Analysis options for sensitivity in molecular project

* Alignment options
  + No alignment
  + MUSCLE
  + ClustalW
  + ClustalOmega
* Nucleic acid vs protein sequence
* Distance methods
  + Hamming
  + Other string methods
  + Log-Det method
  + ML model methods
  + P-Epitope
  + Cartography
  + Year distance
  + Polymorphism p distance
  + Biochemophysical distances like Grantham
* Algorithms for distance trees
* Algorithms for ML tree
* Methods for tree comparison
  + Likelihood
  + Some similarity metric
* With/without MI/85 incomplete strain
* Missing data: match vs nonmatch vs ignored
* H1/H3 separate or together