

FaSTR™ DNA is expert forensic DNA analysis software that rapidly analyses DNA profiles and estimates a Number of Contributors, ensuring consistency and efficiency in DNA analysis. Developed by the makers of the highly successful STRmix™, it simplifies the analysis of DNA profiles generated by capillary electrophoresis and multiplex profiling kits.

FaSTR™ DNA is designed by scientists for scientists, combining a sophisticated and user-friendly graphical interface with easily understandable, transparent and laboratory customisable rules for DNA profile analysis.

INTUITIVE

FaSTR™ DNA's interface helps streamline the otherwise time-consuming workflow of calling alleles.

INTELLIGENT

FaSTR™ DNA incorporates optional artificial neural networks (ANN) for the independent classification of peaks detected [1].

INTEGRATED

FaSTR™ DNA's in-built Number of Contributors (NoC) estimator allows seamless integration with STRmix™ to make the analysis and interpretation process even easier [2].

[1] D. Taylor, A. Harrison, D. Powers, Artificial neural network system to identify alleles in reference electropherograms. *FSI Genetics* 30 (2017) 114-126.

[2] M. Kruijver, H. Kelly, K. Cheng, M.-H. Lin, J. Morawitz, L. Russell, J. Buckleton, J.-A. Bright, Estimating the number of contributors to a DNA profile using decision trees, *Forensic Science International: Genetics* 50 (2021) 102407.

[3] M.-H. Lin, S.-I. Lee, X. Zhang, L. Russell, H. Kelly, K. Cheng, S. Cooper, R. Wivell, Z. Kerr, J. Morawitz, J.-A. Bright, Developmental validation of FaSTR™ DNA: Software for the analysis of forensic DNA profiles, *Forensic Science International: Reports* 3 (2021) 100217.

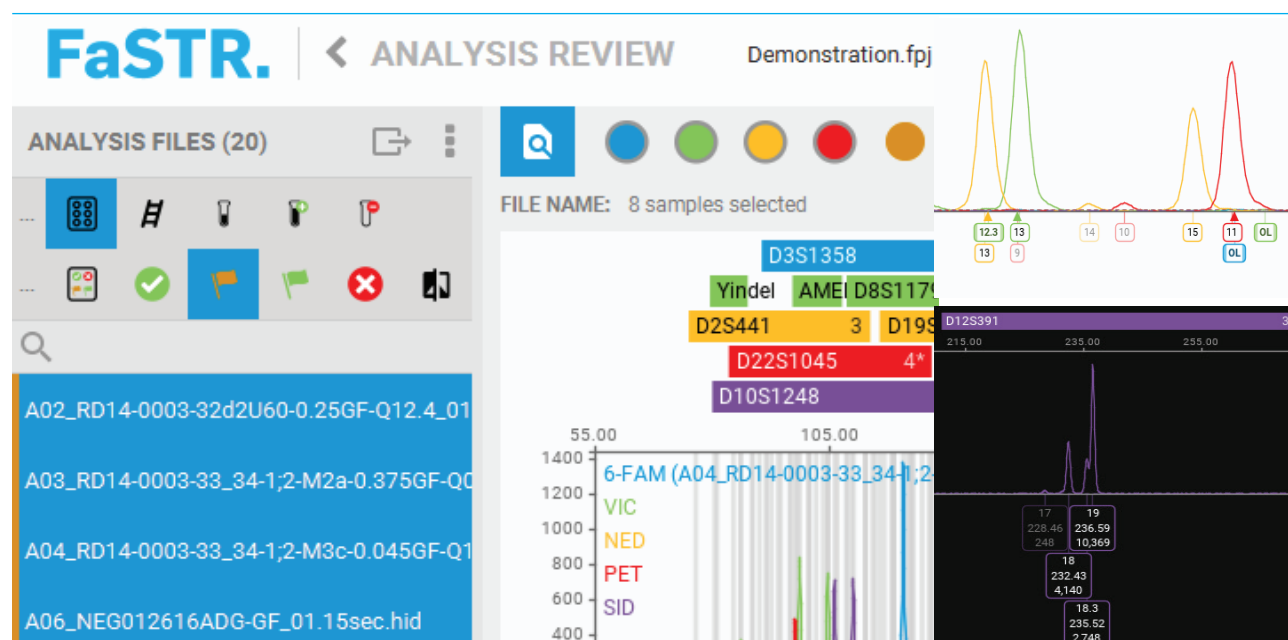
RAPIDLY ANALYSE DNA PROFILES

www.STRmix.com/FaSTR

The software has been developed by the New Zealand Institute for Public Health and Forensic Science (PHF Science), with Forensic Science SA (FSSA) and supported by a published developmental validation study [3].

