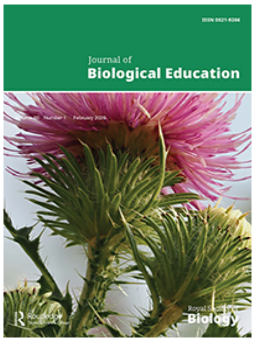

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From reflection to framework: investigating biology pre-service teachers' understanding of genetic information flow, exchange, and storage (IFES)

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ABSTRACT

Understanding genetic information flow, exchange, and storage (IFES) is essential in biology education, yet pre-service teachers (PSTs) often struggle with these core concepts. This small-scale qualitative study explores PSTs' conceptual understanding and misconceptions through an eight-week elective seminar course, where reflective journals were analysed using qualitative content analysis. An IFES conceptual framework was developed, and a rubric-based evaluation assessed PSTs' learning progress, followed by a heatmap visualisation of their conceptual development. Findings reveal that deterministic reasoning persists, particularly in gene expression, inheritance, and environmental regulation of genes. Many PSTs oversimplify protein synthesis, misunderstand RNA's role, and demonstrate limited awareness of epigenetic mechanisms. While some conceptual improvements were observed, none of the PSTs achieved the highest level of integration in any IFES category, highlighting the need for improved instructional strategies in teacher education programmes. This study contributes to biology teacher education by introducing an IFES rubric and framework to assess and enhance PSTs' genetics comprehension. The findings suggest that inquiry-based learning, explicit discussions of misconceptions, and interdisciplinary approaches could support deeper conceptual integration. Future research should examine longitudinal interventions with larger, multi-site samples to confirm these patterns and to better address PSTs' persistent misconceptions and improve genetics instruction in teacher preparation programmes.

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pre-service biology teachers; genetic information flow; exchange and storage (IFES); reflective journals; genetics education

Introduction

National initiatives to enhance science education emphasise the integration of scientific practices with core disciplinary concepts (e.g. Brewer and Smith 2011; National Research Council 2012). These efforts highlight the need to define key biological concepts that all undergraduate students should master. *The Vision and Change in Undergraduate Biology Education: A Call to Action* report stresses the importance of helping students to develop a deep understanding of fundamental biological principles across scales and integrate knowledge across conceptual domains. The report identifies five essential biological concepts that are foundational for scientific literacy: pathways and transformations of

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energy and matter (PTEM), information flow, exchange, and storage(IFES), structure and function (SF), evolution (E), and systems (S) (Cary and Branchaw 2017). These core concepts are essential for both enhancing teaching competency and developing students' scientific literacy, aligning with fundamental biological principles (Liu and Benning 2024; Woodin, Carter, and Fletcher 2010). Over the past several decades, biology education research has emphasised the importance of these core concepts in teaching and learning (Klymkowsky 2010; Quinn and Kohl 2011; Scheiner 2010). However, while these overarching themes provide a structured instructional framework, their broad scope poses challenges in designing learning objectives, instructional materials, and assessments that accurately measure student understanding (Brownell et al. 2014).

This study specifically focuses on IFES (Information Flow, Exchange, and Storage), which encompasses how genetic and molecular information is stored, expressed, and transmitted across biological scales (Brownell et al. 2014). A firm grasp of IFES is fundamental to genetics education, yet pre-service teachers (PSTs) frequently struggle with these interconnected processes. Effectively explaining genetic information flow in molecular and cellular biology requires understanding of mechanistic interactions across different levels of biological organisation, such as transitioning from molecular to submolecular perspectives (van Mil, Boerwinkel, and Waarlo 2013). Prior studies suggest that even after completing formal coursework, students retain a mix of normative and non-normative ideas about genetic information flow (Uhl et al. 2020; Uhl, Shiroda, and Haudek 2022). This persistence of misconceptions indicates that students continue to struggle with the Central Dogma, despite structured instruction. A clear understanding of genetic information flow is critical for comprehending heredity, phenotypic expression, developmental biology, and evolution (Sikumbang, Rakhmawati, and Suwandi 2019).

Research shows that pre-service teachers face significant challenges in understanding RNA's role in protein synthesis, highlighting widespread misconceptions about transcription and translation (Ariesta and Susantini 2021). Many PSTs fail to effectively connect RNA to its function in protein synthesis, exposing critical knowledge gaps that could affect their future teaching effectiveness (Hidayat and Kasmiruddin 2020). Additionally, a study using a three-tier diagnostic test to assess PSTs' comprehension of the Central Dogma of molecular biology revealed low overall understanding, particularly concerning transcription and RNA function (Retone and Prudente 2023). These misconceptions mirror the findings of Prevost et al. (2016), who examined student misunderstandings of stop codons and translation termination, illustrating how fragmented knowledge of one process impacts comprehension of the broader molecular framework. Likewise, Sieke et al. (2019) found that students struggle to grasp the effects of mutations in noncoding regions of DNA, reflecting a persistent misconception that only coding sequences influence gene expression. These findings underscore the critical need for assessment strategies that go beyond traditional multiple-choice testing to capture the depth of students' conceptual understanding.

To address these challenges in teacher education programmes, it is essential to ensure that pre-service teachers develop accurate and comprehensive knowledge of genetics. As advancements in genetics and biotechnology continue, teacher training programmes must evolve to equip educators with the necessary knowledge and pedagogical strategies to teach complex genetic concepts effectively and confidently. Jonsson and Svingby (2007) emphasise that rubric-based assessments can enhance student learning and evaluation reliability, making them an effective tool for capturing conceptual development in PSTs. Given the limitations of standardised multiple-choice assessments, qualitative methods such as reflective journals and rubric-based evaluations provide a more nuanced way to identify and address students' conceptual difficulties.

Building upon these insights, this study examines PSTs' conceptual challenges in IFES through an analysis of reflective journals, allowing for an in-depth exploration of their understanding and misconceptions. Research suggests that teacher educators should focus on identifying and addressing knowledge gaps that persist in PSTs nearing the end of their training (Buma and Nyamupangedengu 2023). While previous studies have investigated PSTs' misconceptions and pedagogical content knowledge (PCK) in genetics, research rarely explores which IFES concepts continue to be problematic at the end of teacher training programmes (e.g. Etobro and Banjoko 2017; Irmak and Yilmaz Tüzün 2018; Kalaycı 2025; Taskin Bedizel 2023). This study aims to fill this gap by analysing reflections from senior biology pre-service teachers, providing insights into IFES-related conceptual difficulties and developing an IFES framework based on their reflections. The study is conducted through an eight-week elective seminar course, where PSTs explore genetics topics they perceive as challenging and engage in structured reflections on their learning progress.

