Relatedness and Kinship Statistics

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Relatedness

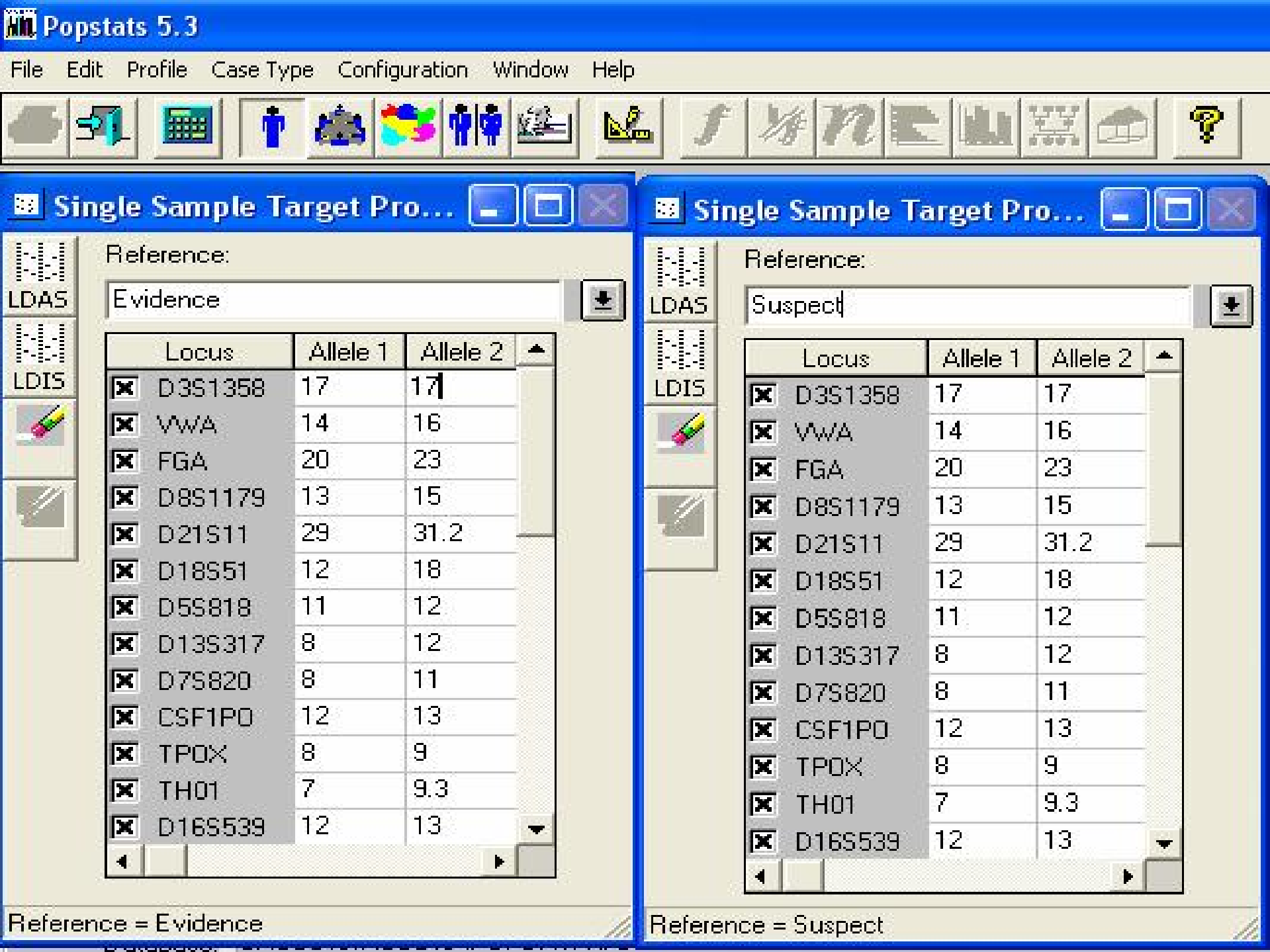
"**Relatedness is a consequence of sharing identical alleles. Alleles that have descended from a single ancestral allele are said to be Identical by Descent (IBD).**"* Alleles that are IBD will have the same base sequence.

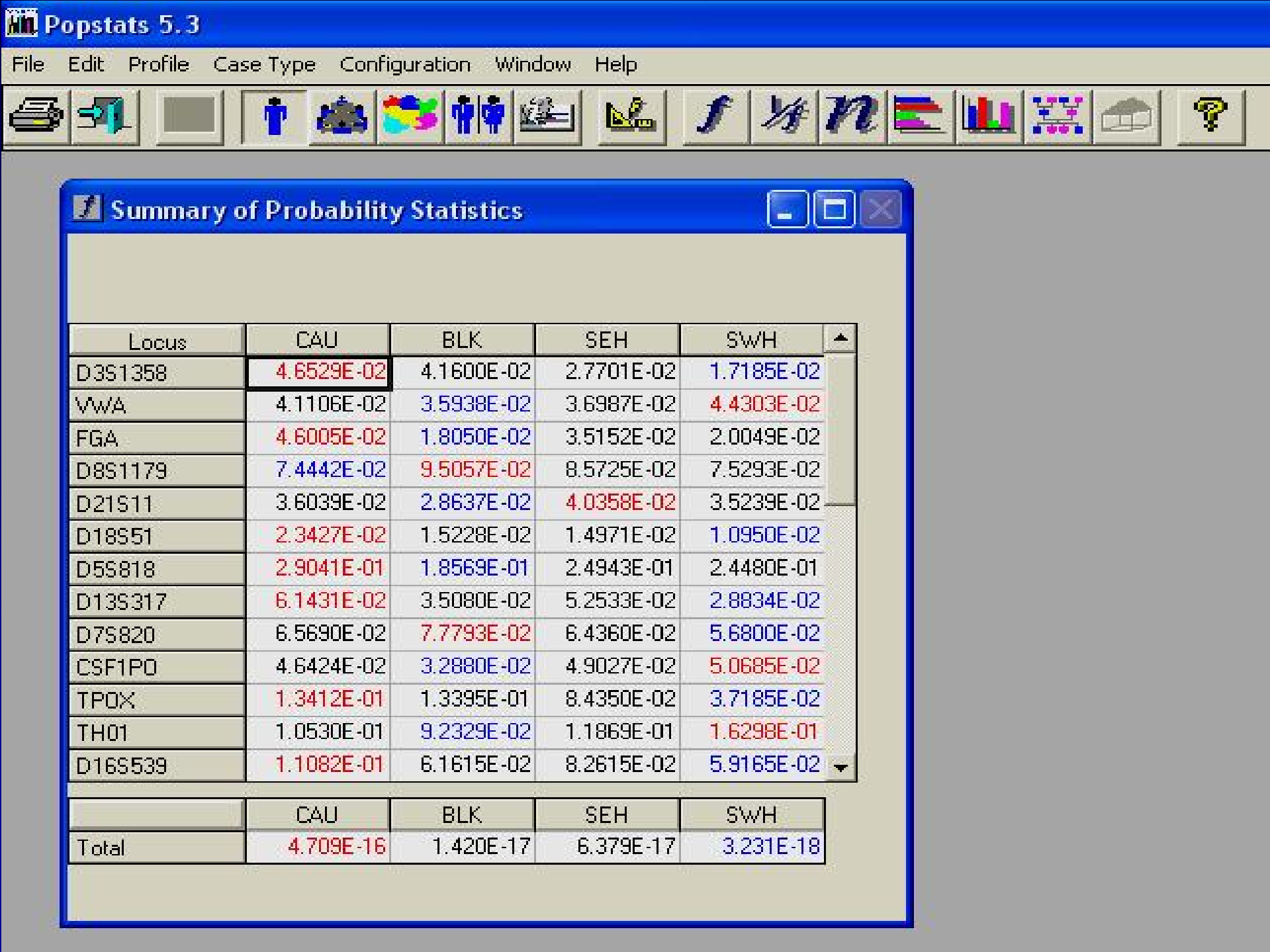
However, alleles with the same base sequence are not necessarily IBD, they can be Identical By State and not originate from the same ancestral allele. This may be true in an individual that is homozygous at a given locus.

* B.S. Weir, 1996. Genetic Data Analysis II. (p 204).

The genetic profile of a suspect matches the genetic profile of an evidentiary sample, therefore, the suspect cannot be excluded as a potential contributor of the biological evidentiary sample.

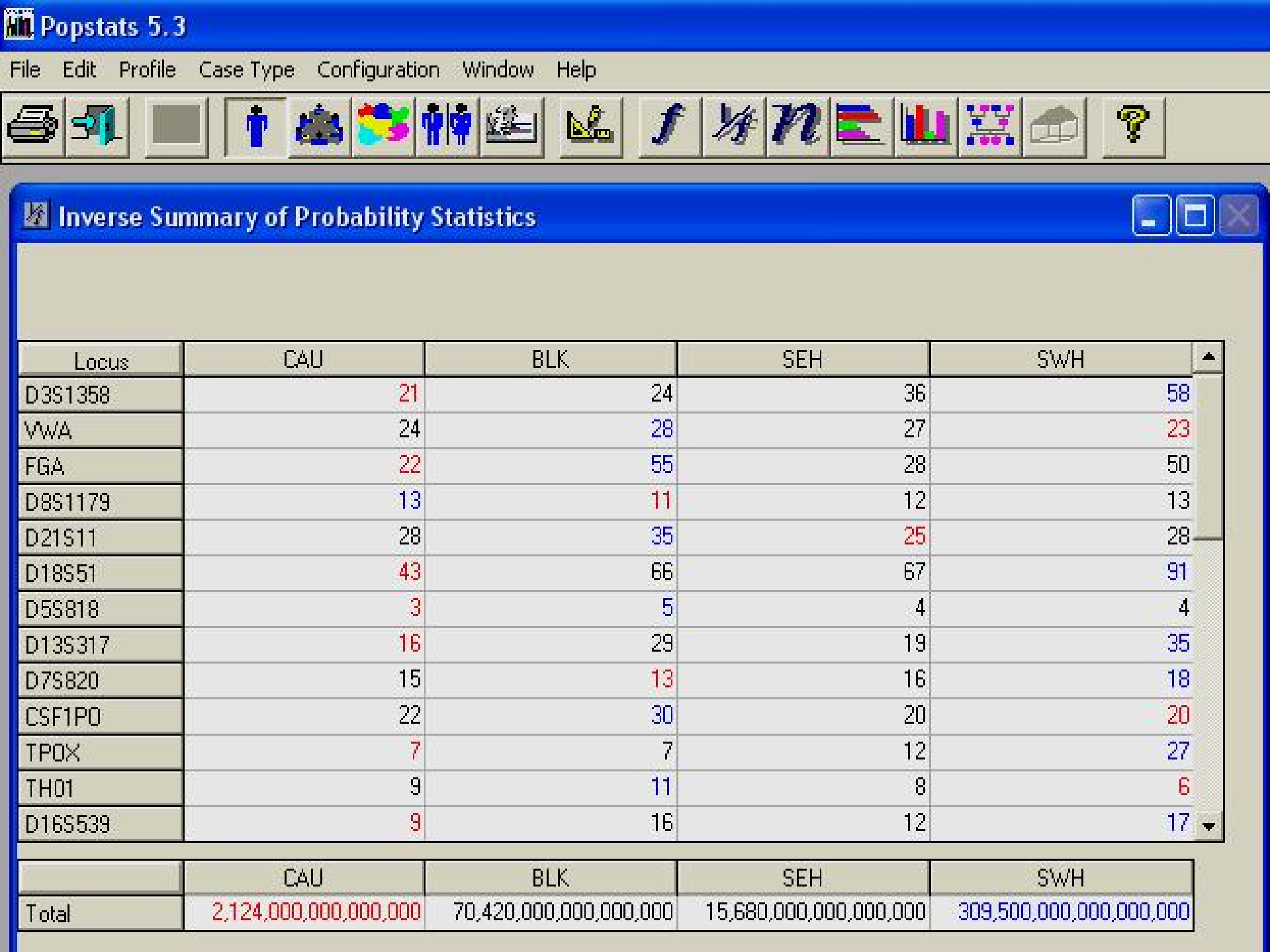
Popstats can then be used to calculate the frequency with which a person taken at random from a population of potential perpetrators has the profile in question?


