**Multiple Sequence Alignment (MSA)**

**MSA Tools and resources:**

* Many different algorithms, most common: MUSCLE, MAFFT, T-coffee, ClustalO, M-coffee (speed vs. accuracy trade-off)
  + **MUSCLE: iterative (slow, more accurate)**
  + T-coffee: progressive (faster)
  + MAFFT: progressive + iterative (faster)
  + ClustalO: progressive but improved accuracy
  + M-coffee: combining multiple MSA
* WEB resources
  + **EBI by EMBL (**[**https://www.ebi.ac.uk/Tools/msa/**](https://www.ebi.ac.uk/Tools/msa/)**):** 
    - several different algorithms
    - parameter adjustment possible
    - sometimes long waiting times
    - more comprehensive output (identical (\*); similar(:,.) AAs)
  + MPI Tübingen (<https://toolkit.tuebingen.mpg.de/>):
    - several algorithms
    - no parameter adjustment possible
    - usually less waiting time
    - minimal output

**MSA output formats:**

* FASTA format
* **CLUSTAL**

**MSA viewer:**

* **Jalview online** (<https://www.jalview.org/jalview-js/JalviewJS/>)**:**
  + A lot of meta data
  + Stable online version
  + Download available
* MView (EBI) / Alignment viewer (MPI) / AlignmentViewer (NCBI)
  + Minimalistic

**Additional Tools for exercises:**

* **Uniprot** (<https://www.uniprot.org/>): get FASTA sequences
* **AlphaFold** (<https://alphafold.ebi.ac.uk/>): visualize known proteins