STRmix Team Launches STRmix™ NGS

New Expert Forensic Software Enables Users to Investigate Interpretation of Complex Next Generation Sequencing Mixtures

WASHINGTON, DC, USA, February 29, 2024 /EINPresswire.com/ -- The team that created STRmix™ – sophisticated forensic software used to resolve mixed DNA profiles previously thought to be too complex to interpret – is launching STRmix™ NGS (Next Generation Sequencing).

NGS, also known as MPS (Massively Parallel Sequencing), is an emergent DNA profiling technology offering ultra-high throughput, scalability, and speed. Used to determine the order of nucleotides in entire genomes or targeted regions of DNA, the technology has the potential to assist forensic laboratories in cases involving human identification, kinship, and ancestral origin at a faster pace and a cheaper cost.

While not currently available for casework, STRmix™ NGS "has the potential to be a game changing technology for laboratories familiar with STRmix™ that are investigating future implementation of emergent NGS/MPS technology," says Dr Jo-Anne Bright, Senior Science Leader at the New Zealand Institute of Environmental Science and Research (ESR). "Pairing NGS with STRmix™ provides the potential to unlock the value of complex mixtures for this emergent technology."

This marks the first application of the ground-breaking STRmix™ technology for NGS, which employs a fully continuous approach for interpretation of NGS-generated Short Tandem Repeat (STR) DNA profiles. This allows users to research the potential implementation and validation path of Probabilistic Genotyping (PG) alongside NGS chemistries and sequencing equipment.

Recognizing that forensic laboratories embarking on the implementation of NGS in casework have a need for a PG solution to interpret complex mixtures, this "Research and Validation" release of STRmix™ NGS can help forensic laboratories to understand future use of such evidence. This is an important first step for laboratories that are keen to adopt this technology in casework in the future.

The STRmix™ NGS workflow and user experience is grounded on the capillary electrophoresis-based STRmix™ technology, which has been extensively validated and used for casework interpretation at ESR, as well as at numerous laboratories in Australia, the United States, Canada,

Europe, Asia, and the United Kingdom.

Initially launched in August 2012, STRmix™ uses well-established statistical methods to build millions of conceptual DNA profiles. These profiles are then graded against the evidential sample, finding the combinations that best explain the DNA profile being analyzed. From there, it provides a range of Likelihood Ratio (LR) options for subsequent comparisons to reference profiles.

STRmix™ NGS has many features in common with standard STRmix™ technology, albeit applied to this emergent DNA profiling technology. These features include the ability to:

- Undertake quality checks for data;
- Model any type of stutter observed within STR profiling kits;
- Calculate multiple LRs from multiple reference inputs to a previously run deconvolution;
- Compare evidence samples with legacy length-based reference data in the LR;
- Batch multiple deconvolutions or other STRmix™ NGS functions (such as Interpretation, LR from Previous, and Database Search) in a queue, allowing the user to run multiple deconvolutions and calculate LRs sequentially;
- Include related individuals as alternate propositions in the LR;
- Carry out familial searches against a database, searching for close relatives of contributors to mixed DNA profiles; and
- Generate fully configurable (and if required, retrospective) reports.

After STRmix™ NGS is made available to selected STRmix™ users, there will be further functionality development and improvement planned as a result of a very active scientific research program.

For more information STRmix™ NGS, visit https://www.strmix.com.

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