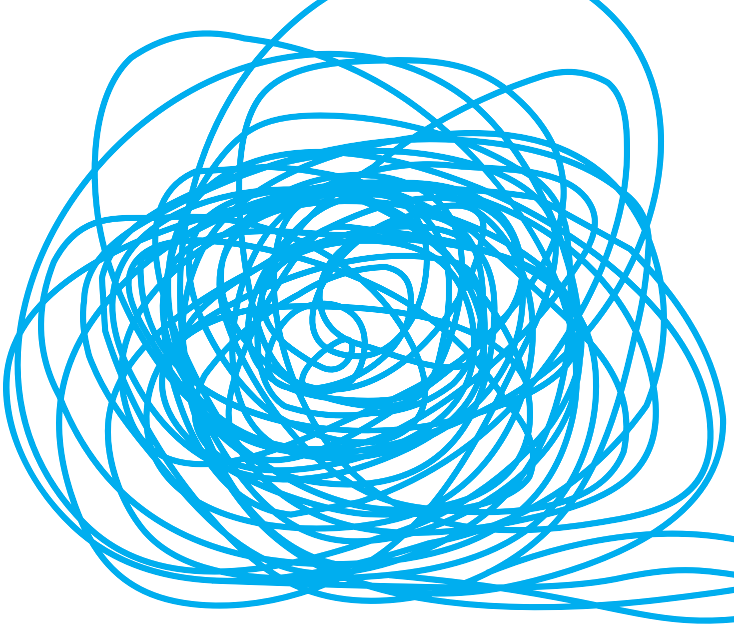


STRmix.™

RESOLVE MORE DNA MIXTURES.

STRmix™ EMPOWERING FORENSIC SCIENCE • Since 2012 •

Telarc. Registered™ Quality ISO 9001

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.

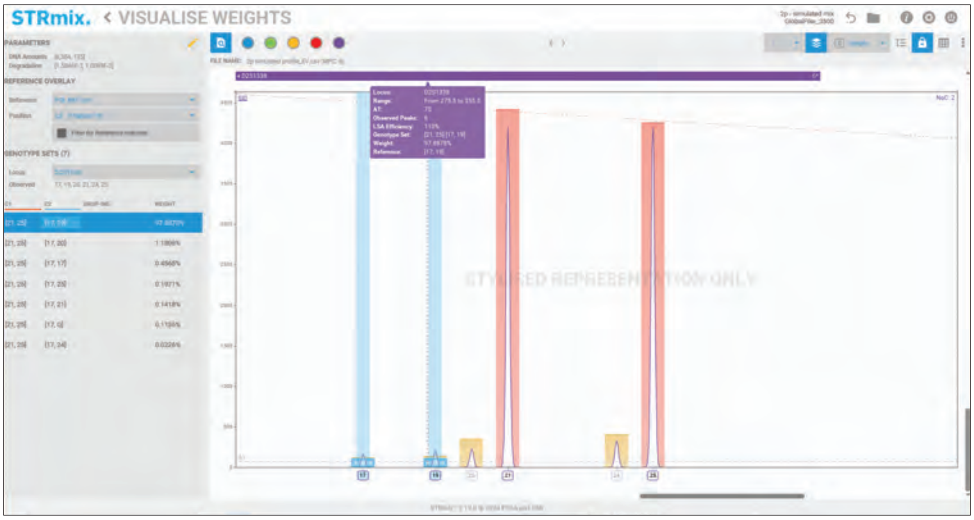
ENABLING

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 Government owned research organisation PHF Science (formerly ESR) with Forensic Science SA (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.



Left: The Visualise Weights module of STRmix™ showing the fit of the person of interest (blue bars) given the interpretation.

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.

UNDERTAKE quality checks for data.

SET the number of major contributors to a mixed DNA profile you are interested in and obtain an *LR* only for these.

MODEL any type of stutter observed within your STR profiling kit, now including improved dropout modelling allowing analysis of DNA profiles with a low, or even no analytical threshold.

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, now including Amelogenin in the interpretation.

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.

SET UP multiple report templates and generate more than one report at the end of each calculation (***new in STRmix™ 2.13***).

REVIEW the deconvolution and explore the accepted genotypes, their weights, and how a person of interest aligns.

VISUALISE a representation of the evidence input and ignore any peak during setup (***new in STRmix™ 2.13***).

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

COLLATE your deconvolution and likelihood ratio data using the in built tools.

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 *LR*s sequentially.

INSTANTLY set up interpretations (including replicate inputs, ***new in STRmix™ 2.13***) with flexible likelihood ratio propositions for multiple profiles using Batch Maker.

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.

OPTIONALLY utilise peak labelling probabilities in STRmix™ deconvolutions (an advanced feature for FaSTR™ DNA users).

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 sophisticated biological modelling and standard 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 PHF Science and multiple Australian, US, European, Canadian, Asian and UK laboratories (first implemented in August 2012). STRmix™ has achieved Certificate of Networthiness (CoN) status on the United States Army Network.

CERTIFICATION

The STRmix team's quality management system is certified to ISO 9001:2015.

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 http://www.strmix.com/strmix/specifications/

SELECTED PUBLISHED DATA

The following selection of papers describing the biological model, mathematics, performance and validation of STRmix™ have been published (for the full list please visit https://www.strmix.com/strmix/published-data/):

[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] D.A. Taylor. Using continuous DNA interpretation methods to revisit likelihood ratio behaviour. Forensic Science International: Genetics, 2014. 11: 144-153.

[4] 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.

[5] 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.

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

[7] 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, https://doi.org/10.1002/wfs2.1354

[8] 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.

[9] H. Kelly, J.-A. Bright, M.D. Coble, J.S. Buckleton. A description of the likelihood ratios in the probabilistic genotyping software STRmix™. Wiley Interdisciplinary Reviews: Forensic Science, https://doi.org/10.1002/wfs2.1377

[10] J. Bright, J. Buckleton, D. Taylor. Probabilistic interpretation of the Amelogenin locus. Forensic Science International: Genetics. 2021;52:102462

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

NEW ZEALAND INSTITUTE FOR PUBLIC HEALTH AND FORENSIC SCIENCE LIMITED (PHF SCIENCE)

PHF Science is a New Zealand Government owned research organisation that plays a critical national role in public health and forensics, and is a key contributor to environment and biosecurity outcomes.

FORENSIC SCIENCE SA (FSSA)

FSSA provides independent, expert scientific evidence, opinion and information to the justice system and carries out award-winning research in forensic science.