

Algoritmi di Bioinformatica

Zsuzsanna Lipták

Laurea Magistrale Bioinformatica e Biotechnologie Mediche (LM9)
a.a. 2013/14, spring term

Organisation

- **email:** `zsuzsanna.liptak@univr.it`
Please put "corso Algoritmi di Bioinformatica" in the subject line
- **office:** CV 2, 1st floor, room 1.79
- **office hours:** Wed 11-13 (to be changed from 9 April)
- **language:** English, but you can ask questions in English or in Italian
- **attendance:** not obligatory but highly recommended
(read what I wrote on the webpage of the course)

Organisation (cont.)

- total grade (voto): 50% Algoritmi, 50% Linguaggi
- grade Algoritmi:
 - 50% **written**: 2 exams (2 hours each) in April+June
 - or** 1 exam (3 hours) June or any other exam session
 - 50% **oral**: presentation of a topic (little project) in front of class (June or July) **or** oral exam (any exam session)
- **webpage**:
<http://profs.sci.univr.it/~liptak/ALBioinfo.html>
will include: current info, materials, projects topics etc.

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Questions?

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Goals of this course

1. to learn about some basic **problems and algorithms** behind common bioinformatics applications (sequence alignment, sequence similarity, phylogenetic reconstruction)
2. to get an idea of some basic **computational issues** involved (complexity, efficiency, limitations, problem specification)

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The differences in background (biology/biotech vs. computer science) will be resolved

- by doing all algorithms in enough detail (comprehensible **and** interesting)
- different levels/difficulty in the project presentation part (also w.r.t. grades)

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Overview

- **Part I: Sequence Analysis**
 - Pairwise sequence alignment
 - **Detour:** Algorithm analysis
 - Multiple sequence alignment
 - String similarity and distance
 - Scoring matrices
 - Heuristics: FASTA, BLAST
 - **Detour:** Basic statistics for bioinformatics
- **Part II: Phylogenetics**
 - algorithms for distance-based data
 - character-based data, Perfect Phylogeny
 - Small Parsimony: Fitch's algorithm
 - Large Parsimony: heuristics

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Erasmus info meeting

next Tuesday, 11 March 2014, at 13.30
in Aula B

We have many exchanges with European universities,
among these Bielefeld (Germany),
particularly good for [bioinformatics](#)

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Announcement

- until 3 April, we may do 4 hours on Wednesdays (9 - 12.30), when possible
- See course announcements on webpage of department

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Books

- **João Setubal, João Meidanis**: Introduction to Computational Molecular Biology (1997).—my favourite, 1 copy in library
- **Neil C. Jones and Pavel A. Pevzner**: An Introduction to Bioinformatics Algorithms (2004).—3 copies in library
- **R. Durbin, S. Eddy, A. Krogh, G. Mitchinson**: Biological Sequence Analysis (1998).—oriented towards probabilistic models
- **Dan Gusfield**: Algorithms on Strings, Trees, and Sequences (1997).—the bible of string algorithms, a bit dated now
- **Hans-Joachim Bckenhauer and Dirk Bongartz**: Algorithmic Aspects of Bioinformatics (2010).—very formal, mathematical
- **Joseph Felsenstein**: Inferring Phylogenies (2004).—important book on phylogenetics
- **Cormen, Leiserson, Rivest (& Stein)**: Introduction to Algorithms (different editions, 1990-onwards).—the bible of algorithms, a must have for anyone interested in algorithms (buy second hand, old editions are also fine)

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Books (2)

More biologically oriented:

- **David M. Mount:** Bioinformatics: Sequence and Genome Analysis (2004).
- **Arthur Lesk:** Introduction to Bioinformatics (2008).

Careful, in these books, often the treatment of algorithms is not in-depth not enough! But closer to applications.

I also use (downloadable from the course webpage):

- Sequence Analysis I+II, lecture notes from Bielefeld University, by Jens Stoye and others
- Phylogenetics, lecture notes from Bielefeld University, by Jens Stoye and others

Mostly much too detailed, do not print! We will assign chapters from these for the projects.