

Hybrid Search Techniques for Multiple Sequence Alignment

Project Description

Multiple Sequence Alignment is a challenging problem in Bioinformatics. Many approaches have been tried with varying degrees of success. This interdisciplinary project will investigate hybrid approaches combining techniques from Constraint Programming, Artificial Intelligence and Operations Research. As well as attacking the standard alignment problem, we will develop methods for interactively improving alignments been generated by other software systems. No software yet exists for this task, which is currently performed manually by biologists.

Project Coordinator

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Project Partners

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