STRmix v2.10 Adds New Features to Groundbreaking Forensic Software

Enhanced DNA Interpretation, Dropout Modelling Among Latest Improvements

WASHINGTON, DC, USA, December 21, 2022 /EINPresswire.com/ -- Following extensive technical development and testing, STRmix™ version 2.10 – the latest iteration of the breakthrough software used by forensic analysts to resolve mixed DNA profiles previously considered too complex to interpret – has been launched.

> STRmix™ v2.10's further integration with FaSTR™ DNA enables forensic labs using both software packages to achieve greater speed and efficiency in the analysis and interpretation of DNA profiles."
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> *Dr. Meng-Han Lin, Senior Scientist, STRmix™ Team.*

Like its predecessors, the newest version of STRmix™ will enable forensic analysts to produce highly usable, interpretable, and admissible DNA results in a wide range of criminal cases, including violent crime, sexual assault, and cold cases.

STRmix™ v2.10 will also contain a number of new features, including the introduction of a Visualize Weights module to help analysts investigate DNA interpretation results and additional improvements to dropout modelling which will allow forensic labs using FaSTR™ DNA to set a low, or even no, analytical threshold.

FaSTR™ DNA, which was developed by the same team that created STRmix™, seamlessly integrates with STRmix™ (when in use) to rapidly analyze DNA profiles and assign a Number of Contributors (NoC) estimate.

"STRmix™ v2.10's further integration with FaSTR™ DNA enables forensic labs using both software packages to achieve even greater speed and efficiency in the analysis and interpretation of raw data generated by genetic analyzers and standard profiling kits," explains Dr. Meng-Han Lin, Senior Scientist, STRmix™ Team.

The new features implemented with in STRmix™ v2.10 were made primarily in response to recommendations made by the forensic laboratories currently using the software, allowing them to better address the on-the-job needs.

Like previous versions of STRmix™, v2.10 works by assessing how closely multitudes of proposed

profiles resemble or can explain an observed DNA mixture. Applying the same statistical methods routinely used in computational biology, physics, engineering, and weather prediction, the probability of the observed DNA evidence can be calculated by assuming the DNA originated from either a person of interest or an unknown donor. These probabilities are then presented as a likelihood ratio (LR), inferring the value of the findings and level of support for one proposition over the other.

Since its introduction in 2012, STRmix™ has been used to interpret DNA evidence in more than 380,000 cases worldwide, including over 210,000 cases in North America, 30,000 in Europe and the United Kingdom, and 135,000 in Australasia.

STRmix™ is currently being used in 101 forensic organizations around the world. These include 75 in the U.S. (including those operated by the FBI and the Federal Bureau of Alcohol, Tobacco, Firearms and Explosives), all nine state and territory forensic laboratories in New Zealand and Australia, and forensic labs in Europe, the United Kingdom, Asia, the Middle East, Canada, and the Caribbean.

In addition to STRmix™ v2.10 and FaSTR™ DNA, the STRmix™ team developed and previously launched DBLR™, an application that when used with STRmix™ allows forensic labs to undertake superfast database searches, visualize the value of DNA mixture evidence, and carry out mixture-to-mixture matches and extensive kinship analyses. Together, FaSTR™ DNA, STRmix™, and DBLR™ complete the full workflow from analysis to interpretation and database matching.

STRmix™ v2.10 has now been released to all qualifying users. For more information, visit http://www.strmix.com.

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