



Minisymposium 26 - Mathematics in the Biosciences

A New View on Multiple Alignment

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Many molecular sequence analyses start with a collection of aligned homologous sequences to infer certain features of the considered group or subgroup of sequences. We focus on the general question: what are the general sequence pattern inside the multiple sequence alignment discriminating and defining subgroups. Such patterns could later be mapped to structural or functional features of the sequence family. The proposed problem becomes more and more challenging when the number resp. the length of the considered sequences increases. We propose a singular value based approach based on parameters of a Hidden Markov Model to give a structured view of the multiple sequence alignment. Finally we show and discuss biological examples.