

Goals of course

- At the interface of computer science and biology
 - Scientific motivation
 - New data and new demands
 - High throughput sequencing
 - Rational drug design
 - Systems view of biology
 - Impact on human health
- Algorithms and data mining in context
- Three points of view
 - Computer scientist: methods & applications domain
 - Biologist: foundations of biological software tools
 - Computational biologist: both

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Course outline

- Introduction (4 hours)
 - Principal datasets
 - Review of the fundamentals of molecular biology and genetics.
- Sequence comparison (~~12~~ 20 hours)
 - Genetic variations
 - Score matrices.
 - Global and local alignment.
 - Alignment statistics.
 - Multiple sequence alignment.
 - Database searching.
 - FASTA, BLAST and other sequence database search tools.

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Course outline

- Motif finding (4-8 hours)
 - EM, Gibbs sampling, HMM
- ~~Microarrays (2 hours)~~
 - Data analysis
- ~~Structure Analysis (6 hours)~~
 - Primary, secondary and tertiary structure.
 - Structure comparison and motif finding
- Phylogenetic trees (~~6-8~~ hours)
 - Distance-based methods
 - Character-based methods
- ~~Pathway synthesis and analysis (4 hours)~~

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Grading

- Paper presentation (5%)
- Homework sets (25%)
- Term project (40%)
 - List of projects
- Final examination (30%)

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Mapping of course outcomes

	Lectures	Reading	Homework	Final	Project
Understand CS-Bio link	x	x	x	x	x
Develop new ideas					x
Programming and expts			x		x
Literature survey	x	x	x		x
Biological knowledge	x	x	x	x	x
Presentation skills		x			x
Algorithms & Data mining techniques	x	x	x	x	x

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What remains?

- Homework 3 (Due Dec 5)
- Project report (Due Dec 12)
 - Presentation to mentor/me
 - Report guidelines posted
- Final examination (Dec 8 12-3)
 - Sample problems to be posted by Dec 4

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