Bioinformatics

CS300

Chap 3

Sequence Alignment with ClustalW

Spring 2021

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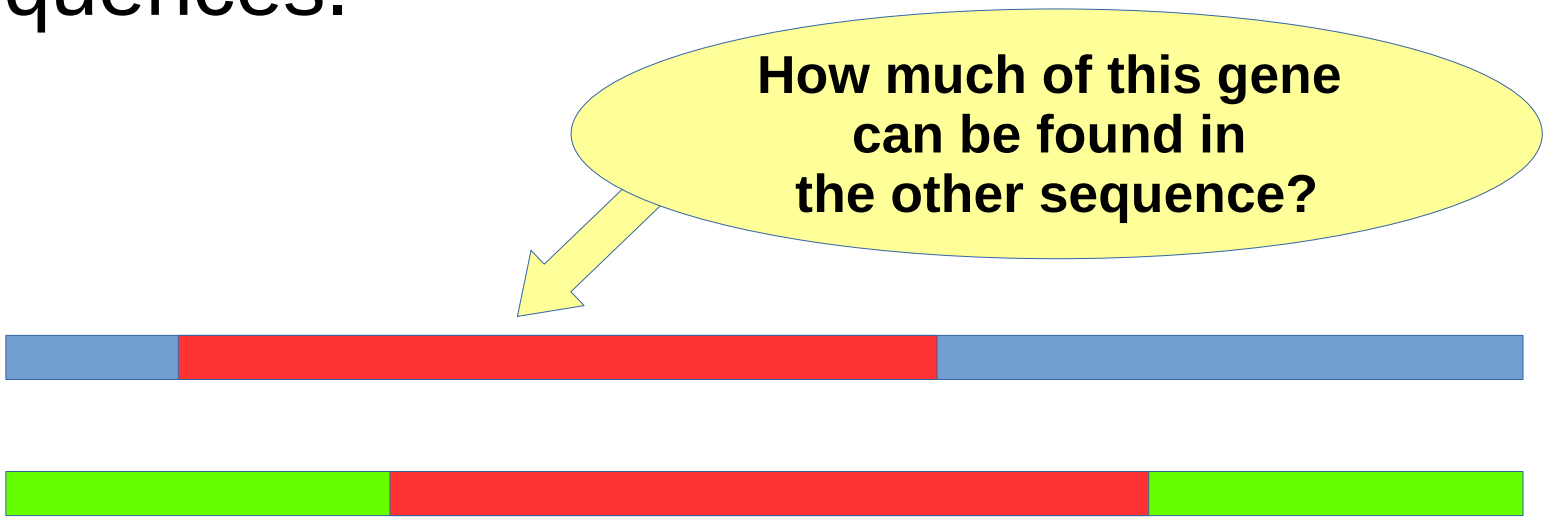
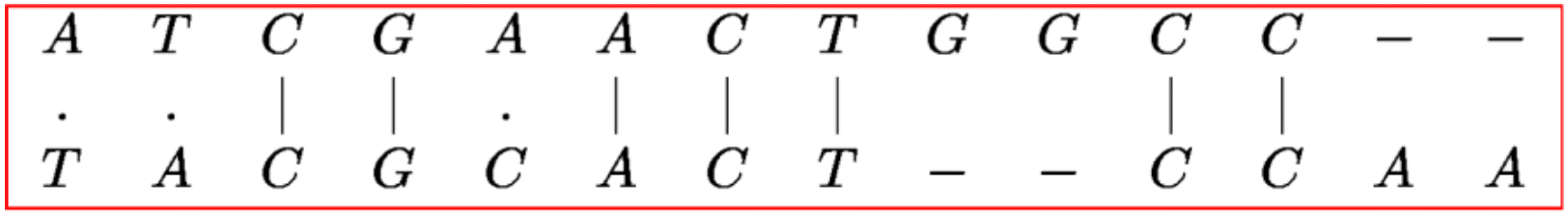
What is Sequence Alignment?

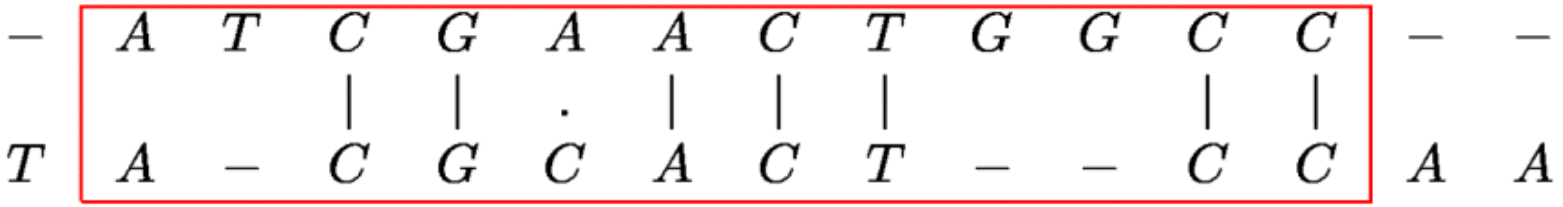
- Sequence alignment is a way of arranging the sequence of genetic material (DNA, RNA or protein) to identify regions of similarity that may be a consequence of functional, structural or evolutional relationships between the sequences.



