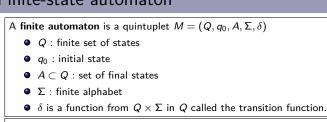
#### CÔTE D'AZUR Finite-state automaton

Algorithmics for Biology



The suffix function associated with a pattern P[1..m]:

$$\sigma : \Sigma^* \longrightarrow \{0, 1, ..., m\}$$

$$t \longrightarrow \sigma(x) = \max\{k \mid P[1..k] \text{ suffix of } t\}$$

$$(1)$$

The number  $\sigma(t)$  is the size of the largest prefix of the pattern being searched for, which is the suffix of the text t.

**Example :** For P = ab, one have  $\sigma(\epsilon) = 0$ ,  $\sigma(ccaca) = 1$ ,  $\sigma(ccab) = 2$ . If x is suffix of y,  $\sigma(x) \leq \sigma(y)$ . b is suffix of ab,  $\sigma(b) < \sigma(ab)$ a is suffix of aa,  $\sigma(a) \leq \sigma(aa)$ .

Automaton associated with a pattern. This is the automaton for which we are in state q if and only if the largest prefix we have just read is P[1..q].

•  $Q = \{0, 1, ..., m\}$ 

• line 4 :  $O(|\Sigma|)$ • line 3 : O(m)

• We can do faster.

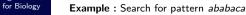
• Global complexity :  $O(m^3|\Sigma|)$ 

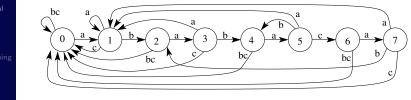
- $q_0 = \{0\}$
- $A = \{m\}$
- $\delta(q, a) = \sigma(P_q a)$  maximum suffix of the concatenation of  $P_q$  with  $a \otimes c_{25/112}$

#### CÔTE D'AZUR Finite-state automaton

Algorithmics

Antomata





Once the automaton has been constructed, the text traversal algorithm is as follows :

1	def FiniteAutomatonSearch(T, delta, m)
2	n = len(T);
3	q = 0;
4	for (i=1; i<=n; i++) {
5	q = delta (q,T[i]);
6	if q = m then
7	<pre>print(''The pattern appears with the offset'', i-m);</pre>
8	}

 $^{A}$ 

## **Complexity** : O(n)

Run the automaton on the string ababacaba.

▲□▶ ▲□▶ ▲ 三▶ ▲ 三 ● ○ Q ○ 26/112

CÔTE D'AZUR		CÔTE D'AZUR	Examp	le :	building the automa	aton <sup>-</sup>	for pat	ttern	AAB
Algorithmics for Biology Jean-Paul Comet Pat. Matching Rabin-Karp Anomata KMP BM Graphs Dyn.Prog. Sequences	<b>Computing the transition function.</b> The idea is based on the meaning of the different states of the automaton : state <i>i</i> corresponds to the state where the first <i>i</i> letters of the searched pattern have just been read. To build the automaton, we go through all the states of the automaton (from 0 to <i>n</i> , where <i>n</i> is the length of the word we're looking for) and for each state <i>i</i> , we go through each letter a of the alphabet. We then calculate the longest prefix of the pattern that is a suffix of <i>P</i> [1 <i>i</i> ]. <i>a</i> . The length of this suffix gives the arrival state of the transition starting from <i>i</i> via letter <i>a</i> . 1 def Transition_Function_computation (P, Sigma) 2 def Transition_function; (P, Sigma) 2 for q in range(m): 3 for q in range(m): 4 for a in Sigma : 5 k = min(m,q+1); 6 delta(q,a) = k; 9 return(delta); For this function to be correct, the following convention must be used : $\varepsilon$ is the suffix for all strings. Complexity analysis : • lines 6-7 : $Q(m^2)$	Algorithmics for Biology Jean-Paul Comet Complexity Pat. Matching Rabin-Karp Antomta KMP BM Graphs Dyn.Prog. Sequences	     	A B A B A A B A B B	k min(m, q + 1) = min(3, 1) = 1 1 0 min(m, q + 1) = min(3, 2) = 2 2 1 0 min(m, q + 1) = min(3, 3) = 3 3 min(m, q + 1) = min(3, 4) = 3 1 3 2 1 0	$\begin{array}{c} P_k \\ A \\ A \\ \varepsilon \\ AAA \\ AA \\ A \\ c \\ AAB \\ A \\ A$	Pq.aABAAABABABAAAAAAAAAAABAABAAABAAABAAABBAABBAABBAABB	suffix yes no yes yes no no yes no no yes no no no yes	$\frac{\delta}{1}$ 0 2 0 2 3 1 0
	5							yes	

