## Machine Learning in Biomedicine (3 Credits)



## 生物医学中的机器学习

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Synopsis	An advanced course for students interested in biomedicine, computing and their intersection, as well as in biomedical engineering. The course aims to demonstrate how fundamental computational and algorithmic methods form the basis and the core of modern methods in computational biomedicine. It presents hard-core topics in machine learning, probability, statistical modeling and algorithms, while focusing on their practical application as building blocks for computational biology and medicine.		
Offering	2014 Summer Semester		
Audience	Year 3 & 4 Undergraduates and Year 1 Graduate Students		
Classroom	Room xxx, Teaching Bldg. No. XX, Peking University		
Schedule	<u>Class</u> : 8-11 AM, M-F, July 7–25, 2014; <u>Final Exam</u> : None		
Objective	By the end of the course students should be able to see and understand how computational (and mathematical) concepts that might have seemed abstract and possibly "arbitrary" when first encountered in introductory math and computer science classes, such as dynamic		

first encountered in introductory math and computer science classes, such as dynamic programming, conditional probability or Bayes rule, are directly applicable to problems in biomedical data analysis. Moreover, students will be able to apply such methods and make new connections between theoretical material in computer science & mathematics and applications in biology and medicine.

## Topics 1. Introduction

- 2. Dynamic programming and biological sequence alignment
- 3. Conditional probability, Bayes' theorem, expectation maximization, their role in clustering and classification, with biomedical and clinical applications.
- 4. Hidden Markov models and their biological/clinical applications.
- 5. Biomedical text mining and the computational methods applied in it.
- 6. Protein subcellular Location Prediction from sequence and from text data.
- 7. Bayesian networks and their application in modeling for biomedicine.

## References 1. Biological Sequence Analysis by R. Durbin, S. Eddy, A. Krogh and G. Mitchison (Cambridge University Press, 1998)

- 2. Introduction to Computational Molecular Biology by C. Setubal and J. Meidanis (Cengage Learning, 1997)
- 3. Mining the Biomedical Literature by H. Shatkay and M. Craven (MIT Press, 2012)
- 4. Molecular Biology of the Cell by B. Alberts et al. (Garland Science, 2007)
- 5. Journal Papers

		Total	100%
	Participation and discussion		10%
	Homework assignments		40%
Grading	Two midterm assessment tes	sts	25% each