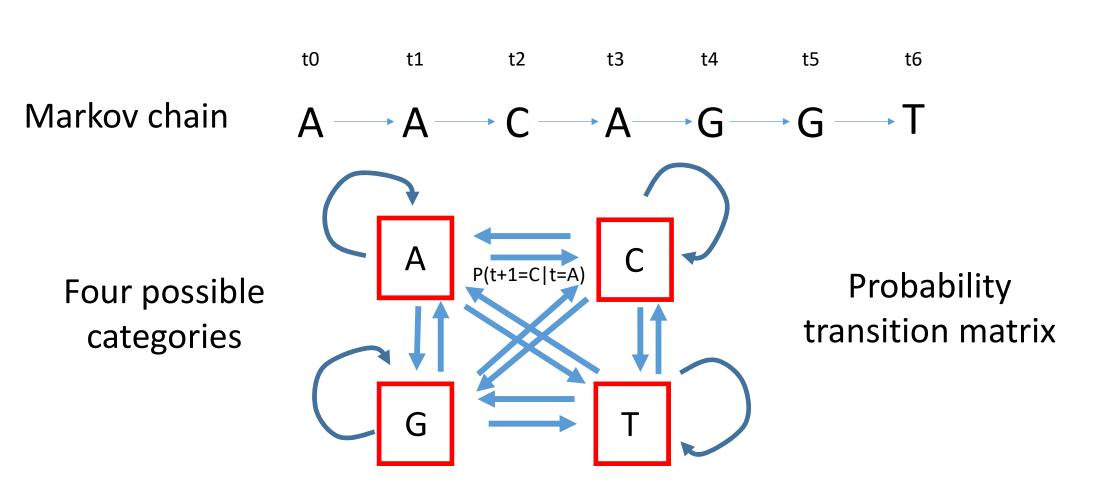
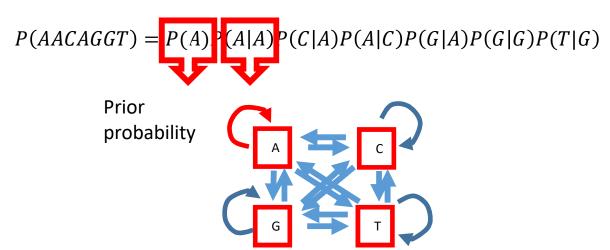
### Session 2

Hidden Markov Models applied to Clustering of Biological Sequences

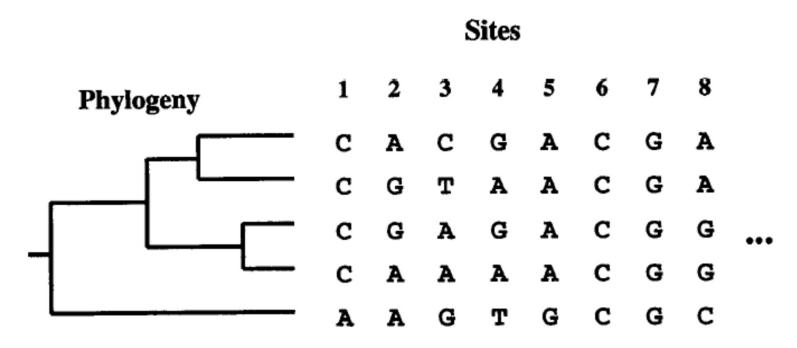
### Markov model



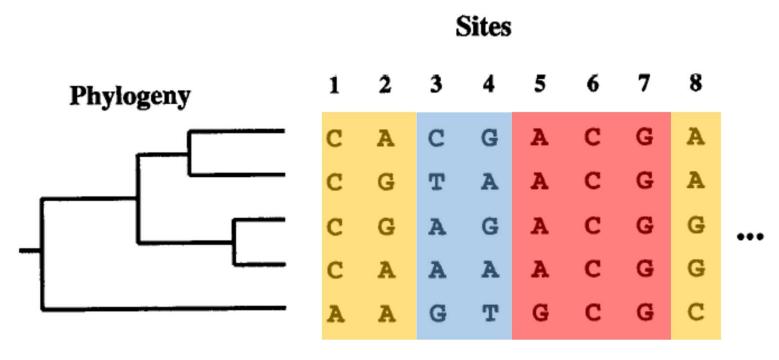
### How to identify a pattern of characters?



How does the rates of evolution change over a sequence?



How does the rates of evolution change over a sequence?

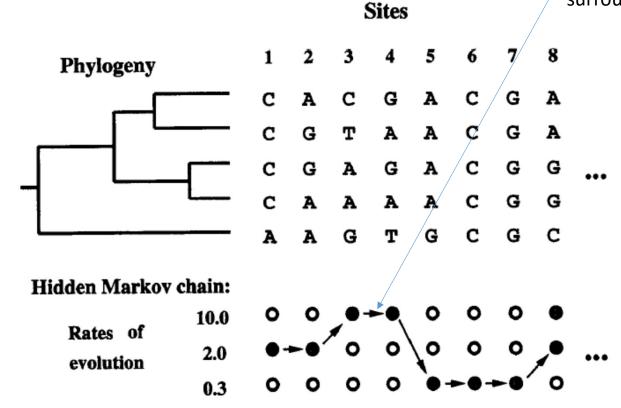


Fast evolving Slow evolving Intermediate evolving

### How does the rates of evolution change over

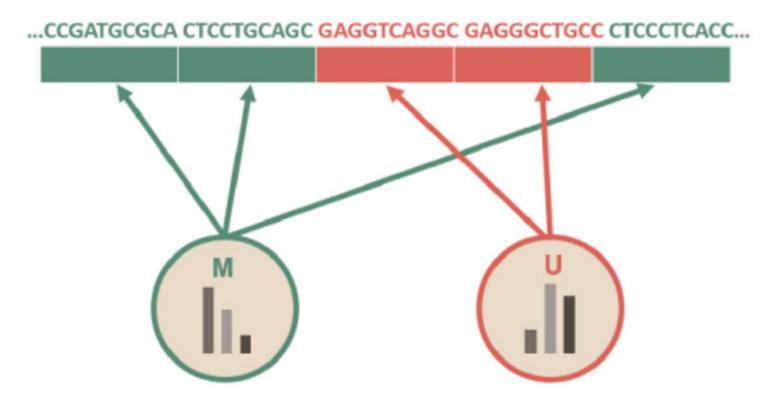
a sequence?

The Probability that I will be in one state or another depends on the surrounding nucleotides



### Other examples of finding a pattern in the sequence: Metilation

#### **DNA Metilation**



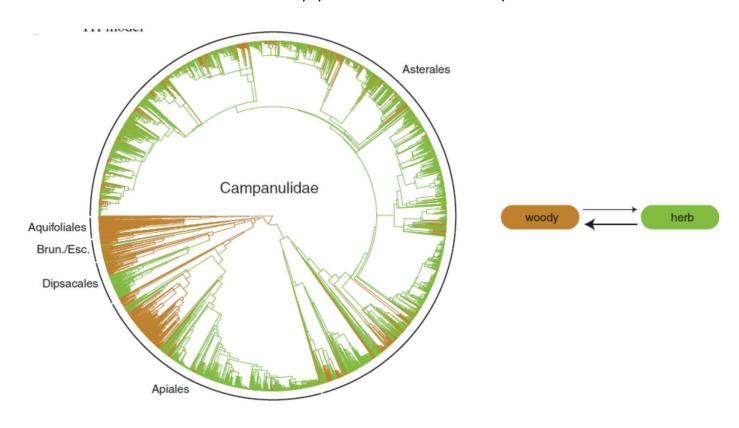
A Review of Three Different Studies on Hidden Markov Models for Epigenetic Problems: A Computational Perspective

### How does a phenotype change over a

phylogeny?

Identifying Hidden Rate Changes in the Evolution of a Binary Morphological Character: The Evolution of Plant Habit in Campanulid Angiosperms

JEREMY M. BEAULIEU1,\*, BRIAN C. O'MEARA2, AND MICHAEL J. DONOGHUE1



### How to identify a pattern of characters?

2) To which rate of evolution each nucleotide belongs to?

Hidden because the state (Fast, Intermediate, Slow) is unknown

#### ATGATTTCAAAAGGACCATCATTAGGA

Observed categories

FFFIIIIIISSS...

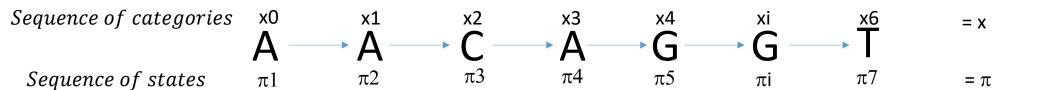
Hidden states

Fast (F), Intermediate (I) or Slow (S) is hidden (in fact, this is what we want to estimate!)

