

BIO 5106 – Bioinformatics

Course description

Major concepts and methods of bioinformatics. Topics may include, but are not limited to: genetics, statistics & probability theory, alignments, phylogenetics, genomics, data mining, protein structure, cell simulation and computing.

Textbook

Deonier RC, Tavaré S and Waterman MS. 2005. *Computational genome analysis*. Springer, New York.

Evaluation

Assignments^(a): 33%

Mini-review papers (two in total)^(b): 33% (15% + 15%)

Final seminar^(c): 33%

- (a) Weekly reading assignments will be followed by short select exercises from the textbook or other sources.
- (b) Students will have to write two short reviews (one per ½ term; up to five pages plus one page of references) on an imposed topic extending the concepts covered in class.
- (c) Students will present a research seminar by groups of twos or threes and will learn to work in an interdisciplinary environment (groups of students with mixed academic background / co-supervision). Research topics will generally be suggested, although groups of students can also propose their own.

Times & location

Mondays 11:30-1:00 (to be confirmed).

Wednesdays 2:30-4:00 (to be confirmed).

Coordinator:

Dr Stéphane Aris-Brosou
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Office hours: Mondays 2-5pm.

Syllabus (Fall 2007)

Non-contractual and subject to change without notice.

Week	Lecture	Date	Topic	Instructor
1	1	Sep 10	– Introduction	Aris-Brosou
	2	Sep 12	– Basics of Genetics (organisms, central dogma, genetics code, promoters)	Aris-Brosou
2	3	Sep 17	– Overview of Statistics I (random variables, distributions, likelihood, conditional probability, estimation, testing)	Aris-Brosou
	4	Sep 19	– Overview of Statistics II (stochastic processes, inference for stochastic processes)	Aris-Brosou
3	5	Sep 24	– Pairwise alignments (evolution, similarity, alignments, dynamic programming, Needleman-Wunsch algorithm, local & global alignments)	Turcotte
	6	Sep 26	– Pairwise alignments and database searches (FASTA, BLAST, PatternHunter, BLAT, etc.)	Aris-Brosou
4	7	Oct 1	– Hidden Markov Models (basic algorithms [Viterbi etc.], gene finding, profile HMMs)	Green
	8	Oct 3	– Multiple sequence alignments [MSA]	Turcotte
5	9	Oct 8	– Application of MSA I: similarity, distance & clustering	Aris-Brosou
	10	Oct 10	– Application of MSA II: parsimonious phylogenies	Aris-Brosou
6	11	Oct 15	– Application of MSA III: model-based phylogenies	Aris-Brosou
	12	Oct 17	– Comparative Genomics	Sankoff
7	13	Oct 22	– Genetic variation in populations: HapMap	Aris-Brosou
	14	Oct 24	– Text Mining (BioNPL, ontologies, annotations)	Andrade
8	15	Oct 29	– RNA folding	Kranakis
	16	Oct 31	– RNA secondary structure prediction, motif inference, pattern matching	Turcotte
9	17	Nov 5	– Protein Structure and Function	Dumontier
	18	Nov 7	– Protein Structure Prediction	Dumontier
10	19	Nov 12	– Interactions and Pathways	Dumontier
	20	Nov 14	– Bioinformatics of Disease	Dumontier
11	21	Nov 19	– Parallel and Distributed Computing	Dehne
	22	Nov 21	– oral presentations	
12	23	Nov 26	– oral presentations	
	24	Nov 28	– oral presentations	