Popstats 5.3
File Edit Profile Case Type Configuration Window Help
Single Sample Target Pro...
LDAS
LDIS
Reference:
Evidence
Locus Allele 1 Allele 2
D3S1358 17 17
VWA 14 16
FGA 20 23
D8S1179 13 15
D21S11 29 31.2
D18S51 12 18
D5S818 11 12
D13S317 8 12
D7S820 8 11
CSF1PO 12 13
TPOX 8 9
TH01 7 9.3
D16S539 12 13
Reference = Evidence
Single Sample Target Pro...
LDAS
LDIS
Reference:
Suspect
Locus Allele 1 Allele 2
D3S1358 17 17
VWA 14 16
FGA 20 23
D8S1179 13 15
D21S11 29 31.2
D18S51 12 18
D5S818 11 12
D13S317 8 12
D7S820 8 11
CSF1PO 12 13
TPOX 8 9
TH01 7 9.3
D16S539 12 13
Reference = Suspect



Locus	CAU	BLK	SEH	SWH
D3S1358	4.6529E-02	4.1600E-02	2.7701E-02	1.7185E-02
VWA	4.1106E-02	3.5938E-02	3.6987E-02	4.4303E-02
FGA	4.6005E-02	1.8050E-02	3.5152E-02	2.0049E-02
D8S1179	7.4442E-02	9.5057E-02	8.5725E-02	7.5293E-02
D21S11	3.6039E-02	2.8637E-02	4.0358E-02	3.5239E-02
D18S51	2.3427E-02	1.5228E-02	1.4971E-02	1.0950E-02
D5S818	2.9041E-01	1.8569E-01	2.4943E-01	2.4480E-01
D13S317	6.1431E-02	3.5080E-02	5.2533E-02	2.8834E-02
D7S820	6.5690E-02	7.7793E-02	6.4360E-02	5.6800E-02
CSF1PO	4.6424E-02	3.2880E-02	4.9027E-02	5.0685E-02
TPOX	1.3412E-01	1.3395E-01	8.4350E-02	3.7185E-02
TH01	1.0530E-01	9.2329E-02	1.1869E-01	1.6298E-01
D16S539	1.1082E-01	6.1615E-02	8.2615E-02	5.9165E-02

	CAU	BLK	SEH	SWH
Total	4.709E-16	1.420E-17	6.379E-17	3.231E-18



Locus	CAU	BLK	SEH	SWH
D3S1358	21	24	36	58
VWA	24	28	27	23
FGA	22	55	28	50
D8S1179	13	11	12	13
D21S11	28	35	25	28
D18S51	43	66	67	91
D5S818	3	5	4	4
D13S317	16	29	19	35
D7S820	15	13	16	18
CSF1PO	22	30	20	20
TPOX	7	7	12	27
TH01	9	11	8	6
D16S539	9	16	12	17

	CAU	BLK	SEH	SWH
Total	2,124,000,000,000,000	70,420,000,000,000,000	15,680,000,000,000,000	309,500,000,000,000,000

Relatedness Statistics

Although, unrelated individuals have a very low probability of sharing the same genetic profile with a suspect, the probability increases for relatives.

Relatedness Statistics

What is the probability of a person with a given degree of relatedness having the identical genotype as the known genotype of our suspect?

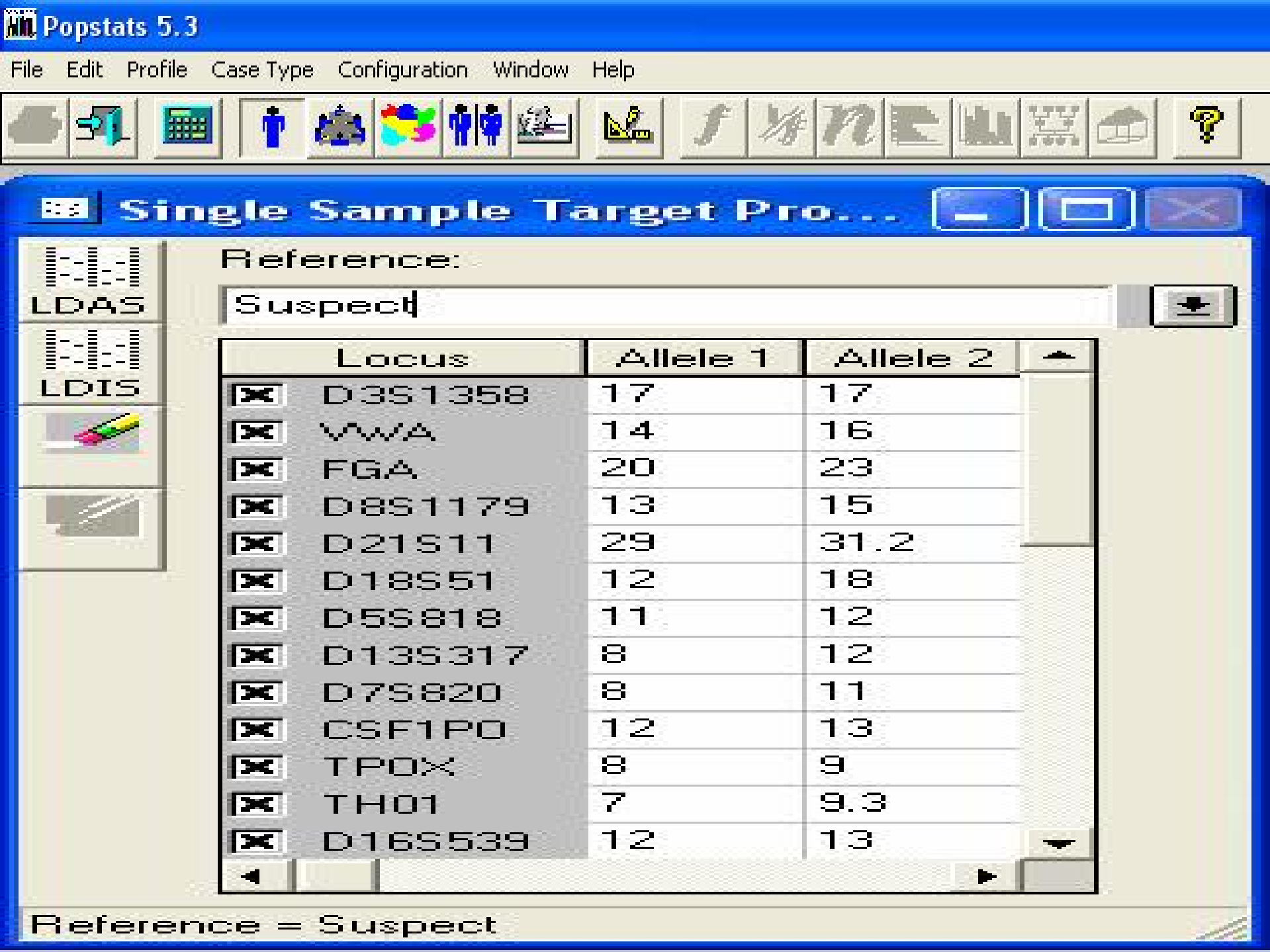
Relatedness Statistics

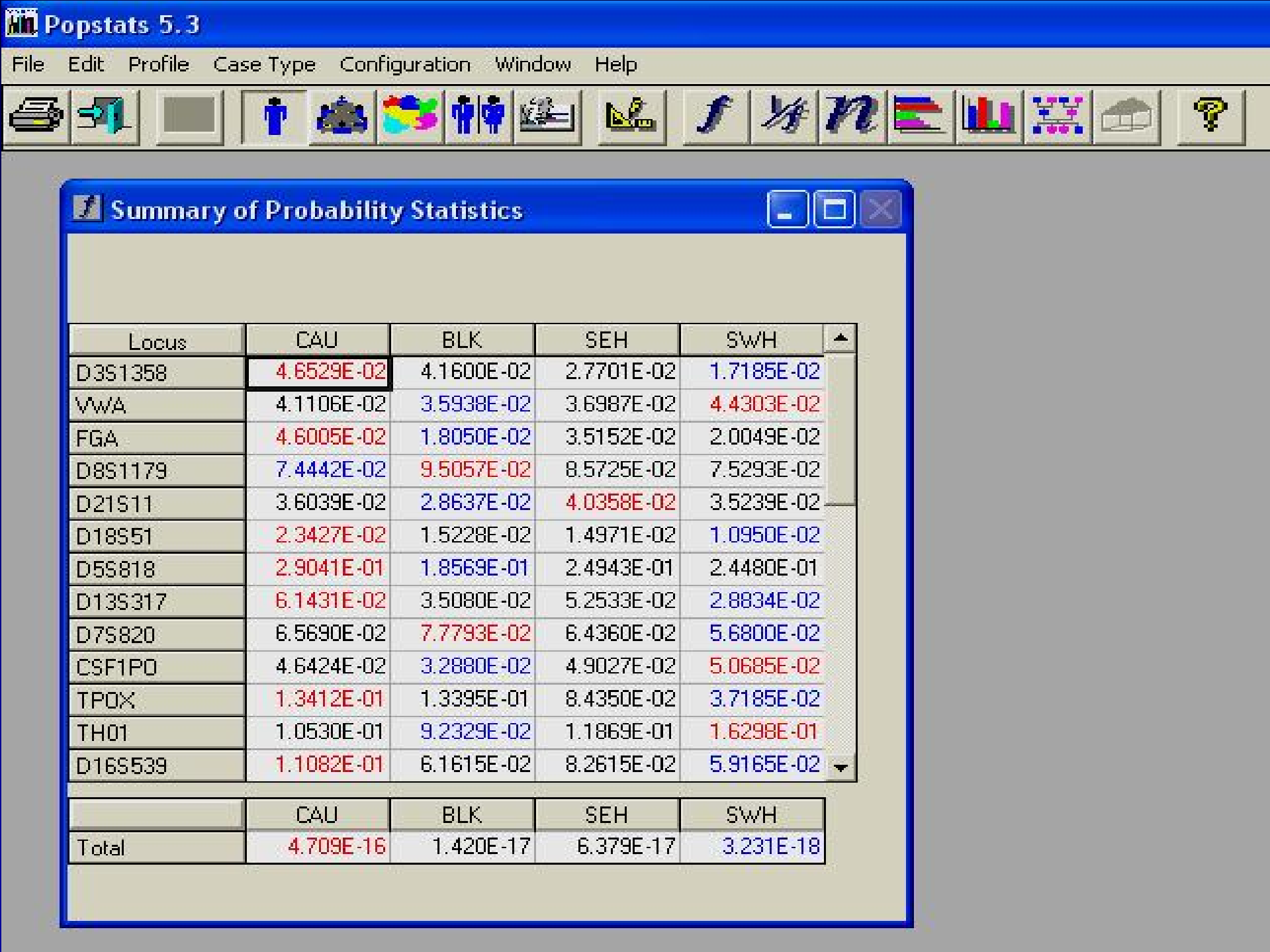
Calculations for related individuals are **conditional probabilities**. They answer the question for a specific genotype

In general, the closest relationship that has an impact on calculations is **full-sibs**

Coefficient of Kinship (F) definition:

- randomly select an allele from each of two individuals
- the probability that the two alleles are identical by descent (IBD) is called F, the coefficient of kinship
- the expected proportion of alleles that are IBD between two people is 2F