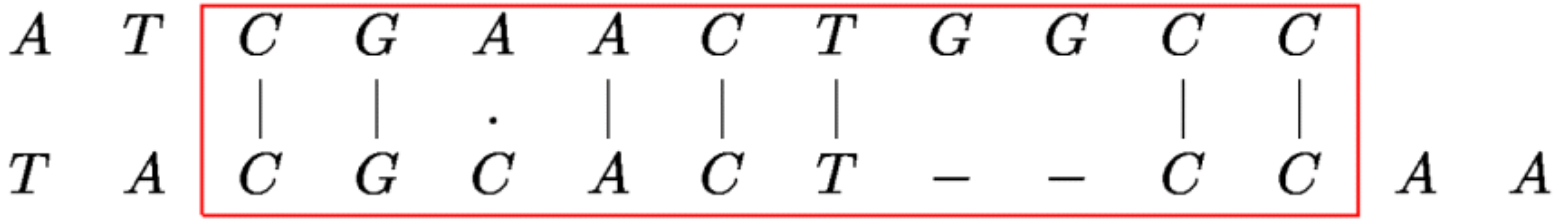
Types of Alignment



(a) Global alignment example



(b) Semi-global alignment example

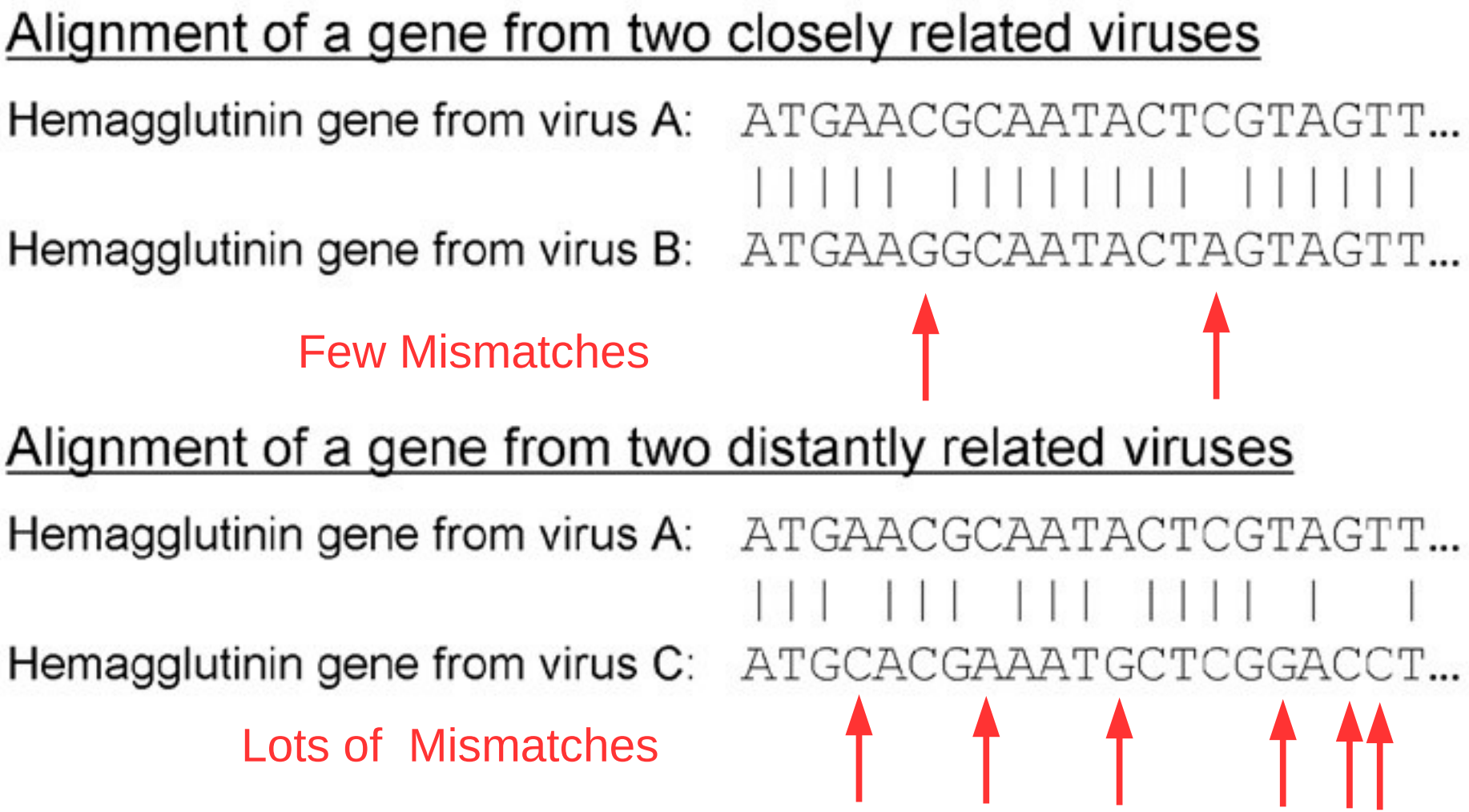


(c) Local alignment example

Needleman-Wunsch Algorithm Background

- **Alignment**: Used to determine which parts of a sequence are in common with another