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science safeguarding society

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Implementation considerations with continuous systems

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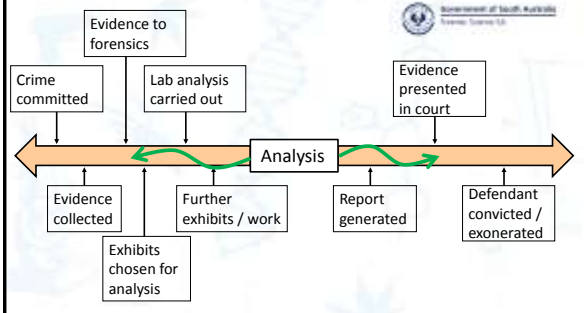

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Before implementation

When considering how to implement STRmix we asked ourselves:

- Why do we even need it ?
- What was wrong with the way that we were doing things ?

Obvious advantage of using a high science system that allowed us to make use of much more information than we could previously

We also recognised that a major problem with current interpretation methods was inconsistency between:

- Practitioners in different labs across Australia
- Different practitioners in the same lab
- The same practitioner at different times

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philosophy

Designed to be a powerful tool that allows forensic scientists to assess DNA evidence in a standard and objective manner

We tried to carry this idea of standardisation and objectivity throughout our workflows

There are two over-arching ideas that guided our implementation

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Contextual bias

No one knowingly biases their opinions, but…

Contextual bias exists, and even worse…

It happens even if we are aware of it !

Opportunity to create workflows to reduce potential for bias

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Overarching idea 1 – decisions early

Before you receive any DNA results

Make as many decisions here as possible – no results to be biased by
-Which samples to analyse
-Which references to compare / calculate LR
-Which PCRs to include
-Who to assume is a contributor
-LR proposition setup

Before you receive references but after receiving evidence

Try to make less decisions here
-Samples requiring reworking
-Decision on suitability for analysis
-Number of contributors

After you have received references and evidence

Area for decision making with most potential for bias – try to avoid
-Whether mutations/trisomy exists in references that could affect analyses

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Overarching idea 2 – avoid grouping

Part of the power of a continuous system is the removal of the need to make a lot of subjective choices

Want to avoid adding a system that re-introduces subjective choices

This usually means that when decisions are made, they are done so in a way where a single idea/rule is used for all profiles

This avoids decision making, which separates profiles into groups which different workflows will be applied

Often decision making is based on subjective assessment of profiles and introduces potential biases

Example

NOTE

I am about to give an example of how these ideas could be implemented

We have done this in South Australia

It is not the only way that a continuous system can be implemented, but just something for you to think about if/when you are implementing a similar system in your lab

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Example

FSSA current workflow is that every profile we obtain is analysed and compared to every reference in the case, regardless of the profile or reference obtained. Unless:

•There has been some problem with the generation of the profile

•We cannot determine how many contributors in the evidence profile

•We are legally unable to do so

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Example

Before you receive any DNA results

Make as many decisions here as possible – no results to be biased by
-Which samples to analyse
-Which references to compare / calculate LR
-Which PCRs to include
-Who to assume is a contributor
-LR proposition setup

We are making these decisions at this point & There is a single workflow for all samples

Before you receive references but after receiving evidence

Try to make less decisions here
-Samples requiring reworking
-Decision on suitability for analysis
-Number of contributors

After you have received references and evidence

Area for decision making with most potential for bias – try to avoid
-Whether mutations/trisomy exists in references that could affect analyses

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Example

Now consider an alternative.

Don't carry out comparison to references that appear excluded as possible contributors

Just decide via human interpretation that they are excluded and report them as such

This has 2 consequences……

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Example

Before you receive any DNA results

Make as many decisions here as possible – no results to be biased by
-Which samples to analyse
~~-Which references to compare / calculate LR~~
-Which PCRs to include
-Who to assume is a contributor
-LR proposition setup

Before you receive references but after receiving evidence

Try to make less decisions here
-Samples requiring reworking
-Decision on suitability for analysis
-Number of contributors

After you have received references and evidence

Area for decision making with most potential for bias – try to avoid
-Whether mutations/trisomy exists in references that could affect analyses
-Which references to compare / calculate LR

We are have moved this decision to here

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Example

Need some basis to decide someone is excluded via human interpretation

Will need:
•Dropout threshold
•Stutter threshold
•Het balance threshold
•Mix proportion threshold
•Drop-in threshold

Will reintroduced a binary, subjective system of thresholds infront of the continuous system that was implemented to remove them!

