Algorithm 1 Marie Curie Genetic Algorithm Overview

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Let $NUM\_GENS = 100$ represent the number of generations to evolve
Let $POP\_SIZE = 100$ represent the size of the total population
Let $NBPG = 50$ represent the number of new candidates to breed every generation
Let $\boldsymbol{S_{min}}$ and $\boldsymbol{S_{max}}$ represent the vectors of servo limits
Let $L_R$ represent the landmarks in the reference image
Let $P = \{C_i, i \in \{0, 1, .., POP\_SIZE\}\}$ where each $C_i$ is a candidate expression
for $i \in \{0, 1, .., POP\_SIZE - 1\}$ do
    Initialize $\mathbf{C_i.chromosome}$ to $\mathcal{U}(\boldsymbol{S_{min}}, \boldsymbol{S_{max}})$
    Score each candidate s.t. $C_i.score = mc\_score()$
end for
for $g \in \{0, 1, .., NUM\_GENS\}$ do
    Let $N = \{N_i, i \in \{0, 1, .., NBPG\}\} = mc\_breed\_new(NBPG)$ be the set of new candidates for this gen
    Score $N$ s.t. $N_i.score = mc\_score(\mathbf{N_i.chromosome}, L_R)$
    Set $C = C \cup N$
    Remove the $NBPG$ elements with the worst score from $C$
end for
return $C_{opt} = C_i$ where $i = \underset{i}{\operatorname{argmin}}\{C_i.score\}$
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Algorithm 2 MC Score Algorithm (mc_score(X, L'_R))

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Let $M = 68$ be the number of landmarks recognized in an image (constrained by dlib landmark recognition algorithm)
Let $D = 2$ be the dimensionality of a single landmark
Let $L \in R^{D,M}$ represent the raw pixel valued landmarks
Let $L'_R$ be the reference landmarks to score against
Let $X$ be the chromosome to score
Actuate X on the face using the Maestro Controller
Capture an image, $I_C$, of the face
Get the bounding box $B$ of the face
Detect the center of a rectangular bounding box, $B_C = [x, y]^T \in \mathbb{R}^2$ of the face
Detect raw landmarks for cand. image $L_C = dlib\_predictor(I_C).landmarks$
Calculate new "centered" landmarks $L_C^C = L_C - (B_C \otimes \mathbf{1}^T)$
Calculate the horizontal scaling by $x_s = B_{Right} - B_{C,x}$
Calculate the vertical scaling by $y_s = B_{Bottom} - B_{C,y}$
Get normalized landmarks $L'_C = L_C^C \oslash ([x_s, y_s]^T \otimes \mathbf{1}^T)$
Calculate difference in corresponding landmarks between the reference image and the candidate image $L_D = L'_C - L'_R$
return $\|L_D\|_F = \sqrt{tr(L_D^T L_D)}$ where $L_D^T L_D \in \mathbb{R}^{(M,M)}$ is the Gramian matrix of $L_D$ and the diagonal elements of $L_D^T L_D$ represent the euclidean distance error of each landmark. This can also be expressed as the square root of the sum of the squared errors.
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Algorithm 3 MC Breed New (mc_breed_new(N_C, N_{CpP}))

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Let $N_C$ be the number of new candidates to breed
Let $N_{CpP}$ be the maximum number of candidates to breed for a single set of parents
Calculate the number of pairs of parents $N_{pP}$
Get the mating pool $M$ which is comprised of the best (lowest) scoring $2N_{pP}$ candidates in $C$
Create $N_{pP}$ pairs of parents, $P_p$, by pairing the highest scoring parents together (i.e. $P_p = \{\{M_0, M_1\}, \{M_2, M_3\}, \dots\}$)
Initialize $N = \emptyset$ where $N$ is the set of all new candidates bred this generation.
for $p \in P_p$ do
    for $j \in \{0, 1, \dots, N_{CpP} - 1\}$ do
        Let $C_N$ represent the new candidate
        Randomize order of $p$
        Randomly select location $i$ in which to perform crossover of chromosomes
        Set $\mathbf{C_N}.\mathbf{chromosome} = [p_0[: i]^T, p_1[i :]^T]^T$ representing the concatenation of the two parent chromosomes sliced at index i
        Set $\mathbf{C_N}.\mathbf{chromosome} = \mathcal{N}(\mathbf{C_N}.\mathbf{chromosome}, 50^2)$ representing a mutation of the inherited chromosome with each gene varying in a normal distribution parameterized by $\boldsymbol{\mu} = \mathbf{C_N}.\mathbf{chromosome}$ and $\sigma^2 = 50^2$ where 50 is the standard deviation in quarter microseconds
        Saturate values in $\mathbf{C_N}.\mathbf{chromosome}$ to safe limits for servos
        Append $C_N$ to $N$ by $N = N \cup C_N$
    end for
end for
return $N$
```