Development of a CODE-Based Teaching Guide on the Central Dogma in Biochemistry: A Study in the Philippines

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ABSTRACT

This study developed and validated the CODE Instructional Approach (Case-Organized, Dramatized, and Embodied) to enhance preservice science teachers' understanding of the Central Dogma of Molecular Biology. A total of twelve (12) third-year BSED Science students enrolled in PHSc108 Biochemistry participated in the implementation phase of the study. Using the ADDIE instructional design model, the Analysis Phase revealed several learning needs, such as students' persistent misunderstandings, difficulty visualizing molecular processes, and a strong preference for visual and hands-on learning strategies. A panel of seven qualified evaluators assessed the instructional materials for validity, clarity, and pedagogical integrity. The overall validity rating for the pretest–posttest instrument was 3.77, and the rating for the Teaching Guide was 3.70, both interpreted as "very highly valid." The mean score for students' conceptual understanding increased from 14.25 to 20.17, representing a substantial improvement. The Wilcoxon Signed-Rank Test confirmed that this increase was statistically significant ($Z = -3.068$, $p = .002$), with a very large effect size ($r = 0.886$). Thematic analysis of student reflections identified four themes: misconceptions regarding the direction of genetic information flow, difficulty understanding molecular processes, incomplete understanding of mutation, and a preference for visual and experiential learning. Overall, the results show that the CODE Approach effectively addresses gaps in understanding by integrating multimodal, contextualized, and embodied learning activities.

Keywords: Central Dogma, CODE Instructional Approach, Embodied Learning, Molecular Biology Education, Multimodal Instruction

INTRODUCTION

The Central Dogma of Molecular Biology explains how genetic information moves from DNA to RNA to protein, and it is considered a foundational concept in biology education. For preservice science teachers, understanding the Central Dogma is essential because it supports learning in genetics, biochemistry, cell and molecular biology, and related fields. Since this concept plays a central role in the curriculum, students need instructional approaches that help them build accurate and coherent mental models of molecular processes.

Despite its importance, the Central Dogma is consistently identified as one of the most challenging topics for learners. Many students struggle to differentiate transcription from translation, describe the roles of mRNA and tRNA, or explain how mutations affect protein structure. Misconceptions such as the idea that DNA directly produces proteins or that replication and transcription refer to the same process have been documented both internationally and locally (Wieseman, 2016). More recent studies indicate that these misunderstandings remain common among biology majors and preservice teachers, suggesting that traditional instructional methods often fail to address them effectively (Dogan and Uzuntiryaki-Kondakci, 2021; Brownell and Freeman, 2021). Similar difficulties have been observed in local classroom contexts, where many students rely heavily on memorization and find it difficult to construct meaningful mental models of molecular events. The diagnostic findings in this study reflected the same pattern of fragmented understanding and persistent misconceptions, which suggests that lecture-based teaching may not sufficiently promote conceptual learning.

In response to these difficulties, a variety of innovations in molecular biology instruction have emerged. Simulation-based and virtual learning tools have been shown to help students visualize abstract molecular interactions that cannot be observed directly (Cano, 2022; Park and Lee, 2024). Contextualized instruction enables learners to relate gene expression concepts to real-world scenarios, while inquiry-based laboratory activities such as GFP plasmid expression provide firsthand experience with transcription and translation (Bujanda and Anderson, n.d.). Other multimodal approaches, including manipulatives, model construction, art-integrated lessons, and case-based exercises, have also improved student understanding. Emerging research shows that embodied and dramatized learning can enhance students' ability to visualize dynamic molecular processes and reason about system-level interactions (Lindgren et al., 2022; Núñez and Fias, 2023). Case-based strategies likewise strengthen higher-order reasoning and help learners apply molecular concepts in authentic situations (Wood and Anderson, 2023).

However, most instructional innovations focus on a single strategy, such as simulation, modeling, or inquiry-based learning, without combining these methods into an integrated framework. Only a few studies have attempted to unify case-based learning, dramatized role-play, and embodied modeling within a single instructional design. Even fewer have formally developed, validated, and pilot-tested such an approach within preservice teacher education in the Philippines. Recent literature continues to emphasize the need for multimodal and research-informed strategies that correct misconceptions and support visualization of molecular phenomena (Mhlongo and Govender, 2024; Abuhassna, 2024; Reyes and Constantino, 2024). This points to a clear gap in the field. There is a lack of comprehensive, classroom-tested instructional models that combine contextualized, dramatized, and embodied learning experiences to address persistent misconceptions about the Central Dogma.

