Supplement

Fig. S1 1: Genotype combinations and varying allele frequencies and error rates $e$. a) Comparison of the likelihood ratios for $H_1 \sim H_2$ (triangles) and $H_3 \sim H_0$ (circles) for $(gt_{x_1}, gt_{x_2}) = (a_1a_1,a_2a_2)$ for increasing $f_1 = f(a_1)$ and different values of $e$. b) Comparison of likelihood ratios for $H_1 \sim H_2$ for different fixed values of $f_1$ and increasing $e$, comparing homozygous genotypes, $a_1a_1$, with heterozygous genotypes, $a_1a_2$. c) Comparison of likelihood ratios for $H_1 \sim H_2$, assuming $f_2 = 1 - f_1$ in a bi-allelic state. d) Comparison of likelihood ratios for $H_3 \sim H_0$, assuming $f_2 = 1 - f_1$ in a bi-allelic state.
Visualization of pedigree information

The code for the visualization of the pedigrees from all generated relationships information can be found at https://gene-talk.de/vcf2ped. A stepwise description for the pedigree shown in Fig. 1 would be as follows:

<table>
<thead>
<tr>
<th>ID</th>
<th>MOTHER</th>
<th>FATHER</th>
<th>CHILDREN</th>
<th>SIBLINGS</th>
<th>GENDER</th>
</tr>
</thead>
<tbody>
<tr>
<td>I3</td>
<td>1_female</td>
<td>1_male</td>
<td>-</td>
<td>I2</td>
<td>female</td>
</tr>
<tr>
<td>III1</td>
<td>2_female</td>
<td>II1</td>
<td>-</td>
<td>-</td>
<td>female</td>
</tr>
<tr>
<td>I1</td>
<td>3_female</td>
<td>3_male</td>
<td>II1</td>
<td>-</td>
<td>female</td>
</tr>
<tr>
<td>III2</td>
<td>II2</td>
<td>4_male</td>
<td>-</td>
<td>III3</td>
<td>female</td>
</tr>
<tr>
<td>III3</td>
<td>II2</td>
<td>4_male</td>
<td>-</td>
<td>III2</td>
<td>female</td>
</tr>
<tr>
<td>II1</td>
<td>II1</td>
<td>II2</td>
<td>III1</td>
<td>-</td>
<td>male</td>
</tr>
<tr>
<td>II2</td>
<td>7_female</td>
<td>I2</td>
<td>II2,III3</td>
<td>-</td>
<td>female</td>
</tr>
<tr>
<td>I2</td>
<td>1_female</td>
<td>1_male</td>
<td>II2,II1</td>
<td>I3</td>
<td>male</td>
</tr>
</tbody>
</table>

Tab. S 1: Most likely relationship states between dyads.

Each sample is a node in a two-dimensional coordinate system. In the following each node will systematically be assigned to coordinates \((x, y)\).

<table>
<thead>
<tr>
<th>ID</th>
<th>x</th>
<th>y</th>
<th>Gender</th>
</tr>
</thead>
<tbody>
<tr>
<td>I3</td>
<td>NA</td>
<td>NA</td>
<td>female</td>
</tr>
<tr>
<td>III1</td>
<td>0</td>
<td>0</td>
<td>female</td>
</tr>
<tr>
<td>I1</td>
<td>NA</td>
<td>NA</td>
<td>female</td>
</tr>
<tr>
<td>III2</td>
<td>NA</td>
<td>NA</td>
<td>female</td>
</tr>
<tr>
<td>III3</td>
<td>NA</td>
<td>NA</td>
<td>female</td>
</tr>
<tr>
<td>II1</td>
<td>NA</td>
<td>NA</td>
<td>male</td>
</tr>
<tr>
<td>II2</td>
<td>NA</td>
<td>NA</td>
<td>female</td>
</tr>
<tr>
<td>I2</td>
<td>NA</td>
<td>NA</td>
<td>male</td>
</tr>
<tr>
<td>1_female</td>
<td>NA</td>
<td>NA</td>
<td>female</td>
</tr>
<tr>
<td>2_female</td>
<td>NA</td>
<td>NA</td>
<td>female</td>
</tr>
<tr>
<td>3_female</td>
<td>NA</td>
<td>NA</td>
<td>female</td>
</tr>
<tr>
<td>7_female</td>
<td>NA</td>
<td>NA</td>
<td>female</td>
</tr>
<tr>
<td>1_male</td>
<td>NA</td>
<td>NA</td>
<td>male</td>
</tr>
<tr>
<td>3_male</td>
<td>NA</td>
<td>NA</td>
<td>male</td>
</tr>
<tr>
<td>4_male</td>
<td>NA</td>
<td>NA</td>
<td>male</td>
</tr>
</tbody>
</table>

