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Linkage analysis, the use of pedigree data to identify genes, has traditionally been used for analysis of binary or continuous traits. We will present a statistical framework for analysis of categorical traits, employing a novel estimator for parameter inference from Markov chain Monte Carlo. We will demonstrate the value of our method by analyzing candidate genes for cardiac arrhythmia in a pedigree of German Shepherd dogs. (Received September 10, 2008)