WITH FaSTR™ DNA YOU WILL BE ABLE TO:

- analyse raw DNA results more rapidly
- fully configure settings, including setting known kit artefacts
- optionally estimate the Number of Contributors to a profile (for both autosomal and Y-STR profiles)
- seamlessly integrate with STRmix™ (when in use) for even greater speed and efficiency
- easily generate informative electropherogram (EPG) reports
- customise export and report settings
- carry out quality checks including control concordance testing, and checks for presence of quality markers and primer flare
- perform sample to sample and sample to database comparison checks
- group samples as replicates for interpretation in STRmix™ and replicate sample comparison checks
- review two separately analysed projects side by side and resolve conflicts
- create a sub-project of analysed data for better case management.



ABOUT FASTR™ DNA

FaSTR™ DNA is expert forensic DNA analysis software that allows DNA analysts to simplify the analysis of DNA profiles generated by capillary electrophoresis instruments and multiplex profiling kits.

FaSTR™ DNA enables forensic laboratories to:

- expedite the otherwise time-consuming process of calling alleles
- ensure consistency in DNA analysis and NoC estimation, which is critical to meeting quality assurance criteria.

FaSTR™ DNA applies a set of fully configurable rules to analyse many DNA profiles automatically. However, DNA analysis is complex, and the rules alone cannot resolve all profiles. At times, the DNA analyst must intervene. FaSTR™ DNA signals when this human intervention (expert judgment) is required. These rules can also be configured to require fully manual data analysis.

As forensic provider to New Zealand Police and custodian of New Zealand's National DNA Database, PHF Science understands the need for speed, accuracy, and simplicity. In developing FaSTR™ DNA, particular attention has been paid to simplifying the procedure. Reliable results can now be gained with minimal effort.

FaSTR™ DNA can analyse profiles generated using the most commonly used instruments and multiplex kits. The software is configurable with easy addition of new kits, dye colours, and internal size standards.

FaSTR™ DNA optionally estimates the Number of Contributors to a profile using an easily replicable decision tree process for autosomal STR profiles, and a heuristics-based estimation for Y-STR profiles. Utilising all information within the profile, FaSTR™ DNA can be coupled with STRmix™ (www.strmix.com/strmix) for seamless interpretation of complex mixed DNA profiles.

CONFIGURATION PARAMETERS

The analysis settings can be general or specific to each profiling kit type and locus. FaSTR™ DNA contains easily customisable default kits and methods. You can also create (and save) customised sets of parameters appropriate to analysing different types of DNA samples (e.g., known reference and crime-scene samples).

SPECIFICATIONS

For guidance on hardware and/or software specifications please go to www.strmix.com/fastr/specifications

CERTIFICATION

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

HOW DOES FASTR™ DNA WORK?

DNA analysis is a process of identifying alleles. The alleles appear as peaks in an electropherogram (EPG) and are identified from their locations within the EPG. The locations are determined using internal size standards and allelic 'ladders'.

FaSTR™ DNA contains the size standard and allelic ladder data for commonly available profiling kits. Additional kits and size standards can easily be added by importing panel, bin, and size standard information, or by manual entry.

Based on an adaptation of the methods implemented in OSIRIS^[4], FaSTR™ DNA applies a set of fully configurable rules to identify and label alleles and remove artefacts within the EPGs of samples.

THE ANALYSIS PROCESS

EPGs are produced by capillary electrophoresis instruments in the form of .fsa, .hid, or .promega data files. FaSTR™ DNA analyses EPG data by:

1. Smoothing and dynamic baselining of the EPG data
2. Detection and assignment of size standard peaks for the accurate sizing of peaks in the allelic ladder and sample
3. Size alignment of peaks detected in the allelic ladder with peaks detected in the sample to apply allele calls
4. Optionally applying a set of analysis rules to distinguish artefactual from allelic peaks
5. Optionally carrying out NoC estimation^[2]
6. Optionally carrying out sample to sample or sample to database comparison checks
7. Carrying out full concordance testing on positive and negative controls, including quality marker checks
8. Exporting the results in various configurable formats
9. Carrying out a project review to compare two analysed projects and resolve conflicts to create a final reviewed project.

OUTPUTS

FaSTR™ DNA displays the results of its analysis (the 'DNA profile'), as a labelled EPG and as a table of locus and peak designations. With FaSTR™ DNA you can:

- Easily print EPGs and include snapshots of areas of interest
- Easily print a report of changes made to peaks during analysis
- Export analysed data to STRmix™, the FaSTR™ DNA CODIS tool, or a genotype table
- Save the analysis as a 'project' (.fpj) for future reference.

CONTACT

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

PHF Science (formerly ESR) is a New Zealand Government-owned research organisation delivering world-class research, knowledge and laboratory services. Our science powers solutions to complex challenges, protecting communities and supporting New Zealand to prosper and grow.

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.

STRmix Limited is a subsidiary of PHF Science, founded to better serve international users of STRmix group software.

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^[4] R.M. Goor, L. Forman Neall, D. Hoffman, S.T. Sherry, *Mathematical approach to analysis of multiplex DNA profiles*, Bull Math Biol 73(8) (2011) 1909-1931