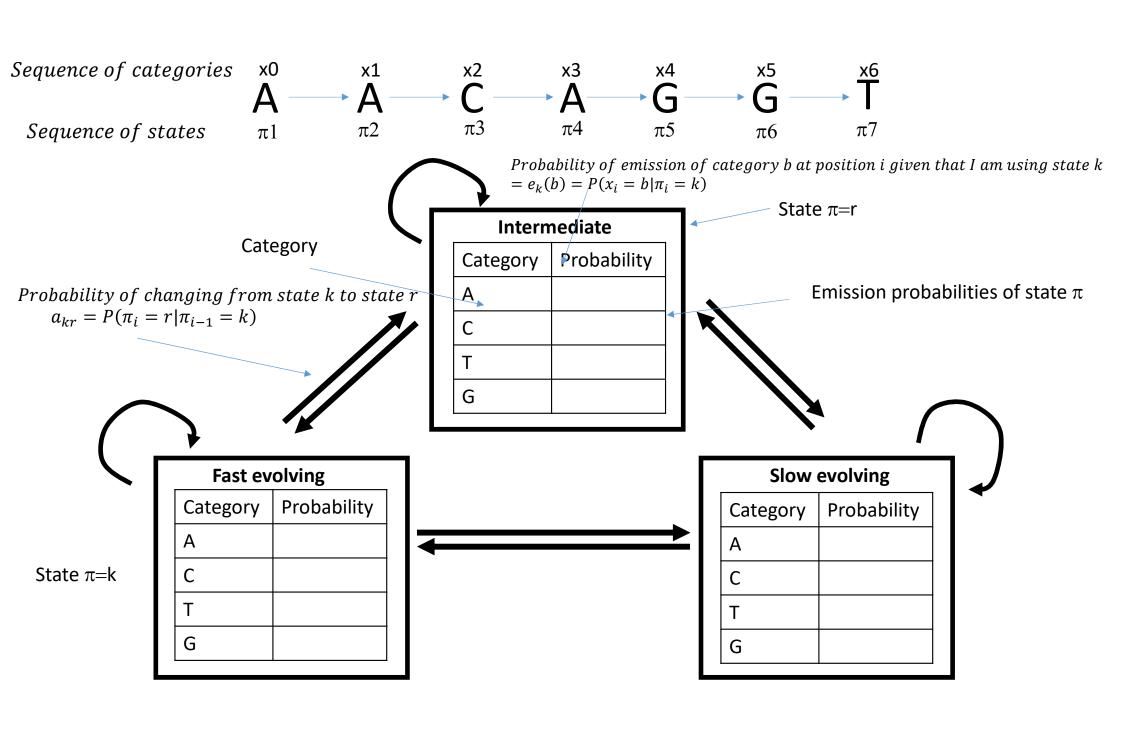
### What am I saying when I use a HMM?

"My data is a mixture of k probability distributions, each determined by its own parameters"

"The probability of using one probability distribution or another depends on which one I used in the previous step"



### SOME NOTATION



### NOTATION HMM

State at position  $i = \pi_i$ 

Sequence of states =  $\pi$ 

Category at position  $i = x_i$ 

Sequence of categories = x

$$P(x,\pi) = a_{0\pi} \prod_{i}^{N} e_{\pi_{i}}(x_{i}) a_{\pi_{i}\pi_{i}+1}$$

Initial state ("Probability that I started the chain at state  $\pi$ ")

Probability of changing from state k to state  $r = a_{kr} = P(\pi_i = r | \pi_{i-1} = k)$ 

Given that I was in the previous position using state k

I am using state r

Transmission matrix

		<u> </u>	Jule K
	Fast Evolving	Intermediate Evolving	Slow Evolving
Fast Evolving			
Intermediate Evolving			
Slow Evolving			

#### Emission Probability matrix for each possible state

Category	Probability
Α	
С	
Т	
G	

**Fast evolving** 

Category	Probability
А	
С	
Т	
G	

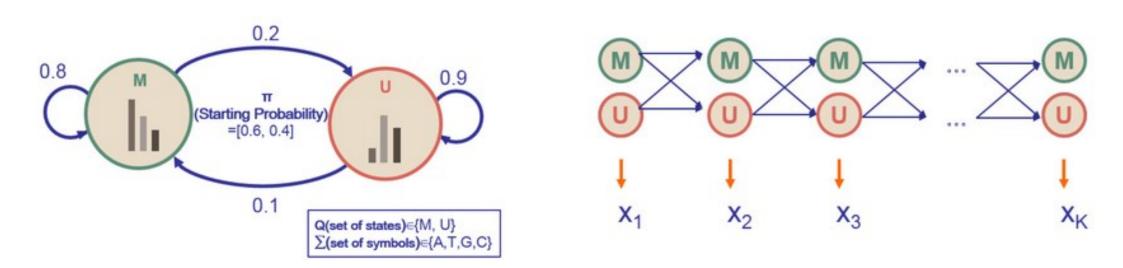
**Intermediate** 

Category	Probability
А	
С	
Т	
G	

Slow evolving

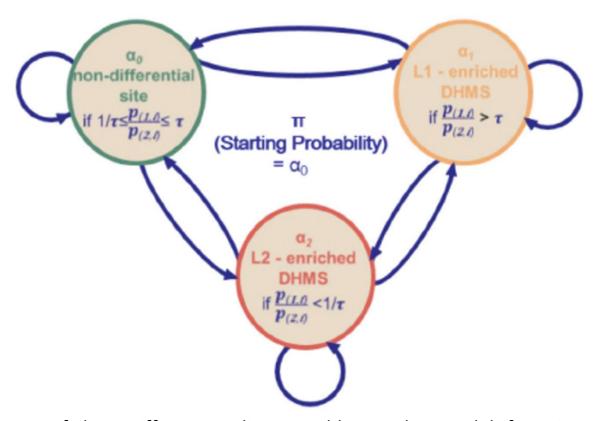
Probability of emission of category b at position i given that I am using state  $k = e_k(b) = P(x_i = b | \pi_i = k)$ 

### HMM: Multiple ways of modelling DNA Metilation



A Review of Three Different Studies on Hidden Markov Models for Epigenetic Problems: A Computational Perspective

### HMM: Multiple ways of modelling DNA Metilation



differential histone modification sites (DHMSs)

A Review of Three Different Studies on Hidden Markov Models for Epigenetic Problems: A Computational Perspective

# HMM: A simple working case The occasionally dishonest casino problem

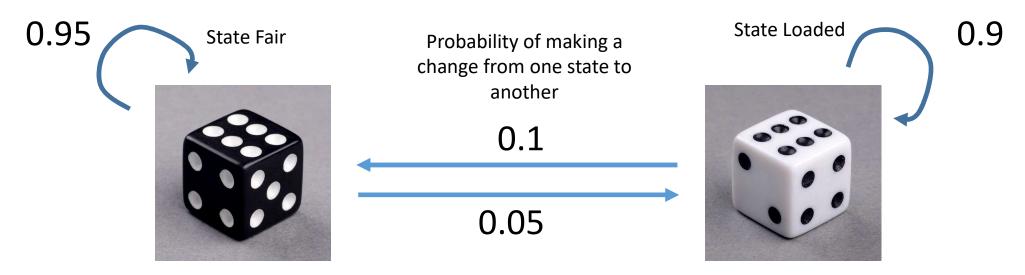




With some probability, the casino uses a dice that is **LOADED** so the number six (the bench wins) occurs more often (P(6)=0.5) than expected at random.

HOW CAN WE KNOW WHEN IT IS LOADED OF FAIR?

### The occasionally dishonest casino problem.



#### Emission probabilities of fair dice

1	2	3	4	5	6
1/6	1/6	1/6	1/6	1/6	1/6

Fair (F) dice

#### Emission probabilities of loaded dice

1	2	3	4	5	6
1/10	1/10	1/10	1/10	1/10	1/2

Loaded (L) dice

### HMM:

### 1,3,4,5,1,2,6,6,3,6,6,2,1,2,4,5

x	P(x F)	
1	1	
	6	
2	1	P(C F)=0.02
	6	
3	1	
	6	D(E C) = 0
4	1	P(F C)=0.
	<del>-</del> 6	•
5	1	
	<del>-</del> 6	
6	1	
	<del>-</del> 6	

x	P(x C)
1	1
	<del>10</del>
2	1
	<del>10</del>
3	1
	<del>10</del>
4	1
	<del>10</del>
5	1
	<del>10</del>
6	1
	$\overline{2}$

x	P(x F)
1	1
2	1
	6
3	1
	6
4	1
	6
5	1
	6
6	1
	6

$$P(C|F) = 0.01$$

$$P(F|C) = 0.1$$

$\boldsymbol{x}$	P(X C)
1	1
	$\overline{10}$
2	1
	$\overline{10}$
3	1
	<del>10</del>
4	1
	$\overline{10}$
5	1
	$\overline{10}$
6	1
	2

It refers to the values of emission and transmission that are used for the k considered states

Probability of a sequence x given that the states of the sequence are known and we have the HMM model

Imagine we observe the sequence x

$$x = \langle x_1, x_2, x_3 \rangle = \langle 6, 1, 6 \rangle$$

Assume that the prior probability of starting at one state or at the other is the same (0.5)

What would be the probability  $P(x,\pi)$  if the state sequence was

$$\pi = \langle \pi_1, \pi_2, \pi_3 \rangle = \langle F, F, F \rangle$$

$$P(x, \pi) = 0.5 * 0.95 * \frac{1}{6} * 0.95 * \frac{1}{6} * 0.95 * \frac{1}{6} = 0.001984664$$

Prior of starting at F

Prob of staying at state F

Emission prob of 6 at state F

We know that in a MC it is just:

P(S|Markov Chain) = P(1)P(3|1)P(4|3)...

