



STRmix™

RESOLVE MORE DNA MIXTURES.

www.STRmix.com

STRmix™ is expert forensic software that can resolve previously unresolvable mixed DNA profiles. Developed by global leaders in the field, it uses a fully continuous approach for DNA profile interpretation, resolving complex DNA mixtures worldwide.

FAST

STRmix™ interprets complex DNA results in minutes.

ACCESSIBLE

STRmix™ software runs on a user's PC, without the need for high-speed computing.

ENABLING

STRmix™ can easily be understood and explained in court by DNA analysts. STRmix™ is a breakthrough for forensic

analysts as it can assist investigations using DNA evidence that was previously considered too complex to interpret. The software has been developed by New Zealand Crown research institute ESR, with Forensic Science South Australia (FSSA).

WITH STRmix™ YOU WILL BE ABLE TO:

- interpret DNA results faster
- combine DNA profiles from different kits in the same interpretation
- compare profiles against a person of interest and calculate a likelihood ratio
- resolve previously unresolvable, complex DNA mixtures with no restriction on the number of contributors
- use more of the information in a DNA profile, and model any type of stutter
- search complex, mixed DNA profiles against a database.

RESOLVE MIXED DNA PROFILES without reference to known contributors.

ENTER contributor number range when performing a deconvolution.

MODEL any type of stutter observed within your STR profiling kit.

COMPARE REFERENCE DNA PROFILES to single source and mixed DNA profiles and provide a statistical weighting.

INTERPRET DNA PROFILING DATA generated by any autosomal STR profiling kit.

INTERPRET DNA PROFILES from a range of starting template DNA concentrations.

USE LABORATORY-SPECIFIC SETTINGS to perform calculations suited exactly to that laboratory's results.

SEARCH A DECONVOLUTED DNA PROFILE directly against a database without the need to interpret a single source component.

CALCULATE multiple LRs from multiple reference inputs to a previously run deconvolution (LR Batch tool).

PERFORM a large number of in-silico specificity tests on a profile-by-profile basis (Hd True Tester tool).

BATCH multiple deconvolutions or other STRmix™ functions (such as interpretation, LR from Previous, and Database Search) in a queue, allowing the user to run them sequentially.

COMBINE multiple amplifications of the same DNA extract - even when generated with different multiplexes - into one interpretation.

ACCOMMODATE DATA generated by protocols demonstrating increased stochastic variation and nonzero allelic drop-in rates, for example elevated PCR cycle number and enhanced CE injection methods.

INCLUDE RELATED INDIVIDUALS as alternate propositions in the likelihood ratio.

CARRY OUT FAMILIAL SEARCHES against a database, searching for close relatives of contributors to mixed DNA profiles.

GENERATE fully configurable (and if required, retrospective) reports including a CODIS report.

PASSWORD PROTECT default settings and kit settings.

HOW DOES STRmix™ WORK?

STRmix™ combines biological modelling and mathematical processes to interpret a wide range of complex DNA profiles. Using well-established statistical methods, the software builds millions of conceptual DNA profiles. It grades them against the evidential sample, finding the combinations that best explain the profile. A range of Likelihood Ratio options are provided for subsequent comparisons to reference profiles. Using a Markov Chain Monte Carlo engine, STRmix™ models any types of allelic and stutter peak heights as well as drop-in and drop out behaviour. It does this rapidly, accessing evidential information previously out of reach with traditional methods.

STRmix™ is supported by comprehensive empirical studies with its mathematics readily accessible to DNA analysts, so results are easily explained in court.

VALIDATION

STRmix™ has been extensively validated and used for casework interpretation at ESR and multiple Australian, US, and UK laboratories (first implemented in August 2012). STRmix™ has achieved Certificate of Networkiness (CoN) status on the United States Army Network.

SPECIFICATIONS

STRmix™ is designed to run on an individual DNA analyst's PC, (either standalone or in a networked environment). For guidance on hardware and software specifications please go to www.strmix.com/#how

PUBLISHED DATA

The following papers describing the biological model, mathematics, performance and validation of STRmix™ have been published:

