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| Match |  |  |
| :---: | :---: | :---: |
| item | questioned evidence | suspect |
| data | $d_{Q}$ | $d_{S}$ |
| type | $Q$ | $S$ |
| $M(Q, S):$ for some value $x \in X$ |  |  |
| $Q=x \& S=x$ |  |  |

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## Inner Product

$\operatorname{Pr}\{M(Q, S)\}=\sum_{x \in \mathcal{X}} q(x) \cdot s(x)$

- standard pattern comparison method
- widely used, powerful math properties

$$
\begin{aligned}
& \operatorname{Pr}\{M(Q, S)\}=\int_{X} q(x) \cdot s(x) d x \\
& \operatorname{Pr}\{M(Q, S)\}=\int_{X} q(x) \cdot s(x) \cdot \mu(x) d x
\end{aligned}
$$

## Match Rarity

for random type $R, \operatorname{Pr}\{R=x\}=r(x)$

Define the Match Likelihood Ratio (MLR) statistic

$$
M L R \equiv \frac{\operatorname{Pr}\{M(Q, S)\}}{\operatorname{Pr}\{M(Q, R)\}}
$$

How to compute the MLR

$$
\begin{aligned}
M L R & =\frac{\operatorname{Pr}\{M(Q, S)\}}{\operatorname{Pr}\{M(Q, R)\}} \\
& =\frac{\sum_{x \in X} q(x) \cdot s(x)}{\sum_{x \in X} q(x) \cdot r(x)}
\end{aligned}
$$

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## MLR is a likelihood ratio

Hypothesis C: suspect S contributed to evidence item Q
$\operatorname{Pr}\{M \mid C\}=\operatorname{Pr}\{M(Q, S)\}$
$\operatorname{Pr}\{M \mid \bar{C}\}=\operatorname{Pr}\{M(Q, R)\}$

$$
M L R=\frac{\operatorname{Pr}\{M(Q, S)\}}{\operatorname{Pr}\{M(Q, R)\}}=\frac{\operatorname{Pr}\{M \mid C\}}{\operatorname{Pr}\{M \mid \bar{C}\}}
$$

MLR assesses match observation M under alternative contributor hypotheses C and $\mathrm{C}^{\prime}$

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## Single Source DNA

likelihood $\operatorname{Pr}\left\{d_{Q} \mid Q=x\right\}=\left\{\begin{array}{cc}1 & x=x_{0} \\ 0 & \text { otherwise }\end{array}\right.$
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prior $\quad \operatorname{Pr}\{Q=x\} \propto 1$
posterior $\quad q(x) \propto \operatorname{Pr}\left\{d_{Q} \mid Q=x\right\} \cdot \operatorname{Pr}\{Q=x\}$

$$
M L R=\frac{\sum_{x \in X} q(x) \cdot s(x)}{\sum_{x \in X} q(x) \cdot r(x)}=\frac{1}{r\left(x_{0}\right)}
$$

## DNA Mixture: Inclusion

$$
\begin{gathered}
\operatorname{Pr}\left\{d_{Q} \mid Q=x\right\}=\left\{\begin{array}{cc}
1 & \text { alleles }(x) \subset \text { alleles }\left(d_{Q}\right) \\
0 & \text { otherwise }
\end{array}\right. \\
\operatorname{Pr}\{Q=x\} \propto 1 \\
q(x) \propto \operatorname{Pr}\left\{d_{Q} \mid Q=x\right\} \cdot \operatorname{Pr}\{Q=x\} \\
M L R=\frac{\sum_{x \in X} q(x) \cdot s(x)}{\sum_{x \in X} q(x) \cdot r(x)}=\frac{1}{\sum_{x \in I} r(x)}
\end{gathered}
$$


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DNA Mixture: Equality
$\operatorname{Pr}\left\{d_{Q} \mid Q=x, V=y\right\}=\left\{\begin{array}{lc}1 & \text { alleles }(x) \cup \text { alleles }(y)=\text { alleles }\left(d_{Q}\right) \\ 0 & \text { otherwise }\end{array}\right.$
$\operatorname{Pr}\{Q=x\} \propto 1$
$q(x) \propto \operatorname{Pr}\left\{d_{Q} \mid Q=x, V=y\right\} \cdot \operatorname{Pr}\{Q=x\}$
$M L R=\frac{\sum_{x \in X} q(x) \cdot s(x)}{\sum_{x \in X} q(x) \cdot r(x)}=\frac{1}{\sum_{x \in J} r(x)}$

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## DNA Mixture: Quantitative

$$
\begin{gathered}
\operatorname{Pr}\left\{d_{Q} \mid Q=x, V=y\right\}=N([w \mathbf{x}+(1-w) \mathbf{y}] \cdot u, \Sigma) \\
\operatorname{Pr}\{Q=x\}=r(x) \\
q(x) \propto \operatorname{Pr}\left\{d_{Q} \mid Q=x, V=y\right\} \cdot \operatorname{Pr}\{Q=x\} \\
M L R=\sum_{x \in X} q(x) \cdot s(x) \quad \begin{array}{l}
1,2 \& 3 \text { unknown } \\
\text { low copynnumber } \\
\text { damaged DNA } \\
\text { case-to-case } \\
\text { method validation }
\end{array}
\end{gathered}
$$

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## Population Substructure

Genotypes are not independent: shared ancestry
Coancestry coefficient 鹵: allele IBD probability Induces a measure 累 on joint genotypes

$$
M L R=\frac{\sum_{x \in X} q(x) \cdot s(x) \cdot \mu(\theta, x)}{\sum_{x \in X} q(x) \cdot r(x) \cdot \mu(\theta, x)}
$$

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| Conclusions |
| :---: |
| - introduced MLR: "match likelihood ratio" <br> - an inner product ratio statistic <br> - agrees with "data likelihood" DNA LR <br> - extends LR to other DNA applications <br> - statistical framework for non-DNA forensics |

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- an inner product ratio statistic
- agrees with "data likelihood" DNA LR
- extends LR to other DNA applications
- statistical framework for non-DNA forensics $\qquad$

