
A hidden Markov model (HMM) is a stochastic process in which the relationship between the number of states and the observations is not one-to-one. HMMs are often used in speech recognition programs, bioinformatics, and scoring protein-ligand interactions in structure-based drug design. Detecting hidden states from noisy data is generally difficult. We illustrate a possible retrieval algorithm using synthetic data which was created in R by implementing a low dimensional HMM. (Received February 28, 2017)