IEEE Access
Multidisciplinary ⋮ Rapid Review ⋮ Open Access Journal

Received 14 June 2024, accepted 17 July 2024, date of publication 29 July 2024, date of current version 9 August 2024.

Digital Object Identifier 10.1109/ACCESS.2024.3434689

RESEARCH ARTICLE

The Emotional State Transition Model Empowered by Genetic Hybridization Technology on Human–Robot Interaction

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This work was supported by Universiti Kebangsaan Malaysia under Tabung Agihan Penyelidikan under Grant TAP-K006873.

This work involved human subjects in its research. Approval of all ethical and experimental procedures and protocols was granted by the Jawatankuasa Etika Penyelidikan IVI (IVI Research Ethics Committee).

ABSTRACT In the rapidly developing field of Human-Robot Interaction (HRI), simulating human emotional states poses significant challenges due to the inherent complexity and unpredictability of human emotions. Addressing the limitations in artificial emotion simulation, such as fuzzy theory, memory mechanism, and etc., we explore the genetic canvas that portrays emotions as an interplay of myriad complex expressions. By simulating emotional states using Genetic Hybridization Technology (GHT) in the Emotional State Transition (EST) model, this study investigates the role of genetics in artificial emotion simulation, outlines the creation of EST morphological genes, and validates their consistency. The results indicate that the Fréchet distance for EST curves ranges between 0.072 and 0.239, suggesting a high level of consistency between the experimentally generated EST curves and the newly generated EST morphological genes. This finding demonstrates the effectiveness of our proposed method and supports its future use in experimental design under various conditions. Additionally, we identified instances of gene mutations that occurred during the gene hybridization process, as highlighted in the results for EST curve (h). Despite this variation, the Fréchet distance remains within a reasonable range, further validating the reliability of our methodology. This study establishes a precedent for the methodology of emotional simulation, providing new research pathways for enriching HRI, through substantive exploration of the relationship between Artificial emotional intelligence (AEI) and GHT.

INDEX TERMS Emotional state transition model, genetic hybridization technology, human-robot interaction, artificial emotional intelligence.

I. INTRODUCTION

In the rapidly advancing field of robotics, the emulation of human-like emotions appears as one of the most intriguing and challenging frontiers [1]. The pursuit to endow robots with the capability to not only perform tasks but also to exhibit and interpret emotional responses has seen significant interest [2]. This paper presents an innovative approach to the emotion simulation in robots through the Emotional State Transition (EST) model driven by Genetic Hybridization technology (GHT). This interdisciplinary nexus aims to bridge the gap between complex biological mechanisms and artificial emotional processing.

The associate editor coordinating the review of this manuscript and approving it for publication was Maurizio Tucci.

Artificial emotional intelligence (AEI) is focused on simulating and extending natural emotion (especially human emotion) to provide robots with the capability to recognize and express emotions in human–robot interaction (HRI) [3]. In the field of HRI, particularly in the context of AEI, the prevailing approach towards artificial EST-related research currently involves methodologies such as fuzzy theory [4], [5], memory mechanism [6], [7], and personalized emotion analysis [8], [9]. These approaches frame the modeling of emotional dynamics in terms of probabilistic and subjective inference, offering valuable insights into the stochastic nature of affective phenomena, and have showcased emotions as complex, and multi-dimensional constructs. Fuzzy theory [10], in particular, has been instrumental in providing a mathematical structure to capture the imprecision inherent in human emotions, while memory mechanism aids in handling incomplete information systems indicative of emotional states [11]. Personalized emotion analysis involves tailoring emotional models to individual idiosyncrasies, thereby, enhancing the pertinence and predictability of interactional outcomes.

Despite the advancements made in these areas, it is obvious that studies delving into the genetic underpinnings of emotions—a crucial biological aspect of affective states—remain relatively emergent. The genetic composition of emotions which entails a mapped gene expression and emotional responses could yield a richer understanding of emotional variants [12]. While genetic factors contributing to emotional traits in humans have been subject to rigorous investigation, their extension to artificial platforms has yet to be extensively explored [13]. This identified gap presents a compelling argument for integrating genetic insights into emotion-related artificial modeling, positing that affective genetics exploration could unravel novel mechanisms for emergence as well as transition of emotions within an artificial entity. Limited existing research for affective genes necessitates a broader, more integrative approach to biological and computational aspects of emotions.

The concept of EST within humans has been extensively studied and is pivotal to understanding the intricacies of human interactions [14], [15]. Based on this, robots can better understand and respond to human emotional needs, thereby, more accurately simulating and expressing human emotions, and ultimately, improving the quality and effectiveness of HRI. To achieve this, hybridization techniques in genetics have unlocked the potential for creating diverse biological attributes. By adopting genetic hybridization approaches, we can develop a nuanced emotional landscape within a robotic framework that better mirrors human emotionality. Further, the application of GHT within EST also introduces an element of mutations, evolution, and adaptation, enabling robots simulate as well as 'learn' emotion dynamics in real-time interactions. GHT thus provides a robust methodological foundation for the development of an EST model in robots.

This paper is structured as follows: we begin with a review of related work in the field of robot emotion simulation and gene hybridization. Next, we delve into the theoretical underpinnings of emotion and its implementations in biological systems, drawing parallels wherever applicable to robotics. Following this, we introduce the EST model, demonstrating GHT integration to enhance its functionality. Finally, we discuss the implementation of the EST model in a robotic context and explore the implications of such systems in the broader scope of HRI. Through this work, we seek to contribute to the ongoing dialogue in HRI by providing a novel perspective on how genetic principles can inform and advance the simulation of emotions in robots. This integration evidence how AEI could transcend beyond current boundaries, catalyzing the genesis of life-like robots that not only simulate human-like emotions but also exhibit an evolved emotional repertoire shaped by both environmental interactions and 'inherited' emotional predilections. In conclusion, bridging the gap between the current focus on AEI and the vital emerging field of affective genetics could chart a transformative course for the future of robot emotion simulation.

II. LITERATURE REVIEW

The field of emotion simulation of HRI is an intersection of distinct but interrelated lines of inquiry, each contributing various perspectives and techniques aimed at enriching interactions between humans and machines. The literature review that follows encompasses the development of emotion simulation and genetic hybridization, emphasizing new distinctive research directions. Initially, the concept of emotional intelligence in machines was theorized for an inanimate audience, however, it has progressively evolved into an active area of robotics research [16], [17]. Early contributions by Velásquez [18] provided one of the pioneering models for generating and expressing emotions in robots, forming a precursor to more complex systems. From there, the idea of simulating emotions advanced through diverse methodologies, as embodied by the Affective Computing group led by Picard [19] at the Massachusetts Institute of Technology. Arbib and Fellous [20] further explored the interplay between emotions and cognition in the context of robot design.

