = \mu_i(x) + \varepsilon_i$$
 ( $i = 1, ..., 1000$ )  
 $\varepsilon_i \sim \text{Normal}(0, \sigma_i)$ 

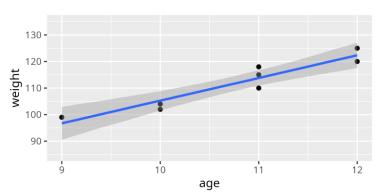
Same as:  $\widehat{y}_i(x) \sim \text{Normal}(\mu_i(x), \sigma_i)$ 

95% intervals are called **prediction intervals.**They quantify uncertainty of newly predicted data.
(Should contain around 95% of observed data.)



## Fitted vs. predictive

#### **Fitted**

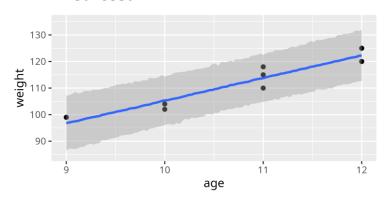


Mean regression line / curve under parameter uncertainty

"Credible intervals"

Uses deterministic model part only

#### **Predicted**



Predictive data distribution under parameter uncertainty and model residuals

"Prediction intervals"

Uses deterministic and stochastic model parts

### Fitted vs. predictive

#### **Fitted**

```
> fitted(fit1)
    Estimate Est.Error Q2.5 Q97.5
[1,] 105.25324 1.813620 101.59634 108.8769
[2,] 122.30603 2.343272 117.55827 127.0220
[3,] 113.77964 1.458628 110.92357 116.6928
[4,] 113.77964 1.458628 110.92357 116.6928
[5,] 96.72685 2.995963 90.55468 102.8774
[6,] 113.77964 1.458628 110.92357 116.6928
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```

Mean regression line / curve under parameter uncertainty

"Credible intervals"

Uses deterministic model part only

#### **Predicted**

Predictive data distribution under parameter uncertainty and model residuals

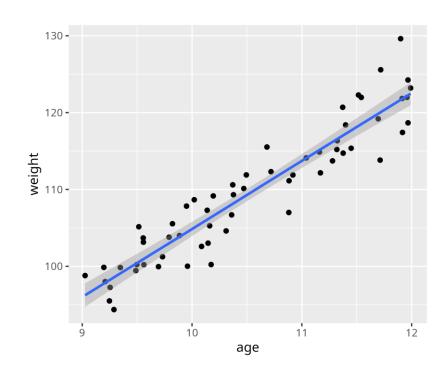
"Prediction intervals"

Uses deterministic and stochastic model parts

Posterior predictive checks

# **Linear regression assumptions**

- Independent observations.
   Systematic differences in y are because of x!
- 2. Trend of y follows (linear) prediction model  $\mu(x) = a + b \cdot x$
- 3. Residuals follow normal distribution  $\varepsilon \sim \text{Normal}(0,\sigma)$
- 4. Constant variance (standard deviation) across whole range of x



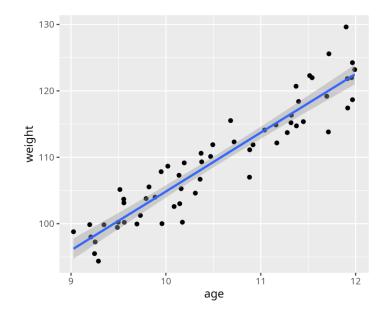
# **Model checking**

Visualization is easy when you have just one predictor!

Need alternative visual tools when dealing with multiple predictors.

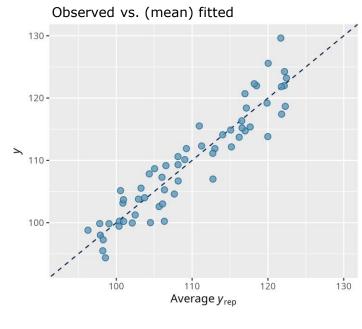
Response / prediction is just 1 variable

- → Compare and plot against each other:
- observations
- (mean) predictions
- residuals (observed predicted)

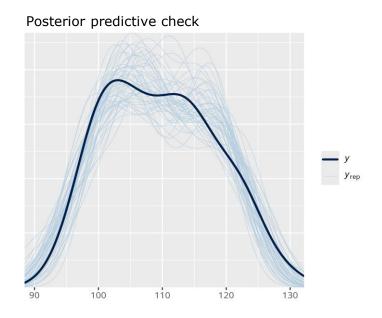


> plot(conditional\_effects(fit1), points=TRUE)

# **Model checking** (from brms package)

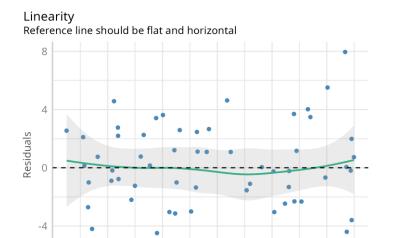


> pp\_check(fit1, type=,,scatter\_avg")



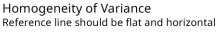
> pp\_check(fit1, ndraws=50)

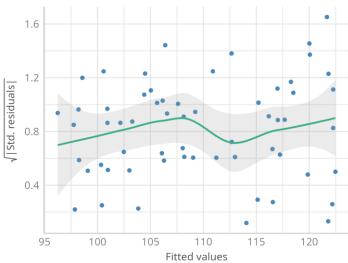
# **Model checking** (from performance package)



Fitted values

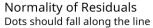
> check model(fit1, check=,,linearity")

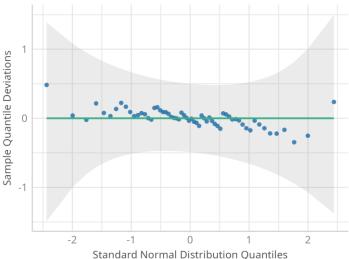




> check model(fit1, check=,,homogeneity")

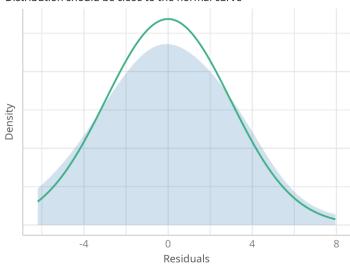
# **Model checking** (from performance package)





> check model(fit1, check=,,qq")

## Normality of Residuals Distribution should be close to the normal curve



> check model(fit1, check=,,normality")

