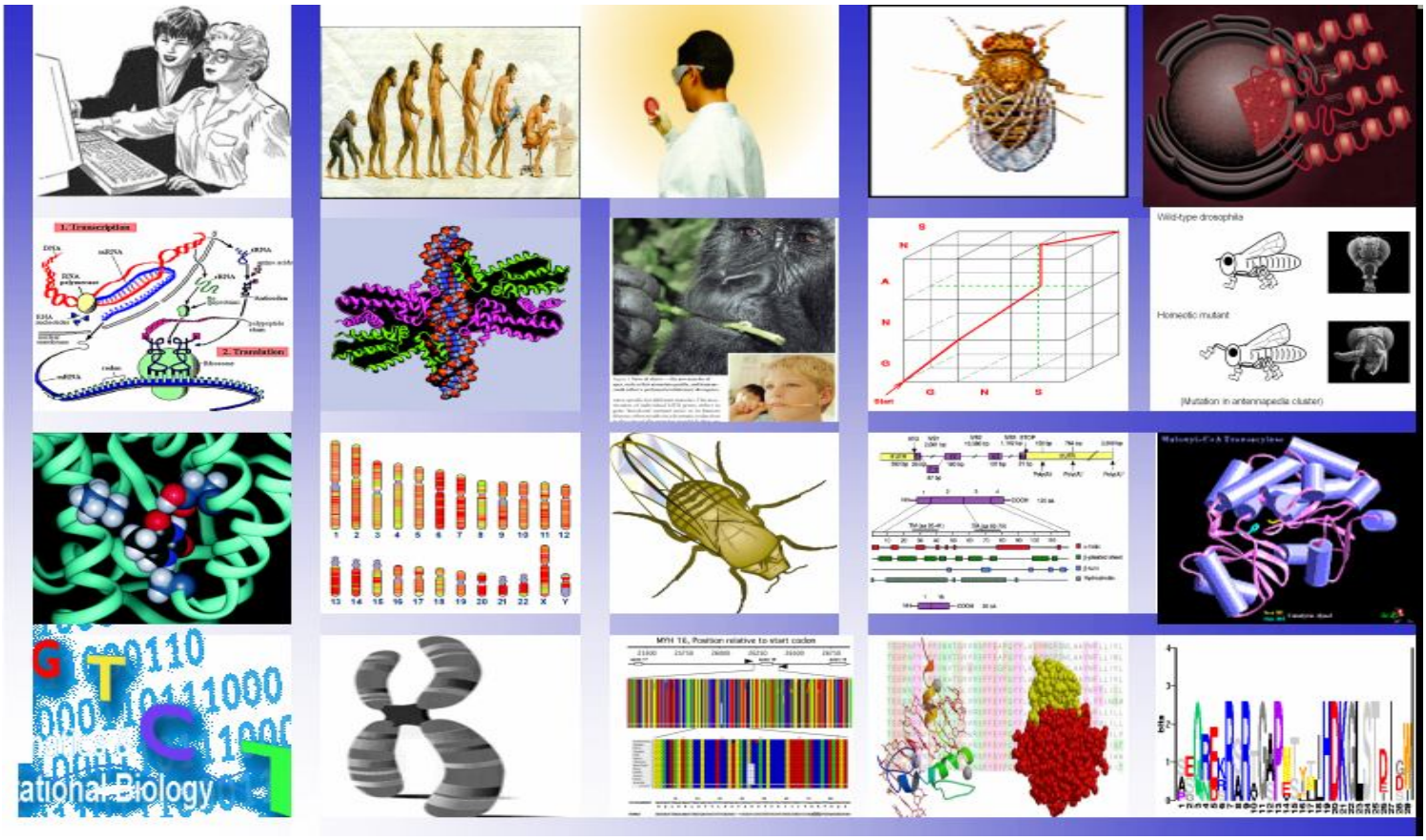
Fall 2009
CS223: Bioinformatics

The course investigates the main algorithms used in the Bioinformatics field. After a brief description of commonly used tools, algorithms, and databases in Bioinformatics, the course describes specific tasks that can be completed using combinations of the tools and databases. The course covers prevalent methods for biological sequence analyses, such as pairwise and multiple sequence alignments, profile and motif searches, gene prediction, RNA secondary structure analysis, fragment assembly, phylogenetic inference, and comparative genomics.
The course is self contained and does not assume any background knowledge in biology. Students will be given programming projects.

Prerequisite: CS160 or permission of the instructor.
Instructor: Sami Khuri www.cs.sjsu.edu/faculty/khuri
Meetings: Tuesdays and Thursdays 12:00 – 13:15 in MH225.



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