Identifying common donors in DNA mixtures

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Budapest, English Speaking Working Group of the ISFG, 2 September 2016

Likelihood ratio

To evaluate whether there is evidence that a Pol S with genotype g has contributed to a mixture M, one evaluates the likelihood ratio

$$LR(M,g) = \frac{P(M \mid S = g, H_p)}{P(M \mid S = g, H_d)},$$

where

- M are the mixture data that are evaluated
- H_p states that S is a contributor
- H_d replaces S by an unknown contributor

Likelihoods

A probabilistic model is needed to compute $P(M \mid H_*)$.

Model types

- Binary/semi-continous models consider M to be the set of recorded alleles, allowing for dropout and drop-in
- Continuous models consider M to be the recorded alleles and their peak heights.

Continuous models treat more data, hence need a more sophisticated probabilistic model.

Semi-continuous

Parameters are:

- number of contributors n
- Dropout probability d_1, \ldots, d_n per donor
- Drop-in parameter c

Parameters can be chosen in several ways

- Based on the mixture data, and uncontested contributors; then used for both hypotheses
- For both hypotheses separately (e.g. using Maximum Likelihood estimates)

Likelihood ratio versus deconvolution

If we take the same model under both hypotheses, then

$$LR(M,g) = \frac{P(M \mid S = g, H_p)}{P(M \mid S = g, H_d)}$$
$$= \frac{P(S = g \mid M, H_p)}{P(S = g \mid M, H_d)}.$$

LR interpretations

The LR says:

- How much more probable the mixture data are when the Pol is supposed to be a donor than if not
- How much more likely the Pol is to have the genotype g if he is a donor than if not

Without θ -correction or relatedness, $P(S = g \mid M, H_d) = p_g$ (population frequency). We continue with this assumption.

LR never more than for single source

$$LR(M,g)p_g = P(S = g \mid M, H_p) \le 1 \Rightarrow LR(M,g) \le \frac{1}{p_g}.$$

LR distributions

Based on the mixture data we can

- Calculate the LR for every genotype
- Equivalently, calculate the probability of every genotype to be that of the searched donor
- ► Obtain LR-distributions both for H_p and H_d (for power calculations)

See also K. Slooten, T. Egeland, Likelihood ratios and exclusion probabilities with applications to mixtures, Int. J. Legal Medicine 130, 2016

MixKin

Calculations have been carried out with Mathematica script MixKin.

- Dropout probability per donor
- LR calculations
- Relatedness under H_p (familial searching) or H_d (discriminate from relative)
- LR distributions to see expected LR's for non-donors, relatives of donors and donors
- Donor genotype probability distribution
- ROC curves

See also

- K. Slooten, Familial Searching on DNA mixtures with dropout, Forensic Science International: Genetics 22, 128–138, 2016
- K. Slooten, Discriminating between donors and their relatives in complex DNA mixtures, Forensic Science International: Genetics 21, 95–109, 2015

Mixture with dropout $(d_1, d_2, d_3) = (0.2, 0.3, 0.5)$ and c = 0.05:

D251338	{17., 21., 23., 24.}	{18., 20., 23., 24.}	{18., 20., 23., 24.}	
D351358	{15., 17.}	{15., 16., 17., 18.}	{15., 16.}	
FGA	{20., 23., 24.}	{21., 23., 24.}	{21., 24.}	
D851179	{12., 13., 14.}	{12., 13., 14.}	{12., 13., 14.}	
THO1	{8., 9., 9.3}	{7., 9.3}	{8., 9.}	
WWA	{16., 19.}	{14., 16., 17., 19.}	{14., 16., 17., 18.}	
D16S539	{11., 12., 13.}	{12., 13.}	{11., 12.}	
D18551	{12., 15., 18.}	{12., 15., 18.}	{12., 13., 15., 18., 19.}	
D195433	{13., 14., 15., 16.2}	{13., 14., 16.2}	{13., 14., 15.}	
D21511	{28., 29., 30., 30.2}	{28., 29., 30.2}	{28., 29., 30.2}	

Donor 1 (with $d_1 = 0.2$):