While numerous studies have explored undergraduate students' misconceptions about genetics, including the Central Dogma, gene regulation, and inheritance (e.g. Prevost, Smith, and Knight 2016; Uhl, Shiroda, and Haudek 2022), far fewer have investigated how these conceptual difficulties persist in pre-service biology teachers nearing the end of their formal education. This distinction is critical, as pre-service teachers are not only expected to understand these concepts but also to teach them accurately. Furthermore, the specific IFES framework – emphasising the interconnectedness of information flow, exchange, and storage – has not been widely used to evaluate teacher candidates' conceptual development. This study addresses this gap by focusing on senior biology pre-service teachers' written reflections in a genetics-focused seminar course, aiming to identify persistent misconceptions and conceptual progress related to IFES. By developing and applying a novel IFES rubric, this research contributes to understanding the specific challenges faced by future educators and offers a tool to guide instruction in teacher preparation programmes.

Research questions

(1) What conceptual understandings and misconceptions do pre-service biology teachers reveal in their reflective journals regarding the IFES concepts?
(2) How was the IFES framework developed based on qualitative data, and how does it categorise pre-service teachers' conceptual understanding?
(3) What do the heatmap results reveal about pre-service teachers' conceptual development across IFES dimensions?

Methods

Research design

This study employed a qualitative research design with a focus on conceptual framework development, specifically using qualitative content analysis to construct the Information

Flow, Exchange, and Storage (IFES) framework. The study followed an interpretivist paradigm, emphasising the meaning-making process of pre-service teachers (PSTs) as they reflected on their conceptual understanding of genetics.

Conceptual framework development studies are commonly used in education research to derive theoretical models from qualitative data (Collins and Stockton 2018). The qualitative content analysis method allows for systematic categorisation of emerging themes (Schreier 2012), making it a suitable approach for analysing PSTs' reflective journals and developing the IFES framework.

Researcher reflexivity

The Author holds a doctoral degree in Biology Education and teaches undergraduate and graduate-level courses in the field. Having conducted multiple independent studies and contributed to various research projects, the researcher is well versed in national and international ethical guidelines. As a qualitative researcher, she acknowledges potential biases and worked alongside expert researchers to incorporate feedback and conduct the study with scientific rigour and ethical responsibility. She attended the 8-week training as a non-participatory observer to gain a deeper understanding of the course content and PSTs while documenting field notes to ensure data integrity. The author also distributed prompt sheets to participants at the end of each week.

Participants and context

This research was conducted during the fall semester of the 2022/2023 academic year in the Faculty of Education, Biology Teacher Education Department, at a university in northwest Turkiye. The participants were 11 biology education senior-year pre-service teachers (all-female, ages between 21–23) who previously completed all genetics related courses in the curriculum (Molecular Biology, Genetics I, Genetics II and Evolution). In our programme – and nationally – biology teacher education cohorts are predominantly female; thus, our all-female sample reflects the typical intake rather than a selection effect. In the national context, the student quota in biology education programmes were typically 21 at that time of the study. During the time of the present study, there were 10 female pre-service teachers in the freshman year, 17 female and 2 male pre-service teachers in the sophomore year, and 18 female and 3 male pre-service teachers in the junior year. We report our findings as context-specific and do not necessarily claim representativeness. Additionally, previous studies conducted with biology teacher candidates on various topics found no significant differences between genders (e.g. Kabasakal and Yel 2020).

The research data were collected as part of a seminar course aimed at helping biology teacher candidates overcome their self-identified gaps in genetics. Before the course, all participants acknowledged having difficulties with certain genetics topics and provided feedback to the instructor on the areas they found challenging. In collaboration with the PSTs, the topics to be covered in the study were determined. They were asked to identify the genetics concepts they needed to review, and based on their responses, an eight-week course plan was designed. The course content focused on genetics topics that they had previously studied and passed but wanted to revisit for further reinforcement. Upon graduation, PSTs were required to take the Teacher Field Knowledge Exam, which includes 75 questions - 60

Table 1. Outline of the follow-up course.

Weeks	Content
1	The nucleoprotein structure of DNA, its function, and the relationships between code, codon, and gene concepts.
2	The advantages of DNA being double-stranded in passing traits to offspring, how DNA regulates vital processes in the cytoplasm, and the one-gene-one-polypeptide concept.
3	The structure and types of RNA, ribosome biogenesis, the stepwise relationship between codon and anticodon, and protein synthesis (introduction)
4	Central dogma, differences between mitosis and meiosis, crossing-over, homolog chromosomes, allele gen, sister chromosomes.
5	Mitosis and meiosis (review of the previous week), the purpose of meiosis, gametogenesis, spermatogenesis, oogenesis, linked genes, and genotype-phenotype concepts.
6	Mendelian laws (law of uniformity, independent assortment, segregation, self-fertilization + dihybrid self-fertilization).
7	The concept of mutation, mutagen factors, types of mutations, autosomes, gonosomes, environmental factors (abiotic + biotic), selection, and isolation.
8	Questions & Answers

on biology content and 15 on biology education - in order to qualify as secondary school biology teachers. In 2023, when the participants of this study sat the exam, the distribution of biology questions was as follows: Cell and Metabolism: 12 questions (16%); Plant Biology: 7–8 questions (10%); Human and Animal Biology: 15 questions (20%); Ecology: 7–8 questions (10%); Classification of Living Organisms: 6 questions (8%); Genetics and Evolution: 12 questions (16%). Given that these PSTs were preparing for the Teacher Field Knowledge Exam, a requirement for teacher certification in Türkiye, their motivation for the lessons was notably high. Therefore, following a molecular first approach, the 8-week-course plan included the topics as shown in Table 1. The course content in each week was completed in a 90-minute session.

