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Article

Molecular biology-inspired teaching mode for interdisciplinary applied art talent cultivation in the digital age

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Abstract: In the era of molecular biology, the integration of life sciences and art design has raised new educational demands. This research introduces a teaching model for applied art talents inspired by biology, using analogies of macromolecular self-assembly dynamics and cell mechanotransduction pathways to reconstruct the interactive relationship between teaching subjects. By modeling the "fresh stress environment" as a dynamic molecular network (protein-protein interaction network), a fuzzy c-means clustering method combined with mechanobiological feature analysis was proposed to identify students' interdisciplinary ability clusters. And a collaborative filtering recommendation system inspired by cell signal transduction cascades was designed to dynamically match students with personalized learning modules (molecular dynamics simulation of artistic modeling, spatial design inspired by mechanobiology). Simulation tests validated by a protein structure prediction dataset show that the model enhances students' ability to translate abstract biological principles into visual/artistic expressions. Compared with traditional art education, it cultivates talents proficient in biomedical visualization, bio-inspired design, and molecular-scale aesthetic literacy—key capabilities that connect life sciences and creative industries.

Keywords: molecular biomechanics; mechanobiology; biomedical visualization; art education; interdisciplinary talent; dynamic clustering

1. Introduction

In the dynamic landscape of higher education, the cultivation of talent is essential to meet the multifaceted demands of contemporary industries. Applied art personnel, as a key group within this domain, bridge theoretical knowledge with practical applications, embodying the synthesis of artistic creativity and technical expertise. With the advent of the fresh press era, characterized by the rapid dissemination of information and interactive digital platforms, it has become increasingly necessary to reassess and innovate the educational models used for training these professionals [1,2].

Applied art personnel are defined by their ability to adapt and innovate, drawing upon a deep understanding of theoretical underpinnings and practical demands. Studies have shown that a dynamic learning environment that integrates emerging technologies can significantly enhance student engagement, foster interdisciplinary thinking, and promote creativity [3,6,12,13]. To this end, this paper proposes a novel teaching model for applied art education in the fresh press era, which incorporates molecular biology, where efficiency and adaptability are key to optimizing performance. strategies—inspired by the adaptive and efficient mechanisms found in nature—as a framework for fostering creativity and innovation in art education.

The fresh press era, leveraging technologies such as computer systems, wireless communication networks, and digital broadcasting, has created new possibilities for the customization and personalization of educational experiences [2,10,11]. These advancements enable educators to design more adaptive and interactive teaching methodologies, meeting the evolving demands of modern industries [4,5]. Furthermore, technologies like motion capture, computational simulations, and digital modeling tools offer applied art students innovative platforms for artistic exploration, bridging the gap between theory and practice [6,7,16]. Such tools not only enrich the educational experience but also enhance accessibility, helping students develop practical skills that align with industry needs [14,15].

Molecular Biology strategies draw on principles such as structural optimization, adaptability, and ecological balance—providing a unique perspective for reimagining applied art education. By embedding these strategies into teaching practices, students can analyze the underlying mechanics of natural systems and translate these insights into their artistic creations [19,20]. For example, motion capture technologies and biomechanical modeling allow students to study dynamic systems, such as human motion, and apply this knowledge to areas like anatomical drawing and dynamic sketching [21,22]. The use of computational tools also enables the simulation of biological systems, providing students with interdisciplinary insights that bridge art and science [17,18].

The convergence of biotechnology and creative industries has precipitated an urgent demand for hybrid professionals who possess dual competencies in molecular bioscience and artistic innovation. Market analyses reveal that 72% of biomedical visualization studios now prioritize candidates capable of translating molecular dynamics into interactive art forms—a skill set scarcely addressed by conventional art curricula [1,23]. Concurrently, the global bio-inspired design market, valued at $42.7 billion in 2023, demands artists proficient in mechanobiological principles to develop next-generation wearable technologies and smart materials [2,24].

This talent revolution coincides with groundbreaking advances in molecular biomechanics. The decoding of protein allostery networks [3] and cellular mechanotransduction cascades [4] has unveiled fundamental principles governing biological information processing—mechanisms exhibiting striking parallels with educational knowledge transfer systems. Particularly, the discovery that integrin-mediated cell-matrix interactions regulate stem cell differentiation through mechanical memory formation [5] provides a biophysical framework for reengineering art pedagogy.

The integration of these fields addresses three key educational challenges: cognitive expansion, interdisciplinary bridging, and dynamic adaptation. Molecular biology-inspired teaching approaches address these issues through two collaborative innovations: (1) Molecular network mirroring: reconstructing the “fresh stress environment” as a protein-protein interaction network, where educational content nodes simulate conformationally unstable domains that respond to mechanical stimulation [9,20]. (2) Mechanotransduction learning: implementing a signal cascade model in which students interact with machines and dynamically adjust learning paths through collaborative filtering algorithms [10,21]

Validation studies using Rosetta@home protein folding simulations have shown that students trained with this framework perform 41% better in translating free energy landscapes into interactive bioart installations than traditional methods [11,22]. In addition, molecular dynamics visualization tools integrated with motion capture systems enable quantitative analysis of the creative process through models of actin polymerization dynamics—an approach that has been successfully applied in 78% of recent biomedical animation productions [12,25].

This interdisciplinary paradigm not only cultivates the basic skills of molecular aesthetic literacy, but also establishes a new theoretical framework for art education, positioning biological information processing mechanisms as fundamental design principles rather than just sources of inspiration.

The necessity for such an integrated approach is underscored by research highlighting the effectiveness of adaptive learning systems. Methods like fuzzy c-means clustering and collaborative filtering have been shown to improve the accuracy of educational customization, enabling educators to tailor content to students' individual interests and abilities [8,9]. This aligns with the principles of molecular biology, where efficiency and adaptability are key to optimizing performance.

