

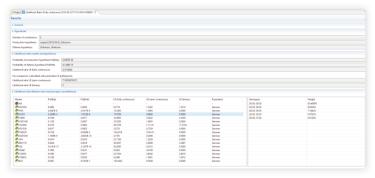
# GenoProof Mixture 3 FACTSHEET

#### FACT 1: Fully continuous approach for likelihood ratio calculation

The likelihood ratio (LR) calculation enables the formulation of hypotheses in order to compare persons of interest to profiles. When employing a fully continuous approach, the explanatory power of calculations in comparison to the binary or the semi-continuous approach is considerably increased.

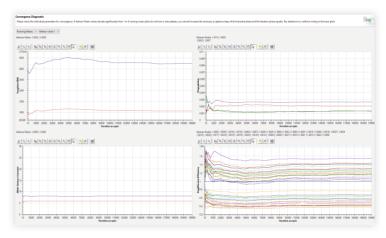
#### FACT 2: Genotypes of major and minor contributors of a stain

The fully continuous approach is based on the estimation of parameters. Thereby, determining the likelihood of a match of the expected peak heights (generated by random genotype constellations and random parameter combinations) with the observed peak heights. The algorithm creates all possible genotype constellations, whereas all not justifiable genotype constellations are previously filtered by heuristics. By executing Monte-Carlo-Markov-chains, statistical weighting of all genotype constellations is performed, as well as the deconvolution of major and minor contributor profiles.



# **FACT 3**: Convergence diagnostics and Gelman-Rubin values to assess the quality of the calculations

To analyse the quality of the results of the LR calculation with the fully continuous approach, convergence diagnostics and Gelman-Rubin values are assessed. These control tools are included to help you to define the correct settings for relevant parameters and step number of burn-in and iteration phase.



# FACT 4: Uses more information of your profiles

The fully continuous approach is based on modelling of peak heights of genotype constellations on the basis of DNA quantity, DNA degradation, allele size, amplification efficiency, variance of replicats, homozygosity and heterozygosity, pre-stutter and allelic drop-in and drop-out events, also depending on contributing persons, DNA markers, test kits and analysis devices.

### FACT 5: Direct comparison of LR calculations

In addition to results calculated with the fully continuous approach, the results of the binary and semi-continuous model are displayed for a direct comparison. A separate LR calculation using the binary or the semi-continuous model is possible. In all calculations, the consideration of subpopulations is optional.

# **FACT 6**: Calculation of number of contributors is based on maximum allele count or maximum likelihood methods

In addition to entering the number of contributors of a stain manually, GenoProof Mixture 3 can automatically calculate this value according to the maximum allele count or the maximum likelihood method.

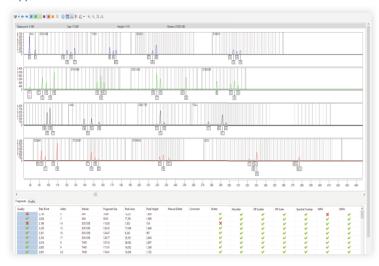


#### FACT 7: Integrated raw data analysis of fsa/hid files

GenoProof Mixture 3 offers high-performance fragment analyses of fsa and hid raw data including size and allele calling, as well as a reliable artifact detection. Thus, there is no need for additional genotyping software.

#### FACT 8: Import of GeneMapper-analyzed data

GeneMapper® analyzed data can be imported into GenoProof Mixture 3, so that all relevant information, including peak heights, alleles and test kits can be considered in a LR calculation using the fully continuous approach.



# **FACT 9**: Multikit functionality to combine PCR replicates of different test kits in one analysis

DNA-Profiles from replicate analyses with different test kits can be combined for all available calculations.

#### FACT 10: Calculate the Probability of identity and the RMP

When calculating the probability of identity, allelic dropouts can be considered using the 2p rule. The RMP (Random match probability) is the probability for a random match in the population. The calculation of the RMP includes the options unrelated, related or same subpopulation.

#### FACT 11: RMNE calculation

GenoProof Mixture 3 enables the calculation of the RMNE (random man not excluded) with the optional consideration of subpopulations.

# FACT 12: Genetic reference database for test kits, size standards and population data

A database with allele frequencies for populations, commercial test kits and size standards is included in the software. The user can also add any relevant reference data, e.g. test kit files (panels, bins, stutter), as well as population data in csv files or from the STRidER database.

#### FACT 13: CODIS import and export of profiles

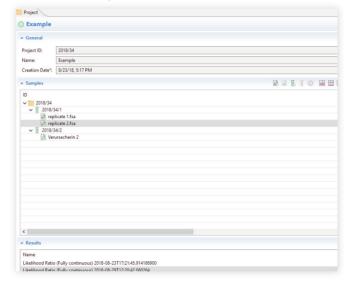
Profiles can be imported and exported in the current CODIS format (Combined DNA Index System). This format is commonly used by US crime labs, as well as in Europe.

#### **FACT 14**: Export information

Results, project data and raw data can be exported in the csv format. An extensive report functionality facilitates individual reports in DOCX and PDF format with a multitude of variables from the calculations. In addition, direct printing of projects, samples, results and electropherograms is possible.

#### FACT 15: Project and sample management

GenoProof Mixture 3 contains a project and sample management. A project is comprised of associated samples, raw data and calculation results. The project overview shows all projects with the possibility to filter and search for relevant projects. Projects can be closed, which disables further editing.



#### FACT 16: User and rights management

The user and rights management defines the access of different user groups (admin, laboratory head and assistant) to the program functionalities.

# FACT 17: Fastest software for fully continuous LR calculations

Advanced algorithms enable interpretation of complex DNA samples within minutes, without the need for high-speed computing and a training of parameters.

#### FACT 18: Validation

Based on hundreds of samples, the fully continuous approach is validated in each GenoProof Mixture 3 version in terms of specifity, sensitivity and precision according to SWGDAM guidelines.

#### FACT 19: Consider kinship for commonly encountered relationships

If an unknown, but related person to the suspect cannot be excluded as a contributor to the stain, results can be calculated considering multiple kinship constellations.