Data collection instrument

The primary data collection instrument was reflective student journals, designed to facilitate reflective thinking and writing (Dewey 1933; Schön 1992). PSTs completed these journals at the end of each lesson. The format of the journals was designed with questions on the left page and student responses on the right page, partially inspired by the Cornell note-taking system (Pauk and Owens 2011). In this system, the left-side column contains prompts or questions, while the right-side column is designated for responses and notes. By adapting this format, the PSTs were able to view, compare, and revise their answers easily.

Development of prompts

The prompts in the journals were developed collaboratively by the researcher, the course instructor, and another expert in the field. The prompts were based on the research model proposed by Towndrow, Ling, and Venthan (2008), with certain adaptations in its structure and implementation. As a result of the discussions, five common prompts were assigned weekly, with additional topic-related questions (see Appendix) included each week for evaluation purposes. After conducting a pilot study to assess the clarity of the prompts and questions, the final set of prompts in the reflective journals was determined as illustrated in Table 2. In addition, Figure 1 shows examples of pre-service teachers' reflective journals.

Data collection procedure

PSTs kept a reflective journal over eight weeks during the fall semester of the 2022/2023 academic year. Throughout this period, PSTs participated in weekly lessons and documented their reflections in their reflective journals. At the end of each session, they stayed in the classroom to complete and submit their journal to the author. The author was present in the class and PSTs were not allowed to confer while writing their journals. All journals were completed individually and instructions emphasised that entries should reflect personal learning, not peer discussions or online sources. The reason for not allowing them to confer was to reduce the risk of influencing the results from others being more outspoken. In addition, we found no indications of duplicated or shared wording across journals.

Data analysis and framework development

Upon completion of the study, all journals were gathered, and their contents were transcribed into a Word document without any alterations. Any drawings included in

Table 2. Prompts in the reflective journals.

	Journal Prompts for each week
1	Summarize the content of the lesson in your own words.
2	Did you encounter any information that was completely new to you, something you had never heard of before?
3	Did you come across any information that challenged what you previously believed, making you feel uncertain or confused?
4	Did you encounter any information that you partially understood but still needed to connect all the pieces?
5	Did you come across any information that helped you correct a misconception or deepen an incomplete understanding?
6	Topic-related questions to be discussed in the 8th week of the course (see Appendix)

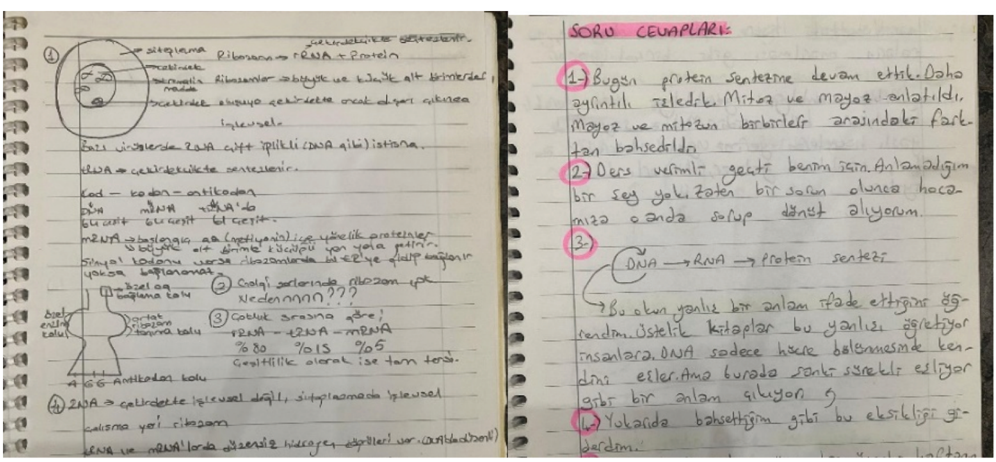

Figure 1. Examples of pre-service teachers' reflective journals.

the journals were photographed and archived in their original format. Data were analysed using qualitative content analysis (Schreier 2012), which involved:

- Familiarisation – Reading and re-reading journal entries to gain an initial understanding.
- Generating initial codes – Assigning preliminary labels to recurring concepts and misconceptions.
- Searching for themes – Identifying patterns across journal entries related to the five core genetics concepts (IFES1–IFES5).
- Developing the IFES Framework – Organising recurring themes into conceptual categories to construct a theoretical framework.
- Refinement and Validation – The framework was reviewed and refined through discussions with an expert panel to ensure coherence and validity.

This method aligns with existing literature on framework development in education research (Collins and Stockton 2018; Creswell 2013), which emphasises deriving conceptual models from qualitative data.

Development of the IFES rubric and heatmap

Once the IFES framework was established, a rubric was developed to categorise PSTs' conceptual understanding across four levels (Beginning, Developing, Proficient, and Advanced). The rubric was informed by:

- Recurring themes from journal analysis.
- Existing conceptual models in genetics education (Duncan, Rogat, and Yarden 2009; Venville and Treagust 1998).
- Expert validation to ensure alignment with recognised learning progressions.

Following rubric development, heatmaps were generated with GraphPad to visually represent the distribution of PSTs' conceptual understanding across the IFES dimensions. This approach provided a structured visualisation of conceptual strengths and challenges within the sample (Hanauer and Dolan 2013).

Trustworthiness and credibility

To strengthen the credibility of the analysis, 25% of the reflective journal entries were independently coded by the author and an experienced biology educator with 25 years of teaching experience, who is also a current PhD student, using the initial coding framework. Cohen's Kappa was calculated to assess interrater reliability, resulting in a moderate to substantial agreement ($\kappa = 0.74$). Discrepancies were discussed and resolved through consensus, and the coding framework was refined accordingly. The remaining data were coded by the lead researcher using the revised framework. A detailed audit trail and memoing were used throughout to ensure consistency, transparency, and replicability of analytical decisions. This process aligns with best practices in qualitative research for ensuring credibility and reliability (Creswell 2013;

Schreier 2012). In addition, PSTs were informed that participation in the study was voluntary, and their responses would not affect their grades or have any negative consequences. They were assured that they could withdraw from the study at any time and that their personal information, including their names, would remain confidential and anonymous. All participants were over 18 years old and provided informed consent both verbally and in writing. The researchers maintained ethical integrity throughout all research stages, including data collection, communication with participants, and data analysis. Additionally, all PST information was anonymised, and they were assigned coded identifiers by different names. The researcher had no conflicts of interest with any institution or organisation. In cases where journal entries were unclear or ambiguous, participant confirmation was sought to clarify the intended meaning. Each PST confirmed that they had personally completed their journals. Because journals were written individually and submitted instantly, the risk of peer influence on written reflections was reduced; nevertheless, we acknowledge that shared classroom experiences may still shape salience and framing. We therefore treat potential social influence as a limitation and report context to support judicious transferability. Furthermore, a record of all analytical decisions was maintained to ensure transparency and replicability.

