

Distribution of paternity index and random man not excluded values from a simulated parentage testing study

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Abstract

The two most commonly used methods of determining paternity relationship in mass disasters and parentage testing on forensic science or clinical medicine is either to generate a paternity index (PI) or to calculate the chance of a random man not excluded (RMNE). The effect of these two calculations was compared using a total of 1,244 family groups that were randomly selected from 10,000 simulated families. The data used 15 STR loci to create duo cases, where the alleles from one parent are compared to that from a child, and trio parentage test, where the genotypes of both parents are compared with that from a child. The distribution range of the resulting PI values was significantly larger than that of 1/RMNE using the duo scenario. This was not the case with trio cases where fewer differences were noted. When the PI and 1/RMNE was performed for each family, the average ratio of PI/(1/RMNE) was 8.56 in a duo case and 1.80 in a trio parentage test. These data highlight the benefit of being able to create large virtual populations to undertake these types of test as well as illustrating the problems with linking a child to a parent. The study further illustrates the variation in the distribution for PI and RMNE values observed in this virtual population.

Keywords: paternity index, random man not excluded, parentage testing, STR loci

Introduction

The evaluation of DNA results for parentage testing is expressed based on a mathematical formula either as a paternity index (PI) or using the random man not excluded (RMNE) calculation. Commonly when calculating a PI and realistic prior probabilities cannot be established, the equal prior probability for all hypotheses was adopted [1], however the assumption is likely open to challenge. To circumvent this problem the RMNE method is used instead of the PI method in some countries [2]. The merits of random man not excluded and likelihood ratios in DNA mixture interpretation have been discussed [3], and the conclusions indicate that

LRs are more difficult to present in court and the RMNE statistic wastes information that should be utilized. On comparison of these two methods for parentage testing, only an expository review was reported by using simple examples to illustrate certain principles or properties [4]. Variations of distribution in parentage testing for these two methods were compared by using simulated families for forensic and medical applications in this study.

Materials and methods

Sampling

A total of 10,000 simulated families were generated using the 15 STR loci that comprise the Identifiler[®] kit

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(Applied Biosystems, Foster City, CA, USA) with allele frequencies taken from the Taiwanese population [5]. From the 10,000 families, 1,244 were selected randomly and a PI or RMNE determined [2, 6] assuming either a trio paternity test or a duo test. To simulate the 1,244 duo tests the “mother” was removed from the calculation.

Data analysis

Calculation of PI and RMNE was performed by Forensic DNA data analysis system [7], and the statistic analysis was performed by the SigmaPlot software [8]. In this study, variations of distribution for PI and RMNE were evaluated in duo and trio cases respectively. The reciprocal of RMNE value (1/RMNE) was adopted for representing the likelihood ratio between alleged father

and random man not excluded. The Kolmogorov-Smirnov goodness of fit test [9] was used to assess the distribution.

Results and discussion

Distribution of PI and 1/RMNE in duo parentage testing

The distribution of the PI and 1/RMNE values from the 1,244 duo families is shown in Table 1. The median, observed value (O) and expected value (E) for 30 intervals are provided in this table. The distribution of observed value and expected value was assessed by the Kolmogorov-Smirnov (KS) test. The KS value was 0.1351 and 0.1531 for PI(log) and 1/RMNE(log) respectively, both of which are lower than the critical P value. The distribution for the duo case is shown in Figure 1. The minimum and maximum value of observed

Table 1. Distributions of PI and 1/RMNE in 1,244 duo and trio families.

