Introduction to Bayesian statistics and Markov Chain Monte Carlo

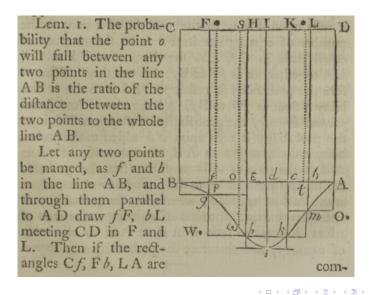
- Brief review of probability concepts
- Bayes theorem
- Bayesian inference (thought experiment)
- Introduction to Markov Chain Monte Carlo (without the theory)
- Understanding MCMC output

Rev. Mr. Thomas Bayes, FRS paper

Bayes, T. and Price, R. (1763). An Essay towards Solving a Problem in the Doctrine of Chances. Philosophical Transactions of the Royal Society of London, 53, 370-418.

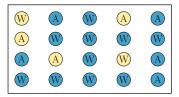
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Rev. Mr. Thomas Bayes, FRS paper



Suppose there are twenty marbles inside a box:

		Material		
		Wooden	Plastic	
Color	Yellow	2	3	
ပိ	Blue	10	5	
				20



• Suppose there are **twenty** marbles inside a box:

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		Wooden	Plastic	
Color	Yellow	2	3	
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We take one marble randomly out of the box

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Suppose there are **twenty** marbles inside a box:

		Mate	Material		
		Wooden	Plastic		
Color	Yellow	2	3		
0	Blue	10	5		
				20	

- We take one marble randomly out of the box
- What is the probability that it is **yellow** and made of **wood**?

•
$$P(\mathbf{C} = Y, \mathbf{M} = W) = P(Y, W) = ?$$

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Suppose there are **twenty** marbles inside a box:

		Material		
		Wooden	Plastic	
Color	Yellow	2	3	
ပိ	Blue	10	5	
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•
$$P(Y,W) = 2/20 = 0.1$$
 or 10%

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Suppose there are **twenty** marbles inside a box:

		Material		
		Wooden	Plastic	
Color	Yellow	2	3	
ပိ	Blue	10	5	
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•
$$P(Y,W) = 2/20 = 0.1$$
 or 10%

 $\blacksquare \ P(Y,W)$ is known as the joint probability of Y and W

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• Suppose there are **twenty** marbles inside a box:

		Material		
		Wooden	Plastic	
Color	Yellow	2	3	
ů	Blue	10	5	
·				20

We place the marble back in the box, shuffle and take out another marble

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• Suppose there are **twenty** marbles inside a box:

		Material		
		Wooden	Plastic	
Color	Yellow	2	3	
ပိ	Blue	10	5	
				20

- We place the marble back in the box, shuffle and take out another marble
- What is the probability that it is blue?
- $\bullet P(B) = ?$

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Suppose there are twenty marbles inside a box: Material				table margin
		Wooden	Plastic	argin
<u>o</u>	Yellow	2	3	5
<u>e</u>	Blue	10	5	15
-	table margin	12	8	20

 $\bullet P(B) = 15/20 = 0.75$

Suppose there are twenty marbles inside a box:				
	Material			table margin
		Wooden	Plastic	V ⁱⁿⁱ
Color	Yellow	2	3	5
S	Blue	10	5	15
-	table margin	12	8	20

•
$$P(B) = 15/20 = 0.75$$

 $\blacksquare \ P(B)$ is known as the marginal probability of W

Suppose there are **twenty** marbles inside a box:

		Material		
		Wooden	Plastic	
Color	Yellow	2	3	5
ပိ	Blue	10	5	15
		12	8	20

NA . . .

Note that:

$$\bullet P(B) = 10/20 + 5/20 = 0.75$$

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• Suppose there are **twenty** marbles inside a box:

		Material		
		Wooden	Plastic	
Color	Yellow	2	3	5
ပိ	Blue	10	5	15
		12	8	20

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Note that:

- P(B) = 10/20 + 5/20 = 0.75 or
- $\bullet \ P(B) = P(B,W) + P(B,P)$
- The marginal is the sum over the joints

Suppose there are **twenty** marbles inside a box:

Material Wooden Plastic Yellow 2 3 5 Blue 10 5 15 12 8 20

Suppose we took out a **blue** marble, what is the probability that it is **wooden**?

$$\bullet P(W \mid B) = ?$$

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Suppose there are **twenty** marbles inside a box:

		Material		
		Wooden	Plastic	
Color	Yellow	2	3	5
ပိ	Blue	10	5	15
		12	8	20

NA . . .

$$P(W \mid B) = 10/15 = 0.667$$

• Suppose there are **twenty** marbles inside a box:

		Material		
		Wooden	Plastic	
Color	Yellow	2	3	5
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		12	8	20

$$P(W \mid B) = 10/15 = 0.667$$

• $P(W \mid B)$ is the conditional probability of W given B

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Suppose there are **twenty** marbles inside a box:

Material Wooden Plastic Yellow 2 3 5 Blue 10 5 15 12 8 20

 $\blacksquare P(W \mid B) \text{ vs } P(W,B)$

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Color	Yellow	2	3	5
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		12	8	20

- $\blacksquare \ P(W \mid B) \text{ vs } P(W,B)$
- **Conditional:** we have information. One variable is not random

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- $\blacksquare \ P(W \mid B) \text{ vs } P(W,B)$
- **Conditional:** we have information. One variable is not random
- Joint: both are random

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		Mate		
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Note that:

• $P(W \mid B) = 10/15$

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• $P(W \mid B) = 10/15$

• $P(W \mid B) = (10/20)/(15/20) = 0.667$ or

• Suppose there are **twenty** marbles inside a box:

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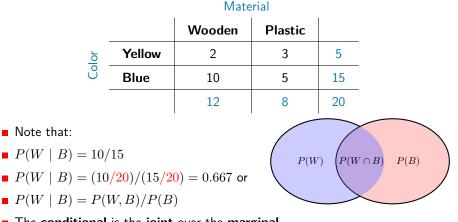
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Suppose there are **twenty** marbles inside a box:

Material Wooden Plastic Yellow 2 3 5 Blue 10 5 15 12 8 20

Note we can reverse the conditional:

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Material Wooden Plastic Yellow 2 3 5 Blue 10 5 15 12 8 20

Note we can reverse the conditional:

$$\blacksquare P(B \mid W) = P(B, W) / P(W)$$

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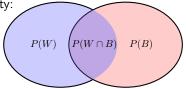
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- Note we can reverse the conditional:
- $\blacksquare P(B \mid W) = P(B, W) / P(W)$

$$P(B \mid W) = (10/20)/(12/20) = 0.833$$

Bayes Theorem

- From the definition of conditional probability:
- $P(B \mid W) = P(B, W)/P(W)$
- $P(W \mid B) = P(B, W)/P(B)$



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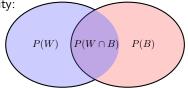
Bayes Theorem

- From the definition of conditional probability:
- $P(B \mid W) = P(B, W)/P(W)$
- $P(W \mid B) = P(B, W)/P(B)$
- We obtain:

$$P(B, W) = P(W) \times P(B \mid W)$$

$$P(B,W) = P(B) \times P(W \mid B)$$

 $\blacksquare P(W) \times P(B \mid W) = P(B) \times P(W \mid B)$



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Bayes Theorem

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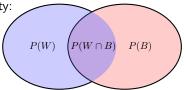
- $P(B, W) = P(B) \times P(W \mid B)$
- $\blacksquare P(W) \times P(B \mid W) = P(B) \times P(W \mid B)$