Popstats 5.3
File Edit Profile Case Type Configuration Window Help
Single Sample Target Pro...
LDAS
LDIS
Reference:
Suspect
Locus Allele 1 Allele 2
D3S1358 17 17
VWA 14 16
FGA 20 23
D8S1179 13 15
D21S11 29 31.2
D18S51 12 18
D5S818 11 12
D13S317 8 12
D7S820 8 11
CSF1PO 12 13
TPOX 8 9
TH01 7 9.3
D16S539 12 13
Reference = Suspect

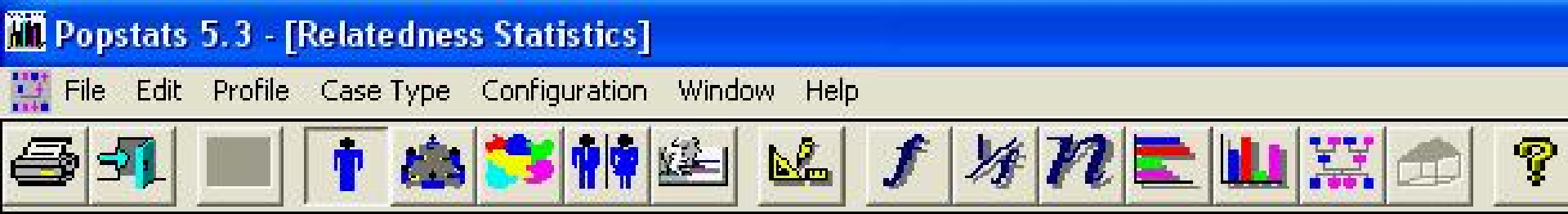


Locus	CAU	BLK	SEH	SWH
D3S1358	4.6529E-02	4.1600E-02	2.7701E-02	1.7185E-02
VWA	4.1106E-02	3.5938E-02	3.6987E-02	4.4303E-02
FGA	4.6005E-02	1.8050E-02	3.5152E-02	2.0049E-02
D8S1179	7.4442E-02	9.5057E-02	8.5725E-02	7.5293E-02
D21S11	3.6039E-02	2.8637E-02	4.0358E-02	3.5239E-02
D18S51	2.3427E-02	1.5228E-02	1.4971E-02	1.0950E-02
D5S818	2.9041E-01	1.8569E-01	2.4943E-01	2.4480E-01
D13S317	6.1431E-02	3.5080E-02	5.2533E-02	2.8834E-02
D7S820	6.5690E-02	7.7793E-02	6.4360E-02	5.6800E-02
CSF1PO	4.6424E-02	3.2880E-02	4.9027E-02	5.0685E-02
TPOX	1.3412E-01	1.3395E-01	8.4350E-02	3.7185E-02
TH01	1.0530E-01	9.2329E-02	1.1869E-01	1.6298E-01
D16S539	1.1082E-01	6.1615E-02	8.2615E-02	5.9165E-02

	CAU	BLK	SEH	SWH
Total	4.709E-16	1.420E-17	6.379E-17	3.231E-18

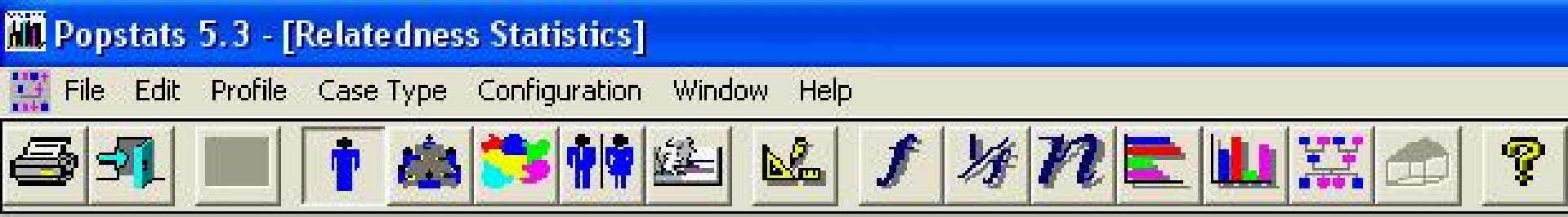
CAU | BLK | SEH | SWH

Locus	Unrelated	Parent/ Offspring	Full Sibling	Half Sibling/ Uncle/Aunt/ Nephew/Niece	First Cousin
D3S1358	4.6529E-02	2.1180E-01	3.6711E-01	1.2833E-01	8.6594E-02
VWA	4.1106E-02	1.5175E-01	3.3615E-01	9.6428E-02	6.8767E-02
FGA	4.6005E-02	1.5180E-01	3.3740E-01	9.8902E-02	7.2453E-02
D8S1179	7.4442E-02	2.2450E-01	3.8086E-01	1.4947E-01	1.1196E-01
D21S11	3.6039E-02	1.4030E-01	3.2916E-01	8.8169E-02	6.2104E-02
D18S51	2.3427E-02	1.0970E-01	3.1071E-01	6.6564E-02	4.4996E-02
D5S818	2.9041E-01	3.8210E-01	5.1365E-01	3.3626E-01	3.1333E-01
D13S317	6.1431E-02	2.0410E-01	3.6741E-01	1.3277E-01	9.7098E-02
D7S820	6.5690E-02	1.8230E-01	3.5757E-01	1.2400E-01	9.4843E-02
CSF1PO	4.6424E-02	1.9825E-01	3.6073E-01	1.2234E-01	8.4381E-02
TPOX	1.3412E-01	3.3375E-01	4.5040E-01	2.3393E-01	1.8402E-01
TH01	1.0530E-01	2.3890E-01	3.9578E-01	1.7210E-01	1.3870E-01
D16S539	1.1082E-01	2.5125E-01	4.0333E-01	1.8103E-01	1.4593E-01
Total	4.709E-16	9.519E-10	2.838E-06	5.299E-12	1.224E-13



CAU | BLK | SEH | SWH

Locus	Unrelated	Parent/ Offspring	Full Sibling	Half Sibling/ Uncle/Aunt/ Nephew/Niece	First Cousin
D3S1358	21	5	3	8	12
VWA	24	7	3	10	15
FGA	22	7	3	10	14
D8S1179	13	4	3	7	9
D21S11	28	7	3	11	16
D18S51	43	9	3	15	22
D5S818	3	3	2	3	3
D13S317	16	5	3	8	10
D7S820	15	5	3	8	11
CSF1PO	22	5	3	8	12
TPOX	7	3	2	4	5
TH01	9	4	3	6	7
D16S539	9	4	2	6	7
Total	2,124,000,000,000,000	1,051,000,000	352,400	188,700,000,000	8,170,000,000,000



CAU | **BLK** | SEH | SWH

Locus	Unrelated	Parent/ Offspring	Full Sibling	Half Sibling/ Uncle/Aunt/ Nephew/Niece	First Cousin
D3S1358	4.1600E-02	2.0000E-01	3.6000E-01	1.2000E-01	8.0000E-02
VWA	3.5938E-02	1.6805E-01	3.4301E-01	1.0199E-01	6.8966E-02
FGA	1.8050E-02	9.8600E-02	3.0381E-01	5.8325E-02	3.8188E-02
D8S1179	9.5057E-02	2.1805E-01	3.8279E-01	1.5655E-01	1.2581E-01
D21S11	2.8637E-02	1.3265E-01	3.2348E-01	8.0643E-02	5.4640E-02
D18S51	1.5228E-02	9.4450E-02	3.0103E-01	5.4839E-02	3.5033E-02
D5S818	1.8569E-01	3.0835E-01	4.5060E-01	2.4702E-01	2.1636E-01
D13S317	3.5080E-02	2.5975E-01	3.8865E-01	1.4742E-01	9.1248E-02
D7S820	7.7793E-02	1.9880E-01	3.6885E-01	1.3830E-01	1.0804E-01
CSF1PO	3.2880E-02	1.7740E-01	3.4692E-01	1.0514E-01	6.9010E-02
TPOX	1.3395E-01	2.7510E-01	4.2104E-01	2.0453E-01	1.6924E-01
TH01	9.2329E-02	2.7265E-01	4.0941E-01	1.8249E-01	1.3741E-01
D16S539	6.1615E-02	1.7585E-01	3.5333E-01	1.1873E-01	9.0174E-02
Total	1.420E-17	3.373E-10	1.909E-06	1.160E-12	1.566E-14

Popstats 5.3 - [Relatedness Statistics]

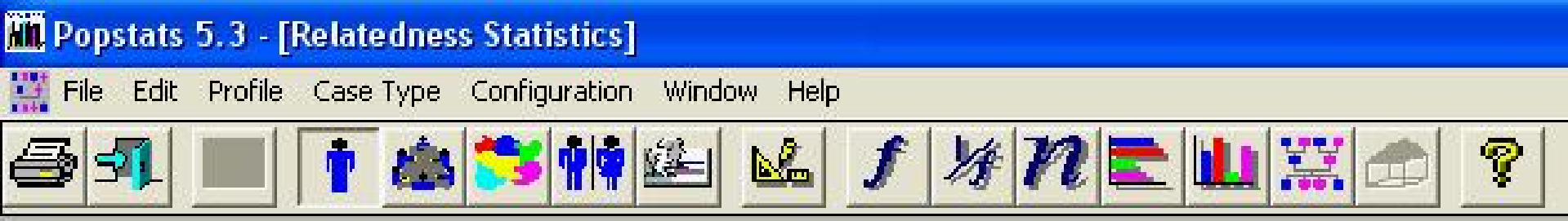
File Edit Profile Case Type Configuration Window Help

CAU | **BLK** | SEH | SWH

Locus	Unrelated	Parent/ Offspring	Full Sibling	Half Sibling/ Uncle/Aunt/ Nephew/Niece	First Cousin
D3S1358	24	5	3	8	13
VWA	28	6	3	10	15
FGA	55	10	3	17	26
D8S1179	11	5	3	6	8
D21S11	35	8	3	12	18
D18S51	66	11	3	18	29
D5S818	5	3	2	4	5
D13S317	29	4	3	7	11
D7S820	13	5	3	7	9
CSF1PO	30	6	3	10	14
TPOX	7	4	2	5	6
TH01	11	4	2	5	7
D16S539	16	6	3	8	11
Total	70,420,000,000,000,000	2,965,000,000	523,800	862,100,000,000	63,860,000,000,000

CAU | BLK | **SEH** | SWH

Locus	Unrelated	Parent/ Offspring	Full Sibling	Half Sibling/ Uncle/Aunt/ Nephew/Niece	First Cousin
D3S1358	2.7701E-02	1.6230E-01	3.3774E-01	9.4321E-02	6.0331E-02
VWA	3.6987E-02	1.6880E-01	3.4365E-01	1.0289E-01	6.9940E-02
FGA	3.5152E-02	1.3350E-01	3.2554E-01	8.4326E-02	5.9739E-02
D8S1179	8.5725E-02	2.3820E-01	3.9053E-01	1.6196E-01	1.2384E-01
D21S11	4.0358E-02	1.6230E-01	3.4124E-01	1.0133E-01	7.0844E-02
D18S51	1.4971E-02	9.5550E-02	3.0152E-01	5.5260E-02	3.5116E-02
D5S818	2.4943E-01	3.5525E-01	4.8998E-01	3.0234E-01	2.7589E-01
D13S317	5.2533E-02	1.7190E-01	3.4908E-01	1.1222E-01	8.2374E-02
D7S820	6.4360E-02	1.8440E-01	3.5829E-01	1.2438E-01	9.4370E-02
CSF1PO	4.9027E-02	2.1255E-01	3.6853E-01	1.3079E-01	8.9908E-02
TPOX	8.4350E-02	2.9480E-01	4.1849E-01	1.8957E-01	1.3696E-01
TH01	1.1869E-01	2.4375E-01	4.0155E-01	1.8122E-01	1.4995E-01
D16S539	8.2615E-02	2.0835E-01	3.7483E-01	1.4548E-01	1.1405E-01
Total	6.379E-17	4.841E-10	2.160E-06	2.047E-12	3.507E-14



