THE EFFECT OF HANDLING ALLELIC DROPOUT IN LIKELIHOOD RATIO COMPUTATIONS FOR DVI KINSHIP ANALYSIS

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In case of a Disaster Victim Identification (DVI) or a Missing Person Identification (MPI), degraded victim DNA may lead to allelic dropout. This may make the identification process more difficult, in particular in large scale cases where many comparisons between victims and pedigrees of relatives have to be made.

The goal of the model study presented in this poster is to get more insight into the possible effects of different ways to handle allelic dropout in likelihood ratio computations for kinship analysis as used in DVI and MPI cases. A way to handle dropout is for example the removal of the locus with a suspected allele dropout. Another way is the use a wild card allele in the genotype at the locus with the dropout. A third way that we consider is to represent the genotype as homozygous.

For this study we simulate a series of DVI cases. In each simulation, data is generated randomly from assumed population statistics, assumed pedigrees, and assumed dropout probabilities. Dropout is simulated as data missing at random.

With the simulated data, in particular with the dropouts, kinship analyses are performed by computing likelihood ratios for victim-family combinations, with the hypothesis of the victim being unrelated as alternative. In these computations the different ways to handle dropout are implemented. The obtained likelihood ratios are compared with the assumed ground truth likelihood ratio, which are computed on the basis of the underlying allele values of the dropouts.

Various scenarios to generate simulated DVI data are considered of which results will be presented.