P(S|Hidden Markov Chain): P(1)P(3|1)P(4|3)...

In our previous HMM notation

 $e_{\pi_i(x_i)}$   $a_{\pi_i\pi_{i+1}}$ 

In a HMC this chain explodes!

P(C)

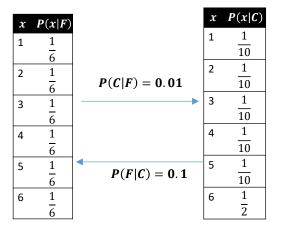
P(F)

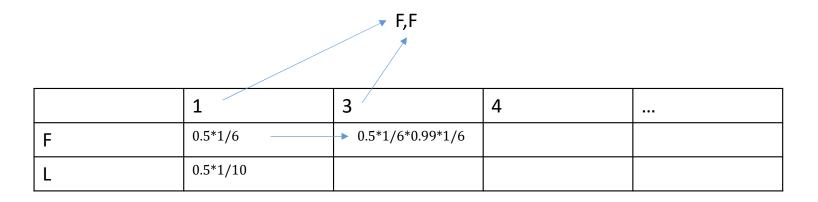
D(1|E)

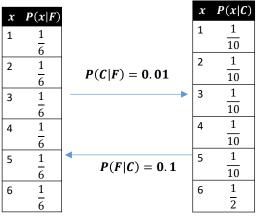
P(3|F)P(F|F

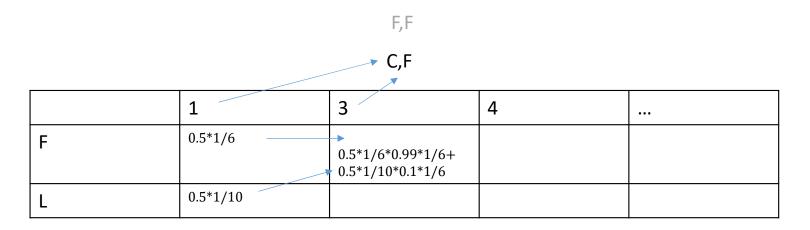
P(3|C)P(C|F

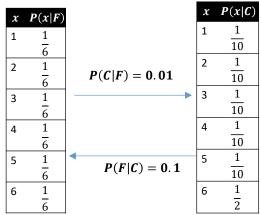
	1	3	4	
F	0.5*1/6			
L	0.5*1/10			





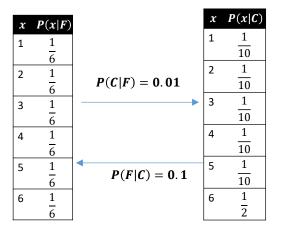


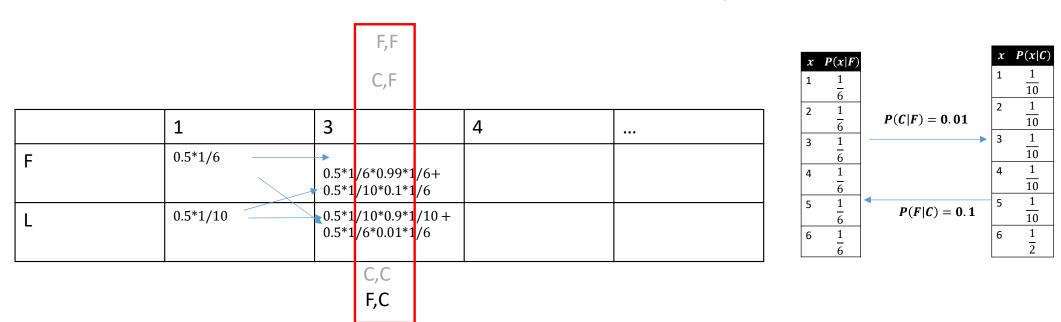




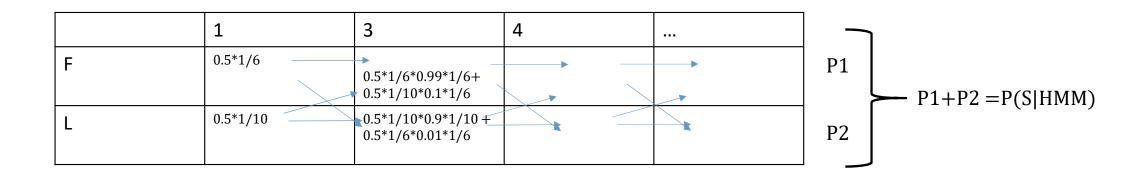
F,F C,F

	1	3	4	
F	0.5*1/6	0.5*1/6*0.99*1/6+ 0.5*1/10*0.1*1/6		
L	0.5*1/10	0.5*1/10*0.9*1/10		





We have searched all the combinations



### Some computational considerations....

- Each step implies multiplying a small number by a number between 0 and 1 (the probability of doing that step).
- We end having VERY small numbers, which ultimately will produce underflow
  - Do a log transformation (you can do this whenever you multiply probabilities)
  - Scale the probability at each step (you do this when you multiply and add probabilities)

• Scale the probability at each step (Rabiner 1989)

State	P(i)	P(i+1)
State1		
State2		
StateK		

$$\widehat{f}_l(i) = \frac{f_l(i)}{\prod_{j=1}^i s_i}$$

Scaling factor

• Scale the probability at each step (Rabiner 1989)

State	$\widehat{f}_l(i)$	$\widehat{f}_l(i+1)$
State1		
State2		
StateK		

$$\widehat{f}_l(i) = \frac{f_l(i)}{\prod_{j=1}^i s_j}$$

New scaled variable

• Scale the probability at each step (Rabiner 1989)

State	$\widehat{f}_l(i)$	$\widehat{f}_l(i+1)$
State1		
State2		
StateK		

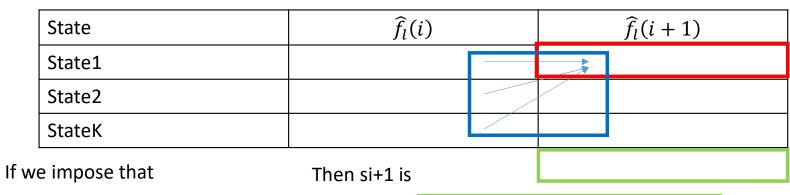
Probability of moving from state r to state I in i+1

$$\widehat{f}_{l}(i+1) = \frac{1}{S_{i+1}} e_{l}(x_{i+1}) \sum_{r=1}^{K} \widehat{f}_{r}(i) a_{rl}$$

Scaled forward

Emission probability of category at xi+1 using state I

• Scale the probability at each step (Rabiner 1989)



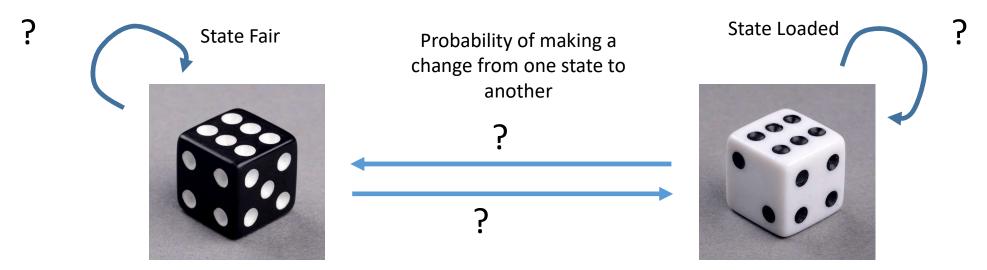
$$\sum_{l} \widehat{f}_{l}(i) = 1$$

$$s_{i+1} = \sum_{l} e_{l}(x_{i+1}) \sum_{k} \widehat{f}_{k}(i) a_{kl}$$

$$P(X|HMM) = \prod_{i}^{L} s_{i}$$

Total of the scaled value

### What happens when the parameters are not known?



#### Emission probabilities of fair dice

1	2	3	4	5	6
?	?	?	?	?	?

Fair (F) dice

#### Emission probabilities of loaded dice

1	2	3	4	5	6
	?		?	?	?