D2S1338	{20., 23.}
D3S1358	{16., 17.}
FGA	{24., 24.}
D8S1179	{13., 14.}
THO1	{9., 9.3}
VWA	{14., 16.}
D165539	{12., 13.}
D18551	{13., 15.}
D195433	{13., 14.}
D21511	{28., 29.}

FGA: donor is (24, 24)

Di65339 3 0.0027767 0.000767205 2.96879 0.472579 0.2371677 D951179 3 0.036803 0.038404 2.28739 6.79076 0.831919 0.2231587 D195433 4 0.000153201 0.00074127 2.06674 57.237 1.44285 0.7275822 D195433 4 0.000153201 0.00074127 2.06674 57.237 1.44285 0.7465320 D351354 4 0.000051271 0.00051114 1.03075 1122.13 3.05004 0.7315215 D18551 5 5.07057×10 ⁻⁷ 5.541×10 ⁻⁷ 0.915099 1026.86 3.01151 1.9253719 vNA 5 8.77879×10 ⁻⁴ 1.98099×10 ⁻⁶ 4.41348 4532.04 3.65629 1.9524050 D251335 6 2.8807×10 ⁻⁶ 7.067505 18468.3 4.26643 4.7773966 FGA [Prob for donor with dropout, 0.2] a priori prob LR {21., 24.} 0.266427 0.0459357 6.48322 [22., 24.] <td< th=""><th></th><th>(Locus</th><th>distinct alleles</th><th>h Hp</th><th>Lh Hd</th><th>LR locus</th><th>cumulative</th><th>LR Log(10, cumu-LR</th><th>time for locus</th><th>(3)</th></td<>		(Locus	distinct alleles	h Hp	Lh Hd	LR locus	cumulative	LR Log(10, cumu-LR	time for locus	(3)
DBS1179 3 0.0316583 0.0006102714 0.0976 0.831919 0.2231587 D21511 4 0.000249157 0.0000610277 1.64285 0.7275322 D195433 4 0.000153201 0.000074127 2.06674 57.2377 1.75814 0.7455309 FGA 4 0.0000527271 0.000051544 1.03075 1122.13 3.05604 0.7315215 D18551 5 5.07057×10 ⁻⁷ 5.541×10 ⁻⁷ 0.915099 1026.86 3.01151 1.9253719 vWA 5 8.77879×10 ⁻⁴ 1.9909×10 ⁻⁶ 4.41348 4532.04 3.65629 1.9524050 D251338 6 2.88807×10 ⁻⁶ 7.0872×10 ⁻⁶ 4.07505 18468.3 4.26643 4.7773906 FGA {Prob for donor with dropout, 0.2} a priori prob LR [21., 24.] 0.266427 0.0459493 5.79827 [23., 24.] 0.14714 0.0189475 7.7657 [21., 23.] 0.113006 0.0491514 2.29915 [20., 21.] 0.038481 <td< td=""><td></td><td>D16S539</td><td>3</td><td>0.00227767</td><td>0.000767205</td><td>2.96879</td><td>2.96879</td><td>0.472579</td><td>0.2371677</td><td></td></td<>		D16S539	3	0.00227767	0.000767205	2.96879	2.96879	0.472579	0.2371677	
D21311 4 0.000249157 0.00001297 4.08256 27.7237 1.44285 0.7245322 D138433 4 0.000153201 0.000074127 2.06674 57.2977 1.75814 0.7445170 TB01 4 5.01194 x10 ⁻⁶ 2.04899 x10 ⁻⁶ 2.44666 140.188 2.14671 0.7455309 FGA 4 0.000051271 0.000051134 1.03075 1122.13 3.05004 0.7315215 D18551 5 5.07057 x10 ⁻⁷ 5.541 x10 ⁻⁷ 0.915099 1026.86 3.01151 1.9253719 vNA 5 8.77879 x10 ⁻⁴ 7.0872 x10 ⁻⁵ 1.8488.3 4.26643 4.7773906 VNA 5 8.77879 x10 ⁻⁴ 7.0872 x10 ⁻⁵ 1.8488.3 4.26643 4.7773906 VNA 5 8.77879 x10 ⁻⁴ 7.0872 x10 ⁻⁵ 1.8488.3 4.26643 4.7773906 C21., 24.1 0.266427 0.0455357 6.48322 422.9915 4.29915 {21., 23.} 0.113006 0.0491514 2.29915 4.20643		D8S1179	3	0.0316583	0.0138404	2.28739	6.79076	0.831919	0.2231587	
D195433 4 0.000015201 0.000074127 2.06674 57.2977 1.75814 0.7465370 TR01 4 5.01194x10*2 2.04649x10*2 2.4666 140.188 2.14671 0.7455309 FGA 4 0.0000527271 0.000051154 1.03075 1122.13 3.05004 0.7315215 D18551 5 5.07057x10* 5.541x10* 0.91509 1026.86 3.01151 1.9253719 vNA 5 8.77879x10* 1.98909x10* 4.41348 4532.04 3.65629 1.9524050 D251338 6 2.88807x10* 7.0872x10* 4.07505 18468.3 4.26643 4.7773906 FGA [Prob for donor with dropout, 0.2] a priori prob LR [21., 24.] 0.266427 0.0459493 5.79827 [23., 24.] 0.14714 0.0189475 7.7657 [21., 23.] 0.113006 0.0491514 2.29915 [20., 24.] 0.0389302 0.0394764 0.986164 [21., 21.] 0.0149037 0.0278578 0.534991 [23., 23.] 0.0131309 0.0216803 <td></td> <td>D21511</td> <td>4</td> <td>0.000249157</td> <td>0.0000610297</td> <td>4.08256</td> <td>27.7237</td> <td>1.44285</td> <td>0.7275322</td> <td></td>		D21511	4	0.000249157	0.0000610297	4.08256	27.7237	1.44285	0.7275322	
