List of Algorithms

Algorithm 1 Marie Curie Genetic Algorithm Overview

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 $i = \underset{i}{\text{argmin}}\{C_i.score\}$

Algorithm 2 MC Breed New (mc_breed_new(N_C, N_{CpP}))

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 $\mathbf{C_N}$**.chromosome** $= [p_0[:i]^T, p_1[i:]^T]^T$ representing the concatenation of the two parent chromosomes sliced at index i
        Set $\mathbf{C_N}$**.chromosome** $= \mathcal{N}(\mathbf{C_N}$**.chromosome**$, 50^2)$ representing a mutation of the inherited chromosome with each gene varying in a normal distribution parameterized by $\boldsymbol{\mu} = \mathbf{C_N}$**.chromosome** and $\sigma^2 = 50^2$ where 50 is the standard deviation in quarter microseconds
        Saturate values in $\mathbf{C_N}$**.chromosome** to safe limits for servos
        Append C_N to N by $N = N \cup C_N$
    end for
end for
return N

Algorithm 3 MC Score Algorithm (mc_score(X, L'_R))

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.