

Introduction to Bioinformatics

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Course Information

• Course Description

- This course covers computational techniques for mining the large amount of information produced by recent advances in biology, such as genome sequencing and microarray technologies. Main topics of the course include:
 - DNA and protein sequence alignment,
 - sequence motifs/patterns,
 - phylogenetic trees,
 - protein structures: prediction, alignment, classification
 - microarray data analysis: normalization, clustering
 - and biological networks.

• Lecture Time/Place

- Monday - 13:40 to 15:30 in BMB-5.
- Thursday - 11:40 to 12:30 in BMB-5.

• Reading Material

- Textbook:
 - M. Zvelebil and J. O. Baum, *Understanding Bioinformatics*, Garland Science, 2008.
- Reference Books:
 - D.E. Krane and M.L. Raymer, *Fundamental Concepts of Bioinformatics*, Pearson Education, 2003.
 - N. C. Jones and P. A. Pevzner, *An Introduction to Bioinformatics Algorithms*, MIT press, 2004.
 - C.A. Orengo, D.T. Jones and J.M.Thornton, *Bioinformatics: Genes, Proteins and Computers*, Routledge, 2003.
 - A. M. Lesk, *Introduction to Bioinformatics*, Oxford University Press, 2002.
 - D. Mount, *Bioinformatics: Sequence and genome analysis*, Cold Spring Harbor Laboratory Press, 2001.
 - P. A. Pevzner, *Computational Molecular Biology: An Algorithmic Approach*, MIT press, 2000.
 - P. Baldi and S. Brunak, *Bioinformatics: the machine learning approach (2nd edition)*, MIT press, 2001.
 - T. Jiang, Y. Xu, and M. Zhang, eds. *Current Topics in Computational Molecular Biology*, MIT press, 2002.
 - S. Karlin, *Frontiers of Bioinformatics: Unsolved Problems and Challenges*, National Academy Press, 2005

• Prerequisites

- None.

• Goals

- The main objective of the course is to provide the student with a solid foundation for conducting further research in bioinformatics. By the end of the course, the students will have learned:
 - the bioinformatics terminology,
 - main bioinformatics problems,
 - and the key methods and tools used in bioinformatics.

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