Therefore:

$$P(B \mid W) = \frac{P(B) \times P(W \mid B)}{P(W)}$$

This is known as the Bayes theorem

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Marginal Probability

$$P(W) = P(Y, W) + P(B, W)$$

$$P(W) = P(W \mid Y)P(Y) + P(W \mid B)P(B)$$

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Marginal Probability

$$P(W) = P(Y, W) + P(B, W)$$

•
$$P(W) = P(W \mid Y)P(Y) + P(W \mid B)P(B)$$

Suppose there are marbles of n different colours in the box, then::
P(W) = P(W | C₁)P(C₁) + ... + P(W | C_n)
P(W) = \sum_{i}^{n} P(W | C_{i})P(C_{i})

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Marginal Probability

$$P(W) = P(Y, W) + P(B, W)$$

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P(W) = \sum_{i}^{n} P(W | C_{i})P(C_{i})

• $P(W) = \int P(W \mid X)P(X)dX$ if X is continuous

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Rev. Mr. Bayes thought experiment (modified)

- We have a **billiard table** (or flat plane)
- A white ball \bigcirc is thrown onto the table at an unknown position (x, y)
- The position (x, y) is **unknown** to us (not revealed)
- A second **black** ball is thrown randomly onto the table and we are told if:
 - \blacksquare The ball lands to the left or right of the unknown position \boldsymbol{x}
 - \blacksquare The ball lands to the front or behind of the unknown position y
- After *n* throws of the **black** ball, can we guess the position of the **white** ball?

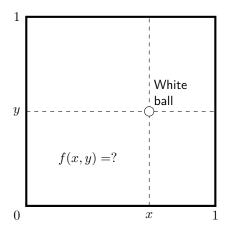
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Rev. Mr. Bayes thought experiment (modified)

- Thomas Bayes showed how to estimate the probability of the white ball's location based on observed data (inverse probability problem)
- He further showed that with sufficient throws (data), we would eventually become almost certain of the white balls's position
- We will go through the example

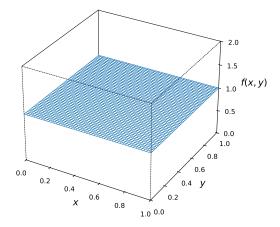
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We throw the white ball

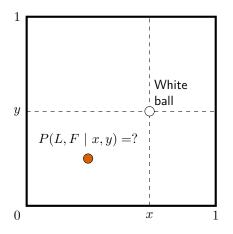


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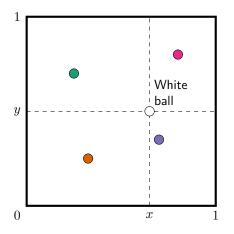
We assume a uniform distribution over x and y: f(x, y) = 1



- L: LeftR: RightF: Front
- B: Back

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The probability, after **one throw**, is the landing area:

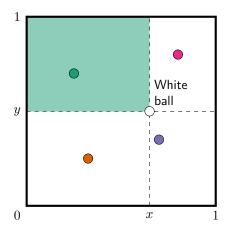
 $\bullet P(L,F \mid x,y) = xy$

$$P(L,B \mid x,y) = x(1-y)$$

$$P(R,F \mid x,y) = (1-x)y$$

•
$$P(R, B \mid x, y) = (1 - x)(1 - y)$$

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The probability, after **one throw**, is the landing area:

 $\bullet P(L,F \mid x,y) = xy$

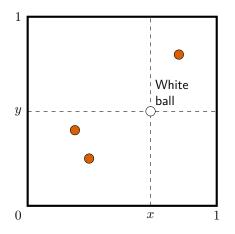
$$P(L,B \mid x,y) = x(1-y)$$

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The probability, of a **sequence of ball throws**, is the product of the single throw probabilities:

Data (ball throws):

$$D = \{ (L, F), (L, F), (R, B) \}$$

Probability of observing data given (x, y):

 $P(D|x,y) = P(L,F \mid x,y)^2 P(R,B \mid x,y)$

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The probability of a **sequence of throws** is the product of the single throw probabilities:

■ $D = \{(L, F), (L, F), (R, B)\}$ ■ $P(D \mid x, y) = P(L, F \mid x, y)^2 P(R, B \mid x, y)$ ■ $P(D \mid x, y) = (xy)^2 (1 - x)(1 - y)$

In general, the probability after $n\ {\rm throws}$ is:

- $P(D \mid x, y) = x^a (1-x)^{(n-a)} y^b (1-y)^{(n-b)}$
- |D| = n: number of throws (size of data)
- *a*: number of left landings
- **b**: number of front landings

We have defined the marginal density of x and y, and calculated the conditional probability of D given $x,y{:}$

•
$$f(x,y) = 1$$

• $P(D \mid x, y) = x^a (1-x)^{(n-a)} y^b (1-y)^{(n-b)}$

Therefore, we can now define the **joint density** of D, x, y:

$$f(D, x, y) = f(x, y)P(D \mid x, y)$$

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According to the Bayes theorem:

$$f(x, y \mid D) = \frac{f(x, y)P(D \mid x, y)}{P(D)}$$

The difficulty is in calculating the marginal probability P(D)

Recall that the marginal probability is the sum over the joint probabilities. Here, x and y are continuous, so instead of a double sum, we have a double integral:

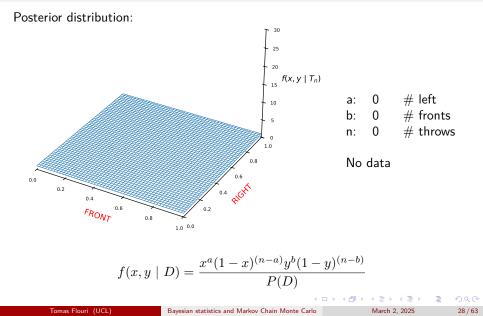
$$P(D) = \iint f(D, x, y) \, dx \, dy$$
$$= \frac{a!(n-a)!b!(n-b)!}{((n+1)!)^2}$$

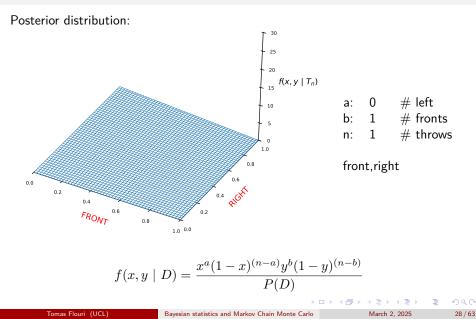
Tomas Flouri (UCL)

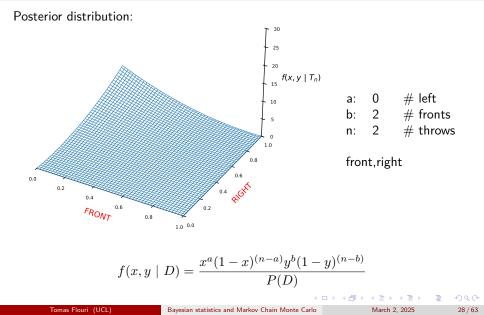
Simulation for the modified Bayes thought experiment:

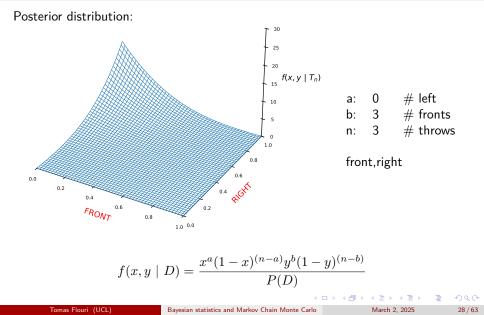
- **1** Sample x and y from the join uniform f(x, y). This is the position of the **white ball**
- **2** Initilize a = b = n = 0
- **3** Sample two numbers, w and z, from the joint uniform. This is the position of the ball after one throw.
- 4 Set a = a + 1 if w < x (ball is at left)
- **5** Set b = b + 1 if z < y (ball is at front)
- 6 Repeat steps 3 to 5
- **7** Calculate $f(x, y \mid D)$. Note: Our data is $D = \{a, b, n\}$

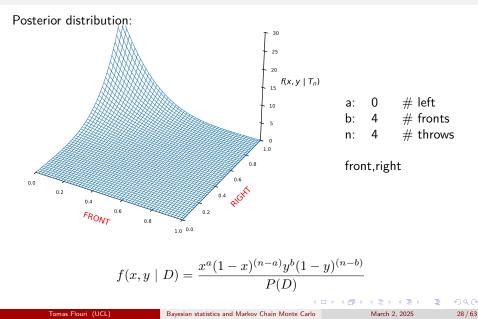
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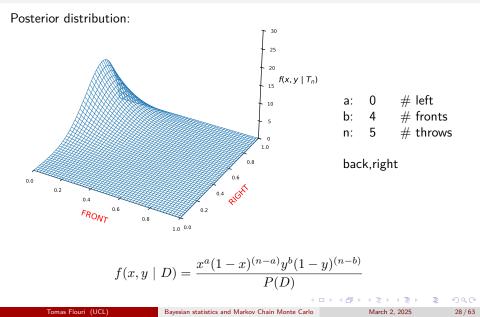


