Research and Validation version release
NOT FOR CASEWORK USE

STRmix™ NGS
RESOLVE MORE DNA MIXTURES.

www.STRmix.com/NGS

STRmix™ NGS Research and Validation is expert forensic software for laboratories familiar with STRmix™ that are investigating the future implementation of emergent Next Generation Sequencing (NGS) / Massively Parallel Sequencing (MPS) technology.

Developed by global leaders in the field, this first application of the ground-breaking STRmix™ technology to NGS uses a fully continuous approach for interpretation of NGS-generated Short Tandem Repeat (STR) DNA profiles. Not currently for casework use, it allows users to research the potential implementation and validation path of Probabilistic Genotyping alongside NGS chemistries and sequencing equipment.

FAST
STRmix™ NGS interprets complex STR DNA results in minutes.

ACCESSIBLE
STRmix™ NGS can be run on a user's PC, without the need for high-speed computing.

ENABLING
STRmix™ NGS can easily be understood by DNA analysts.

STRmix™ NGS is a breakthrough for forensic laboratories embarking on the implementation of NGS as it can help laboratories plan for the future use of NGS DNA mixture evidence in casework.

The software has been developed by New Zealand Crown Research Institute ESR, with Forensic Science SA (FSSA).

WITH STRmix™ NGS YOU WILL BE ABLE TO:
- investigate the interpretation of complex mixed STR DNA results generated with NGS technology
- compare profiles against a person of interest and calculate a likelihood ratio (*LR*)
- resolve complex NGS STR DNA mixtures
- use more of the information in an NGS DNA profile, and model any type of stutter
- search complex, mixed DNA profiles against a database.

WHAT CAN STRmix™ NGS DO?

INTERPRET DNA PROFILING DATA generated at STR profiling loci.

RESOLVE MIXED DNA PROFILES without reference to known contributors.

UNDERTAKE quality checks for data.

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 PROFILES from a range of starting template DNA concentrations.

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

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

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

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 *LR*s sequentially.

CONSIDER RELATED INDIVIDUALS as alternate contributors 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.

PASSWORD PROTECT default settings and kit settings.

STRmix™ EMPOWERING FORENSIC SCIENCE 10 YEARS Since 2012

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HOW DOES STRMIX™ NGS WORK?

STRmix™ NGS combines sophisticated biological modelling and standard mathematical processes to interpret a wide range of complex NGS STR 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™ NGS models allelic and stutter sequences as well as drop-in and dropout behaviour.

VALIDATION

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 and multiple Australian, US, Canadian, European, Asian, and UK laboratories (first implemented in August 2012).

CERTIFICATION

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

SPECIFICATIONS

STRmix™ NGS 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 https://www.strmix.com/ngs/specifications/

SELECTED PUBLISHED DATA

The following selection of papers describing the biological model and mathematics of STRmix™ NGS have been published (for updates please also visit https://www.strmix.com/ngs/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] K. Cheng, J. Skillman, S. Hickey, R. Just, L. Moreno, J.-A. Bright, H. Kelly, M.-H. Lin, J.M. Curran, J.S. Buckleton. Variability and additivity of read counts for aSTRs in NGS DNA profiles. Forensic Science International: Genetics. 48 (2020) 102351.

[4] K. Cheng, M.-H. Lin, L. Moreno, J. Skillman, S. Hickey, D. Cuenca, W.R. Hudlow, R. Just, J.-A. Bright, J.S. Buckleton, J.M. Curran. Modeling allelic analyte signals for aSTRs in NGS DNA profiles. Journal of Forensic Sciences. 66(4) (2021) 1234-1245.

[5] 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.

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

[7] 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.

[8] 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.

[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] 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.

[11] K. Cheng, J.-A. Bright, H. Kelly, Y.Y. Liu, M.H. Lin, M. Kruijver, D.A. Taylor, J.S. Buckleton, Developmental validation of STRmix™ NGS, a probabilistic genotyping tool for the interpretation of autosomal STRs from forensic profiles generated using NGS. Forensic Science International: Genetics 62 (2023) 102804.

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