1. Each node starts with undefined coordinates (NA), except for one starting node (light blue \((x, y) = (0, 0)\)). This node is a randomly chosen sample without any children but with at least one parent, e.g. III1.

2. For every node without defined parents (MOTHER or FATHER), new parent-nodes will be created (light violet).

3. The current node (here: III1) will be checked for a) children, b) siblings and c) parents and new coordinates will be assigned depending on the relationship state.

4. The current node does not have children or siblings. The next coordinates will be assigned to the parent nodes.
5. The y-coordinates for both parents will be shifted +1 compared to the y-coordinate from III1 and the x-coordinate will be shifted with a difference of $-0.5/0.5$, since III1 does not have siblings.

6. Repeat step 3. for sample II1.

7. Set coordinates for I1 and I2 according to step 5., but shift the x-coordinates with a difference of $-1/1$ since both nodes have parents and need more space.

8. Repeat step 3. for sample I2.

9. Set coordinates for II2 (child of I2).

10. Set coordinates for I3 (sibling of I2). Coordinates of I3 would overlap with parents of II2 → shift x-coordinate of I3 + 1 compared to I2.

11. Set coordinates for 1 female and 1 male (parents of I2).

12. Repeat step 3. for sample I3 → nothing to do.

13. Repeat step 3. for sample II2.

14. Set coordinates for III2 and III3 (children of II2)

15. Set coordinates for 7 female (mother of II2)


<table>
<thead>
<tr>
<th>ID</th>
<th>x</th>
<th>y</th>
<th>Gender</th>
<th>ID</th>
<th>x</th>
<th>y</th>
<th>Gender</th>
</tr>
</thead>
<tbody>
<tr>
<td>III1</td>
<td>0</td>
<td>0</td>
<td>female</td>
<td>III1</td>
<td>0</td>
<td>0</td>
<td>female</td>
</tr>
<tr>
<td>II1</td>
<td>0.5</td>
<td>1</td>
<td>male</td>
<td>I1</td>
<td>-0.5</td>
<td>2</td>
<td>female</td>
</tr>
<tr>
<td>2 female</td>
<td>-0.5</td>
<td>1</td>
<td>female</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>I3</td>
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<td>2</td>
<td>female</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>III1</td>
<td>0</td>
<td>0</td>
<td>female</td>
<td>III2</td>
<td>2.0</td>
<td>0</td>
<td>female</td>
</tr>
<tr>
<td>III3</td>
<td>3.0</td>
<td>0</td>
<td>female</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>I1</td>
<td>0.5</td>
<td>1</td>
<td>male</td>
<td>I1</td>
<td>0.5</td>
<td>1</td>
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<tr>
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<td>1.0</td>
<td>1</td>
<td>female</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>II2</td>
<td>1.5</td>
<td>2</td>
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<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
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<td>3</td>
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<tr>
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<td>female</td>
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<tr>
<td>7 female</td>
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</tr>
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<td>ID</td>
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<td>------</td>
<td>--------</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
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<td>2</td>
<td>female</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
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<td>0</td>
<td>female</td>
<td></td>
<td></td>
<td></td>
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<tr>
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<td></td>
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<tr>
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<td>0</td>
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<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>I1</td>
<td>0.5</td>
<td>1</td>
<td>male</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>II2</td>
<td>1.0</td>
<td>1</td>
<td>female</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>I2</td>
<td>1.5</td>
<td>2</td>
<td>male</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
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<td>1</td>
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</tr>
</tbody>
</table>