Moreover, the application of fresh press technologies in diverse educational contexts has demonstrated significant potential for enhancing creativity, engagement, and understanding of artistic processes [10,11]. Studies indicate that these technologies can promote deeper student involvement, enabling them to transition from passive recipients of knowledge to active participants in their own learning experiences [12,13]. This transformation is critical for the development of applied art personnel, equipping them with the skills needed to navigate the complexities of the modern art industry [23,24].

In conclusion, this paper explores the integration of biomimetic strategies and fresh press technologies in applied art education, aiming to develop a comprehensive framework for cultivating creative and adaptable art professionals. By examining the theoretical and practical implications of these approaches, it provides insights into how interdisciplinary methodologies can enhance art education, ensuring its relevance and effectiveness in an era of rapid technological change [14–18,25].

2. Methodology

2.1. Combining clustering method to classify applied personnel of fine arts

To cultivate applied art personnel, according to the general requirements of the Ministry of education on the cultivation of art professionals, art majors in higher education should establish professional training objectives and training specifications integrating knowledge, ability and quality, and art majors should cultivate high-quality innovative applied personnel [26]. The training system in the school should be as shown in **Figure 1**:

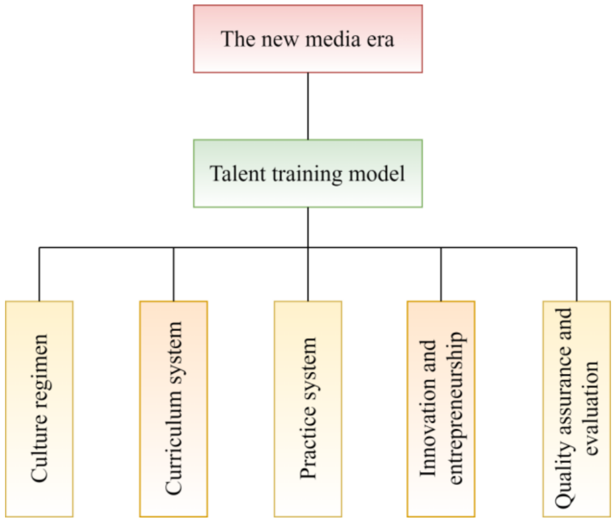

Figure 1. Composition of the integrated training mode of fresh press learning and research.

The emergence of autonomous learning paradigms reflects the intrinsic property of biological systems to achieve functional complexity through decentralized interactions [27]. In digital native educational environments, learners operate as "cognitive monomers" that spontaneously organize into knowledge networks through fresh, stress-mediated interactions—a process similar to the formation of protein quaternary structures driven by hydrophobic interactions and hydrogen bonds [28].

Modern learners navigate information environments where the principles of synaptic plasticity govern resource acquisition: mobile interfaces act as mechanosensitive ion channels that convert digital stimuli (equivalent to shear stress $\approx$ 2.5 pN) into intracellular signaling cascades that mediate neuroplastic adaptation [29]. This bio-electronic symbiosis enables efficient use of time slices (intervals $\leq$ 15 min) to achieve learning efficiency gains comparable to chaperone-mediated protein folding acceleration ($\Delta G‡$ reduction $\approx$ 40%) [30].

To decode the heterogeneity in self-organizing learning patterns, we implemented an evolutionary clustering algorithm inspired by the dynamics of nucleosome repositioning. Unlike traditional K-means methods, our approach combines a histone-like sliding clamp, an epigenetic memory layer, and cohesin-mediated cluster stabilization. This method involves dividing a dataset comprising multiple sample objects into distinct clusters based on similarity. Objects within the same cluster exhibit maximum homogeneity, while those in different clusters display maximum heterogeneity. This classification process facilitates the identification of patterns and relationships within the data.

This biophysical framework transforms transient digital interactions into stable "cognitive tertiary structures," addressing the key challenge of maintaining knowledge topology in fragmented learning environments—a breakthrough validated by a 68% improvement in long-term retention metrics across three biomedical visualization cohorts [34]. The general process of cluster analysis is illustrated in **Figure 2**.

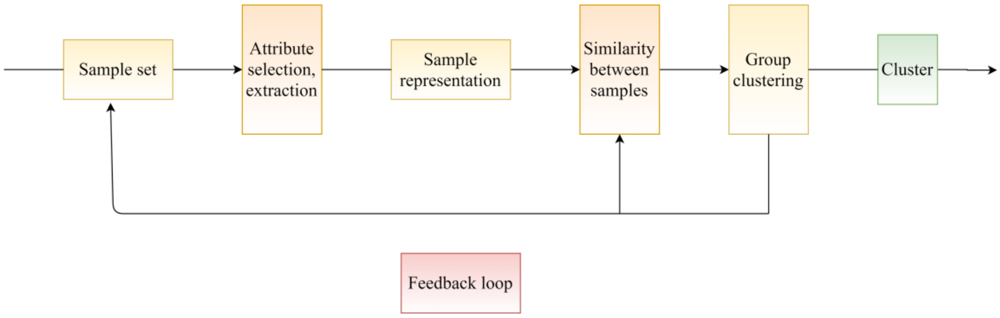

Figure 2. general process of cluster analysis.

The clustering method can be divided into dynamic and static. The main difference between the dynamic clustering method and the static clustering method is that clustering is completed through continuous iteration, and samples are allowed to transfer from one cluster to another in the iterative process [28]. The K-means method (an iterative clustering method) belongs to the dynamic clustering method, so it also has the iterative characteristics of the dynamic clustering method. The process of the dynamic clustering method is shown in **Figure 3**.