sequence; used to measurement similarity between sequences.
- Developed by Saul B. Needleman and Christian D. Wunsch in 1970.
- Dynamic programming to find optimal solution for matching the characters of the two sequences.

Ex: Pairwise Alignment



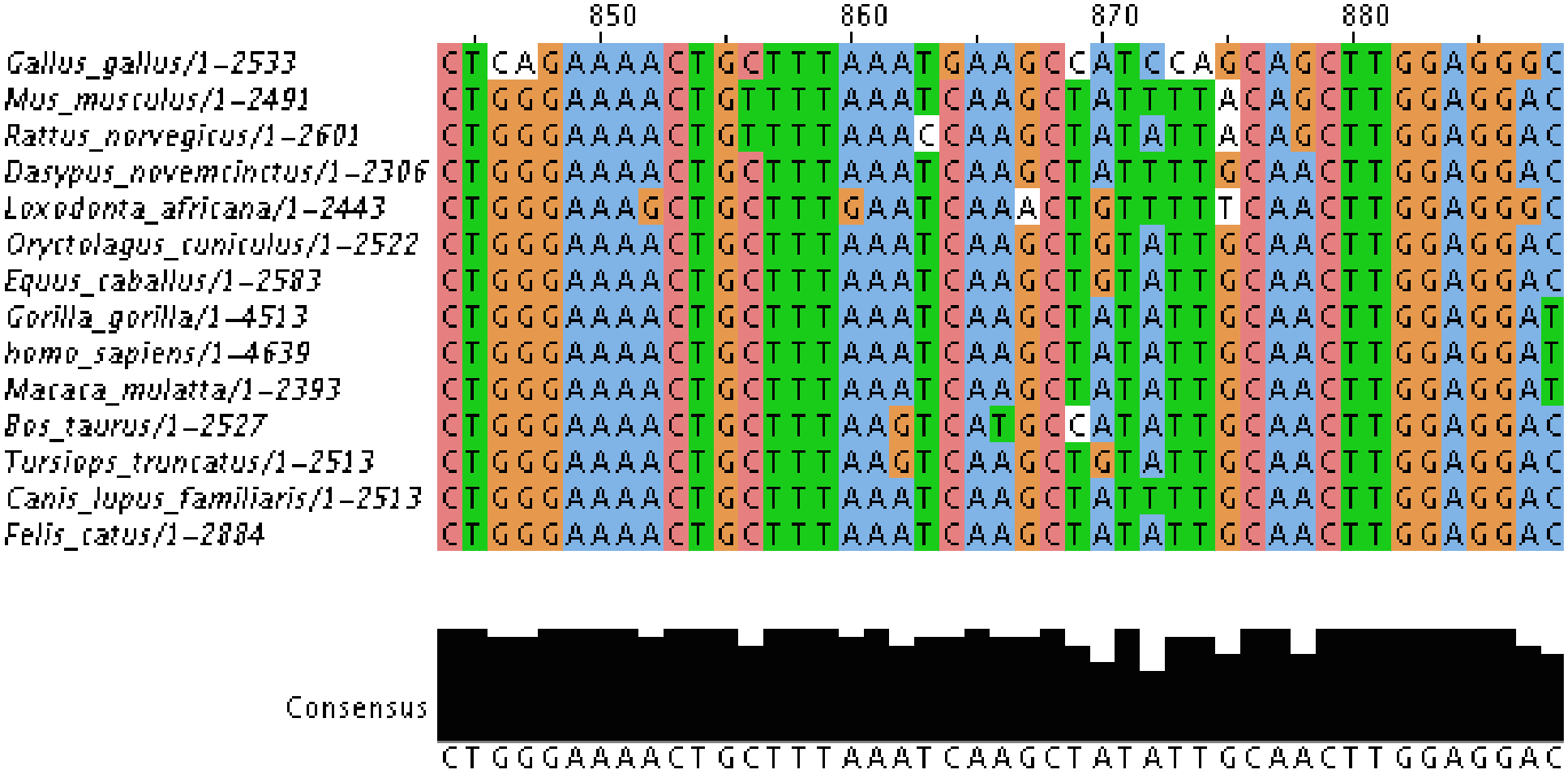
What is Global Sequence Alignment?