Interval	Duo ^a						Trio ^a					
	PI (log)			1/RMNE (log)			PI (log)			1/RMNE (log)		
	Median	O	E	Median	O	E	Median	O	E	Median	O	E
1	1.80	1	3.92	2.68	6	7.37	4.21	3	7.34	4.09	1	5.42
2	2.04	1	6.57	2.79	6	11.82	4.48	2	11.44	4.35	1	9.12
3	2.28	3	10.51	2.90	11	18.10	4.74	7	17.11	4.60	6	14.61
4	2.53	5	16.12	3.01	24	26.46	5.00	19	24.55	4.85	14	22.27
5	2.77	20	23.64	3.13	32	36.95	5.27	27	33.83	5.11	22	32.31
6	3.02	33	33.20	3.24	59	49.27	5.53	47	44.74	5.36	46	44.61
7	3.26	49	44.61	3.35	56	62.73	5.79	65	56.80	5.62	64	58.63
8	3.50	63	57.37	3.46	80	76.26	6.05	70	69.22	5.87	68	73.35
9	3.75	71	70.62	3.57	92	88.53	6.32	87	80.97	6.12	110	87.34
10	3.99	83	83.19	3.69	104	98.14	6.58	95	90.92	6.38	85	98.99
11	4.23	91	93.80	3.80	94	103.88	6.84	101	98.00	6.63	128	106.78
12	4.48	108	101.22	3.91	115	104.99	7.10	102	101.39	6.89	100	109.64

Table 1. (continued)

Interval	Duo ^a						Trio ^a					
	PI (log)			1/RMNE (log)			PI (log)			1/RMNE (log)		
	Median	O	E	Median	O	E	Median	O	E	Median	O	E
13	4.72	114	104.54	4.02	101	101.33	7.37	104	100.69	7.14	107	107.15
14	4.96	96	103.34	4.13	96	93.38	7.63	83	95.99	7.39	100	99.68
15	5.21	95	97.77	4.25	70	82.17	7.89	83	87.84	7.65	80	88.26
16	5.45	82	88.52	4.36	64	69.04	8.16	70	77.16	7.90	59	74.38
17	5.69	69	76.72	4.47	55	55.40	8.42	65	65.06	8.16	59	59.66
18	5.94	65	63.63	4.58	45	42.44	8.68	56	52.65	8.41	50	45.55
19	6.18	50	50.51	4.69	31	31.05	8.94	43	40.91	8.66	34	33.10
20	6.42	52	38.37	4.80	21	21.69	9.21	41	30.51	8.92	40	22.90
21	6.67	29	27.90	4.92	25	14.47	9.47	33	21.84	9.17	22	15.08
22	6.91	15	19.42	5.03	13	9.21	9.73	6	15.01	9.43	19	9.45
23	7.16	21	12.93	5.14	15	5.60	9.99	14	9.90	9.68	7	5.64
24	7.40	9	8.25	5.25	8	3.25	10.26	6	6.27	9.93	7	3.20
25	7.64	6	5.03	5.36	9	1.80	10.52	5	3.81	10.19	6	1.73
26	7.89	6	2.94	5.48	4	0.96	10.78	2	2.22	10.44	4	0.89
27	8.13	2	1.64	5.59	2	0.48	11.05	5	1.24	10.70	2	0.44
28	8.37	1	0.88	5.70	4	0.23	11.31	1	0.67	10.95	1	0.20
29	8.62	3	0.45	5.81	1	0.11	11.57	1	0.35	11.20	1	0.09
30	8.86	1	0.22	5.92	1	0.05	11.83	1	0.17	11.46	1	0.04
Mean		4.88	4.78		3.95	3.88		7.32	7.19		7.06	6.90
SD		1.14	1.16		0.55	0.52		1.25	1.30		1.17	1.14
KS			0.1351			0.1531			0.1822			0.1379
P			0.6121			0.4501			0.2456			0.5857

^aMedian was for each interval. O and E represented observed and expected value respectively.

PI was 47.39 and 1.18E+09 respectively. The minimum and maximum value of observed 1/RMNE was 419.65 and 9.53E+05 respectively. The observed standard deviation (SD) of PI (1.14) was 2 folds more than 1/RMNE (0.55) (Table 1), indicating that the distribution range of PI was larger than that of 1/RMNE. The distribution range was concentrated within 748.36 to 1.05E+05 for 95 % of 1/RMNE values. The distributions of PI and 1/RMNE ratio (PI/(1/RMNE)) for these families are shown in Table 2. The means of observed and expected values for PI were both slightly higher than those of 1/RMNE. The ratios were 8.56 (log 8.56=0.93) and 6.61 (log 6.61=0.82) respectively.

