



Functionality offered by BLAST+ applications

The functionality offered by the BLAST+ applications has been organized by program type, as to more closely resemble Web BLAST.

As an example, to run a search of a nucleotide query (translated “on the fly” by BLAST) against a protein database one would use the `blastx` application. The `blastx` application will also work in “Blast2Sequences” mode (i.e.: accept FASTA sequences instead of a BLAST database as targets) and can also send BLAST searches over the network to the public NCBI server if desired.

The BLAST+ package offers three categories of applications: 1.) search tools, 2.) BLAST database tools, and 3.) sequence filtering tools. The `blastn`, `blastp`, `blastx`, `tblastx`, `tblastn`, `psiblast`, `rpsblast`, and `rpstblastn` are considered search applications, as they execute a BLAST search, whereas `makeblastdb`, `blastdb_aliastool`, `makeprofiledb`, and `blastdbcmd` are considered BLAST database applications, as they either create or examine BLAST databases.

There is also a new set of sequence filtering applications described in the section [Sequence filtering applications](#) and an application to build database indices that greatly speed up megablast in some cases (see section titled [Megablast indexed searches](#)).