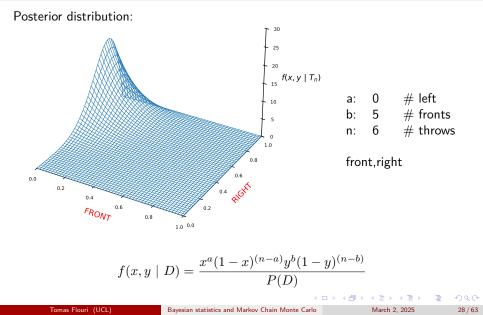


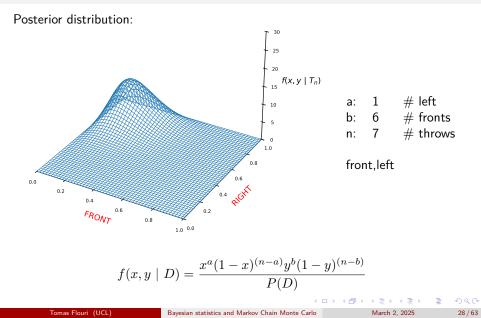


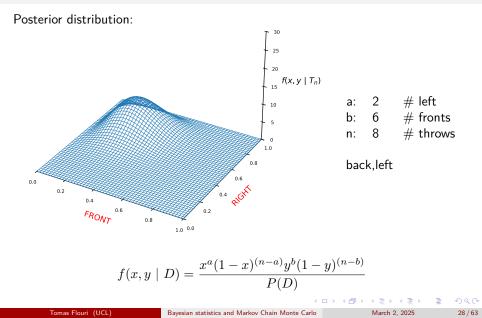


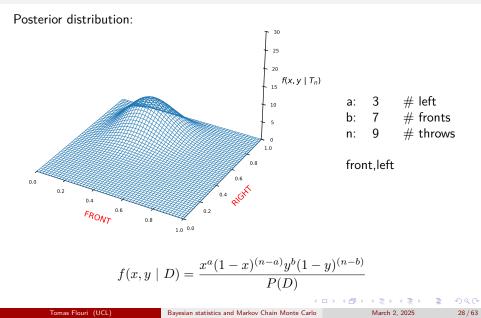


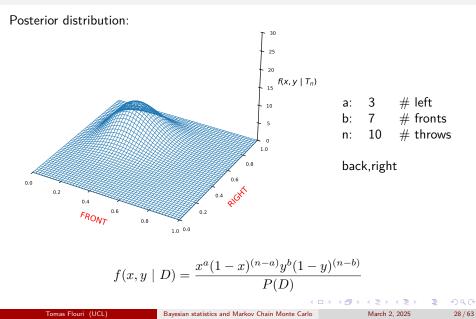


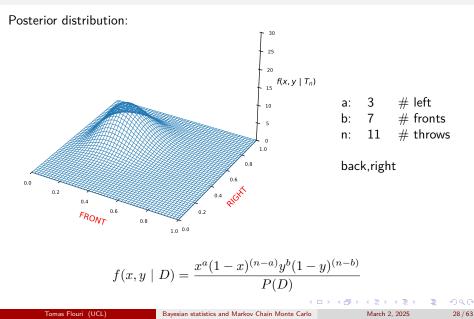


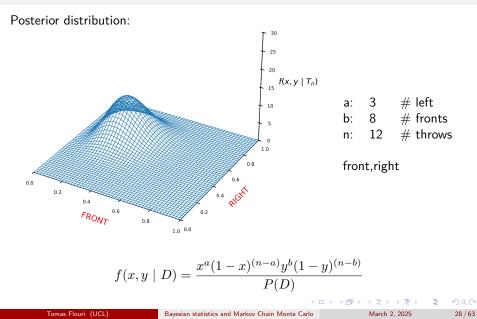


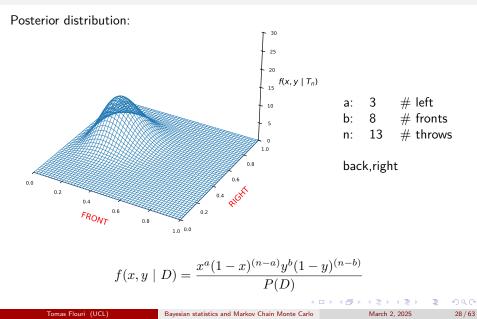


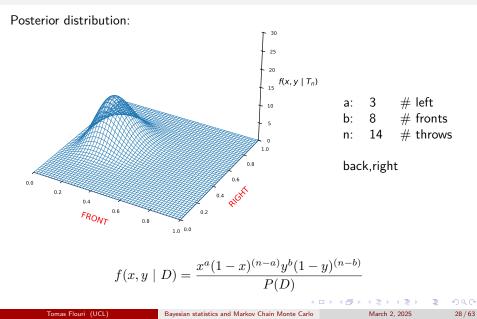


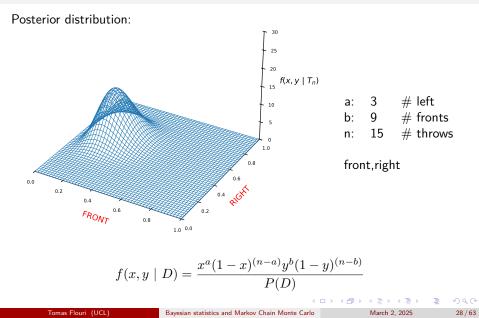


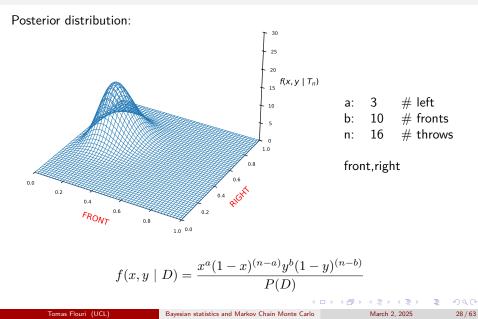


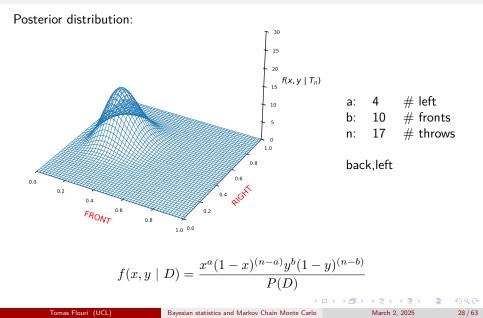


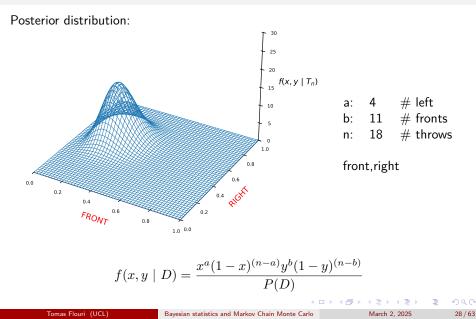


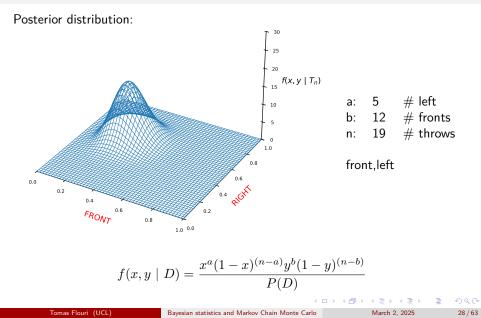


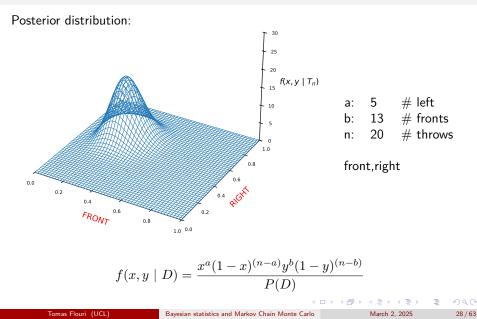


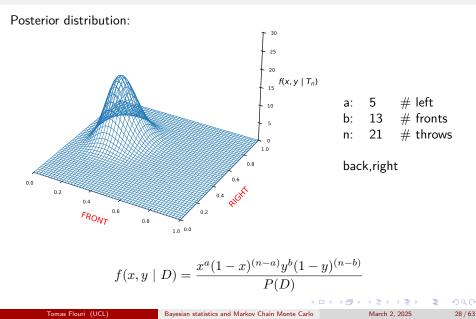


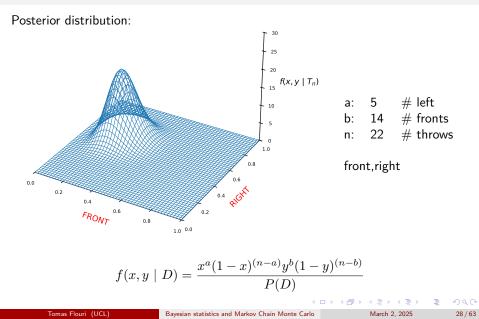


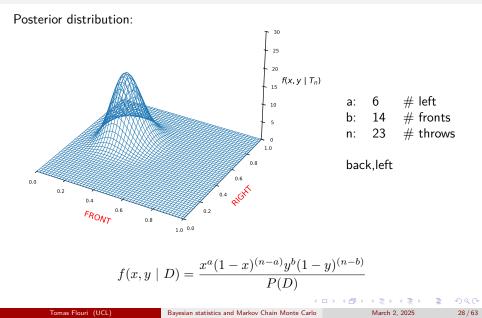


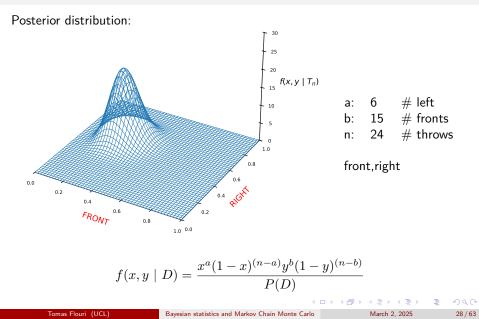


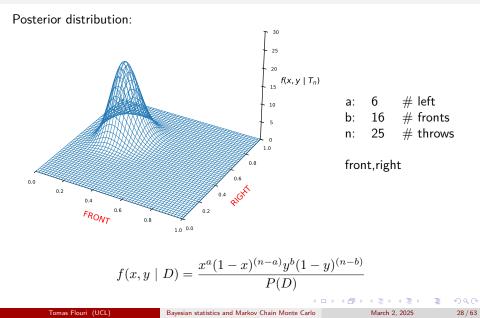


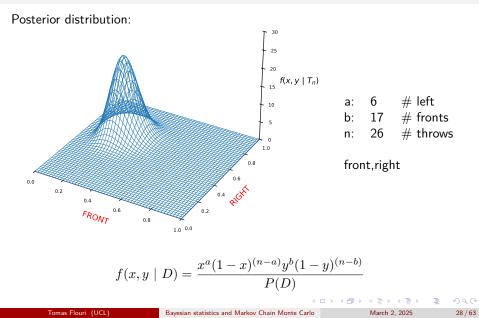


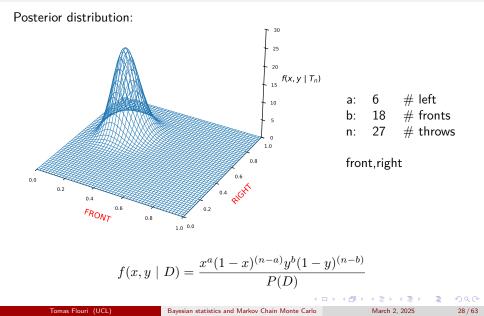


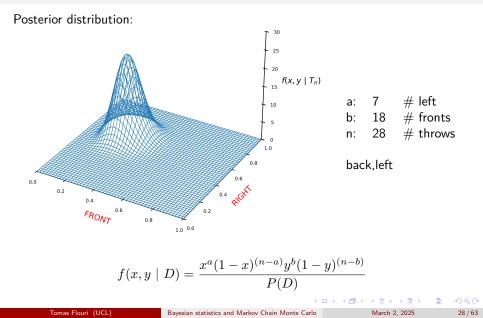


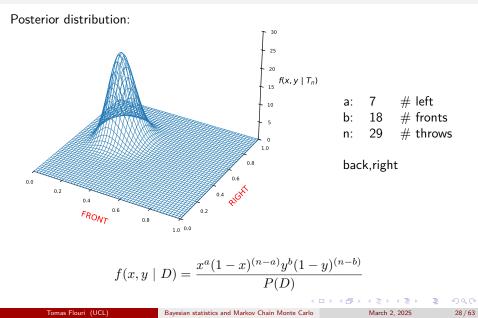


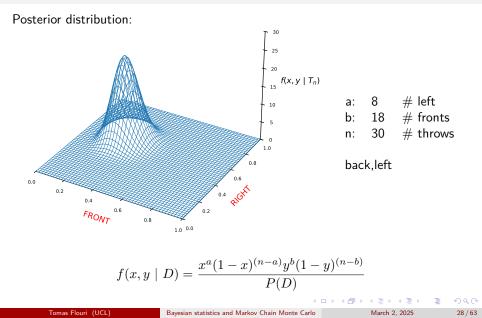


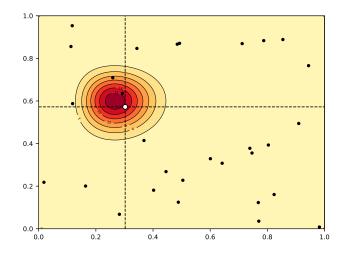












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Bayesian Terminology

$$f(x, y \mid D) = \frac{f(x, y)f(D \mid x, y)}{P(D)}$$

- The marginal of x and y, f(x, y), is known as the **prior** distribution of x and y
- The prior f(x, y) reflects our **prior knowledge** about x and y before any data has been observed