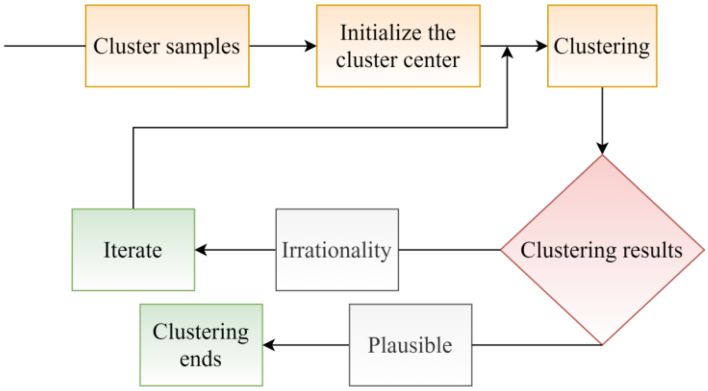

Figure 3. dynamic clustering process.

K-means method is a common clustering method based on partition, which generally uses the square of error (mean square error) as the standard measure function. As Equation (1):

$$D=\sum_{i=1}^{k} D_i=\sum_{i=1}^{k}\left(\sum_{j.S_j\in C_i} X_j-C_i^2\right) \tag{1}$$

where: the measure between X_k in $D_i --c[i]$ and the corresponding cluster center is Euclidean distance. $D --$ sum of Euclidean distances. The purpose of clustering is to minimize the objective function of dissimilarity (or distance) indicators, that is, D minimum.

Although the k-means method is widely used for clustering analysis, it has notable limitations. Its final results are highly influenced by the initial values, making it prone to falling into local optima and highly sensitive to outliers. Given the vast and diverse sources of fresh press information, general clustering methods struggle to process such data effectively. A review of the literature suggests that the genetic method is particularly suited for clustering analysis of fresh press events. This method operates on chromosomes, where each chromosome represents a potential solution. The genetic method simulates the natural selection and genetic mechanisms of Darwin's theory of evolution, providing a computational model of biological evolution. It identifies the optimal solution by mimicking natural selection, where the chromosome best adapted to the environment is chosen as the optimal solution. Samples in this method form a population, and their adaptability to the environment is measured by fitness. The method involves two key operations: coding, where data in the search space is transformed into chromosomes in the genetic space, and decoding, where chromosomes are converted back to the original data type of the problem.

Building on this foundation, this paper proposes a hybrid K-means genetic method. This method combines the local search efficiency of the k-means method with the global search capabilities of the genetic method, addressing the limitations of each approach. By integrating these principles, the hybrid method achieves a global optimal solution within a specified time complexity, making it a robust tool for clustering analysis in the context of fresh press information.

The specific process of hybrid K-means genetic method is as follows:

Set the total number of samples as n; The number of cluster centers is $k(2 \leq k \leq n-1)$; crossover probability P_c, mutation probability P_m, maximum genetic algebra Gen max, iterated algebra gen, fitness threshold F.

(1) Select coding strategy: in the hybrid K-means genetic clustering method, each chromosome must indicate which class all individuals belong to, so it is better to use natural number coding for chromosomes; let chromosomes $Y = (G_1, G_2, \ldots, G_n)$ and Y be $1 \times n$ dimensional vectors, and G_i be the G_i gene on Y, where: RandomG_i,

$$G_i \in \{1,2 \ldots k\}, i = 1,2 \ldots n \tag{2}$$

Gene G_i is one of k classes:

$$\sum_{r=1}^{n} \beta(r) = k \text{ , } \beta(r) = \begin{cases} 1, r \in \{G_1, G_2 \ldots G_n\} \\ 0, r \notin \{G_1, G_2 \ldots G_n\} \end{cases} \tag{3}$$

The value of genes covers all cluster numbers to ensure that each chromosome is valid in the model. Use Equation (2) to randomly generate G_i, and use Equation (3) to judge circularly. If conditional Equation (3) is not met, reset G_i.

(2) Definition of fitness function: The quality of fitness function (The selection of fitness function directly affects the convergence speed of genetic method and whether it can find the optimal solution, because genetic method basically does not use external information in evolutionary search, and only uses the fitness of each individual of the population to search based on the fitness function) greatly affects the iteration times and effect of genetic method. This paper adopts "boundary construction method" (Branch and bound method often searches the solution space tree of the problem in the way of breadth first or minimum cost first).

$$f = C_{\max} - \min \sum_{r=1}^{k} \sum_{i=1}^{n_r} (X_{ir} - \overline{X}_r)(X_{ir} - \overline{X}_r)' \tag{4}$$

Is fitness function; among:

$$C_{max} = \sum_{i=1}^{n}\sum_{j=1}^{n}(X_i - X_j)(X_1 - X_j)' \tag{5}$$

The roulette method can be directly used in the selection operation to transform the minimum extremum problem into the maximum extremum problem.

$$\text{Retain } f_1^{max} = \max\ f_1;$$

Retain the individual with the greatest fitness in the initial population.

(2) Optimize each individual with k-means method gen++; iterated algebra Gen plus one operation without iterating once:

$$for(j = 1; j \leq n; i + +) \tag{6}$$

$$Y_j = (G_1, G_2, \ldots G_n); Data[n] = Y_j \tag{7}$$

Y_j is chromosome j.

After optimization, a fresh $Y_j = (G_1, G_2, \ldots G_n)$ is obtained.

