

## Bioinformatics Algorithms

(Fundamental Algorithms, module 2)

Zsuzsanna Lipták

Masters in Medical Bioinformatics  
academic year 2018/19, II semester

### Organisation

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- Title of course: **Bioinformatics Algorithms** (Fundamental Algorithms, module 2)  
Master of Medical Bioinformatics (MB)  
**6 CFU** of a total of 12 CFU
- This course doubles as (*mutuato*) **Algorithms for Computational Biology** in the Master in Medical and Molecular Biotechnology (MMB)  
**6 CFU**

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### Organisation (cont.)

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- **course times:** Tue 12:30 - 14:30 (aula L), Thu 11:30 - 14:30 (aula A)
- **email:** [zsuzsanna.liptak@univr.it](mailto:zsuzsanna.liptak@univr.it)  
Please include the course title and your name in the email
- **office:** CV 2, 1st floor, room 1.79
- **student hours:** Wed 10-12 (**9:30-11:30?**) and by appointment
- **webpage of course:**  
<http://profs.scienze.univr.it/~liptak/FundBA/>

- **exam:** written and oral,  
admitted to oral only if you pass the written test
- **different exams** for students of MB and MMB
- There will be **two extra lectures** for students of MMB on computational complexity
- **takehome exercises** during term: will be discussed but not marked
- for Fundamental Algorithms **final grade** is 50% mod.1, 50% mod.2

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- **Pairwise sequence analysis**
  - Pairwise sequence alignment (global, local, other variants)
  - Pairwise alignment in practice: BLAST, Scoring matrices
  - String distances (edit distance, LCS distance,  $q$ -gram distance)

### Questions?

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  - Sanger shotgun sequencing: SCS (recap)
  - Sequencing with de Bruijn graphs

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- Multiple sequence alignment
  - DP-algorithm, SP-score
  - Heuristic and approximation algorithms

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- Basics of Phylogenetics
  - distance-based data: UPGMA, Neighbor Joining
  - character-based data: Perfect Phylogeny, Small and Large Parsimony

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  - distance-based data: UPGMA, Neighbor Joining
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- Introduction to string data structures
  - Basics of Suffix Trees and Suffix Arrays
  - Some applications

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## Books

- **Enno Ohlebusch**: Bioinformatics Algorithms: Sequence Analysis, Genome Rearrangements, and Phylogenetic Reconstruction. Oldenbusch Verlag (2013) —*recent, detailed, covers some but not all topics of this course, 3 copies in library*
- **H.-J. Böckenhauer, D. Bongartz**: Algorithmic Aspects of Bioinformatics (2010)
- **V. Mäkinen, D. Belazzougui, F. Cunial, A.I. Tomescu**: Genome-Scale Algorithm Design. Cambridge University Press (2015)—*very recent, advanced*
- **Neil C. Jones and Pavel A. Pevzner**: An Introduction to Bioinformatics Algorithms (2004)—3 copies in library
- **David M. Mount**: Bioinformatics: Sequence and Genome Analysis (2004)—*biologically oriented book, detailed, not always sufficiently algorithmic*
- **João Setubal, João Meidanis**: Introduction to Computational Molecular Biology (1997)—*my old favorite but a bit dated, 1 copy in library*
- **Dan Gusfield**: Algorithms on Strings, Trees, and Sequences (1997)—*the bible of string algorithms, a bit dated now*
- **Joseph Felsenstein**: Inferring Phylogenies (2004)—*important book on phylogenetics, very understandably written*
- **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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