

# Evaluating Individual Admixture Estimation through Plasmode Data

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## Abstract

Admixture mapping has recently garnered attention as a potentially useful method for gene mapping. Structured association testing, where admixture estimates are used as a control variable, has been advanced as a means of controlling for confounding induced by population stratification in genetic association studies. Both techniques depend on the use of individual ancestry estimates as covariates. Many admixture estimation methods have been proposed, but most have been evaluated only with simulated data. An attractive method to supplement the evaluation of these methodologies is the use of plasmodes. Plasmode datasets are simply those generated by natural processes, and not through computer simulation, but still have some aspect of the truth known. Here we use plasmodes consisting of mice from two inbred line crosses. Each cross shares a common founding inbred line so that the ancestry proportion, which is equivalent to individual admixture minus some error, for each mouse is known. This allows us to compare the effectiveness of different algorithms (*Structure*, *AdmixMap*, and *FRAPPE*) at estimating individual admixture proportions.