

Unaligned sequences (input)



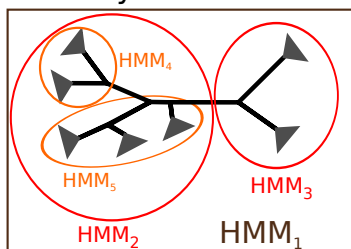
Randomly selected backbone



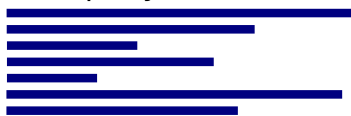
Backbone alignment and tree



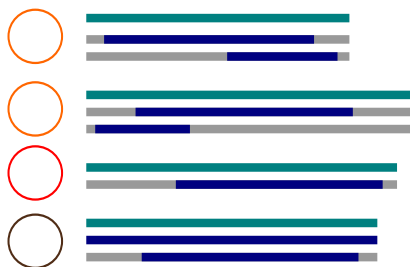
Family of HMMs



Remaining sequences (query set)



Alignment of query sequences to the best scoring model



Final merged alignment of all sequences

