

Quick Start Guide for switching from BLAST to BLAST+ command line tools

BLAST	BLAST+	Speciality
megablast	blastn -task megablast	For very similar nucleotide sequences
bl2seq -i -j	blast -query -subject	Align one sequence against another
blastpgp	psiblast deltablast	Position Specific Initiated BLAST
rpsblast -p F	rpstblastn	Translated Reverse Position Specific BLAST

BLAST	BLAST+	Description
blastall	blastn, blastp, ...	
-p	n/a	BLAST program: blastn, blastp, blastx, tblastn, ...
-i	-query	Input sequence file
-d	-db	BLAST database
-o	-out	Output file
-m	-outfmt	Output format: BLAST XML:7 TAB:8 BLAST+ XML:5 TAB:7
-e	-evalue	Expectation value threshold
-a	-num_threads	Number of CPU cores to use
-F F	-dust no -seg no	Disable low complexity filtering: DNA:dust AA:seg
formatdb	makeblastdb	
-i	-in	Input sequence file
-p T/F	-dbtype prot/nucl	Molecule type
-o T	-parse_seqids	Parse and index sequence IDs
-n	-out	Base name for output files
fastacmd	blastdbcmd	
-d	-db	BLAST database
-s	-entry	Search string
-D 1	-entry all	Dump database in FASTA format

Query	Database	Comparison Space	Program to use
nuc	nuc	/nuc/	blastn
nuc	nuc	/Prot/	tblastx
Prot	Prot	/Prot/	blastp
Prot	nuc	/Prot/	tblastn
nuc	Prot	/Prot/	blastx