

**Input:** cluster\_fittest<sub>1..i</sub>

**Output:** new\_cluster\_fittest<sub>1..i</sub> in sorted order with population\_fittest on top

**Procedure:** inter-cluster evolution

1. number of crossover points = 4
2. new\_cluster\_fittest<sub>1..i</sub> = recombination(cluster\_fittest<sub>1..i</sub>)
3.  $p_m$  = mutation probability
4. new\_cluster\_fittest<sub>1..i</sub> = mutate(new\_cluster\_fittest<sub>1..i</sub>,  $p_m$ )
5. evaluate\_fitness([new\_cluster\_fittest<sub>1..i</sub> + cluster\_fittest<sub>1..i</sub>])
6. new\_cluster\_fittest<sub>1..i</sub> = select the fittest from [new\_cluster\_fittest<sub>1..i</sub> + cluster\_fittest<sub>1..i</sub>] equal to the input size