- We search for matches, matches and gaps between two sequences to determine their **relatedness**.
- (*) indicate matches or similar nucleotides (bases) along sequence
- Here, the sequences may have a common ancestor

```
ACGTACT    ACGTAC-T    ACGTACT----
ACTACGT    AC-TACGT    ----ACTACGT
**    *    ** *** *        ***
```

Ex: Comparing DNA

- We compare DNA samples from several different organisms.

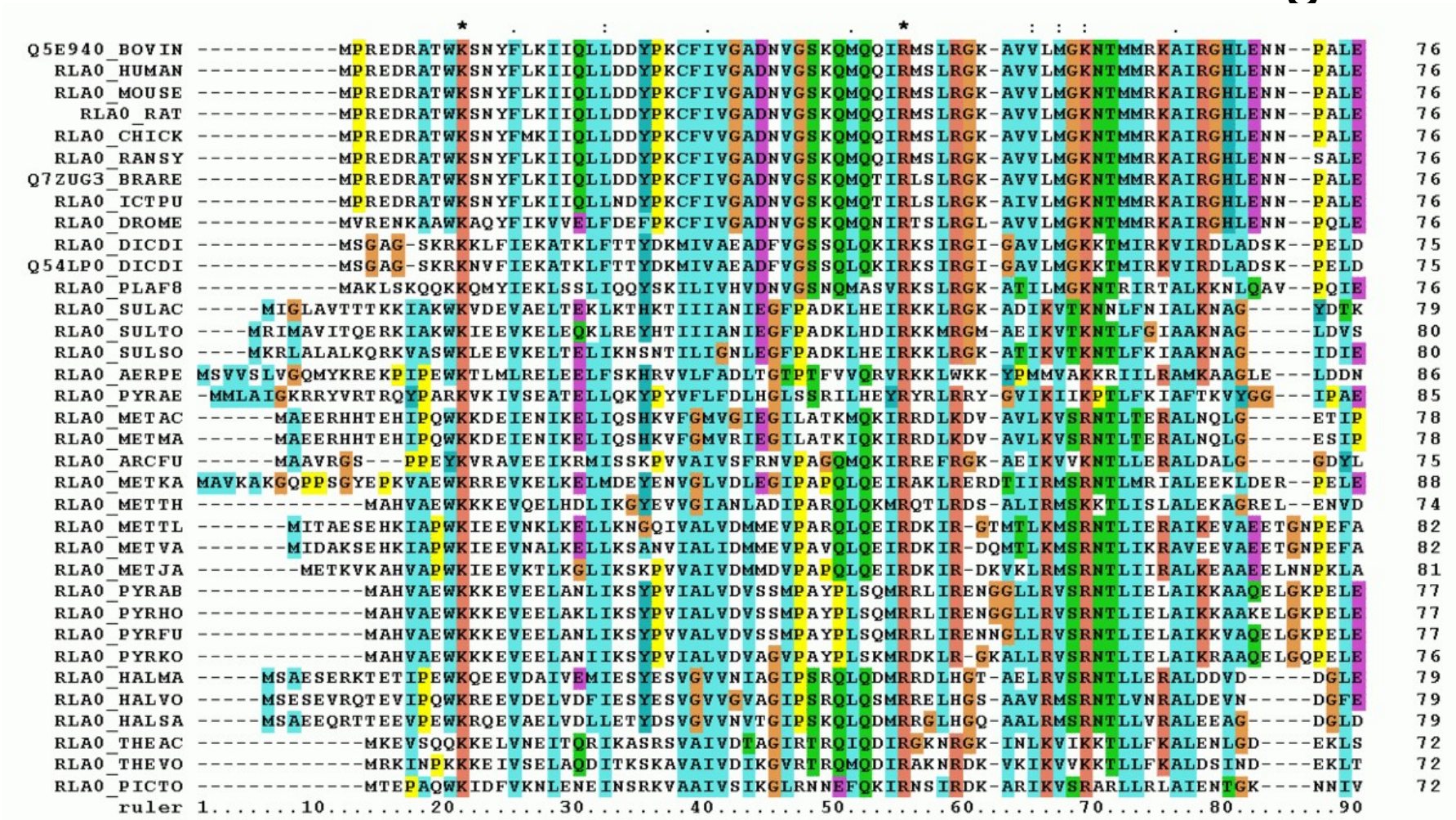


Ex: Comparing Protein

- We compare protein samples from several different organisms.

Ex: Comparing Protein

- The common code have same nucleotides but there are still breaks in these common regions.



Terms

- Alignment is divided up unto sub problems
- Solutions are scored; the best solutions for char by char comparison are kept in the overall solution.
- **Match** – bases of each sequence at position ARE same
- **Mismatch** – bases of each sequence at position are NOT same
- **Gap** – bases are not the same, some insert or deletion may have occurred.