Findings

Senior biology pre-service teachers' conceptual understandings and misconceptions in IFES concepts

IFES 1: information flow across biological scales

The main challenge in understanding information flow across biological scales (IFES1) was that PSTs initially held species-specific misconceptions, assuming that genetic information was exclusive to humans or certain organisms rather than universally conserved across species. This misconception was reflected in statements such as *'I thought that only humans have unique genetic codes, but some genes are shared across species'*. (Sena) and *'I didn't know that glucose-related genes are common in all living organisms'* (Eda).

As the follow-up course progressed, some PSTs moved away from this rigid perspective, beginning to recognise that genes are present in all cells but are differentially expressed. This conceptual shift was evident in statements like *'All chromosomes exist in all cells, but not all are expressed; only the necessary ones are activated'* (Tuana), indicating progress towards a more refined understanding of gene regulation and expression.

Additionally, many PSTs had prior misunderstandings about the hierarchical organisation of genetic material, including confusion between genes, alleles, chromosomes, and DNA. Some conceptualised chromosomes as containers for genes, similar to objects stored inside a box (e.g. *'Genes are like items stored inside chromosomes'* – Selin), while others perceived genes, DNA, and chromosomes as interchangeable, failing to recognise that genes are functional sequences embedded within the DNA strand.

A common misconception was that DNA is simply a component of chromosomes, without recognising that chromosomes consist of both DNA and histone proteins. Buse, for example, reflected on this realisation, stating, *'I realized that I had misunderstood the size order of DNA, genes, and chromosomes, and through this lesson, I learned the correct sequence'.*

Figure 2 shows examples of PSTs drawings of the relationship between genes, DNA and chromosomes at the beginning of the follow-up course.

However, none of the PSTs demonstrated a fully integrated understanding of IFES1. The findings indicate that conceptual connections between gene regulation at different biological levels (cells, organisms, populations) and their role in evolutionary processes remained underdeveloped.

IFES 2: genetic and epigenetic information storage

The primary challenge in understanding genetic and epigenetic information storage (IFES2) was the underestimation of RNA's role in storing genetic information. Many PSTs initially believed that only DNA carries genetic information, struggling to comprehend RNA-based genetic systems and epigenetic regulation. For instance, Ceylan initially wrote in their reflective journal, *'RNAs do not contribute to amino acid diversity. They have no contribution to protein synthesis'.*

Furthermore, RNA-based genetic systems were largely overlooked, reinforcing a DNA-centric perspective of molecular biology. This misconception was evident in Meriç's reflection: *'It is very surprising that some plants have RNA-mediated epigenetic inheritance and that some viruses have double-stranded RNA'.*

As the course progressed, some PSTs began to acknowledge the role of epigenetic modifications, recognising that gene regulation does not always require changes in DNA

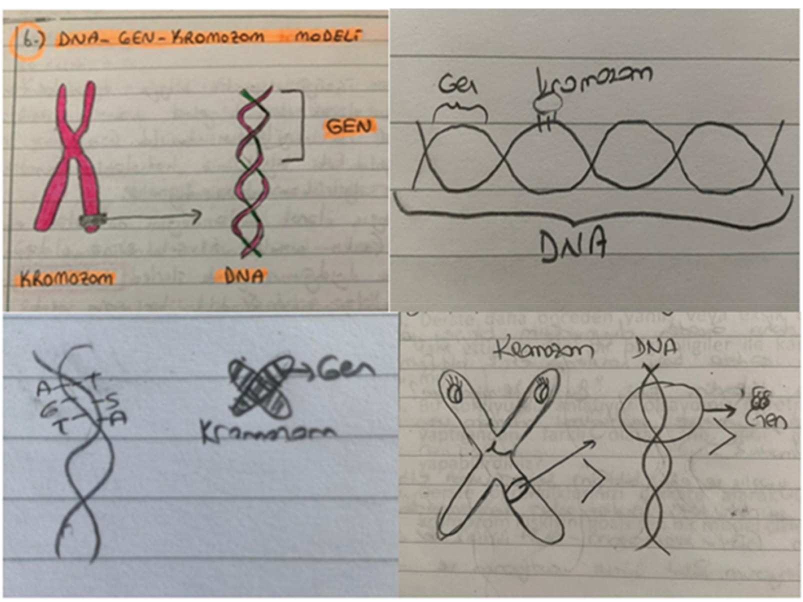

Figure 2. Biology PSTs drawings of DNA, gene, and chromosome relationships (from upper left to lower right; Ceylan, Tuana, Ozge, Dilara).

sequence (e.g. *'Epigenetic modifications like DNA methylation can influence gene expression without changing the DNA sequence'* – Ceren).

However, none of the PSTs demonstrated a fully integrated understanding of epigenetic regulation. While a few recognised its importance, very few explicitly connected it to developmental biology or environmental influences, suggesting the need for further emphasis on the broader implications of epigenetics in inheritance and gene expression.

IFES 3: protein synthesis and its regulation

The primary challenge in understanding protein synthesis and its regulation (IFES3) was the oversimplification of protein function, with PSTs assuming that proteins directly determine traits without considering post-translational modifications or molecular interactions. This static view of protein function was evident in statements such as *'I learned that an enzyme being produced or not is also a trait'*. (Meriç). Similarly, Ayla and Selin expressed a limited understanding of protein roles, stating, *'Proteins have open ends, meaning they can form bonds, which is why many traits emerge'*. (Ayla) and *'I just realized that proteins contribute to trait formation, but they are not only structural proteins'*. (Selin).

As the course progressed, some PSTs moved beyond this simplified view, recognising that protein function is influenced by modifications, structure, and cellular context (e.g. *'Post-translational modifications affect protein folding and function'*. – Selin). However, many still viewed proteins as static molecules, rather than as dynamic regulators of cellular processes.