17. Set coordinates for 4_male

18. Repeat step 3. for sample I1 (only remaining node with undefined coordinates for relatives.)

<table>
<thead>
<tr>
<th>ID</th>
<th>x</th>
<th>y</th>
<th>Gender</th>
</tr>
</thead>
<tbody>
<tr>
<td>I3</td>
<td>2.5</td>
<td>2</td>
<td>female</td>
</tr>
<tr>
<td>III1</td>
<td>0</td>
<td>0</td>
<td>female</td>
</tr>
<tr>
<td>I1</td>
<td>-0.5</td>
<td>2</td>
<td>female</td>
</tr>
<tr>
<td>III2</td>
<td>2.0</td>
<td>0</td>
<td>female</td>
</tr>
<tr>
<td>III3</td>
<td>3.0</td>
<td>0</td>
<td>female</td>
</tr>
<tr>
<td>I1</td>
<td>0.5</td>
<td>1</td>
<td>male</td>
</tr>
<tr>
<td>II2</td>
<td>1.0</td>
<td>1</td>
<td>female</td>
</tr>
<tr>
<td>I2</td>
<td>1.5</td>
<td>2</td>
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</tr>
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<td>3</td>
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</tr>
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</tr>
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<td>2.5</td>
<td>3</td>
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<tr>
<td>7</td>
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<td>2</td>
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</tr>
<tr>
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</tr>
<tr>
<td>4</td>
<td>3.0</td>
<td>1</td>
<td>male</td>
</tr>
</tbody>
</table>

19. Set coordinates for 3_female and 3_male (parents of I1)

20. All coordinates are set. Draw nodes and edges between nodes.
Likelihood ratios $LR(H_i, H_0)$ for all subject-query genotype combinations $gt$ for hypotheses $H_2$ and $H_3$.

The highlighted equations are summarized in Table 1 in the main text.

$H_2$: **Full Sibling** (known child$_1$ - known child$_2$ - alleged parent$_1$ - alleged parent$_2$)

(1) $H_2$, Case$_1$: child$_1 = a_1a_1$, child$_2 = a_1a_1$

Possible genotypes for parents:

a) parent$_1 = a_1a_1$, parent$_2 = a_1a_1$

b) parent$_1 = a_1a_1$, parent$_2 = a_1a_2$

c) parent$_1 = a_1a_2$, parent$_2 = a_1a_2$

\[
Pr(\text{Case}_1|H_2, a)Pr(a) = f_1^2 f_1^2 = f_1^4 \\
Pr(\text{Case}_1|H_2, b)Pr(b) = 2(f_1^2 \frac{1}{4} 2f_1f_2) = f_1^3 f_2 \\
Pr(\text{Case}_1|H_2, c)Pr(c) = (\frac{1}{4} 2f_1f_2)^2 = \frac{1}{4} f_1^2 f_2^2 \\
Pr(\text{Case}_1|H_0) = f_1^2 f_1^2 = f_1^4
\]

$\rightarrow LR(H_2, H_0|\text{Case}_1) = \frac{Pr(\text{Case}_1|H_2)}{Pr(\text{Case}_1|H_0)} = \frac{f_1^4 + f_1^3 f_2 + \frac{1}{4} f_1^2 f_2^2}{f_1^4}$

$= \frac{\frac{1}{4} f^2(4f_1^4 + 4f_1f_2 + f_2^4)}{f_1^4}$

$= \frac{\frac{1}{4} f^2(2f_1 + f_2)^2}{f_1^4}$

$= \frac{\frac{1}{4} f^2(1 + f_1)^2}{f_1^4}$

(bi-allelic: $f_1 + f_2 = 1$)

