STRmix™ Basics for DCI Crime Lab Stakeholders

Iowa DCI Crime Lab
DNA Section
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What is STRmix™?

- A commercially available software created by the Institute of Environmental Science and Research (ESR) in New Zealand
  - Fully continuous **probabilistic genotyping** (PG) software which combines biological modeling with mathematical processes in order to (1) interpret and deconvolute DNA profiles and (2) compare known reference samples to forensic evidence samples and provide statistical weight in the form of a likelihood ratio (LR)
  - https://www.strmix.com/strmix

What is probabilistic genotyping (PG)?

- The use of biological modeling, statistical theory, computer algorithms, and probability distributions to calculate likelihood ratios and/or infer genotypes for the DNA typing results of forensic samples
  - STRmix™ is one software that utilizes PG
  - Other PG software exist (True Allele®, EuroForMix, etc.), however the Iowa DCI Crime Lab validated and is using STRmix™ v2.7

Why change?

- STRmix™ allows Criminalists to analyze, interpret, and investigate DNA profiles more efficiently and effectively
- STRmix™ allows for interpretation of some DNA profiles previously considered too weak or too complex to interpret
- The Iowa DCI Crime Lab is the 92nd lab in the US to implement STRmix™

STRmix™ Introductory Video

Below is a link to a ~2-minute video from the STRmix™ Developers (ESR) which gives a brief introduction to STRmix™

https://vimeo.com/173566540/0af0b13406?&login=true#_=_

How does STRmix™ work?

- DNA Criminalist reviews forensic evidence DNA profile to determine the number of contributors and if the profile is interpretable
- STRmix™ is utilized for the DNA profile interpretation and the comparison of known reference samples (i.e. known buccal swabs or known bloodstain cards)
  - STRmix™ utilizes mathematical and biological modeling to determine genotype combinations for contributor(s) to a forensic evidence profile
  - If a known reference profile can be included as a contributor(s) to the forensic evidence profile, STRmix™ then calculates a statistic called a likelihood ratio.
    - Statistics will not be calculated for individuals that are assumed to be present in DNA mixture
      - Example: body swab donor
- DNA Criminalist reviews STRmix™ outputs to ensure the deconvolution meets their scientific expectations

DNA Statistics

- Gives weight to the evidence (i.e., strength to the association(s))
- Required for legal system & is useful for law enforcement, attorneys, judges, and juries
- Three qualitative categories where DNA associations can fall:
  1. <u>Inclusion</u>: an individual is included as a contributor to a profile
  2. <u>Exclusion</u>: an individual is excluded as a contributor to a profile
  3. <u>Inconclusive</u>: not enough information to include or exclude an individual as a contributor to a profile
- Without giving a statistic, <u>all</u> inclusions would have the <u>same</u> weight regardless of the strength of the association.

Comparison of DNA Statistics

Random Match Probability (RMP)

- Estimates of the rarity of a profile in a population

- Can be applied to:
  - Single source profiles
  - Partial profiles
  - Mixtures

Likelihood Ratio (LR)

- Comparing the probability of observing a profile under two alternate hypotheses
  - Example: This DNA profile originated from PERSON 1 and PERSON 2 as opposed to the DNA profile originating from two unknown individuals

- Can be applied to:
  - Single source profiles
  - Partial profiles
  - Mixtures
  - Paternity/kinship cases

What does STRmix™ mean for previous interpretations that used RMP statistics?

- Those interpretations and reported associations are still valid
    - RMP methods are still used in numerous forensic DNA laboratories across the United States
    - The Iowa DCI Crime Lab will still utilize RMP in some cases at least through the end of 2025
- STRmix™ vs previous interpretation/statistical methods
    - Both methods of interpretation and applying statistics are scientifically valid and legally accepted today in courtrooms across the United States
    - STRmix™ is more efficient and effective in the interpretation of complex and low-level mixtures
- STRmix™ has been validated, used, and accepted in legal jurisdictions across the United States for nearly a decade