Regarding IFES3, another major misconception was the belief that DNA replication must occur before each instance of protein synthesis, reflecting a misunderstanding of the sequence of molecular events in the central dogma. Meriç illustrated this misconception, stating, *'I once thought that DNA replication took place before every protein synthesis in the central dogma'*.

Additionally, some PSTs assumed that DNA replication occurs without errors, showing a lack of awareness of mutation rates and DNA repair mechanisms (e.g. *'I thought DNA replication always happens without errors'* – Ayla, Tuana). This misconception overlooks the stochastic nature of replication errors and the role of proofreading enzymes in correcting mutations.

Furthermore, some PSTs misunderstood base pairing, initially perceiving it as a random process rather than a chemically specific interaction. Ozge later addressed this misconception in her journal, stating, *'I learned that chemical analyses have shown that Adenine pairs with Thymine because they complement each other, so Cytosine cannot pair with Adenine'* – Ozge.

Despite some conceptual progress, many PSTs still struggled with the complexities of protein synthesis, regulation, and the broader molecular interactions involved in gene expression and trait formation.

IFES 4: the influence of environmental signals on gene regulation

In relation to the influence of environmental signals on gene regulation (IFES4), the primary challenge was the deterministic belief that gene expression is fixed at birth, leading to a static view of genetics. Statements such as *'Gene expressions are fixed at birth'* (Ceren) and *'All genes are expressed in all cells'* (Tuana) exemplified this misconception, as PSTs initially struggled to recognise the dynamic nature of gene regulation. Many assumed that all genes are active in all cells, demonstrating difficulty in understanding differential gene expression (e.g. *'I assumed that all my cells should have the same active genes because they all have the same DNA'* – Tuana).

Regarding IFES4, PSTs' oversimplified understanding of genetic variation limited their ability to connect mutations with evolutionary processes, inheritance patterns, and disease mechanisms – all of which involve complex interactions between genetic and environmental influences. For example:

> I learned that mutations could occur between genes on the same chromosome. I used to think that mutations only happened between homologous genes. – Buse, Sena, Eda

> Xeroderma pigmentosum: It is a mutation that can be repaired in the eye, but when it occurs in the skin, it cannot be repaired and becomes carcinogenic. – Sena, Eda

Some PSTs also tend to categorise mutations as strictly good or bad, rather than recognising neutral mutations and their role in genetic diversity. The deterministic assumption that mutations are always either harmful or beneficial (e.g. *'Whether a mutation is beneficial or harmful is decided by the environment'* – Ceylan) reflects a lack of understanding of stochastic genetic processes.

As the course progressed, some PSTs began to recognise that genes can be activated or deactivated in response to environmental factors. Ceren later reflected on this shift in understanding, stating, *'I learned that genes can be activated or deactivated at different stages of life because of lifestyle'* – Ceren.

Despite these conceptual improvements, many PSTs still struggled to fully grasp the intricate pathways linking environmental signals to gene regulation. Among all IFES concepts, IFES4 had the highest number of PSTs at the beginning level, indicating that understanding gene-environment interactions remains a significant challenge.

IFES 5: inheritance beyond DNA sequence

In relation to understanding inheritance beyond DNA sequence (IFES5), the primary challenge was the Mendelian-dominant perspective held by PSTs, where they assumed all mutations are inherited and directly result in speciation. For instance, Ayla initially stated, *'Mutations are always passed to future generations'*, while Ozge expressed the misconception that *'Some mutations create entirely new species instantly'*.

Additionally, many PSTs exhibited an oversimplified view of inheritance, failing to account for incomplete dominance, epistasis, or polygenic traits. This was evident in statements such as *'If an allele is dominant, it always shows in the phenotype'*. (Eda) and *'Dominant diseases always appear in individuals'* (Sena).

Some PSTs also misconstrued genetic information as something that physically moves through the body, reinforcing a mechanistic rather than molecular view of inheritance. For example, Ayla believed that *'If a child gets more chromosomes from the grandfather, they will look more like him'*.

As the course progressed, some PSTs began recognising that mutations are not always inherited and that epigenetic modifications can influence inheritance (e.g. *'Epigenetic changes can influence inheritance'* – Ceren). However, a further misconception was the belief that genes are inherited as complete, indivisible units, rather than undergoing recombination and independent assortment during meiosis. Tuana reflected on this shift in understanding, stating, *'I used to think that each parent's genes are inherited without mixing'*.

Development of the IFES framework: categorizing conceptual understanding

Drawing from PSTs' reflections after each follow-up class, we developed the IFES Rubric, presented in Table 3. It is essential to highlight that none of the senior biology PSTs achieved a fully comprehensive understanding of any IFES concept. As a result, the advanced category remains hypothetical, representing the idealised, complete understanding of each concept rather than an attained level of comprehension among the participants.

The IFES Rubric allowed us to categorise the conceptual understanding of senior biology pre-service teachers (PSTs) across five core dimensions of information flow, exchange, and storage. By analysing the placement of their responses within Beginning, Developing, Proficient, and Advanced levels, we interpreted the strengths and persistent challenges in their learning.

Heatmap analysis: visualizing conceptual development in IFES

After creating the IFES rubric, we scored each PST across IFES dimensions and categorised conceptual development into four levels as indicated in the data analysis section. These rubric scores were used to generate a heatmap to compare individual PSTs strengths, weaknesses, and misconceptions across IFES dimensions. Figure 3 shows the conceptual understanding levels of Biology PSTs across IFES dimensions.

As depicted in the heatmap in Figure 3, none of the PSTs achieved a fully comprehensive understanding in any IFES category, indicating that even the most advanced learners did not reach the highest level of conceptual integration. At the same time, no PSTs remained at the beginning level in any category, suggesting that they were able to correct their initial misconceptions throughout the follow-up course.

Among all IFES dimensions, IFES4 (Environmental Regulation of Gene Expression) posed the greatest challenge, as many PSTs struggled to grasp the complex pathways connecting environmental cues to gene regulation. Additionally, deterministic reasoning remained prevalent across multiple categories, such as the belief that all genes are active in all cells (IFES4), that all mutations are inherited (IFES5), and that proteins directly determine traits without regulation (IFES3).

