EINPRESSWIRE

New Version of Groundbreaking Forensic Software Released

STRmix™ v2.12 Improvements Make It Easier to Produce Usable, Interpretable DNA Results

WASHINGTON, DC, UNITED STATES, December 4, 2024 /EINPresswire.com/ -- The latest version of STRmix™ – groundbreaking software for resolving low-level, degraded, or mixed DNA samples from multiple contributors – will be released today.

> **STRmix™ v2.12™ will make it easier for labs to produce highly usable, interpretable, and legally admissible DNA results in criminal cases, including violent crime, sexual assault, and cold cases."**
>
> *Dr. Jo-Anne Bright*

Like its predecessors, STRmix™ v2.12 builds on previous versions of STRmix™, while adding several significant new features. These include support for peak label probabilities in varNOC calculations and inclusion of results collation tools for database searches and interpretations and likelihood ratios (LRs) in the Reporting module.

STRmix™ v2.12 also features:
• The ability to visualize the evidence input in a stylized plot and ignore loci from the graph if required;
• Extension to the Visualize Weights module to include the ability to visualize genotypes corresponding to person(s) of interest and evidence;
• Improvements to the varNOC LR assignment calculation when data is missing from a reference for consistency with varNOC implementation in DBLR™ v1.4.

"The new enhancements incorporated into STRmix™ v2.12 are in direct response to recommendations made by forensic labs to better address on-the-job needs they regularly encounter," explains STRmix team Senior Science Leader Dr. Jo-Anne Bright. "These changes will make it easier for labs to produce highly usable, interpretable, and legally admissible DNA results in a wide range of criminal cases, including violent crime, sexual assault, and cold cases."

The latest version of STRmix™ comes after a full year of technical development and testing.

Since its introduction in 2012, STRmix™ has been used to interpret DNA evidence in more than 690,000 cases worldwide. STRmix™ is now being used in 119 forensic laboratories worldwide, including 90 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 20 forensic labs in Europe, the United Kingdom, Asia, the Middle East,

Canada, and the Caribbean.

Unlike previous methods of DNA analysis, which depended entirely on the application of fixed stochastic thresholds and other biological parameters to manually analyze DNA samples, STRmix™ assesses how closely a multitude of potential DNA profiles resemble or can explain an observed DNA mixture.

Relying on proven methodologies routinely used in computational biology, physics, engineering, and weather prediction, STRmix™ calculates the probability of observed DNA evidence by assuming the DNA originated from either a person of interest or an unknown donor. These two probabilities are then presented as a LR, which infers the value of the findings and the level of support for one proposition over the other.

In addition to STRmix™ v2.12, the STRmix team has developed and previously launched three related software applications:
• DBLR™, an application which when used with STRmix™ allows forensic laboratories to undertake extensive kinship analysis, carry out rapid database searches, visualize the value of their DNA mixture evidence, and carry out mixture to mixture matches;
• FaSTR™ DNA, expert forensic software which seamlessly integrates with STRmix™ (when in use) to rapidly analyze raw DNA data generated by genetic analyzers and standard profiling kits and assigns a number of contributors (NoC) estimate; and
• STRmix™ NGS, fully continuous mixture interpretation and likelihood ratio generation software for profiles generated using Next Generation Sequencing (NGS).

In combination with STRmix™, FaSTR™ DNA and DBLR™ complete the full workflow from analysis to interpretation and database matching, while STRmix™ NGS broadens the range of profile types that can be interpreted.

Because the latest version of DBLR™ (v1.4) uses amelogenin in the mixture to mixture LR function, it was decided that unlike previous versions STRmix™ v2.12 would not include mixture to mixture matching. Labs currently using mixture to mixture matching with STRmix™ should contact the STRmix team directly about adopting DBLR™ to continue using this function.

For more information about STRmix™ v2.12, visit http://www.strmix.com. A preview video highlighting the changes in STRmix™ v2.12 is now live at https://www.strmix.com/news/sneak-preview-of-strmix-v2-12/.

Ray Weiss
Pugh & Tiller PR
+1 4103035019
email us here

This press release can be viewed online at: https://www.einpresswire.com/article/765968050

EIN Presswire's priority is source transparency. We do not allow opaque clients, and our editors try to be careful about weeding out false and misleading content. As a user, if you see something we have missed, please do bring it to our attention. Your help is welcome. EIN Presswire, Everyone's Internet News Presswire™, tries to define some of the boundaries that are reasonable in today's world. Please see our Editorial Guidelines for more information.