## A Bayesian nonparametric decision theoretic approach to inference of copy-number variation in heterogeneous cancer samples

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We present a Bayesian nonparametric approach to the problem of inferring copy-number, variation (CNV) within heterogeneous cancer samples. CNV refers to stretches of DNA > 1000 bases long which are found in varying copies within genomes, such as deleted or duplicated states. We have developed a Bayesian Hidden Markov model where the conditional sampling density (or likelihood) within state follows a mixture model; including a mixture of Dirichlet Process (MDP) model. The HMM structure causes difficulties for conventional computational sampling approaches for MDP and we have devised a novel slice sampling method to allow for efficient computation. Given a posterior distribution on the underlying (hidden) state sequence we make use of decision theory and maximum expected utility to make an "optimal" call for the underlying state sequence.