$\begin{array}{cccccccccccccccccccccccccccccccccccc$		D195433	4	0.000153201	0.000074127	2.06674	57.2977	1.75814	0.7445170	
FGA 4 0.000389945 5.02138×10 ⁻⁶ 7.7657 1088.66 3.03689 0.7465320 D351358 4 0.000051271 0.000051141 1.03075 1122.13 3.05004 0.7315215 D18551 5 5.07057×10 ⁻⁷ 5.541×10 ⁻⁷ 0.915099 1026.86 3.01151 1.9253719 vNA 5 8.77879×10 ⁻⁴ 1.98909×10 ⁻⁶ 4.41348 4532.04 3.65629 1.9524050 D251338 6 2.88807×10 ⁻³ 7.0872×10 ⁻⁶ 4.07505 18468.3 4.27643 4.7773966 FGA [Prob for donor with dropout, 0.2] a priori prob LR {21., 24.} 0.266427 0.0459493 5.79827 {23., 24.} 0.262802 0.0405357 6.48322 24., 24. 0.14714 0.0189475 7.7657 {21., 23.} 0.113006 0.0491514 2.29915 {20., 24.} 0.0389302 0.0389407 2.53531 {20., 23.} 0.0131309 0.0278578 0.534991 {23., 23.}		THO1	4	5.01194×10-6	2.04849×10-6	2.44666	140.188	2.14671	0.7455309	
$\begin{array}{c c c c c c c c c c c c c c c c c c c $		FGA	4	0.0000389945	5.02138×10^{-6}	7.7657	1088.66	3.03689	0.7465320	
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$		D3S1358	4	0.0000527271	0.000051154	1.03075	1122.13	3.05004	0.7315215	
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$		D18551	5	5.07057×10-7	5.541×10^{-7}	0.915099	1026.86	3.01151	1.9253719	
$\begin{tabular}{ c c c c c c c c c c c c c c c c c c c$		WWA	5	8.77879×10 ⁻⁶	1.98909×10^{-6}	4.41348	4532.04	3.65629	1.9524050	
$\begin{array}{c c c c c c c c c c c c c c c c c c c $		D2S1338	6	2.88807×10 ⁻⁸	7.0872×10^{-9}	4.07505	18468.3	4.26643	4.7773906	
{21., 24.} 0.266427 0.0459493 5.79827 {23., 24.} 0.262802 0.0405357 6.48322 {24., 24.} 0.14714 0.0189475 7.7657 {21., 23.} 0.113006 0.0491514 2.29915 {20., 24.} 0.039481 0.0447485 0.881551 {20., 21.} 0.0394937 0.0394764 0.986164 {21., 23.} 0.0113009 0.0278578 0.534991 {23., 23.} 0.0131309 0.0216803 0.605659 {24., Unseen} 0.00215517 0.138248 0.0155892 {23., Unseen} 0.00214067 0.12196 0.0175522 {20., 20.} 0.000704931 0.0179701 0.0392279 {Unseen, Unseen} 0.0000100735 0.171519 0.0000587309	1	(FGA	{Prob for	donor with	dropout	, 0.2}	a priori prob	LR	3
{23., 24.} 0.262802 0.0405357 6.48322 {24., 24.} 0.14714 0.0189475 7.7657 {21., 23.} 0.113006 0.0491514 2.29915 {20., 24.} 0.0935648 0.0369047 2.53531 {20., 21.} 0.0394481 0.0447485 0.881551 {20., 23.} 0.0389302 0.0394764 0.986164 {21., 21.} 0.0149037 0.0278578 0.534991 {23., 23.} 0.0131309 0.0216803 0.65659 {24., Unseen} 0.00215517 0.138248 0.0155892 {23., Unseen} 0.00214067 0.12196 0.0175522 {20., 20.} 0.000704931 0.0179701 0.0392279 {Unseen, Unseen} 0.0000100735 0.17519 0.0000587309		{2	1., 24.}		0.266427	7		0.0459493	5.79827	
{24., 24.} 0.14714 0.0189475 7.7657 {21., 23.} 0.113006 0.0491514 2.29915 {20., 24.} 0.0935648 0.0369047 2.53531 {20., 21.} 0.039481 0.0447485 0.881551 {20., 23.} 0.0389302 0.0394764 0.986164 {21., 21.} 0.0149037 0.0278578 0.534991 {23., 23.} 0.00131309 0.0216803 0.605659 {24., Unseen} 0.00215517 0.138248 0.0155892 {23., Unseen} 0.00214067 0.12196 0.0175522 {20., 20.} 0.000704931 0.0179701 0.0392279 {Unseen, Unseen} 0.000100735 0.17519 0.0000587309		{2	3., 24.}		0.262802	2		0.0405357	6.48322	
{21., 23.} 0.113006 0.0491514 2.29915 {20., 24.} 0.0935648 0.0369047 2.53531 {20., 21.} 0.039481 0.0447485 0.881551 {20., 23.} 0.0389302 0.0394764 0.986164 {21., 21.} 0.0149037 0.0278578 0.534991 {23., 23.} 0.0131309 0.0216803 0.605659 {24., Unseen} 0.00215517 0.138248 0.0155892 {23., Unseen} 0.00214067 0.12196 0.0175522 {20., 20.} 0.000704931 0.0179701 0.0392279 {Unseen} 0.0000100735 0.171519 0.0000587309		{2	4., 24.}		0.14714			0.0189475	7.7657	
