Reform and Practice of Bioinformatics Experimental Teaching Based on Project-based Learning: A Case Study of "Influenza Virus Analysis"

Shuying FU[1], **Linqi HUANG**[1], **Yu MEN**[1], **Wenwu TANG**[2], **Meiying FENG**[1]*

1. School of Life Sciences, Zhaoqing University, Zhaoqing 526061, China; 2. Principal's Office, Zhaoqing Industrial and Trade School, Zhaoqing 526060, China

Abstract To meet the need for cultivating application-oriented talents in local universities, this study introduced a project-based learning approach into the reform of bioinformatics experimental teaching. The course was structured around a project titled "Influenza Virus Analysis", comprising four progressive modules: database utilization and information retrieval, sequence alignment and phylogenetic analysis, functional and structural prediction, and omics data analysis. These modules were integrated into a coherent research workflow that connected fragmented knowledge and technical skills. During implementation, flipped classroom and group collaboration methods were employed, alongside the establishment of a diversified assessment system emphasizing process evaluation. Teaching practice indicates that the reform effectively enhances students' professional application skills, learning experience, and scientific literacy, facilitating a shift from "tool operation" to "problem-solving" capabilities. This study provides a reference model for the reform of bioinformatics experimental teaching in local universities.

Key words Bioinformatics experiment; Project-based learning; Teaching reform; Teaching practice; Influenza virus

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With the rapid development of life science research, bioinformatics, as an interdisciplinary field integrating biology, computer science, and mathematics, has become an important link between experimental data and scientific discovery. The core task of bioinformatics is to develop and apply computational methods to extract useful information from massive biological data and uncover underlying biological patterns[1]. At the fundamental research level, bioinformatics facilitates the integration and functional annotation of multidimensional data, from genome sequences to protein structures. At the applied level, it plays a key role in medicine, biotechnology, agriculture, and environmental science[2]. In particular, in precision medicine and drug discovery, computational models and biomarker screening significantly enhance target identification and the development of individualized treatment strategies[3]. In recent years, with the emergence of advanced technologies such as single-cell sequencing and spatial transcriptomics, combined with deep integration of artificial intelligence, bioinformatics is driving life science research toward higher resolution and greater systematic understanding[4]. As a result, the ability to perform bioinformatics analysis has become an essential competency for students in biological sciences[5].

For local universities, cultivating application-oriented bioinformatics talents who possess both practical analytical skills and a certain level of research thinking is crucial for improving students' core competitiveness and supporting regional scientific research innovation and industrial transformation[6]. However, due to limitations in computing resources, experimental conditions, and curriculum design, the bioinformatics experimental teaching in many local universities remains at the level of tool operation and lacks systematic training[7-8]. Such an "instruction-driven" teaching model often leads students to follow procedures step-by-step without understanding the underlying logic or appropriate contexts of the analytical methods. Consequently, they struggle to apply what they have learned. Moreover, traditional experimental courses usually organize content around software functions rather than scientific questions, leaving students with fragmented skills and little sense of a complete research workflow. This hinders the development of systematic research thinking and comprehensive analytical ability, weakening the course's support for the goal of cultivating application-oriented talents.

To address these issues, it is essential to explore teaching models that fit the practical context of local universities while fostering both systematic thinking and practical competence. Project-based learning (PBL), which uses real scientific research problems to drive learning through project implementation, has achieved strong outcomes in engineering, medicine, and computer science education[9-10]. Introducing the PBL model into the bioinformatics experimental course can help overcome the fragmentation and passivity of traditional instruction. It can guide students in developing a scientific research logic chain from problem identification to data analysis and then to conclusions through hands-on tasks. Based on this idea, the present study integrated the PBL approach into the experimental teaching of the biotechnology major at Zhaoqing University. By developing a project centered on "influenza virus analysis", we established a problem-driven, ability-oriented teaching framework. This framework aims to provide a

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Shuying FU (1992 -), female, P. R. China, PhD, lecturer, devoted to research on bioinformatics and metabolic diseases.

* Corresponding author.

practical and transferable strategy for reforming bioinformatics experimental teaching, thereby supporting the cultivation of application-oriented talents at local universities.

Teaching Reform Framework and Design Principles

This teaching reform focuses on enhancing students' applied abilities in bioinformatics. It follows a progressive sequence of " task-driven learning, skill acquisition, problem solving, and reflective improvement" and systematically restructures the experimental teaching system. The overall reform strategy includes three key components. First, projects act as the main thread, integrating scattered knowledge points and analytical methods into a complete scientific task, allowing students to understand the internal connections of knowledge through coherent practice. Second, teaching approaches such as flipped classrooms and group collaboration are incorporated to strengthen self-directed learning and teamwork, creating an open and interactive learning environment[11]. Third, a diversified assessment system centered on process evaluation is established, guiding students to transfer what they learn in class to practical application scenarios such as graduation projects and research competitions.