The CODE Instructional Approach was developed to address this gap. CODE refers to Case-Organized, Dramatized, and Embodied learning. It combines real-world biological case scenarios, dramatized simulations in which students act out transcription and translation, and embodied modeling activities that involve constructing and manipulating representations of DNA, RNA, and proteins. These strategies are intended to create a coherent, immersive, and student-centered learning experience that helps students refine their understanding and overcome misconceptions. The approach is grounded in constructivist learning theory, case-based learning, and embodied cognition, which emphasize active engagement, contextual meaning-making, and physical involvement in learning. Its development followed the ADDIE Model, an instructional design framework that is widely used to produce effective science instructional materials (Martin and Sun, 2022).

The local educational context strengthens the need for such an approach. Many preservice science teachers in regional institutions begin their Biochemistry courses with limited prior knowledge of molecular biology and often rely on memorization rather than conceptual reasoning. Recent findings indicate that multimodal and interactive teaching strategies can substantially improve molecular biology understanding across different learning environments (Mhlongo and Govender, 2024). These observations highlight the importance of designing contextualized, embodied, and interactive instructional tools that match the learning needs of Filipino preservice teachers.

To ensure curricular relevance, the CODE Instructional Approach was aligned with the learning outcomes of Module 2, Lesson 2.5 of the PHSc108 Biochemistry course. These outcomes include explaining how DNA encodes genetic information, distinguishing among transcription, translation, and mutation, and relating the Central Dogma to genetic disorders and biotechnology. These objectives guided the development of the case tasks, dramatized activities, and embodied modeling components of the teaching guide.

With this context in mind, the study aimed to develop and validate the CODE Instructional Approach and determine its effectiveness in improving preservice teachers' understanding of the Central Dogma. Specifically, the study sought to:

1. develop and validate the CODE teaching materials using the ADDIE Model,
2. determine the change in students' conceptual understanding before and after the intervention, and
3. explore students' perceptions and learning experiences with the CODE Approach.

Overall, this research presents a multimodal instructional framework for molecular biology education and provides a replicable model for preservice science teacher training in the Philippines.

METHODOLOGY

Research Design

This study used a developmental research design guided by the ADDIE instructional model, which involves the stages of Analysis, Design, Development, Implementation, and Evaluation. The model was applied to create and validate the CODE Instructional Approach. To determine the effectiveness of the intervention, a one-group pretest–posttest design was employed to measure changes in students' conceptual understanding of the Central Dogma of Molecular Biology. A qualitative descriptive approach supported the quantitative analysis by documenting students' perceptions and learning experiences through written reflections.

Participants

The participants were twelve third-year BSED Science students who were officially enrolled in PHSc108 Biochemistry during the First Semester of Academic Year 2025–2026 at Visayas State University–Isabel Campus. This group represented the entire population of third-year BSED Science students enrolled in the course for that semester.

Purposive sampling was used because PHSc108 covers Module 2, Lesson 2.5, which focuses on the Central Dogma. Since the intervention specifically targeted this lesson, these students were the most relevant participants for the development, validation, and pilot testing of the teaching guide. Participation was voluntary, and informed consent was obtained from all students before data collection.

Development of the CODE Instructional Approach

The CODE (Case-Organized, Dramatized, and Embodied) Approach was developed using the ADDIE Model as follows:

1) **Analysis:** Students' prior knowledge and misconceptions were identified using a diagnostic test and three open-ended questions. Additional input from biology educators emphasized the need for multimodal, contextualized, and embodied strategies to support learning of abstract molecular concepts.

2) **Design:** The CODE Teaching Guide was structured to align with the PHSc108 Biochemistry course syllabus and constructivist learning principles. The design involved planning real-world case scenarios, dramatized simulations of transcription and translation, and embodied molecular modeling tasks. Assessment tools, including the pretest–posttest instrument and reflection prompts, were also prepared.

3) **Development:** All instructional materials were created by the researcher, including the full teaching guide, role-play scripts, case narratives, embodied activity guides, and molecular modeling tasks. The pretest–posttest assessment and validation rating sheets were developed in this phase. Adopted rubrics were used by the panel of evaluators to examine content accuracy, clarity, pedagogical alignment, feasibility, and scientific correctness.

4) **Implementation:** The CODE Approach was implemented through three instructional sessions. These included case analysis, dramatized simulations of transcription and translation, and embodied modeling of molecular interactions. The teaching guide served as the primary reference for activity flow and sequencing.