# **Pitfalls of prediction: Multivariate posterior**

If you posterior (parameters a,b) was shaped like Croatia, (nonlinear correlation), then the mean  $(\bar{a},\bar{b})$  in 2d-space would not be part of the posterior sample

Parameter combination  $(\bar{a}, \bar{b})$  is **highly unlikely** 

Prediction  $\mu(\bar{a}, \bar{b})$  is not the mean prediction, but rather meaningless!

→ Always use full posterior for making predictions!



Due to its shape, the centre of Croatia is actually located in Bosnia and Herzegovina

Post übersetzer



# Pitfalls of prediction: Jensen's inequality

For linear models  $\mu$  (as in linear regression  $\mu = a + bx$ )

$$\mathrm{mean}\big(\mu(\theta_1),...,\mu(\theta_{1000})\big) = \mu\big(\mathrm{mean}(\theta_1,...,\theta_{1000})\big)$$

$$\mathrm{Distribution\ of}_{\mathrm{predictions}}$$

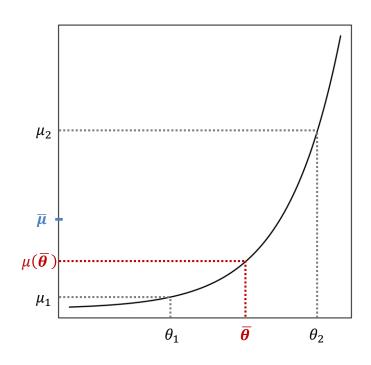
$$\mathrm{Prediction\ with}_{\mathrm{point\ estimate\ }\overline{\theta}}$$

#### For **nonlinear functions** $\mu$

$$\operatorname{mean}\big(\mu(\theta_1), \dots, \mu(\theta_{1000})\big) \neq \mu\big(\operatorname{mean}(\theta_1, \dots, \theta_{1000})\big)$$

Relevant for nonlinear statistical models, GLMs, link functions, parameter or data transformations

→ Always use full posterior for making predictions!



Summary

# **Summary**

- Priors → you choose!
- Likelihood → given by data & statistical model
- MCMC samples from posterior → check convergence!
- Informative priors can decrease uncertainty in posterior
- More datapoints can decrease uncertainty in posterior
- Use posterior predictions to check model assumptions and model fit
- In Bayesian statistics, everything is a distribution
- → Use full posterior (samples) for everything

## **Further reading**

Banner, K. M., Irvine, K. M., & Rodhouse, T. J. (2020). The use of Bayesian priors in Ecology: The good, the bad and the not great. *Methods in Ecology and Evolution*, 11(8), 882–889. <a href="https://doi.org/10.1111/2041-210X.13407">https://doi.org/10.1111/2041-210X.13407</a>

Bürkner, P. (2024). The brms Book [in progress]. <a href="https://paulbuerkner.com/software/brms-book/">https://paulbuerkner.com/software/brms-book/</a>

Conn, P. B., Johnson, D. S., Williams, P. J., Melin, S. R., & Hooten, M. B. (2018). A guide to Bayesian model checking for ecologists. *Ecological Monographs*, 88(4), 526–542. <a href="https://doi.org/10.1002/ecm.1314">https://doi.org/10.1002/ecm.1314</a>

Gabry, J., Simpson, D., Vehtari, A., Betancourt, M., & Gelman, A. (2019). Visualization in Bayesian workflow. *Journal of the Royal Statistical Society. Series A, (Statistics in Society)*, 182(2), 389–402. <a href="https://doi.org/10.1111/rssa.12378">https://doi.org/10.1111/rssa.12378</a>

Lemoine, N. P. (2019). Moving beyond noninformative priors: why and how to choose weakly informative priors in Bayesian analyses. *Oikos*, 128(7), 912–928. <a href="https://doi.org/10.1111/oik.05985">https://doi.org/10.1111/oik.05985</a>

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