

Decision theoretic decoding of Hidden Markov
Models with applications to signal segmentation
in cancer genomics

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Hidden Markov models (HMMs) are widely used tools for change-point analysis and signal segmentation. However, methods for providing predictions of the hidden state sequence given data are poorly developed, principally relying either on the Viterbi algorithm to find the most probable state sequence or the forward-backward algorithm for the sequence of most probable marginals. In this talk we will present new results on the use of decision theoretic loss functions to derive flexible predictions that minimize an expected loss. This includes a new algorithm using auxiliary counting variables that allows for exact linear-time reporting of the optimal hidden state sequence conditioned on a user-specified number of transitions or change-points of a particular type. The techniques are motivated and demonstrated using on-going real world studies in cancer genomics surrounding the detection of copy-number-aberrations, stretches of DNA that are duplicated or deleted in tumour cells, which are key drivers of cancer initialisation and progression.