Republic of Iraq

Ministry of Higher Education and

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University of Babylon

College of Information Technology

Network Department

Media Encryption and

Decryption using DNA algorithm in

A project

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University of Babylon in Partial Fulfillment of the Requirements for the Group

Project

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Abstract

For aligning DNA sequences that differ only by sequencing errors, or by equivalent errors from other sources, a greedy algorithm can be much faster than traditional dynamic programming approaches and yet produce an alignment that is guaranteed to be theoretically optimal. We introduce a new greedy alignment algorithm with particularly good performance and show that it computes the same alignment as does a certain dynamic programming algorithm, while executing over 10 times faster on appropriate data. An implementation of this algorithm is currently used in a program that assembles the UniGene database at the National Center for Biotechnology Information.