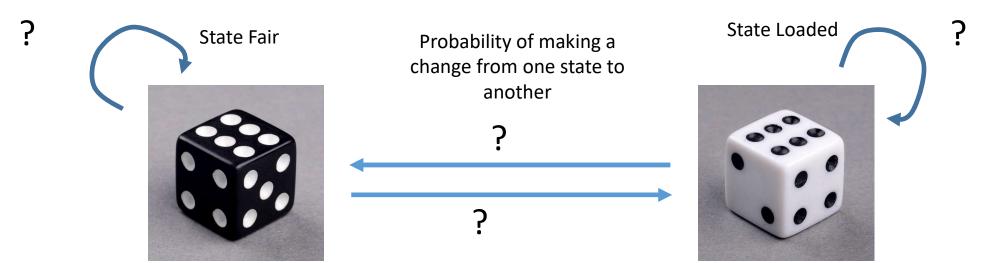
Loaded (L) dice

### What happens when the parameters are not known?

1 We have a training dataset where we know the hidden state

- *x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

- *x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4



#### Emission probabilities of fair dice

1	2	3	4	5	6
?	?	?	?	?	?

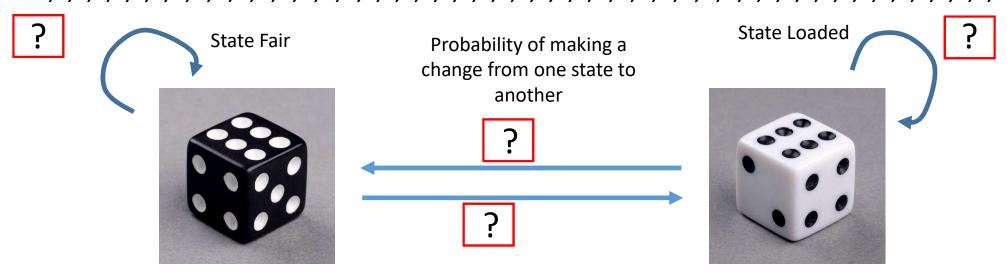
Fair (F) dice

#### Emission probabilities of loaded dice

1	2	3	4	5	6
?	?	٠:	?	?	?

### Loaded (L) dice

- *x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4



Emission probabilities of fair dice

1	2	3	4	5	6
?	5	?	?	?	?

Fair (F) dice

Emission probabilities of charged dice

1	2	3	4	5	6
?	?	?	?	?	?

Loaded (L) dice

- *x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

## How would you do it?

- *x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

Come from->Goes to	F	L
F		
L		

*x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

Come from->Goes to	F	L
F	1	
L		

- *x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

Come from->Goes to	F	L
F	2	
L		

*x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

Come from->Goes to	F	_
F	α	β
L	γ	δ

 $a_{FF}$ 

 $a_{FC}$ 

 $a_{CF}$ 

 $a_{CC}$ 

7

- 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

### Marginal of the row

Come from->Goes to	F	С	Total
F	α	β	α+β
С	γ	δ	γ+δ

Counts in cell row k, column I

Maximum likelihood estimates

$$a_{FF} = \frac{\alpha}{\alpha + \beta}$$

$$a_{FC} = \frac{\beta}{\alpha + \beta} \qquad a_{kl} = \frac{A_{ll}}{\sum_{ll} A_{ll}}$$

$$a_{kl} = \frac{A_{kl}}{\sum_{l}, A_{kl}}$$

Counts in row k (Marginal)

Row k

"come from"

Column I "go to"

Why the maximum likelihood can be computed like this?

For a given "I come from" state, we have two possible movements

"I stay at the state" with probability p

"I move to the other state" with probability 1-p

We observe "I stay at the state" y observations out of n observations

Which is the statistical distribution that could model this process?

$$P(y|p;n) = \frac{n!}{y!(n-y)!}(p)^{y}(1-p)^{n-y}$$

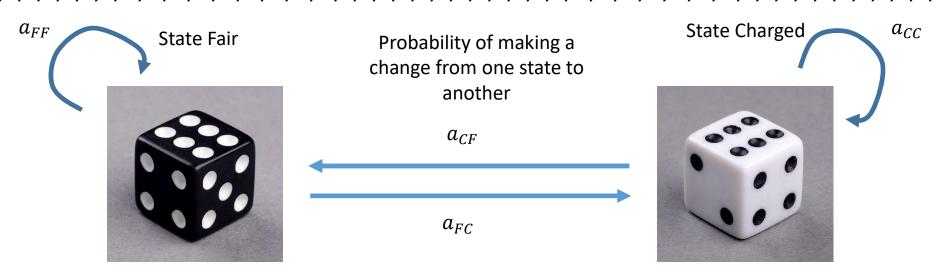
$$P(y|p;n) = \frac{n!}{y!(n-y)!}(p)^{y}(1-p)^{n-y}$$

$$\log(L(p)) = \log(C) + y\log(p) + (n-y)\log(1-p)$$

$$\frac{dL}{dp} = \frac{h}{p} - \frac{n - y}{1 - p}$$

$$\frac{dL}{dp} = 0; p = \frac{y}{n}$$

- *x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4



### Emission probabilities of fair dice

1	2	3	4	5	6
?	?	?	?	?	?

Fair (F) dice

Emission probabilities of charged dice

1	2	3	4	5	6
?	?	?	?	?	?

Loaded (L) dice

- *x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4



### Emission probabilities of fair dice

1	2	3	4	5	6
?	?	?	?	?	?

Fair (F) dice

### Emission probabilities of loaded dice

1	2	3	4	5	6
?	?	?	?	?	?

Loaded (L) dice

- *x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

## How would you do it?

x	F
1	$n_{1F}$
2	$n_{2F}$
3	$n_{3F}$
4	$n_{4F}$
5	$n_{5F}$
6	$n_{6F}$

x	P(x F)
1	$n_{2F}/N_F$
2	$n_{2F}/N_F$
3	$n_{3F}/N_F$
4	$n_{4F}/N_F$
5	$n_{5F}/N_F$
6	$n_{6F}/N_F$

$$e_k(b) = \frac{E_k(b)}{\sum_{b'} E_k(b')}$$

Can you identify the different variables?

# Once the parameters have been estimated in training, they must be validated in a different dataset not used for training (replication)

Confusion matrix. In classification tasks, it allows to estimate how good is the model

Viterbi	F is predicted given HMM	C is predicted given HMM	
F is true in replication	<b>↑</b>		
C is true in replication			

I would like this to be as close as possible to 100%

Check also P(S|HMM)

## The occasionally dishonest casino problem Unknown paths

*x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

How to find HMM that maximizes P(X|HMM)?

## The occasionally dishonest casino problem Unknown paths

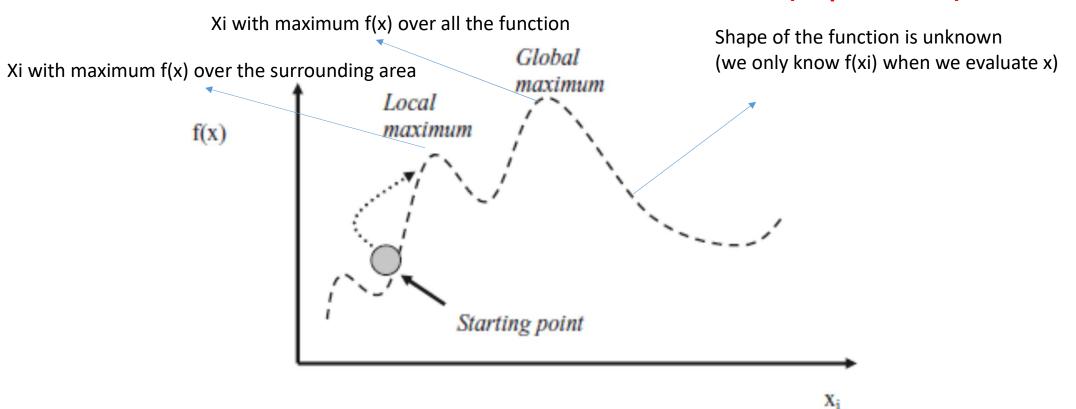
*x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

 $P(x|HMM=a_{rk};e_k(b))$ 

Likelihood of an observed sequence given a set of transition and emission probabilities from a given HMM, computed using the forward algorithm

How to find HMM that maximizes P(X|HMM)?

