BLAST Help Manual Overview

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Created: January 28, 2011.

The Basic Local Alignment Search Tool (BLAST) is the most widely used sequence similarity tool. There are versions of BLAST that compare protein queries to protein databases, nucleotide queries to nucleotide databases, as well as versions that translate nucleotide queries or databases in all six frames and compare to protein databases or queries. PSI-BLAST produces a position-specific-scoring-matrix (PSSM) starting with a protein query, and then uses that PSSM to perform further searches. It is also possible to compare a protein or nucleotide query to a database of PSSM's. The NCBI supports a BLAST web page at blast.ncbi.nlm.nih.gov as well as a network service. The NCBI also distributes stand-alone BLAST applications for users who wish to run BLAST on their own machines or with their own databases. This document describes the stand-alone BLAST applications and will concentrate on the latest generation of such applications included in the BLAST+ package.

The first two sections of this document are "quick start" guides that address setting BLAST+ up under UNIX (including LINUX and MacOSX) and Windows. The third section is a more in-depth look at the BLAST+ applications. These documents are currently being revised and may change substantially in coming releases.

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