In terms of design principles, the reform is driven by real scientific questions, situating experimental content within concrete and coherent biological scenarios. This approach encourages students to actively construct knowledge systems while addressing authentic research problems. To address the disconnect between tool-based teaching and problem analysis often found in traditional teaching, the course adopts "influenza virus analysis" as a central theme and builds a continuous task chain. Students are guided to develop systematic thinking as they work through data acquisition, sequence alignment, structure prediction, and omics data analysis. This process deepens their understanding of the applicability and limitations of various analytical methods and fosters the ability to apply them comprehensively in solving biological problems.

Design of Teaching Reform Content

Based on the above principles, the teaching team integrated the experimental content into a comprehensive project centered on "influenza virus analysis" (Table 1). This topic provides abundant publicly accessible data resources and moderate computational requirements. It not only reflects real scientific research scenarios in virology and public health, but also matches the teaching conditions and student backgrounds in most local universities. On this basis, the course was organized into four stages, forming a progressive training sequence that gradually develops students' knowledge, analytical skills, and research thinking. Each stage is guided by a core scientific question, aligned with clear learning objectives, and supported by targeted tools and databases.

Table 1 Design of the *Bioinformatics Experiment* course based on influenza virus analysis

Stage	Key questions	Main tasks	Databases & tools
Stage 1: Database utilization and acquisition of basic viral information	What are the structural features of influenza viruses, and which strains are currently circulating in the local region?	1. Retrieve and download influenza virus genome sequences and their annotation information. 2. Identify and extract nucleotide and amino acid sequences of key virulence genes. 3. Search for and identify prevalent viral strains in the local region.	Databases: PubMed, Genome, GenBank, Gene, Protein, UniProt, ViralZone; Tools: NCBI Entrez Programming Utilities.
Stage 2: Sequence alignment and evolutionary analysis	Why does the influenza vaccine need to be updated regularly?	1. Analyze variations in key influenza virus genes based on sequence alignment. 2. Identify mutation hotspots and conserved regions within major antigenic sites. 3. Construct a phylogenetic tree to infer evolutionary relationships of influenza viruses.	Alignment Tools: EMBL-EBI Needle/Water, BLAST, Clustal Omega; Evolutionary Analysis: MEGA; Visualization: Weblogo, iTOL.
Stage 3: Functional and structural prediction	Do gene mutations in the influenza virus affect protein structure and function?	1. Perform sequence translation and predict protein tertiary structures using homology modeling and AI-based approaches. 2. Compare the structural differences between wild-type and mutant proteins. 3. Analyze the interaction network and perform functional annotation of key influenza virus genes.	Translation & Modeling: Expasy, AlphaFold2, SWISS-MODEL; Visualization & Analysis: PyMOL; Interaction Network: STRING database.
Stage 4: Omics data analysis	How to decipher the genomic information of newly emerged influenza virus strains?	1. Perform quality assessment and filtering of raw sequencing data. 2. Conduct *de novo* genome assembly and evaluate assembly quality. 3. Execute functional annotation and validation of the assembled viral genome.	QC & Assembly: Fastp, SPAdes; Visualization: IGV; Annotation: Prokka, NCBI VADR.

Stage 1: Database utilization and acquisition of basic viral information. Focusing on the question, "What are the structural features of influenza viruses, and which strains are currently circulating in the local region?", students learn to use core databases such as PubMed, Genome, GenBank, and ViralZone. They practice retrieving genome sequences, annotation information, and

key virulence gene and protein sequence data. To ensure that students can transfer these skills, instructors provide structured search tasks, such as locating specific segments of the hemagglutinin or neuraminidase genes and extracting related functional annotations. By analyzing gene sequences from locally circulating strains, students develop a systematic understanding of the research subject, including subtype classification, host range, and basic pathogenic features. Meanwhile, they begin to build the ability to refine scientific questions, select appropriate databases, and efficiently obtain professional information, laying the groundwork for subsequent stages.

Stage 2: Sequence alignment and evolutionary analysis. Guided by the central question, "Why does the influenza vaccine need to be updated regularly?", students use BLAST, Clustal Omega, and other tools to perform sequence alignment, identify mutation hotspots and conserved regions of antigenic sites, and analyze variations in key influenza virus genes. On this basis, they construct phylogenetic trees using MEGA to infer evolutionary relationships among strains and to understand the molecular mechanisms of antigenic drift and its influence on vaccine updates. Mutation trends in strains such as H1N1 and H3N2 are incorporated as case studies, helping students appreciate how bioinformatics analysis supports surveillance and decision-making in public health. Through this stage, students not only become familiar with basic alignment and phylogenetic tools but also learn to interpret evolutionary trees, connect sequence variation with epidemiological phenomena, and formulate evidence-based explanations for vaccine updates.

