# Algorithms and Data Structures in Biology

Introduction to the Course

Ugo Dal Lago





University of Bologna, Academic Year 2018/2019

#### Section 1

Organization

#### Organization

- Webpage
  - http://www.cs.unibo.it/~dallago/ADSB1819/
- ► Email
  - ▶ ugo.dallago@unibo.it
- ▶ Office Hours
  - ▶ Where: see http://www.cs.unibo.it/~dallago
  - ▶ When: there is no fixed office hours, just write me an email and we will fix an appointment.
- ► Teaching Assistant
  - ► Thomas Leventis, thomas.leventis@irif.fr
  - ▶ He takes care of the lab sessions.

#### Structure and Schedule

- ► First Module: **Theory** 
  - ► Monday 11.00am-1.00pm, Friday 9.00am-11.00am.
  - ▶ The basics of the theory of algorithms, and some design patterns: exhaustive search, dynamic programming, divide et impera, etc.
  - ▶ All lectures will be given by Ugo Dal Lago.
- ► Second Module: Lab
  - ► *Monday*, 2.00pm-6.00pm.
  - ▶ Performance evaluation of algorithms as implemented in the Python programming language through the cProfile library. You will also learn how to write a report by way of the LATEX system.
  - ▶ Initially, both teachers will be present at the lab, while later on only Thomas Leventis will be there.

#### Textbooks and Exams

#### Textbook

- ▶ The first module, being theoretical, requires a textbook.
- Neil C. Jones, Pavel A. Pevzner. An Introduction to Bioinformatics Algorithms (Computational Molecular Biology). The MIT Press. 2004.

#### Exams

- ▶ The first module's exam will be written, and will be given at the end of the course.
- ▶ The second module's exam will consist in three assignments, that needs to be completed in a week each. In *very* exceptional cases, in which students cannot complete one or more assignments on time, the teachers will decide how to

#### Section 2

The "What" and the "Why"

# The Course's Objectives

#### ▶ Problems and Algorithms

▶ Algorithms are the middle ground between problems and programs.

#### ▶ Measuring Algorithms' Complexity

- Different algorithms (solving the same problem) may do so quite differently.
- ▶ How should we decide *which one* of the possibly many algorithms is the right one for our needs?

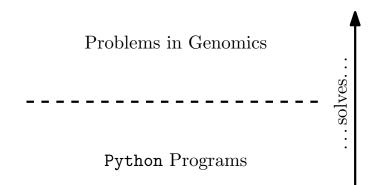
#### ▶ How to Design Algorithms

- ▶ Although designing algorithmics requires a nontrivial dose of creativity, there are *a few recipes* that work remarkably well in many cases.
- ▶ We will learn a few of them.

#### ▶ Proving Algorithms Correct

▶ Suppose you designed an algorithm for a

# "Why Should I Learn Algorithmics?"



### "Why Should I learn Algorithmics?"

- ► The workflow you have in mind is, very likely, the following one:
  - 1. In my daily work as an expert in genomics, I **stumble upon a problem** which seems to have a nice, nontrivial, computational content.
  - 2. I have some ideas about how to solve it via Python, but the problem seems to be **too complicated** to be solved *directly*.
  - 3. I thus **look for** a module which provides some dedicated function solving the kind of problem I encountered. Hey! There should be one, shouldn't it?
  - 4. Once I find it, I simply **import** the module, **invoke** the function, and that's it.
- ▶ But is all this going to *always* work?
  - ► The set of problems you will encounter is not fixed once and for all: it changes over time.
  - ▶ You cannot just wait until *someone* implements a module for you!

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# "Why Should I Learn Algorithmics?"

Problems in Genomics solves or implement. Combinatorial Problems Algorithms Python Programs

### An Example: a Problem from Genomics

▶ Suppose you want to verify whether a strand of DNA you obtained from a database contains (or not, and how many times) a sub-strand which looks *similar* to a given sequence of interest, for example

#### **AACTTCGG**

▶ In other words, we not only want to look for exact occurrences of the sequence, but also for approximate ones, like the following:

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### An Example: Approximate String Matching

- Given an alphabet  $\Sigma = \{a_1, \dots, a_n\}$ , the expression  $\Sigma^*$  indicates the set of all finite sequences of elements from  $\Sigma$ , called *strings from*  $\Sigma$ .
- ightharpoonup Examples of strings from  $\{0,1\}$  are:

 $\varepsilon$  0101 00000 1 01101001

▶ Given two strings  $s, t \in \Sigma^*$ , their edit distance  $\delta(s, t)$  is minimum number of insertions, erasure and modifications (of simbols from  $\Sigma$ ) necessary to turn s into t. As an example

$$0001010 \rightarrow 000010 \rightarrow 000000 \rightarrow 1000000$$
$$\delta(00010101, 1000000) \le 3$$

- ▶ Approximate String Matching (ASM)
  - ▶ Input: two strings s, t and a natural number n.
  - ▶ Output: all the substrings  $s_1, ..., s_k$  of s such that  $\delta(s_i, t) \leq n$ .

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#### Combinatorial Problems

- ▶ Approximate string matching is a typical example of a **combinatorial problem**.
- ▶ It generalises, thus helping to solve, the problem from genomics we mentioned a few slides ago.
- ▶ It is dubbed **combinatorial**, because it is formulated in the language of finite structures, and in particular as a problem on strings.
- ▶ We of course can try to solve the problem by directly writing some Python code, or by looking at a module providing a function which fits our needs.
- ▶ We could instead look at the problem in a principled way, and look for an *algorithm* which *efficiently* solves the ASM problem.
  - ▶ This is what we will do in this course.

Thank You!

Questions?