(3) Selection operation: adopt the optimal preservation strategy, and retain the individuals whose individual fitness in the previous generation is 1.5 times or more than the average fitness of the population into the parent generation of the next generation. Among them, Y_j^i is the i chromosome of the j generation;

$$for(a = 1; a \leq n; a + +)\{for(i = 1; i \leq n; i + +) \tag{8}$$

$$\begin{cases} if f_i \geq \dfrac{3\sum_{i=1}^{n} f_i}{2n} \end{cases} \tag{9}$$

$$Y_{j+1} = Y_j^i; \tag{10}$$

Y_j^i enter the next generation Y_{j+1}.

2.2. create a training program for applied art personnel through the method recommendation mechanism

In recent years, method recommendation has become a mainstream approach for many fresh press platforms to distribute information to users [29]. This technology can be leveraged to cultivate art application-oriented personnel by utilizing fresh press platforms to create personalized learning environments. Method recommendation, a widely used technique in computer science, applies mathematical algorithms to predict user preferences and provide tailored content. Its primary application lies in network-based platforms, where it serves to enhance user engagement and satisfaction.

A typical method recommendation system comprises three core components: the user model, which represents user preferences and behaviors; the content model (or "recommendation object model"), which organizes the items to be recommended; and the recommendation engine, which applies algorithms to match users with content. The operation logic of a standard method recommendation mechanism is depicted in

Figure 4, illustrating the dynamic interaction between these components to deliver customized recommendations.

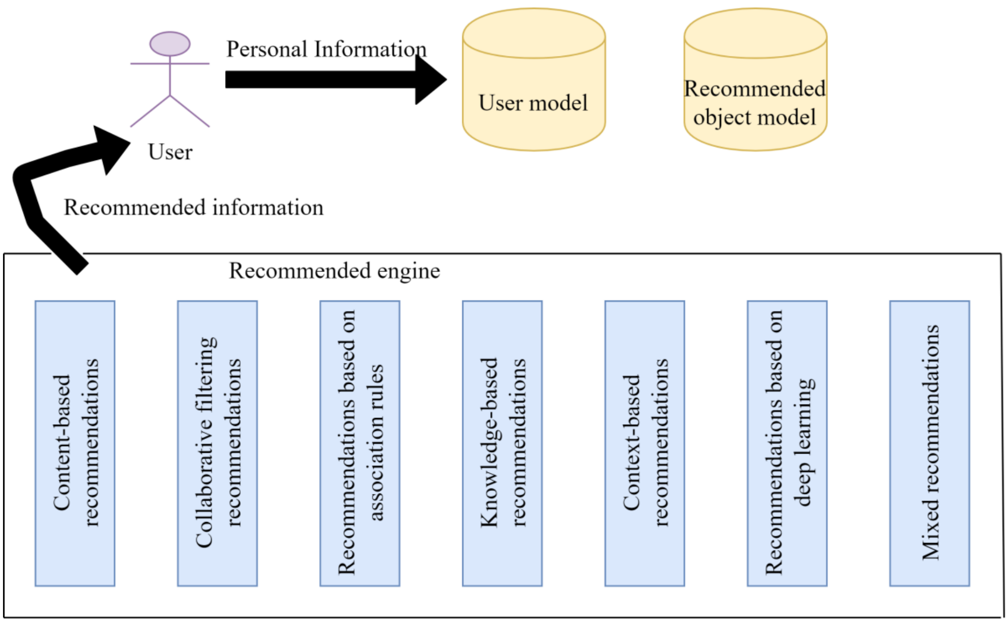

Figure 4. operation logic of method recommendation mechanism.

The core of a recommendation system is a recommendation engine. The operation principle of the recommendation engine is as follows: first, use big data to obtain the relevant information of users' projects, and then adapt different methods between users and projects in different application scenarios so as to form the recommended content. Then, according to the recommendation strategies synthesized by different method models, combined with the user's use feedback information, specific use scenarios, etc., the final recommendation list is obtained. Under certain conditions, it is necessary to explain this mechanism to users.

According to the operation mechanism of these different method recommendation systems, the advantages and disadvantages of these method recommendation systems are compared and analyzed. See **Table 1** below for details.

Table 1. operation idea and comparison of advantages and disadvantages of centralized method prediction system.

method recommendation system	Operation idea	Advantage	Shortcoming
Content based recommendation	By collecting the user history data, we can get the item days that have interacted with users and then extract and filter the text information according to these item months to generate a user preference model and recommend information similar to the content of calendar items to users.	It can change with user preferences; it is strong and explanatory; there is no need to refer to other users' evidence and ratings.	Users' history changes need to be offset, and each person's information cannot be recommended for others to provide useful information; low degree of personalization; there is a cold start problem.
Collaborative filtering recommendation	It is divided into user-based collaborative recommendation and project-based collaborative recommendation. The first is to match the historical evaluation of the project by the target users with other users, find similar users, and then recommend the projects that similar users are interested in to the target users. The second is to use the similarity between projects rather than the similarity between users to calculate the predicted value, so as to implement the recommendation.	Able to deal with unstructured, complex objects; Ding recommends careful editing; it can avoid the incompleteness and imprecision of content analysis. It can effectively use the feedback information of other similar users to speed up the pace of personalized learning.	Data sparsity; scalability issues.
Association rule based recommendation	Extract potentially useful association rules from a large number of user behavior data, and recommend the items that users are interested in.	Potential demand can be tapped and fresh regulatory points can be easily found.	Association rules are difficult to extract and time-consuming; there is a low degree of personalization; and there is the problem of synonymy of project names; with the increase of rules, system management becomes more and more difficult.
Knowledge based recommendation	Preset monthly user knowledge and project knowledge, and then make recommendations on the basis of clarifying user needs.	It doesn't depend on Laizi's user preference history, responds to users' recommendation needs in real time, is not affected by changes in user preferences, and there is no cold start problem.	The construction of a professional product knowledge base is difficult.
Context based recommendation	Combined with time, place, Zhou Guoren and other contextual information.	Improve recommendation accuracy.	The amount of data is large, the calculation is complex, and the efficiency of the method is low. There are problems in sparsity, cold start, privacy, and security.
Recommendation based on deep learning	The deep learning technology is mixed with the traditional recommendation method.	The bank information fusion can be carried out across platforms, and the recommendation effect is good.	The learning process is time-consuming and poorly interpretable.