- [1] D.A. Taylor, J.-A. Bright, J. S. Buckleton, The interpretation of single source and mixed DNA profiles, *Forensic Science International: Genetics*. 7(5) (2013) 516-528.
- [2] J.-A. Bright, D.A. Taylor, J. M. Curran, J. S. Buckleton, Developing allelic and stutter peak height models for a continuous method of DNA interpretation, *Forensic Science International: Genetics*. 7(2) (2013) 296-304.
- [3] J.-A. Bright, D.A. Taylor, J. Curran, J. Buckleton, Degradation of forensic DNA profiles, *Australian Journal of Forensic Sciences*. 45(4) (2013) 445-449.
- [4] J.-A. Bright, D.A. Taylor, J. M. Curran, J. S. Buckleton, Searching mixed DNA profiles directly against profile databases *Forensic Science International: Genetics*. 9 (2014) 102-110.
- [5] D.A. Taylor. Using continuous DNA interpretation methods to revisit likelihood ratio behaviour. *Forensic Science International: Genetics*, 2014. 11: 144-153.
- [6] J.-A. Bright, J.M. Curran and J.S. Buckleton, The effect of the uncertainty in the number of contributors to mixed DNA profiles on profile interpretation. *Forensic Science International: Genetics*, 2014. 12: 208-214.
- [7] J.-A. Bright, I.W. Evett, D.A. Taylor, J.M. Curran and J.S. Buckleton, A series of recommended tests when validating probabilistic DNA profile interpretation software. *Forensic Science International: Genetics*, 2015. 14: 125-131.
- [8] J.-A. Bright, K.E. Stevenson, J.M. Curran and J.S. Buckleton, The variability in likelihood ratios due to different mechanisms. *Forensic Science International: Genetics*, 2015. 14:187-190.
- [9] D.A. Taylor, J.-A. Bright and J.S. Buckleton, Considering relatives when assessing the evidential strength of mixed DNA profiles. *Forensic Science International: Genetics*, 2014. 13: 259-263.
- [10] T.W. Bille, S.M. Weitz, M.D. Coble, J.S. Buckleton and J.-A. Bright, Comparison of the performance of different models for the interpretation of low level mixed DNA profiles. *ELECTROPHORESIS*, 2014. 35:3125-33.
- [11] D.A. Taylor, J.-A. Bright and J.S. Buckleton, The 'factor of two' issue in mixed DNA profiles. *Journal of Theoretical Biology*, 2014. 363: p. 300-306.
- [12] D.A. Taylor and J.S. Buckleton, Do low template DNA profiles have useful quantitative data? *Forensic Science International: Genetics*, 2015. 16:13-6.
- [13] D.A. Taylor, J.S. Buckleton and I. Evett, Testing likelihood ratios produced from complex DNA profiles. *Forensic Science International: Genetics*, 2015. 16:165-171.
- [14] S.J. Cooper, C.E. McGovern, J.-A. Bright, D. A. Taylor and J.S. Buckleton, Investigating a common approach to DNA profile interpretation using probabilistic software. *Forensic Science International: Genetics*, 2015. 16:121-131.
- [15] J.-A. Bright, D.A. Taylor, C.E. McGovern, S.J. Cooper, L.J. Russell, D. Abarno, J.S. Buckleton, Developmental validation of STRmix™, expert software for the interpretation of forensic DNA profiles. *Forensic Science International: Genetics*, 2016. 23:226-239.
- [16] D.A. Taylor, J.-A. Bright, C.E. McGovern, C. Hefford, T. Kalafut, J.S. Buckleton, Validating multiplexes for use in conjunction with modern interpretation strategies. *Forensic Science International: Genetics*, 2016. 20:6-19.
- [17] D.A. Taylor, J.S. Buckleton, J.-A. Bright, Factors affecting peak height variability for short tandem repeat data. *Forensic Science International: Genetics*, 2016. 21:126-33.
- [18] T.R. Moretti, R.S. Just, S.C. Kehl, L.E. Willis, J.S. Buckleton, J.-A. Bright, D.A. Taylor, Internal validation of STRmix™ for the interpretation of single source and mixed DNA profiles. *Forensic Science International: Genetics*, 2017. 29:126-144.
- [19] D.A. Taylor, J.-A. Bright, H. Kelly, M.-H. Lin, J.S. Buckleton. A fully continuous system of DNA profile evidence evaluation that can utilise STR profile data produced under different conditions within a single analysis. *Forensic Science International: Genetics*, 2017. 31:149-154.
- [20] D.A. Taylor, J.S. Buckleton, J.-A. Bright, Does the use of probabilistic genotyping change the way we should view sub-threshold data? *Australian Journal of Forensic Sciences*, 2017. 49(1):78-92.
- [21] J.-A. Bright, et al., Internal validation of STRmix; A multi laboratory response to PCAST. *Forensic Science International: Genetics*, 2018. 34:11-24.

CONTACT

FOR MORE INFORMATION ABOUT STRmix™ OR TO REQUEST A QUOTE:

Björn Sutherland
STRmix Limited

Private Bag 50348, Porirua 5240, New Zealand
E: bjorn.sutherland@esr.cri.nz
T: +64 4 914 0681
M: +64 27 612 7378

NORTH/SOUTH/CENTRAL AMERICA DISTRIBUTOR:

Vic Meles
NicheVision Inc.

526 So Main St Ste 714-G, Akron OH 44311, USA
E: vic@nichevision.com
T: +1-866-840-3758 (US Only) or
T: +1-330-252-2711 (International)

INSTITUTE OF ENVIRONMENTAL SCIENCE AND RESEARCH (ESR)

ESR uses the power of science to solve complex problems with the potential to affect the lives of all New Zealanders. It is the sole source provider of forensic services to the New Zealand Police while its comprehensive knowledge of the presence and interpretation of DNA is utilised across the country and around the world.

FORENSIC SCIENCE SOUTH AUSTRALIA (FSSA)

FSSA provides independent, objective expert scientific opinions and evidence to the justice system and community of South Australia undertaking a comprehensive range of forensic case work in pathology, biology, toxicology and chemistry.

STRmix LIMITED

STRmix Limited is a newly formed subsidiary of ESR, and was founded to better serve international customers of STRmix™.