Title: A Two-Phase Dynamic Programming Algorithm Tool for DNA Sequences

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Abstract: Sequence alignment has to do with the arrangement of DNA, RNA, and protein sequences to identify areas of similarity. Technically, it involves the arrangement of the primary sequences of DNA, RNA, or protein to identify regions of similarity that may be a consequence of functional, structural, or evolutionary relationships between the sequences. Similarity may be a consequence of functional, structural, or evolutionary relationships between the sequences. If two sequences in an alignment share a common ancestor, mismatches can be interpreted as mutations, and gaps as insertions. Such information becomes of great use in vital areas such as the study of diseases, genomics and generally in the biological sciences. Thus, sequence alignment presents not just an exciting field of study, but a field of great importance to mankind. In this light, we extensively studied about seventy (70) existing sequence alignment tools available to us.

Most of these tools are not user friendly and cannot be used by biologists. The few tools that attempted both Local and Global algorithms are not ready available freely. We therefore implemented a sequence alignment tool (CU-Aligner) in an understandable, user-friendly and portable way, with click-of-a-button simplicity. This is done utilizing the Needleman-Wunsh and Smith-Waterman algorithms for global and local alignments, respectively which focuses primarily on DNA sequences. Our aligner is implemented in the Java language in both application and applet mode and has been efficient on all windows operating systems.