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Number of Contributors

At the moment we still need knowledge of these DNA profile behaviors in order to assess the number of contributors to a DNA profile
•Dropout threshold
•Stutter threshold
•Het balance threshold
•Mix proportion threshold
•Drop-in threshold

This is something that we hope to reduce or remove in the near future with work we are doing on a continuous system that can handle a range of possible contributor numbers

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Number of Contributors

This is something that we hope to reduce or remove in the near future with work we are doing on a continuous system that can handle a range of possible contributor numbers

$$LR = \frac{\sum_n \Pr(N = n \mid H_1) \sum_j w_j \Pr(S_j \mid N = n, H_1)}{\sum_n \Pr(N = n \mid H_2) \sum_j w_j \Pr(S_j \mid N = n, H_2)}$$

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Reporting results

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Reporting results

There are many aspects of implementation that must be considered and I am happy to talk to anyone about FSSA experience in mind numbing detail

I will just go through a couple of issues that will need to be considered when implementing a continuous system

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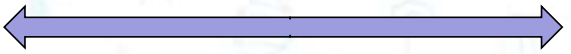
How do you report results ?



Result expressed comprehensibly

Result expressed statistically

•Need to strike some balance between maintaining ultimate statistical purity in the way we express our results and expressing results so that they will be understood in court

•There's no point giving a correct result if no-one's listening

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Reporting LRs that favour exclusion

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Reporting negative likelihood ratios

Typically the numerator of a LR will be the prosecution hypothesis and the denominator of the LR will be the defence hypothesis

Continuous systems have the ability to produce LR that favour a hypothesis of inclusion, i.e. LR > 1

Also have the ability to produce LR that favour a hypothesis of exclusion, i.e. 0 < LR < 1

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Reporting negative likelihood ratios

LRs in the second category are often termed 'negative LRs' as their log is a negative number

Up to this point we generally haven't had LRs that favour exclusion

There has been some questions that arise about what to do with them

i.e. how should we report them ?

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Reporting negative likelihood ratios

Option 1
LR > 1 - report 'not excluded' interpretation and give LR
LR < 1 - report 'excluded' interpretation only and no LR

Option 2
LR > n - report 'not excluded' interpretation and LR
1/n < LR < n - report 'inconclusive' interpretation
LR < 1/n - report 'excluded' interpretation and no LR

Option 3
Any value for LR - report interpretation and LR

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Reporting negative likelihood ratios

A quick scenario

Person 1 has genotype [A,B]
Person 2 has genotype [C,D]

Hp: They are siblings
Hd: They are unrelated

LR = 0.25

How should this results be reported ?
-They are excluded as being brothers
-Not excluded as brothers
-Provide LR or not ?

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Reporting negative likelihood ratios

Option 1
LR > 1 - report 'not excluded' interpretation and LR
LR < 1 - report 'excluded' interpretation only and no LR

Pros
1) Simple to understand and apply and simply to explain in court

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Reporting negative likelihood ratios

Cons
1) LR mildly < 1 is not strong evidence of exclusion and 'excluded' may not be appropriate
2) There are many examples of LR < 1 even though contribution is known to be true – the interpretation would be wrong
3) Creates a bias in reporting: 'we only report LR that support the prosecution'
4) Examples when 'exclusion' is either not conservative or is nonsensical
– e.g. exclusion of an alternative suspect to the accused is not conservative with respect to the accused
6) Not supported by any leading international commentators

Reporting negative likelihood ratios

Option 2
LR > 100 - report 'not excluded' interpretation and LR
1/n < LR < n - report 'inconclusive' interpretation and no LR
LR < 1/n - report 'excluded' interpretation and no LR

Pros
1) Simple to understand and apply and simply to explain in court

2) Less bias in the reporting scales than with other options

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Reporting negative likelihood ratios

Cons
1) Can't standardised DNA evidence with all other evidence (e.g. glass, fibre, shoeprint, etc) as many of these trace evidence types don't obtain very big statistical weightings

2) Would cause many problems with relative/paternity/DVI situations where lower LR can commonly be obtained

3) Can be seen as hiding evidence, especially if LR favours exclusion

4) Wastes potentially important information

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Reporting negative likelihood ratios

Option 3
Any value for LR - report interpretation and LR

Pros
1) Provides the least biased and most statistically supported way of reporting results
2) Supported by all international commentators polled.