CAU | BLK | **SEH** | SWH

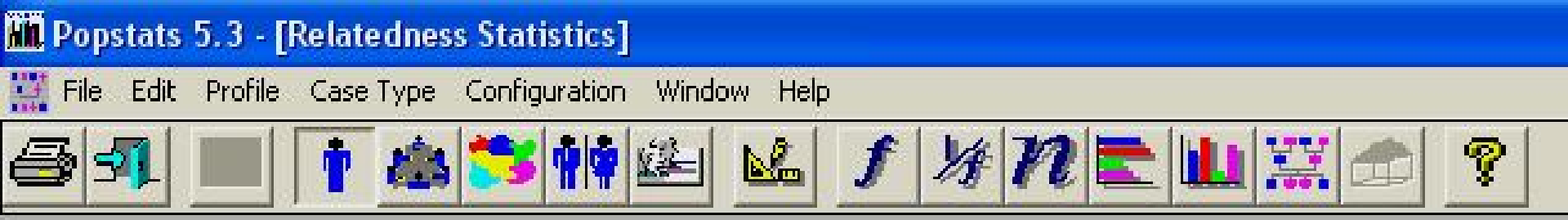
Locus	Unrelated	Parent/ Offspring	Full Sibling	Half Sibling/ Uncle/Aunt/ Nephew/Niece	First Cousin
D3S1358	36	6	3	11	17
VWA	27	6	3	10	14
FGA	28	7	3	12	17
D8S1179	12	4	3	6	8
D21S11	25	6	3	10	14
D18S51	67	10	3	18	28
D5S818	4	3	2	3	4
D13S317	19	6	3	9	12
D7S820	16	5	3	8	11
CSF1PO	20	5	3	8	11
TPOX	12	3	2	5	7
TH01	8	4	2	6	7
D16S539	12	5	3	7	9
Total	15,680,000,000,000,000	2,066,000,000	463,000	488,500,000,000	28,510,000,000,000

Popstats 5.3 - [Relatedness Statistics]

File Edit Profile Case Type Configuration Window Help

CAU | BLK | SEH | SWH

Locus	Unrelated	Parent/ Offspring	Full Sibling	Half Sibling/ Uncle/Aunt/ Nephew/Niece	First Cousin
D3S1358	1.7185E-02	1.2680E-01	3.1742E-01	7.1439E-02	4.3759E-02
VWA	4.4303E-02	2.1060E-01	3.6638E-01	1.2745E-01	8.5877E-02
FGA	2.0049E-02	1.0590E-01	3.0796E-01	6.2975E-02	4.1512E-02
D8S1179	7.5293E-02	2.2045E-01	3.7905E-01	1.4787E-01	1.1158E-01
D21S11	3.5239E-02	1.4530E-01	3.3146E-01	9.0269E-02	6.2754E-02
D18S51	1.0950E-02	7.8800E-02	2.9214E-01	4.4875E-02	2.7913E-02
D5S818	2.4480E-01	3.5590E-01	4.8915E-01	3.0035E-01	2.7258E-01
D13S317	2.8834E-02	1.4165E-01	3.2803E-01	8.5242E-02	5.7038E-02
D7S820	5.6800E-02	1.9380E-01	3.6110E-01	1.2530E-01	9.1050E-02
CSF1PO	5.0685E-02	2.2845E-01	3.7690E-01	1.3957E-01	9.5126E-02
TPOX	3.7185E-02	2.9425E-01	4.0642E-01	1.6572E-01	1.0145E-01
TH01	1.6298E-01	2.8945E-01	4.3547E-01	2.2622E-01	1.9460E-01
D16S539	5.9165E-02	1.9475E-01	3.6217E-01	1.2696E-01	9.3062E-02
Total	3.231E-18	2.643E-10	1.840E-06	7.319E-13	7.543E-15



CAU | BLK | SEH | **SWH**

Locus	Unrelated	Parent/ Offspring	Full Sibling	Half Sibling/ Uncle/Aunt/ Nephew/Niece	First Cousin
D3S1358	58	8	3	14	23
VWA	23	5	3	8	12
FGA	50	9	3	16	24
D8S1179	13	5	3	7	9
D21S11	28	7	3	11	16
D18S51	91	13	3	22	36
D5S818	4	3	2	3	4
D13S317	35	7	3	12	18
D7S820	18	5	3	8	11
CSF1PO	20	4	3	7	11
TPOX	27	3	2	6	10
TH01	6	3	2	4	5
D16S539	17	5	3	8	11
Total	309,500,000,000,000,000	3,784,000,000	543,500	1,366,000,000,000	132,600,000,000,000

Relatedness Statistics
Brothers
Prob (Full-Sibs have same given genotype)

$A_i A_i$ (homozygous locus): $(1 + p_i)^2 / 4$

$A_i A_j$ (heterozygous locus): $(1 + p_i + p_j + 2 p_i p_j) / 4$

LOCUS	ALLELE i	ALLELE j	ALLELE FREQ p_i	ALLELE FREQ p_j	FORMULA FULL SIBLING	FULL SIBLING
D3S1358	17		0.2118		$(1+p_i)^2 / 4$	0.36711
VWA	14	16	0.1020	0.2015	$(1+p_i+p_j+2p_ip_j) / 4$	0.33615
FGA	20	23	0.1454	0.1582	$(1+p_i+p_j+2p_ip_j) / 4$	0.33740
D8S1179	13	15	0.3393	0.1097	$(1+p_i+p_j+2p_ip_j) / 4$	0.38086
D21S11	29	31.2	0.1811	0.0995	$(1+p_i+p_j+2p_ip_j) / 4$	0.32916
D18S51	12	18	0.1276	0.0918	$(1+p_i+p_j+2p_ip_j) / 4$	0.31071
D5S818	11	12	0.4103	0.3538	$(1+p_i+p_j+2p_ip_j) / 4$	0.51361
D13S317	8	12	0.0995	0.3087	$(1+p_i+p_j+2p_ip_j) / 4$	0.36741
D7S820	8	11	0.1626	0.2020	$(1+p_i+p_j+2p_ip_j) / 4$	0.35757
CSF1PO	12	13	0.3251	0.0714	$(1+p_i+p_j+2p_ip_j) / 4$	0.36073
TPOX	8	9	0.5443	0.1232	$(1+p_i+p_j+2p_ip_j) / 4$	0.45040
TH01	7	9.3	0.1724	0.3054	$(1+p_i+p_j+2p_ip_j) / 4$	0.39578
D16S539	12	13	0.3391	0.1634	$(1+p_i+p_j+2p_ip_j) / 4$	0.40333
frequency (*f*)						2.838E-06
1 / frequency (1/*f*)						352,334

Probability that a Brother would have the same profile is 1 in 352,334

Relatedness Statistics
Brothers
Prob (Full-Sibs have same given genotype)

Probability is approximately 1/4 per locus, Therefore, for "L" loci,

The Probability that two full-sibs would have the same given genotype is approximately

$(1/4)^{L}$

Relatedness Statistics
Brothers
(Full-Sibs)

L	$(1/4)^L$
4	1 / 256
5	1 / 1024
:	:
9	1 / 262,144
:	:
13	1 / 67,108,864

Relatedness Statistics
Father and Son
Prob (Parent-Child have same given genotype)

$A_i A_i$ (homozygote): p_i

$A_i A_j$ (heterozygote): $(p_i + p_j) / 2$

LOCUS	ALLELE i	ALLELE j	ALLELE FREQ p_i	ALLELE FREQ p_j	FORMULA PARENT CHILD	PARENT & CHILD
D3S1358	17		0.2118		p_i	0.21180
VWA	14	16	0.1020	0.2015	$(p_i + p_j) / 2$	0.15175
FGA	20	23	0.1454	0.1582	$(p_i + p_j) / 2$	0.15180
D8S1179	13	15	0.3393	0.1097	$(p_i + p_j) / 2$	0.22450
D21S11	29	31.2	0.1811	0.0995	$(p_i + p_j) / 2$	0.14030
D18S51	12	18	0.1276	0.0918	$(p_i + p_j) / 2$	0.10970
D5S818	11	12	0.4103	0.3538	$(p_i + p_j) / 2$	0.38205
D13S317	8	12	0.0995	0.3087	$(p_i + p_j) / 2$	0.20410
D7S820	8	11	0.1626	0.2020	$(p_i + p_j) / 2$	0.18230
CSF1PO	12	13	0.3251	0.0714	$(p_i + p_j) / 2$	0.19825
TPOX	8	9	0.5443	0.1232	$(p_i + p_j) / 2$	0.33375
TH01	7	9.3	0.1724	0.3054	$(p_i + p_j) / 2$	0.23890
D16S539	12	13	0.3391	0.1634	$(p_i + p_j) / 2$	0.25125
frequency (*f*)						9.517E-10
1 / frequency (1/*f*)						1,050,718,457

Probability that a Father or Son would have the same profile is 1 in 1,050,718,457

Relatedness Statistics
Half-Brothers
Prob (Half-Sibs have same given genotype)

$A_i A_i$ (homozygous locus): $p_i (1 + p_i) / 2$

$A_i A_j$ (heterozygous locus): $(p_i + p_j + 4 p_i p_j) / 4$

LOCUS	ALLELE i	ALLELE j	ALLELE FREQ p_i	ALLELE FREQ p_j	FORMULA HALF SIBLING	HALF SIBLING
D3S1358	17		0.2118		$p_i (1+ p_i) / 2$	0.12833
VWA	14	16	0.1020	0.2015	$(p_i + p_j + 4p_ip_j) / 4$	0.09643
FGA	20	23	0.1454	0.1582	$(p_i + p_j + 4p_ip_j) / 4$	0.09890
D8S1179	13	15	0.3393	0.1097	$(p_i + p_j + 4p_ip_j) / 4$	0.14947
D21S11	29	31.2	0.1811	0.0995	$(p_i + p_j + 4p_ip_j) / 4$	0.08817
D18S51	12	18	0.1276	0.0918	$(p_i + p_j + 4p_ip_j) / 4$	0.06656
D5S818	11	12	0.4103	0.3538	$(p_i + p_j + 4p_ip_j) / 4$	0.33619
D13S317	8	12	0.0995	0.3087	$(p_i + p_j + 4p_ip_j) / 4$	0.13277
D7S820	8	11	0.1626	0.2020	$(p_i + p_j + 4p_ip_j) / 4$	0.12400
CSF1PO	12	13	0.3251	0.0714	$(p_i + p_j + 4p_ip_j) / 4$	0.12234
TPOX	8	9	0.5443	0.1232	$(p_i + p_j + 4p_ip_j) / 4$	0.23393
TH01	7	9.3	0.1724	0.3054	$(p_i + p_j + 4p_ip_j) / 4$	0.17210
D16S539	12	13	0.3391	0.1634	$(p_i + p_j + 4p_ip_j) / 4$	0.18103
frequency (*f*)						5.298E-12
1 / frequency (1/*f*)						188,748,573,845

Probability that a Half Brother would have the same profile is 1 in 188,748,573,845

Relatedness Statistics
Uncle-Nephew

Prob (Uncle and Nephew have same given genotype)