$= \frac{(1 + f_1)^2}{4f_1^2}$
(2) \( H_2, Case_2 \): child\(_1 = a_1a_1\), child\(_2 = a_1a_2\)

Possible genotypes for parents:
  
a) parent\(_1 = a_1a_1\), parent\(_2 = a_1a_2\)
  
b) parent\(_1 = a_1a_2\), parent\(_2 = a_1a_2\)

\[
Pr(Case_2|H_2, a) Pr(a) = 2(f_1^2 \frac{1}{2} 2f_1f_2) = 2f_1^3 f_2
\]
\[
Pr(Case_2|H_2, b) Pr(b) = (\frac{1}{2} 2f_1f_2)^2 = f_1^2 f_2^2
\]
\[
Pr(Case_2|H_0) = 2(f_1^2 2f_1f_2) = 4f_1^3 f_2
\]

\[
\rightarrow LR(H_2, H_0|Case_2) = \frac{Pr(Case_2|H_2)}{Pr(Case_2|H_0)} = \frac{2f_1^3 f_2 + f_1^2 f_2^2}{4f_1^3 f_2}
\]
\[
= \frac{f_1^2 f_2(2f_1 + f_2)}{4f_1^3 f_2}
\]
\[
= \frac{f_1^2 f_2(f_1 + 1)}{4f_1^3 f_2} \quad \text{(bi-allelic: } f_1 + f_2 = 1)\]
\[
= \frac{f_1 + 1}{4f_1}
\]

(3) \( H_2, Case_3 \): child\(_1 = a_1a_1\), child\(_2 = a_2a_2\)

Possible genotypes for parents:
  
a) parent\(_1 = a_1a_2\), parent\(_2 = a_1a_2\)

\[
Pr(Case_3|H_2, a) Pr(a) = \frac{1}{4} 2f_1f_2 \frac{1}{4} 2f_1f_2 = \frac{1}{4} f_1^2 f_2^2
\]
\[
Pr(Case_3|H_0) = f_1^2 f_2^2
\]

\[
\rightarrow LR(H_2, H_0|Case_3) = \frac{Pr(Case_3|H_2)}{Pr(Case_3|H_0)} = \frac{1}{4} \frac{f_1^2 f_2^2}{f_1^2 f_2^2}
\]
\[
= \frac{1}{4}
\]
(4) $H_2$, Case 4: \( \text{child}_1 = a_1a_2, \text{child}_2 = a_1a_2 \)

Possible genotypes for parents:

a) parent 1 = \( a_1a_1 \), parent 2 = \( a_1a_2 \)
b) parent 1 = \( a_1a_1 \), parent 2 = \( a_2a_2 \)
c) parent 1 = \( a_1a_2 \), parent 2 = \( a_1a_2 \)
d) parent 1 = \( a_1a_2 \), parent 2 = \( a_2a_2 \)

\[
Pr(Case_4|H_2,a)Pr(a) = 2(f_2^3)^2 = f_1^3f_2 \\
Pr(Case_4|H_2,b)Pr(b) = 2f_1^2f_2^2 \\
Pr(Case_4|H_2,c)Pr(c) = 2(\frac{1}{4}2f_1f_2)^2 = f_1^2f_2^2 \\
Pr(Case_4|H_2,d)Pr(d) = 2*(\frac{1}{4}2f_1f_2f_2) = f_1f_2^2 \\
Pr(Case_4|H_0) = 2f_1f_22f_1f_2 = 4f_1^2f_2^3
\]

