



Multiple Sequence Alignments

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Multiple sequence alignments

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A common approximation: **Progressive Alignments.**

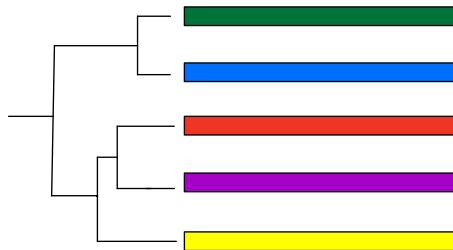
1. Calculate the pairwise scores of all your sequences
2. Align the two most similar sequences
3. Replace the two aligned sequences with their alignment
4. If more than one sequence remain, reiterate from 1.



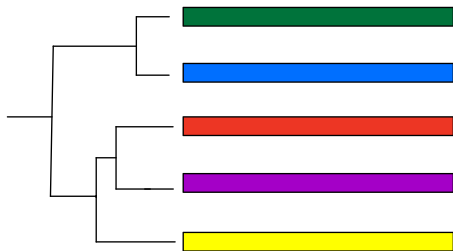
An example of progressive alignments



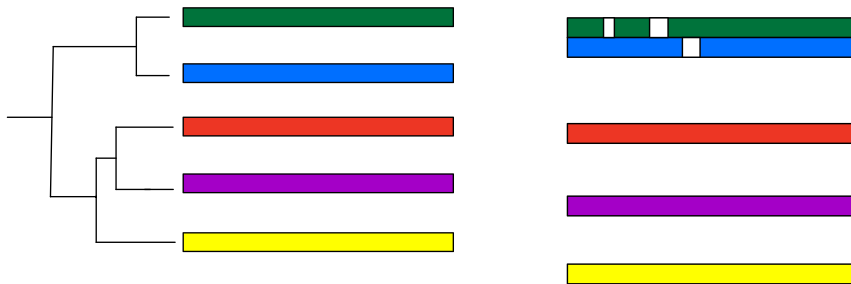
An example of progressive alignments



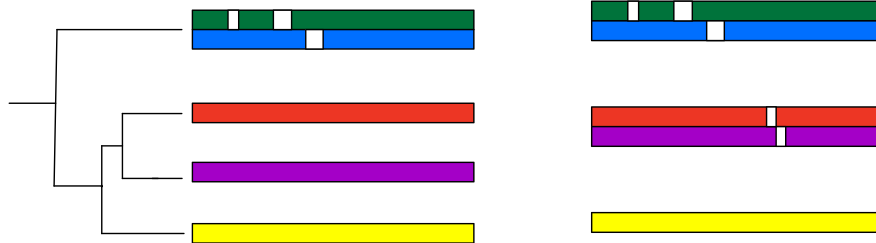
An example of progressive alignments



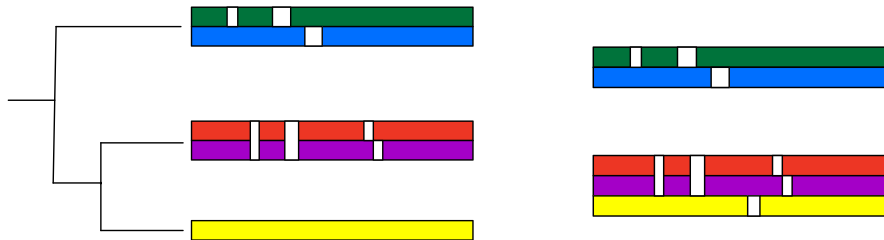
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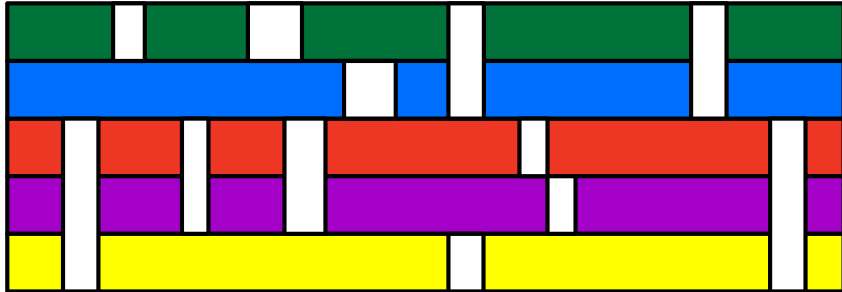
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Some commonly available MSA methods

- ▶ Kalign, <https://www.ebi.ac.uk/Tools/msa/kalign/>
- ▶ MaFFT, <https://mafft.cbrc.jp/>
- ▶ Clustal Omega, <https://www.ebi.ac.uk/Tools/msa/clustalo/>
- ▶ Muscle, <https://www.ebi.ac.uk/Tools/msa/muscle/>
- ▶ T-Coffee, <http://tcoffee.crg.cat/>
- ▶ ProbConc, <http://probcons.stanford.edu/>



Thanks!