Emotional models established by Marsella and Gratch [21] were pivotal in integrating psychological theories of emotion into computational frameworks for robots. The synthesis of psychological principles and artificial intelligent (AI) has significantly influenced the current landscape of robot emotion simulation. The efforts to comprehend and replicate the subtle shifts in emotional states has led Cañamero [22] to investigate the role of homeostatic mechanisms and their potential utility in robotic systems, contributing to a layer of physiological grounding to emotional expressions. Early work in evolutionary robotics by Nolfi and Floreano [23] threw light on how genetic algorithms could be leveraged to evolve

TABLE 1. Summary and analysis of previous studies.

Authors	Results/Findings	Limitations
Bentley [24]	Merge genetic principles with emotion simulation in robotics	Focused more on genetic optimization of robotic traits rather than simulation of emotion methods
Nolfi and Floreano [23]	Genetic algorithms could be leveraged to simulate robotic behaviors	Lacking in specific emotional simulation methods
Fernando, et al. [31]	Principles of natural evolution can be used to enhance learning and adaptation in artificial systems	Proposed principles of natural evolution, but lacking in further explorations of emotional simulation methods
Jiang, et al. [5]	Draw an emotional state transition tube for Artificial emotion simulation based on fuzzy theory	Required extensive computational processing, increasing implementation difficulty and processor performance demands
Xiao, et al. [28]	Establish a customized system for machine emotion expression based on the proposed emotion transfer model	Lacked generalization
Chuah and Yu [27]	Effective simulation of emotions in robots can be enhanced by utilizing Instagram data through the integration of multidisciplinary theories	Findings could be biased due to the specific user demographic on Instagram
Sijin, et al. [7]	Apply emotional memory mechanism to understand and express uncertain emotions	May not have accurately replicated all memory characteristics in simulating human memory processes
Abdollahi, et al. [29]	Integrating AEI into a social robot and explores the robot's effectiveness in engaging with older adults	Real-time detection and interpretation of complex human emotions remained challenging
Liu, et al. [8]	Introduce a novel emotion-based personalized music recommendation (hereinafter EPMR) framework	While addressing personalization, it might not have fully accounted for the wide spectrum and nuances of emotions

robotic behaviors. While not directly addressing emotional states, these works set the stage for considering genetic approaches in robot design. It was from here that the idea to merge genetic principles with emotion simulation in robotics began to take hold, although initial explorations such as those by Bentley [24] focused more on the genetic optimization of robotic traits rather than the direct simulation of emotions. The study of bio signal processing techniques for emotion recognition in machines, as demonstrated by Schuller [25], underscores the growing sophistication of emotion detection and the potential for these methods to inform genetic algorithms. The use of deep learning for emotional state classification in robotics, as illustrated by Rao et al. [26], further pushes the boundaries of how machines can interpret human affective signals.

In recent years, AEI has made significant progress in the HRI field. Incorporating relevant psychology theories and data science within the framework of HRI, Chuah and Yu [27] used Instagram data to explore the impact of emotional robots on the affective responses of potential consumers. A probability and integrated learning method is proposed by Jiang et al. [5] for constructing artificial emotion models by simulating human thinking. Xiao et al. [28] introduced a machine emotion transfer model to establish a customized system for machine emotion expression. It also strives to create a dynamic emotional interaction model between humans and machines within an intelligent interactive environment. Abdollahi et al. [29] presented research on integrating AEI into a social robot and explored the robot's effectiveness in engaging with older adults. The robot identifies users' emotional states using various input modalities for emotion in real-time, such as facial expression and speech sentiment. It then employs a dialogue manager to generate emotional responses. Ojha et al. [30] suggests that an emotional model should identify the relationship between mood and emotions dynamically, using emotion related data collected from human subjects to enable AI to generate emotions of their own.

To sum up, Current research related to the application of GHT to robotics is limited. However, the integration of hybridizing genetic principles into cognitive architectures, holds extensive and promising potential. For example, a concept derived from biologically inspired computing, Fernando et al. [31] explores how principles of natural evolution could be used to enhance learning and adaptation in artificial systems. This study aims to undertake this under-explored research direction, in order to address the inherent complexity and unpredictability of human emotions. In the following sections, we will build upon existing literature, introducing the EST model, detailing its integration with GHT, and illustrating the transformative potential that this synergy holds for robotics and AEI. In doing so, we aim to contribute a novel perspective to the ongoing development of this field. Table 1 lists the current studies on AEI.

III. MORPHOLOGY FUNCTION OF EST MODEL

A. EXPERIMENT

1) EXPERIMENTAL PREPARATION

Participant Recruitment: Recruiting 30 undergraduate students at a university in China to ensure equal gender representation for 15 males and 15 females.

Selection Criteria: The students are selected based on predefined criteria, such as age range and absence of known affective disorders that could influence their emotional responses.

Exclusion criteria: Participants are excluded from the experiment if they meet any of the following conditions. known neurological or psychiatric disorders affecting responses to emotional stimuli; use of medications or

substances interfering with neural or affective responses; lack of language ability, which could affect understanding and interaction; uncorrected vision or hearing problems, as the experiment may involve visual or auditory stimuli; participation in similar experiments in the past six months to avoid bias; and inability or unwillingness to give informed consent or adhere to the experimental process. These exclusion criteria are established to ensure the reliability of the collected data and minimize the impact of confounding factors on the results.

2) EQUIPMENT AND ENVIRONMENT SETUP

Laboratory Environment: The experiment is conducted in a quiet, closed laboratory free from external disturbances to maintain a controlled environment and ensure accuracy in data collection.

Equipment: High-resolution desktop computer for video presentation, EEG system with 32 electrodes, ECG monitor, Galvanic Skin Response (GSR) sensors, and a high-definition camera focused on the participant's face for facial emotion recognition.

Video Stimuli: More than 200 video clips ranging from comedic to sad content, sourced from popular Chinese video websites, pre-screened to elicit clear emotional responses. Use video editing software to clip these clips into a 1-minute experimental sample. These samples should include both positive and negative emotion clips.

3) EXPERIMENTAL PROCEDURE

Initial Briefing and Consent: Before the experiment, participants are briefed about the procedure and provided with informed consent forms detailing the study's purpose and outlining their right to withdraw at any time.

Baseline Data Collection: Participants are first allowed to familiarize themselves to the lab environment. Baseline physiological data are collected while the participant is at rest to establish a control measure for emotional states prior to any stimuli exposure.

Stimuli Exposure: A preselected 1 min video clips are played to each participant in a predetermined order, while data collection equipment records their physiological responses in real-time.

Continuous Monitoring: Throughout the experiment, participants are monitored to ensure comfort and data fidelity.

4) DATA COLLECTION (EXAMPLE)

Participant 1: Male, 21, indicated visible laughter during comedic clips, shown in amplified facial movements. GSR levels elevated, and EEG data suggested high engagement.

Participant 2: Female, 19, revealed a pronounced emotional response to a sad clip, with a significant ECG rate increase and dampened movement.

5) DATA PROCESSING AND ANALYSIS

Signal Processing: After the experiment, the collected physiological data is processed using signal processing methods to remove noise and artefacts. For example, the raw EEG data, which is often noisy and contains artefacts, is first subjected to band-pass filtering. This filtering is done to constrain the signal into the frequency band of interest that is relevant for emotion recognition tasks, usually ranging from 0.5Hz to 50Hz. Following the initial band-pass filtering stage, the data undergoes artifact removal. Artifacts in EEG data can originate from various sources, such as muscle activity, eye blinks, and other physiological or external electrical noises. We employ Independent Component Analysis (ICA), a widely used technique for artefact removal in EEG data. ICA works by separating the multivariate signal into additive subcomponents that are maximally independent.

