KONGOH: OPEN SOURCE SOFTWARE FOR DNA MIXTURE INTERPRETATION BASED ON A CONTINUOUS MODEL

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We developed an open source software called *Kongoh* (named after the Japanese word "mixture") using R language to interpret mixed DNA profiles. The software is based on a continuous model that uses peak heights and can be used in the case of low-template DNA with allelic drop-out. A profile typed by means of the Identifiler Plus Kit can be interpreted using the software. The software implements five biological parameters: the mixture ratio, DNA degradation, locus-specific amplification efficiency, heterozygote balance, and stutter ratio. To estimate distributions of expected peak heights, a Monte Carlo simulation is performed on the basis of probability distributions of the biological parameters determined by means of empirical data, and then the peak heights generated by the simulation are approximated by gamma distributions. Likelihood ratio is calculated as the weight of evidence from the ratio of maximum likelihood in a prosecutor hypothesis and that in a defense hypothesis. Because likelihood values in both hypotheses of 1–4 contributor(s) are calculated automatically, the number of contributors does not need to be determined manually prior to the analysis in the software. We validated the software using nine two-person mixtures, nine three-person mixtures, and two four-person mixtures with various mixture ratios. The software generated greater likelihood ratios than binary and semi-continuous models did and produced accurate estimates of the number of contributors and of the mixture ratio. Therefore, this new tool should be especially useful for interpretation of three- or four-person mixtures.