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- P(D) is known as the marginal likelihood

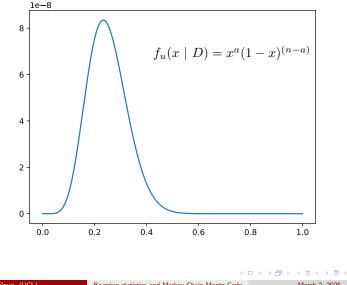
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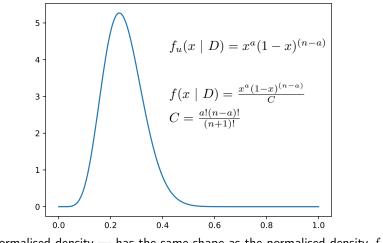
Bayesian Terminology

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- \blacksquare The conditional $f(D \mid x,y)$ is known as the **likelihood** of the data D
- $\blacksquare \ P(D)$ is known as the marginal likelihood
- $\blacksquare \ P(x,y \mid D)$ is the posterior distribution of x and y
- The posterior f(x, y | D) reflects our **updated (posterior) knowledge** after the data has been observed



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 f_u : unnormalised density — has the same shape as the normalised density f

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• Can we ignore the marginal likelihood P(T)?

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- Can we ignore the marginal likelihood P(T)?
- No.

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- Can we ignore the marginal likelihood P(T)?
- No.
- The density must be normalised because the probability is the area under the curve:

$$P(a < x < b) = \int_{a}^{b} f(x \mid D) dx$$

Note:

$$\bullet P(0 \le x \le 1) = 1$$

 For multi-dimensional densities, the probability is the volume under the surface

2

0

0.0

0.2

0.4

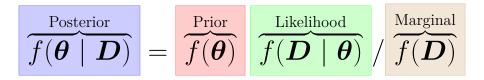
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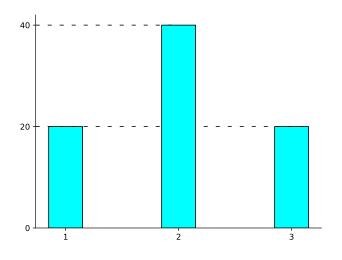
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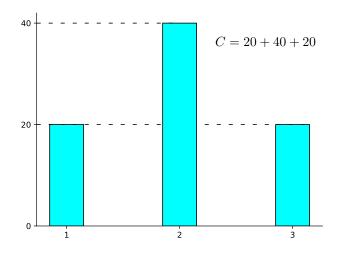
General Bayesian Model

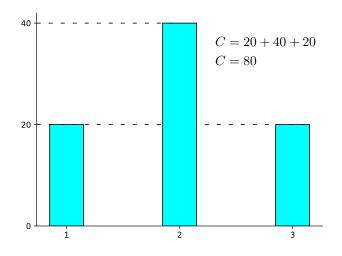


- D is the data
- $\boldsymbol{\theta} = (\theta_1, \theta_2, \dots, \theta_n)$ is the set of model parameters
- $f(D) = \int f(\theta) f(D \mid \theta) \, d\theta$ is the marginal likelihood
- f(D) is an *n*-dimensional integral
- Usually, this integral does not have an analytical solution or is hard to calculate
- What do we do?

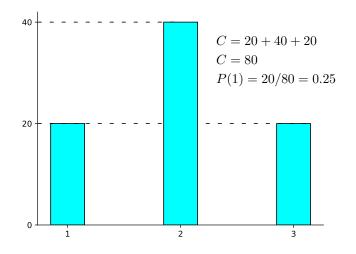
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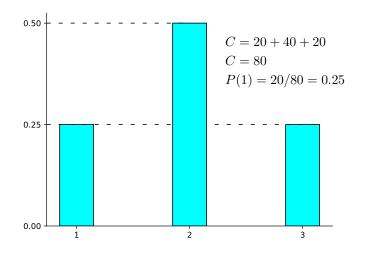




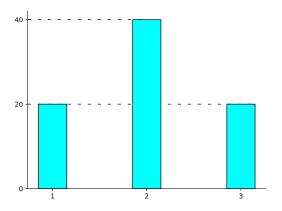
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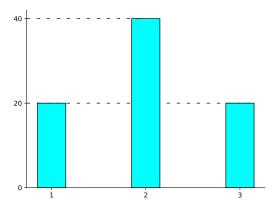
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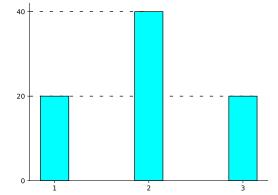
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Algorithm:



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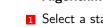


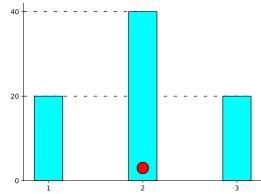
Algorithm:

1 Select a starting point (x)

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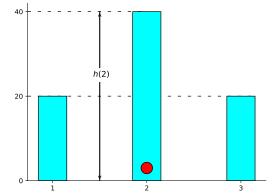


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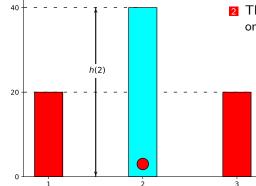
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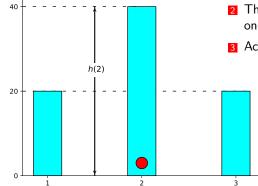
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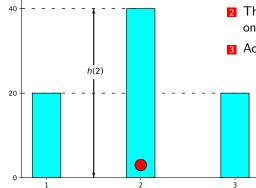
Algorithm:

- **1** Select a starting point (x)
- 2 Throw a coin to propose a visit to one of the adjacent bars (x*)



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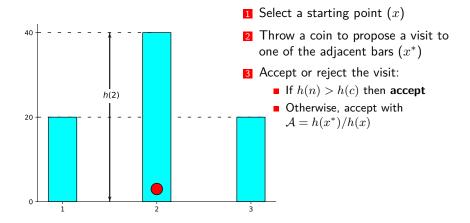


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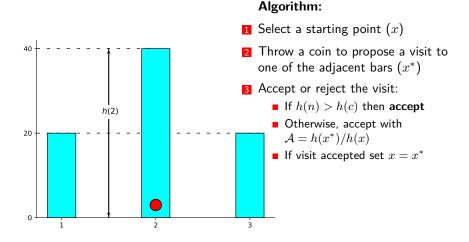
- **1** Select a starting point (x)
- 2 Throw a coin to propose a visit to one of the adjacent bars (x*)
- 3 Accept or reject the visit:
 - If h(n) > h(c) then accept

Algorithm:

Sampling from histograms

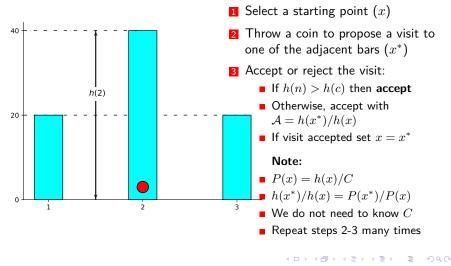


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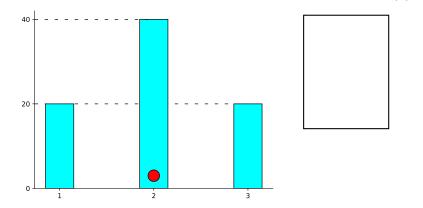
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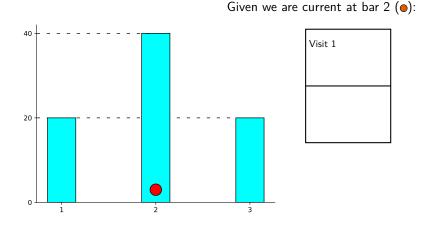
Sampling from histograms



Given we are current at bar 2 (\bullet) :

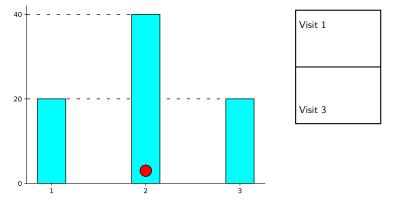
Sampling from histograms





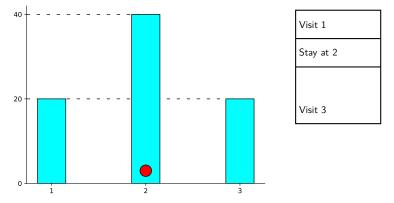
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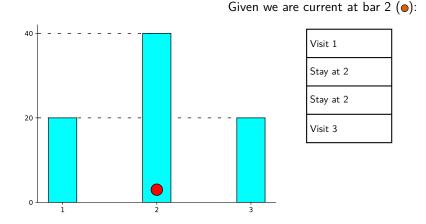


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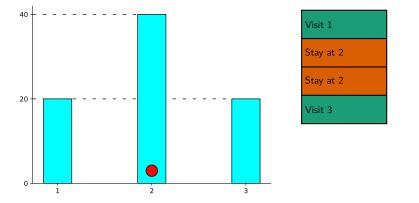


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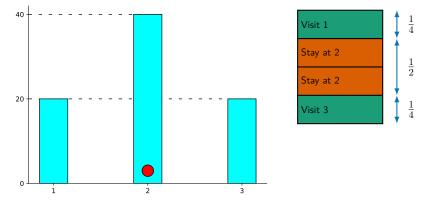
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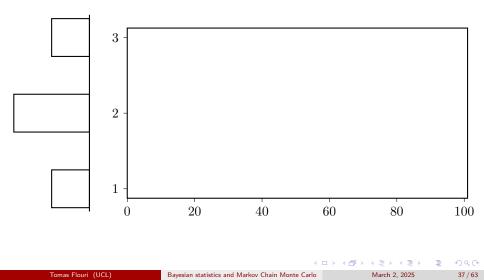
Tomas Flouri (UCL) Bayesian stati

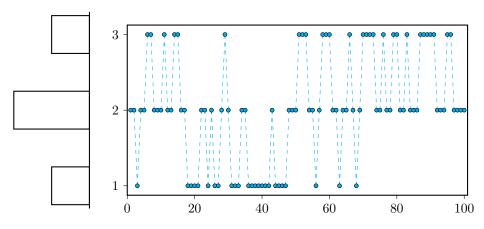
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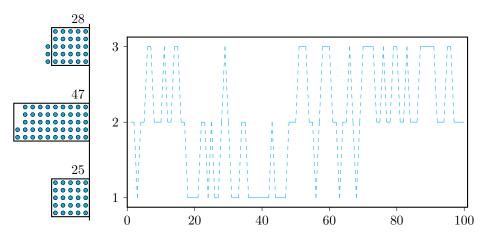
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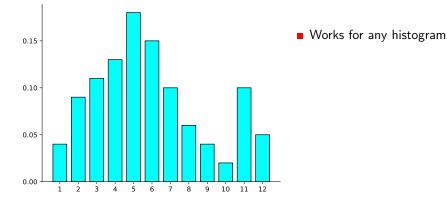
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Expectation: 25:50:25

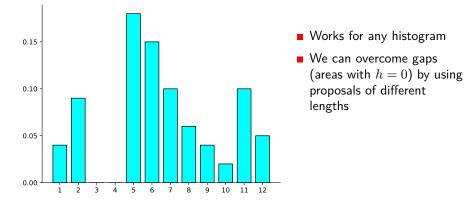
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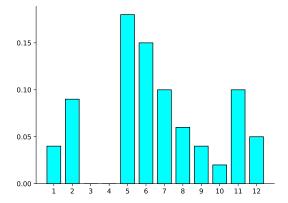
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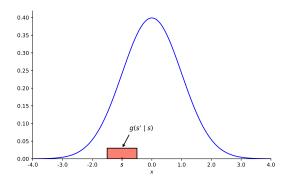
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- Works for any histogram
- We can overcome gaps (areas with h = 0) by using proposals of different lengths
- This class of algorithms is known as Markov Chain Monte Carlo or MCMC

March 2, 2025

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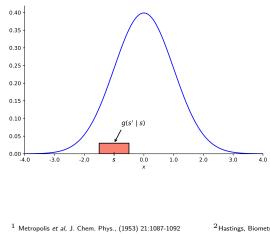


MCMC

- Also works for continuous densities
- Start at some point s
- Use a density g(s' | s) to propose the next point s'
- Accept or reject with $P = \min\{1, f(s')/f(s)\}$

Algorithm

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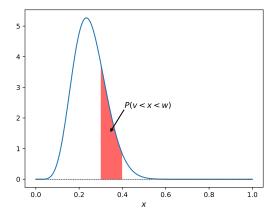
Make sure that:

- $\blacksquare \ g(s' \mid s) = g(s \mid s')$
- This is known as the Metropolis algorithm¹

Asymmetric proposals²

²Hastings, Biometrika, (1970) 57:97-109

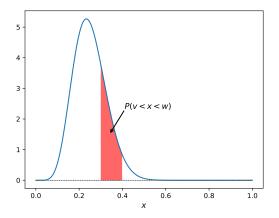
How do we calculate
$$P(v < x < w) = \int_{v}^{w} f(x) dx$$
 ?



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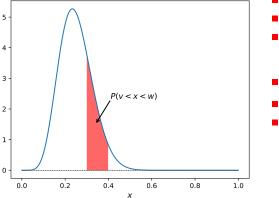


- $P(v < x < w) \approx \frac{n_a}{N}$
- n_a: times red area was visited
- N: total number of MCMC iterations

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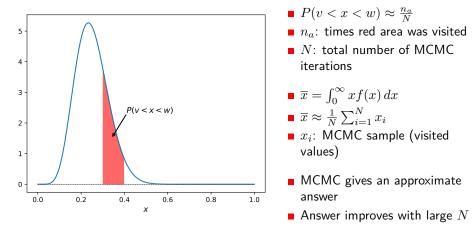


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$$\overline{x} = \int_0^\infty x f(x) \, dx$$
$$\overline{x} \approx \frac{1}{N} \sum_{i=1}^N x_i$$

x_i: MCMC sample (visited values)

How do we calculate
$$P(v < x < w) = \int_{v}^{w} f(x) dx$$
 ?



Bayesian Phylogenomics

When analysing phylogenomic data, we are typically interested in estimating:

- A tree topology T
- \blacksquare The branch lengths \pmb{b} given the topology T
- Other model parameters heta

Our data is typically in the form of an alignment matrix D.