Feature Selection: Emotional features are extracted from the physiological data, which include heart rate variability, GSR changes, and EEG patterns associated with emotional responses.

Emotion Indexing: Using emotion recognition algorithms [32], the data is synthesized to assign an emotional index score to each participant's response to the video stimuli. with positive scores for joy and negative scores for sadness (typically from 1 to -1).

6) EST CURVE GENERATION

Data Alignment: Align these values with the corresponding timestamps of the video stimuli to create a coherent time series of emotional data.

Curve Plotting: Plot the emotional indices on the y-axis against the time (in seconds) during which the video stimulus was watched on the x-axis, thereby plotting the EST curve.

Curve Analysis: Evaluate the resulting EST curve for patterns of emotional transition throughout the stimuli exposure and identify any variations between the genders or individual participants.

7) VALIDATION

Result Interpretation: Interpret the results of the EST curve in the context of the emotional stimuli presented, considering the gender distribution and individual differences.

Result Validation and Reporting: Correlate the physiological data with any self-reported measures of emotion for validation. The part of experimental results is shown in Figure 1.

Where the dashed line in the figure represents the confidence interval of EST curve [5].

B. GENE CODE TECHNOLOGY ON EST MORPHOLOGY

1) INTRODUCTION

During the development of an EST model constructed by GHT, encoding the EST curve genes is particularly crucial. To enhance the efficiency of EST curve gene encoding, we process the EST curves obtained during the experiment using a computer and then encode the extracted lines. The curve encoding method based on binary trees can be used to construct an intuitive tree structure [33], as shown in Table 2.

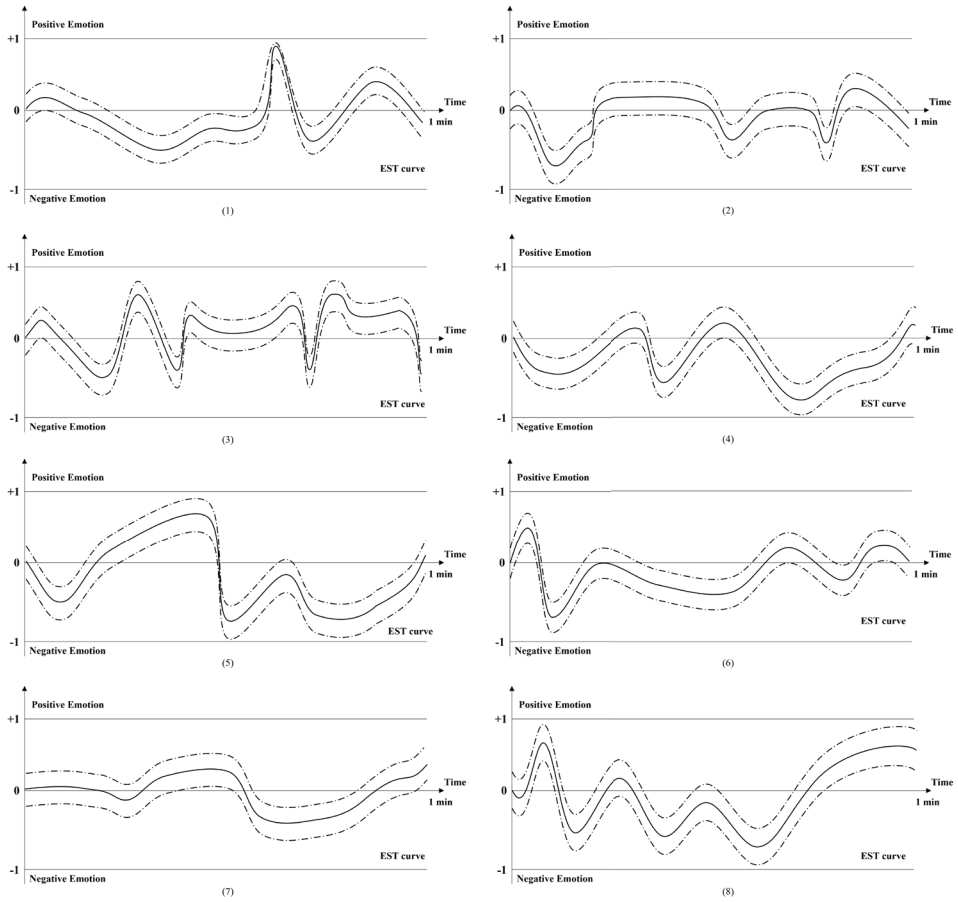


FIGURE 1. EST curve of partial experimental results.

TABLE 2. Complete binary tree and full binary tree.

	Complete binary tree	Full binary tree
Total node k	$2^{h-1} \ll k \ll 2^{h-1}$-1	$k = 2^{h-1}$-1
Tree height h	$h = log_2 k + 1$	$h = log_2 (k+1)$

These parameters pertain to the total number of nodes (k) and tree height (h) in both complete binary trees and full binary trees. Importantly, the nodes and heights are significantly linked to the magnitude and complexity of the genetic data encoded. The encoding process takes advantage of a binary tree method to conveniently and effectively manage the complexity and volume of genetic information in the EST curve. A binary tree enables us to structure the encoded information in a hierarchical and intuitive manner. This organizational structure makes it easier for us to handle and manage the encoded EST curve genes in the subsequent stages of our analysis and facilitates the selection of key points for curve fitting in MATLAB.

2) ENCODING PROCESS

The encoding of morphological genes for the EST model is an essential process in our study. The justification encoding

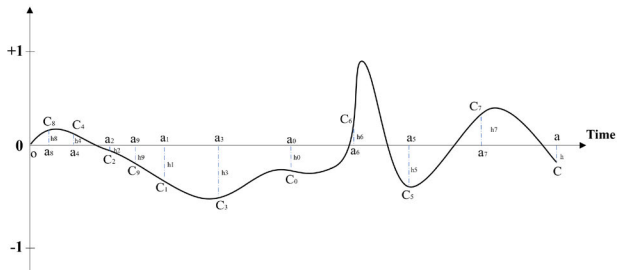
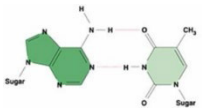


FIGURE 2. EST curve coding.

the EST curve genes is to streamline the process of analyzing and deciphering the genetic data collected during our experiment. The encoding process begins with the computerized processing of the EST curves obtained from the experiment. The significant lines within these curves are then subject to encoding. Taking the EST curve obtained in the experiment as an example, extract the contour line from Figure 1 (1), as shown in Figure 2. At the end of the EST curve, point C is perpendicular to point a on the time axis. Connect the first and last points, labelled as o and a. Next, find the midpoint a_0 on the time axis, and draw a vertical line perpendicular to the time axis through a_0 that intersects the EST curve at

TABLE 3. Comparison of EST morphology and biological gene composition.

