Algorithm 1 Marie Curie Genetic Algorithm Overview

- 1: Let $NUM_GENS = 100$ represent the number of generations to evolve
- 2: Let $POP_SIZE = 100$ represent the size of the total population
- 3: Let NBPG = 50 represent the number of new candidates to breed every generation
- 4: Let S_{min} and S_{max} represent the vectors of servo limits
- 5: Let L_R represent the landmarks in the reference image
- 6: Let $P = \{C_i, i \in \{0, 1, ..., POP_SIZE\}\}$ where each C_i is a candidate expression
- 7: for $i \in \{0, 1, .., POP_SIZE 1\}$ do
- 8: Initialize $C_i.chromosome$ to $\mathcal{U}(S_{min}, S_{max})$
- 9: Score each candidate s.t. $C_i.score = mc_score()$
- 10: end for
- 11: **for** $g \in \{0, 1, ..., NUM_GENS\}$ **do**
- 12: Let $N = \{N_i, i \in \{0, 1, ..., NBPG\}\} = mc_breed_new(NBPG)$ be the set of new candidates for this gen
- 13: Score N s.t. $N_i.score = mc_score(N_i.chromosome, L_R)$
- 14: Set $C = C \cup N$
- 15: Remove the NBPG elements with the lowest score from C
- 16: end for
- 17: **return** $C_{opt} = min(C)$

Algorithm 2 MC Score Algorithm (mc_score(X, L'_R))

- 1: Let M = 68 be the number of landmarks recognized in an image
- 2: Let D=2 be the dimensionality of a single landmark
- 3: Let $L \in \mathbb{R}^{M,N}$ represent the raw pixel valued landmarks
- 4: Let L'_R be the reference landmarks to score against
- 5: Let X be the chromosome to score
- 6: Actuate X on the face using the Maestro Controller
- 7: Capture an image, I_C , of the face
- 8: Get the bounding box B of the face
- 9: Detect the center of a rectangular bounding box, $B_C = [x, y] \in \mathbb{R}^2$ of the
- 10: Detect raw landmarks $L_C = dlib_predictor(I_C).landmarks$
- 11: Calculate new "centered" landmarks $L_C^C = L_C (\mathbf{1} \otimes B_C)$
- 12: Calculate the horizontal scaling by $x_s = B_{Right} B_{C,x}$

- 13: Calculate the vertical scaling by $y_s = B_{Bottom} B_{C,y}$ 14: Get normalized landmarks $L'_C = L^C_C \oslash (\mathbf{1} \otimes [x_s, y_s])$ 15: Calculate difference in corresponding landmarks $L_D = L'_R L'_C$
- 16: **return** $||L_D||_F = \sqrt{tr(L_D^T L_D)}$ where $L_D^T L_D$ 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

Algorithm 3 MC Breed New (mc_breed_new(num_to_breed))