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Our data is typically in the form of an alignment matrix D.

In a Bayesian framework, we are inferring the **posterior distribution** of T, b, θ given the data D:

 $f(T, \boldsymbol{b}, \boldsymbol{\theta} \mid D) = \frac{f(\boldsymbol{\theta}) P(T) f(\boldsymbol{b} \mid T) \times P(D \mid \boldsymbol{\theta}, T, \boldsymbol{b})}{P(D)}$

Bayesian Phylogenomics

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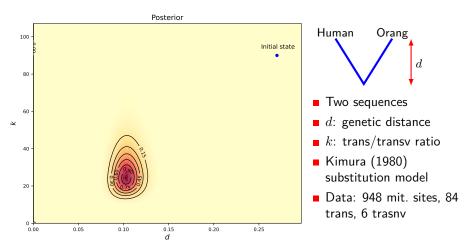
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Our data is typically in the form of an alignment matrix D.

In a Bayesian framework, we are inferring the **posterior distribution** of T, b, θ given the data D:

$$f(T, \boldsymbol{b}, \boldsymbol{\theta} \mid D) = \frac{f(\boldsymbol{\theta})P(T)f(\boldsymbol{b} \mid T) \times P(D \mid \boldsymbol{\theta}, T, \boldsymbol{b})}{P(D)}$$

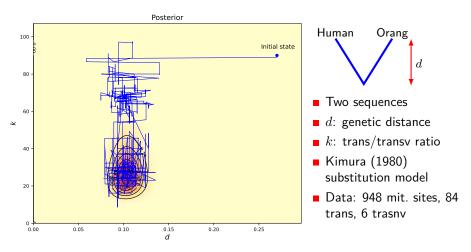
- $P(D) = \sum_{i} \iint f(\boldsymbol{\theta}, T_{i}, \boldsymbol{b}) P(D \mid \boldsymbol{\theta}, T_{i}, \boldsymbol{b}) d\boldsymbol{\theta} d\boldsymbol{b}$
- $\blacksquare \ P(D)$ is impossible to calculate, and so we need MCMC
- \blacksquare For example, $P(T \mid D) \approx n_T/N$



Data from: Yang 2014, p.7, Table 1.3

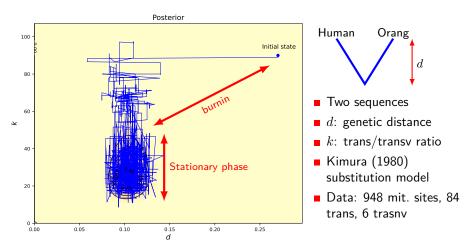
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Data from: Yang 2014, p.7, Table 1.3

42/63

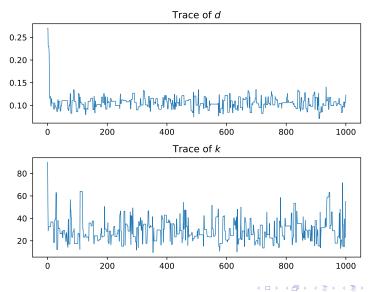


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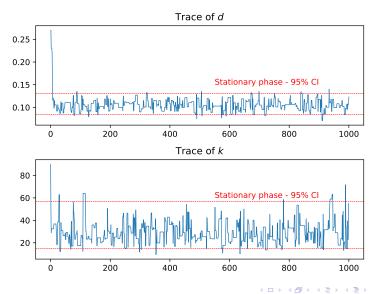
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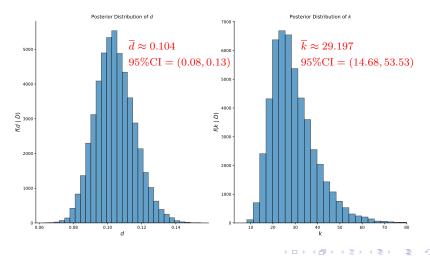
42/63



March 2, 2025



The sample from the stationary phase can be summarised to obtain the approximation to the posterior distribution



Bayesian statistics and Markov Chain Monte Carlo

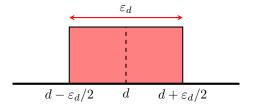
Proposal step size

In this example, we use uniform distributions to propose new values:

$$d' \sim U(d - \varepsilon_d/2, d + \varepsilon_d/2)$$

•
$$k' \sim U(k - \varepsilon_k/2, k + \varepsilon_k/2)$$

 \bullet $\varepsilon_d, \varepsilon_k$ are known as the proposal step sizes



Mixing and convergence rate

Mixing: refers to how quickly a chain explores the state space.

- Rejecting too many proposals means we stay in the same place too long
- If we accept too many proposals usually means we are moving slowly, remaining in the same region too long.

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Proposal step size affects mixing:

- Step is too big: we reject most proposals
- Step is too small: we accept most proposals (baby steps)

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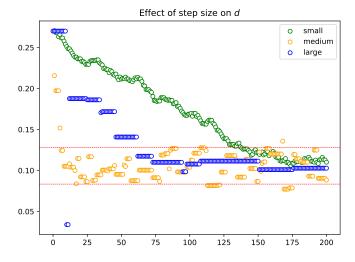
Proposal step size affects mixing:

- Step is too big: we reject most proposals
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Convergence rate: refers to how quickly the chain moves into the stationary phase

- Proposal step size also affects convergence rate
- Small sizes lead to low convergence rate

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Mixing (acceptance %): Small: 82%, Medium: 34%, Large: 7%

Tomas Flouri (UCL)

47 / 63

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Mixing and fine tuning

Fine-tuning: The process of adjusting step sizes to achieve optimal mixing

- Analysis of normal distribution indicates that mixing is best at \sim 23.4% (20% 40%)^{1,2}
- Most MCMC software will do this automatically, but sometimes it is useful to do it manually:
 - is too high: increase step size
 - is too low: decrease step size

¹Gelman et al, Ann. Appl. Probab. 7(1):110-120, 1997

²Roberts and Rosenthal, Statist. Sci 16(4):351-367, 2001

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Mixing and fine tuning

Fine-tuning: The process of adjusting step sizes to achieve optimal mixing

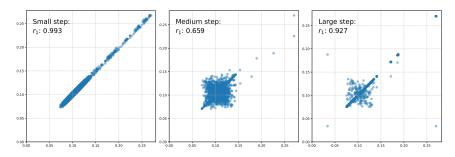
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- Most MCMC software will do this automatically, but sometimes it is useful to do it manually:
 - is too high: increase step size
 - is too low: decrease step size
- Recall MCMC estimates are approximate, e.g. $\overline{d} \approx \sum_i d_i / N$
- For two chains of the same length, the errors in the estimates are larger for the chain with poorest mixing
- Note: calculations are done after removing burn-in samples

²Roberts and Rosenthal, Statist. Sci 16(4):351-367, 2001

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Autocorrelation

- MCMC samples are autocorrelated because accepted values are modifications of the previous values
- K80 example, $r_L = \operatorname{corr}(d_i, d_{i+L})$
- L indicates the lag. Plots below are for L = 1

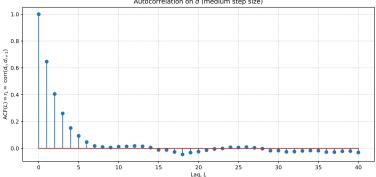


Mixing (acceptance %): Small: 82%, Medium: 34%, Large: 7%

49/63

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Autocorrelation Function



Autocorrelation on d (medium step size)

Chains that mix well have ACF that decays fast!

