

# Blum, Rosenberg 2007c

## Article ...

▼ ... in a Journal

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### Title:

Estimating the number of ancestral lineages using a maximum-likelihood method based on rejection sampling

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### Abstract:

Estimating the number of ancestral lineages of a sample of DNA sequences at time  $t$  in the past can be viewed as a variation on the problem of estimating the time to the most recent common ancestor. To estimate the number of ancestral lineages, we develop a maximum-likelihood approach that takes advantage of a prior model of population demography, in addition to the molecular data summarized by the pattern of polymorphic sites. The method relies on a rejection sampling algorithm that is introduced for simulating conditional coalescent trees given a fixed number of ancestral lineages at time  $t$ . Computer simulations show that the number of ancestral lineages can be estimated accurately, provided that the number of mutations that occurred since time  $t$  is sufficiently

large. The method is applied to 986 present-day human sequences located in hypervariable region 1 of the mitochondrion to estimate the number of ancestral lineages of modern humans at the time of potential admixture with the Neanderthal population. Our estimates support a view that the proportion of the modern population consisting of Neanderthal contributions must be relatively small, less than approximately 5%, if the admixture happened as recently as 30,000 years ago.

▼ ...in a Conference Proceeding

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