EXPLORING THE STATE SEQUENCE SPACE FOR HIDDEN MARKOV AND SEMI-MARKOV CHAINS

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Once a hidden Markovian model has been estimated, it is generally of interest to understand the hidden state sequence structure underlying an observed sequence. Questions of interest are: Is the most probable state sequence most probable by a long way or are there other state sequences with near-optimal probability? Do these near-optimal sequences have state structures very similar to the most probable state sequence or do they differ greatly? The knowledge of state sequences that explain a given observed sequence for a known hidden Markovian model is the basis of methods that may be divided into two categories: (i) enumeration of state sequences, (ii) state profiles i.e. state sequences summarized in a $J \ge J$ τ array where J is the number of states and τ the length of the sequence. Various methods belonging to these two categories are presented for different families of hidden Markovian models. In particular, we propose a new type of state and state change profiles that can be viewed as the superposition (from the less probable to the most probable) of all the state sequences. Finally, the use of the entropy of the state sequence for a given observed sequence as a global measure of the state sequence uncertainty is discussed. These methods are illustrated by the analysis of plant topological structures (succession of growth phases along tree trunks and branching structures).