Norwegian Institute of Public Health

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ISFG DNA commission recommendations

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Statistical methods in forensic genetics 7-10 October 2013, Copenhagen

(slides adapted from Peter Gill)
(Advanced DNA Interpretation workshop ISFG 2013, Melbourne)

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DNA commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures

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N. Morling [g], M. Prinz [h], P.M. Schneider [i], B.S. Weir [j]

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ISFG DNA commission recommendations

- *Recommendation 1: The likelihood ratio is the preferred approach to mixture interpretation. The RMNE approach is restricted to DNA profiles where the profiles are unambiguous. If the DNA crime stain profile is low level and some minor alleles are the same size as stutters of major alleles, and/or if drop-out is possible, then the RMNE method may not be conservative.*

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ISFG DNA commission recommendations

- *Recommendation 2: Even if the legal system does not implicitly appear to support the use of the likelihood ratio, it is recommended that the scientist is trained in the methodology and routinely uses it in case notes, advising the court in the preferred method before reporting the evidence in line with the court requirements. The scientific community has a responsibility to support improvement of standards of scientific reasoning in the court-room.*

ISFG DNA commission recommendations

- *Recommendation 3: The methods to calculate likelihood ratios of mixtures (not considering peak area) described by Evett et al [13] and Weir et al [14] are recommended.*

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ISFG DNA commission recommendations

- *Recommendation 4: If peak height or area information is used to eliminate various genotypes from the unrestricted combinatorial method, this can be carried out by following a sequence of guidelines based on Clayton et al* [17].

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ISFG DNA commission recommendations

- *Recommendation 5: The probability of the evidence under Hp is the province of the prosecution and the probability of the evidence under Hd is the province of the defence. The prosecution and defence both seek to maximise their respective probabilities of the evidence profile. To do this both Hp and Hd require propositions. There is no reason why multiple pairs of propositions may not be evaluated* (Appendix 3*).*

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Example of generalisation

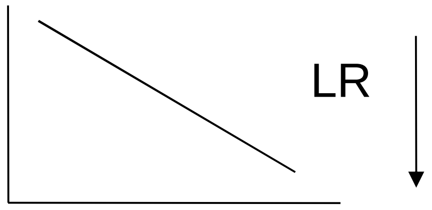
- How many contributors in a DNA profile?
- Classically we decide on the number of contributors by counting the number of alleles present per locus
- By consideration of the casework circumstances

Anchoring the prosecution hypothesis

$$LR = \frac{\Pr E \mid Hp}{\Pr E \mid Hd}$$

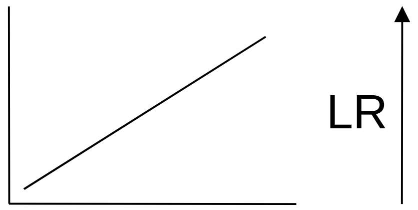
Not anchored – the number of propositions is the same in numerator and denominator:

$$\frac{S + U_1 + U_2 + U_3}{U_0 + U_1 + U_2 + U_3}$$



Anchored - the number of propositions is different in numerator and denominator:

$$\frac{S + U_1}{U_0 + U_1 + U_2 + U_3}$$



Contributors under Hd

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How does this help?

- Usually the scientist decides the number of contributors on behalf of both prosecution and defence
- Minimising the number of contributors usually maximises the Probability on behalf of the defence
- The foregoing is a *generalisation* which may not always be true (Buckleton et al 2007).
- Is the generalisation true in this case?
- **check the *trend* by analysing multiple propositions**

ISFG DNA commission recommendations

- *Recommendation 6: If the crime-profile is a major/ minor mixture, where minor alleles are the same size (height or area) as stutters of major alleles, then stutters and minor alleles are indistinguishable. Under these circumstances alleles in stutter positions that do* <u>*not*</u> *support Hp should be included in the assessment.*

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ISFG DNA commission recommendations

- *Recommendation 7: If drop-out of an allele is required to explain the evidence under Hp: (S = ab; E = a), then the allele should be small enough (height/area) to justify this (i.e. the allele should be below a predetermined threshold).*

- Basically, this means that if an allele found in the reference sample is missing in the crime stain then it is not necessarily neutral evidence.
- Reworking the sample is always important to see if we can recover the missing alleles.

ISFG DNA commission recommendations

- *Recommendation 8: When a DNA profile is at a level that is dominated by background noise, then a biostatistical interpretation should not be attempted.*

