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Admixed individuals, such as many Latinos, have DNA from multiple ancestries. Identifying the ancestry of small regions of DNA can enhance statistical tests for association between genes and diseases or other traits. In this work, we compare 6 methods of incorporating ancestry into genetic association mapping for simulated binary and quantitative traits. We also compare two approaches to extend each method from two-population admixture to three-population admixture. Surprisingly, for 5 of the methods, the naïve approach of comparing each ancestry versus the other two is as powerful as modeling all three ancestries jointly. However, it is also more computationally intensive due to the need for permutation testing. (Received September 11, 2014)