Distribution of PI and 1/RMNE in trio parentage testing

For the 1,244 families, the distribution of PI and 1/RMNE in trio parentage testing showed that the minimum observed PI value was 12117.07 and maximum

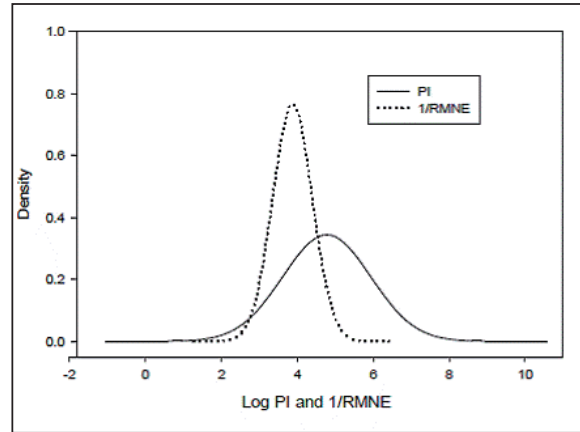


Fig.1 The distribution plot of PI and 1/RMNE in duo parentage testing. The x axis represents the log of the PI data and the 1/RMNE value. The y axis represents the Density (the normal probability density function). A higher mean value is observed for the PI data compared to the 1/RMNE and there is wider variation.

Table 2. Distributions of PI and 1/RMNE ratio in 1,244 duo and trio families.

Duo				Trio			
Interval	PI/(1/RMNE) (log)			Interval	PI/(1/RMNE) (log)		
	Median	O	E		Median	O	E
1	-1.70	2	2.86	1	-0.93	3	8.13
2	-1.49	4	5.14	2	-0.84	8	12.09
3	-1.27	6	8.78	3	-0.74	7	17.37
4	-1.06	15	14.26	4	-0.65	18	24.09
5	-0.85	18	21.99	5	-0.55	19	32.25
6	-0.64	27	32.21	6	-0.46	42	41.67
7	-0.43	42	44.80	7	-0.36	54	51.97
8	-0.22	56	59.20	8	-0.27	78	62.57
9	-0.01	74	74.29	9	-0.17	87	72.72
10	0.20	93	88.56	10	-0.08	72	81.58
11	0.42	101	100.26	11	0.02	95	88.35
12	0.63	113	107.81	12	0.11	97	92.36

Table 2. (continued)

Duo				Trio			
Interval	PI/(1/RMNE) (log)			Interval	PI/(1/RMNE) (log)		
	Median	O	E		Median	O	E
13	0.84	128	110.10	13	0.21	83	93.19
14	1.05	98	106.81	14	0.30	90	90.78
15	1.26	93	98.41	15	0.40	78	85.35
16	1.47	72	86.12	16	0.49	74	77.47
17	1.68	67	71.58	17	0.59	62	67.87
18	1.89	58	56.51	18	0.68	68	57.40
19	2.11	44	42.37	19	0.78	51	46.86
20	2.32	35	30.18	20	0.88	32	36.93
21	2.53	26	20.41	21	0.97	27	28.09
22	2.74	20	13.11	22	1.07	23	20.63
23	2.95	19	8.00	23	1.16	12	14.62
24	3.16	9	4.64	24	1.26	23	10.00
25	3.37	7	2.55	25	1.35	13	6.61
26	3.58	6	1.34	26	1.45	6	4.21
27	3.79	4	0.66	27	1.54	5	2.59
28	4.01	2	0.31	28	1.64	9	1.54
29	4.22	2	0.14	29	1.73	5	0.88
30	4.43	3	0.06	30	1.83	3	0.49
Mean		0.93	0.82	Mean		0.25	0.19
SD		1.00	0.93	SD		0.51	0.51
KS			0.1489	KS			0.0942
P			0.4858	P			0.9423

observed value was $9.22E+11$, whereas the minimum and maximum value of observed $1/RMNE$ was 9239.40 and $3.84E+11$ respectively. The KS value was 0.1822 for $PI(\log)$ and 0.1379 for $1/RMNE(\log)$, both of which were lower than the critical P value. Figure 2 shows the distribution in trio parentage testing. Comparing with the result reported by Buckleton J et al. [10], Figure 2 shows

