

Scientific Combination of DNA Evidence: A Handgun Mixture in Eight Parts

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Cybergenetics

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Handgun Evidence

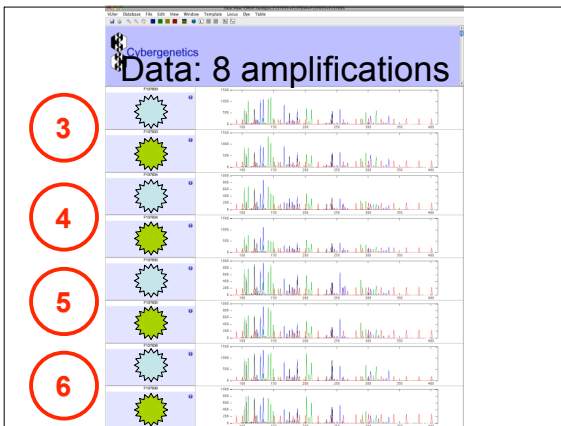


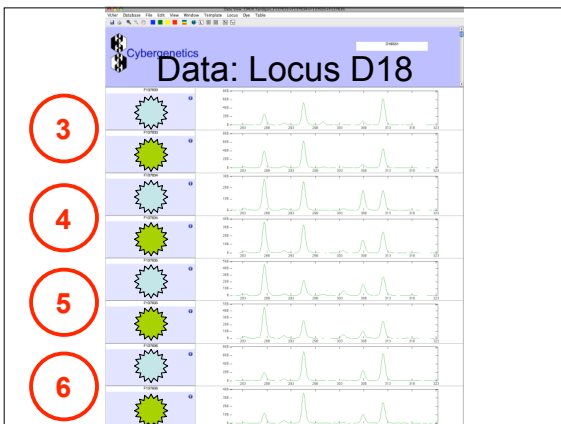
DNA Swabs



Duplicate Amplifications







3

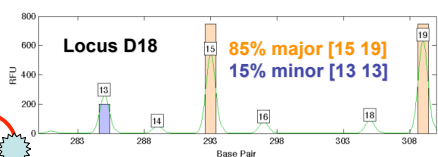
Human Review: Major

STR PROFILE COMPONENTS										
D3	VWA	D16	D2	AMEL	D8	D21	D18	D19	TH01	FGA
15,17	14,19	8,11	18,25	X,Y	12,13	26,30	15,19	10,11	7,10	24,24
15,17	14,19	F,F	18,25	X,Y	12,13	F,F	F,F	F,F	F,F	24,F

CPI: LR = 17,000
log(LR) = 4.23

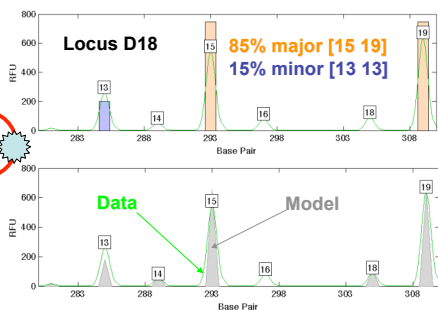
Quantitative Likelihood Function

3



Quantitative Likelihood Function

3



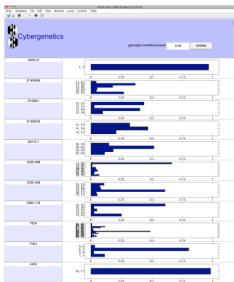
Computer Infers Major Genotype



Definite genotype
at every locus
100% probability
at one allele pair

Full RMP
 $\log(LR) = 16.72$
trillion-fold increase
 $4.23 \rightarrow 16.72$
over CPI

Computer Infers Minor Genotype

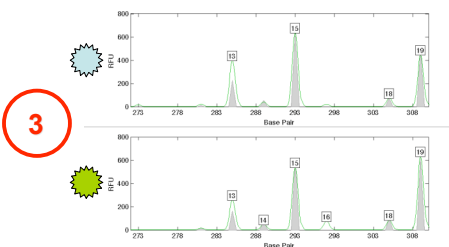


Uncertain genotype
at every locus
< 100% probability
at multiple allele pairs

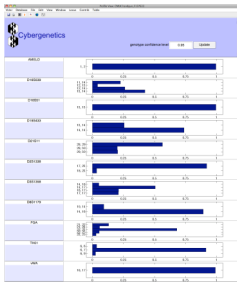
Finds match strength
 $\log(LR) = 4.99$
100,000-fold increase
 $0 \rightarrow 4.99$
over no result

Joint Likelihood Function

Locus D18
85% major [15 19]
15% minor [13 13]



Infer Minor Genotype

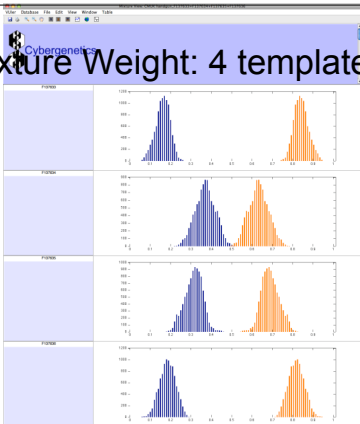


More genotype certainty with two amplifications of one PCR template

Greater match strength
 $\log(LR) = 5.25$
 some increase
 $0 \rightarrow 4.99 \rightarrow 5.25$