$A_i A_i$ (homozygous locus): $p_i (1 + p_i) / 2$

$A_i A_j$ (heterozygous locus): $(p_i + p_j + 4 p_i p_j) / 4$

LOCUS	ALLELE i	ALLELE j	ALLELE FREQ p_i	ALLELE FREQ p_j	FORMULA UNCLE NEPHEW	UNCLE & NEPHEW
D3S1358	17		0.2118		$p_i (1+ p_i) / 2$	0.12833
VWA	14	16	0.1020	0.2015	$(p_i + p_j + 4p_ip_j) / 4$	0.09643
FGA	20	23	0.1454	0.1582	$(p_i + p_j + 4p_ip_j) / 4$	0.09890
D8S1179	13	15	0.3393	0.1097	$(p_i + p_j + 4p_ip_j) / 4$	0.14947
D21S11	29	31.2	0.1811	0.0995	$(p_i + p_j + 4p_ip_j) / 4$	0.08817
D18S51	12	18	0.1276	0.0918	$(p_i + p_j + 4p_ip_j) / 4$	0.06656
D5S818	11	12	0.4103	0.3538	$(p_i + p_j + 4p_ip_j) / 4$	0.33619
D13S317	8	12	0.0995	0.3087	$(p_i + p_j + 4p_ip_j) / 4$	0.13277
D7S820	8	11	0.1626	0.2020	$(p_i + p_j + 4p_ip_j) / 4$	0.12400
CSF1PO	12	13	0.3251	0.0714	$(p_i + p_j + 4p_ip_j) / 4$	0.12234
TPOX	8	9	0.5443	0.1232	$(p_i + p_j + 4p_ip_j) / 4$	0.23393
TH01	7	9.3	0.1724	0.3054	$(p_i + p_j + 4p_ip_j) / 4$	0.17210
D16S539	12	13	0.3391	0.1634	$(p_i + p_j + 4p_ip_j) / 4$	0.18103
frequency (*f*)						5.298E-12
1 / frequency (1/*f*)						188,748,573,845

Probability that a Uncle or a Nephew would have the same profile is 1 in 188,748,573,845

Relatedness Statistics
First Cousins
Prob (First Cousins have same given genotype)

$A_i A_i$ (homozygous locus): $p_i (1 + 3p_i) / 4$

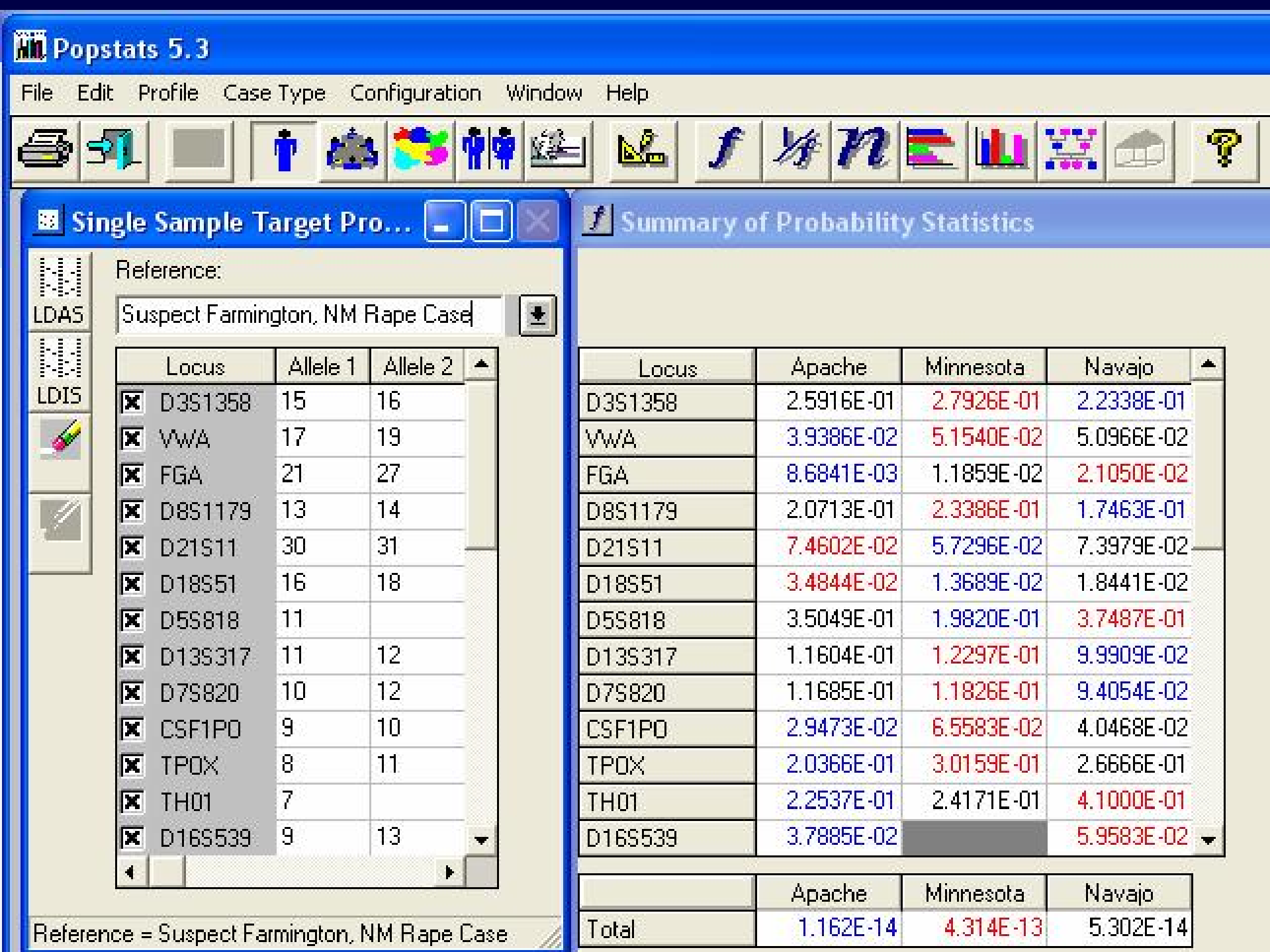
$A_i A_j$ (heterozygous locus): $(p_i + p_j + 12 p_i p_j) / 8$

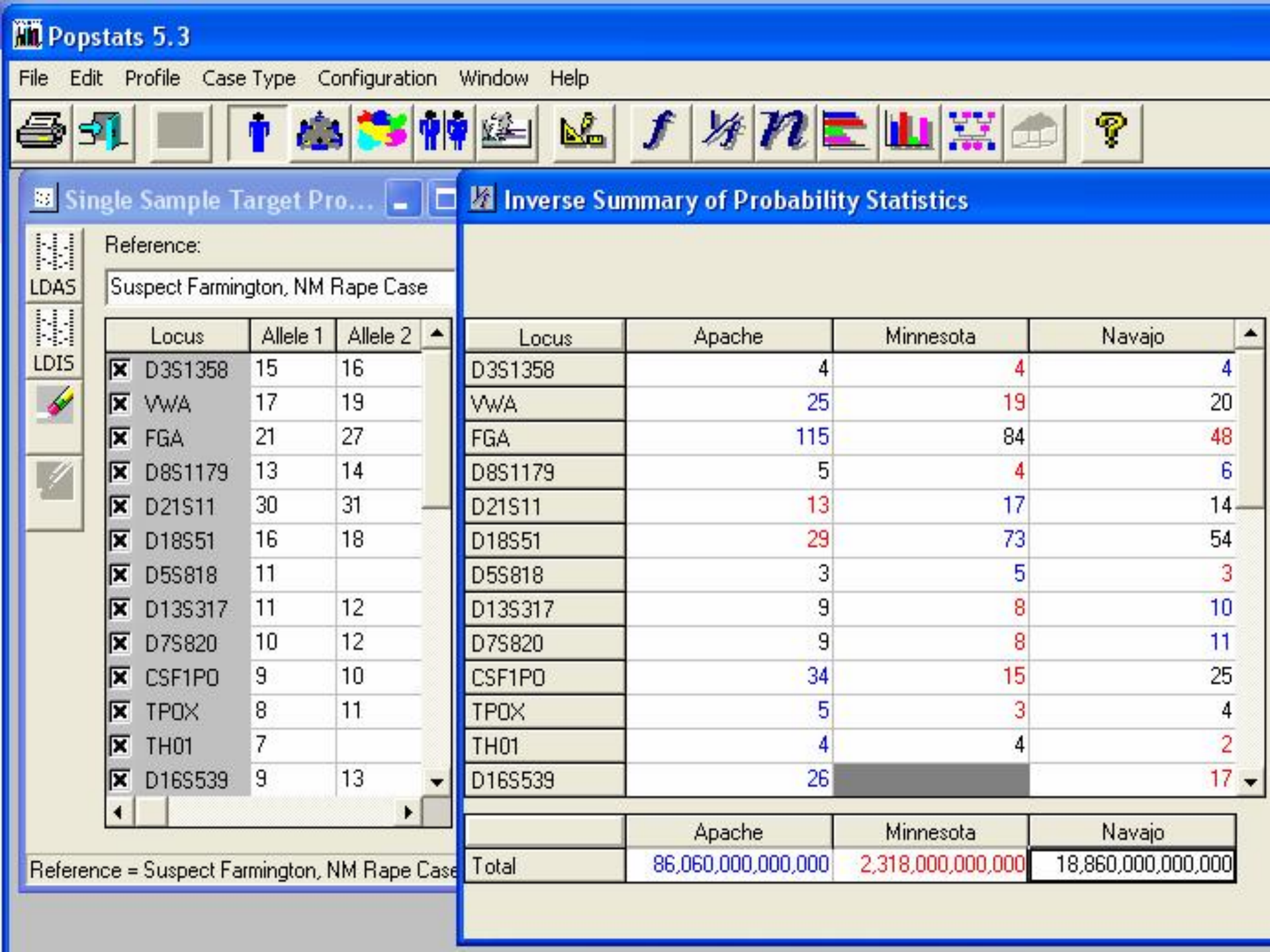
LOCUS	ALLELE i	ALLELE j	ALLELE FREQ p_i	ALLELE FREQ p_j	FORMULA FIRST COUSIN	FIRST COUSIN
D3S1358	17		0.2118		$p_i (1 + 3p_i) / 4$	0.08659
VWA	14	16	0.1020	0.2015	$(p_i + p_j + 12p_ip_j) / 8$	0.06877
FGA	20	23	0.1454	0.1582	$(p_i + p_j + 12p_ip_j) / 8$	0.07245
D8S1179	13	15	0.3393	0.1097	$(p_i + p_j + 12p_ip_j) / 8$	0.11196
D21S11	29	31.2	0.1811	0.0995	$(p_i + p_j + 12p_ip_j) / 8$	0.06210
D18S51	12	18	0.1276	0.0918	$(p_i + p_j + 12p_ip_j) / 8$	0.04500
D5S818	11	12	0.4103	0.3538	$(p_i + p_j + 12p_ip_j) / 8$	0.31326
D13S317	8	12	0.0995	0.3087	$(p_i + p_j + 12p_ip_j) / 8$	0.09710
D7S820	8	11	0.1626	0.2020	$(p_i + p_j + 12p_ip_j) / 8$	0.09484
CSF1PO	12	13	0.3251	0.0714	$(p_i + p_j + 12p_ip_j) / 8$	0.08438
TPOX	8	9	0.5443	0.1232	$(p_i + p_j + 12p_ip_j) / 8$	0.18402
TH01	7	9.3	0.1724	0.3054	$(p_i + p_j + 12p_ip_j) / 8$	0.13870
D16S539	12	13	0.3391	0.1634	$(p_i + p_j + 12p_ip_j) / 8$	0.14593
frequency (*f*)						1.224E-13
1 / frequency (1/*f*)						8,171,074,738,912

Probability that a First Cousin would have the same profile is 1 in 8,171,074,738,912

Sexual Assault Case Processed by the Arizona Department of Public Safety, Southern Regional Crime Laboratory in Tucson for the Farmington, New Mexico Police Department

Sexual Assault Case in which the suspects DNA profile matched the DNA profile from the male fraction of the vaginal swab collected from victim


