37th Annual ISHI Symposium Will Feature Presentations by STRmix Scientists

Conference Will Focus on Profiling the Future of DNA Forensics

WASHINGTON, DC, UNITED STATES, September 30, 2026 /EINPresswire.com/ -- STRmix™ Co-Developer Jo Bright, STRmix team Training and Support Lead Cat McGovern, and Senior Scientists Meng-Han Lin and Richard Wivell will be among the featured speakers when the 37th International Symposium on Human Identification (ISHI) – the largest annual conference dedicated exclusively to forensic DNA innovation – takes place from October 26-29 at the Rhode Island Convention Center, Providence, RI.

This year's symposium, whose theme is "Profiling the Future of Forensics," will draw hundreds of global experts, lab directors, and law enforcement professionals for interactive workshops and presentations covering the latest advancements, methodologies, and breakthroughs in such core areas as probabilistic genotyping (PG), DNA mixture interpretation, next-generation sequencing, and forensic investigative genetic genealogy.

STRmix scientists will be featured in two key ISHI workshops:

• DNA Profile Analysis in a Validated Process for Efficiency and Interpretation will offer a fresh perspective on DNA analysis, focusing on enhanced efficiency and accuracy of the analysis process and PG integration. Co-chaired by Meng-Han Lin and supported by Cat McGovern, this session will cover such key topics as algorithmic variations across different analysis software, stutter modelling and its role in interpretation and number of contributors (NoC) determination, development of workflows, and internal implementation and validation. This workshop will be run in collaboration with Helena Wong of the Oakland Police Department and Megan O'Donnell from the New Hampshire State Police Forensic Laboratory. (October 25, 8:30 a.m.-5:00 p.m.)

• Bayes to Bench: Understanding Likelihood Ratios and Probabilistic Genotyping from Foundations to Legal Challenges will examine legal challenges at admissibility hearings, including the scope of internal validation, the assigned number of contributors, relatives, and the likelihood ratio (LR). Featuring presentations by Jo Bright and Richard Wivell, the workshop, chaired by Professor Mike Coble of the University of North Texas Health Science Center will build foundational understanding of Bayes Theorem and the LR, its use within forensic DNA interpretation, explanation in court, and common challenges to PG use. (October 26, 8:00 a.m.-4:00 p.m.)

In addition, Dr. Bright will deliver two presentations:

- A Paradigm Shift in Forensic DNA Analysis: Investigation into the Reduced Stutter Chemistry and its Implications for Profile Interpretation with Professor Coble will evaluate the performance of Reduced Stutter Polymerase (RSP) on ground-truth, single-source, and mixed DNA profiles, including an assessment of allele concordance and locus and allele-specific stutter rates. The presentation will also examine how low-stutter chemistry performs when assessing the NoC and the results of sensitivity and specificity testing of complex mixed DNA profiles using PG methods. (October 27, 10:30-10:50 a.m.)

- It's Ys: Probabilistic Genotyping of Y-STR Profiles will explore the development and performance of a PG method for interpretation of Y-STR profiles, including modelling of stutter, peak height variance and dropout, and treatment of multi-copy loci. The presentation will provide results of sensitivity and specificity studies for a range of mixtures of varying quality and quantity, and review the assigned LRs. (October 29, 9:56-10;16 a.m.)

Dr. Bright is a Senior Science Leader within the STRmix team at the New Zealand Institute for Public Health and Forensic Science Limited (PHF Science), where she has worked since 1999. The co-author of numerous papers and a regular speaker at major conferences around the world, Dr. Bright co-developed STRmix™, sophisticated forensic software capable of resolving mixed DNA profiles previously regarded as too complex to interpret.

Catherine McGovern is a Science Leader at PHF Science with over 30 years of experience in the forensic biology discipline. Her current role is as Team Leader of customer training and support services within the STRmix team.

Meng-Han Lin is a Senior Scientist at PHF Science and has been part of the STRmix team since 2016. He is primarily responsible for the science development, testing, and validation of FaSTR™ DNA analysis software, as well as providing training and scientific support services for FaSTR™ DNA software to forensic laboratories internationally. He is a molecular biologist by training.

Richard Wivell is a Senior Scientist within the STRmix team at PHF Science, where he has worked since 2008. Before moving to New Zealand, he was a forensic scientist for the Metropolitan Police Service and the Forensic Science Service in the UK.

PHF Science is a New Zealand government research organization, of which STRmix Limited is a wholly owned subsidiary, founded to better serve international users of STRmix™ software.

Since its introduction in 2012, STRmix™ has proven to be a highly effective tool in producing usable, interpretable, and admissible DNA results in more than 700,000 criminal cases worldwide. It has been particularly effective in helping to resolve violent crime and sexual assault cases, as well as cold cases in which evidence was originally dismissed as inconclusive.

The worldwide success of STRmix™ has led the team behind its development to create and

regularly update three related software applications:
• FaSTR™ DNA, expert forensic software which seamlessly integrates with STRmix™ (when in use) to rapidly analyze raw DNA data and assign a NoC estimate;
• DBLR™, an application which when used with STRmix™ allows forensic laboratories to undertake extensive kinship analysis, carry out rapid database searches and mixture-to-mixture matches, and visualize the value of their DNA mixture evidence;
• STRmix™ NGS, fully continuous mixture interpretation and LR generation software for profiles generated using Next Generation Sequencing.

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. For more information about STRmix™, visit http://www.strmix.com.

STRmix – A global leader in forensic DNA interpretation, trusted by more than 120 forensic laboratories worldwide.

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

This press release can be viewed online at: https://www.einpresswire.com/article/946103124

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.
© 1995-2026 Newsmatics Inc. All Right Reserved.