{20., 24.} 0.0935648 0.0369047 2.53531 {20., 21.} 0.039481 0.0447485 0.881551 {20., 23.} 0.0389302 0.0394764 0.986164 {21., 21.} 0.0149037 0.0278578 0.534991 {23., 23.} 0.0131309 0.0216803 0.605659 {24., Unseen} 0.00215517 0.138248 0.0155892 {23., Unseen} 0.00214067 0.12196 0.0175522 {20., Unseen} 0.000731383 0.111036 0.00658692 {20., 20.} 0.000704931 0.0179701 0.0392279 {Unseen} 0.0000100735 0.171519 0.0000587309		{2	1., 23.}		0.113000	6		0.0491514	2.29915	
{20., 21.} 0.0394481 0.0447485 0.881551 {20., 23.} 0.0389302 0.0394764 0.986164 {21., 21.} 0.0149037 0.0278578 0.534991 {23., 23.} 0.0131309 0.0216803 0.605659 {24., Unseen} 0.00490455 0.114015 0.0430167 {21., Unseen} 0.00215517 0.138248 0.0155892 {23., Unseen} 0.000731383 0.111036 0.00658692 {20., 20.} 0.000704931 0.0179701 0.0392279 {Unseen, Unseen} 0.0000100735 0.171519 0.0000587309		{2	0., 24.}		0.093564	8		0.0369047	2.53531	
{20., 23.} 0.0389302 0.0394764 0.986164 {21., 21.} 0.0149037 0.0278578 0.534991 {23., 23.} 0.0131309 0.0216803 0.605659 {24., Unseen} 0.00490455 0.114015 0.0430167 {21., Unseen} 0.00215517 0.138248 0.0155892 {23., Unseen} 0.000731383 0.111036 0.00658692 {20., Unseen} 0.000704931 0.0179701 0.0392279 {Unseen, Unseen} 0.0000100735 0.171519 0.0000587309		{2	0., 21.}		0.039448	1		0.0447485	0.881551	
{21., 21.} 0.0149037 0.0278578 0.534991 {23., 23.} 0.0131309 0.0216803 0.605659 {24., Unseen} 0.00490455 0.114015 0.0430167 {21., Unseen} 0.00215517 0.138248 0.0155892 {23., Unseen} 0.00214067 0.12196 0.0175522 {20., Unseen} 0.0007031383 0.111036 0.00658692 {20., 20.} 0.000704931 0.0179701 0.0392279 {Unseen, Unseen} 0.0000100735 0.171519 0.0000587309		{2	0., 23.}		0.038930	2		0.0394764	0.986164	
{23., 23.} 0.0131309 0.0216803 0.605659 {24., Unseen} 0.00490455 0.114015 0.0430167 {21., Unseen} 0.00215517 0.138248 0.015892 {23., Unseen} 0.00214067 0.12196 0.0175522 {20., Unseen} 0.000731383 0.111036 0.00658692 {20., 20.} 0.000704931 0.0179701 0.0392279 {Unseen, Unseen} 0.000100735 0.171519 0.0000587309		{2	1., 21.}		0.014903	7		0.0278578	0.534991	
{24., Unseen} 0.00490455 0.114015 0.0430167 {21., Unseen} 0.00215517 0.138248 0.015892 {23., Unseen} 0.00214067 0.12196 0.0175522 {20., Unseen} 0.000731383 0.111036 0.0058692 {20., 20.} 0.000704931 0.0179701 0.0392279 {Unseen, Unseen} 0.000100735 0.171519 0.0000587309		{2	3., 23.}		0.013130	9		0.0216803	0.605659	
{21., Unseen} 0.00215517 0.138248 0.0155892 {23., Unseen} 0.00214067 0.12196 0.0175522 {20., Unseen} 0.000731383 0.111036 0.00658692 {20., 20.} 0.000704931 0.0179701 0.0392279 {Unseen, Unseen} 0.0000100735 0.171519 0.0000587309		{24	., Unseen}		0.0049045	55		0.114015	0.0430167	
{23., Unseen} 0.00214067 0.12196 0.0175522 {20., Unseen} 0.000731383 0.111036 0.00658692 {20., 20.} 0.000704931 0.0179701 0.0392279 {Unseen, Unseen} 0.0000100735 0.171519 0.0000587309		{21	., Unseen}		0.0021551	17		0.138248	0.0155892	
{20., Unseen} 0.000731383 0.111036 0.00658692 {20., 20.} 0.000704931 0.0179701 0.0392279 {Unseen, Unseen} 0.0000100735 0.171519 0.0000587309		{23	., Unseen}		0.0021406	67		0.12196	0.0175522	
{20., 20.} 0.000704931 0.0179701 0.0392279 {Unseen, Unseen} 0.0000100735 0.171519 0.0000587309		{20	., Unseen}		0.0007313	83		0.111036	0.00658692	
{Unseen, Unseen} 0.0000100735 0.171519 0.0000587309		{2	0., 20.}		0.0007049	31		0.0179701	0.0392279	
		{Unse	en, Unseen}		0.00001007	735		0.171519	0.0000587309	9/