### How to find HMM that maximizes P(X|HMM)?



### The occasionally dishonest casino problem

### Optimization of a and e using The Genetic Algorithm

```
Program Genetic Algorithm ()

{
    initialize population;
    evaluate population;
    while (termination conditions not reached)
    {
        select solutions for next population;
        perform crossover and mutation
        evaluate population;
    }
}
```

$$chromosome = [p_1, p_2, p_3, \dots, p_{N_{var}}]$$

### Algorithm 3.1: Canonical Genetic Algorithm

Determine how the solution is to be encoded as a genotype and define the fitness function;

Create an initial population of genotypes;

Decode each genotype into a solution and calculate the fitness of each of the n solution candidates in the population;

#### repeat

Select n members from the current population of encodings (the *parents*) in order to create a mating pool;

#### repeat

Select two parents randomly from the mating pool;

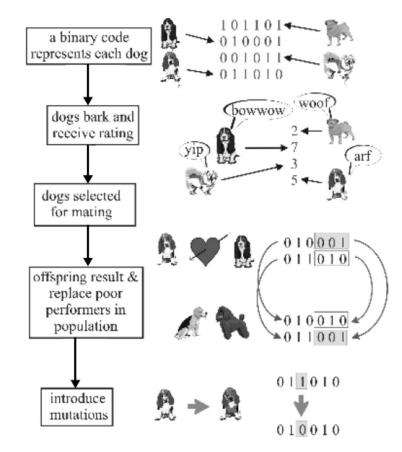
With probability  $p_{\text{cross}}$ , perform a crossover process on the encodings of the selected parent solutions, to produce two new (child) solutions; Otherwise, crossover is not performed and the two children are simply copies of their parents;

With probability  $p_{\text{mut}}$ , apply a mutation process to each element of the encodings of the two child solutions;

until n new child solutions have been created;

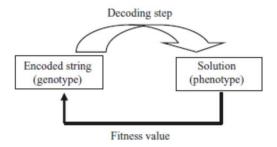
Replace the old population with the newly created one (this constitutes a generation);

until terminating condition;



- What do we need?
  - A chromosome based representation of the solution that we are searching for:

$$chromosome = [p_1, p_2, p_3, \dots, p_{N_{var}}]$$



$$y = -3.12 + 23.11 \times 3.93$$

- What do we need?
  - A way to generate new solutions by recombination from previous ones (Mating & Recombination):

$$parent_1 = [p_{m1}, p_{m2}, p_{m3}, p_{m4}, p_{m5}, p_{m6}, \dots, p_{mN_{var}}]$$
$$parent_2 = [p_{d1}, p_{d2}, p_{d3}, p_{d4}, p_{d5}, p_{d6}, \dots, p_{dN_{var}}]$$

By setting few crossover points Binary

By setting random uniform crossovers

offspring<sub>1</sub> =  $[p_{m1}, p_{m2}, p_{d3}, p_{d4}, p_{m5}, p_{m6}, \dots, p_{mN_{var}}]$ offspring<sub>2</sub> =  $[p_{d1}, p_{d2}, p_{m3}, p_{m4}, p_{d5}, p_{d6}, \dots, p_{dN_{var}}]$ offspring<sub>1</sub> =  $[p_{m1}, p_{d2}, p_{d3}, p_{d4}, p_{d5}, p_{m6}, \dots, p_{dN_{var}}]$ offspring<sub>2</sub> =  $[p_{d1}, p_{m2}, p_{m3}, p_{m4}, p_{m5}, p_{d6}, \dots, p_{mN_{var}}]$ 

Not allowing repeated values within each offspring

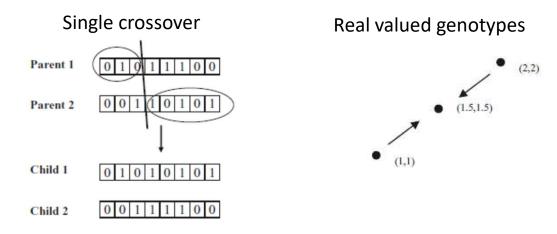
 $p_{new} = \beta p_{mn} + (1 - \beta) p_{dn}$ 

By mixing at each gene the proportions of the parents

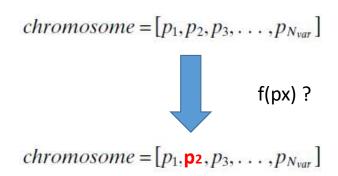
 $p_{new} = \beta(p_{mn} - p_{dn}) + p_{mn}$ 

Clustering based labeling

- What do we need?
  - A way to generate new solutions by recombination from previous ones (Mating & Recombination):



How to introduce new solutions (mutation)?



## Classical Genetic algorithm Other hyperparameters to consider

Which fitness? F(x) = g(f(x))

Which elitism?

(too small = a lot of bad solutions

Too high = risk of ending in a local solution)

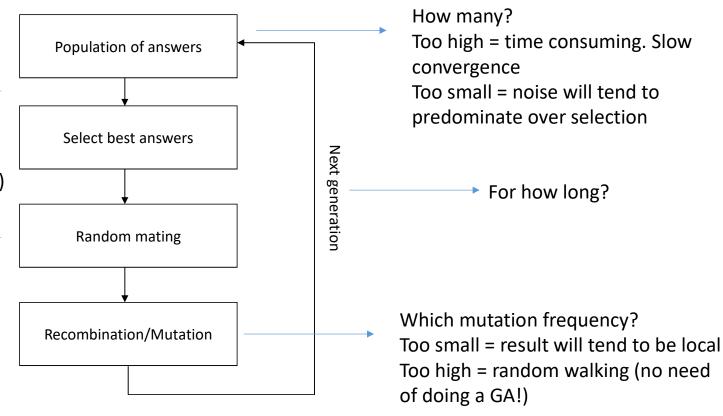
How do I allow the best to mate? -

At random?

Best have the higher frequency of mating?

$$f_{\text{rank}} = 2 - P + 2(P - 1) \frac{(\text{rank} - 1)}{(n - 1)}.$$

Tournament selection?



### The occasionally dishonest casino problem

### Optimization of a and e using The Genetic Algorithm

Chromosome structure

"Put in a vector the parameters you want to estimate"

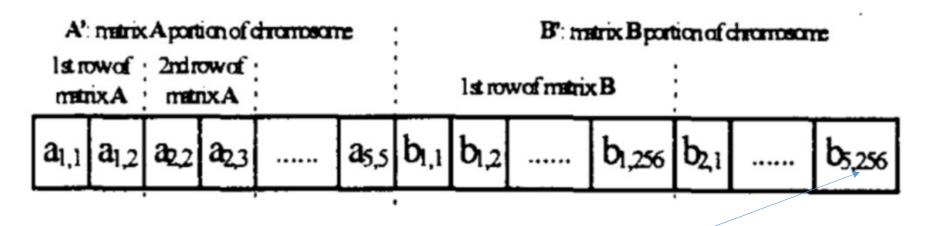
Which are the parameters?

$x \qquad P(x F)$		x	P(x C)
1		1	
2		2	
3	P(C F)	3	
4		4	
5	D(FIG)	5	
6	P(F C)	6	

### The occasionally dishonest casino problem

### Optimization of a and e using The Genetic Algorithm

Coding of the matrices in a vector (=Chromosome in GA). Example



This is because in this case they are using characters for speech recognition problems

### The occasionally dishonest casino problem

### Optimization of a and e using The Genetic Algorithm

Chromosome structure

	Which are the parameters?				
"Put in a vector the parameters you want to estimate"	$x \qquad P(x F)$	$x \qquad P(x C)$			
"taking into account possible conditions"	1	1			
taking into account possible conditions	2	2			
All these variables must	3 P(0	:  <b>F</b> ) 3			
add to one	4	4			
	5	5			
	6	<b>F</b> ( <b>C</b> ) 6			

### The occasionally dishonest casino problem

### Optimization of a and e using The Genetic Algorithm

### Chromosome structure

1				
1				
1				
1				

Which are the parameters?

"Put in a vector the parameters you want to estimate"

"taking into account possible conditions"

All these variables must add to one

$x \qquad P(x F)$		$\boldsymbol{x}$	P(x C)
1		1	
2		2	
3	P(C F)	3	
4	,	4	
5	D(E C)	5	
6	P(F C)	6	

### The occasionally dishonest casino problem

### Optimization of a and e using The Genetic Algorithm

### Chromosome structure

l			l	
1				
1				
1				
1				

Which are the parameters?

"Put in a vector the parameters you want to estimate"

"taking into account possible conditions"

All these variables must add to one

States P(Sj Si)	$S_1$	$S_2$	$S_n$
$S_1$			
$S_2$			
$S_n$			

### The occasionally dishonest casino problem

### Optimization of a and e using The Genetic Algorithm

Chromosome structure

	Which are the parameters?				
"Dut in a vector the parameters you want to estimate"	$x \qquad P(x F)$	$x \qquad P(x C)$			
"Put in a vector the parameters you want to estimate"  "taking into account possible conditions"	1	1			
taking into account possible conditions	2	2			
How many independent	3 P	(C F) 3			
variables do we have	4	4			
here?	5	5			
	6	6			

### The occasionally dishonest casino problem

### Optimization of a and e using The Genetic Algorithm

Which are the parameters?

