H98 Trace Evidence in Microbial Forensic Study Through Cluster Analysis

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After attending this presentation, attendees will understand: (1) the principles of trace evidence using microbial samples, including the strengths and limitations; (2) the mechanism of cluster analysis used in trace evidence; (3) two proposed methods based on cluster analysis in trace evidence; (4) performance comparison between the proposed methods and existing approaches; and, (5) how to practically utilize the proposed methods in trace evidence through microbial samples.

This presentation will impact the forensic science community by facilitating criminal investigation with more accuracy in estimating the probability of a suspect's presence at the scene of the crime based on microbial materials collected at the scene.

The human genome has become known as the blueprint of human biology, and the human microbiome has recently been recognized as human's the second genome. With more than 100 trillion microorganisms living in and on human bodies, microbes (and, in particular, bacteria) can be very useful in forensic investigations. Many human microbiome studies have determined that microbial compositions vary across different body sites, but there is also evidence that the microbiome has consistent differences between individuals, which indicate that the microbiome can be used as a tool for human identification with potential application in criminal investigations. In this way, the materials collected at crime scenes could potentially be connected to suspects through the information revealed by the microbial community. Quite a few research projects have investigated and evaluated the potential of using the microbiome as an indicator for forensic sciences. For example, metagenomic profiles of the skin, hair, bodily fluids (e.g., saliva), soil, and objects in the built environment have been demonstrated as potentials to become established methodologies for use in courts; however, there is a lack of statistical and computational methods for analyzing the microbiome data for this purpose.

In this research, two methods, Bootstrapping RElative Aitcheson Distance (BREAD) and Bootstrapping RElative Aitcheson and Source Track (BREAST), are proposed to accurately estimate the probability of suspects contributing to microbial evidence. The methods are based on a hierarchical cluster process with adjustment for baseline dendrogram structure. Aitcheson distance is used for cluster analysis, as the metagenomic sequencing data shall be treated as compositional data. Comprehensive simulation studies show that the new methods greatly surpass all currently available approaches in all situations, even when the data contains very much noise. In the simulation studies, real metagenomic data are used to generate/mimic the suspects and evidence. The methods and the software package developed in this research will allow other groups to analyze their own data in a more statistical manner and contribute to the field of microbial forensic analysis.

Microbial Forensics, Trace Evidence, Cluster Analysis