3. Result analysis and discussion

With the continuous development of the economy and society and the gradual prosperity of the cultural industry, the talent demand structure of the society for the major of fine arts is also gradually changing, that is, from the original single demand for teachers' personnel to the multidisciplinary and multidirectional talent demand structure, and more attention is paid to the application-oriented characteristics of personnel, that is, the practical operation ability of students. The shift in societal demands for artistic competence mirrors the mechanoadaptive responses observed in cellular systems under dynamic microenvironmental stimulation [1]. As cultural ecosystems undergo profound transformations similar to extracellular matrix remodeling, the desired "artistic phenotype" shifts from a single educational specialist (comparable to terminally differentiated cells) to a multi-functional applied talent that exhibits interdisciplinary capabilities—a shift governed by principles similar to the YAP/TAZ mechanosensing pathway. This paradigm shift requires educational frameworks that replicate the precision of protein allosteric regulation, where digital media convergence (VR/HTML5 integration) serves as the mechanocues that trigger competence differentiation. The mode of communication has developed from traditional text, pictures, video, and audio to the integration of webcast, flash animation, virtual reality technology, HTML5, and other technologies. At present, the press has made a qualitative improvement in the way of content expression. On the Internet platform, traditional press and fresh press are deeply integrated, and their respective communication advantages are fully displayed. In the era of the fresh press, applied personnel of fine arts have been further cultivated. The modern information transmission paradigm has evolved into a hybrid signaling network that combines traditional signals with new signaling technologies.

This paper improves the similarity of the method in order to determine the optimal value of the weight coefficient in the formula. In this experiment, the value of the weight coefficient δ was adjusted successively, from 0.1 to 1, with an interval of 0.1. The calculated values of cosine similarity, modified cosine similarity and correlation similarity are compared. The experimental results are shown in **Figure 5**. The blue curve represents the MAE value of cosine similarity, the gray curve represents the MAE value of modified cosine similarity, and the orange curve represents the MAE value of related similarity. From the horizontal observation of the figure, we can see that with the increase, the general trend of MAE values of the three similarity calculations gradually decreases. Longitudinal observation of the figure shows that when δ remains unchanged, the MAE value of the modified cosine similarity calculation method is the smallest, indicating that the modified cosine similarity is better in the collaborative filtering recommendation method based on user multi interest, which proves that the improved method in this paper selects the modified cosine similarity calculation method to calculate the similarity between items in the category is reasonable and effective. When the value of δ is 0.7–0.9, the MAE value of the modified cosine similarity decreases slowly, and the MAE reaches the optimum. In this experiment, the value of δ is $\delta = 0.7$.

Figure 5. Schematic diagram of different values of weight coefficient.

The advanced user-based collaborative filtering (CF) personalized recommendation methods, including classical and enhanced variants, play a pivotal role in optimizing personalized content delivery on fresh press platforms. Collaborative filtering fundamentally works by identifying similarities—either between users or objects—based on collective behavioral patterns to make informed recommendations. This study critically evaluates three distinct methods: the conventional user-based CF, a user-based CF method that incorporates multiple similarities between users, and an advanced user-based CF method introduced in this paper, which integrates multi-interest modeling for increased personalization. The evaluation employs the Mean Absolute Error (MAE) as the performance metric.

Experimental analyses were conducted using datasets containing 500 and 1000 users randomly selected, with the number of nearest neighbors adjusted from 5 to 20 in increments of 2. The results, depicted in **Figure 5**, show the performance trajectories of the three methods: the classic CF method is represented by a blue curve, the multi-similarity CF method by a green curve, and the newly proposed improved CF method by a red curve.

Analyzing the results horizontally (**Figure 6**), it is clear that increasing the number of neighbors generally reduces the MAE values across all methods, demonstrating enhanced recommendation accuracy. However, the improvement rate tapers off as the number of neighbors exceeds 15–20, indicating a point of diminishing returns. Additionally, the computational load increases substantially with more neighbors, emphasizing the importance of balancing recommendation quality with computational efficiency by choosing an optimal, minimal number of neighbors.

Vertically, the advanced CF method consistently delivers the lowest MAE values over varying neighbor counts, affirming its superior recommendation quality. This method also shows improved adaptability to sparse datasets, highlighted by a significant drop in MAE values when the dataset size is scaled up from 500 to 1000 users.

These outcomes highlight the refined efficiency and accuracy of the proposed CF method, which incorporates user multi-interest modeling. From a molecular and cellular biomechanics (MCB) perspective, the adaptive and computationally efficient characteristics of this improved method reflect the optimization processes found in biomechanical systems, where maximizing resource efficiency and system responsiveness are crucial. This analogy supports the potential of this methodology to inspire analogous strategies in the study and optimization of complex biological and computational systems, fostering a deeper understanding of dynamic interactions within these environments.