AGGCTATCACCTGACCTCCAGGCCGATGCCC
TAGCTATCACGACCGCGGTCGATTTGCCCGAC

-AGGCTATCACCT**GACCTC**CA**GGCCGA--TGCCC---**
TAG-CTATCAC--GACCGC**--GG**TCGA**TTGCCC**GAC

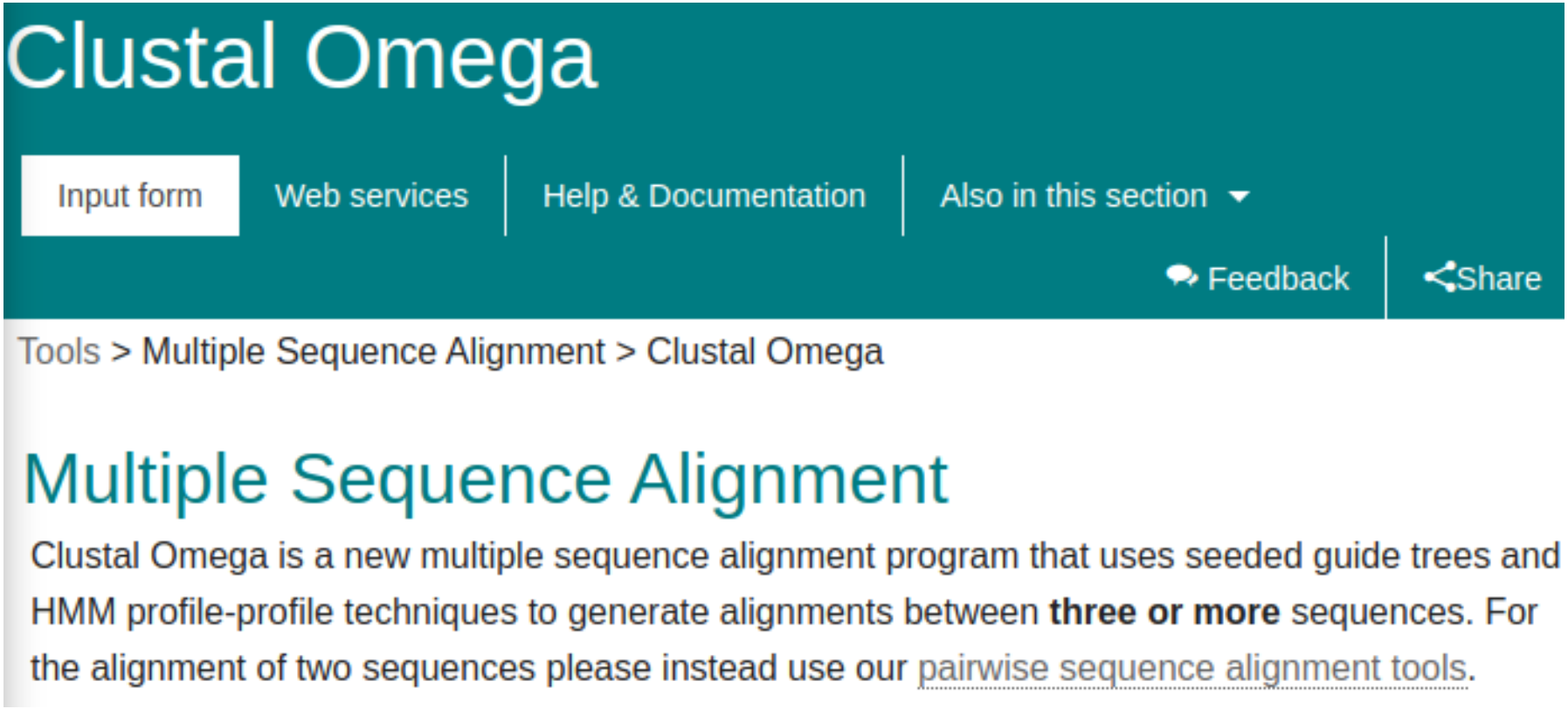
Terms

- **Homology** – Two or more sequences have a common ancestor
- **Similarity** – Two sequences are similar in terms of base arrangements. Note: this similarity does not refer to any specific evolutionary process; the sequences show *similarity* as they are compared.
- **Conserved regions** – Regions in code which are very similar (or the same) across a wide group of organisms. Having code which has not changed, in light of mutations, in all the organisms suggests that the region have been maintained by natural selection (and may serve an important function.)
- **DNA Coding Regions** – Contains code that is more likely to make protein, often less likely to change genetically. Mutations in these areas may cause danger.
- **DNA NonCoding Regions** – Contains DNA that does not necessarily code for protein, but may serve in gene regulation, such as the binding or recognition sites of ribosomes and transcription factors. May still be be conserved within a genome.

Bring the Tool!

Up Next!