Changes for Stakeholders

- Reporting of statistics
  - Likelihood ratios will be used instead of RMPs in DNA reports and court testimony
  - Introduction of a verbal scale – intended to aid the audience with conceptualizing the LR statement
    - Verbal scale: “very strong support, strong support, moderate support, limited support, uninformative.”
  - Upper limit of LR reporting at the Iowa DCI Crime Lab
    - Statistical associations that exceed an LR of 1 decillion (1.0 X 10^{33}) will be reported as “…at least 1 decillion times more likely if…”
- Reporting language
  - Will no longer using terms such as “match”, “major”, “minor”, etc.
- There may be multiple statistics given for one profile and this can be expected in DNA mixtures:
  - Will be dependent on the profile that is obtained, the evidence item, and case scenario
  - There may be multiple alternative hypotheses to consider
  - A request for additional alternative hypothesis can be done if requested in timely manner and is relevant to the evidence/profile

Difference in Report Wording -Single Source Example

Binary/RMP

The DNA profile developed from the sperm fraction of the vaginal sample (1.6S) matched the known DNA profile of PERSON 1. The probability of finding this profile in a population of unrelated individuals, chosen at random, would be less than one out of 24 octillion.

STRmix™/ LR

The DNA profile from the sperm fraction of the vaginal sample (1.6S) was interpreted as a single source profile. The DNA results are approximately 2.1 septillion times more likely if it originated from PERSON 1 than if it originated from an unknown, unrelated individual.

This analysis provides very strong support for the proposition that PERSON 1 is the source of the DNA profile obtained from the sperm fraction of the vaginal sample (1.6S).

Difference in Report Wording- Mixture Example

Binary/RMP

The DNA profile developed from the epithelial fraction of the underwear sample (1.2E) indicated a mixture of two individuals. Assuming the presence of PERSON 1, the profile of the second contributor matched the known DNA profile of PERSON 2. The probability of finding this profile in a population of unrelated individuals, chosen at random, would be less than 1 out of 19 nonillion.

STRmix™/LR

The DNA profile from the epithelial fraction of the underwear sample (1.2E) was interpreted as a mixture of two individuals. The probability of the evidence has been calculated by considering multiple propositions.

- The DNA results are approximately 190 septillion times more likely if it originated from PERSON 1 and one unknown, unrelated individual than if it originated from two unknown, unrelated individuals.
  - This analysis provides very strong support for the proposition that PERSON 1 is a contributor to the DNA profile obtained from the epithelial fraction of the underwear sample (1.2E).

- The DNA results are approximately 24 quadrillion times more likely if it originated from PERSON 1 and PERSON 2 than if it originated from PERSON 1 and one unknown, unrelated individual.
  - This analysis provides very strong support for the proposition that PERSON 2 is a contributor to the DNA profile obtained from the epithelial fraction of the underwear sample (1.2E).

When thinking about this for the above report language:

Consider that PERSON 1 is the underwear owner

Consider that PERSON 2 is the person of interest (POI)

What profiles are eligible for STRmix™?

- Samples processed at the Iowa DCI Crime Laboratory after April 14, 2025
- 2- & 3-person mixture DNA profiles
- Single source DNA profiles

Note:

- RMP statistics will still be utilized for certain DNA cases through at least the end of 2025 depending on the nature of the evidence and complexity of the forensic evidence profile(s).
- All forensic evidence profiles are evaluated prior to determining the interpretation/statistic method that will be used.
- If a case is reported with RMP statistics, there is no reason to believe that STRmix™ interpretation would have resulted in a different association.

What profiles are not eligible for STRmix™?

- 4 (or more) person mixtures
- Profiles that are too weak
- Profiles that are too complex
- Mixtures with an unknown number of contributors
- Profiles that previously been interpreted and reported
  - The **evidence** may be re-submitted for additional testing after consultation with the DNA Casework Technical Leader and/or DNA Criminalist Supervisor
    - Since evidence *may* be consumed permission to consume must be provided prior to re-submission

Please use us as a resource!
Direct Inquiries to:

Mike Halverson Criminalist Supervisor

- mhalvers@dps.state.ia.us
- 515-559-7055

Sabrina Seehafer, PhD, ABC-MB Criminalist, DNA Casework Technical Leader

- seehafer@dps.state.ia.us
- 515-313-1138

Karlee Schneider, MSFS Criminalist

- schneide@dps.state.ia.us
- 515-559-7053

DCI Laboratory DNA Section

- 515-725-1500
- Ask to speak with the DNA Criminalist who authored the report