

Solutions for exercises using Familias

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There are also some [videos](#) available for some other exercises.

Exercise S1

Answers:

a) We can write

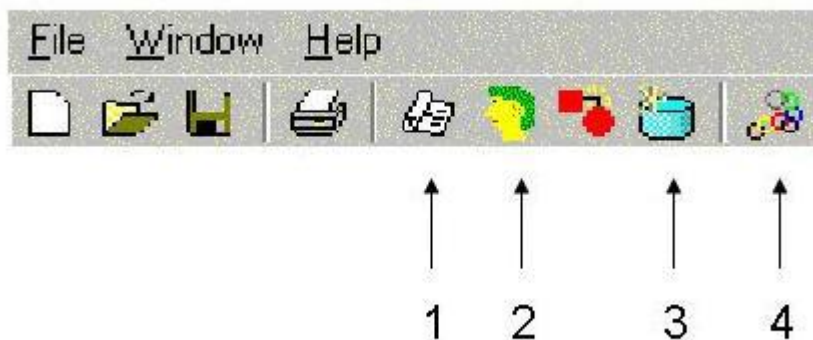
$$LR = \frac{P(child | mother, AF)}{P(child | mother)}.$$

Consider first the numerator. The only possible genotype for the child, given the mother and the AF, is A/B, and therefore the probability is 1. For the denominator, the father must have passed on the A allele, and therefore the probability is p_A . Hence

$LR = 1 / p_A$. The standard interpretation is

“The data is 20 times more likely assuming AF to be the father compared to the alternative that some unknown man is the father”.

b) The buttons labeled 1, 2, 3 and 4 below will be used as explained under.

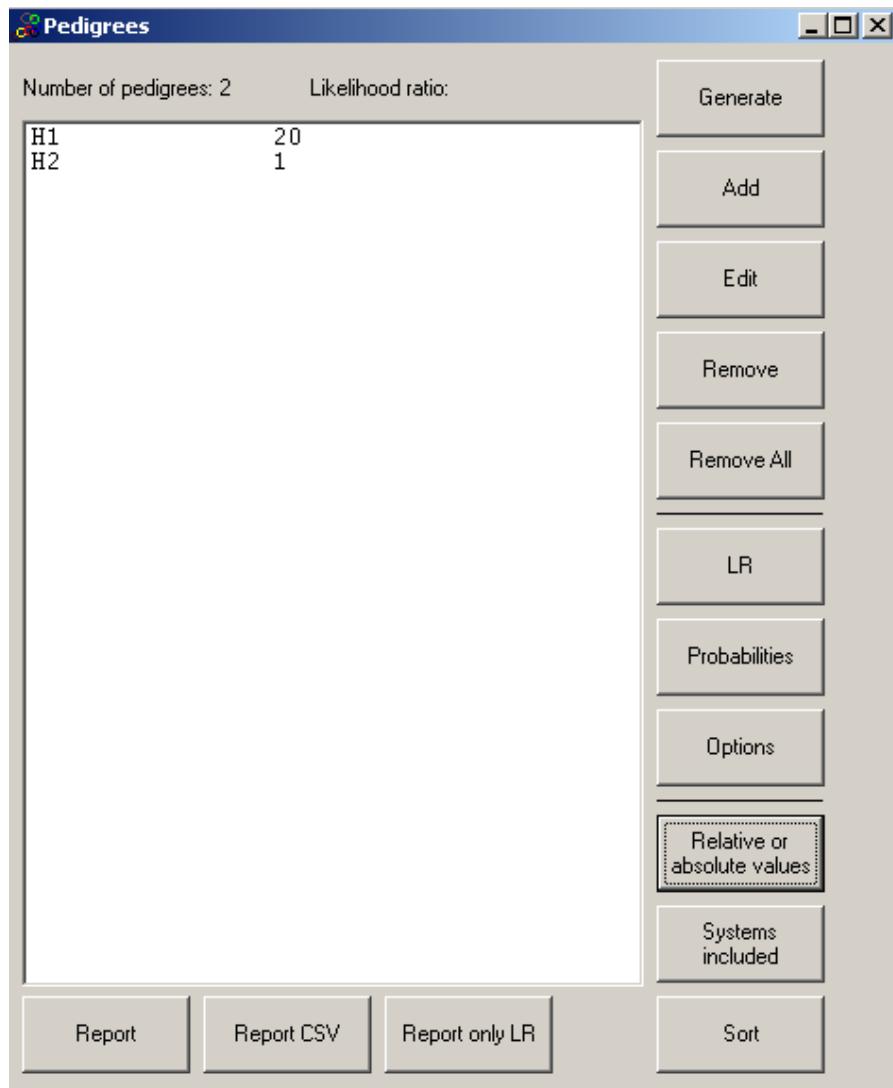


How to do it:

1. **General DNA data:** Click Add to enter an allele system. In the new window, enter allele system name S1 and the two alleles A and B, both with frequencies 0,05. Enter the C allele with frequency 0,9. Press OK.
2. **Persons:** Enter the persons: mother, AF and child and their gender.
3. **Case-Related DNA data:** Double-click each person to enter his or her DNA data. In the new window, enter the appropriate allele system (use the pull-down menu) and the observed alleles for this person, then press Add and OK.
4. **Pedigrees:** Click Add to enter the pedigree corresponding to hypothesis H_1 . Enter H1 as Pedigree name. Enter the mother as the parent of the child in the pull-down menu and click Add. Enter the AF as the parent of the child in the pull-down menu and click Add. Click OK to finish the definition of the pedigree corresponding to hypothesis H1. Click Add in the pedigree window once more to add the pedigree corresponding to hypothesis H_2 . Enter H2 as Pedigree name. Press LR. (Normally

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one would answer Yes when asked to save.) This gives relative values. It remains to specify the denominator, H_2 in this case, by marking the line corresponding to H_2 . Press the button **Relative or absolute values**. The pedigree window should now appear as



- c) Repeat step 1 above to define the marker S2 and step 3 to define the genotypes for all individuals. Steps 2 and 4 need not be repeated. The LR is then obtained as before and the answer is: $LR=200$.
- d) $(1/p_A) * (1/p_a) = (1/0.05) * (1/0.10) = 200$
- h) $LR = (1 + 3 * 0.02) / (2 * 0.02 + (1 - 0.02) * 0.05) = 11.91$
- i) To be discussed in class. We note now, however, that *Hardy-Weinberg equilibrium* is required for the LR derivation for each marker. This assumption is not needed when we use theta-correction. Furthermore, *linkage disequilibrium* is needed. We have also assumed that there are no mutations or silent alleles.

Exercise S2

- a) The numerator, $P(child | AF) = 0$ and therefore $LR=0$ as confirmed by **Familias**.

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- b) The General DNA data is used to specify the mutation model and should be completed as below

Allele system

System name:

Silent frequency:

Alleles:	Frequencies:
14	0,072
15	0,082
16	0,212
17	0,292
18	0,222
19	0,097
20	0,02
21	0,003

Female mutations:

Mutation rate:

☐ Prob. decreasing with range (stable)

☐ Prob. decreasing with range (equal)

Mutation range:

☐ Probability proportional to frequency (stable)

☒ Equal probability (simple and fast)

Male mutations:

Mutation rate:

☐ Prob. decreasing with range (stable)

☐ Prob. decreasing with range (equal)

Mutation range:

☐ Probability proportional to frequency (stable)

☒ Equal probability (simple and fast)

Buttons: Apply, OK, Remove Allele, Edit Allele, Add

Answer $LR=4.07E-03=0.00407$

c) $LR=0.01*(0.212+0.292)/(2*0.212*0.292)=0.00407$

Exercise S3

The pedigree corresponding to H_1 , Figure 3, is specified as follows

Pedigree

Pedigree Name:

Parent	Child
Alleged mother	Bone
Alleged Father	Bone
Alleged mother	Alleged Sibling
Alleged Father	Alleged Sibling

Buttons: OK, Persons, Remove, Add

Add section: Parent Child

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Most answers are given in the rightmost column of the below table from the report generated by **Familias**. “D7S820, gives a very large LR, namely 11189” since 11.1 is so rare. If this marker is omitted the new LR is $530437141/11189=47407$.