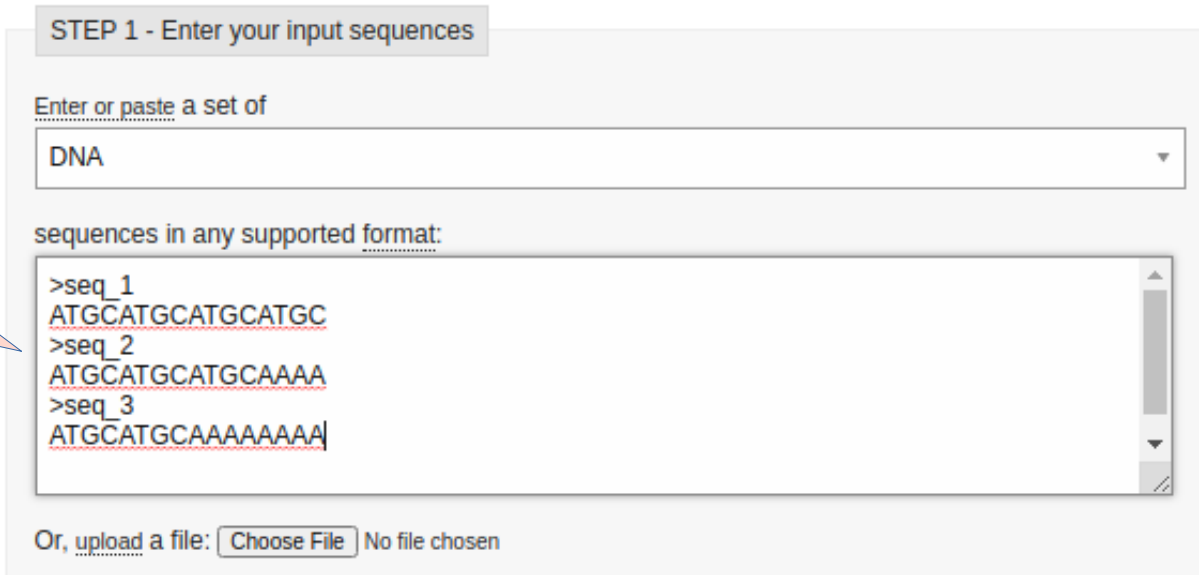
Clustal Omega
Multiple Sequence Alignment