Popstats 5.3
File Edit Profile Case Type Configuration Window Help
Single Sample Target Pro...
LDAS
LDIS
Reference:
Suspect Farmington, NM Rape Case
Locus | Allele 1 | Allele 2
D3S1358 15 16
VWA 17 19
FGA 21 27
D8S1179 13 14
D21S11 30 31
D18S51 16 18
D5S818 11
D13S317 11 12
D7S820 10 12
CSF1PO 9 10
TPOX 8 11
TH01 7
D16S539 9 13
Reference = Suspect Farmington, NM Rape Case
Summary of Probability Statistics
Locus | Apache | Minnesota | Navajo
D3S1358 2.5916E-01 2.7926E-01 2.2338E-01
VWA 3.9386E-02 5.1540E-02 5.0966E-02
FGA 8.6841E-03 1.1859E-02 2.1050E-02
D8S1179 2.0713E-01 2.3386E-01 1.7463E-01
D21S11 7.4602E-02 5.7296E-02 7.3979E-02
D18S51 3.4844E-02 1.3689E-02 1.8441E-02
D5S818 3.5049E-01 1.9820E-01 3.7487E-01
D13S317 1.1604E-01 1.2297E-01 9.9909E-02
D7S820 1.1685E-01 1.1826E-01 9.4054E-02
CSF1PO 2.9473E-02 6.5583E-02 4.0468E-02
TPOX 2.0366E-01 3.0159E-01 2.6666E-01
TH01 2.2537E-01 2.4171E-01 4.1000E-01
D16S539 3.7885E-02 5.9583E-02
Apache Minnesota Navajo
Total 1.162E-14 4.314E-13 5.302E-14


Popstats 5.3
File Edit Profile Case Type Configuration Window Help
Single Sample Target Pro...
LDAS
LDIS
Reference:
Suspect Farmington, NM Rape Case
Locus Allele 1 Allele 2
D3S1358 15 16
VWA 17 19
FGA 21 27
D8S1179 13 14
D21S11 30 31
D18S51 16 18
D5S818 11
D13S317 11 12
D7S820 10 12
CSF1PO 9 10
TPOX 8 11
TH01 7
D16S539 9 13
Reference = Suspect Farmington, NM Rape Case
Inverse Summary of Probability Statistics
Locus Apache Minnesota Navajo
D3S1358 4 4 4
VWA 25 19 20
FGA 115 84 48
D8S1179 5 4 6
D21S11 13 17 14
D18S51 29 73 54
D5S818 3 5 3
D13S317 9 8 10
D7S820 9 8 11
CSF1PO 34 15 25
TPOX 5 3 4
TH01 4 4 2
D16S539 26 17
Apache Minnesota Navajo
Total 86,060,000,000,000 2,318,000,000,000 18,860,000,000,000

The approximate frequency of this profile in the Native American (Navajo) Population

is

1 in 18.86 trillion (1.886×10^{13})

The probability of finding an unrelated, random individual from the Native American (Navajo) population that matches the male fraction of the vaginal swab is

1 in 18.86 trillion (1.886×10^{13})

THE BROTHER DID IT?

Defense argued that the suspects brother committed the crime. Defense called Dr. Dan Krane from Wright State University in Ohio to testify to probability of a brother having the same profile.

Popstats 5.3

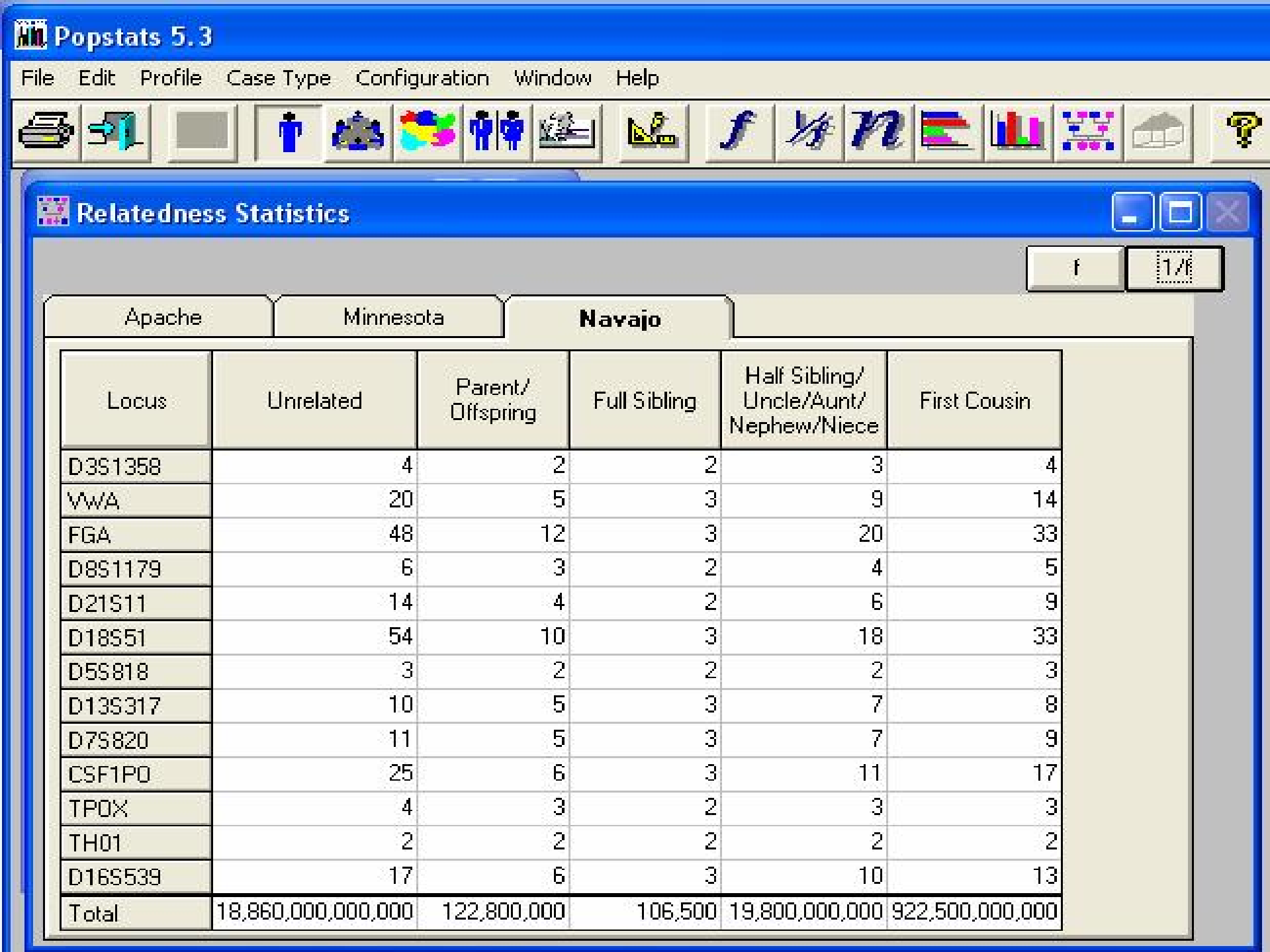
File Edit Profile Case Type Configuration Window Help

Relatedness Statistics

f 1/f

Apache | Minnesota | **Navajo**

Locus	Unrelated	Parent/ Offspring	Full Sibling	Half Sibling/ Uncle/Aunt/ Nephew/Niece	First Cousin
D3S1358	2.2338E-01	4.3820E-01	5.1987E-01	3.2064E-01	2.6186E-01
VWA	5.0966E-02	1.8410E-01	3.5066E-01	1.0928E-01	7.1864E-02
FGA	2.1050E-02	8.6550E-02	2.9623E-01	4.9178E-02	3.0492E-02
D8S1179	1.7463E-01	2.9595E-01	4.3900E-01	2.3003E-01	1.9708E-01
D21S11	7.3979E-02	2.7840E-01	4.0157E-01	1.6394E-01	1.0672E-01
D18S51	1.8441E-02	1.0135E-01	3.0241E-01	5.4149E-02	3.0548E-02
D5S818	3.7487E-01	5.8240E-01	6.2600E-01	4.6079E-01	3.9999E-01
D13S317	9.9909E-02	2.1015E-01	3.7708E-01	1.4909E-01	1.1855E-01
D7S820	9.4054E-02	2.1295E-01	3.7670E-01	1.4692E-01	1.1390E-01
CSF1PO	4.0468E-02	1.5525E-01	3.3408E-01	9.0544E-02	5.8192E-02
TPOX	2.6666E-01	3.6265E-01	4.9699E-01	3.1265E-01	2.8765E-01
TH01	4.1000E-01	6.1260E-01	6.5012E-01	4.9394E-01	4.3461E-01
D16S539	5.9583E-02	1.5540E-01	3.3970E-01	1.0170E-01	7.4850E-02
Total	5.302E-14	8.145E-09	9.387E-06	5.051E-11	1.084E-12



Locus	Unrelated	Parent/ Offspring	Full Sibling	Half Sibling/ Uncle/Aunt/ Nephew/Niece	First Cousin
D3S1358	4	2	2	3	4
VWA	20	5	3	9	14
FGA	48	12	3	20	33
D8S1179	6	3	2	4	5
D21S11	14	4	2	6	9
D18S51	54	10	3	18	33
D5S818	3	2	2	2	3
D13S317	10	5	3	7	8
D7S820	11	5	3	7	9
CSF1PO	25	6	3	11	17
TPOX	4	3	2	3	3
TH01	2	2	2	2	2
D16S539	17	6	3	10	13
Total	18,860,000,000,000	122,800,000	106,500	19,800,000,000	922,500,000,000

THE BROTHER DID IT?

The probability of finding a brother of the suspect that matches the male fraction of the vaginal swab is

1 in 106,500

If the suspect had 106,500 brothers,
1 would be expected to have the same profile as the suspect

THE BROTHER DID IT?

However, it is **1.77×10^8** times more likely to see this profile in an untested brother as opposed to an untested, randomly chosen individual from the Native American (Navajo) population

This is an answer to a different question other than the match probability for the evidentiary sample

THE BROTHER DID IT?

The problem was that the suspects brother was deceased and not available for testing

Even though the chance of the untested brother having the same profile was very low;

The trial ended with a hung jury

Relatedness Statistics

We can calculate a Likelihood Ratio (for any given profile) in which the probability that the suspect is the contributor of the evidence is compared with the probability that a specified relative is the contributor of the evidence

In the following example the profile at a given locus is either homozygous or heterozygous and the allele frequency is 0.1

Formulas: B.S. Weir, 1996. Genetic Data Analysis II. Table 5.7 (p 221).

Relationship	Homozygous Locus	Heterozygous Locus
Unrelated	100.00	50.00
Full-Sibs	3.31	3.28
Parent-Child	10.00	10.00
Half-Sibs	18.18	16.67
Uncle-Nephew	18.18	16.67
First Cousins	30.76	25.00

Kinship Determination From Genotype Data On Two Individuals

Currently Popstats does not have the capability of calculating the most likely kinship relationship between two individuals whose genotypes are known.

Kinship Determination From Genotype Data On Two Individuals

There are a number of programs that are available to provide statistical support for the kinship relationship between two individuals with observed genotypes.

Currently the FBI has released a contract to develop the appropriate software which would be included in future versions of Popstats.

Kinship Determination From Genotype Data On Two Individuals

The programs that are available to provide statistical support for the kinship relationship between two individuals with observed genotypes essentially make use of the same algorithm.

Let Gx(l) and Gy(l) be the genotypes of two individuals X and Y, the algorithm finds the best support for the kinship relationship between individuals X and Y based upon genotypes Gx(l) and Gy(l) for L loci (l = 1,2,....,L)

Kinship Determination From Genotype Data On Two Individuals

The algorithm requires two sets of information.

First, the kinship of two individuals dictate with what probabilities the genotypes of two individuals will have two, one or zero alleles IBD. These three quantities are denoted by:

$$\phi_2,\ \phi_1, \text{ and } \phi_0,\ (0 \leq \phi_i \leq 1,\ \phi_2 + \phi_1 + \phi_0 = 1),$$

IBD status 2, 1, and 0 are called as events I, T, and O.

Kinship Determination From Genotype Data On Two Individuals

The algorithm requires two sets of information.

