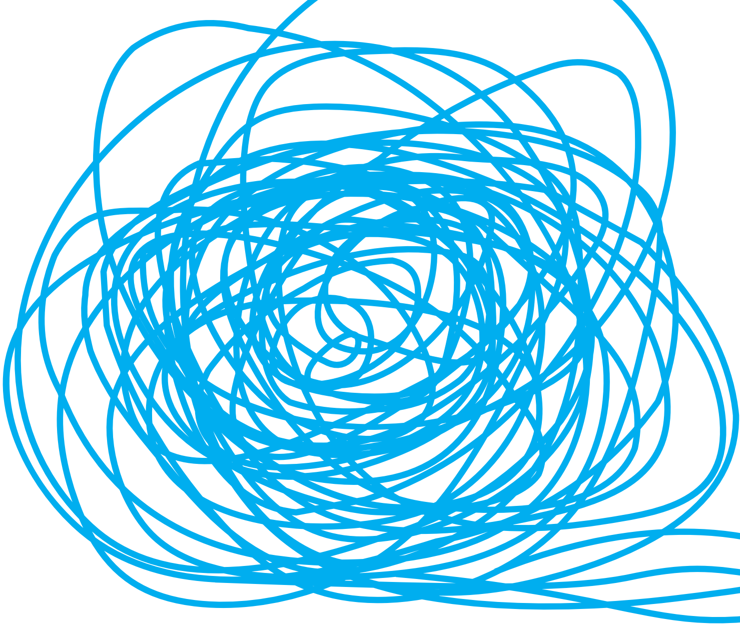

STRmix™

RESOLVE MORE DNA MIXTURES.

PRIME MINISTER'S SCIENCE PRIZE
WINNER
2018

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 (LR)
- 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.

WHAT CAN STRmix™ DO?

RESOLVE MIXED DNA PROFILES without reference to known contributors.

ENTER contributor number range when performing a deconvolution.

ASSIGN an LR varying the number of contributors under the prosecution and defence propositions (***New in STRmix™ v2.7***).

UNDERTAKE quality checks for data (***New in STRmix™ v2.7***).

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.

COMPARE mixtures to other mixtures to find common contributors (***New in STRmix™ v2.7***).

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 multiple deconvolutions and calculate LRs 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 LR.

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, Middle East, Europe and UK laboratories (first implemented in August 2012). STRmix™ has achieved Certificate of Networthiness (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 and J.S. Buckleton, Do low template DNA profiles have useful quantitative data? Forensic Science International: Genetics, 2015. 16:13-6.

[12] 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.

[13] 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.

[14] 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.

[15] 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.

[16] 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.

[17] 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.

[18] 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.

[19] 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.

[20] J.-A. Bright, et al., Internal validation of STRmix; A multi laboratory response to PCAST. Forensic Science International: Genetics, 2018. 34:11-24.

[21] L. Russell, S.J. Cooper, R. Wivell, Z.B. Kerr, D. Taylor, J.S. Buckleton, J.-A.Bright, A guide to results and diagnostics within a STRmix™ report. Wiley Interdisciplinary Reviews: Forensic Science.

[22] J.S. Buckleton, J.-A. Bright, S. Gittelson, T. R. Moretti, A.J. Onorato, F.R. Bieber, B. Budowle, D.A. Taylor. The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity. Journal of the Forensic Sciences, 2018. 64(2):393-405.

[23] J.-A. Bright, K. Cheng, Z. Kerr, C. McGovern, J.S. Buckleton. STRmix™ collaborative exercise on DNA mixture interpretation, Forensic Science International: Genetics. 2019. 40: 1-8.

[24] T. Bille, S. Weitz, J.S. Buckleton, J.-A. Bright. Interpreting a major component from a mixed DNA profile with an unknown number of minor contributors. Forensic Science International: Genetics. 2019. 40:150-159.

[25] J.A. Bright, D. Taylor, Z. Kerr, J.S. Buckleton, M. Kruijver. The efficacy of DNA mixture to mixture matching. Forensic Science International: Genetics. 2019. 41:64-71.

CONTACT

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

NORTH/SOUTH/CENTRAL AMERICA:
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)

CHINA:
Resonant Limited
421 N Milpas St,
Santa Barbara, CA 93103
E: info@resonantltd.com
T: +1-805-962-3080

UK/EUROPE/ROW:
Adam McCarthy
E: adam.mccarthy@esr.cri.nz
T: +44(0)7590 405 501

INSTITUTE OF ENVIRONMENTAL SCIENCE AND RESEARCH (ESR)

ESR is New Zealand's Crown Research Institute that specialises in science relating to people and communities. It's our science that helps safeguard people's health, protect food-based economies, improve the safety of freshwater and groundwater resources, and contributes expert forensic science to justice systems.

FORENSIC SCIENCE SOUTH AUSTRALIA (FSSA)

FSSA provides services to some of South Australia's largest government departments and undertakes award-winning research in forensic science.

STRMIX LIMITED STRmix Limited is a subsidiary of ESR, founded to better serve international users of STRmix™.