Cons
1) Can be difficult for juries to understand and may cause confusion if not properly explained

This is the option that we use in SA

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Reporting negative likelihood ratios

Also recommended by others in the forensic field:

"*I believe that an LR less than one must be reported. If it has a numerical value then that value must be given*"..... "*It is not logical to report a LR of less than one as an exclusion; indeed, it might be seriously misleading.*"
- Dr Ian Evett

"*LR below 1 should be reported as such.*"..... "*Reporting all likelihood ratios below 1 as "exclusions" does not make any sense to me. "Exclusion" can only be used when the LR is assigned to 0.*"
- Professor Christophe Champod

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Reporting negative likelihood ratios

Also recommended by others in the forensic field:

"*I dont think it makes any sense to decide an exclusion or an inclusion based on LR=1. It's really a jury question. This thinking is rooted in the RMNE approach which forces decisions to be made by scientists about inclusion/exclusion."*
- Professor Peter Gill

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Reporting negative likelihood ratios

Also recommended by others in the forensic field:

"*As you wrote, one view is that the value of the LR is what it is and should be reported. So, if a result is greater than 1 it supports the hypothesis specified at the numerator of the LR. If the value is less than one, the alternative hypothesis is supported. This guarantees a balanced and transparent way to present the value of the evidence.*"
- Professor Franco Taroni

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Reporting negative likelihood ratios

Also recommended by others in the forensic field:

"*Simplifying a LR to a decision negates the entire logical framework.*

In the short time that we have been applying LRs to casework, we have already experienced situations where changing one variable (in our case drop-out probability) generates LRs spanning 1. I think it demonstrates how quickly attempting to translate a LR to a decision loses credibility."
- Dr. Norah Rudin

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Function creep

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BEWARE of function creep

It is totally logical that:

Probably OK

Getting iffy

Very subjective

- We don't need to analyse single source profiles because their results are so simple we know what analysis is going to give. Lets just upload them
- If there is a clear major component in a 2p mix and only a couple of weak minor alleles then we can just manually upload the major without analysis
- If we are confident we can see major in any mixture, lets just manually interp/upload
- If we don't think analysis will be able to resolve a single component then let's not waste our time trying
- Let's just use analyse when we think it will lead to a 'good' result

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Some further considerations

- What exhibits do you accept ?
- How do you read profiles ?
- What do you do about artefacts ?
- Which samples do you analyse ?
- Which samples don't you analyse ?
- Which replicates do you include ?
- Which settings to use ?
- When can data be ignored?
- Determining # of contributors
- Reviewing results
- Reviewing results
- Which propositions do you use ?
- When to assume someone
- Which results do you report ?
- How do you deal with unknowns ?
- Do you re-analyse old cases ?
- How does QA work ?
- Training
- What goes in the casefile ?
- Continual protocol review
- Database use
- Electronic file flow
- Etc etc etc

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Expertise

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Are we still experts ?

•This was put to me by a respected lawyer in SA

"If you have technicians that carry out exhibit examinations and technicians that do lab work and now STRmix to do your profile interpretations, then what is it that you are an expert of ?"

•This is a good questions and worthy of some discussion

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Are we still experts ?

• This comment was related directly at STRmix and the way we have implemented it in SA

•I consider STRmix a tool, and would argue that it takes more than feeding in profiles and blindly transposing the numbers in order to be a expert

•A critical part of our roles as scientific experts is to understand the working of the tools we use and to critically review the results

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Are we still experts ?

•A bigger concern to me is how future generations of scientists will review results from continuous systems

•We all have the advantage of working before and after these systems and so have needed to use threshold based systems to interpret profiles

•We can then use these skills to review the results of any analysis

•What will new scientists base their decisions on if all they have ever known is a continuous system output ??

•This is a problem I envisage appearing over the next 10 years

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Database searching in a continuous world

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Database Searches

- DNA database comparisons traditionally involve direct comparisons:
  - scene to scene – common offender?
  - person to scene – offender?
- Limitation to DNA database searching – you need a single source profile
- What can be done with 'non-resolvable' mixtures?
  - There is no profile for uploading to a database
  - We have been forced to 'file' them

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Database Searches

Presentation so far has shown how an LR can be calculated for comparisons between evidence DNA profiles and references

Can use any hypotheses but as example I will use:

H1: POI + (N-1) unknowns
H2: N unknowns

For a N person profile

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Database Searches

For example a 3 person profile could be analysed and compared to a reference using hypotheses:

H1: POI + 2 unknowns
H2: 3 unknowns

If you can do this then you also have the ability to compare a profile to a list of people in a database in exactly the same way

Just compares each person on the database one at a time using the above hypotheses

