

MasterMix

Peter Gill

A freeware solution to aid the interpretation of mixtures using peak height / or area information

Note that this software is not validated for casework and no warranty is provided for such a purpose

This software is described in the paper below



ELSEVIER

Forensic Science International
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Interpreting simple STR mixtures using allele peak areas

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Spreadsheets

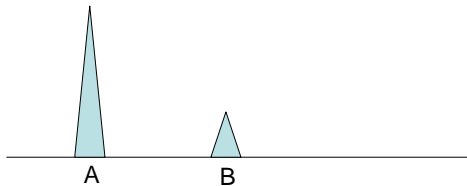
- There are three spreadsheets
- Each spreadsheet can be used to solve 2, 3, 4 banded mixtures
- Two person mixtures only.

Step 1

- Input the peak heights only

Two allele simulation

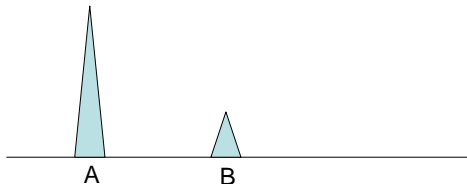
Height Information here		
	Height	Proportions
A	2183	0.708
B	899	0.292
SUM	3082	
Mx	1-Mx	
0.2	0.8	



INPUT THE HEIGHT DATA HERE

Two allele simulation

Height Information here		
	Height	Proportions
A	2183	0.708
B	899	0.292
SUM	3082	
Mx	1-Mx	
0.2	0.8	

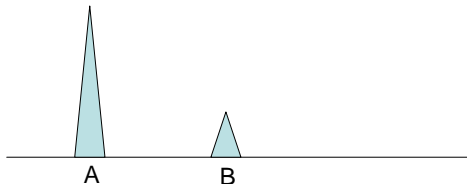


INPUT THE HEIGHT DATA HERE

INPUT Mx value (the mixture proportion) here

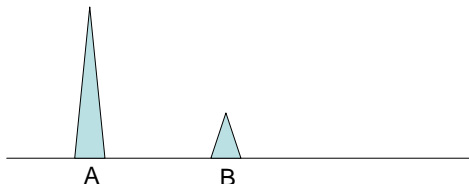
Two allele simulation

Height Information here		
	Height	Proportions
A	2183	0.708
B	899	0.292
SUM	3082	
Mx	1-Mx	
0.2	0.8	



Proportions are automatically calculated

Two allele simulation



This table is calculated automatically

combination	Expected proportions		observed proportions		difference (residuals)	Mx (conditioned)			Heterozygote balance	
	A	B	A	B		Mx	1-Mx	PHR1	PHR2	
AA,AB	0.6	0.4	0.708	0.292	0.023	0.42	0.583	NA	0.00	
AB,AB	0.5	0.5	0.708	0.292	0.087	NA	NA	0.41	NA	
AA,BB	0.2	0.8	0.708	0.292	0.517	0.71	0.292	NA	0.41	
AB,AA	0.9	0.1	0.708	0.292	0.073	0.58	0.417	NA	NA	
BB,AA	0.8	0.2	0.708	0.292	0.017	0.29	0.708	NA	NA	
AB,BB	0.1	0.9	0.708	0.292	0.740	1.42	-0.417	NA	NA	
BB,AB	0.4	0.6	0.708	0.292	0.190	-0.42	1.417	NA	NA	

↑ All possible combinations
 ↑ Expected proportions conditional on the Mx.
 ↑ Observed from epg
 ↑ Sum of squares dif.
 ↑ Conditioned on Mx

The underlying formulae can be examined – simply click on the cell

F3 $=($A$10/2)+0.5$

Height information here			combination		Expected proportions		observed proportions		difference	Mz (conditioned)		Heterozygote balance	
A	B	C	A	B	A	B	A	B	(residuals)	Mz	1-Mz	PHR1	PHR2
A	2183	0.789	AA,AB	0.6	0.4	0.708	0.292	0.023	-0.42	0.583	NA	0.00	
B	899	0.292	AB,AB	0.5	0.5	0.708	0.292	0.087	NA	NA	0.41	NA	
SUM	3082		AA,BB	0.2	0.8	0.708	0.292	0.517	0.71	0.292	NA	0.41	
			AB,AA	0.9	0.1	0.708	0.292	0.073	0.58	0.417	NA	NA	
			BB,AA	0.8	0.2	0.708	0.292	0.017	0.29	0.708	NA	NA	
			AB,BB	0.1	0.9	0.708	0.292	0.740	1.42	-0.417	NA	NA	
			BB,AB	0.4	0.6	0.708	0.292	0.190	-0.42	1.417	NA	NA	
Mz	1-Mz												
0.2	0.8												