Likelihood ratio versus H2: 530437140,978139

System:	Likelihood:	LR versus H2:
D3S1358	0,002107356328	24,3295665373587
D21S11	0,00106135425	4,42583732057416
D18S51	0,0008102440125	26,7722473604827
D7S820	5,037122916E-07	11189,4499975311
D16S539	0,000811482	0,899280575539568
CSF1PO	0,0130390037415	2,25229008488432
F13B	0,001423488512	5,88485536018151
LPL	0,0007365230775	1,37960642346607

Exercise S4

- $LR(\text{grand father/unrelated}) = 0.98$ for D3S1358.
- $LR(\text{grand father/unrelated}) = 0.0085$ for all markers.
- Whether autosomal and haplotype markers can be combined and in case how is a big question and there appears to be no consensus

Exercise S5

- $W=20/(1+20)=0.952$
- $W=200/(1+200)=0.995$
- Same answers as above.
- This is again a big question. Most recommendations are in favor of LR . The problem with W is to decide on the prior. W may be easier to interpret.

Exercise S6

- $LR=10$. *Comment:* The formula provided follows from

$$LR = \frac{P(\text{data} | H_1)}{P(\text{data} | H_2)} = \frac{P(\text{child} | AF, \text{mother})}{P(\text{data} | \text{mother})} = \frac{\frac{1}{4}}{\frac{1}{2} p_2} = \frac{1}{2 p_2}$$

The same result is obtained in *this particular* case if inbreeding is ignored.

- $LR(H1/H2) = 10$, $LR(H1/H3) = 1.905$. We are asked to verify that

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$$LR = \frac{2}{1 + p_2} = \frac{2}{1 + 0.05} = 1.905 \text{ OK!}$$

$$c) P(H_1 | data) = 0.615, P(H_2 | data) = 0.0615, P(H_3 | data) = 0.323$$

Exercise S7

Most answers are given in problem.

Regarding question f. We can add the following: If a model is unstable, allele frequencies change with generations. This adds some intuition as to why introducing an extra person, say a grandparent, typically changes results slightly for an unstable model.

Regarding question g. Consider the first model listed in **Familias** Probability decreasing with range (stable) which gave $LR=6.4E-03=0.0064$. Remove alleles so that only 14,15, 16,17 and a 'Rest allele' remains. Then $LR=7.8E-03=0.0078$, a change. Again this effect does not have to with Familias; there are two different models, one with 8 alleles and one with alleles (which constrains mutations within those five alleles) and different models typically give different results.

Exercise S8

a)

$$LR = \frac{P(data | H_1)}{P(data | H_2)} = \frac{P(data | H_1)}{4 p_{16} p_{17}}$$

$$= \frac{p_{16}(m_{14,17} + m_{15,17}) + p_{17}(m_{14,16} + m_{15,16})}{4 p_{16} p_{17}}$$

b) The formula in Exercise S2 follows by setting $m_{14,17} = m_{15,17} = m_{14,16} = m_{15,16} = m$ and the numerical result $LR=0.0029$ follows.

c)

$$LR = \frac{P(data | H_1)}{P(data | H_2)} = \frac{p_{16}(kp_{17} + kp_{17}) + p_{17}(kp_{16} + kp_{16})}{4 p_{16} p_{17}} = k$$

$$1 - R = \sum_{i=1}^n p_i(1 - k(1 - p_i)) \Rightarrow k = \frac{R}{\sum_{i=1}^n p_i(1 - p_i)} = 0.0063$$

Exercise S9

- $LR(H1: father/H2: not father)=0$ from **Familias**.
- $LR=0$ for PENTA_E as can be seen from report from **Familias**.
- $LR= 4515433$
- See Familias file ExS9Brother.txt which gives $LR=1.4$.
- To be discussed.

Exercise S10

- $LR=0.791/0.209=3.8$ Details on Familias implementation, including definition of pedigrees, can be seen from ExS10.txt.

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b) To be discussed.

Exercise S11

The LR is 1.36

How to do it:

Enter the allele system setting the silent allele frequency to 0.05. Enter the persons and their DNA data as usual. Construct the pedigrees manually. Use LR and Relative and Absolute values as previously

A theoretical argument, not requested, is given below: Let $p_A = p_B = 0.1$ and $p_S = 0.05$. According to <http://dna-view.com/patform.htm>,

$$LR = \frac{p_s (p_A + p_s)}{(p_A + p_s)^2 (p_B + 2 p_s) + p_s p_A (p_B + 2 p_s)} = \frac{0.05 \cdot 0.15}{0.15^2 \cdot 0.2 + 0.05 \cdot 0.1 \cdot 0.2} = 1.36,$$

which coincides with **Familias**.

Exercise S12

See pages 36-37 of the [manual](#).

Exercise S13

$LR=0.0068$

Exercise S14

Explained in problem.