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mixtures by integrating the likelihood ratio

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Accurate assessment of the weight of evidence for DNA mixtures by integrating the likelihood ratio

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Abstract

Several methods exist for weight of evidence calculations on DNA mixtures. Especially if dropout is a possibility, it may be difficult to estimate mixture specific parameters needed for the evaluation. For semi-continuous models, the LR for a person to have contributed to a mixture depends on the specified number of contributors and the probability of dropout for each. We show here that, for the semi-continuous model that we consider, the weight of evidence can be accurately obtained by applying the standard statistical technique of integrating the likelihood ratio against the parameter likelihoods obtained from the mixture data. This method takes into account all likelihood ratios belonging to every choice of parameters, but LR's belonging to parameters that provide a better explanation to the mixture data put in more weight into the final result. We therefore avoid having to estimate the number of contributors or their probabilities of dropout, and let the whole evaluation depend on the mixture data and the allele frequencies, which is a practical advantage as well as a gain in objectivity. Using simulated mixtures, we compare the LR obtained in this way with the best informed LR, i.e., the LR using the parameters that were used to generate the data, and show that results obtained by integration of the LR approximate closely these ideal values. We investigate both contributors and non-contributors for mixtures with various numbers of contributors. For contributors we always obtain a result close to the best informed LR whereas non-contributors are excluded more strongly if a smaller dropout probability is imposed for them. The results therefore naturally lead us to reconsider what we mean by a contributor, or by the number of contributors.

Keywords: Likelihood ratios, DNA mixtures, Semi-continuous model, Allelic dropout, Low Template DNA, Deconvolution, Weight of evidence

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1. Introduction

Several methods exist for weight of evidence calculations on DNA mixtures where dropout is a possibility. Broadly speaking, there are two types of such methods: the semi-continuous models that take into account the set of recorded alleles of the mixture and calculate a mixture likelihood using as parameters the number of contributors to the mixtures and parameters that describe dropout and possibly also drop-in probabilities; and continuous models that take also the peak heights into account and need a more refined probabilistic model that allow to compute a likelihood for the observed peak heights, also needing as input parameter the number of contributors. In this article we will focus on the semi-continuous models. Several of these exist, e.g. LRmixStudio (www.lrmixstudio.org, see also [1]), LabRetriever (cf. [2]), LikeLTD (cf. [3]), and our own implementation MixKin (cf. [4]). In practice it may be difficult to assess the number of contributors and the probabilities of dropout. The latter are sometimes (e.g., for LRmixStudio) chosen by the user and can then be varied to carry out a sensitivity analysis, or they can be estimated by the software (as is the case for LikeLTD). It is therefore logical that estimating and modelling the probability of dropout has received considerable attention in the literature, cf. [5], [6], [7], and so has the question how well the number of contributors to a mixture can be estimated (cf. [8], [9], [10], [11]).

On the other hand, the notion of number of contributors is perhaps less useful in case the contributors do not have all their alleles recorded in the mixture. It should intuitively not make much difference

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