Reproduced from 'An efficient algorithm for segregation analysis in large populations', Kerr & Kinghorn, J. Anim. Breed. Genet. 113 (1996), 457-469.

$$Pr(u_i|\mathbf{y}) = \frac{a_i(u_i)g(y_i|u_i)\prod\limits_{j\in S_i} p_{ij}(u_i)}{L} \tag{1}$$

Anterior probability:

$$\begin{aligned}
a(u_i) = \sum_{u_m}\Big\{ & a_m(u_m)g(y_m|u_m)\prod_{k\in S_m, k\neq f} p_{mk}(u_m)\\
& \times \sum_{u_f}\Big\{ a_f(u_f)g(y_f|u_f)\prod_{k\in S_f, k\neq m} p_{fk}(u_f)\\
& \times tr(u_i|u_m, u_f)\\
& \times \prod_{s\in C_{mf}, s\neq i}\Big[\sum_{u_s} tr(u_s|u_m, u_f)g(y_s|u_s)\prod_{k\in S_s} p_{sk}(u_s)\Big]\Big\}\Big\}
\end{aligned} \tag{2}$$

Posterior probability:

$$\begin{aligned}
p_{ij}(u_i) = \sum_{u_j}\Big\{ & a_j(u_j)g(y_j|u_j)\prod_{k\in S_j, k\neq i} p_{jk}(u_j)\\
& \times \prod_{o\in C_{ij}}\Big[\sum_{u_o} tr(u_o|u_i, u_j)g(y_o|u_o)\prod_{k\in S_o} p_{ok}(u_o)\Big]\Big\}
\end{aligned} \tag{3}$$

Where:

- i: focal individual

- m, f: parents of i

- j: mate to i

- o: offspring of i

- $S.$: Set of mates of 1 individual

- $C..$: Set of offspring of 2 individuals

and

- $a(u_i)$ anterior probability: information from parents and full sibs

- $p_{ij}(u_i)$ posterior probability: information from mates and progeny

- $g(y_i|u_i)$ penetrance value; information from self: conditional probability that i has phenotype (observed genotype) y_i given it has (actual) genotype u_i.

- $tr(u_i|u_m, u_f)$ Inheritance; conditional probability that i has genotype u_i, given that parents m and f have genotypes u_m and u_f.