


Exploring Forensic Scenarios
with TrueAllele® Mixture Automation
59th Annual Meeting
American Academy of Forensic Sciences
February, 2007

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Pittsburgh, PA USA

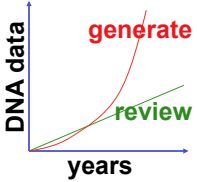

Employee, Shareholder, and Discussion
of Commercial Products or Services



Cybergenetics

Cybergenetics © 2003-2007

So many cases, so little time



meeting the data challenge

Do the *best* job possible

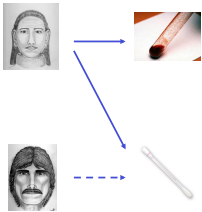
- Look at all the good data
- Ignore the bad data
- Consider every possibility
- Obtain the most match information

DNA evidence



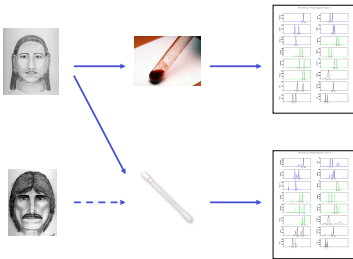
person

DNA evidence

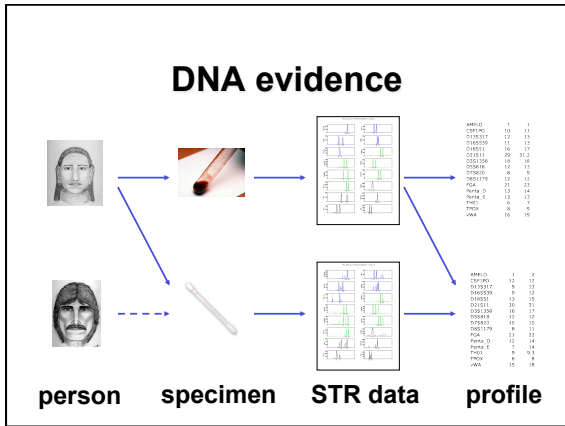


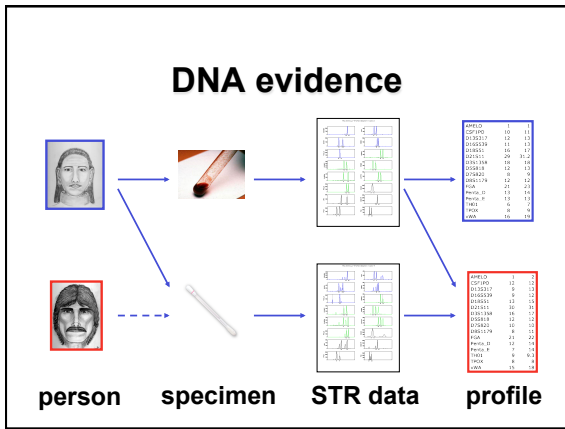
person specimen

DNA evidence



person specimen STR data

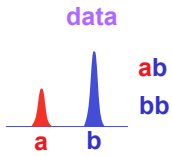




Consider every possibility

- every allele call
- all mixing weights
- stochastic effects
- stutter artifact
- peak imbalance
- specimen combinations

DNA profile ambiguity



Use wild card
[* b]

List possibilities
[a b], [b b]

Attach probability
0.6 0.4

Match DNA profiles

$$\text{Match Information} = \frac{\text{Prob}(\text{specific})}{\text{Prob}(\text{random})}$$

Match Information logarithm –
Very large number:
“billion billion” or 10^{18}
Use the exponent:
18

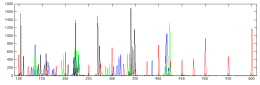
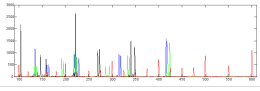
Comparing interpretation via match information

	<u>Information</u>
Wildcards	11.9
Listing	15.9
Probability	17.2

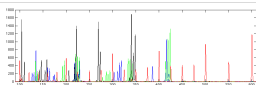
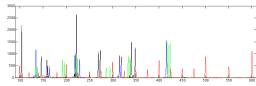
Obtain DNA data



100%	
70%	30%



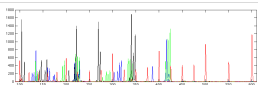
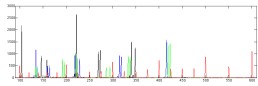
Infer DNA profile



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Match DNA profile



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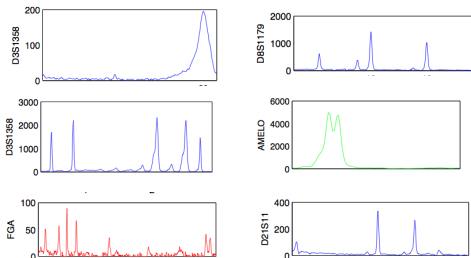
17.3

How many contributors?