Efficiency

Chains that lead to estimates with small errors with respect to the chain's size are said to be **efficient**

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Chains that lead to estimates with small errors with respect to the chain's size are said to be **efficient**

Efficiency relates to the autocorrelation of the chain:

Eff =
$$\frac{1}{1 + 2(r_1 + r_2 + r_3 + \ldots)}$$

- High (+) autocorrelation: Low efficiency
- **Moderate (+) autocorrelation:** Efficient chain
- **No autocorrelation:** Independent sampling (very efficient)
- (-) autocorrelation: Super-efficient chain

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- High (+) autocorrelation: Low efficiency
- Moderate (+) autocorrelation: Efficient chain
- No autocorrelation: Independent sampling (very efficient)
- (-) autocorrelation: Super-efficient chain
- Eff = 1: as efficient as independent sampling
- Eff = 0.2: 20% as efficient as independent sampling

Algorithm

Effective Sample Size

Effective Sample Size is the chain size \times efficiency

$ESS = N \times Eff$

Example:

- \blacksquare We have an MCMC chain with N=1000 samples and ${\rm Eff}=20\%$
- Then, ESS = 200, meaning the chain has the same estimate error as an equivalent, independent chain of size 200

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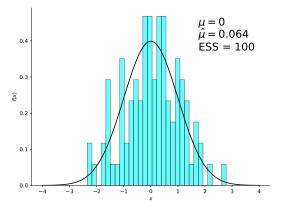
Example:

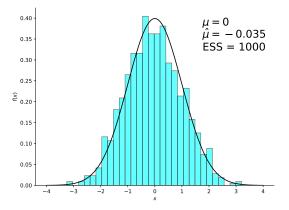
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Stachastic simulation theory recommendation:

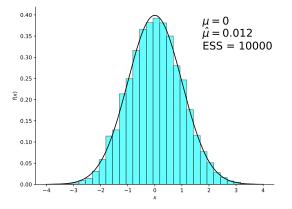
- $\blacksquare~N$ should be between $1\,000$ to $10\,000$ for independent sampling
- \blacksquare Thus, ESS should be between $1\,000$ to $10\,000$
- This is typically hard to achieve in Bayesian phylogenomics
- We aim to have at least ESS > 200

- MCMC is a class of stochastic algorithms
- An MCMC histogram is just an approximation of the posterior density
- \blacksquare This approximation improves as $N \to \infty$
- We must use convergence diagnostics to assess whether the MCMC sample has converged to the posterior





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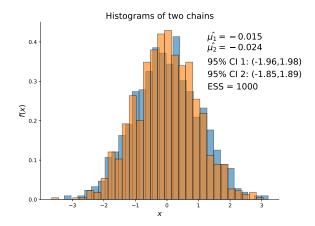
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- In practice the shape of the posterior density is not known
- Thus, we cannot compare the MCMC histogram to the true posterior

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- In practice the shape of the posterior density is not known
- Thus, we cannot compare the MCMC histogram to the true posterior
- The way around this is to run two or more MCMC chains and compare their histograms, traces, posterior means, and credibility intervals
- If they are similar, it is likely we have converged

Important: The chains must start from different starting points

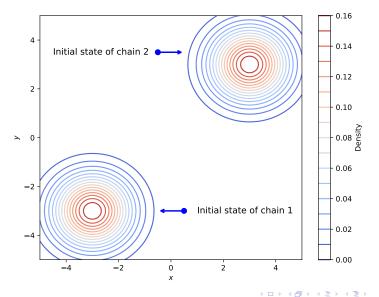


Chains that have converged can be merged into a larger chain

 $ESS_L = ESS_1 + ESS_2$

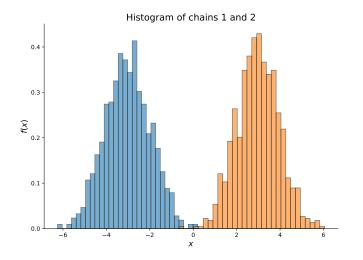
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Multi-modal densities



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Multi-modal densities



No convergence! Chains failed to cross the posterior valley

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 Running many chains with random starting points is a good way to detect multi-modal posteriors

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 Running many chains with random starting points is a good way to detect multi-modal posteriors

If we detect a multi-modal posterior:

- Run the chains for a very long time
- Eventually the chains will cross the valley back and forth and the histograms will converge
- **Do not merge** short chains that are stuck at different modes

 Running many chains with random starting points is a good way to detect multi-modal posteriors

If we detect a multi-modal posterior:

- Run the chains for a very long time
- Eventually the chains will cross the valley back and forth and the histograms will converge
- Do not merge short chains that are stuck at different modes

Important:

- Avoid using fixed starting points (or seeds)
- ESS is not a measure of convergence

Algorithm

Thinning the chain

- In phylogenomics it is difficult to construct efficient chains
- That is because we usually have too many parameters in our models
- Phylogenomic MCMC chains are thus highly correlated
- To get good estimates, we need to run the chains for a very long time
- If we store every chain visit, we would run out of hard disk space very quickly.
- Thinning: Writing down only a fraction of all chain visits (e.g. every 100th or 1000th visit)

Bayesian Phylogenomics

In phylogenomics, we are interested in estimating the topology T, branch lengths b and model parameters θ , given the alignment D

•
$$f(T, \boldsymbol{b}, \boldsymbol{\theta} \mid D) = \frac{f(T, \boldsymbol{b}, \boldsymbol{\theta})f(D \mid T, \boldsymbol{b}, \boldsymbol{\theta})}{f(D)}$$

•
$$f(D) = \sum \iint f(T, \boldsymbol{b}, \boldsymbol{\theta}) f(D \mid T, \boldsymbol{b}, \boldsymbol{\theta}) d\boldsymbol{b} d\boldsymbol{\theta}$$

f(D) is typically not available analytically and thus we use MCMC

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Bayesian Phylogenomics

The likelihood of the data $D[1,\ldots,n]$ (alignment) is the product of the likelihood of sites

$$f(D \mid T, \boldsymbol{b}, \boldsymbol{\theta}) = \prod_{i=1}^{n} f(D[i] \mid T, \boldsymbol{b}, \boldsymbol{\theta})$$

■ D[i] is the *i*-th site pattern

 \blacksquare *n* is the number of site patterns

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Algorithm

Bayesian Phylogenomics

The likelihood of the data $D[1,\ldots,n]$ (alignment) is the product of the likelihood of sites

$$f(D \mid T, \boldsymbol{b}, \boldsymbol{\theta}) = \prod_{i=1}^{n} f(D[i] \mid T, \boldsymbol{b}, \boldsymbol{\theta})$$

• D[i] is the *i*-th site pattern

n is the number of site patterns

MCMC algorithm:

- **1** Choose random initial state for T, b, θ
- **2** Propose topology T and accept/reject
- **3** Propose branch lengths \boldsymbol{b} and accept/reject
- **4** Propose model parameters heta and accept/reject
- 5 Store the current values of parameters into a sample file
- 6 Repeat steps 2-5 many many times

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Additional resources

- Holder & Lewis (2003) Phylogeny estimation: Traditional and Bayesian approaches. Nat. Rev. Genet., 4:275
- Yang (2014) Molecular evolution: A statistical approach. Oxford University Press
- Chen, Kuo, Lewis (2014) Bayesian phylogenetics: Methods, algorithms, and applications. CRC Press
- Kapli et al (2020) Phylogenetic tree building in the genomic age. Nat. Rev. Genet., 21(7):428-444

THE END

Thanks to Mario dos Reis for several lecture materials

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