D16S539: donor is (12, 13)

(Locus	distinct alleles	Lh Hp	Lh Hd	LR locus	cumulative	LR Log(10, cumu-LR)	time for locus (3)
D16S539	3	0.00227767	0.000767205	2.96879	2.96879	0.472579	0.2371677	care c
D8S1179	3	0.0316583	0.0138404	2.28739	6.79076	0.831919	0.2231587	
D21511	4	0.000249157	0.0000610297	4.08256	27.7237	1.44285	0.7275322	
D195433	4	0.000153201	0.000074127	2.06674	57.2977	1.75814	0.7445170	
THO1	4	5.01194×10^{-6}	2.04849×10^{-6}	2.44666	140.188	2.14671	0.7455309	
FGA	4	0.0000389945	5.02138×10-6	7.7657	1088.66	3.03689	0.7465320	
D3S1358	4	0.0000527271	0.000051154	1.03075	1122.13	3.05004	0.7315215	
D18551	5	5.07057×10-7	5.541×10^{-7}	0.915099	1026.86	3.01151	1.9253719	
VWA	5	8.77879×10-6	1.98909×10 ⁻⁶	4.41348	4532.04	3.65629	1.9524050	
D251338	6	2.88807×10 ⁻⁸	7.0872×10^{-9}	4.07505	18468.3	4.26643	4.7773906	- 1
1	D165539	{Prob for	donor wit	h dropo	out, 0.2}	a priori prol	b LR	1
{	11., 12.}		0.3082	15		0.169968	1.81337	
	12., 13.}		0.2814	62		0.0948071	2.96879	
(12., 12.) {11., 13.} {11., 11.} {13., 13.} {12., Unseen} {11., Unseen}		0.252317 0.112117				0.0698379	3.6129	
						0.115369	0.971817	
		0.0262545				0.103415	0.253874	
		0.0143993 0.00291212 0.00119586				0.0321759	0.447517	
						0.124086	0.0234686	6
						0.150997	0.00791975	5
{13	3., Unseen}	0.0011222				0.0842252	0.0133238	8
Uns	een. Unseenl		4.10177×	10-6		0.055118	0.00007441	8

