Reference haplotypes

h_1	1	1	0	0	1	0
h_2	1	1	0	0	1	0
h_3	1	1	0	0	1	0
h_4	1	0	1	0	0	1
h_5	1	0	1	0	0	1
h_6	1	0	1	0	0	1
h_7	0	0	0	0	0	1
h_8	0	0	0	0	0	1

1. Find unique haplotypes

Unique reference haplotypes

h_1	1	1	0	0	1	0
h_4	1	0	1	0	0	1
h_7	0	0	0	0	0	1

$$||x'_1 - h_1 - h_4||^2 = 2$$
$$||x'_1 - h_1 - h_7||^2 = 2$$
$$||x'_1 - h_4 - h_7||^2 = 3$$

Target genotype

2. Initialize missings

x_1 | 2 | 1 | ? | 0 | ? | 1 |

$\longrightarrow$ x'_1 | 2 | 1 | 0 | 0 | 0 | 1 |

3. Find (possibly many) haplotype pairs using BLAS3 with least squares objective

$$x'_1 \approx h_1 + h_4$$
$$x'_1 \approx h_1 + h_7$$

4. R-calculating error on x_1 instead of x'_1:

$$||x_1 - h_1 - h_4||^2 = 0$$
$$||x_1 - h_1 - h_7||^2 = 1$$

x_1's **optimal hap-pair(s)** $= (h_1, h_4)$

5. Find all matching haplotypes in original reference panel

$$h_1 = h_2 = h_3$$
$$h_4 = h_5 = h_6$$

6. Form **Candidate haplotype pairs**

$$(h_1, h_4), (h_1, h_5), (h_1, h_6)$$
$$(h_2, h_4), (h_2, h_5), (h_2, h_6)$$
$$(h_3, h_4), (h_3, h_5), (h_3, h_6)$$