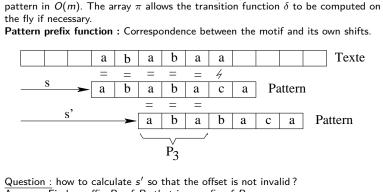
◆□ ▶ < @ ▶ < E ▶ < E ▶ ○ E り < C 27/112</p>



E ∽ Q ( 28/112

#### CÔTE D'AZUR Knuth-Morris-Pratt algorithm

Algorithmics for Biology КМР



This algorithm achieves complexity in  $\Theta(n+m)$  by avoiding the transition

function  $\delta$ . It computes an auxiliar function  $\pi[1..m]$  precomputed from the

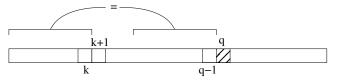
Answer : Find a suffix  $P_k$  of  $P_q$  that is a prefix of P.

The prefix function for the P pattern :  $\Pi : \{1, 2...m\} \longrightarrow \{0, 1...m-1\}$  $\longrightarrow \Pi[q] = max\{k/k < q \text{ and } P_k \text{ is suffix of } P_q\}$ q  $\Pi[q]$  is in fact the size of the longest prefix of P which is a proper suffix of  $P_q$ .

### Intuition for calculating the prefix function CÔTE D'AZUR

• We construct the array  $\Pi$  starting from index 0. The initialisation is simple :  $\Pi[1] = 0$ 

• Now let's assume that we have calculated  $\prod[i]$  from i = 1 to q - 1. To calculate  $\Pi[q]$  we have the following situation :



• Since k is the longest prefix that is a suffix of  $P_{q-1}$ , the longest prefix that is also a suffix of  $P_a$  cannot be longer than  $P_{k+1}$ . Furthermore, we have

$$P[k+1] = P[q] \iff \Pi[q] = k+1$$

• If  $P[k+1] \neq P[q]$ , look for the largest prefix-suffix of  $P_q$ . If we don't look at the last letter, the largest prefix-suffix of  $P_q$  is also a suffix of  $P_k$ . Now we know the largest prefix-suffix of  $P_k$ , which is  $\Pi[k]$ , already constructed. Once we have  $P_{\prod[k]}$ , we need to check if it can be extended to the next letter.

