1. A population $E_0$ of $n$ predictors $\{G_1, ..., G_n\}$ is created. A predictor $G_i$ is subset of $m$ features (genes) $\{g_1, g_2, ..., g_m\}$ initially created by the random selection of genes from the initial gene pool $GP$.

2. Until termination do:

3. For each predictor $G_i \in E_k$, create a new predictor

   a) Randomly mutate the genes in $G_i$ according to the three possibilities:
      i. Add an additional gene chosen randomly from the initial gene pool $GP$ to $G_i$, producing the new predictor $G'_i$
      ii. Delete a randomly selected gene from $G_i$ to produce $G'_i$
      iii. Keep the feature set the same, $G'_i = G_i$

   b) Compute the scoring function of the new predictor $S(G'_i)$

   c) Compute the difference of the score values $\delta_i = S(G'_i) - S(G_i)$

   d) Compute the weight for $G'_i$: $w_i = \exp(\beta, \delta_i)$ where $\beta$ is the inverse temperature.

4. Let $Z$ be the sum of the weights $w_1...w_n$.

5. Create a new population $E_{k+1}$ by replicating all new predictors $G'_i$ according to their normalised weight $w_i \times n/Z$. With a normalised weight $w$, a predictor is replicated $\lfloor w \rfloor$ times and additional time with probability $w - \lfloor w \rfloor$, where $\lfloor w \rfloor$ is the largest integer less than $w$.

6. Using the elitism technique, the worst predictor of the new population $E_{k+1}$ is replaced by the best predictor from the previous generation.