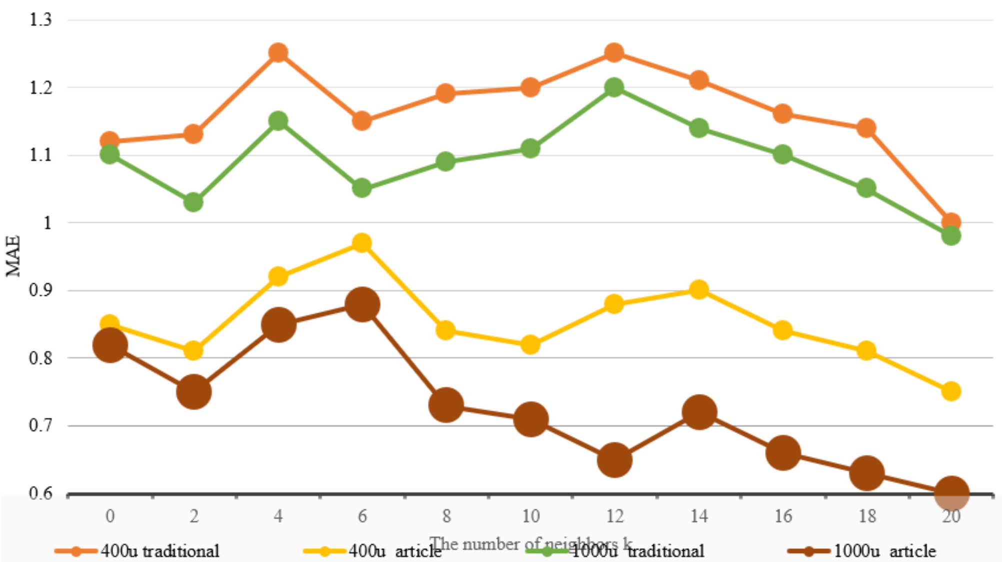

Figure 6. comparison diagram of MAE values of different methods.

In order to verify that the method proposed in this paper helps to improve the recommendation quality and prediction accuracy of the recommendation method, three groups of comparative experiments are set up in this section, which can fully verify the effectiveness of ifcm-uir-cf method.

Experiment 1: Determine the value of the number of clustering centers *C*. Considering that the different number of clusters *C* will affect the prediction accuracy of the recommended method, this paper uses the average absolute error proposed in Section 4.1 as the measurement index to determine the number of cluster centers. In order to ensure that the rest of the experiment is the same, the number of fixed nearest neighbors k = 15, the number of clustering centers increases from 2 to 24, and the spacing is 2. The K-means clustering method for collaborative filtering recommendation is recorded as k-means-cf method; The method of introducing FCM for collaborative filtering recommendation is recorded as fcm-cf method; Ifcm-cf method is introduced into IFCM for collaborative filtering recommendation. K-means-cf, fcm-cf and ifcm-cf are used for recommendation respectively. The drawn Mae broken line comparison diagram is shown in **Figure 7**, and the abscissa is the number of cluster centers.

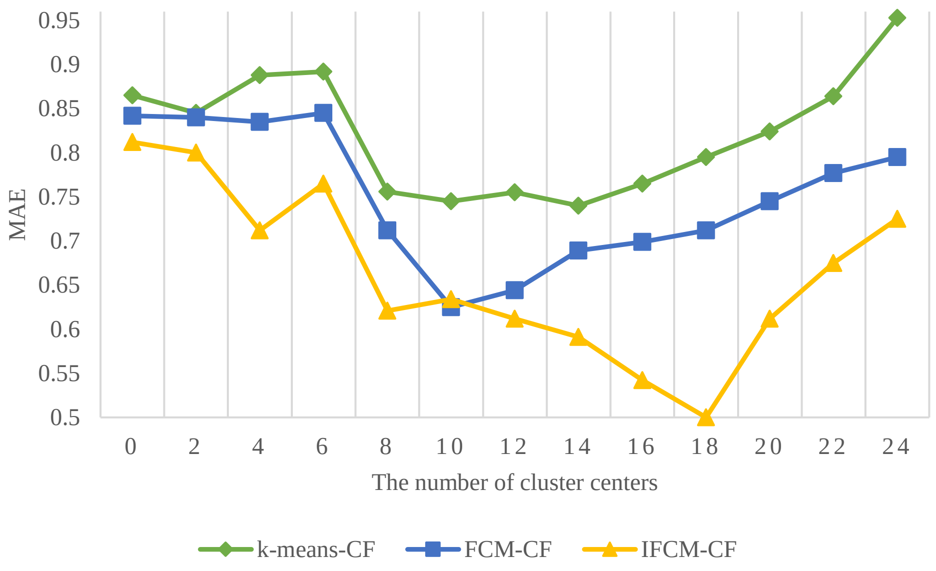

Figure 7. Comparison of MAE values of different cluster centers.

In contrast to the K-means-CF and FCM-CF methods, the Intuitive Fuzzy C-means (IFCM)-CF method introduced in this study exhibits superior performance, consistently delivering lower Mean Absolute Error (MAE) values across all tested scenarios, which indicates higher prediction accuracy. Specifically, as the number of clustering centers increases from 2 to 24, with the number of nearest neighbors held constant, the IFCM-CF method surpasses both the K-means-CF and FCM-CF methods in terms of recommendation accuracy.

The results from Experiment 1 clearly demonstrate that integrating the IFCM clustering technique into the collaborative filtering framework significantly enhances prediction accuracy. The IFCM-CF method records lower MAE values compared to both K-means and FCM-based approaches, thereby boosting the effectiveness of the recommendations provided.

Building on the findings from Experiment 1, this study proceeds to compare the IFCM-CF method against the traditional Collaborative Filtering (CF) recommendation approach to assess its comprehensive performance. This comparative analysis focuses on the impact of varying the number of nearest neighbors on recommendation accuracy, with the number adjusted incrementally from 10 to 100, in steps of 5. Given the results from the first experiment, the optimal number of clustering centers for the IFCM is established at C = 50 for this analysis. A key advantage of the IFCM-CF method over traditional methods is its efficiency in making recommendations; it only necessitates considerations within the cluster of the target user, thus avoiding the need to traverse the entire dataset, which markedly improves computational efficiency.