EST morphology genes		Description	Biological gene		Description
●	Point	Points in geometry only represent positions, while in EST they represent a certain emotional state at a certain point in time		Base	Nucleosides combine with phosphate to form nucleotides, and the phosphate group is attached to the 5th carbon atom of a pentose sugar. Bases are components of nucleic acids, nucleosides, and nucleotides.
▮	Line	Dotting forms a line, which is a continuation of a point. Different types of curves in EST represent changes in emotional states over a period of time		Gene segment	Genes are DNA fragments with specific genetic effects.
■	Surface (3D)	Linear motion forms a surface. The surface in EST is the complete EST surface formed by a person receiving different emotional stimuli during multiple identical time periods.		Chromosome	Genes have a certain position on chromosomes and exhibit linear arrangement.

the point C_0. Following this, locate the midpoint a_1 between points a_0 and o on the time axis. Next, draw a vertical line through the midpoint a_1 that is perpendicular to the time axis and intersects the EST curve at point C_1. Repeat the above operation to obtain perpendicular lines h_2, h_3, and h_4. Establish a unit coordinate system with point o as the origin, place the EST curve within the range of [0,60] on x-axis and $[-1,1]$ on y-axis. Obtain the coordinates of points C, C_0, C_1, C_2, C_3, C_4, C_5, C_6, C_7, and C_8, C_9 on the curve.

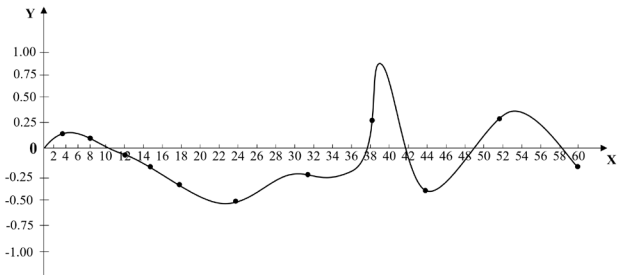


FIGURE 3. Function code of morphology genes of EST curve.

3) EXTRACTION PROCESS

The extraction process works in tandem with the encoding process. After encoding the EST curve gene data, the process involves extracting significant contour lines from the curves using MATLAB. By obtaining the coordinates of points o (0,0), C (60, y_c), C_0 (x_{C_0}, y_{C_0}), C_1 (x_{C_1}, y_{C_1}), C_2 (x_{C_2}, y_{C_2}), C_3 (x_{C_3}, y_{C_3}), C_4 (x_{C_4}, y_{C_4}), C_5 (x_{C_5}, y_{C_5}), C_6 (x_{C_6}, y_{C_6}), C_7 (x_{C_7}, y_{C_7}), C_8 (x_{C_8}, y_{C_8}), and C_9 (x_{C_9}, y_{C_9}) on the curve, function code the encoded curve in MATLAB software, as shown in Figure 3. MATLAB, as a powerful tool for engineering computing, plays a crucial role in fitting functions to gene images in this study. It facilitates the analysis of gene graphical characteristics by fitting the EST curve and deciphering the gene's functional representation. This capability enhances the study of gene graphics and offers a more efficient means to manipulate genes represented by the EST curve from a graphical standpoint.

IV. GENE THEORY ON MORPHOLOGY FUNCTION OF EST MODEL

A. CONCEPT OF MORPHOLOGY GENE OF EST MODEL

According to modern biology, a gene is a nucleotide sequence that contains specific genetic information [34]. It serves as the basis for the transmission of genetic information and traits development. When genes pass on genetic information to the next generation, they not only replicate but also express that information during transmission. Gene engineering involves introducing foreign genes into recipient cells through in vitro recombination, allowing these foreign genes to replicate, transcribe, and translate within the recipient cells. Therefore, biotechnological gene engineering can selectively modify biological traits, endowing organisms with desirable characteristics. In this study of EST morphology genes, we approach the concept from the perspective of the currently popular Multimodal Sentiment Analysis (MSA). By integrating theories related to genetic control of traits in biology and drawing inspiration from biological gene manipulation experiences, we conduct a detailed comparison between the structural elements of EST and those of biological genes. Refer to Table 3 for an illustration.

It is not difficult to find EST morphological genes and biological genes having many similar characteristics in composition. Table 4 depicts selection criteria for operating objects in biological genetic engineering, as well as analysis, comparison, and selection of the operating objects for EST genetic engineering. 'Point' is a visual unit with spatial positional features. When expressing EST morphological features, due to the insufficient information contained in a single element, its operation will greatly increase the workload, and the number of operating objects. On the contrary, the element 'surface' contains too much information, and its operation

TABLE 4. EST morphology composition operation object analysis.

Morphology	Amount of information	Workload	Number of operands	Ease of operation
Point	Less	More	More	Harder
Line	Mid	Mid	Mid	Mid
Surface (3D)	More	More	More	Easy

process will be interfered by a large amount of irrelevant information, thereby, reducing the accuracy of trait control and is not the best choice for morphological gene operation objects.

Therefore, 'line' is the most suitable operating object due to its moderate amount of information and relatively complete structure in the process of EST morphological gene hybridization. The rationale for this selection method can be supported by a large number of cases in the engineering drawing field. From a practical application perspective, the widespread use of the three views evidence that "lines" have sufficient ability to express and control EST morphological features with relatively better operability. Therefore, by combining biological GHT, comparing, and analyzing other studies as well as related concepts of EST genes, it is concluded that EST morphological genes are parameterized morphological representation line segments that contain heritable information of EST morphology that can control EST evolution. By extracting and encoding EST morphological genes, performing cross iteration and mutation operations, EST can undergo morphological changes and construct evolved emotional repertoire.

B. MORPHOLOGICAL GENE HYBRIDIZATION PROCESS OF EST MODEL

Biological gene hybridization is the pairing of two single stranded DNA or RNA bases, which is a method for obtaining individuals which have recombined certain parental genes through mating between individuals of different genotypes. GHT uses gene fragments as operating objects to recombine the genes of parents, forming various types and providing rich materials for selection. In addition, it is noteworthy that gene mutations may occur during the gene recombination process [35]. The application of GHT on EST morphological uses the EST function curve as the operating object to combine the morphological genes of EST, multiple new genes, and prepare for the ultimate provision of an evolutionary emotion pool shared by environmental interactions and future "genetic" emotion prediction. It includes operational techniques such as morphological gene extraction, coding, recombination, cross iteration, and gene mutation. This is a crucial step in the EST morphology gene hybridization process. The technical route and key steps are depicted in Figure 4.

C. GENE ITERATIVE RECOMBINATION

When combining morphological genes, nodes are key elements that interrupt and recombine morphological genes.