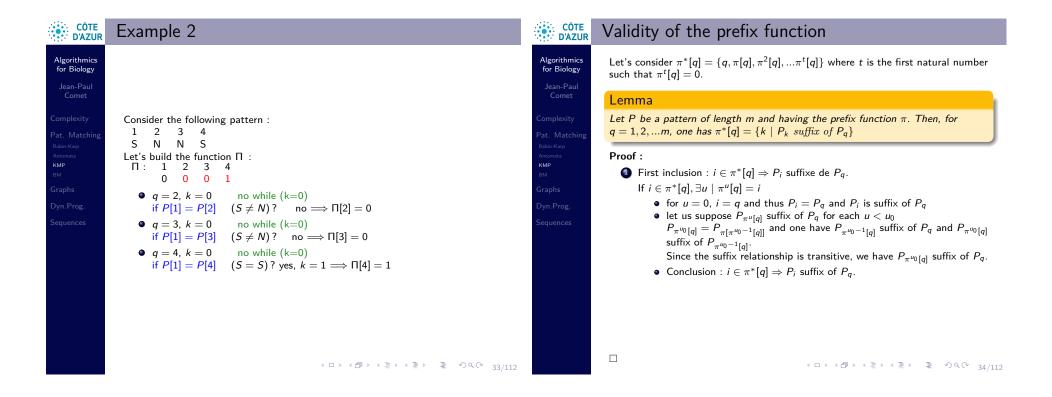
▲□▶ ▲□▶ ▲ 三▶ ▲ 三▶ 三三 のへで 30/112

COTE Algorithm for calculating the prefix function	CÔTE Example 1
Algorithmics for Biology Jean-Paul Comet Complexity 'at. Matching Marconata KAP WA Soft Display (a) Soft Soft Soft Soft Soft Soft Soft Soft	Algorithmics for Biology Jan-Paul Comet Complexity Pat. Matching Refer Key Automats Kup Graphs Dyn.Prog. Sequences $ \begin{array}{c} 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 \\ a & b & a & b & a & b & c & a \\ 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 \\ 0 & 0 & 1 & 2 & 3 & 4 & 5 & 6 & 0 & 1 \\ 0 & 0 & 1 & 2 & 3 & 4 & 5 & 6 & 0 & 1 \\ e & q = 2, k = 0 & \text{no while } (k=0) & \text{if } P[1] = P[2] & (a=b)? & \text{no, } k = 0 \Longrightarrow \Pi[2] = 0 \\ e & q = 2, k = 0 & \text{no while } (k=0) & \text{if } P[1] = P[3] & (a=a)? & \text{yes, } k = 1 \Longrightarrow \Pi[3] = 1 \\ e & q = 4, k = 1 & \text{no while } (P[k+1]=P[q]) \\ if P[2] = P[4] & (b=b)? & \text{yes, } k = 2 \Longrightarrow \Pi[4] = 2 \\ e & q = 5, k = 2 & \text{no while } (P[k+1]=P[q]) \\ if P[3] = P[5] & (a=a)? & \text{yes, } k = 3 \Longrightarrow \Pi[5] = 3 \\ e & q = 6, k = 3 & \text{no while } (P[k+1]=P[q]) \\ if P[4] = P[6] & (b=b)? & \text{yes, } k = 4 \Longrightarrow \Pi[6] = 4 \\ e & q = 7, k = 4 & \text{no while } (P[k+1]=P[q]) \\ if P[5] = P[7] & (a=a)? & \text{yes, } k = 5 \Longrightarrow \Pi[7] = 5 \\ e & q = 8, k = 5 & \text{no while } (P[k+1]=P[q]) \\ if P[6] = P[8] & (b=b)? & \text{yes, } k = 6 \Longrightarrow \Pi[8] = 6 \\ e & q = 9, k = 6 & \text{enter into the while} \\ while P[7] \neq P[9] & (a \neq c) k = \Pi[6] = 4 \\ while P[3] \neq P[9] & (a \neq c) k = \Pi[2] = 0 \\ if P[1] = P[9] & (a=c)? & \text{no, } k = 0 \Longrightarrow \Pi[9] = 0 \\ e & q = 10, k = 0 & \text{no while } (k=0 \& P[k+1]=P[q]) \end{array}$

Algorithmics

for Biology

КМР



CÔTE D'AZUR	Validity of the prefix function	CÔTE D'AZUR	Validity of the prefix fu
Algorithmics for Biology Jean-Paul	Let's consider $\pi^*[q] = \{q, \pi[q], \pi^2[q],\pi^t[q]\}$ where t is the first natural number such that $\pi^t[q] = 0$ .	Algorithmics for Biology Jean-Paul	
Comet	Lemma	Comet	Lemma
Complexity Pat. Matching Rabin-Karp	Let P be a pattern of length m and having the prefix function $\pi$ . Then, for $q = 1, 2,m$ , one has $\pi^*[q] = \{k \mid P_k \text{ suffix of } P_q\}$	Complexity Pat. Matching Rabin-Karp	Let P be a pattern of length m and $\int dr f(q) = 0$ the
Antomata Antomata KMP BM Graphs Dyn.Prog. Sequences	Proof : Iet us prove that : {k   P <sub>k</sub> suffix of P <sub>q</sub> } ⊆ $\pi^*[q]$ Proof by contradiction : let us assume that there is an integer in the set {k   P <sub>k</sub> suffix of P <sub>q</sub> } \ $\pi^*[q]$ . We denote <i>j</i> the largest of the values. As $q \in \pi^*[q] \cup \{k   P_k$ suffix of P <sub>q</sub> } $\Rightarrow j < q$ . Let <i>j'</i> be the smallest integer in $\pi^*[q]$ that is greater than <i>j</i> . • P <sub>j</sub> is a suffix of P <sub>q</sub> since it belongs to {k   P <sub>k</sub> suffix of P <sub>q</sub> } • P <sub>j'</sub> is a suffix of P <sub>q</sub> since it belongs to $\pi^*[q]$ Thus P <sub>j</sub> suffix of P <sub>j'</sub> (trivial because <i>j'</i> > <i>j</i> ) Moreover <i>j</i> is the largest value of {k   P <sub>k</sub> suffixe de P <sub>q</sub> } \ $\pi^*[q]$ We should then have $\pi[j'] = j$ and then $j \in \pi^*[q]$ . Contradiction.	Antomata KMP BM Graphs Dyn.Prog. Sequences	<b>Proof :</b> If $k = \pi[q] > 0$ then $P_k$ suffix of $P_q$ . Thus $P_{k-1}$ suffix of $P_{q-1}$ (by deletin According to the previous lemma : $k$ For $q = 2, 3,, m$ , we define the sub $E_{q-1} = \{k \mid k \in \pi^*$ Intuitively, $E_{q-1}$ is made up of values extend $P_k$ to $P_{k+1}$ and obtain a sufficient