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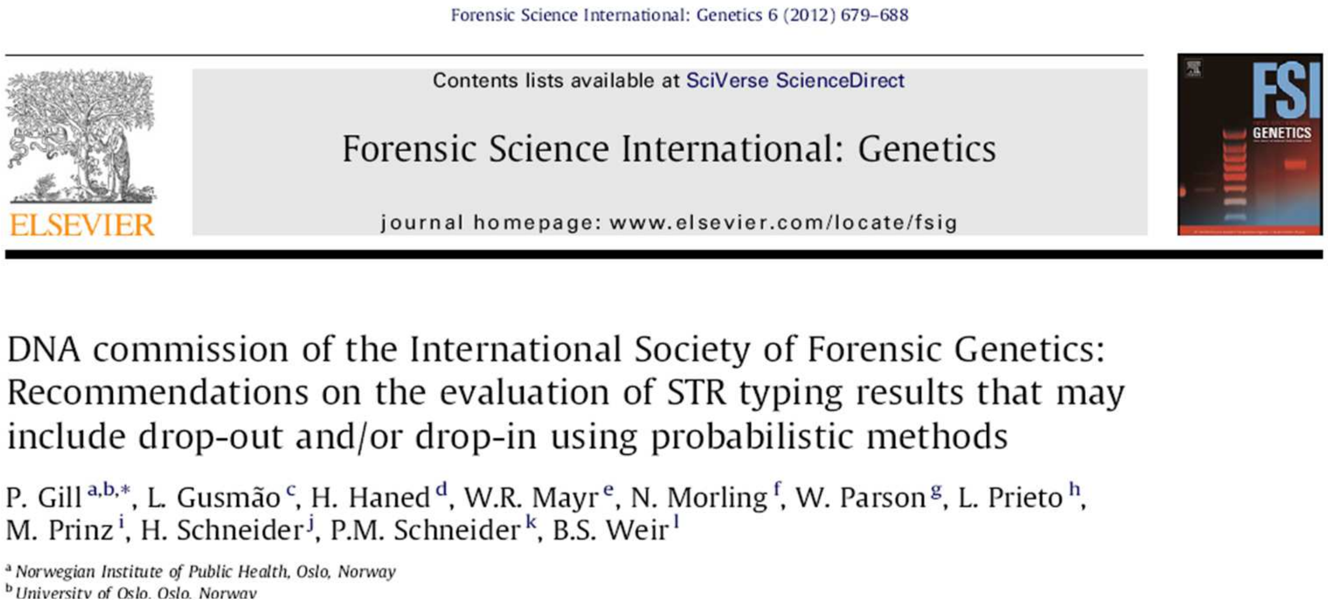
ISFG DNA commission recommendations

- *Recommendation 9: In relation to low copy number, stochastic effects limit the usefulness of heterozygous balance and mixture proportion estimates. In addition, allelic drop-out and allelic drop-in (contamination) should be taken into consideration of any assessment.*

New ISFG DNA commission

- New commission recently reported and recommends the incorporation of dropin and drop-out into probabilistic calculations



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DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR typing results that may include drop-out and/or drop-in using probabilistic methods

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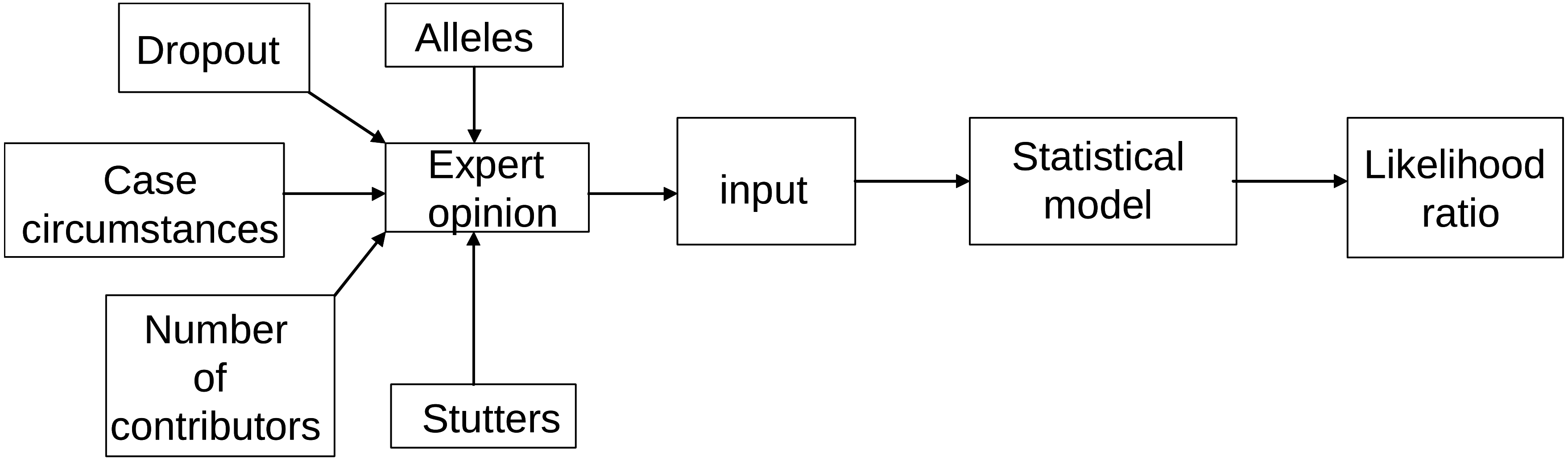
Interpretation process is an interaction of the expert with a statistical model



Dropout

Alleles

Case circumstances

Expert opinion

input

Statistical model

Likelihood ratio

Number of contributors

Stutters

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Numbers of contributors

- There is no need to anchor the number of contributors to be the same under Hp and Hd – they will often be different
- There will be differences between prosecution and defence hypotheses that courts will wish to explore. Software will facilitate the exploration

More generalisations

- Don’t ignore inconvenient (to the prosecution) events.
- Use statistical tools to explore the data so we can understand what is going on
- The statistical analysis may suggest that samples need to be reworked as a preferable option

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Summary of New ISFG DNA commission recommendations

- Probabilistic methods following the *‘basic model’* described here can be used to evaluate the evidential weight of DNA results considering drop-out and/or drop-in.
- Estimates of drop-out and drop-in probabilities should be based on validation studies that are representative of the method used.
- The weight of the evidence should be expressed following likelihood ratio principles.
- The use of appropriate software is highly recommended to avoid hand-calculation errors.