Alignement of homologous characters

- multiple sequence alignment (MSA)
- optimal pairwise alignments (OPAs)
- pairwise, from induced alignments (IPAs)

ML distances estimation

- jointly, on a tree
- pairwise, from induced alignments (IPAs)
- pairwise, from OPAs

Covariance estimation

- estimator from ML theory
- bootstrapping
- models based on common branch lengths (needs topology)
- Susko (2003)
- bootstrapping
- models based on common branch lengths (needs topology)
- Dessimoz et al. (2006), for triplets only.
- present article