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Database Searches

Database

Person 1	H1: Person 1 + two unknown H2: 3 unknowns	LR 1
Person 2	H1: Person 2 + two unknown H2: 3 unknowns	LR 2
Person 3	H1: Person 3 + two unknown H2: 3 unknowns	LR 3
Person 4	H1: Person 4 + two unknown H2: 3 unknowns	LR 4
…		…
Person n	H1: Person n + two unknown H2: 3 unknowns	LR n

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Database Searches

Any LR calculated that falls above the designated cutoff is listed

An example given of an unresolvable 3 person NGM SElect mixture analysed using STRmix

Searched against database of 57 000 spiked with the three known contributors

56 000 of these were outright excluded (LR = 0)

Remaining 1000 gave an LR > 0

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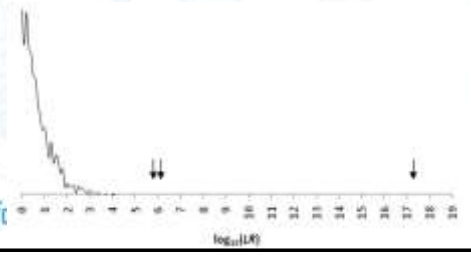
Database Searches

Known contributors shown with arrows

- Database search of this sample would have identified all 3 contributors without ability to interpret a single component



Database Searches

FSSA already does this for contamination checks:

General workflow is:
•Analyse sample
•Run contamination check
•Upload profiles if possible
•Calculate evidentiary LRs

We have done some work investigating known contaminations

Obtained from trawl back through QA records

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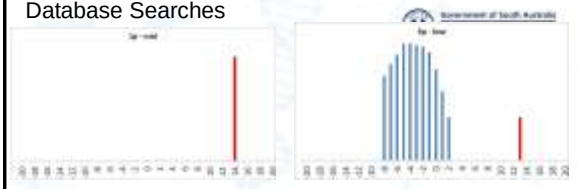
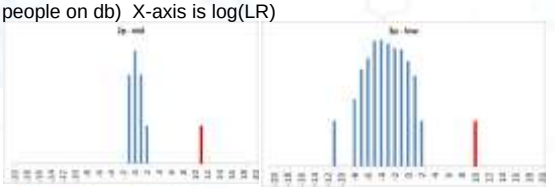
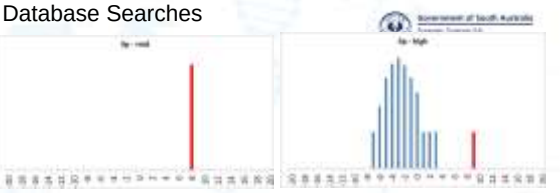
Database Searches



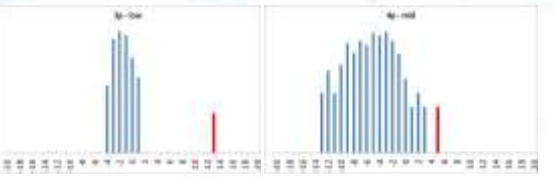
Red shows LR of contaminator – blue shows rest (approx 350 people on db) X-axis is log(LR)



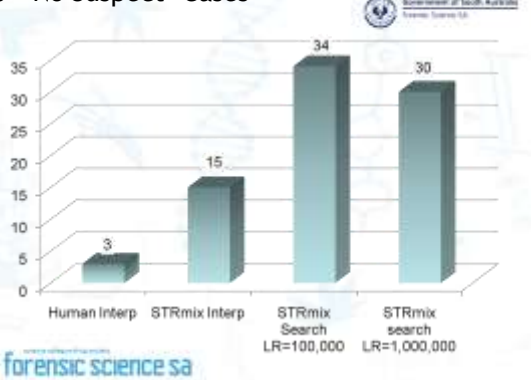
Database Searches



Etc, etc - LR cutoff used currently is 10 000



60 'No Suspect' Cases



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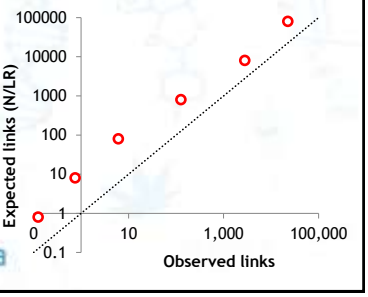
Adventitious matches

Always been a possibility but now must be considered seriously in relation to searching LR cutoff

For a complex mixture the number of matches on a database of 'N' people at an LR cutoff is approximately equal to N/LR



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Database search future

- Could extend this to carry out familial searching to complex mixtures
- Not just searching a database for a relative who may have deposited DNA at a crime scene ('normal' familial search)
- But searching a database for a relative who may be one of the contributors to a complex mixture of DNA at a crime scene

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