5) **Evaluation:** The teaching guide and assessment tools were evaluated by seven qualified experts. Data from the pretest–posttest and student reflections were analyzed to determine the validity, effectiveness, and acceptability of the instructional model, completing the ADDIE cycle.

Instruments

Three sets of instruments were used: (1) researcher-developed instructional and assessment tools, (2) *adopted validation rubrics*, and (3) student reflection instruments. Full copies of these instruments are not included in this article to maintain conciseness and in keeping with IJRISS publication guidelines.

1) Pretest–Posttest Conceptual Understanding Test:

A researcher-developed 25-item test measured students' understanding of DNA, RNA, transcription, translation, and mutation. Seven evaluators reviewed the instrument using an adopted validation rating sheet that assessed content relevance, clarity, scientific accuracy, cognitive demand, grammar, fairness, and feasibility.

2) CODE Teaching Guide Validation Rubric:

The teaching guide was evaluated using an adapted validation rubric based on established instructional design tools. It examined ten criteria, including accuracy, alignment with learning outcomes, sequencing, engagement, contextualization, differentiation, assessment integration, material feasibility, and visual presentation.

3) Student Reflection Instrument:

A semi-structured reflection form allowed students to describe their experiences with the CODE Approach. The tool guided them to reflect on challenges, conceptual changes, engagement in activities, and the usefulness of the case-based, dramatized, and embodied strategies.

Panel of Evaluators

Seven evaluators reviewed the pretest–posttest instrument, teaching guide, and perception tools. Selection criteria included:

(1) holding at least a master's degree in Biology, Science Education, Biochemistry, Curriculum Studies, or related fields;

(2) having expertise or teaching experience in molecular biology, biochemistry, or science education;

(3) having three to five years of tertiary-level teaching experience;

(4) involvement in research, curriculum review, or instructional materials validation; and

(5) willingness and availability to provide feedback.

The panel consisted of faculty members and academic heads from multiple campuses within a state university system, representing strong expertise in biology education, curriculum development, and instructional design.

Data Collection Procedure

Data collection proceeded in three phases:

1) Development Phase: Needs analysis, activity planning, and material development were completed following the ADDIE model. The panel of evaluators reviewed the teaching guide and the pretest–posttest instrument.

2) Implementation Phase: A pretest was given one week before the intervention. The CODE lessons were implemented through three instructional sessions, and the posttest was administered two weeks after the intervention.

3) Qualitative Phase: Students submitted written reflections immediately after the final session. These were collected and prepared for thematic analysis.

Data Analysis

Quantitative data were analyzed using JAMOVI statistical software Version 2.4. Descriptive statistics, including mean, range, and standard deviation, were computed. Normality was tested using the Kolmogorov–Smirnov and Shapiro–Wilk tests. Since the pretest scores were not normally distributed and the sample size was small, the Wilcoxon Signed-Rank Test was used to assess the significance of the difference between pretest and posttest scores. Effect size (r) was computed using the Z-value produced by JAMOVI.

Validation ratings from the evaluators were analyzed using mean scores and standard deviations. Qualitative data from student reflections were examined using Braun and Clarke's six-phase thematic analysis. Themes were triangulated with quantitative results to enhance the interpretation of findings.

Ethical Considerations

Ethical approval was obtained from the Office of the Campus Chancellor. Participation was voluntary, and confidentiality was maintained throughout the research process. Students were informed that they could withdraw from the study at any time without penalty.

RESULTS AND DISCUSSION

Analysis Phase: Needs Assessment for CODE Development

The Analysis Phase of the ADDIE Model examined students' prior knowledge, misconceptions, and learning preferences related to the Central Dogma of Molecular Biology. A 10-item diagnostic test and three open-ended questions were administered to twelve third-year BSED Science students. The diagnostic test produced a mean score of 7.25 out of 10, with scores ranging from 4 to 9, which indicates a moderate level of understanding. Although most students recognized the basic relationship among DNA, RNA, and proteins, weaknesses were evident in items related to transcription output, mutation effects, and the direction of genetic information flow.

Item-level analysis showed that questions involving mutation, transcription products, and identifying incorrect statements about the Central Dogma had the lowest percentages of correct responses. Qualitative answers supported these findings, with several students showing confusion about the distinctions among replication, transcription, and translation, or expressing uncertainty about the origin and consequences of mutations.

