**Sequence alignment and Phylogenetics\_P4**

1. Download Mega
2. Download a pair of homologous sequences from NCBI
3. Perform Global alignment in EMBOSS needle and Local alignment in EMBOSS water.
4. Compare the results.
5. Download 10 related homologous sequences from NCBI
6. Perform Multiple sequence alignment of the sequences
7. Determine the conserved and variable regions
8. Use the aligned sequences to create phylogenetic tree.