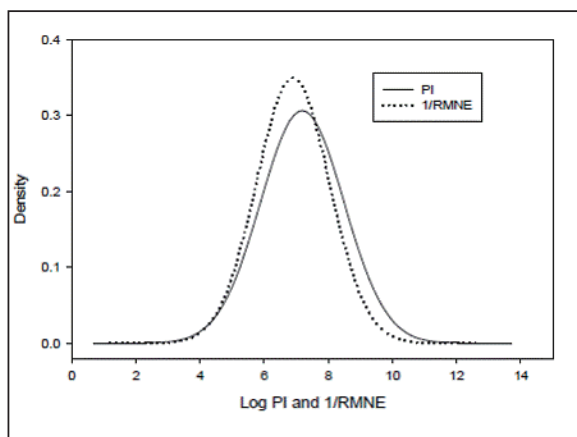


Fig.2 The distribution plot of PI and $1/RMNE$ in trio parentage testing. The x axis represents the log of the PI data and the $1/RMNE$ value. The y axis represents the Density (the normal probability density function). The two sets of data show much similarity with only minor increase in the mean of the PI data compared to that of the $1/RMNE$.

a distribution with slightly lower than it. This is expected to be resulted from the nature of different populations (African and Taiwanese). In this study, the expected mean of distribution for PI was 7.19 ($\log 15488166$) and for $1/RMNE$ was 6.90 ($\log 7943282.3$); with a SD of 1.30 for the PI and 1.14 for the $1/RMNE$ (Table 1). The distributions of PI and $1/RMNE$ ratio for these families are shown in Table 2. The mean of observed values for $PI/(1/RMNE)$ was 1.78 ($\log 1.78=0.25$) and the expected was 1.55 ($\log 1.55=0.19$). These data indicate that there are minor variations between PI and $1/RMNE$ values in trio parentage testing compared with the results in duo parentage testing.

Variations of PI and $1/RMNE$ for each family

In duo parentage testing, the minimum and maximum ratio of $PI/(1/RMNE)$ was 0.0158 and 34191.50 respectively with an average of 8.56. In trio parentage testing, the minimum and maximum ratio of

$PI/(1/RMNE)$ was 0.1047 and 74.82 respectively with an average of 1.80. The distribution curve in Figure 3 and SD in Table 2 indicates that the ratio ranges more extensively in duo than in trio parentage testing.

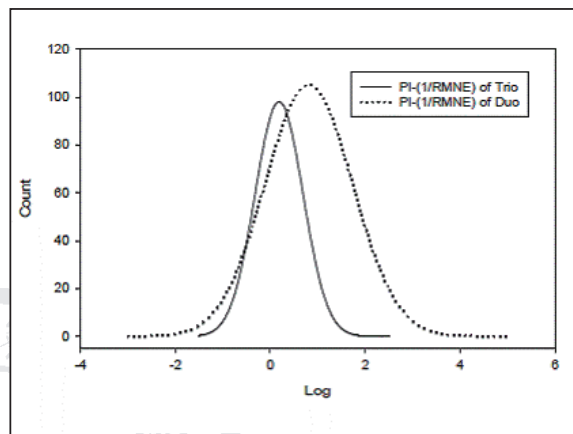


Fig.3 The distribution plot of $PI/(1/RMNE)$ ratio in duo and trio parentage testing. The x axis represents the log of the $PI/(1/RMNE)$ value. The y axis represents the Count (family numbers). The data indicate that there is a higher mean and larger distribution value for the duo compared to that of the trio cases using this virtual population.