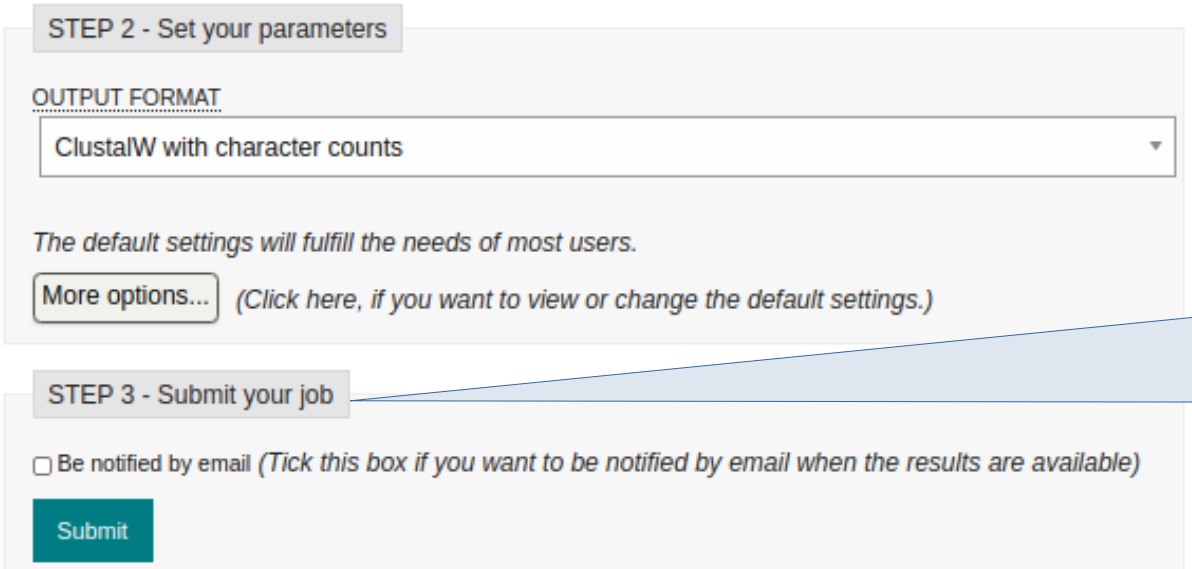


Link:
https://www.ebi.ac.uk/Tools/msa/clustalo/

Clustal Omega
Multiple Sequence Alignment

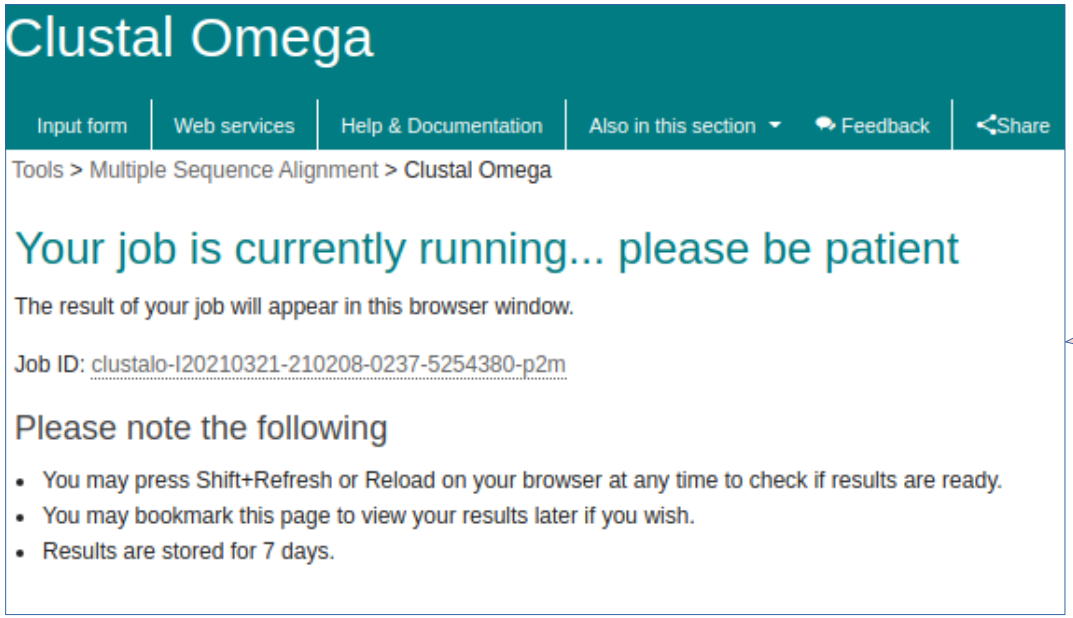
Enter DNA sequences in this **FASTA** format.





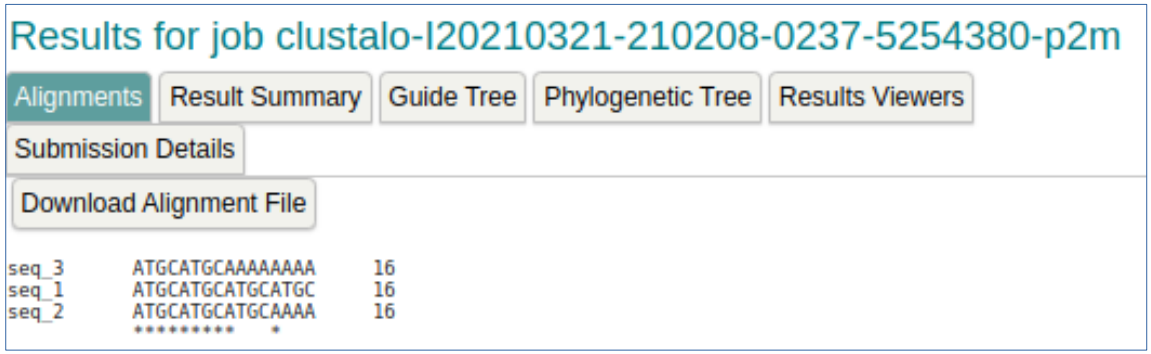
Submit your job with the *Character Counts* option.

Clustal Omega Results

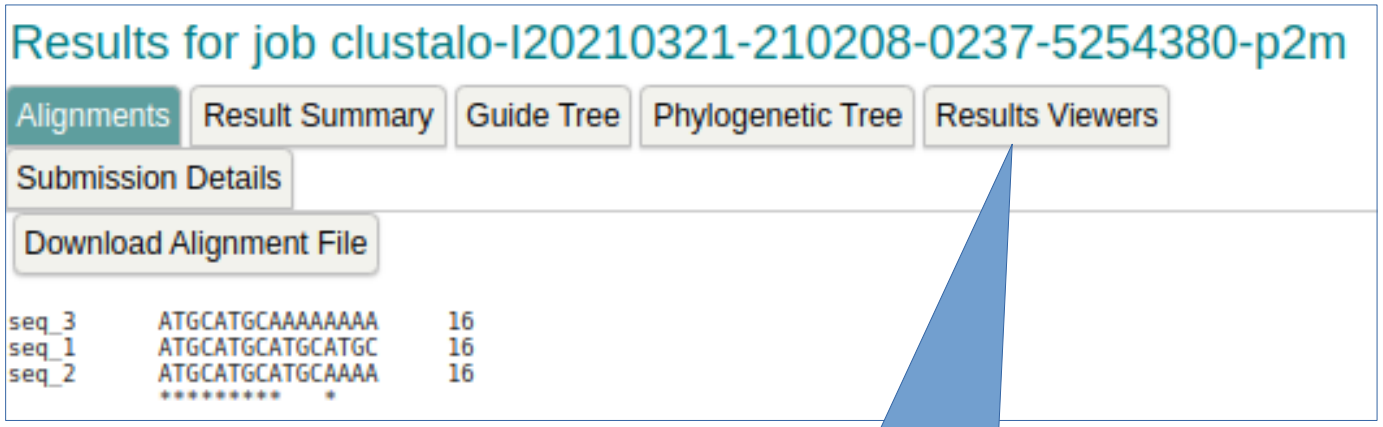


Depending the number of seqs, you may have to wait...