CLICK FOR TWO-ALLELE SIMULATION

Macro button

Step 2

- Press the macro button and the rest is automatic

Simulation

Height information here			combination	Expected proportions		observed pro
A	Height	Proportions		A	B	A
A	2183	0.708	AA,AB	0.8	0.4	0.708
B	899	0.292	AB,AB	0.5	0.5	0.708
SUM	3082		AA,AB	0.2	0.8	0.708
			AB,AA	0.9	0.1	0.708
			BB,AA	0.8	0.2	0.708
			AB,BB	0.1	0.9	0.708
Mx	1-Mx		BB,AB	0.4	0.6	0.708
0.2	0.8					

CLICK FOR TWO-ALLELE SIMULATION

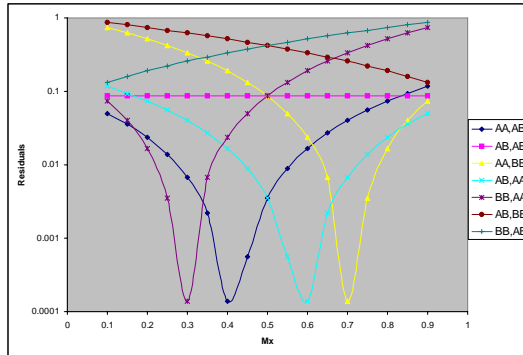
PRESS THIS BUTTON AFTER FILLING IN DETAILS ABOUT PEAK HEIGHT

The program simulates residuals (in cells J3:J9) between Mx= 0.1 – 0.9

Genotype	Mx	0.1	0.15	0.2	0.25	0.3	0.35	0.4	0.45	0.5	0.55	
AA,AB		0.05012177	0.03554114	0.02346051	0.01387968	0.00679925	0.00221862	0.00013799	0.00055736	0.00347673	0.0088961	0.01
AB,AB		0.08678302	0.08678302	0.08678302	0.08678302	0.08678302	0.08678302	0.08678302	0.08678302	0.08678302	0.08678302	0.08
AA,BB		0.7400731	0.62341184	0.51675058	0.42009932	0.33342806	0.2567668	0.19010554	0.13344428	0.08678302	0.05012177	0.00
AB,AA		0.11683169	0.09391232	0.07349295	0.05557358	0.04015421	0.02723484	0.01681547	0.0088961	0.00347673	0.00055736	0.00
BB,AA		0.07349295	0.04015421	0.01681547	0.00347673	0.00013799	0.00679925	0.02346051	0.05012177	0.08678302	0.13344428	0.16
AB,BB		0.86673436	0.80215373	0.7400731	0.68049247	0.62341184	0.56883121	0.51675058	0.46716995	0.42008932	0.37550869	0.30
BB,AB		0.13344428	0.16052491	0.19010554	0.22218617	0.2567668	0.29384743	0.33342806	0.37550869	0.42008932	0.46716995	0.51

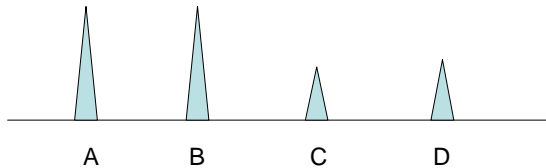
Plots

- The residuals are plotted
- Note log10 scale on x-axis.