For the individual family which had the minimum ratio of 0.0158 in duo parentage testing, the PI value was low when the alleged father and child were both heterozygote (Table 3). The PI was even lower when the shared allele of the alleged father and child was of common type; see TH01 data in Table 3. For the individual family with the maximum ratio (34191.50) in duo parentage testing, the PI value was high when the alleged father and child were both of heterozygote and have the same genotype (Table 3). The PI was even higher when a rare allele was shared; see TPOX and D21S11 data in Table 3. In duo parentage testing, where only the shared allele frequencies are used, the RMNE increases (or the $1/RMNE$ decreases) when the child is a heterozygote. The reverse was noted when the child was a homozygote for the locus where the alleles is shared. The variation range of $1/RMNE$ was narrow in duo parentage testing (Table 1) indicating that the variation of PI and $1/RMNE$ between individual families was primarily related to the genotype of alleged father and child and the frequency of the shared allele.

For the individual family which had the minimum ratio (0.1047) in trio parentage testing, the PI value

was low when the alleged father was a heterozygote (Table 4). The PI was even lower when the genotype of the mother and child were shared and the alleles were common; see TPOX in Table 4. For the individual family

with the maximum ratio (74.82) in trio parentage testing, the PI was usually higher when the alleged father was a homozygote rather than a heterozygote. The PI increased with the rarity of the shared allele. The ratio of PI and 1/

Table 3. The minimum and maximum ratios of PI/(1/RMNE) for each family in duo parentage testing.

STR marker	Minimum ^a					Maximum ^a				
	AF	C	PI	1/RMNE	PI/(1/RMNE)	AF	C	PI	1/RMNE	PI/(1/RMNE)
vWA	16, 18	16, 16	3.17	3.45	0.92	14, 17	14, 17	2.06	1.36	1.52
TH01	7, 9	9, 9.3	0.53	1.33	0.40	9, 9	6, 9	1.05	1.21	0.87
TPOX	8, 8	8, 8	1.80	1.25	1.45	8, 10	8, 10	12.47	1.22	10.22
CSF1PO	10, 12	10, 11	1.02	1.35	0.75	11, 11	10, 11	2.05	1.35	1.52
D5S818	9, 10	7, 10	1.24	2.44	0.51	10, 12	10, 12	2.41	1.52	1.59
D13S317	8, 9	9, 11	1.83	1.64	1.12	9, 11	9, 11	2.87	1.64	1.76
D7S820	8, 9	8, 8	3.88	4.14	0.94	8, 10	10, 11	1.63	1.33	1.23
D16S539	9, 11	9, 10	0.94	1.56	0.60	9, 12	9, 12	2.11	1.37	1.54
D2S1338	20, 24	20, 22	2.24	3.40	0.66	23, 23	19, 23	2.53	1.60	1.58
D8S1179	12, 13	10, 13	1.20	1.83	0.66	12, 15	12, 15	3.44	1.99	1.73
D21S11	29, 29	28, 29	1.97	1.93	1.02	28, 34	29, 34	208.33	2.25	92.55
D18S511	15, 17	15, 15	2.71	2.99	0.91	15, 18	13, 15	1.36	1.68	0.81
D19S433	12, 13	13, 15	0.82	1.65	0.50	13, 15.2	15, 15.2	1.66	2.56	0.65
D3S1358	16, 17	16, 16	1.61	1.91	0.84	14, 17	15, 17	1.07	1.21	0.88
FGA	23, 25	23, 24	1.16	1.60	0.73	20, 23	20, 23	5.84	2.15	2.71
Cumulative			566.538	35931.95	0.0158			33772729	987.7521	34191.50

^aAF and C represented alleged father and child respectively.

RMNE was greater than one when the alleged father was a homozygote; this is independent of the genotype of the child. If the alleged father was a heterozygote, the ratio of PI and 1/RMNE was more than one only when all shared the same genotype; see vWA in Table 4.