The thematic analysis of the open-ended responses produced four major themes:

1. Misconception on the Direction and Location of Genetic Information Flow (1 of 12 students; 8.3 percent)

A small number of students held explicit misconceptions, such as believing that transcription occurs in the cytoplasm or that DNA produces proteins directly. These reveal inaccurate views about the sequence and location of gene expression processes.

2. Difficulty in Understanding Molecular Processes and Components (12 of 12 students; 100 percent)

All students indicated difficulty with at least one molecular process. Translation was the most challenging (6 of 12; 50.0 percent), followed by mutation (5 of 12; 41.7 percent) and transcription (3 of 12; 25.0 percent). Students struggled with codon–amino acid relationships, roles of mRNA and tRNA, and the intracellular mechanisms involved.

3. Limited Understanding of Mutation and Its Biological Implications (5 of 12 students; 41.7 percent)

Almost half of the students were unsure how mutations arise and how they affect protein structure and traits, which suggests weak integration between molecular-level events and phenotype expression.

4. Preference for Visual and Experiential Learning Approaches (12 of 12 students; 100 percent)

All students preferred visual, interactive, or hands-on learning activities. Videos and animations were favored by most students (10 of 12; 83.3 percent), followed by model-building activities (7 of 12; 58.3 percent). Several emphasized the value of role-playing and embodied tasks in understanding abstract molecular processes.

Overall, the Analysis Phase showed that while students possessed some factual knowledge, they experienced substantial difficulty visualizing molecular processes and connecting abstract ideas to observable biological phenomena. Their strong preference for visual and experiential approaches supported the development of the CODE Instructional Approach, which integrates contextualized cases, dramatized simulations, and embodied modeling. These findings align with Research Objective 1 by providing the empirical basis for designing the teaching guide.

Validation of Instruments and Teaching Guide

The CODE Instructional Approach and its associated materials were evaluated by a panel of seven experts. The pretest–posttest instrument received an overall mean rating of 3.77, which is interpreted as Very Highly Valid. Scientific correctness, grammatical clarity, and fairness received perfect mean scores of 4.00, indicating that the tool was appropriate for measuring conceptual understanding of the Central Dogma.

The teaching guide received an overall mean rating of 3.70, interpreted as Very Highly Acceptable. Evaluators identified strengths in instructional sequencing, contextualization, and the use of multimodal strategies. Minor improvements were suggested for differentiation strategies and visual layout. These results confirm the instructional and scientific quality of the materials and support the Development and Evaluation phases of the ADDIE Model under Research Objective 1.

Table 1. Validation Results for the Pretest-Posttest Instrument

Criterion	Mean Rating	Verbal Interpretation
Content Relevance	3.83	Very Highly Valid
Item Clarity	3.50	Highly Valid
Scientific Correctness	4.00	Very Highly Valid
Cognitive Level	3.50	Highly Valid
Item Format	3.33	Highly Valid
Grammar & Language	4.00	Very Highly Valid
Bias / Fairness	4.00	Very Highly Valid
Feasibility & Time Allocation	3.83	Very Highly Valid
Overall Mean	3.77	Very Highly Valid

Improvement in Conceptual Understanding

A pretest was given one week prior to the intervention, and a posttest was administered two weeks after. All twelve students completed both assessments.

1) Descriptive Statistics:

Pretest scores ranged from 9 to 21, while posttest scores ranged from 17 to 23. The mean pretest score was 14.25, increasing to 20.17 in the posttest, resulting in a gain of 5.92 points. Every student showed improvement, indicating an overall increase in conceptual understanding.