4-allele simulation

Height Information here		
	Height	Proportions
A	2000	0.411
B	2000	0.411
C	400	0.082
D	466	0.096
SUM	4866	
Mx	1-Mx	
0.9	0.1	



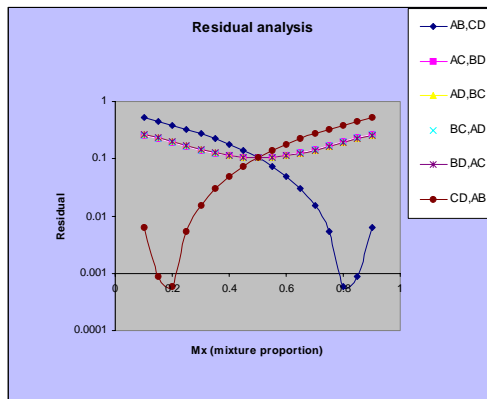
4-allele simulation

Height Information here		
	Height	Proportions
A	2000	0.411
B	2000	0.411
C	400	0.082
D	466	0.096
SUM	4866	
Mx	1-Mx	
0.9	0.1	

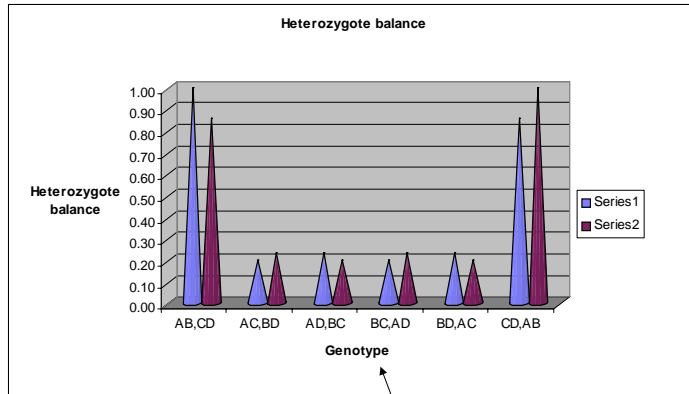
combination	Expected proportions				observed proportions				difference (residuals)	Mx (conditioned)			Heterozygote balance	
	A	B	C	D	A	B	C	D		Mx	1-Mx	PHR1	PHR2	
AB,CD	0.100	0.100	0.400	0.400	0.411	0.411	0.082	0.096	0.387	0.822	0.178	1.00	0.86	
AC,BD	0.100	0.400	0.100	0.400	0.411	0.411	0.082	0.096	0.190	0.493	0.507	0.20	0.23	
AD,BC	0.100	0.400	0.400	0.100	0.411	0.411	0.082	0.096	0.198	0.507	0.493	0.23	0.20	
BC,AD	0.400	0.100	0.100	0.400	0.411	0.411	0.082	0.096	0.190	0.493	0.507	0.20	0.23	
BD,AC	0.400	0.100	0.400	0.100	0.411	0.411	0.082	0.096	0.198	0.507	0.493	0.23	0.20	
CD,AB	0.400	0.400	0.100	0.100	0.411	0.411	0.082	0.096	0.001	0.178	0.822	0.86	1.00	

Simulation

Genotypes	Mx										
	0.1	0.15	0.2	0.25	0.3	0.35	0.4	0.45	0.5	0.55	
AB,CD	0.52136714	0.45166776	0.38696837	0.32726899	0.27256961	0.22287022	0.17817084	0.13847146	0.10377207	0.07407269	0.04
AC,BD	0.25826334	0.22145193	0.18964052	0.16282911	0.14101777	0.1242063	0.11239489	0.10558348	0.10377207	0.10696066	0.11
AD,BC	0.26911637	0.23094833	0.19778029	0.16961226	0.14644422	0.12827618	0.11510815	0.10694011	0.10377207	0.10560404	0
BC,AD	0.25842778	0.22159581	0.18976385	0.16293189	0.14109992	0.12426796	0.112436	0.10560404	0.10377207	0.10694011	0.11
BD,AC	0.26928081	0.23109222	0.19790362	0.16971503	0.14652644	0.12833785	0.11514926	0.10696066	0.10377207	0.10558348	0.11
CD,AB	0.00617701	0.00087639	0.00057577	0.00527516	0.01497454	0.02967392	0.04937331	0.07407269	0.10377207	0.13847146	0.11



Heterozygote balance (conditioned on Genotype peak heights)



Most likely combinations conditioned on Mx