CSE 308-408 Bioinformatics: Issues and Algorithms Professor Daniel Lopresti • Spring 2007 • TuTh 2:35 - 3:50

"Biology easily has 500 years of exciting problems to work on." – Donald Knuth (Stanford Professor & famous Computer Scientist)

18/	Genetic	→ Molecular	Biochemical	 Phenotype
	Information	Structure -	Function	(Symptoms)
http://cmgm.stanford.edu/biochem2	TGCTTTAGCTTT AAACTACAGGCC TCACTGGAGCTA GAGACAAGAAGG TAAAAAACGGCT GACAAAAGAAGT CCTGGTATCCTC TATGATGGGAGA AGGAAACTAGCT AAAGGGAAGAAT AAATTAGAGAAA AACTGGAATGAC GCTTATACCTGG		OH CH2 CH CH NH3 COŌ L-Phenylalanine OH CH2 CH2 CH2 CH NH3 COŌ L-Tyrosine	

By applying methods from Computer Science to the analysis of sequence data and related structures, we can help in understanding genetic nature of disease.

Topics we study in CSE 308-408:

- sequence comparison & alignment
- sequence assembly
- physical mapping of DNA
- phylogenetic (evolutionary) trees
- genome rearrangements
- RNA & protein structure prediction
- DNA microarray analysis
- DNA computing

No prior knowledge of biology is required. For more details: dal9@lehigh.edu.