Second, the probabilities of Gy(l) given Gx(l) at the l-th locus, under the scenarios of I, T, and O (i.e., under the scenario that Gx(l) and Gy(l) have 2, 1, or 0 alleles IBD)

The three conditional probabilities are:

$P_2(xy)$ = probability of $G_y(l)$ given $G_x(l)$ with 2 of their alleles IBD

$P_1(xy)$ = probability of $G_y(l)$ given $G_x(l)$ with 1 of their alleles IBD

$P_0(xy)$ = probability of $G_y(l)$ given $G_x(l)$ with 0 of their alleles IBD

Kinship Determination From Genotype Data On Two Individuals

The three conditional probabilities are:

$P_2(xy)$ = probability of $G_y(l)$ given $G_x(l)$ with 2 of their alleles IBD

$P_1(xy)$ = probability of $G_y(l)$ given $G_x(l)$ with 1 of their alleles IBD

$P_0(xy)$ = probability of $G_y(l)$ given $G_x(l)$ with 0 of their alleles IBD

The likelihood of observing $G_y(l)$ given $G_x(l)$ for a given kinship (i.e., for a given set of ϕ_2, ϕ_1, and ϕ_0 is computed by

$$[P_2(xy) \times \phi_2] + [P_1(xy) \times \phi_1] + [P_0(xy) \times \phi_0]$$

Kinship Determination From Genotype Data On Two Individuals

$$[P_2(xy) \times \phi_2] + [P_1(xy) \times \phi_1] + [P_0(xy) \times \phi_0]$$

The likelihoods that are computed for each locus can be multiplied over all L loci to compute the combined likelihood under a specified kinship relationship. The kinship that provides the maximum likelihood is the best-supported kinship relationship for the observed genotype profiles of individuals X and Y.

At a Single Locus, Two Individuals Can Have the Following Genotypes

#1	#2	
AB	AB	2 alleles shared
AA	AA	
AA	AB	1 allele shared
AB	AC	
AB	CD	0 alleles shared
AA	BB	
AA	BC	

Identity By Descent (IBD) Coefficients:

	ϕ_2	ϕ_1	ϕ_0
• Full sibs	1/4	1/2	1/4
• Parent-child	0	1	0
• Half-sibs	0	1/2	1/2
• Cousins	0	1/4	3/4
• Unrelated	0	0	1

How Are The Identity By Descent (IBD) Coefficients Determined:

	ϕ_2	ϕ_1	ϕ_0
Full sibs	1/4	1/2	1/4

Lets say we have two parents AB and CD, their offspring are either AC, AD, BC, or BD

	AC	AD	BC	BD
AC	2	1	1	0
AD	1	2	0	1
BC	1	0	2	1
BD	0	1	1	2

2 alleles IBD = 4/16 or ¼

1 alleles IBD = 8/16 or ½

0 alleles IBD = 4/16 or ¼

How Are The Identity By Descent (IBD) Coefficients Determined:

	ϕ_2	ϕ_1	ϕ_0
Parent - Child	0	1	0

Lets say we have two parents AB and CD, their offspring are either AC, AD, BC, or BD

	AB	CD
AC	1	1
AD	1	1
BC	1	1
BD	1	1

2 alleles IBD = 0/8 or 0

1 alleles IBD = 8/8 or 1

0 alleles IBD = 0/8 or 0

How Are The Identity By Descent (IBD) Coefficients Determined:

	ϕ_2	ϕ_1	ϕ_0
Half-sibs	0	1/2	1/2

Lets say we have three parents AB (m), CD (af1), and EF (af2) their offspring are either AC, AD, BC, BD or AE, AF, BE, BF

	AE	AF	BE	BF
AC	1	1	0	0
AD	1	1	0	0
BC	0	0	1	1
BD	0	0	1	1

2 alleles IBD = 0/16 or 0

1 alleles IBD = 8/16 or 1/2

0 alleles IBD = 8/16 or 1/2

The Identity By Descent (IBD) Coefficients

	ϕ_2	ϕ_1	ϕ_0
Half-Sibs	0	1/2	1/2
Uncle/Aunt/Nephew/Niece	0	1/2	1/2
Grandparent-Grandchild	0	1/2	1/2

IBD Coefficients are the same for these kinship relationships

Kinship Formula:

C.C. Li and L.Sachs, 1954.
Method of ITO stochastic matrices

Transition matrix for 2 alleles IBD

$$I = \begin{array}{c|ccc} & A_1A_1 & A_1A_2 & A_2A_2 \\ A_1A_1 & 1 & 0 & 0 \\ A_1A_2 & 0 & 1 & 0 \\ A_2A_2 & 0 & 0 & 1 \end{array}$$

Kinship Formula

Transition matrix for 1 allele IBD

$$T = \begin{array}{c|ccc} & A_1A_1 & A_1A_2 & A_2A_2 \\ A_1A_1 & p_1 & p_2 & 0 \\ A_1A_2 & 0.5p_1 & 0.5(p_1+p_2) & 0.5p_2 \\ A_2A_2 & 0 & p_1 & p_2 \end{array}$$

Kinship Formula:

Transition matrix for 0 alleles IBD

$$O = \begin{array}{c|ccc} & A_1A_1 & A_1A_2 & A_2A_2 \\ A_1A_1 & p_1^2 & 2p_1p_2 & p_2^2 \\ A_1A_2 & p_1^2 & 2p_1p_2 & p_2^2 \\ A_2A_2 & p_1^2 & 2p_1p_2 & p_2^2 \end{array}$$

Kinship Formulas:

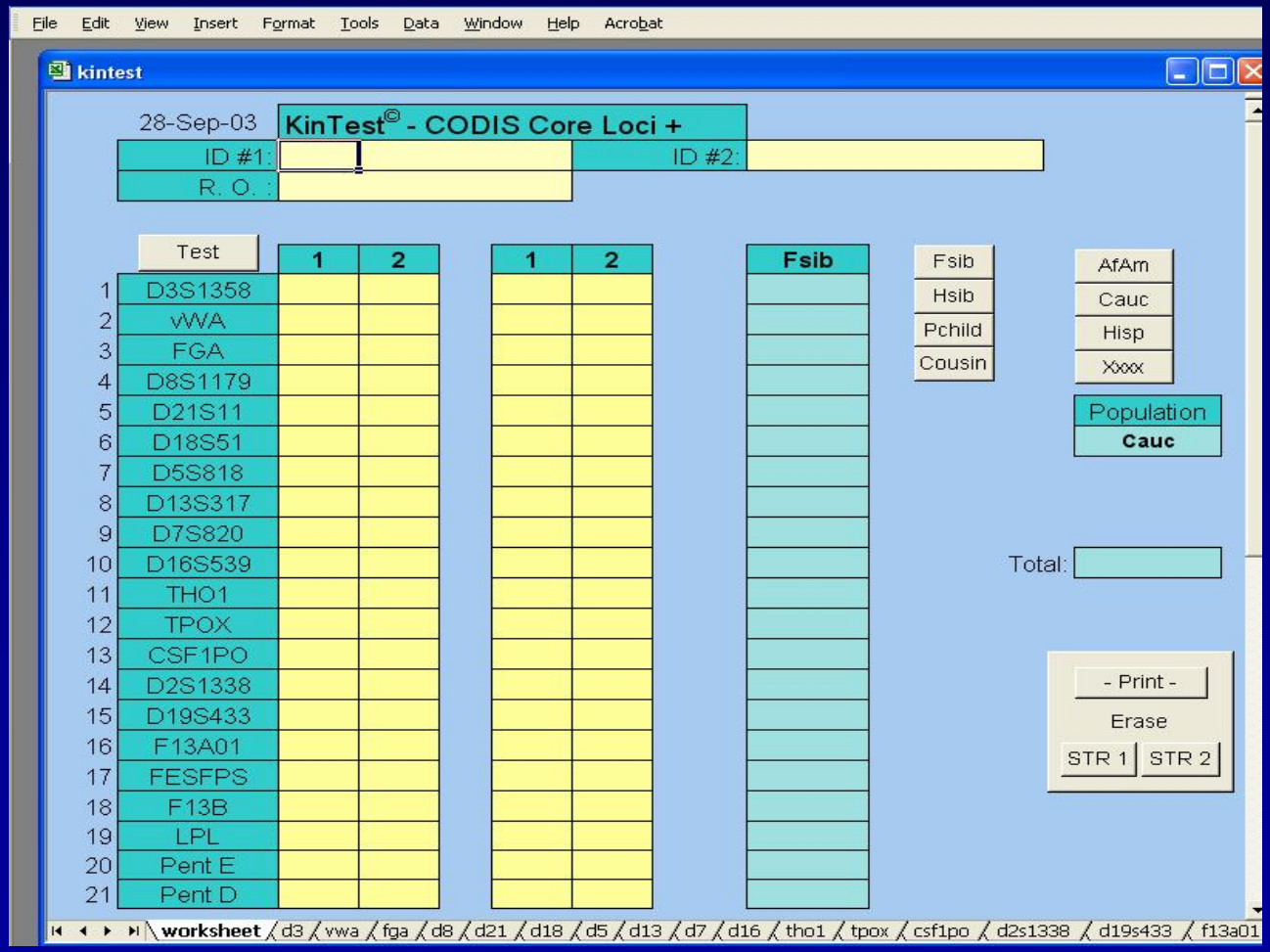
$$[P_2(xy) \times \phi_2] + [P_1(xy) \times \phi_1] + [P_0(xy) \times \phi_0]$$

#1	#2	frequency
AB	AB	$\phi_2 + 0.5\phi_1(p_A + p_B) + 2\phi_0 p_A p_B$
AA	AA	$\phi_2 + \phi_1 p_A + \phi_0 p_A^2$
AA	AB	$\phi_1 p_B + 2\phi_0 p_A p_B$
AB	AC	$0.5\phi_1 p_C + 2\phi_0 p_A p_C$
AB	CD	$2\phi_0 p_C p_D$
AA	BB	$\phi_0 p_B^2$
AA	BC	$2\phi_0 p_B p_C$

Likelihood Ratios for Full- & Half-Sibs

		full-sib	:	half-sib	:	unrelated
AB	AB	$(1+p+q+2pq)$	:	$(p+q+4pq)$	:	$8pq$
AA	AA	$(1+p)^2$	:	$2p(1+p)$	:	$(2p)^2$
AA	AB	$(1+p)$	:	$(1+2p)$	:	$4p$
AB	AC	$(1+2p)$	:	$(1+4p)$	:	$8p$
AB	CD	1	:	2	:	4
AA	BB	1	:	2	:	4
AA	BC	1	:	2	:	4

KinTest Program Created by George Carmody, Carleton University, Canada



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27-Sep-03

KinTest© - CODIS Core Loci +

ID #1:	P-61692	ID #2:	
R. O. :			

	Test	1	2	1	2	Fsib
1	D3S1358	17	18	16	16	0.25
2	vWA	15	20	16	20	10.05
3	FGA	24	25	22	25	2.06
4	D8S1179	12	15	12	15	10.09
5	D21S11	27	30	29	30	0.79
6	D18S51	16	17	17	17	1.86
7	D5S818	8	13	8	13	77.57
8	D13S317	11	12	11	12	2.32
9	D7S820	10	11	10	12	0.68
10	D16S539	11	12	11	13	0.71
11	THO1	8	8	8	8	20.07
12	TPOX	9	10	9	9	2.28
13	CSF1PO	9	10	10	10	1.24
14	D2S1338	19	23	19	19	1.98
15	D19S433	14.2	16	14	14.2	7.85
16	F13A01	3.2	15	3.2	15	124.46
17	FESFPS	11	12	11	12	2.36
18	F13B	6	10	9	10	0.56
19	LPL	11	12	11	12	3.45
20	Pent E					
21	Pent D					

Fsib
Hsib
Pchild
Cousin

AfAm
Cauc
Hisp
Xxxx

Population
Cauc

Total: 3.3E+09

- Print -
Erase
STR 1 STR 2

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27-Sep-03

KinTest© - CODIS Core Loci +

ID #1:	P-61692	ID #2:	
R. O. :			