CÔTE D'AZUR	Validity of the prefix function
Algorithmics for Biology	
Jean-Paul Comet	Lemma
Complexity Pat. Matching Rabin-Karp	Let P be a pattern of length m and prefix function $\pi$ . For $q = 1, 2,, m$ , if $\pi[q] > 0$ then $\pi[q] - 1 \in \pi^*[q - 1]$ .
Antomata KMP BM Graphs Dyn.Prog. Sequences	<b>Proof :</b> If $k = \pi[q] > 0$ then $P_k$ suffix of $P_q$ . Thus $P_{k-1}$ suffix of $P_{q-1}$ (by deleting the last character of $P_k$ and $P_q$ ) According to the previous lemma : $k - 1 \in \pi^*[q - 1]$ . $\Box$
	For $q=2,3,,m$ , we define the subset $E_{q-1}\subseteq \pi^*[q-1]$ by :
	$E_{q-1} = \{k \mid k \in \pi^*[q-1] \text{ by } P[k+1] = P[q]\}$
	Intuitively, $E_{q-1}$ is made up of values $k \in \pi^*[q-1]$ such that it is possible to extend $P_k$ to $P_{k+1}$ and obtain a suffix of $P_q$ .

#### CÔTE D'AZUR Validity of the prefix function

# corrolary

Let P be a pattern of length m and prefix function pi. For q = 2, 3, ..., m,

 $\pi[q] = 0$  if  $E_{q-1} = \{\}$  $\pi[q] = 1 + \max\{k \in E_{q-1}\} \text{ if } E_{q-1} \neq \{\}$ 

Proof :

If  $r = \pi[q] > 0$  then  $P_r$  suffix of  $P_q$ . And  $r \ge 1 \Rightarrow P[r] = P[q]$ According to the previous lemma, if  $r \ge 1$ , we have :

$$r = 1 + \max\{\underbrace{k \in \pi^*[q-1] \mid P[k+1] = P_q}_{E_{q-1}}\}$$

If r = 0, there is no  $k \in \pi^*[q - 1]$  for which we can extend  $P_k$  to  $P_{k+1}$  to obtain a suffix of  $P_q$ , since we would then have  $\pi[q] > 0$ . Thus  $E_{a-1} = \{\}$ 

◆□▶ ◆□▶ ◆ ■▶ ▲ ■ ▶ ■ のへで 36/112

CÔTE D'AZUR

КМР

Algorithmics for Biology Algorithm validity : **1**  $\pi[1] = 0$  correct because  $\pi[q] < q$  for all q2 At the start of each loop iteration, we have  $k = \pi[q - 1]$ • for the first loop : imposed by  $\pi[1] = 0$  and k = 0• for the others : imposed by  $\pi[q] = k$ 3 while loop : we run through all the values of  $\pi^*[q-1]$  until we find one for which P[k+1] = P[q]. At this point, we know that k is the largest value of  $E_{q-1}$ ; and from the corollary, we can give to  $\pi[q]$  the value k+1If no such k is found, k = 0

◆□ ▶ < @ ▶ < E ▶ < E ▶ E りへで 37/112</p>

CÔTE D'AZUR	Global procedure	
Algorithmics for Biology Jean-Paul Comet Complexity Pat. Matching Rabin-Karp Antomata KMP BM Graphs Dyn.Prog. Sequences	<pre>1 KMP1(T,P) 2 n = long[T]; 3 m = long[P]; 4 PI = Calcul_fonct_prefixe(P); 5 q = 0; 6 7 Pour i=1 à n faire 8 tant que q&gt;0 &amp; P[q+1]!=T[i]; 9 q = PI[q]; 10 si P[q+1]=T[i]: 11 q = q+1; 12 si q = m alors 13 print(''hit at '', i-m); 14 q = PI[q];</pre>	<pre>1 KMP2(T,P) 2 n = long[T]; 3 m = long[P]; 4 PI = Compute_prefix_Function(P) ; 5 i = q = 0; 6 while (i<n): 8 if T[i] == P[q]: 9 i++; q++; 10 else 11 if q==0: 12 i++; 13 else: 14 q = PI[q-1]; 15 if q==m 16 print(''hit at '', i-m); 17 q = PI[q-1];</n): </pre>

The first version is based on the same idea as the prefix function. The second version manages two indices in a single loop : one to indicate progress in the text and another to indicate progress in the pattern.

Complexity analysis : requires amortized analysis...