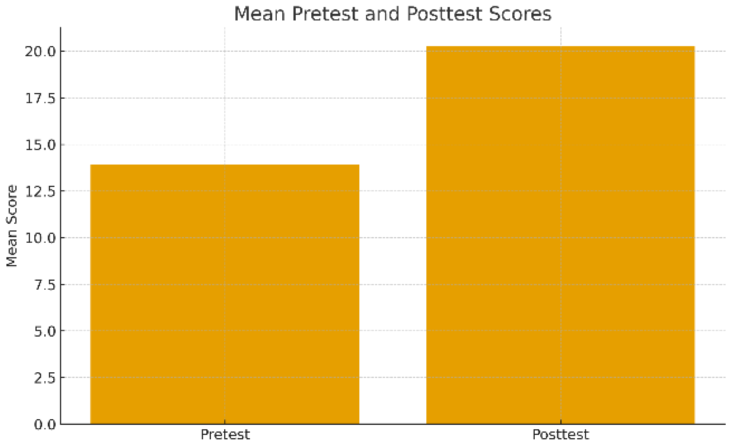

Figure 1. Mean Pretest and Posttest Scores

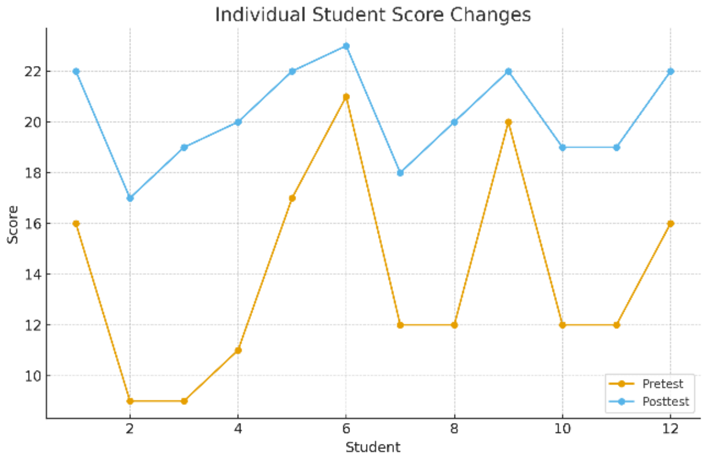

Figure 2. Individual Student Score Changes

2) Test of Normality:

Normality was assessed using the Kolmogorov–Smirnov (K–S) and Shapiro–Wilk (S–W) tests. While Shapiro–Wilk indicated approximate normality for both score distributions ($p > .05$), the K–S test revealed that the pretest distribution significantly deviated from normality ($p = .018$). Given the small sample size ($n = 12$), bounded score scale, the Wilcoxon Signed-Rank Test was deemed appropriate for analyzing the difference between pretest and posttest scores.

Table 2. Test of Normality for Pretest and Posttest Scores

Test	Score Set	p-Value	Interpretation
Kolmogorov–Smirnov	Pretest	0.018	Not Normal
Kolmogorov–Smirnov	Posttest	0.062	Approximately Normal
Shapiro–Wilk	Pretest	0.174	Approximately Normal

Shapiro–Wilk	Posttest	0.255	Approximately Normal

3) Wilcoxon Signed-Rank Test:

To determine whether the observed improvement was statistically significant, the Wilcoxon Signed-Rank Test was performed. All twelve students obtained higher posttest scores, resulting in 12 positive ranks, 0 negative ranks, and 0 ties.

The Wilcoxon test produced a Z-value of –3.068 with a p-value of .002, indicating a statistically significant increase in conceptual understanding after exposure to the CODE Instructional Approach.

Table 3. Wilcoxon Signed-Rank Test: Ranks Summary

Category	N	Mean Rank	Sum of Ranks
Negative Ranks	0	0.00	0.00
Positive Ranks	12	6.50	78.00
Ties	0	–	–
Total	12	–	–

Table 4. Wilcoxon Signed-Rank Test: Test Statistics

Statistic	Value
Z-value	–3.068
p-value	0.002
Interpretation	Significant at $\alpha = 0.05$

4) Effect Size:

Effect size was computed using the formula $r = Z/\sqrt{N}$, yielding $r = 0.886$, which represents a very large effect. This confirms the strong and meaningful impact of the CODE Instructional Approach on student learning and addresses Research Objective 2.

Students' Experiences and Perceptions

Thematic analysis of students' post-intervention reflections identified four major themes that describe how learners experienced the CODE Approach.

1) Emerging Themes:

1. Misconception on the Direction of Genetic Information Flow: Students initially misordered or conflated replication, transcription, and translation, with some believing that DNA directly produces proteins. Sample Quote: “DNA makes proteins directly without RNA.”
2. Difficulty in Understanding Molecular Processes and Components: Students struggled to visualize cellular locations and molecular functions of mRNA, tRNA, ribosomes, and enzymes. *Sample Quote:* “Replication happens in the nucleus, transcription in the cytoplasm.”

3. Limited Understanding of Mutation and Its Biological Implications: Students expressed uncertainty about how mutations arise and how they influence protein structure and traits. Sample Quote: "Even though the process is correct, mutation still appears."

4. Preference for Visual and Experiential Learning Approaches: Learners favored hands-on modeling, role-playing, and visual aids that helped them engage with abstract molecular concepts. Sample Quote: "I prefer to learn through interactive videos and model-building."