	Test	1	2	1	2	Hsib
1	D3S1358	17	18	16	16	0.50
2	vWA	15	20	16	20	10.30
3	FGA	24	25	22	25	2.31
4	D8S1179	12	15	12	15	2.50
5	D21S11	27	30	29	30	1.04
6	D18S51	16	17	17	17	2.11
7	D5S818	8	13	8	13	11.11
8	D13S317	11	12	11	12	1.30
9	D7S820	10	11	10	12	0.93
10	D16S539	11	12	11	13	0.96
11	THO1	8	8	8	8	4.48
12	TPOX	9	10	9	9	2.53
13	CSF1PO	9	10	10	10	1.49
14	D2S1338	19	23	19	19	2.23
15	D19S433	14.2	16	14	14.2	8.10
16	F13A01	3.2	15	3.2	15	11.59
17	FESFPS	11	12	11	12	1.34
18	F13B	6	10	9	10	0.81
19	LPL	11	12	11	12	1.55
20	Pent E					
21	Pent D					

Fsib
Hsib
Pchild
Cousin

AfAm
Cauc
Hisp
Xxxx

Population
Cauc

Total: 5.0E+06

- Print -
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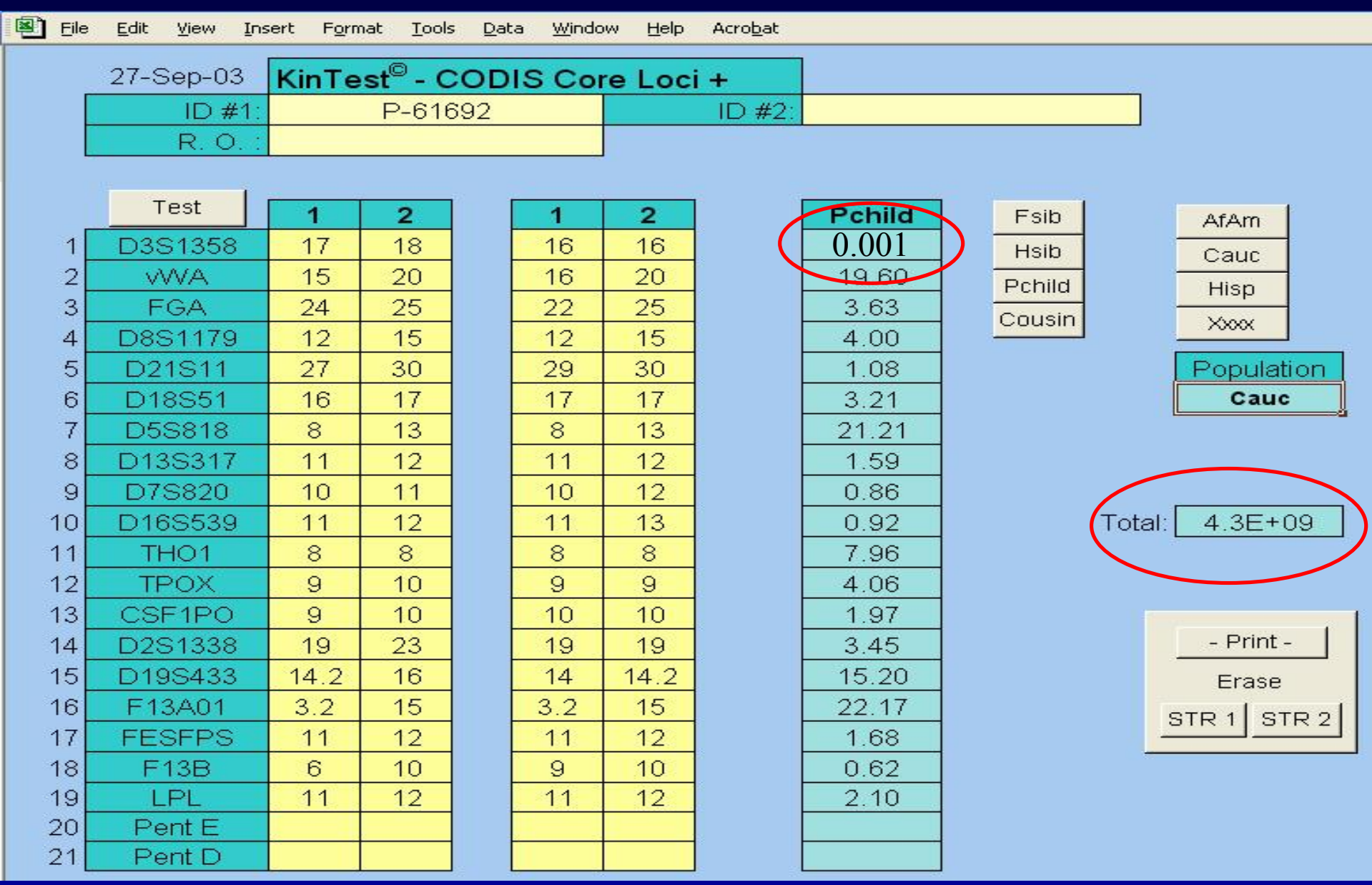
STR 1 STR 2



Residual CPI = 4.3E+9 X 0.001 = 4.3E+6

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27-Sep-03

KinTest© - CODIS Core Loci +

ID #1:	P-61692	ID #2:	
R. O. :			

	Test	1	2	1	2	Cousin
1	D3S1358	17	18	16	16	0.75
2	vWA	15	20	16	20	5.65
3	FGA	24	25	22	25	1.66
4	D8S1179	12	15	12	15	1.75
5	D21S11	27	30	29	30	1.02
6	D18S51	16	17	17	17	1.55
7	D5S818	8	13	8	13	6.05
8	D13S317	11	12	11	12	1.15
9	D7S820	10	11	10	12	0.97
10	D16S539	11	12	11	13	0.98
11	THO1	8	8	8	8	2.74
12	TPOX	9	10	9	9	1.77
13	CSF1PO	9	10	10	10	1.24
14	D2S1338	19	23	19	19	1.61
15	D19S433	14.2	16	14	14.2	4.55
16	F13A01	3.2	15	3.2	15	6.29
17	FESFPS	11	12	11	12	1.17
18	F13B	6	10	9	10	0.91
19	LPL	11	12	11	12	1.28
20	Pent E					
21	Pent D					

Fsib
Hsib
Pchild
Cousin

AfAm
Cauc
Hisp
Xxxx

Population
Cauc

Total: 4.8E+04

- Print -
Erase
STR 1 STR 2

Kinship Determination For Genotype Data On Two Individuals in Case P-61692

Full – Sibs	3.3E+9
Half – Sibs	5.0E+6
Parent – Child	4.3E+6
First Cousins	4.8E+4

The likelihood ratio comparing Full-Sib to Half-Sib is

3.3E+9 / 5.0E+6 = 660

It is **660 times more likely** given the genotype of individual one, and the genotype of individual two, that the two individuals are Full-Sibs as opposed to Half-Sibs

Kinship Analysis P-61692 at the D5S818 Locus

Individual 1	Individual 2	Allele Freq
8	8	0.0128
13	13	0.1462

	ϕ_2	ϕ_1	ϕ_0
Full - Sib	0.25	0.5	0.25
Half - Sib	0	0.5	0.5
Parent - Child	0	1	0
First Cousins	0	0.25	0.75
Unrelated	1	0	0

$$\phi_2 + 0.5\phi_1(p_A + p_B) + 2\phi_0 p_A p_B$$

Kinship Analysis P-61692 at the D5S818 Locus

$$\phi_2 + 0.5\phi_1(p_A + p_B) + 2\phi_0 p_A p_B$$

Full – Sibs = 0.25 + (0.5*0.5(0.0128+0.1462)) + (2*0.25*0.0128*0.1462)

Half – Sibs = (0.5*0.5(0.0128+0.1462)) + (2*0.5*0.0128*0.1462)

Parent – Child = (0.5*(0.0128+0.1462))

First Cousins = (0.5*0.25(0.0128+0.1462)) + (2*0.75*0.0128*0.1462)

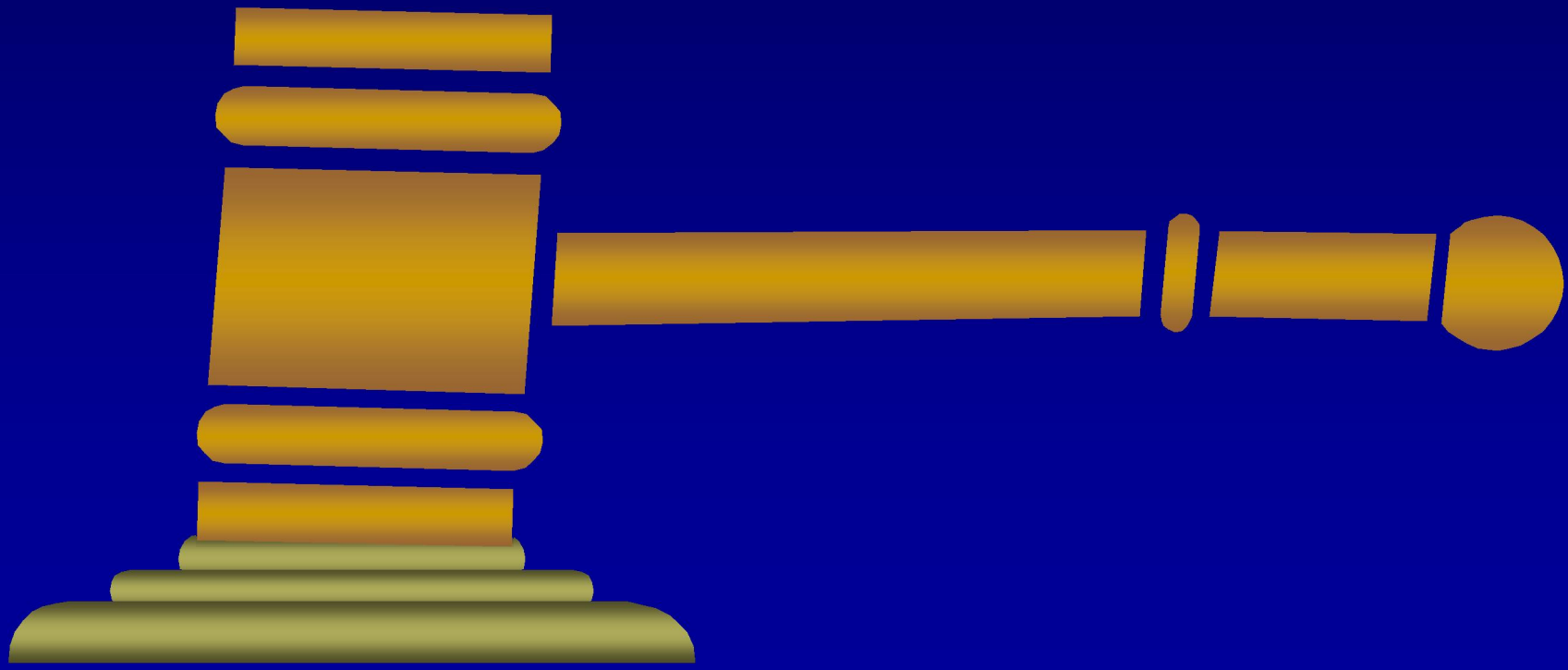
Unrelated = 2*0.0128*0.1462

Kinship Analysis P-61692 at the D5S818 Locus

Full – Sibs	0.291
Half – Sibs	0.042
Parent – Child	0.080
First Cousins	0.023
Unrelated	0.004

Divide each of the kinship likelihood by the likelihood for Unrelated

Kinship Analysis P-61692 at the D5S818 Locus

Full – Sibs	77.67
Half – Sibs	11.12
Parent – Child	21.24
First Cousins	6.06
Unrelated	1

Thank you!