6

### Chromosome structure

"Dut in a vector the parameters you want to estimat	$x \qquad P(x F) \qquad \qquad x \qquad P(x C)$
"Put in a vector the parameters you want to estimat	1 1
"taking into account possible conditions"	2
How many independent	P(C F) 3
variables do we have	4
here? 5 (because all the	5 P(F C)

In statistical jargon we would say n-1 degrees of freedom

variables must add to 1)

## The occasionally dishonest casino problem Optimization of a and e using The Genetic Algorithm

Chromosome structure

		l		
		l .		
		l .		
1		l		
		l .		
	l	I		ĺ

"Put in a vector the parameters you want to estimate"

"taking into account possible conditions"

Some subsets of parameters must add to 1 (we can exclude one)

All parameters cannot be greater than 1

Conditions of this particular problem

Find a way how to transform the variables so the conditions are fulfilled

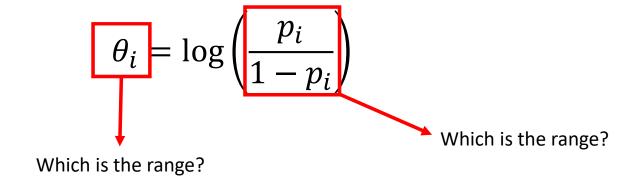
Discrete probability function

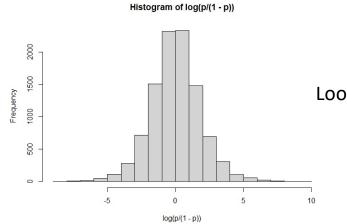
Logit transformation for a binary variable

$$P(i) = p_i$$

$$\sum_{i}^{K} p_i = 1$$







 $p{\sim}U(0{,}1)$  Looks like a Normal distribution, but it is not

### Discrete probability function

$$P(i) = p_i$$

$$\sum_{i}^{K} p_{i} = 1$$

Logit transformation for a binary variable

$$\theta_i = \log\left(\frac{p_i}{1 - p_i}\right)$$

How to estimate pi?

### Discrete probability function

$$P(i) = p_i$$

$$\sum_{i}^{K} p_i = 1$$



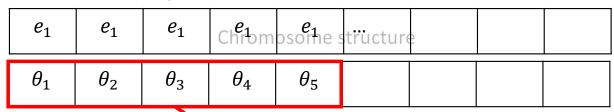
"Logit transformation of multinomial distribution"

$$p_i = \frac{e^{\theta_i}}{1 + \sum_{j}^{K-1} e^{\theta_j}}$$

$$p_K = 1 - \sum_{j}^{K-1} p_j$$

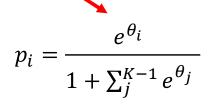
### The occasionally dishonest casino problem

### Optimization of a and e using The Genetic Algorithm

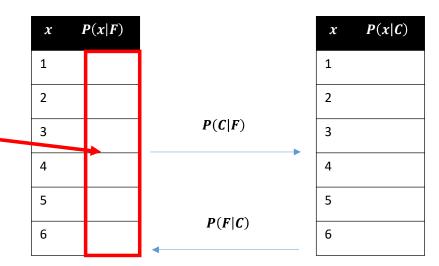


We need to keep track to which table each parameter refers to (BUT IT IS NOT CODED IN THE chromosome)

Which are the parameters?



Decode the information of the chromosome



### The occasionally dishonest casino problem

### Optimization of a and e using The Genetic Algorithm

#### **Breakpoints**

		 $\theta_{3,1}$	$\theta_{2,1}$	$\theta_{1,1}$	$\theta_{5,1}$	$\theta_{4,1}$	$\theta_{3,1}$	$\theta_{2,1}$	$\theta_{1,1}$
Parents									
		 $\theta_{3,2}$	$\theta_{2,2}$	$\theta_{1,2}$	$\theta_{5,2}$	$\theta_{4,2}$	$\theta_{3,2}$	$\theta_{2,2}$	$\theta_{1,2}$
	_								
Offspring		 $\theta_{3,1}$	$\theta_{2,1}$	$\theta_{1,2}$	$\theta_{5,2}$	$\theta_{4,2}$	$\theta_{3,1}$	$\theta_{2,1}$	$\theta_{1,1}$
550		 $\theta_{3,2}$	$\theta_{2,2}$	$\theta_{1,1}$	$\theta_{5,1}$	$\theta_{4,1}$	$\theta_{3,2}$	$\theta_{2,2}$	$\theta_{1,2}$

### The occasionally dishonest casino problem

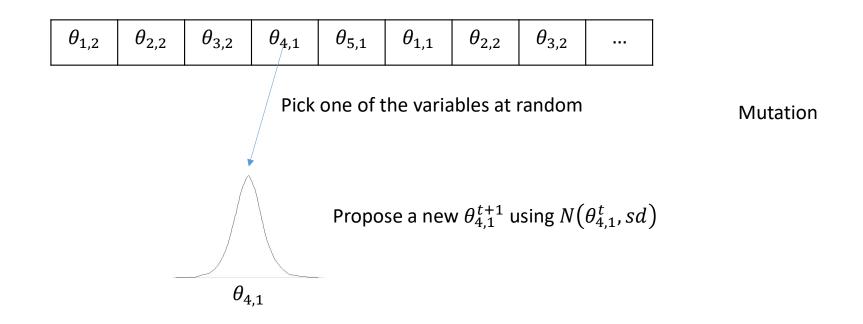
### Optimization of a and e using The Genetic Algorithm

#### **Breakpoints**

		 $\theta_{3,1}$	$\theta_{2,1}$	$\theta_{1,1}$	$\theta_{5,1}$	$\theta_{4,1}$	$\theta_{3,1}$	$\theta_{2,1}$	$\theta_{1,1}$
Parents									
		 $\theta_{3,2}$	$\theta_{2,2}$	$\theta_{1,2}$	$\theta_{5,2}$	$\theta_{4,2}$	$\theta_{3,2}$	$\theta_{2,2}$	$\theta_{1,2}$
	_								
Offspring		 $\theta_{3,1}$	$\theta_{2,1}$	$\theta_{1,2}$	$\theta_{5,2}$	$\theta_{4,2}$	$\theta_{3,1}$	$\theta_{2,1}$	$\theta_{1,1}$
550		 $\theta_{3,2}$	$\theta_{2,2}$	$\theta_{1,1}$	$\theta_{5,1}$	$\theta_{4,1}$	$\theta_{3,2}$	$\theta_{2,2}$	$\theta_{1,2}$

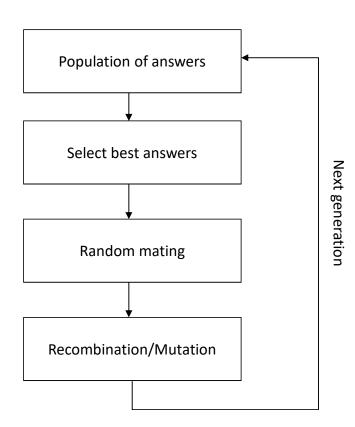
### The occasionally dishonest casino problem

### Optimization of a and e using The Genetic Algorithm



# Classical Genetic algorithm Other hyperparameters to consider

Which fitness?



### The occasionally dishonest casino problem

### Optimization of a and e using The Genetic Algorithm

Experimen	#1	#2	#3	#4	#5
		Genetic A	lgorithm		
Psame	-4.9473	-3.5693	-3.2932	-3.0982	-4.2345
Pdifferent	-7.4982	-8.9727	-8.6473	-8.5291	-9.1483
	Forwa	rd-Backw	ard Proce	dure	
Prame	-4.7359	-4.2125	-4.9843	-4.3908	-4.3876
Pdifferent	-7.2714	-8.6137	-7.5914	-7.7634	-7.1007

Experimen	#6	#7	#8	#9	#10
		Genetic A	lgorithm		
Prame	-3.3281	4.1869	-4.2322	-4.3872	-3.1539
Pdifferent	-7.5581	-7.6257	-8.6274	-8.7812	-8.3641
	Forwa	rd-Backw	ard Proce	dure	
Prame	-4.9811	-4.3481	-4.0567	-4.4860	4.9251
Pdifferent	-7.3825	-7.7351	-7.9328	-7.7514	-8.2254

### The occasionally dishonest casino problem

### Baum-Welch algorithm

*x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

 $P(x|HMM=a_{rk};e_k(b))$ 

Likelihood of an observed sequence given a set of **transition** and **emission** probabilities from a given HMM, computed using the forward algorithm

Imagine I could establish the probability of observing F,F given the sequence and the observed symbols and a proposed  $a_{kl}$ 

- *x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

Which is the probability of observing this sequence given a transition  $a_{kl}$  probability and all the observed sequence?

$$P(\pi_i = k; \pi_{i+1} = l | x; HMM) = \frac{P(\pi_i = k | x_1...x_i; HMM)P(x_i | \pi_i = k; HMM)P(\pi_{i+1} = l | \pi_i = k; HMM)P(\pi_{i+1} = l; HMM)P(\pi_{i+1} = l | x_{i+1}...x_L; HMM)}{P(x)}$$
Probability of observing state k at position I, state I at osition i+1 given the observed sequence of symbols and a proposal of parameters

Emission probability of symbol x at position i using state k at position i

$$P(\pi_i = k; \pi_{i+1} = l | x; HMM) = \frac{P(\pi_i = k | x_1...x_i; HMM)e_k(b = x_i)a_{kl}e_l(b = x_{i+1})P(\pi_{i+1} = l | x_{i+1}...x_L; HMM)}{P(x)}$$

Knowing that, I would be able to get a new estimate of the expected number of times that I expect to see such combination of k and I and, given that, propose a new  $a_{kl}$  to maximize the likelihood of the data given the parameters.