The cumulative PI is calculated based on the product of the frequency of shared alleles and, as shown by the

data, will result in a large variation between PI and 1/RMNE within the same family. It is the number of matching alleles used in the 1/RMNE calculation rather than the frequency of the shared alleles that is the major factor that affects the values. In contrast to the PI data, the value of RMNE is stable.

Table 4. The minimum and maximum ratios of PI/(1/RMNE) for each family in trio parentage testing.

STR marker	Minimum ^a					
	AF	M	C	PI	1/RMNE	PI/(1/RMNE)
vWA	14, 17	14, 16	16, 17	2.03	2.31	0.88
TH01	7, 9	7, 7	7, 9	1.05	1.38	0.76
TPOX	9, 11	8, 11	8, 11	0.59	1.03	0.58
CSF1PO	10, 11	11, 12	10, 12	2.04	2.32	0.88
D5S818	10, 12	10, 10	10, 10	2.48	2.76	0.90
D13S317	9, 11	8, 11	9, 11	3.67	3.93	0.93
D7S820	9, 12	9, 12	12, 12	2.08	2.36	0.88
D16S539	9, 10	9, 12	9, 9	1.88	2.17	0.87
D2S1338	18, 23	19, 24	18, 24	5.04	5.30	0.95
D8S1179	12, 14	13, 15	12, 15	3.88	4.15	0.94
D21S11	30, 31.2	29, 30	30, 30	1.90	2.19	0.87
D18S511	14, 15	16, 16	14, 16	2.49	2.76	0.90
D19S433	13, 15.2	15.2, 15.2	15.2, 15.2	3.33	3.60	0.92
D3S1358	15, 16	15, 17	15, 15	1.44	1.74	0.83
FGA	19, 24	23.2, 24	23.2, 24	2.73	3.01	0.91
Cumulative				111087.4	1060808	0.1047

^aAF, M and C represented alleged father, mother and child respectively..

Table 4. (continued)

STR marker	Maximum ^a					
	AF	M	C	PI	1/RMNE	PI/(1/RMNE)
vWA	14, 19	14, 19	14, 19	3.05	1.82	1.67
TH01	9, 9	7, 7	7, 9	2.11	1.38	1.53
TPOX	8, 8	8, 12	8, 12	1.74	1.22	1.42
CSF1PO	11, 12	11, 12	11, 11	2.05	2.34	0.88
D5S818	10, 11	11, 13	11, 13	1.08	1.40	0.77
D13S317	13, 13	12, 13	13, 13	29.67	15.09	1.97
D7S820	8, 8	9, 11	8, 9	7.75	4.14	1.87
D16S539	11, 11	9, 12	9, 11	3.74	2.16	1.73
D2S1338	19, 21	20, 22	19, 22	2.63	2.91	0.90
D8S1179	12, 12	12, 13	12, 12	7.76	4.15	1.87
D21S11	28, 30	27, 29	28, 29	9.42	9.67	0.97
D18S511	14, 19	13, 15	13, 19	13.70	13.95	0.98
D19S433	12, 12	14, 14.2	12, 14.2	28.01	14.26	1.96
D3S1358	16, 16	15, 17	16, 17	3.22	1.91	1.69
FGA	23, 24	22, 22	22, 23	2.32	2.60	0.89
Cumulative				1.17E+10	156350754	74.82

Conclusions

This study establishes a model for analyzing the variations in the distribution for PI and RMNE values in parentage testing on forensic science or clinical medicine. The distributions were obtained for the PI and RMNE data using 1,244 virtual families. The distribution of $PI/(1/RMNE)$ for duo families was more

dispersed than that for trio families highlighting the effect that different mathematic methods will have on the results using either of these tests; this is especially in the duo cases. These data highlight the benefit of being able to create large virtual populations to undertake these types of test as well as illustrating the problems with linking a child to a parent. The study further

illustrates the variation in the distribution for PI and RMNE values observed in this virtual population. This information is highly valuable for forensic and medical applications.

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