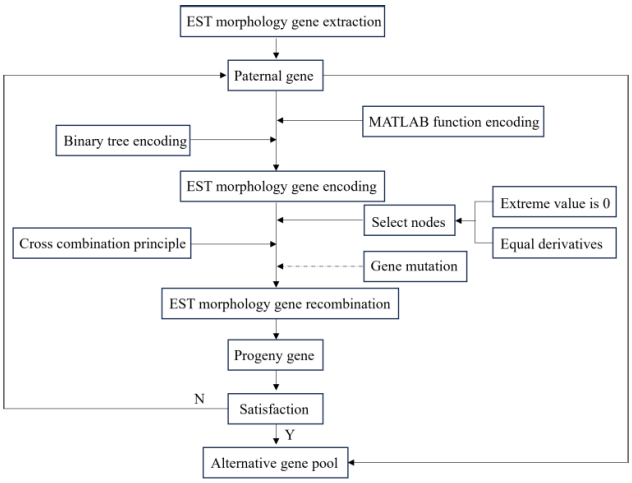


FIGURE 4. 4 Diagram of EST morphology gene hybridization process.

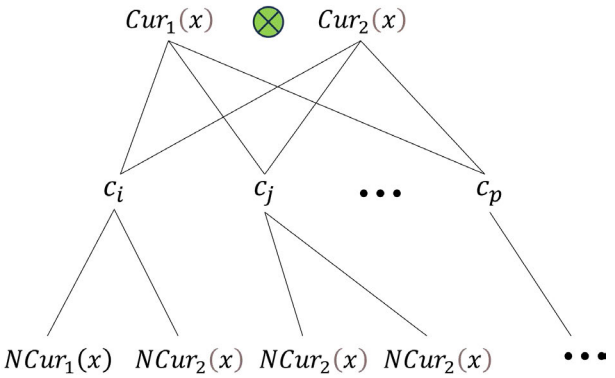


FIGURE 5. Diagram of gene cross recombination.

Selecting equidistant nodes or special equidistant nodes with extreme values of zero for crossover and recombination can generate a new piecewise function with continuous curvature. The function image is the new EST morphological gene, and the newly generated morphological gene can well inherit the morphological characteristics of the previous generation gene. It is noteworthy that gene mutations occur when positive (negative) emotional curve segments are combined with negative (positive) emotional curve segments.

In order to express the functional transformation of EST morphological genes more clearly, two curves, $\mathrm{Cur}_1(x)$ and $\mathrm{Cur}_2(x)$, are set up, where $x \in [0, 60]$. There are two points C_i and C_j, C_i, $C_j \in [0,60]$, making $\mathrm{Cur}_1'(C_i) = \mathrm{Cur}_2'(C_j)$. Taking C_i and C_j as nodes, the two curves are broken and regrouped into two new piecewise functions $\mathrm{NCur}_1(x)$ and $\mathrm{NCur}_2(x)$ as shown in Figure 5.

$$N\mathrm{Cur}_1(x) = \begin{cases} \mathrm{Cur}_1(x), & x \in [0, C_i] \\ \mathrm{Cur}_2(x), & x \in [C_i, C_i + 60 - C_j] \end{cases} \quad (1)$$

$$N\mathrm{Cur}_2(x) = \begin{cases} \mathrm{Cur}_2(x), & x \in [0, C_j] \\ \mathrm{Cur}_2(x), & x \in [C_j, C_j + 60 - C_i] \end{cases} \quad (2)$$

Gene mutation occurs if there have two points C_m that satisfy $\mathrm{Cur}_1(x) > 0$ ($x \in [0, C_i]$) and $\mathrm{Cur}_2(x) < 0$

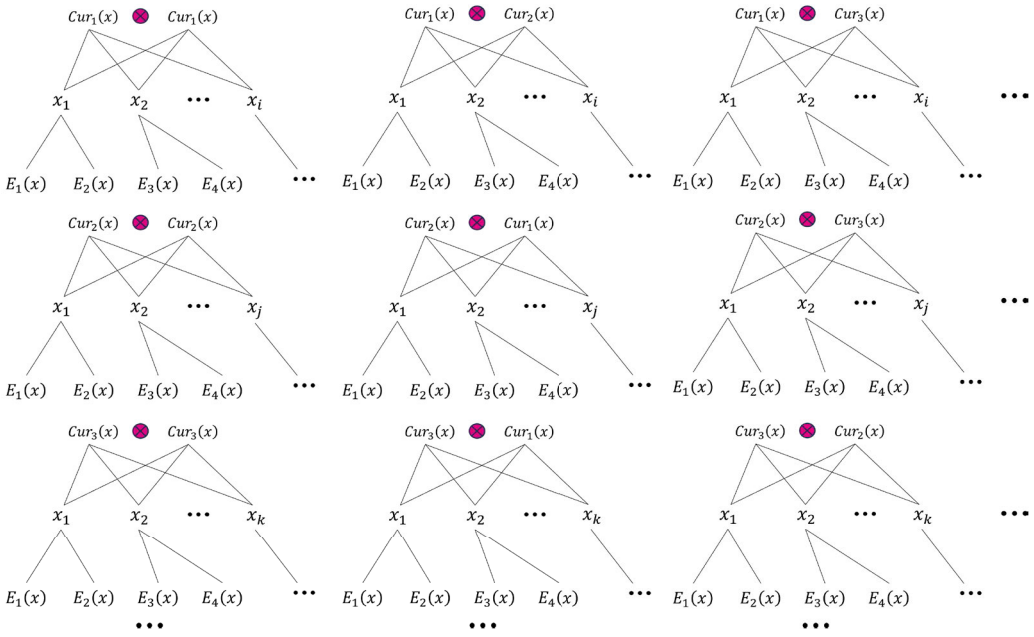


FIGURE 6. Diagram of iterative recombination of EST morphological gene.

$(x \in [C_j, C_m])$; or $\mathrm{Cur}_1(x) < 0$ $(x \in [0, C_i])$ and $\mathrm{Cur}_2(x) > 0$ $(x \in [C_j, C_m])$ and C_n that satisfy $\mathrm{Cur}_1(x) > 0$ $(x \in [0, C_i])$ and $\mathrm{Cur}_2(x) < 0$ $(x \in [C_j, C_n])$; or $\mathrm{Cur}_1(x) < 0$ $(x \in [0, C_i])$ and $\mathrm{Cur}_2(x) > 0$ $(x \in [C_j, C_n])$. Please refer another two equations:

$$\mathrm{NCur}_1(\mathrm{x}) = \begin{cases} \mathrm{Cur}_1(x), & x \in [0, C_i] \\ -\mathrm{Cur}_2(x), & x \in [C_j, C_m] \\ \mathrm{Cur}_2(x), & x \in [C_k, C_k + 60 - C_j] \end{cases} \tag{3}$$

$$\mathrm{NCur}_2(x) = \begin{cases} \mathrm{Cur}_2(x), & x \in [0, C_j] \\ -\mathrm{Cur}_1(x), & x \in [C_i, C_n] \\ \mathrm{Cur}_1(x), & x \in [C_n, C_n + 60 - C_i] \end{cases} \tag{4}$$

D. FUNCTIONAL OPERATION OF ITERATIVE RECOMBINATION

In the above transformation, only one iso-derivative node in each curve is considered, but in the actual recombination process, each morphological gene often has multiple iso-derivative nodes cross combination, so the above recombination function is named RF, the iterative function is named F, the initial parent gene is $\{E\}$, $\{E_i\}$ represents the i generation morpho-child gene, then:

$$\begin{aligned} E_1 &= \mathrm{RF}\{E\}, \{E_2\} = \mathrm{RF}\{\mathrm{RF}\{E\}\}, \ldots, \{E_i\} \\ &= FF_{i-1}, \ldots, \{F\{\mathrm{RF}\{E\}\}\} \end{aligned} \tag{5}$$

As shown in Figure 6, the newly generated progeny genes of each generation go through iterative function operation again, so that the cross combination of multiple isogenic nodes can be achieved. In this way, a large number of comprehensive morphogenetic genes can be obtained, and the set $\{\mathrm{EE_i}\}$ of its original parent genes is the complete candidate gene pool generated.

