B187 Validation of Probabilistic Genotyping Software for Use in Forensic DNA Casework

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After attending this presentation, attendees will better understand the scientific foundation of software validation. Attendees will receive both theoretical and practical guidance on implementing validation of probabilistic genotyping software in a forensic DNA laboratory.

This presentation will impact the forensic science community by assisting forensic DNA laboratories in validating probabilistic genotyping software, which fills a current and critical need.

Complex profiles may encompass a multitude of confounding factors resulting from DNA profiling of a low quantity and/or low quality biological sample. The resulting profile may contain multiple contributors, may lack information from the true contributors (allelic drop-out), may include extraneous information unrelated to the crime-sample information (allelic drop-in), and may suffer from degradation or inhibition. It is now accepted throughout the worldwide forensic DNA community that a likelihood ratio approach is required to reliably interpret these types of profiles.

Accordingly, recent years have seen a proliferation of probabilistic models, implemented via software, offered to the community as solutions to this problem. Acceptance of such software in the user community, and subsequent acceptance by the court, relies heavily on their validation. Although these probabilistic models rely on different assumptions and make use of different types of information, they all enable the evaluation of evidence within a likelihood framework. While these software programs have proven generally useful to facilitate the interpretation of complex DNA profiles, few guidelines exist that describe the appropriate and sufficient validation of such software used in forensic DNA casework.[1,2] The validation of probabilistic models for use in forensic casework is not straightforward because the true weight of the DNA evidence cannot be determined; there is no “right” answer. Indeed, the generated likelihood ratio always depends on the model’s assumptions. No “gold standard” exists in the form of a true likelihood ratio that can serve as a comparison.

Forensic science is not the first discipline to face the challenges of model and software validation. Consequently, the field can draw on the collective wisdom of other disciplines to guide its inquiry. This presentation will discuss general principles of software validation and how they could be applied to the interpretation software now being introduced into the forensic community. This presentation will first introduce some general definitions of model and software validation taken from existing fields. Importantly, the relationship between a statistical model and its implementation via software will be clarified. This presentation will then illustrate how these ideas can be translated into use for forensic casework. A set of considerations that seek to provide guidance in validating probabilistic genotyping software for casework use will be offered.

Finally, this presentation will make the case for transparency in software. Concerns about the reliability and reproducibility of software used in scientific computing have grown over the past few years. There is a strong movement for researchers to make the source code used for analyses freely available to the community at the time of publication. Easily accessible source code implementing a statistical method will allow scientists to perform all aspects of software validation. Finally, such transparency will promote standardization and will facilitate improvements and extensions to existing software, which will be a further benefit to the community.

Reference(s):

1. Scientific Working Group on DNA Analysis Methods. *Guidelines for the Validation of Probabilistic Genotyping System.* www.swgdam.org (2015).
2. Haned H., Gill P., Lohmueller K., Inman K., Rudin, N. Validation of probabilistic genotyping software for use in forensic DNA casework: Definitions and illustrations. *Science and Justice.* 56 (2016) 104–108

Probabilistic Genotyping, Software, Forensic DNA