The heatmap analysis highlights persistent gaps in conceptual understanding, particularly in epigenetics, gene regulation, and environmental influences on inheritance. While some PSTs made notable progress, especially in protein synthesis and genetic information flow, many misconceptions persisted across IFES categories.

Discussion

This small-scale, qualitative, context-bound study offers an in-depth view of IFES-related conceptual challenges that may persist among senior biology pre-service teachers (PSTs), despite prior coursework in genetics. The findings are not intended to generalise but to

Table 3. IFES rubric.

IFES Concept	Beginning (Misconceptions & Gaps in Understanding)	Developing (Partial Understanding)	Proficient (Correct but Simplistic Understanding)	Advanced (Comprehensive Understanding)
IFES1: Information exists in many forms and is relayed within and across biological molecules, cells, tissues, organisms, populations, and ecosystems.	Believes genetic information is unique to humans or specific species. Confuses genes, alleles, chromosomes, and DNA as interchangeable. Thinks DNA is just a component of chromosomes.	Recognizes that genes are present in all cells but struggles with the concept of differential gene expression. Views chromosomes as simple containers for genes rather than organized structures.	Understands that genetic material is hierarchically organized and that different genes are expressed in different cells. However, struggles with applying this understanding to different biological scales.	Fully comprehends the multi-level nature of genetic information, recognizing that gene expression varies across cells, organisms, and evolutionary processes. Can relate gene regulation to larger biological systems.
IFES2: Genetic information is stored in nucleic acids (DNA and RNA); epigenetic information is stored in proteins that associate with DNA and in reversible DNA modifications.	Does not recognize RNA as a genetic material. Assumes only DNA carries genetic information. Does not understand epigenetics.	Acknowledges RNA's existence but believes it plays only a passive role. Struggles to understand histones, methylation, and gene regulation.	Recognizes that RNA has functional roles and that epigenetic modifications can regulate gene expression but does not fully integrate these into a broader framework.	Fully understands that genetic information is stored in both DNA and RNA, and gene expression is regulated by histones, methylation, and other epigenetic modifications. Recognizes the role of epigenetics in inheritance.
IFES3: The process of protein synthesis results from the flow of genetic information through various pathways.	Believes proteins directly determine traits without considering modifications. Thinks DNA replication must occur before each protein synthesis event. Assumes base pairing is random.	Understands that mRNA carries information for protein synthesis but does not recognize regulation at multiple levels. Struggles with post-translational modifications.	Knows that proteins are synthesized from mRNA templates but has a simplistic view of protein function. Recognizes DNA replication errors but does not fully grasp mutation mechanisms.	Recognizes that protein synthesis involves transcription, translation, post-translational modifications, and dynamic regulation of gene expression. Understands the role of protein interactions in cellular processes.
IFES4: Information from the environment regulates protein synthesis and activity, which control cellular processes and thereby organismal and population-level activity.	Believes gene expression is fixed at birth and that all genes are expressed in all cells. Views genetic activity as static rather than dynamic.	Understands that gene expression can change in response to environmental factors but struggles to identify mechanisms (e.g. transcription factors, epigenetics).	Recognizes that environmental signals regulate gene expression but does not fully connect this to adaptation, disease, or cellular responses.	Fully understands how external factors such as stress, nutrients, and temperature regulate gene expression through signaling pathways and epigenetic changes. Can apply this knowledge to real-world scenarios.
IFES5: Organisms transmit genes and epigenetic information to their offspring.	Assumes inheritance is strictly Mendelian and only DNA-based. Believes all mutations are inherited and cause immediate speciation.	Understands genetic inheritance but does not recognize non-DNA factors such as epigenetics. Views dominant traits as always appearing in the phenotype.	Acknowledges epigenetic influences but does not fully integrate them into classical inheritance models. Struggles with concepts like recombination and polygenic traits.	Comprehends that inheritance involves both DNA sequences and epigenetic factors that can be influenced by the parental environment and passed to offspring. Recognizes genetic diversity beyond Mendelian inheritance.

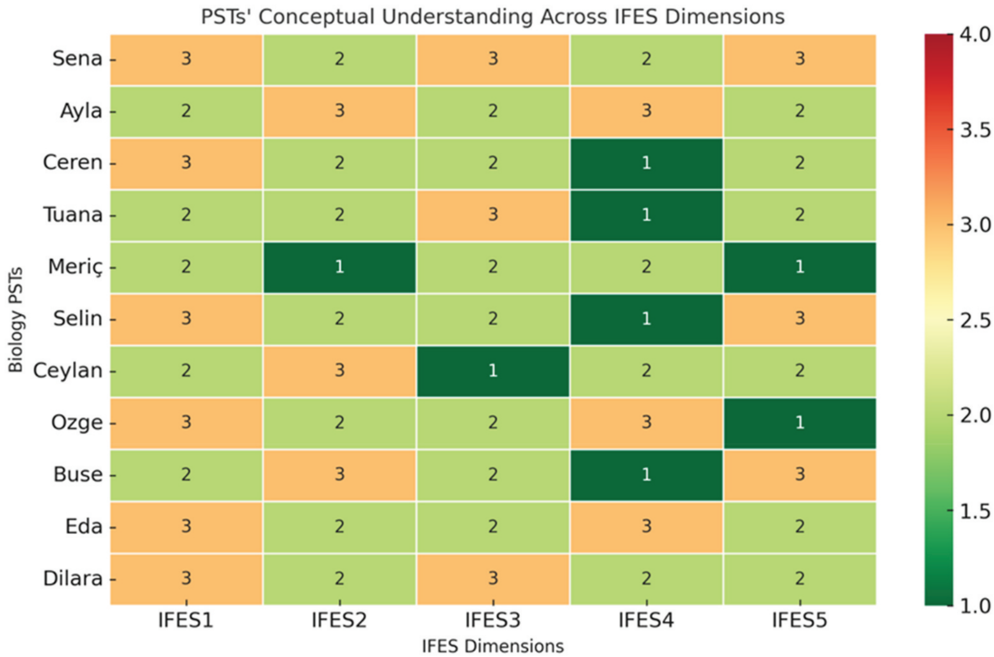

Figure 3. Biology PSTs′ conceptual understanding across IFES dimensions.

illuminate that the PSTs in our study group are not yet fully prepared to teach IFES concepts, as they still struggle with key topics such as epigenetics, gene-environment interactions, protein regulation, and probability-based reasoning inheritance. While conceptual progress was observed, deterministic reasoning persisted across multiple IFES categories, hindering these PSTs' ability to grasp the probabilistic nature of mutations, gene regulation, and evolutionary mechanisms.