## $HMM_{i}$

*x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

$$P(\pi_i = k | x) = \frac{P(\pi_i = k, x)}{P(x)}$$

"I want to know the probability of state k at position i given that I have observed the whole sequence x"

1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,<mark>2</mark>,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

$$P(\pi_i = k, x_1 \dots x_i)$$

$$P(x_{i+1} ... x_L | \pi_i = k, x_1 ... x_i)$$

$$P(\pi_i = k, x) = P(\pi_i = k, x_1 \dots x_i) P(x_{i+1} \dots x_L | \pi_i = k, x_1 \dots x_i)$$

1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,<mark>2</mark>,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

$$P(\pi_i = k, x_1 \dots x_i)$$

$$P(x_{i+1} \dots x_L | \pi_i = k)$$

Because it only depends on the last element!

$$P(\pi_i = k, x) = P(\pi_i = k, x_1 ... x_i) P(x_{i+1} ... x_L | \pi_i = k)$$

#### HMM i

x 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,<mark>2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4</mark>

$$P(\pi_i = k, x_1 \dots x_i) \qquad P(x_{i+1} \dots x_L | \pi_i = k) = b_k(i)$$

$$P(\pi_i = k | x) = \frac{P(\pi_i = k)P(x | \pi_i = k)}{P(x)}$$

### The occasionally dishonest casino problem

*x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

Imagine we have observed this part of the sequence Imagine we know the parameters of the HMM (A, B)

$$P(X_1, X_2 ... X_i, \pi_i = l | HMM)$$

"Which is the probability that I observe the sequence of symbols and at position i the state is I given the parameters of my HMM?"

### The occasionally dishonest casino problem

*x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

Imagine we have observed this part of the sequence Imagine we know the parameters of the HMM (A, B)

Transition probability matrix

Emission probability matrix

$$P(X_1, X_2 ... X_i, \pi_i = l | HMM)$$

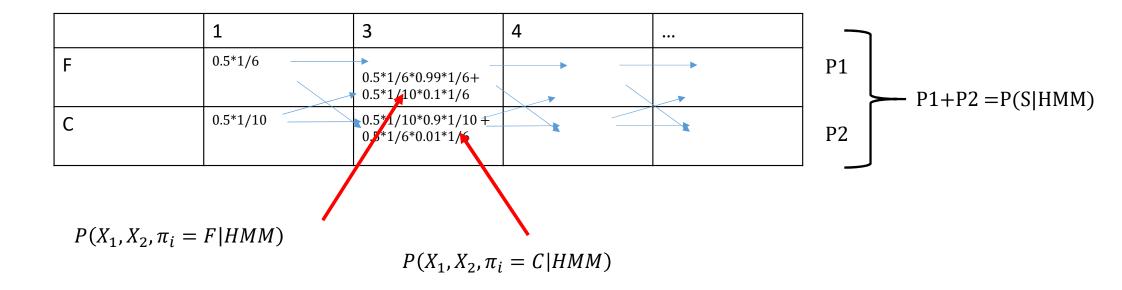
"Which is the probability that I observe the sequence of symbols and at position i the state is I given the parameters of my HMM?"

Forward algorithm: how to estimate the probability of a sequence ending in state k given a HMM

$$P(X_1, X_2 \dots X_i, \pi_i = l | HMM)$$

"Which is the probability that I observe the sequence of symbols and at position i the state is k given the parameters of my HMM?"

Forward algorithm: how to estimate the probability of a sequence ending in state k given a HMM



Forward algorithm: how to estimate the probability of a sequence ending in state k given a HMM

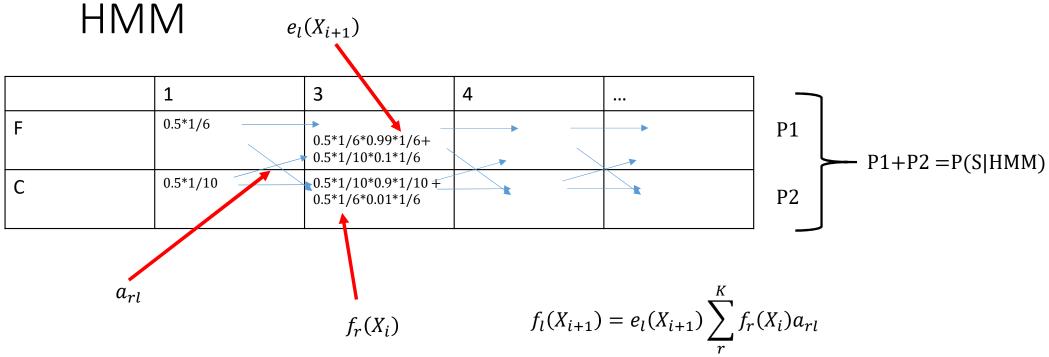
$$P(X_1,X_2\dots X_{i+1},\pi_{i+1}=l|HMM)=f_l(X_{i+1})=e_l(X_{i+1})\sum_{r}^K f_r(X_i)a_{rl}$$
 Transition probability to move from state  $r$  to  $l$ 

Emission probability of X at time i+1 given that the state is 1

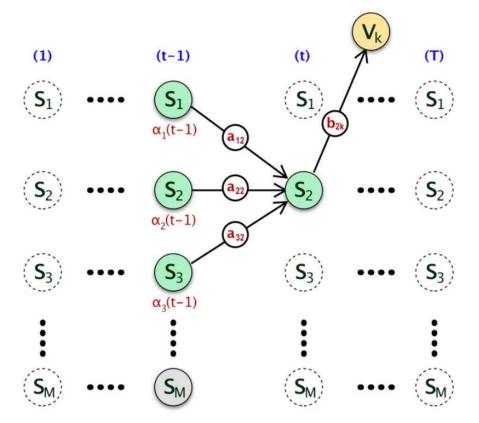
Probability of the sequence up to *i*, ending at *i* in state *r* 

"Which is the probability that I observe the sequence of symbols and at position i the state is k given the parameters of my HMM?"

Forward algorithm: how to estimate the probability of a sequence ending in state k given a



# Another way of visualizing the forward algorithm



http://www.adeveloperdiary.com/data-science/machine-learning/forward-and-backward-algorithm-in-hidden-markov-model/

Forward algorithm: how to estimate the probability of a sequence ending in state k given a HMM. Pseudocode (From the book of Durbin)

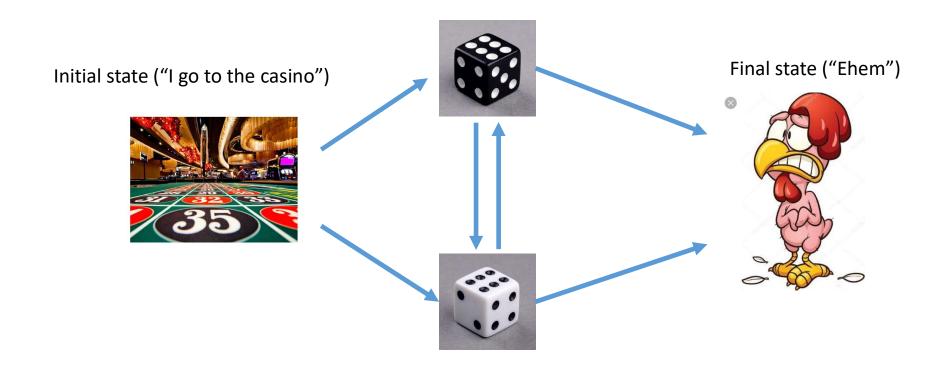
#### Algorithm: Forward algorithm

Initialisation 
$$(i = 0)$$
:  $f_0(0) = 1$ ,  $f_k(0) = 0$  for  $k > 0$ .

Recursion 
$$(i = 1 ... L)$$
:  $f_l(i) = e_l(x_i) \sum_{k} f_k(i-1) a_{kl}$ .

