STRmix Launches New Version of Investigative App for Calculating Likelihood Ratios

DBLR™ v1.5 Enables Use of Variable Number of Contributor Inputs, Updates to Reporting

WASHINGTON, DC, UNITED STATES, April 14, 2025 /EINPresswire.com/ -- The team that created ground-breaking forensic software STRmix™ has launched DBLR™ v1.5, the newest version of its investigative application for rapidly calculating millions of likelihood ratios (LRs) in DNA evidence.

> The latest version of DBLR™ contains a new pre-check feature. While configuring propositions in Kinship, DBLR™ will use a simplified model to continuously run checks on the setup as changes are made. ”
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> *Dr. Maarten Kruijver*

DBLR™ enables forensic laboratories to achieve superfast database searches, visualize the value of DNA mixture evidence, carry out mixture-to-mixture matches, determine whether there is a common donor between samples, and calculate any conceivable kinship relationship when used in conjunction with STRmix™.

DBLR™ v1.5 improves upon previous versions of the software by enabling the use of variable number of contributor (varNOC) inputs (utilizing the stratified LR) in the Automated Searching, Kinship, and Simulation (Explore deconvolution) modules. Updates to reporting to align the formatting more with other STRmix™ software are also now included.

“In addition, the latest version of DBLR™ contains a new pre-check feature added to the Kinship module,” explains Dr. Maarten Kruijver, developer of DBLR™. “While configuring propositions in Kinship, DBLR™ will use a simplified model to continuously run checks on the setup as changes are made. A warning is shown if the proposition can no longer explain the evidence or if a mutation would be needed to explain genotypes in the pedigree. This helps to flag input errors, incorrect known biological relationships, and genuinely exclusionary results.”

DBLR™ enables forensic laboratories using STRmix™ to explore the interpretation results from a DNA profile given different hypotheses. Thousands of LRs can be calculated and plotted to determine the expected range for different hypotheses, quickly helping to inform whether a profile is suitable for comparison with a person of interest or suitable for entry onto a database for matching.

Since having gone live in casework, DBLR™ has proven to be extremely useful, with multiple

potential applications including performing unidentified human remains identification, saving analysts hours of manual kinship calculations. It is also effective in generating intelligence for cold cases when looking at profiles that span multiple items and may contain related or common DNA donors.

DBLR™ enables the Amelogenin locus to be included in LR calculations in all modules if it is present in the Allele Frequency file(s), a feature initially added to v1.4.

DBLR™ v1.5 also allows STRmix™ users to:
- Apply population stratification and utilize sequence-based data from STRmix™ NGS in the Kinship, Search Database, and Explore Deconvolution modules;
- Leverage probabilistic links within the Kinship module to probabilistically condition on the presence of a sample donor;
- Undertake direct comparison of one or many components of a forensic DNA mixture to a database of known individuals;
- Determine the genotypes of the most likely contributors to a profile;
- Combine multiple evidence profiles under the assumption that there is a common contributor within different samples;
- Build any pedigree imaginable and calculate LRs given different propositions; and
- Model linkage, mutation, and FST in the Kinship module.

STRmix™, DBLR™, and a third software package developed by the STRmix™ team, FaSTR™ DNA, complete the full workflow from analysis to interpretation and database matching. FaSTR™ DNA rapidly analyzes raw DNA data generated by genetic analyzers and standard profiling kits and assigns a number of contributors (NoC) estimate.

STRmix™ can be used to carry out interpretations on the analyzed data and DBLR™ can be used for further investigations. DBLR™ can also take inputs from STRmix™ NGS, an additional software package in the STRmix suite.

The effectiveness of these solutions, coupled with the highly successful track record STRmix™ has established in producing usable, interpretable, and legally admissible DNA evidence in more than 690,000 criminal cases, has led to their widespread adoption in forensic labs worldwide.

Currently, 91 federal, state, local, and private organizations in the U.S. regularly use STRmix™ for DNA analyses. Internationally, STRmix™ is now being used by 29 forensic laboratories, including labs in Canada, the United Kingdom, Europe, Asia, the Middle East, and the Caribbean, as well as all state and territory forensic labs in New Zealand and Australia.

For more information about STRmix products, visit www.strmix.com.

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