\[
\rightarrow LR(H_2,H_0|Case_4) = \frac{Pr(Case_4|H_2)}{Pr(Case_4|H_0)} = \frac{f_1^3f_2 + 2f_1^2f_2^2 + f_1f_2^3 + f_1^3f_2^2}{4f_1^2f_2^2} \\
= \frac{\frac{1}{2}f_1f_2(2f_1^2 + 4f_1f_2 + 2f_1f_2 + 2f_2^2)}{4f_1^2f_2^2} \\
= \frac{\frac{1}{2}f_1f_2((f_1 + f_2)^2 + f_1^2 + f_2^2 + 4f_1f_2)}{4f_1^2f_2^2} \\
= \frac{\frac{1}{2}f_1f_2(1 + f_1^2 + f_1f_2 + f_2^2 + f_1f_2 + 2f_1f_2)}{4f_1^2f_2^2} \\
= \frac{\frac{1}{2}f_1f_2(1 + f_1 + f_2 + 2f_1f_2)}{4f_1^2f_2^2} \\
= \frac{\frac{1}{2}f_1f_2(1 + f_1 + f_2 + 2f_1f_2)}{8f_1f_2} \\
= \frac{1 + f_1f_2}{4f_1f_2}
\]
(5) $H_2, Case_5$: child$_1 = a_1a_1$, child$_2 = a_2a_3$

Possible genotypes for parents:

a) parent$_1 = a_1a_2$, parent$_2 = a_1a_3$

$$Pr(Case_5|H_2, a)Pr(a) = \frac{1}{2} f_1 f_2 * \frac{1}{2} f_1 f_3 = f_1^2 f_2 f_3$$

$$Pr(Case_5|H_0) = 2(f_1^2 f_2 f_3) = 4f_1^2 f_2 f_3$$

$$\rightarrow LR(H_2, H_0|Case_5) = \frac{Pr(Case_5|H_2)}{Pr(Case_5|H_0)} = \frac{f_1^2 f_2 f_3}{4f_1^2 f_2 f_3} = \frac{1}{4}$$

(6) $H_2, Case_6$: child$_1 = a_1a_2$, child$_2 = a_1a_3$

Possible genotypes for parents:

a) parent$_1 = a_1a_1$, parent$_2 = a_2a_3$

b) parent$_1 = a_1a_2$, parent$_2 = a_1a_3$

c) parent$_1 = a_1a_2$, parent$_2 = a_2a_3$

d) parent$_1 = a_1a_3$, parent$_2 = a_2a_3$

$$Pr(Case_6|H_2, a)Pr(a) = f_2^2 \frac{1}{2} 2f_2 f_3 + 2f_2^2 \frac{1}{2} 2f_2 f_3 = 2f_2^2 f_2 f_3$$

$$Pr(Case_6|H_2, b)Pr(b) = \frac{1}{2} f_1 f_2 \frac{1}{2} 2f_1 f_3 + \frac{1}{2} f_1 f_2 \frac{1}{2} 2f_1 f_3 = f_1^2 f_2 f_3$$

$$Pr(Case_6|H_2, c)Pr(c) = \frac{1}{2} f_1 f_2 \frac{1}{2} 2f_2 f_3 + \frac{1}{2} f_1 f_2 \frac{1}{2} 2f_2 f_3 = f_1^2 f_2 f_3$$

$$Pr(Case_6|H_2, d)Pr(d) = \frac{1}{2} f_1 f_3 \frac{1}{2} 2f_2 f_3 + \frac{1}{2} f_1 f_3 \frac{1}{2} 2f_2 f_3 = f_1 f_2^2 f_3$$

$$Pr(Case_6|H_0) = 2(2f_1 f_2 f_3) = 8f_1^2 f_2 f_3$$

$$\rightarrow LR(H_2, H_0|Case_6) = \frac{Pr(Case_6|H_2)}{Pr(Case_6|H_0)} = \frac{2f_2^2 f_2 f_3 + f_1^2 f_2 f_3 + f_1 f_2^2 f_3}{8f_1^2 f_2 f_3} = \frac{f_1 f_2 f_3 (2f_1 + f_1 + f_2 + f_3)}{8f_1^2 f_2 f_3} = \frac{f_1 f_2 f_3 (2f_1 + 1)}{8f_1^2 f_2 f_3} = \frac{2f_1 + 1}{8f_1}$$
(7) $H_2$, Case 7: child$_1 = a_1a_2$, child$_2 = a_3a_4$

