CÔTE D'AZUR		CÔTE D'AZUR	Teaching organiz	ation			
Algorithmics for Biology Jean-Paul Comet Complexity Pat. Matching	Algorithmics for Biology Département Génie Biologique	Algorithmics for Biology Jean-Paul Comet Complexity Pat. Matching	 Lectures : 9 session TDs : 9 sessions of teachers : Jean-Paul Comet Lisa Guzzi 	s of 1 hours 30 1 hours 30 Jean-F lisa	Paul.Comet@ .guzzi@etu.	univ-cot	edazur.fr
Graphs	GB4 – year 2023–2024	Graphs	Date	hours	Lecture	TDs	
Dyn.Prog.		Dyn.Prog.		2024 13h30-16h45	JPC	LG	
Sequences		Sequences	2 09/02	2024 8h30-11h45	JPC	LG	
	POLYTECH' sophia antipolis		3 16/02	2024 8h30-11h45	JPC	LG	
			4 08/03	2024 8h30-11h45	JPC	LG	
			5 12/03	2024 15h15-16h45*	JPC	LG	
	Ioan Paul Comet		6 29/03	2024 8h30-11h45	JPC	LG	
	Jean-Faur Connet			2024 13h30-16h45	JPC	LG	
			8 11/04	2024 8h30-11h45	JPC	LG	
	Université Côte d'Azur		9 19/04	2024 8h30-11h45	JPC	LG	
			• Evaluation : Final e	xam (3 hours), 23/04/2	2024 13h30-:	16h30	70%
	19/01/2024		4 TD report, to fin	sh at home			30%
			 course material + https://w 	D + annals : ww.i3s.unice.fr/~co	met/SUPPOR	TS/ 🗆	
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CÔTE D'AZUR	Plan	CÔTE D'AZUR	Generality		
Algorithmics for Biology Jean-Paul Complexity Generality Complexity analysis Notations Divide and Conquer Pat. Matching Graphs Dyn.Prog. Sequences	 Introduction to algorithm complexity Generality Complexity analysis Notations Divide and Conquer Exact Pattern Matching Graph algorithms 	Algorithmics for Biology Jean-Paul Complexity Complexity Complexity analysis Notations Divide and Conquer Pat. Matching Graphs Dyn.Prog. Sequences	An algorithm is a sequence of actions to be performed by a machine or auto- maton in a finite amount of time, to achieve the desired result. • finite sequence of instructions • inputs / outputs sort an array - insertion sort 1 insertion_sort (double A[], int n) 2 { 1 insertion_sort (double A[], int n) 2 { 3 for (j=1; j <n; j++)="" {<br="">4 key = A[]]; 5 /* insertion of A[j] in the sorted sequence A[0(j-1)] */ 6 i=j-1; 7 while (i>=0) && (A[i]>key) { 8 A[i+1] = A[i]; 9 i = i-1; 10 } 11 A[i+1] = key; 12 }</n;>		
	 ④ Dynamic Programming ⑤ Sequence Comparison 		$ \begin{array}{cccccccccccccccccccccccccccccccccccc$		

COTE Complexity analysis

Algorithmics for Biology

Comet

- Complexity Generality Complexity analysis Notations Divide and Conquer Pat. Matching Graphs Dyn.Prog.
- Complexity analysis shows whether one algorithm is more efficient than another.
- This analysis must be independent of the physical resources used (processor, memory access time).

Complexity \equiv number of steps **required** to solve the problem for an input of a given size.

What's the point of complexity?

- Plan the resources required for an algorithm
- What are the critical resources ? the <u>time</u>, the <u>memory</u>, (the bandwidth of a communication)
- $\bullet \ \mbox{Complexity}$ will depend on the machine model. Generally
 - random access memory (RAM)a single processor

If this model changes, so does the complexity, since you may have to take into account communication times between processors and/or the time it takes to access information in memory.

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COTE Complexity analysis

Algorithmics for Biology

Complexity analysis

1976	1 Mhz	8 Ko	1 core
1984	8 Mhz	512 Ko	1 core
1992	33 Mhz	4 Mo	1 core
1998	400 Mhz	64 Mo	1 core
2000	1 Ghz	512 Mo	1 core
2007	3 Ghz	4 Go	1/2 cores
2012	3.5 Ghz	8 Go	1/2/4 cores
2014	3.5 Ghz	8 Go	2/4/8 cores
2018	3.6 Ghz	16 Go	8 cores
2021	3.7 Ghz	32 Go	10 cores



Insertion sort execution time depends on the input :

- on the number of elements to be sorted
- on the nature of the array :
- if the elements are already sorted, very quickly the shifting is no longer necessary, and the # of comparisons is very low.
 - if sorted in reverse : much longer

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Algorithmics for Biology Jean-Paul Comet Complexity Generality Complexity snalysis Notations Divide and Conquer Pat. Matching Graphs Dyn.Prog. Sequences	 In general, execution time increases with input size. execution time = f(input size) input size for an array : number of elements for a graph : (number of vertices, number of arcs) To estimate execution time : execution time for each elementary instruction Example : Tri_insertion def Tri_insertion (array): for j in range(n): key = array[j] for j in range(n): key = array[j] cost no. of passes for j in range(n): key = array[j] cost no. of passes for j in range(n): for j	Algorithmics for Biology Jean-Paul Comet Jaan-Paul Comet Remarks : Complexity Co
	$t = c_1(n-1) + c_2(n-1) +$	

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CÔTE Notations



COTE Divide and Conquer

Many algorithms have a recursive structure :

- recursive calls to very similar sub-problems,
- these calls separate the problem into several similar subproblems of smaller size.
- they solve the sub-problems recursively
- then combine the solutions of the sub-problems to calculate the solution to the problem.

There are three steps to each level :

- Divide the problem,
- Reign in the sub-problems by solving them recursively,
- Combine sub-problem solutions.

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CÔTE D'AZUR	An atypical sorting algorithm
Algorithmics for Biology	
Jean-Paul Comet	
Complexity Generality Complexity analysis Notations Divide and Conquer	A sorting algorithm NOT based on the comparison of its elements : • Assumption : the array to be sorted is composed only of integers $\in [0, 63]$.
Pat. Matching Graphs Dyn.Prog.	 An array of size 64 is created (initialized to 0). We browse the initial array, and when we find the value k, we update the array C : C[k]++;.
Sequences	The sorted array is then reconstructed.
	Complexity : $O(n)$.