E. DESCRIPTION EXAMPLE OF OPERATION PROCESS

This section uses two EST curves obtained from experiments of participant 1 (Figure 7) to obtain new genotypes as an example to illustrate the actual operation process of this technology This technology primarily starts from the key techniques of extracting, encoding, and cross iteration of morphological genes of EST model. It selects morphological genes and recombines them to form new EST morphological genotypes, providing interactive system with a more diverse emotional repertoire.

It is important to note the iterative nature of our gene hybridization process. Although this section only shows the process starting from two parent morphological genes, in practical operation, the number of parent morphological genes is not limited to these few. Additionally, in each iteration, we introduce more genetic variability not only by recombining the original genes but also by recombining the newly formed offspring. This significantly diversifies the gene pool. Our hybridization method involves cross-combination at multiple iso-derivative nodes, which increases genetic variations in every iteration. So, even though we start with few parent genes, the subsequent multiple recombination generates a multitude of unique and diverse morphological genes.

1) MORPHOLOGY GENE CODING

Before recombining and iterating the parental morphological genes of the extracted EST curve, it is necessary to encode the obtained curve using binary tree method and fit it with MATLAB to obtain the function expression of the curve.

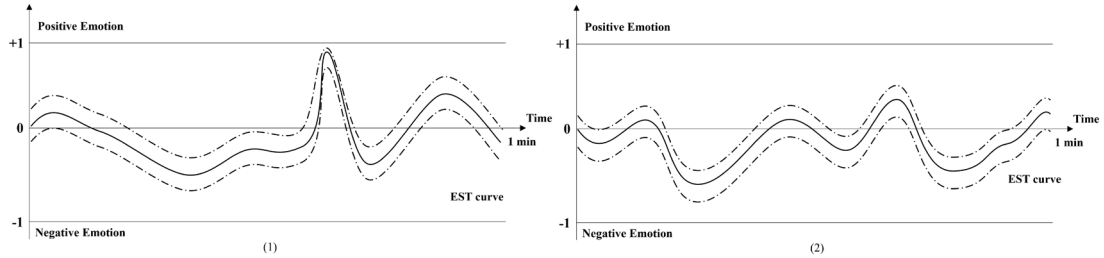


FIGURE 7. Parent morphological gene of EST curve.

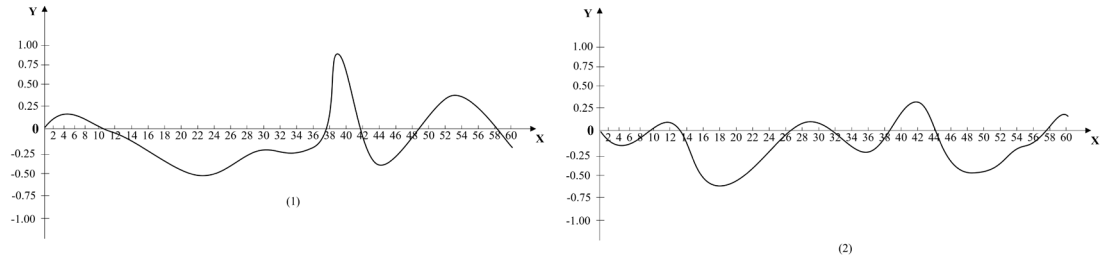


FIGURE 8. Parent EST curve function code.

Encode the curve genes using a binary tree method, establish a coordinate system, place the encoded morphological genes in the unit coordinate system, control the length of the x-axis of the two curve segments to be 60, and use MATLAB software to fit the extracted parental morphological genes of the EST curve, as shown in Figure 8.

The function formula of each curve is obtained by MATLAB fitting, respectively:

$$\begin{aligned} f(x_1) = {} & 1.55 * 10^{-12} * x^9 - 4.31 * 10^{-10} * x^8 \\ & + 5.02 * 10^{-8} - 3.17 * 10^{-6} * x^5 + 10^{-4} * x^5 \\ & - 2 * 10^{-3} * x^4 + 3 * 10^{-2} * x^3 - 0.26 * x^2 \\ & + 0.944 * x - 0.99 \end{aligned} \tag{6}$$

$$\begin{aligned} f(x_2) = {} & -2.41 * 10^{-12} * x^9 + 6.73 * 10^{-10} * x^8 \\ & - 7.94 * 10^{-8} + 5.14 * 10^{-6} * x^5 - 1.98 * 10^{-4} \\ & * x^5 + 4.64 * 10^{-3} * x^4 - 6.39 * 10^{-2} * x^3 + 0.47 \\ & * x^2 - 1.66 * x + 1.79 \end{aligned} \tag{7}$$

Polynomial fitting enables us to capture the complexity of the curve trends without excessively complicating the model or introducing potential errors. In particular, we compared polynomials of various orders and found that a 9th order polynomial provided a fitting match with the experimental data, accurately mapping out the EST curve while minimizing the risk of overfitting. The 9th order polynomial was thus an optimal choice as it struck a balance between accuracy and simplicity.

2) MORPHOLOGICAL GENE CROSS-ITERATIVE RECOMBINATION

The process of finding points lists equations $f'(x) = g'(x)$, and solve the function in pairs. Due to the complexity of the equation and the possibility of multiple solutions, Newton iterative method is used to solve the equation principle [36], [37]: Given the equation $f(t) = 0$ for the complex number t, taking the derivative of $f(t)$ and we get $f'(t) = 0$; First guess a complex value t_0, by $t_1 = t_0 - \frac{f(t_0)}{f'(t_0)}$ can get t_1; Similarly, by $t_2 = t_1 - \frac{f(t_1)}{f'(t_1)}$ can get t_2; Such repeated iterations are iterative: $t_{n+1} = t_n - \frac{f(t_n)}{f'(t_n)}$. For the selected starting point, most iterations converge to some root of the equation $f(t) = 0$. The qualified real number solution within the interval [0, 60] is obtained by the function derivation formula. By taking the iso-derivative nodes of two curves or the special iso-derivative nodes with the extreme value of 0 for cross-combination transformation, a new piecewise function with continuous derivative and curvature can be generated, and the new piecewise function is cross-recombined to generate a new morphological gene. The newly generated morphologic genes of EST model can better inherit the morphological characteristics of the previous generation genes, as shown in Figure 9.