D21S11: donor is (28, 29)

/ Locus disting	st alleles Lh	Hp Lh Hd	LR locus	cumulative	LR Log(10,cumu-LR)	time for locus (s)
D165539	3 0.002	227767 0.000767205	2.96879	2.96879	0.472579	0.2371677
D851179	3 0.03	16583 0.0138404	2.28739	6.79076	0.831919	0.2231587
D21511	4 0.000	249157 0.0000610297	4.08256	27.7237	1.44285	0.7275322
D195433	4 0.000	153201 0.0000/412/	2.06674	57.2977	1.75814	0.7445170
THOI	4 5.0119	94×10 ° 2.04849×10 °	2.44666	140.188	2.14671	0.7455309
FGA	4 0.0000	0389945 5.02138×10"	7.7657	1088.66	3.03689	0.7465320
D351358	4 0.0000	527271 0.000051154	1.03075	1122.13	3.05004	0.7315215
D18551	5 5.0705	57×10- 5.541×10-	0.915099	1026.86	3.01151	1.9253719
VWA	5 8.7787	79×10 ⁻ 1.98909×10 ⁻	4.41348	4532.04	3.65629	1.9524050
D251338	6 2.8880	07×10 ⁻⁶ 7.0872×10 ⁻⁹	4.07505	18468.3	4.26643	4.7773906
(D21511	{Prob	for donor wit	h dropou	it, 0.2}	a priori prol	b LR
{28., 29	. }	0.2781	36		0.0681278	4.08256
{29., 30	.2}	0.2485	75		0.0132203	18.8025
{28., 30	.2}	0.2420	65		0.0111246	21.7595
{29., 29	. }	0.05875	79		0.0404811	1.45149
{28., 28	. }	0.05012	02		0.028664	1.74854
{29., 30	. }	0.03765	63		0.104122	0.361657
{28., 30	. }	0.03694	27		0.0876161	0.421643
{30., 30	.2}	0.03393	06		0.017002	1.99569
{30.2, 30	.2}	0.01028	77		0.00107937	9.53124
{29., Uns	een}	0.00105	602		0.135966	0.00776681
{28., Uns	een}	0.00104	596		0.114413	0.00914204
{30.2, Uns	een}	0.001002	293		0.0222019	0.0451731
{30., 30	.}	0.000293	695		0.0669531	0.00438658
{30., Uns	een}	0.000128	995		0.17486	0.000737704
{Unseen, Un	seen}	9.05262×	10-7		0.114169	7.92911×10^{-6}

