COMPOSITE LIKELIHOOD IN FINE GENETIC MAPPING

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We present here some developments and extensions to a fine mapping method using the ancestral recombination graph (ARG), an extension of the coalescent process which includes recombination, to map a trait influencing mutation. We consider a model for the evolution of microsatellites markers, and some approximations to this model, in the ARG. We propose a new way to estimate the likelihood using the composite likelihood methodology, explore ways to use only pairs of markers, or windows of markers over the sequence, and show advantages and disadvantages of such approaches. Finally, we test these developments with some simulated data, and show that the method works, at least in simple cases.