V. METHOD VALIDATION

A. RESULTS

In order to validate the newly generated EST morphological genes (as shown in Figure 9), we designed a series of detailed experimental steps to ensure the high reliability and accuracy of our research results through intuitive video analysis and accurate data comparison.

Firstly, the preliminary preparation for this validation experiment involves retrieving the combination nodes of all newly generated EST morphological genes. These nodes, such as C_i, and C_j represent specific developmental or morphological time points. In order to capture these critical moments, our team search for the specific locations of the

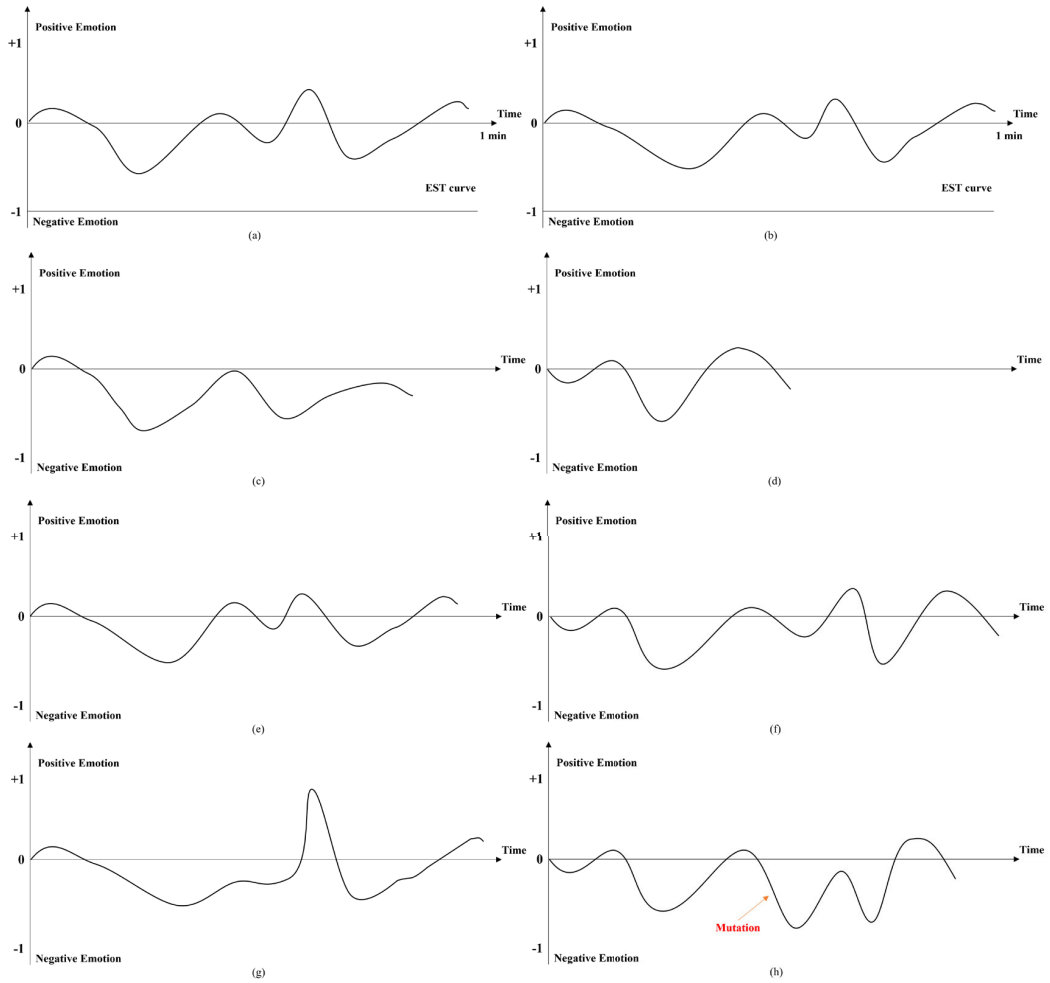


FIGURE 9. The newly generated progeny morphological gene.

corresponding time points in the experimental video samples. After successful retrieval, we used professional video editing software to edit the original samples and generate new experimental video clips. These fragments were named and stored for subsequent steps to call and analyze. This process ensures that we can accurately observe and record the biological events corresponding to each EST morphological gene.

According to the aforementioned experimental methods, we conducted experimental operations on participant No.1 using newly edited experimental samples. During the experiment, the experimental process was closely monitored, and necessary data and results were recorded for subsequent analysis. To evaluate the similarity between the newly generated EST morphological genes and the experimentally generated EST curves, we introduced the average Fréchet distance as a measure. By mathematically comparing two curves, the average Fréchet distance can quantify their differences in shape. It is an important index to measure the spatial similarity between two curves of different lengths, defined as the lower bound of the maximum distance between two curves [38]. Thus, the consistency between the EST morphological genes obtained through GHT and the experimental results was verified.

Suppose $(t_k)_{k=0}^{n+1}$ is a monotonic succession of distinct numbers on the unit interval [0,1], The definition of $(\mathrm{A}(t_k))_{k=0}^{n+1}$ and $(\mathrm{B}(t_k))_{k=0}^{n+1}$ are the points of the series $(t_k)_{k=0}^{n+1}$ on the curve A and B, respectively, given by the large black dots in Figure 10, and the line between the large black dots indicates the distance between them, defined as d $(\mathrm{A}(t_k), \mathrm{B}(t_k))$. Introducing the reparametrized functions α and β of the curve, acting on curves A and B, the corresponding reparametrized curve is A′ and B′, then the distance between A′ (t_k) and B′(t_k) can be defined as d $(\mathrm{A}'(t_k), \mathrm{B}'(t_k))$,That is d $(\mathrm{A}(\alpha(t_k))), \mathrm{B}(\beta(t_k)))$, given by the small black dot and dotted line in Figure 10. Then the Fréchet distance F (A, B) of curves A and B is defined as:

$$F(\mathrm{A}, \mathrm{B}) = \inf_{\alpha,\beta} \max_{t\in[0,1]} \{d(A(\alpha(t)), B(\beta(t)))\} \tag{8}$$

The average Fréchet distance is defined as:

$$\bar{F} = \frac{1}{M} \sum_{m=1}^{M} F(R, X_m) \tag{9}$$

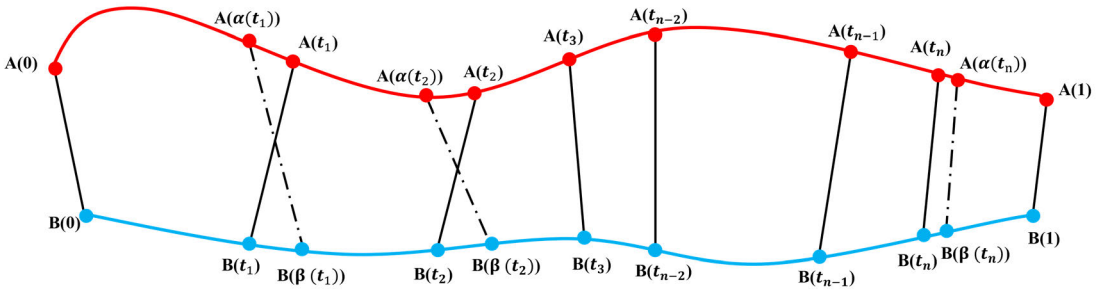


FIGURE 10. Diagram of Fréchet distance calculation.

