

Sequence comparisons: practical sessions

Explore pair-wise local and global sequence alignments (see ebi server <https://www.ebi.ac.uk/Tools> and fasta server: https://fasta.bioch.virginia.edu/fasta_www2/fasta_list2.shtml) and save the output files with appropriate identifications.
Consider 2 protein sequences: KLTH0D17710g.prt and KLTH0G02794g.prt and 2 nucleotide sequences: KLTH0D17710g.dna and KLTH0G02794g.dna

Local alignment

https://www.ebi.ac.uk/Tools/psa/emboss_water/

Water uses the Smith-Waterman algorithm to calculate the local alignment of two sequences (protein or dna)

Nucleotide sequences:

https://www.ebi.ac.uk/Tools/psa/emboss_water/nucleotide.html

LALIGN

Two protein sequences

<https://www.ebi.ac.uk/Tools/psa/lalign/>

Two nucleotide sequences

<https://www.ebi.ac.uk/Tools/psa/lalign/nucleotide.html>

Consider using the FASTA server:

https://fasta.bioch.virginia.edu/fasta_www2/fasta_list2.shtml

LALIGN finds non-overlapping local alignments (protein or dna sequences)

https://fasta.bioch.virginia.edu/fasta_www2/fasta_www.cgi?rm=lalign&pgm=lal

Interesting to explore: *PLALIGN* (plot protein:protein sequences or DNA:DNA sequences)

Blast 2 sequences

allows to get local alignments of 2 sequences:

blastp -query Seq1.prt -subject Seq2.prt -out Seq2sequences.blp

Global alignment

- Consider 2 protein sequences: KLTH0D17710g.prt and KLTH0G02794g.prt

Use this URL to get their global alignment

https://www.ebi.ac.uk/Tools/psa/emboss_needle/

- Consider 2 nucleotide sequences: KLTH0D17710g.dna and KLTH0G02794g.dna

Use this URL to get their global alignment

https://www.ebi.ac.uk/Tools/psa/emboss_needle/nucleotide.html

- Blast Global Alignment: Needleman-Wunsch Global Align Protein/Nucleotide Sequences (ncbi server):

https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE_TYPE=BlastSearch&PROG_DEF=blastn&BLAST_PROG_DEF=blastn&BLAST_SPEC=GlobalAln&LINK_LOC=BlastHomeLink

Explore the dot matrix view (dotplot) and the detailed global alignment.

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