

**Supplementary Table S1.** The overview of tools and methods mentioned in the review.

Tools or Methods	Typical Features	Working on	Year
<b>HHalign</b>	pairwise alignment of profile HMMs	protein sequences	2005
<a href="#">COVID-Align</a>	pre-built HMM	COVID sequences	2021
<b>MAGUS+eHMMs</b>	MAGUS and HMM	fragmentary sequences	2021
<a href="#">MAFFT-addfragments</a>	designed for adding fragmentary sequences to an alignment	fragmentary sequences addition	2012
<a href="#">MUMmer</a>	suffix trees and maximal unique matching subsequences	pairwise alignment of DNA sequences of very large scale	1999
<a href="#">Minimap</a>	seed-chain-align	pairwise alignment for nucleotide sequences	2016
<a href="#">ViralMSA</a>	massively scalable	viral genomes	2021
<a href="#">MAFFT</a>	FFT	general use	2002
<a href="#">FAME</a>	vertical division	general use	2020
<a href="#">FMAAlign</a>	vertical division	nucleotide sequences	2021
<a href="#">MAGUS</a>	horizontal division and Graph Clustering Merger	large-scale alignments	2020
<a href="#">Super5</a>	horizontal division	large datasets	2021
<a href="#">mBed</a>	embedding methods	rough guide tree construction	2010
<a href="#">PartTree</a>	length-based clustering	rough guide tree construction	2006
<a href="#">MACSE</a>	frameshifts and stop codons	coding sequences	2011
<b>GPCRtm</b>	specific to GPCR	scoring systems for GPCR	2015
<a href="#">MAHDS</a>	sophisticated mathematical process	highly divergent nucleotide sequences	2021
<a href="#">HAlign</a>	suffix trees	sequences of very large scale	2015
<a href="#">MASC</a>	suffix trees and Spark Parallel Framework	nucleotide sequences	2017
<b>chained guide trees</b>	simple topology	protein families of large number of sequences for structure-based benchmarks	/
<b>PRANK</b>	phylogeny-aware progressive alignment	alignments for evolutionary analyses	2008
<a href="#">PAGAN</a>	phylogeny-aware progressive alignment	alignments for evolutionary analyses	2012
<a href="#">ProPIP</a>	Poisson Indel Process (explicit mathematical model)	alignments for evolutionary analyses	2021
<a href="#">T-Coffee</a>	consistency objective function	general use	2000
<a href="#">ProbCons</a>	Probabilistic consistency	protein sequences	2005
<a href="#">M-Coffee</a>	consistency objective function	alignments combination	2006
<b>SATé</b>	iteration between re-aligning and tree re-construction	simultaneous alignment and tree estimation for DNA	2009
<a href="#">FAMSA</a>	division strategy based on gaps for iterative refinement	thousands of protein sequences	2016
<b>SpliVert</b>	vertical division strategy for iterative refinement	refinement of protein sequence alignments	2020
<a href="#">MO-SAStrE</a>	multi-objective metaheuristic	general use	2013
<a href="#">M2Align</a>	multi-objective metaheuristic and its parallelization	general use	2017
<b>SAGA</b>	genetic algorithms	general use	1996