

The statistical evaluation of DNA crime stains in R

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Suppose a crime has been committed and a blood stain was collected from the crime scene. It is believed the stain was left by an offender. A suspect is arrested and it is found out that his DNA profile matches the DNA profile of the crime stain. In forensic science, it is common to consider DNA profile match probabilities under the hypothesis that the offender was someone else than the suspect. The problem was investigated, e.g., in [1], under general assumptions allowing for population substructure and relatedness.

In case of DNA mixtures (from more than one person), the weight of the DNA evidence is assigned in terms of likelihood ratio of match probabilities, comparing two hypotheses about origin of the mixture. Authors in [2] obtained a general formula for calculation of match probabilities under assumption of independent alleles in DNA profiles. The result was further extended by [3] and [4] to allow for population substructure and dependence. The DNA mixture problems with presence of relatives were discussed, e.g., in [5].

The aim of this talk is to introduce an R package called *forensic* where the calculations of match probabilities mentioned above are implemented. The functionality of the package will be demonstrated using data from real situations.

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References

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