



DNA “Exclusion Calculator” in DNA-VIEW

Simplified mixture calculation

The *exclusion probability*, denoted A , is the probability that a randomly selected person would have an allele not detected in the specified crime stain profile, at any locus.

The *probability of inclusion* or RMNE (proportion of *random men not excluded*) is $1 - A$.

Profile of 2252-00521

race: c Probability to exclude: 0.9999974
 theta: 0.03 to include: 1/380000

Locus	Alleles								RMNE
DQAI	1•1	2	3	4					0.5535
LDLR	A	B							1
GYP A	A	B							1
HBGG	A	B							0.9989
D7S8	A	B							1
Gc	A	B	C						1
D3S1358	14	15	16	17	18				0.9938
VWA	14	16	17	18					0.6481
D8S1179	10	12	13	14	16				0.6252
D21S11	29	30	31						0.3116
D18S51	6	7	7•2	8	9				1/1482
D5S818	10	11	12	13					0.9551
D13S317	9	10	11	12					0.5333
D7S820	11	12							0.1103

Add to rpt Clear rpt
 Print rpt Clr alleles Options

Hints: Ctrl-Enter for Options; # for next locus

computes the *exclusion probability* for a DNA mixture quickly on one screen

- sensitive to “theta” per NRC II formula 4.4a (Recommendation 4.1)
- allows for null alleles (i.e. primer dropout)
- Operation
 - instantly call up the profile for any defined person
 - “spreadsheet” operation also allows manual entry
 - For loci, type any abbreviation and the program will guess the locus or pop up a choice box.
 - Race – To compute with a different set of databases, click on the race letter and type a new race letter.
 - Theta – To compute with a different value of θ , click on the theta box and type in a new value. 0.01 may be entered by typing 100.

The exclusion calculation is a simpler – though theoretically less valid,[‡] and typically much less powerful – alternative to the likelihood ratio approach of the *mixed stain calculator*.

[‡] It ignores the type of a particular suspect. If the stain has four alleles at some locus, two common and two rare, then the computation impugns a suspect with the two common alleles just as strongly as a suspect with the two rare ones. That might overstate the strength of the evidence against a suspect who has common alleles in common with the stain.

Thus the exclusion probability might be unfair to the suspect. However, while that can happen for one or two loci, it is unlikely that the net effect over all loci is unfair to a suspect.