Triangulation of Quantitative and Qualitative Findings

Triangulation revealed strong alignment between diagnostic test weaknesses and thematic patterns. Items with the lowest pretest accuracy, such as those assessing information flow and mutation, directly corresponded to themes showing misconceptions and limited understanding. Students' stated preference for visual and experiential learning validated the multimodal design of the CODE Approach.

Table 5. Triangulation of Quantitative and Qualitative Findings

Theme	Quantitative Support	Qualitative Support	Integrated Interpretation
Misconception on the Direction of Information Flow	Lowest score in Item 9 (50% correct)	Students confused DNA → RNA → Protein; some believed DNA makes proteins directly	Confirms conceptual gaps in the direction of genetic information flow
Difficulty in Understanding Molecular Processes	Moderate difficulty in Items 5, 7, and 8	Confusion about location and function of transcription, translation, and enzymes	Indicates the need for diagramming, modeling, and embodied simulations
Limited Understanding of Mutation	Item 6 at 58% correct	Students unsure how mutations arise or affect proteins	Shows fragmented understanding requiring contextualized examples
Preference for Visual and Experiential Learning	Moderate initial performance; strong gains after intervention	Students preferred role-play, modeling, videos, and interactive resources	Supports the effectiveness of multimodal and embodied learning strategies

Integrated Interpretation

Overall results show that students initially exhibited fragmented understanding and misconceptions regarding the Central Dogma. The CODE Instructional Approach significantly improved their conceptual understanding, with a very large effect size and consistent qualitative support. The integration of contextualized cases, dramatized simulations, and embodied modeling enhanced visualization, engagement, and conceptual clarity. These findings validate the theoretical foundations of the CODE Approach and demonstrate that all research objectives were achieved within the ADDIE Model.

CONCLUSION

This study developed, validated, and evaluated the CODE Instructional Approach using the ADDIE Model with the goal of improving preservice science teachers' understanding of the Central Dogma of Molecular Biology. Findings from the Analysis Phase showed that many students held persistent misconceptions about transcription, translation, and mutation, and that they preferred visual and experiential modes of learning. These results guided the creation of a teaching guide that incorporated contextualized case examples, dramatized simulations, and embodied modeling activities.

Validation results from the panel of evaluators indicated that the instructional materials possessed high scientific accuracy, clarity, alignment with learning outcomes, and pedagogical soundness. The implementation of the CODE Approach led to substantial gains in conceptual understanding, reflected in the significant difference between pretest and posttest scores ($p = .002$) and a very large effect size ($r = 0.886$). Students' written reflections further affirmed that the multimodal and embodied learning activities made abstract molecular processes more engaging and easier to comprehend.

Overall, the study demonstrates that the CODE Instructional Approach provides an effective, contextually grounded, and multimodal framework for teaching the Central Dogma. It successfully addresses common misconceptions, enhances students' ability to visualize molecular events, and promotes deeper conceptual learning among preservice science teachers.

RECOMMENDATIONS

Recommendations for Teaching Practice

- Integrate the CODE Approach when teaching topics involving gene expression, transcription, translation, and mutation.
- Use multimodal strategies such as case-based learning, role-play, embodied simulations, and molecular modeling to support conceptual clarity.
- Implement diagnostic assessments to identify misconceptions early and apply conceptual-change strategies accordingly.
- Incorporate animations, 3D models, diagramming activities, and interactive simulations to facilitate visualization of microscopic processes.

Recommendations for Curriculum and Instructional Design

- Embed embodied and dramatized learning activities within biology curricula to enhance learner engagement and comprehension.
- Utilize the CODE Teaching Guide as a model for developing instructional materials for other topics in molecular biology and related life sciences.
- Provide professional development programs focused on embodied cognition, multimodal instruction, and innovative teaching methodologies for pre-service and in-service teachers.

Recommendations for Future Research

Given that this study involved a small group of twelve (12) preservice teachers from a single institution and was implemented over a short instructional period, future research may extend and strengthen the present findings by:

- Replicating the study with larger and more diverse samples across multiple institutions to enhance generalizability.
- Conducting comparative or quasi-experimental studies to determine how the CODE Approach performs relative to traditional or other multimodal instructional strategies.
- Examining long-term retention by administering delayed posttests, as this study measured only immediate learning gains.
- Investigating the approach's influence on scientific reasoning, procedural skills, creativity, and student engagement.

- Developing digital, virtual, or hybrid versions of the CODE Approach—including VR/AR-based embodied simulations—to broaden access and further enhance experiential learning.

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