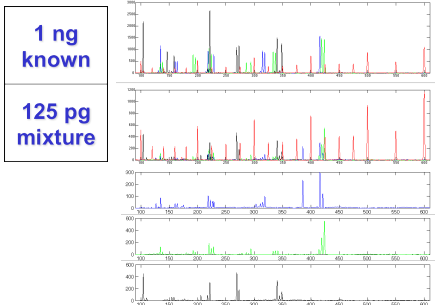
"What if" scenarios

Number	Match Information
1	0.0
2	17.3
3	9.7

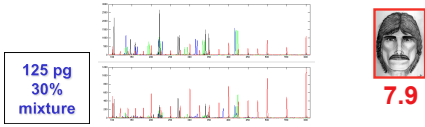
Discard bad data



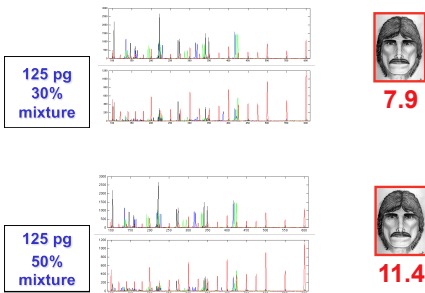
Low-level informative data



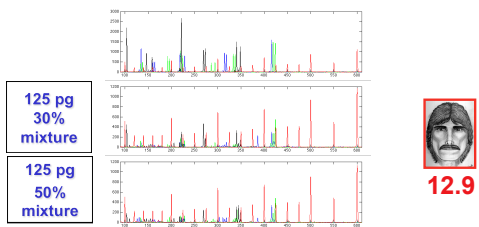
Using informative data



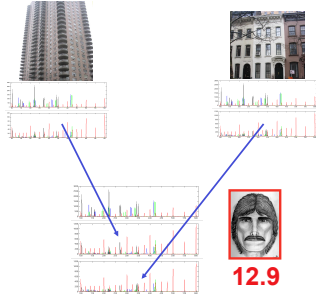
Using informative data



Combine informative data

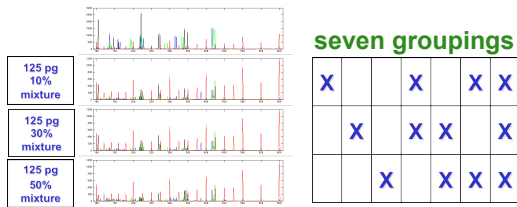


Serial crime investigation

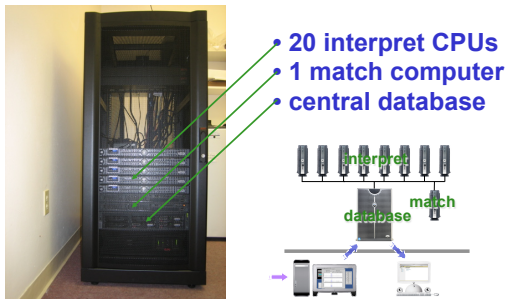


Many sample combinations

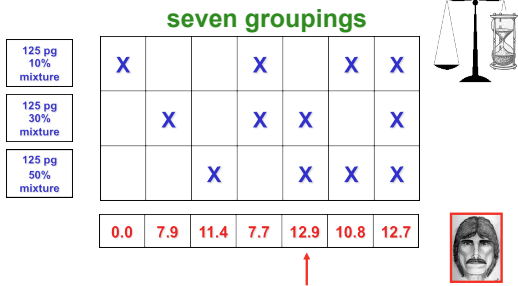
Which subset of DNA samples gives the most informative result?



TrueAllele scientific calculator



Combining low level data



Do the *best* job possible

- Look at all the good data
- Ignore the bad data
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