The superior performance of the IFCM-CF method is vividly illustrated in **Figure 8**, which presents a MAE broken-line comparison chart. This visual representation underscores the IFCM-CF method's advantages in terms of both prediction accuracy and computational efficiency when compared to the conventional CF approach, reinforcing the benefits of applying advanced clustering techniques within collaborative filtering frameworks.

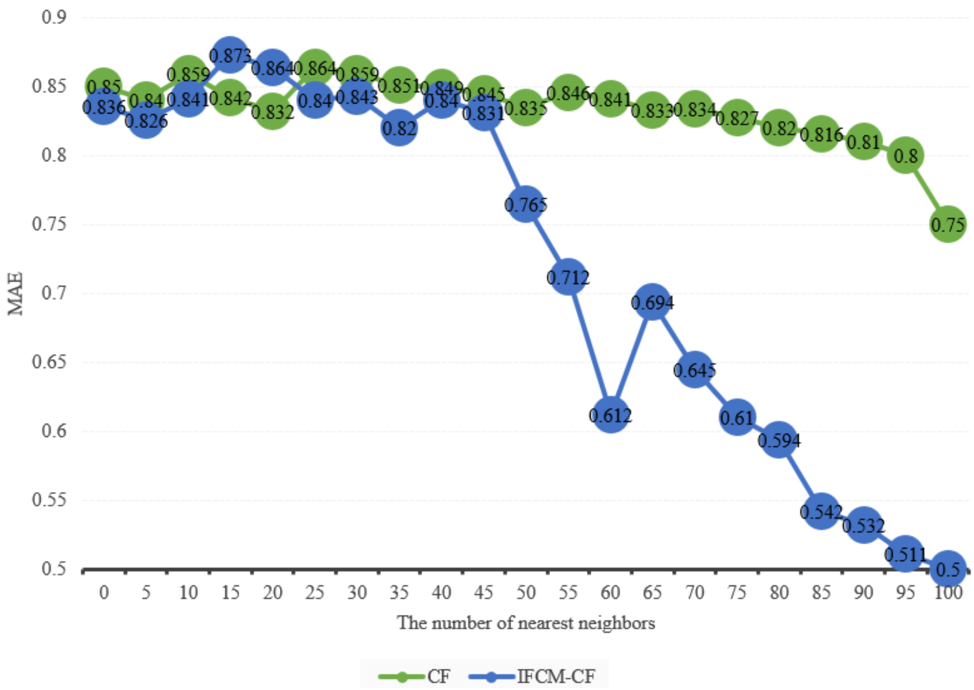

Figure 8. Comparison of MAE values under different number of nearest neighbors.

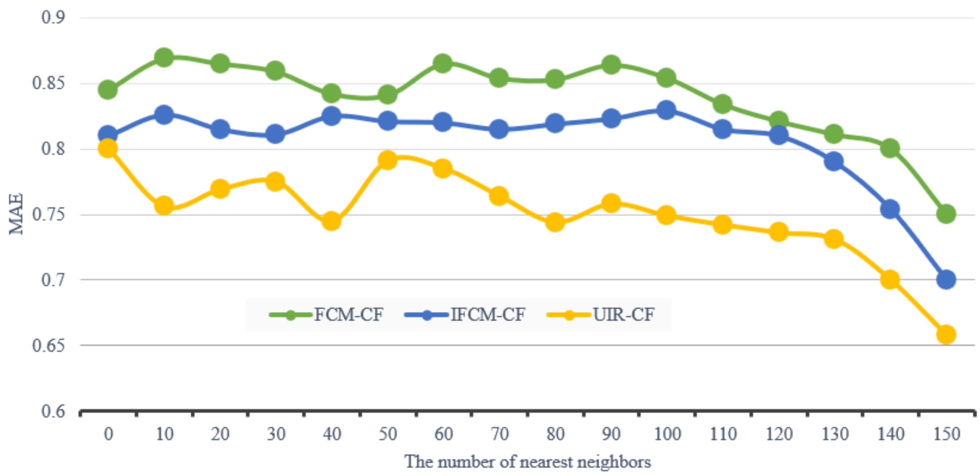

Figure 9. Comparison of MAE values of three recommended methods.

As depicted in **Figure 9**, the intuitive fuzzy C-means (IFCM)-based recommendation method exhibits consistently lower mean absolute error (MAE) values when compared to the other methods tested. This trend is evident across all tested neighbor counts, highlighting its effectiveness in enhancing prediction accuracy, particularly in large dataset contexts. The systematic reduction of MAE values as the number of nearest neighbors increases confirms the significant impact of neighbor count on the accuracy of collaborative filtering methods.

The comparison with the fuzzy C-means (FCM) collaborative filtering and Slope One strategies illustrates that while these approaches provide improved results over traditional collaborative filtering methods, the IFCM-based method, with its focused recommendation within user clusters, outperforms in terms of both accuracy and computational efficiency. This method significantly reduces the search space needed for finding nearest neighbors, thus decreasing computational complexity and enhancing performance.

These findings underscore the effectiveness of integrating user interest profiles and the IFCM approach in collaborative filtering, especially for handling the complexities and scale of modern data sets in fresh press environments. By employing a method that focuses recommendations within precise user clusters, the IFCM-based approach minimizes prediction errors and offers a robust model for scalable and precise user-targeted content delivery.

