COMP 680. MINING BIOLOGICAL SEQUENCES.

Credits: 4

Offered by: Computer Science (Graduate Studies)

This course is not offered this catalogue year.

Description

Advanced algorithms for the annotation of biological sequences. Algorithms and heuristics for pair-wise and multiple sequence alignment. Gene-finding with hidden Markov models and variants. Motifs discovery techniques: over representation and phylogenetic footprinting approaches. RNA secondary structure prediction. Detection of repetitive elements. Representation and annotation of protein domains.

- Prerequisite: COMP 462 or with instructor's permission.

Most students use Visual Schedule Builder (VSB) to organize their schedules. VSB helps you plan class schedules, travel time, and more.

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