TABLE 5. Accuracy comparison of the two types of EST curve.

Type	(a)	(b)	(c)	(d)	(e)	(f)	(g)	(h)
Dis.	0.093	0.072	0.126	0.153	0.161	0.156	0.179	0.239

where R mean reconstructing curves, while $\{X_m\}_{m=1}^{M}$ represents the presentation curve sets.

The average Fréchet distance of EST curve obtained through experiments and newly generated EST morphological genes was calculated and the results in Table 5 were obtained.

From the results, the Fréchet distance of EST curves (a) - (g) is generally small, while the distance of EST curves (h) is due to gene mutations that occurred during the gene hybridization process, but it is also within a reasonable range. This final validation experiment results provide key information on the actual expression and function of newly generated EST morphological genes. The high consistency between the obtained curve and the theoretical prediction further supports the effectiveness of our gene combination technology and provide a basis for future experimental design in more samples or under different conditions. Through these comprehensive experimental measures and detailed data analysis, we can ensure the accuracy of the validation experiment, thereby providing valuable reference for researchers in this field.

B. DISCUSSIONS

The Fréchet distance measure shows impressive versatility in various applications. Not only has it been successfully employed for determining graph similarity in algorithmic frameworks, but its unique application within a phylogeographic tree context has also been highlighted [39], [40]. Expanding on these uses, in a recent innovative approach to deal with challenges in unsupervised learning, the brilliant incorporation of the Fréchet distance concept into a novel Uncertainty Fréchet (UF) Clustering Internal Validity Indices (CIVI) proves crucial [41]. This measure, specifically designed to assess the certainty of well-defined partitions, effectively navigates through issues such as ambiguity, non-convex distributions, outliers, and overlapping data. Therefore, these collective applications truly demonstrate the broad potential and adaptability of the Fréchet distance measure.

When juxtaposing these diverse studies with ours, it is essential to understand that while their usage of the Fréchet distance pertains to varied instances, our application is specifically engineered towards the comparison of gene curves. In our findings, we note a strong correlation in the Fréchet distance of most EST curves, which indicates similar spatial congruities and sequence consistencies. The validation of our technique, however, gleans profound reinforcement from both the practical applications and quantification methodologies manifested in these prior studies. In particular, the minimal Fréchet distance computation in our study mirrors the intimate correspondence amidst objects in the aforementioned investigations. Furthermore, our research also identifies certain divergences on EST curve predominantly attributable to genetic mutations. In coherence with their discoveries, our outcomes offer further testimony to the expansive adaptability and reliability of the Fréchet distance across diverse research domains and experimental paradigms.

To further explain, the Fréchet distance quantifies the greatest of all point-to-point distances between two curves, measured from the start to the end of each. In other words, it quantifies the greatest separation between the experimentally obtained EST curves and the theoretical estimates obtained from our gene hybridization method. A low Fréchet distance indicates a strong correlation between the experimental and theoretically predicted EST curves, thereby validating the accuracy and reliability of our GHT. Conversely, higher values signal potential discrepancies, potentially attributable to genetic mutations during the hybridization process. In the context of our results, the Fréchet distances were generally small (as presented in Table 4), suggesting robust alignment between our theoretical EST morphological genes and the experimental EST curves. This provides strong evidence that our gene hybridization technique can expectantly generate EST morphological genes that are congruent with real, empirical outcomes.

The interpretation and implications of these results are multifold. First, it clearly demonstrates the reliability and efficacy of our GHT in predicting the EST morphological

gene structures, which are in close agreement with the empirical EST curves. Second, the high consistency between the obtained and predicted curves reassures the accuracy of our experimental setup and the reproducibility of our results. Lastly, such convergence bodes well for the future application of our technology in broader or differing conditions, making it a versatile tool in the study and application of EST morphological genes.

VI. LIMITATION AND DISCUSSION

This study presents several noteworthy limitations associated with our research scope and implications. Firstly, the representation of the population is limited as the subjects of our experiments hail only from a single country, which may not adequately represent a broader global population. Secondly, the utilization of GHT, although innovative, adds a layer of complexity and potential unpredictability in gene-emotion correlations. This is evident from discrepancies such as the one noted in curve (h). Lastly, the study does not extensively probe the causal link between specific genes and emotional outcomes, thus calling for deeper exploration in this vein.

In light of these limitations, this study initiates important discussions for the field. It highlights potential progression in HRI that could unfold from enabling robots to mirror human emotional states with enhanced accuracy. It also points to opportunities for future exploration to address these limitations, including widening the representativeness of samples, refining gene hybridization methods, and enhancing analytical algorithms for improved precision. Significantly, the intersection of genetics and AEI facilitated by the study opens avenues for promising cross-disciplinary collaborations to further knowledge in this innovative field. The study also raises ethical considerations, especially in light of the potential implications of applying genetic insights in creating emotionally responsive robots, underscoring the need for safeguarding emotional integrity and preventing manipulative applications.

VII. CONCLUSION AND FURTHER RESEARCH

The integration of GHT with EST model presents a transformative approach to robot emotion simulation. This study addresses the current research gap related to the application of affective genetics to artificial platforms, advocating for a broader, more integrative approach that synthesizes biological theories with AEI computational models. By harnessing techniques from genetic hybridization, the EST model can be enhanced to facilitate a more nuanced emotional simulation within robots. This would enrich the emotional repertoire of robots and enable more natural and human-like interactions. Our study successfully implemented the EST model integrated with GHT. The encoding of EST curves using a binary tree method allowed for precise segmentation and representation, facilitating accurate analysis and simulation. The model exhibited high fidelity in validating EST observed in experimental data.

The results of our method validation exhibit a strong correlation between the encoded curves and the actual emotional transitions. The EST model, in conjunction with GHT, displayed a high degree of accuracy in predicting emotional states, consistently matching theoretical predictions. Robots can adjust their emotional responses based on encoded EST genetic data, which leads to nuanced and contextually appropriate behavior. This approach deepens our understanding of the genetic basis of emotions and their application in robotic emotional simulations. The findings of our study bear practical implications for the development of emotionally intelligent robots capable of engaging in more natural and effective HRI. It represents a novel contribution in the field of AEI. Furthermore, our research sets the stage for future studies exploring the application of genetic principles in artificial systems, which could potentially lead to further advancements in HRI.

However, this study acknowledges the inherent complexities and limitations, including limited sample representativeness and the intricate nature of gene technology, which may impact the generalizability and consistency of findings. These considerations, along with the need for ethical vigilance, provide a roadmap for future research. To further advance this field, there is a need for exploration into the direct relationships between genetics and emotional expression, as well as improvements in experimental methodologies and technologies. A more profound and broad understanding of these relationships will ultimately contribute to the development of robots that can interact with humans in a more sophisticated and emotionally intelligent manner.

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