The pseudo-code of three optimisation methods are given below.

1. **Optimisation on Success Rate [Optimisation 1]**

   Initialisation;
   
currentGene ← 2
   
geneList ← classifying probesets
   
   while currentGene ≤ totalGenes do
   
   Perform LOOCV using 1,…,currentGene
   
   Record SR
   
   if current SR ≤ previous SR then
   
   Eliminate currentGene from the geneList
   
   endif
   
   currentGene ← currentGene + 1
   
   endwhile

2. **Performance Improvement and Random Crossover [Optimisation 2]**

   Initialisation;
   
currentGene ← 2
   
Create initial population
   
repeat
   
   while current subset ≤ total subsets do
   
   Temporary ← current subset
   
   while currentGene ≤ size of the subset do
   
   Perform LOOCV using 1,…,currentGene of Temporary
   
   Record SR and ∆SR
   
   if current SR ≤ previous SR do
   
   Eliminate currentGene from Temporary
   
   endif
   
   currentGene ← currentGene + 1
   
   endwhile
   
   Rank genes of Temporary according to ∆SR
Perform LOOCV using top 25 genes of Temporary

If SR of 25 genes ≥ acceptable do
    Retain the subset
    endif
endwhile
Perform 2 point crossover
Create new population
until a predefined number of iterations

3. Performance Improvement and Crossover of the Fittest [Optimisation3]

    Initialisation;
    currentGene ← 2
    Create initial population
    repeat
        while current subset ≤ total subsets do
            Temporary ← current subset
            while currentGene ≤ size of the subset do
                Perform LOOCV using 1,…,currentGene of Temporary
                Record SR and ∆SR
                if current SR ≤ previous SR do
                    Eliminate currentGene from Temporary
                endif
                currentGene ← currentGene + 1
            endwhile
            Rank genes of Temporary according to ∆SR
            Perform LOOCV using top 25 genes of Temporary
            If SR of 25 genes ≥ acceptable do
                Retain the subset
                endif
            endwhile
while subset < total subsets do
    Rank genes of all subsets according to $\Delta$SR
    Perform crossover of top genes
endwhile

Create new population

until a predefined number of iterations