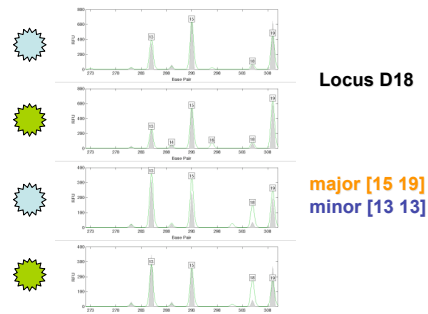
Mixture Weight: 4 templates

- 3
- 4
- 5
- 6

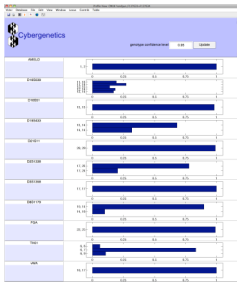


Joint Likelihood Function

- 3
- 4



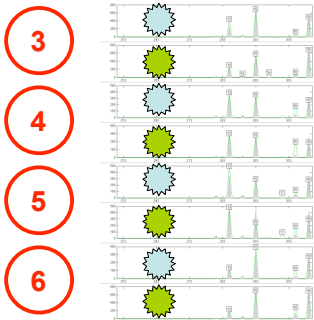
Infer Minor Genotype



Higher genotype certainty with two amplifications of two PCR templates

Greater match strength
 $\log(LR) = 9.73$
large increase
 $0 \rightarrow 4.99 \rightarrow 5.25 \rightarrow 9.73$

Joint Likelihood Function



Locus D18

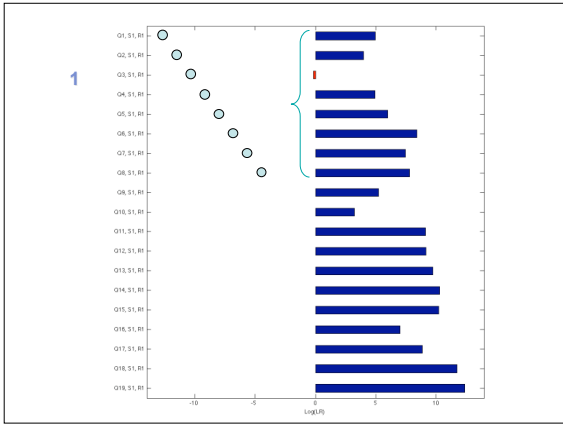
major [15 19]
minor [13 13]

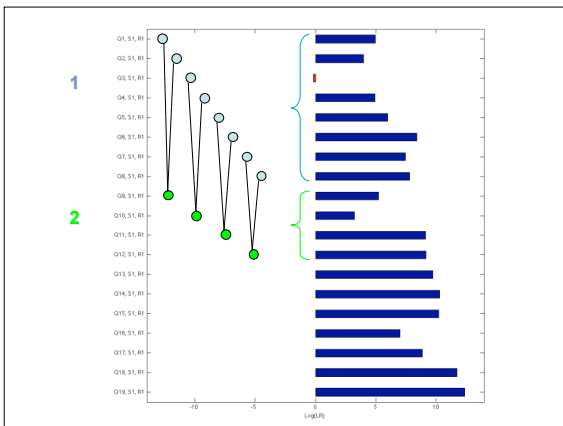
Infer Minor Genotype

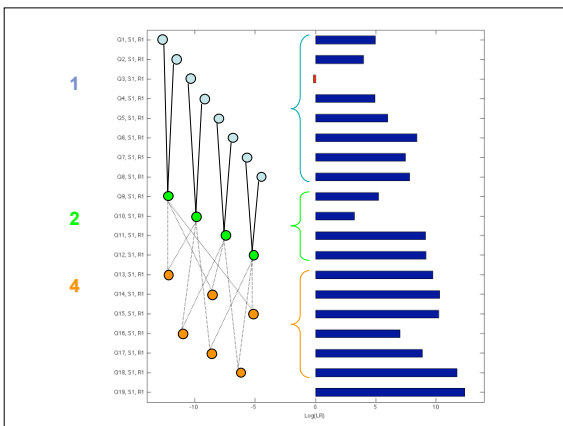


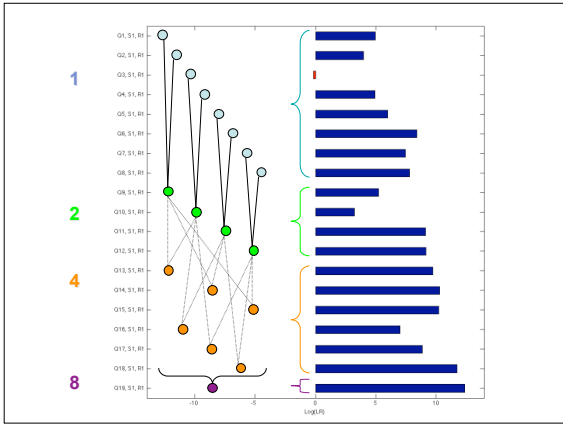
Definite genotype at every locus
two amplifications of four PCR templates

Full match strength
 $\log(LR) = 12.39$
reaches RMP
 $0 \rightarrow 4.99 \rightarrow 5.25 \rightarrow 9.73 \rightarrow 12.39$









Observations

- Coancestry - half a log unit
- Three unknown contributors
- Multiple amplifications are good, multiple templates are better
- Data constrains genotypes; more data, more constraints
- *Complementarity*: combining "unlike data" is more informative

Conclusions

Two mixture genotype examples

Major contributor **Quantitative likelihood** modeling that uses all of the data is *more informative* than qualitative threshold methods

Minor contributor **Combining DNA evidence using a joint likelihood function** is *more informative* than separately examining data in isolation

Trillion-fold increase in identification information