Deterministic reasoning and conceptual challenges in IFES

The results indicate that deterministic thinking remains a fundamental cognitive barrier in our programme. Despite some conceptual improvements, none of the PSTs demonstrated an advanced understanding of how both genetic and epigenetic mechanisms shape inheritance and facilitate adaptive changes across generations. While some acknowledged epigenetic inheritance, they struggled to integrate it into broader evolutionary concepts. Many PSTs retained gene-trait determinism, believing that genes directly and exclusively determine phenotypic traits. Others exhibited molecular determinism, assuming that DNA is the only functional genetic molecule while overlooking the regulatory roles of RNA and epigenetics. These findings are consistent with prior research (e.g. Gericke and Smith 2014), which has documented how fragmented, reductionist, and deterministic reasoning persists despite formal instruction. This reinforces the need for pedagogical strategies that explicitly address intuitive reasoning patterns in genetics education (Donovan 2022; Ojo 2024). In addition, a human-centric tendency was noted in PSTs' examples (e.g. blood groups, disease risk). While human contexts can be seen to increase motivation (Donovan et al. 2019), over-reliance might narrow the application of IFES concepts across taxa and levels. It is recommended that examples be deliberately diversified (microbial regulation, plant responses, population/ecosystem-scale information flow) to strengthen cross-scale reasoning.

The IFES Rubric, developed in this study, offers a preliminary framework for describing and tracking PSTs' understanding. This rubric aligns with Vision and Change in Undergraduate Biology Education (AAAS 2011), offering insights into the essential knowledge of genetics required for teaching IFES effectively. By tracking conceptual development, it allows for targeted interventions to enhance PSTs' understanding of molecular genetics and its broader applications. Additionally, this framework can inform the development of assessments to examine students' understanding of genetic information flow, exchange and storage.

Key conceptual challenges in IFES

Rigid, linear interpretation of the central dogma

Consistent with previous studies (Bujanda and Anderson 2022; Shahoy et al. 2024), many PSTs conceptualised the central dogma of molecular biology (DNA replication, transcription, and translation) as a fixed, sequential process, rather than recognising the dynamic, interconnected nature of gene regulation. This rigid interpretation is well-documented in genetics education literature (Briggs et al. 2016; Lewis and Kattmann 2004; Newman et al. 2016; Reinagel and Bray Speth 2016; Smith and Knight 2012; Uhl et al. 2020; Uhl, Shiroda, and Haudek 2022; Wright, Fisk, and Newman 2014). Prevost et al. (2016) found that undergraduate students often misinterpret the role of stop codons in translation, believing that they universally terminate protein synthesis rather than understanding their role in different regulatory contexts. Similarly, Sieke et al. (2019) reported that students struggle with the effects of mutations in noncoding regions, often assuming that only mutations in coding sequences influence gene expression. Additionally, Duncan, Castro-Faix, and Choi (2014) suggest that introducing the central dogma before Mendelian inheritance could improve learning outcomes, challenging traditional sequencing in genetics instruction.

To address PSTs' fixed, sequential understanding of the central dogma, teacher education programmes could:

- Introduce alternative sequencing of content by teaching molecular mechanisms (DNA → RNA → protein) before classical inheritance models to support mechanistic reasoning, as suggested by Duncan et al. (2016).
- Emphasise the dynamic and regulated nature of gene expression through instructional tools such as annotated diagrams, temporal simulations, or case-based examples of gene regulation in different contexts (e.g. stress responses, development).

Molecular determinism and the role of RNA

Many PSTs neglected RNA's regulatory and catalytic functions, viewing DNA as the sole genetic molecule. This oversimplified, DNA-centric perspective has been widely reported (e.g. Martins and Ogborn 1997; Todd, Romine, and Correa-Menendez 2017). Studies show that students often overlook the importance of non-coding RNAs, RNA modifications, and RNA-based viral genomes, resulting in fragmented conceptual models of molecular genetics (Etobro and Banjoko 2017; Jalmo and Suwandi 2018).

To address this misconception, incorporating RNA-based gene regulation (e.g. RNA interference, riboswitches) through interactive simulations can reinforce the understanding that RNA is an active regulator in cellular processes (Kitt 2023). Additionally, using real-world applications such as mRNA vaccines (Bujanda and Anderson 2022) and CRISPR-Cas systems can make RNA's functional significance more tangible.

Given that PSTs often overlooked RNA's regulatory functions and retained DNA-centric views, curricula may benefit from:

- Including RNA-focused modules that explicitly explore regulatory and catalytic roles (e.g. siRNA, ribozymes, RNA interference).
- Embedding current applications such as mRNA vaccines or CRISPR-Cas technologies to demonstrate RNA's relevance in real-world biotechnology.
- Using interactive simulations or animations to show RNA behaviour, helping PSTs understand its roles beyond messenger functions.

Oversimplification of gene expression and epigenetics

Many PSTs oversimplified gene expression, assuming that all genes are permanently active or inactive from birth, without recognising the influence of epigenetics and environmental regulation (Fahmi et al. 2024; Lewis and Kattmann 2004; Snyder et al. 2020). Since epigenetics is often absent in national curricula in many countries (Zudaire and Napal Fraile 2021), its integration into biology education is crucial for helping students understand gene-environment interactions (N. Gericke and McEwen 2023; McEwen, Gericke, and Thörne 2025; Thörne, Gericke, and McEwen 2025).

Research suggests that incorporating virtual lab simulations on chromatin remodelling, DNA methylation, and histone modifications can significantly enhance students' understanding (Drits-Esser et al. 2014). Additionally, discussing case studies on epigenetic inheritance (e.g. the Dutch Hunger Winter study, twin studies) can illustrate how environmental factors shape gene expression (Gericke and McEwen 2023).