Possible genotypes for parents:

a) parent$_1 = a_1a_3$, parent$_2 = a_2a_4$

b) parent$_1 = a_1a_4$, parent$_2 = a_2a_3$

\[
Pr(Case_7|H_2, a)Pr(a) = 2\left(\frac{1}{2}f_1f_3\frac{1}{2}f_2f_4\right) = 2f_1f_2f_3f_4
\]

\[
Pr(Case_7|H_2, b)Pr(b) = 2\left(\frac{1}{2}f_1f_4\frac{1}{2}f_2f_3\right) = 2f_1f_2f_3f_4
\]

\[
Pr(Case_7|H_0) = 2(2f_1f_22f_3f_4) = 8f_1f_2f_3f_4
\]

\[
\rightarrow LR(H_2, H_0|Case_7) = \frac{Pr(Case_7|H_2)}{Pr(Case_7|H_0)} = \frac{2f_1f_2f_3f_4 + 2f_1f_2f_3f_4}{8f_1f_2f_3f_4} = \frac{4f_1f_2f_3f_4}{8f_1f_2f_3f_4} = \frac{1}{4}
\]
**H₃: Parent-Child** (known child - known parent₁ - alleged parent₂)

(1) **H₃, Case₁**: child = a₁a₁, parent₁ = a₁a₁

Possible genotypes for parent₂:

a) parent₂ = a₁a₁

\[
Pr(\text{Case₁}|H₃,a)Pr(a) = f₁^2 f₂^2 = f₁^4
\]

\[
Pr(\text{Case₁}|H₃,b)Pr(b) = f₁^2 f₂ \frac{f₁^2}{2} = f₁^3 f₂
\]

\[
Pr(\text{Case₁}|H₀) = f₁^2 f₂^2 = f₁^4
\]

\[→ LR(H₃,H₀|\text{Case₁}) = \frac{Pr(\text{Case₁}|H₃)}{Pr(\text{Case₁}|H₀)} = \frac{f₁^4 + f₁^3 f₂}{f₁^4} \]

\[= \frac{f₁ + f₂}{f₁} \]

\[= \frac{1}{f₁} \quad \text{ (bi-allelic: } f₁ + f₂ = 1)\]

(2) **H₃, Case₂**: child = a₁a₁, parent₁ = a₁a₂

Possible genotypes for parent₂:

a) parent₂ = a₁a₁

\[
Pr(\text{Case₂}|H₃,a)Pr(a) = \frac{1}{2} f₁ f₂ f₂^2 = f₁^3 f₂
\]

\[
Pr(\text{Case₂}|H₃,b)Pr(b) = \frac{1}{2} f₁ f₂ \frac{f₁^2}{2} f₁ f₂ = f₁^3 f₂^2
\]

\[
Pr(\text{Case₂}|H₀) = 2 f₁ f₂ f₂^2 = 2 f₁^3 f₂
\]

\[→ LR(H₃,H₀|\text{Case₂}) = \frac{Pr(\text{Case₂}|H₃)}{Pr(\text{Case₂}|H₀)} = \frac{f₁^3 f₂ + f₁^3 f₂^2}{2 f₁^3 f₂} \]

\[= \frac{f₁ + f₂}{2 f₁} \]

\[= \frac{1}{2 f₁} \quad \text{ (bi-allelic: } f₁ + f₂ = 1)\]
(3) $H_3, Case_3$: child = $a_1a_1$, parent$_1 = a_2a_2$