The '*'s denote same bases across sequences.



Percent Identity Matrix
How similar are the seqs?



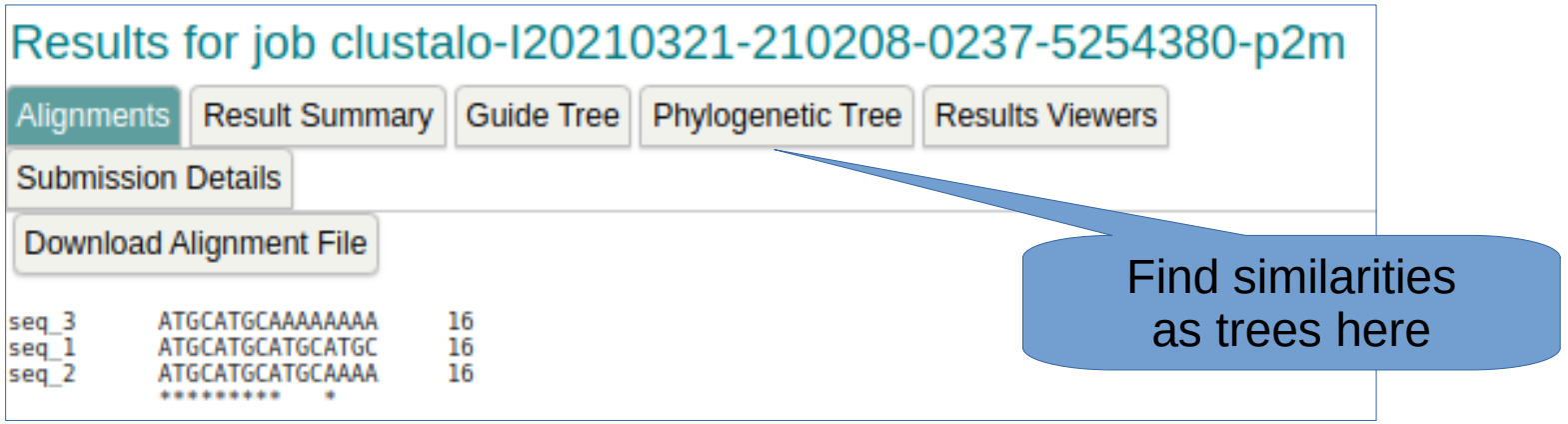
Find percent Identity results here

How similar are the sequences?.

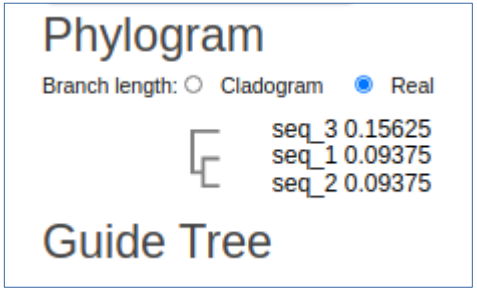
```
#
#
#  Percent Identity  Matrix - created by Clustal2.1
#
#                          Seq_3  Seq_1  Seq 2
     1: seq_3           100.00   62.50   81.25
     2: seq_1            62.50  100.00   81.25
     3: seq_2            81.25   81.25  100.00
```

Percent Identity Matrix

How similar are the seqs?



View similarity in a tree from.

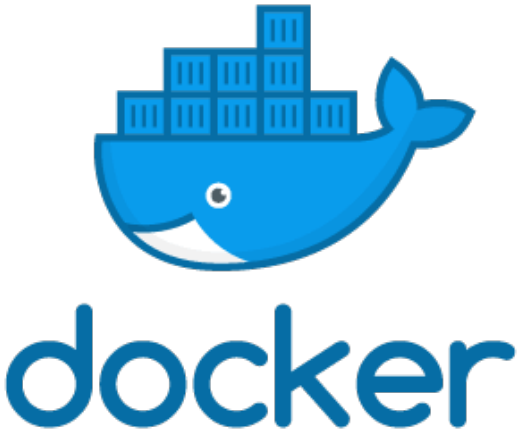


Please rebuild your container!!

New Dockerfile

(for Docker Desktop)

Adds a tool called ClustalW for sequence comparison.




```
FROM ubuntu:20.04

RUN apt-get update && apt-get -y
install git htop vim python3 python3-pip
clustalw


RUN \
pip3 install --upgrade pip \
pip install bioPython

WORKDIR /root

CMD ["bash"]
```

ClustalW On Your Own Machine

Enter sequences in a FASTA format:

```
>seq_1
ATGCATGCATGCATGC
>seq_2
ATGCATGCATGCAAAA
>seq_3
ATGCATGCAAAAAAAA
```