

DESIGN OF A NOVAL ALGORITHM FOR DNA SEQUENCE ANALYSIS

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Abstract

An Algorithm is a recipe or systematic method containing a sequence of instructions to solve a computational problem. It takes some inputs, performs a well defined sequence of steps and produces some outputs. Algorithm Design forms a central theme in computer science. We are proposing an algorithm which tries to find a solution regarding both using Indexing approach. If we see a human genome pattern then it itself is too long to be accommodated in a single go in the system memory. Also if we try to search it more than one time then all our effort of traversing the sequence gets lost. It would be better if we can just bring the necessary data in the memory and search it Part-by-Part. We are also proposing an idea of parallel processing by working on multiple files. We are trying to deal with the problem of recursion by limiting its domain of search. We have seen that multiple file handlers can't be used on a single file. But it would be better if we could use many using multiple threads. This enforces idea of parallelism. We have applied this in the case of DNA Sequences.