Termination: 
$$P(x) = \sum_{k} f_k(L)a_{k0}.$$

### In fact, there is an initial state and a final state



# Forward algorithm: There are two other states!

"After we start the sequence, the probability of going to initial state is 0"

"Before we start the sequence, we are at the initial state"

	NA	1	3	4		L+1
Initial State	1	0	0	0	0	0
F	0					0
С	0					0
Final State	0	0	0	0	0	P(S HMM)

## Forward algorithm: There are two other states!

"After we finish the sequence, the probability akl of going to the final state is 1"

	NA	1	3	4		L+1
Initial State	1	0	0	0	0	0
F	0					0
С	0					0
Final State	0	0	0	0	0	P(S HMM)

### HMM i

*x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,<mark>2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4</mark>

$$P(x_{i+1} ... x_L | \pi_i = k) = b_k(i)$$

$$\underset{i}{\mathsf{HMM}}$$

*x* 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,<mark>2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4</mark>

$$P(x_{i+1} ... x_L | \pi_i = k) = b_k(i)$$

	 5	5	4
F			
С			

Backward algorithm: how to estimate the probability of a sequence given an initial k state

HMM i

1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

$$P(x_{i+1} ... x_L | \pi_i = k) = b_k(i)$$

	 5	5	4
F			1
С			1

Starting at the last element, the entries in this column denote the probability moving to the end state from each state after generating the entire sequence.

### HMM i

x 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,<mark>2,1,3,5,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4</mark>

$$P(x_{i+1} ... x_L | \pi_i = k) = b_k(i)$$

	 5	5	4
F		•	-1
С			1

$$a_{kr}e_r(X_i)b_k(i)$$

$$0.95 * \frac{1}{6} * 1$$

### HMM i

x 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,<mark>2,1,3,5,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4</mark>

$$P(x_{i+1} ... x_L | \pi_i = k) = b_k(i)$$

	 5	5	4
F		$0.95 * \frac{1}{6} * 1$	1
С			1

$$a_{kr}e_r(X_i)b_k(i)$$

$$0.05 * \frac{1}{6} * 1$$

### HMM i

x 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,<mark>2,1,3,5,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4</mark>

$$P(x_{i+1} ... x_L | \pi_i = k) = b_k(i)$$

	 5	5	4
F		$0.95 * \frac{1}{6} * 1 + 0.05 * \frac{1}{6} *$	1
С			1

$$a_{kr}e_r(X_i)b_k(i)$$

$$0.05 * \frac{1}{6} * 1$$

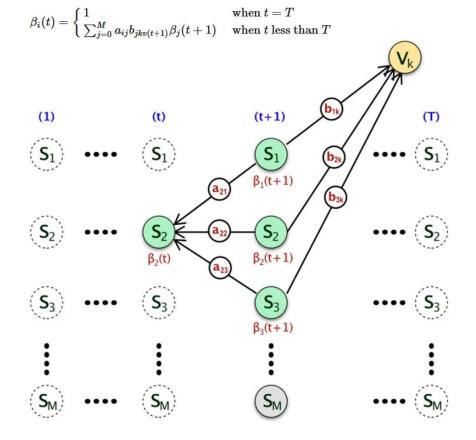
### HMM i

x 1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,2,3,4,5,1,4,3,6,<mark>2,1,3,5,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4</mark>

$$P(x_{i+1} ... x_L | \pi_i = k) = b_k(i)$$

	 5	5	4
F		$\begin{array}{c c} 0.95 * \frac{1}{6} * 1 + 0.05 * \frac{1}{6} \\ * 1 \end{array}$	1
С		$0.9 * \frac{1}{10} * 1 + 0.1 * \frac{1}{10} *$	1

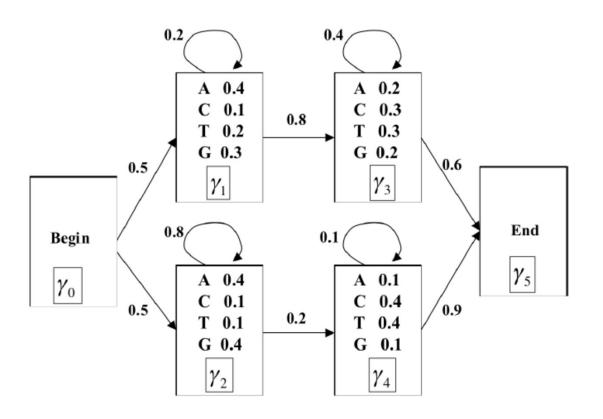
Another way of visualizing the backward algorithm



http://www.adeveloperdiary.com/data-science/machine-learning/forward-and-backward-algorithm-in-hidden-markov-model/

### **HMM**

Remember: Even if we have not explicitly stated, beginning and end are also states



What is strange in this HMM compared to the ones we have been using?

### **HMM**

If our subsequence was TAGA, which is the probability that we have ended at that each stage?

Time Step, t	0	1 (T)	2 (A)	3 (G)	4 (A)
$\gamma_0$	1	-	-	-	0
$\gamma_1$	1	-	-	-	0
$\gamma_2$	1	-	-	-	0
$\gamma_3$	ı	-	-	-	0.6
$\gamma_4$	1	_	_	-	0.9
γ <sub>5</sub>	•	-	-	-	0

### **HMM**

#### Algorithm: Backward algorithm

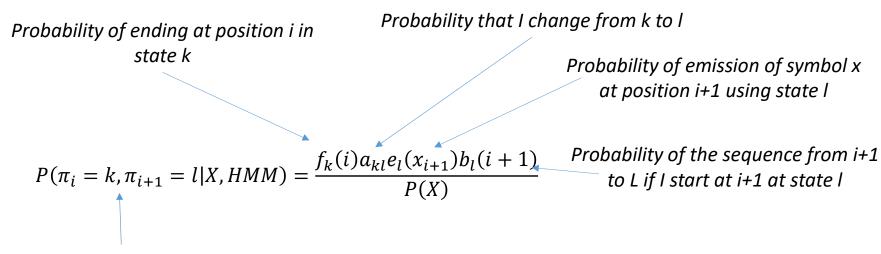
Initialisation 
$$(i = L)$$
:  $b_k(L) = a_{k0}$  for all  $k$ .

Recursion 
$$(i = L - 1, ..., 1)$$
:  $b_k(i) = \sum_l a_{kl} e_l(x_{i+1}) b_l(i+1)$ .

Termination: 
$$P(x) = \sum_{l} a_{0l} e_l(x_1) b_l(1).$$

### The occasionally dishonest casino problem

### Baum-Welch algorithm



Probability of a transition from state k at position i to state l in position i+1

### The occasionally dishonest casino problem

### Baum-Welch algorithm

We can do this for each position. Adding over all the positions, we have an estimate of "how often would occur a transition from state k to l if the parameter  $a_{kl}$  that we are using was the one that generated the data"

$$A_{kl} = \sum_{i}^{L} P(\pi_i = k, \pi_{i+1} = l | X, HMM)$$

 $a_{kl}^{(t+1)} = \frac{A_{kl}^t}{\sum_{l'}^K A_{kl'}^t}$ 

Posterior probability of akl(t+1) given akl(t) and the observed data

"Given that I come from state k, which is the probability of moving to any other state"

When the state was not hidden, this was the maximum likelihood estimate of the transition akl!

### The occasionally dishonest casino problem

### Baum-Welch algorithm

How can we estimate the emission probabilities?

1,4,5,1,3,2,1,6,6,4,1,6,6,6,6,6,6,2,3,4,5,1,4,3,6,2,1,3,5,6,6,6,6,6,6,6,6,6,1,2,3,1,1,1,1,2,3,4,5,5,4

Pick one of the symbols (for example, b = 6)

The index i of this position is 8

$$E_k(b) = \frac{1}{P(x)} \sum_{\{i \mid x_i = b\}} f_k(i) b_k(i)$$
 Probability that we are at state k in position in New emission probabilities

For all the positions where we observe 6

$$e_k^{t+1}(b) = \frac{E_k(b)}{\sum_{b'} E_k(b')}$$

### Baum-Welch algorithm

- 1) Propose a set of transition (a..) and emission (b.(.)) matrices
- 2) Until change of likelihood P(X|HMM) is not smaller than threshold, do
- 3) Using the forward and backward algorithm, estimate the new A.. and B.. variables
- 4) Estimate the new a.. and b.(.) matrices
- 5) Go to 2)

# The Baum-Welch is a special case of the EM algorithm

#### Two steps

- Expectation: missing data are estimated given the observed data and current estimate of the model parameters.
- Maximization: the likelihood function is maximized under the assumption that the missing data are known.

# How does a phenotype change over a phylogeny? Identifying Hidden Rate Changes in the Evolution of a Bina

Identifying Hidden Rate Changes in the Evolution of a Binary Morphological Character: The Evolution of Plant Habit in Campanulid Angiosperms

JEREMY M. BEAULIEU1,\*, BRIAN C. O'MEARA2, AND MICHAEL J. DONOGHUE1

Model adequacy is a different concern than model fit: the latter determines which of a set of models is least bad (or "best") for the data, whereas the former determines whether a single model adequately describes the data. For example, a model that says humans, chimps, and mice all diverged simultaneously 70 million years ago is a better fit to the data than one that puts that divergence 700 million years ago, but neither model adequately describes the data. Adequacy is often evaluated by simulating under the focal model to see if it generates data indistinguishable from the empirical data using one or more measures.