Two mixtures

Deconvolute each mixture

- ► Mixture M: obtain probabilities P_{d,c}(D = g | M) based on the chosen dropout probabilities d and drop-in c
- ▶ Mixture *M*': obtain probabilities $P_{\vec{d'},c'}(D' = g \mid M')$ based on the chosen dropout probabilities $\vec{d'}$ and drop-in c'

Match the donors

- H_1 : D = D', i.e., common donor
- H_2 : $D \neq D'$, i.e., no common donor
- Then the LR becomes

$$LR(M, M') = \frac{P(M, M' \mid H_1)}{P(M, M' \mid H_2)}$$

= $\sum_{g} \frac{P_{\vec{d}, c}(D = g \mid M) P_{\vec{d}', c'}(D' = g \mid M')}{p(g)}$.

Properties

Special case: person-mixture

If M' is a single source trace (e.g. reference sample) with genotype g_0 then

$$LR(M, M') = \sum_{g} \frac{P_{\vec{d}, c}(D = g \mid M) P_{\vec{d'}, c'}(D' = g \mid M')}{p(g)}$$

reduces to

$$LR(M, g_0) = rac{P_{\vec{d}, c}(D = g_0 \mid M)}{p(g_0)} = rac{P_{\vec{d}, c}(M \mid D = g_0)}{P_{\vec{d}, c}(M)},$$

which is the previously discussed LR to test contribution of a Pol.

Therefore LR(M, M') can be seen as a natural extension of the LR method, for comparison of any pair of traces, each of which may but need not be a mixed one.

Power for two-person mixtures, no dropout, on the 15 NGM loci



True positive rate $TPR(t) = P(LR(M, M') \ge t | H_1)$ and false positive rate $FPR(t) = P(LR(M, M') \ge t | H_2)$ for various thresholds *t*; dots labelled by $Log_{10}(t)$.

Power for two-person mixtures, no dropout, on the 21 GlobalFiler loci



True positive rate $TPR(t) = P(LR(M, M') \ge t | H_1)$ and false positive rate $FPR(t) = P(LR(M, M') \ge t | H_2)$ for various thresholds *t*; dots labelled by $Log_{10}(t)$.

Dutch DNA database

Data

1417 two-person mixtures





(a) Histogram of the number of loci for which the mixtures from the database are typed. (b) Histogram of the number of loci for which the mixture pairs are compared.

Figure 1: Breakdown of database mixtures and mixture comparisons according to number of loci

Results

Parameters

- Dropout (0,0.5), c = 0, test for major donor to be the same
- Reason: sometimes a partly derived profile is entered instead of whole mixture

Results

 $1,417\cdot 1,416/2=1,003,236$ LR's calculated, of which 204,870 non-zero:



Matches above $Log_{10}(LR)$ -threshold t

/	t	Matches	
	0	3558	
	1	1288	
	2	410	
	3	118	
	4	43	
	5	32	
	6	26	
	7	26	
	8	22	
	9	16	
	10	12	
	11	7	
	12	6)

True positives

- All matches with $LR > 10^5$ were investigated
- In all cases, these turned out to indeed correspond to mixtures with a common donor

False negatives

- Two pairs were not found above the threshold
- ▶ These had *LR* equal to 6 resp. 1200

Conclusions

Summary

- LR calculation for contribution of a donor amounts to deconvolution of the mixture
- One can then 'match' two deconvoluted mixtures
- This yields LR for the mixtures to have/not to have a common donor
- This LR is a generalization of the trace-person LR usually considered
- Provides additional investigative information to connect cases with each other.
- False positive rate can be controlled by LR-threshold

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