

The posterior-Viterbi: a new decoding algorithm for hidden Markov models

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Motivation

Hidden Markov models (HMM) are powerful machine learning tools successfully applied to problems of computational Molecular Biology. In a predictive task, the HMM is endowed with a decoding algorithm in order to assign the most probable state path, and in turn the class labeling, to an unknown sequence. The Viterbi and the posterior decoding algorithms are the most common. The former is very efficient when one path dominates, while the latter, even though does not guarantee to preserve the automaton grammar, is more effective when several concurring paths have similar probabilities. A third good alternative is 1-best, which was shown to perform equal or better than Viterbi.

Methods

In this paper we introduce the posterior-Viterbi (PV) a new decoding which combines the posterior and Viterbi algorithms. PV is a two step process: first the posterior probability of each state is computed and then the best posterior allowed path through the model is evaluated by a Viterbi algorithm.

Results

We show that PV decoding performs better than other algorithms first on toy models and then on the computational biological problem of the prediction of the topology of beta-barrel membrane proteins.

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