NEW METHOD AND SOFTWARE TO RESOLVE COMPLEX DNA MIXTURES

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Resolving complex DNA mixtures is still one of the greater challenges for DNA experts. Today different biostatistical methods like discrete or fully-continuous models are used for the interpretation of DNA mixtures.

Especially full-continuous models are growing in acceptance and have shown their practical potential in different cases. By the transition from the binary, through the semi- continuous, through fully-continuous mixture model the significance of the likelihood ratio calculation can be increased.

During our research and ongoing development of our software GenoProof Mixture we developed a full-continuous model following different approaches. The weighting of the probabilities of contributor genotype constellations were a central component of our evaluation.

The method for calculating the weights of all possible genotype constellations which can explain the given DNA mixture is using a Markov Chain Monte Carlo method. The method considers peak heights, stutter-quotient, allele drop - in / drop-out and many other parameters to deliver the best results.
The algorithms were optimized to deliver an excellent run-time behavior also on ordinary desktop computers.

To improve also the quality assurance and the transparency of the mixture analysis we developed graphical tools which facilitate the experts working with complex mixtures clearly, so that they easily can explain the results in court.

We provide insights into our developed model and show examples of how to massively strengthen the effectiveness of complex DNA mixture analysis.