Struggles with probability-based reasoning in inheritance

PSTs demonstrated difficulties in understanding inheritance beyond Mendelian genetics, often assuming that dominant traits are always more common (dominance = frequency) or that genes are inherited as complete, indivisible units without recombination. These misconceptions align with prior research (Duncan and Reiser 2007; Lewis and Kattmann 2004). PSTs' deterministic thinking about dominant traits and allele transmission could be mitigated by implementing problem-based learning (PBL) scenarios that require application of population genetics models (e.g. Hardy-Weinberg equilibrium), encouraging simulation-based activities where students predict and observe outcomes under varying genetic and environmental conditions and using data interpretation tasks that challenge students to think statistically and move beyond trait determinism (e.g. exploring polygenic traits, variable expressivity).

Misconceptions about mutations and evolution

PSTs struggled to grasp the stochastic nature of mutations, often categorising them as strictly beneficial or harmful, rather than recognising neutral mutations and their role in genetic diversity (Nadelson 2009). Some also assumed that mutations directly lead to speciation, failing to understand the gradual nature of evolutionary change. Prior studies (Uhl et al. 2020; Uhl, Shiroda, and Haudek 2022) confirm that students often struggle with integrating mutations into broader evolutionary models, reinforcing the need for targeted interventions. The tendency of PSTs to view mutations as inherently beneficial or harmful – and as directly responsible for speciation – highlights the need to incorporate evolutionary case studies that illustrate gradual change (e.g. antibiotic resistance, genetic drift, founder effects) and emphasise the role of neutral mutations. Addressing this misconception may also require explicit instruction on the random and context-dependent nature of mutation outcomes, using visual models and real data sets, as well as engaging PSTs in hypothetical scenarios or role-play tasks that allow them to explore how different mutations may – or may not – affect survival and reproduction.

Conclusion

This study underscores the pervasive influence of deterministic reasoning in pre-service biology teacher education, even after formal coursework in genetics. The IFES rubric and heatmap analysis offer a structured framework for assessing conceptual development, allowing for targeted instructional interventions.

While some conceptual progress was observed, elements of fragmentation and deterministic reasoning remained evident across several IFES categories, particularly in gene-environment interactions, epigenetics, and RNA regulation. Moving forward, teacher education programmes must incorporate interdisciplinary, model-based, and inquiry-driven approaches to help PSTs develop a mechanistic, system-level understanding of genetics. Without such instructional reforms, PSTs may pass on misconceptions to their future students, limiting the next generation's comprehension of molecular biology and its broader implications.

Implications for secondary teaching

Although no mentions of their own experiences in secondary school were found in the reflective journals, deterministic reasoning that persists into teacher preparation may nevertheless be seeded by PSTs' own schooling. It is recommended that: (i) the sequence be rebalanced so that molecular mechanisms and regulation precede or interleave with classical inheritance; and (ii) genetic essentialism be explicitly countered in human-genetics units by emphasising polygenic, probabilistic, and environmental influences. This aligns with calls to reduce Mendelian dominance in school curricula (Johnston 2023; McEwen, Gericke, and Thörne 2025) and to address how teaching can inadvertently amplify determinism/essentialism (Donovan 2022; Thörne, Gericke, and McEwen 2025).

Implications for teacher education

The IFES rubric and heatmap analysis developed in this study offer a context-specific lens for exploring how senior pre-service biology teachers (PSTs) conceptualise genetic information flow, exchange, and storage. Although the findings cannot be generalised beyond this small sample, they highlight persistent misconceptions and reasoning patterns that may inform instructional improvements within similar teacher education contexts. Based on the patterns observed in the reflective journals, the following context-driven implications are proposed:

- Aligned assessment tools based on the IFES framework may offer teacher educators a structured means of identifying and monitoring PSTs' conceptual understanding in genetics. The rubric developed in this study has potential as a formative assessment tool to pinpoint specific areas of difficulty and inform targeted instruction. Nonetheless, further validation across varied educational settings is needed before broader adoption.
- Reflective journaling showed promise as a formative assessment tool, offering insights into how PSTs' conceptual understanding develops over time. This method allowed for the identification of persistent misconceptions and may be a useful supplement to traditional assessments in genetics-focused courses.

Future research

Building on this exploratory work, multi-site replication, development of a rubric-derived questionnaire, mixed-methods designs integrating performance tasks, and longitudinal tracking across cohorts are planned and recommended.

Limitations

While reflective journals offered rich insights into PSTs' conceptual understanding, relying solely on written reflections presents certain limitations. Participants with stronger writing abilities may have been better able to articulate their ideas and misconceptions, whereas others may have struggled to express their thinking clearly, potentially masking underlying conceptual difficulties. Classroom-level social influences cannot be fully excluded despite individual submissions. Additionally, the study was conducted within a specific institutional and curricular context, focusing on a small, convenience sample of senior biology PSTs who had already completed coursework in genetics. As such, the findings may not generalise to earlier-stage teacher candidates or to populations in different cultural or educational settings. Moreover, the study captures a limited timeframe – spanning eight weeks – which provides only a snapshot of conceptual development. PSTs' understandings are likely to evolve through continued coursework, practicum experiences or professional development, underscoring the need for longitudinal research to track changes in understanding over time. These limitations reinforce the study's transferability, not generalisability, and motivate the future research agenda above.

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Appendix. Topic-related questions to be discussed in the 8th week of the course

(Lesson 1)

Draw a model showing the relationship between DNA – gene – chromosome, taking into account what you have learned in class.

(Lesson 2)

What is the distinctive advantage of DNA as genetic material? What would happen if RNA, instead of DNA, were the controlling molecule in humans and other complex organisms?

(Lesson 3)

Why do you think DNA is sometimes called the genetic code?

(Lesson 4)

What can you say about the change in chromosome potential in cells undergoing mitosis? Why is this mechanism important for the continuity of life?

(Lesson 5)

What is the connection between the proteins we take in with food and the proteins present in our cells? Can we use the proteins we take in directly? Can we incorporate them into our structure? What must happen for them to be incorporated or functionally used?

(Lesson 6)

Why are heterozygous individuals diseased in dominant disorders, whereas heterozygous individuals are not diseased in recessive disorders? Explain. Sometimes certain traits do not appear in one generation but may appear in later generations, i.e. they may ‘skip’ a generation. What do you think is the reason for this? Studies on identical twins reveal which aspect of the genotype – phenotype relationship? Explain.

(Lesson 7)

Explain the statement: ‘The closer two individuals are related, the more similar their genomes are’. Under what conditions is natural selection possible? Explain.