There are no possibilities for the genotypes of the parents, therefore

$$Pr(Case_3|H_3) = e$$
$$Pr(Case_3|H_0) = f_1^2f_2^2$$

whereas the parameter $e$ would be zero assuming perfect data quality, but is set to $e = 0.001$ in this work. This leads to:

$$\rightarrow LR(H_3, H_0|Case_3) = \frac{Pr(Case_3|H_3)}{Pr(Case_3|H_3)} = \frac{e}{f_1^2f_2^2}$$

(4) $H_3, Case_4$: child = $a_1a_2$, parent$_1 = a_1a_2$

Possibilities for parent$_2$:

a) parent$_2 = a_1a_1$

b) parent$_2 = a_1a_2$

c) parent$_2 = a_2a_2$

$$Pr(Case_4|H_3,a)Pr(a) = \frac{f_1^2}{2}f_1f_2 = f_1^3f_2$$
$$Pr(Case_4|H_3,b)Pr(b) = \frac{1}{2}(2f_1f_2f_1f_2) = 2f_1^2f_2^2$$
$$Pr(Case_4|H_3,c)Pr(c) = \frac{1}{2}2f_1f_2f_3 = f_1f_2^3$$
$$Pr(Case_4|H_0) = 2f_1f_2f_1f_2 = 4f_1^2f_2^2$$

$$\rightarrow LR(H_3, H_0|Case_4) = \frac{Pr(Case_4|H_3)}{Pr(Case_4|H_3)} = \frac{f_1^3f_2 + 2f_1^2f_2^2 + f_1f_2^3}{4f_1^2f_2^2}$$
$$= \frac{(f_1 + f_2)^2}{4f_1f_2}$$
$$= \frac{1}{4f_1f_2} \quad \text{(bi-allelic: } f_1 + f_2 = 1)$$

(5) $H_3, Case_5$: child = $a_1a_1$, parent$_1 = a_2a_3$

$$Pr(Case_5|H_3) = e$$
$$Pr(Case_5|H_0) = 2(f_1^2f_2f_3)$$

$$\rightarrow LR(H_3, H_0|Case_5) = \frac{Pr(Case_5|H_3)}{Pr(Case_5|H_3)} = \frac{e}{4f_1^2f_2f_3}$$
(6) \( H_3, Case_6 \): child = \( a_1a_2 \), parent_1 = \( a_1a_3 \)

Possibilities for parent_2:

a) parent_2 = \( a_1a_2 \)
b) parent_2 = \( a_2a_2 \)
c) parent_2 = \( a_2a_3 \)

\[
Pr(Case_6|H_3, a) = \frac{1}{2}2f_1f_2f_2f_1f_3 = f_1^2f_2f_3
\]
\[
Pr(Case_6|H_3, b) = \frac{1}{2}2f_1f_3f_2 = f_1f_2^2f_3
\]
\[
Pr(Case_6|H_3, c) = \frac{1}{2}2f_2f_3f_1f_3 = f_1f_2f_3^2
\]
\[
Pr(Case_6|H_0) = 2(2f_1f_2f_1f_3) = 8f_1^2f_2f_3
\]

\[
\rightarrow LR(H_3, H_0|Case_6) = \frac{Pr(Case_6|H_3)}{Pr(Case_6|H_0)} = \frac{f_1^2f_2f_3 + f_1f_2f_3 + f_1f_2f_3^2}{8f_1^2f_2f_3} = \frac{f_1f_2f_3(f_1 + f_2 + f_3)}{8f_1^2f_2f_3} = \frac{1}{8f_1}
\]

(7) \( H_3, Case_7 \): child = \( a_1a_2 \), parent_1 = \( a_3a_4 \)

\[
Pr(Case_7|H_3) = e
\]
\[
Pr(Case_7|H_0) = 2(2f_1f_2f_3f_4)
\]

\[
\rightarrow LR(H_3, H_0|Case_7) = \frac{Pr(Case_7|H_3)}{Pr(Case_7|H_0)} = \frac{e}{8f_1f_2f_3f_4}
\]