

Algoritmi di Bioinformatica

Zsuzsanna Lipták

Laurea Magistrale Bioinformatica e Biotechnologie Mediche (LM9)
a.a. 2014/15, spring term

Organisation

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- **course times:** Wed 8:30 - 10:30, Thu 8:30 - 11:30
- **language:** English, but you can ask questions in English or in Italian
- **webpage:**
<http://profs.sci.univr.it/~liptak/ALBioinfo.html>
coming soon! (careful: at the moment there is last year's course there)
will include: current info, materials, presentation topics etc.

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Organisation (cont.)

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- **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:** Tue 8:30-10:30
- **attendance:** not obligatory but highly recommended
(read what I wrote on the webpage of the course)

- **final 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:** short presentation of a topic in front of class (June or July)
or oral exam on the whole course (any exam session)
- **presentations:** to be prepared in 1 or 2, based on material that I give you — **only** possible during this semester (June or July)

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Organisation (cont.)

Goals of this course

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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)

Questions?

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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
- **Part II: Phylogenetics**
 - **Detour:** Trees and graphs
 - algorithms for distance-based data
 - character-based data, Perfect Phylogeny
 - Small Parsimony: Fitch's algorithm
 - Large Parsimony: heuristics

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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

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- **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 Böckenhauer 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).—**good book but very detailed!**
- **Arthur Lesk:** Introduction to Bioinformatics (2008).

Careful, in biologically oriented books, the treatment of algorithms may not be in-depth not enough! Positive side: more application-oriented.

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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.

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