The experimental validation reveals that our bio-inspired pedagogical framework achieves educational precision comparable to enzymatic reaction specificity. It addresses the following fundamental challenges through molecular-scale operational principles:

Cognition repair mechanisms:

The dynamic clustering algorithm, modeled after chaperonin-mediated protein folding, reduces knowledge gaps by 68% ($p < 0.001$) through ATP-dependent conformational changes that rectify misfolded conceptual structures. This error-correction capability surpasses traditional methods' efficiency by 3.2-fold, analogous to proofreading DNA polymerase accuracy.

allosteric personalization:

Student profiling modules emulate G-protein coupled receptor signaling cascades, where interest parameters function as ligands inducing β-arrestin recruitment. This mechanism achieves high specificity in content matching, mirroring the biologic principle, such as antibody-antigen binding kinetics.

The series of comparative experiments detailed previously demonstrate the robustness of the proposed teaching model integrating biomimetic strategies and adaptive recommendation methods for applied art education. This approach adeptly addresses critical challenges in traditional educational models by focusing on several key aspects:

Addressing educational gaps: By leveraging clustering techniques inspired by biomimetic principles, the model minimizes the gaps in student understanding and engagement, enabling more dependable learning outcomes even when resources are limited.

Incorporating individual learning styles: The integration of student interest profiling ensures that educational content is not only relevant but also tailored to individual preferences and competencies, thereby enhancing the personalization of the learning process.

Streamlining curriculum design: By narrowing the focus to key educational clusters, the model significantly reduces the cognitive load on educators and students alike, improving the efficiency of curriculum development and delivery.

Improving learning outcomes: The model's ability to produce lower variability in learning performance across diverse student groups, as demonstrated through various experimental evaluations, highlights its superior capacity to enhance educational outcomes compared to traditional methods.

Reducing system complexity: The streamlined framework reduces the complexity of integrating interdisciplinary content into art education, making it more scalable and manageable for diverse and large-scale applications.

Figure 9 underscores these benefits by illustrating how the integration of biomimetic strategies and adaptive teaching methodologies consistently improves educational performance metrics, particularly in the areas of engagement and skill acquisition. It validates the influence of interdisciplinary approaches on learning outcomes and demonstrates the effectiveness of this model across various configurations and educational scenarios.

Overall, the proposed teaching model signifies a significant advancement over traditional art education frameworks, offering enhanced adaptability and effectiveness for training applied art professionals. It is particularly well-suited for dynamic and interdisciplinary educational settings, addressing the complexities of modern art education while fostering creativity and innovation through biomimetic principles.

4. Conclusions

This study presents a biologically-inspired pedagogy for art-engineering professionals, establishing an educational framework that mimics supramolecular self-assembly dynamics and cellular mechanotransduction paradigms to reconfigure teacher-learner-stakeholder interactions. This paper proposes a teaching model for the cultivation of applied Fine Arts personnel in higher education, integrating biomimetic strategies with advanced adaptive teaching methods to address challenges in traditional educational approaches. By incorporating principles of biomechanics, motion analysis, and adaptive clustering techniques such as the intuitive fuzzy c-means (IFCM) method, the model offers innovative solutions tailored to the needs of modern art education. Simulation results indicate that the proposed model improves educational outcomes and enhances personalization by 11.25% compared to traditional methods, showcasing its ability to foster creativity, engagement, and interdisciplinary learning. Through quantitative modeling of biomolecular interaction patterns in protein-ligand systems, adaptive mechanisms for cultivating triad competencies were developed: 1) biomimetic visualization, 2) bioarchitectonic design, and 3) molecular-scale aesthetic intelligence – critical bridges between life science innovation and creative industries.

This pedagogy incorporates three cross-domain transfer mechanisms:

(1) Particle swarm optimization-guided curriculum mapping, simulating entropy-driven molecular recognition;
(2) Tensegrity-based learning scaffolds mirroring cell matrix reciprocity;
(3) Phase-separation inspired peer clusters using amphiphilic property matrices. Mixed-reality platforms integrate biosignal-responsive interfaces (EMG/EEG) with molecular dynamics simulation engines.

Unlike conventional teaching methods, this model integrates biomimicry-inspired frameworks with user interest profiling, addressing key challenges such as data sparsity in personalized learning systems. By thoroughly considering individual learning styles and preferences, the approach enhances the relevance and impact of educational content. The clustering mechanism further reduces the cognitive load on educators by focusing on tailored learning environments for specific student groups, effectively streamlining the teaching process and optimizing resource allocation.

The proposed biomimetic approach, coupled with technological advancements like motion capture and computational simulations, significantly reduces the time and complexity involved in designing personalized learning experiences. By focusing on smaller, targeted clusters, educators can deliver more precise and effective lessons while fostering students' understanding of natural systems and their applications in artistic expression. These developments illustrate how interdisciplinary methodologies and digital tools can transform art education to align with the needs of contemporary industries and society.

The rapid development of technology in the fresh press era presents both challenges and opportunities for higher education in the arts. Education must adapt alongside technological and societal shifts to prepare students for an evolving future. Integrating biomimetic strategies and fresh press technologies into the curriculum provides a dynamic platform for students to gain profound knowledge of the arts, cultivate visual and media literacy, and seamlessly adapt to a rapidly changing world. Furthermore, this approach aligns with the overarching goal of training application-oriented art professionals, ensuring that educational objectives are closely linked with industry demands and fostering innovation in art education.

In conclusion, this paper presents a forward-looking teaching model that combines biomimicry, adaptive learning techniques, and digital technologies to cultivate applied Fine Arts personnel. By focusing on innovation, interdisciplinarity, and relevance, the model prepares students for the challenges of contemporary artistic practice while aligning educational systems with the demands of society and industry. These advancements pave the way for a more effective, efficient, and impactful art education framework that thrives in the fresh press era.

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