Stage 3: Functional and structural prediction. Addressing the question, "Do gene mutations in the influenza virus affect protein structure and function?", students use Expasy, SWISS-MODEL, and AlphaFold2 to perform protein structure prediction and modeling. PyMOL is then applied for three-dimensional visualization, allowing students to compare structural differences between wild-type and mutant proteins, with particular attention to changes in known functional or antigenic regions. Students also use the STRING database to construct protein interaction networks and explore the potential functional consequences of key amino acid substitutions. This stage trains students to establish cross-level analytical thinking that links "sequence variation, structural change, and functional impact", providing a foundation for understanding complex biological phenomena.

Stage 4: Omics data analysis. Centered on the question, "How to decipher the genomic information of newly emerged influenza virus strains?", students conduct a full workflow analysis of the latest influenza genome data. They follow the pipeline from raw data quality control and de novo assembly to genome annotation and result visualization. Through hands-on use of tools such as Fastp, SPAdes, Prokka, and NCBI VADR, they complete quality filtering, genome assembly, functional annotation, and validation. IGV is then used to visualize read mapping and assembly quality, enabling students to critically evaluate their own analysis results. Where possible, different parameter settings or datasets are compared to highlight the impact of analytical choices on final outcomes. This process not only enables students to systematically master key omics data analysis techniques but also, through functional annotation and visualization, trains their ability to extract biological insights from sequence features. By the end of this stage, students are expected to propose preliminary biological hypotheses about new strains based on their genomic characteristics, thereby comprehensively enhancing their data analysis, result interpretation, and scientific reporting skills.

Implementation Process of Teaching Reform

During the implementation of the teaching reform, a learner-centered principle was fully applied, emphasizing a dynamic balance between teacher guidance and student inquiry. Teachers acted as task designers, technical supporters, and process supervisors. They were responsible for constructing the framework of scientific problems, selecting and organizing data resources, and providing key technical guidance at critical steps of the project. Students, in turn, worked in collaborative groups to carry out data analysis, advance project progress, and present interim and final results around real scientific tasks. Through this process, they gradually completed knowledge construction and skill enhancement within an authentic, project-based learning environment.

In terms of instructional organization, the flipped classroom model was integrated, and the overall teaching process was restructured. Basic knowledge delivery was moved to pre-class activities. Students were required to independently complete theoretical learning and basic tool operation exercises based on reading materials, micro-lectures, and demonstration videos provided by the teacher. Short online quizzes and pre-class assignments were used to check learning progress and identify common difficulties. Classroom time was then mainly reserved for project advancement and problem-solving. At the beginning of each class, the teacher briefly summarized key concepts and addressed frequent mistakes identified from pre-class work. This was followed by group-based experimental operations and data analysis, during which the teacher circulated among groups to provide on-demand, individualized support. To strengthen interaction and reflection, each group was required to deliver periodic progress reports in either written or oral form. These reports included problem definition, data processing steps, preliminary results, and encountered difficulties. Based on these presentations, the teacher offered targeted feedback, guided students in refining their analytical strategies, and encouraged them to compare different approaches across groups. Peer questioning and group discussion were also incorporated to help students articulate their thinking, defend their methodological choices, and learn from one another. This interactive teaching model effectively stimulated students' initiative and problem awareness, and helped promote the transfer of knowledge to new contexts as well as the internalization of analytical skills.

To comprehensively assess learning outcomes, the course established a diversified evaluation system with a strong emphasis on process assessment. Evaluation was no longer limited to the accuracy of operations or the correctness of final answers. Instead, it comprehensively examined students' abilities in problem analysis, method selection, logical reasoning, data interpretation, and result presentation. Process assessment ran throughout the entire teaching period and covered multiple dimensions, including classroom participation, quality and timeliness of stage task completion, documentation of analytical procedures, and teamwork performance. Clear rubrics were provided in advance to make assessment criteria transparent and to guide students' self-monitoring and peer evaluation. The final assessment focused on the scientific rigor, innovation, and practical value of the project report and final presentation. Students were expected to integrate methods and results from all stages into a coherent research narrative, explain the biological significance of their findings, and reflect on the limitations of their analyses. This combination of formative and summative evaluation enabled dynamic monitoring of the whole learning process and supported a more objective and comprehensive judgment of student performance.

In addition, the teaching team developed a multi-dimensional support system to ensure smooth implementation of the reform. This system included structured teaching materials, step-by-step task guides, demonstration datasets of varying difficulty, and standardized templates for recording and reporting analytical procedures. An online Q&A platform and discussion forum were also set up to provide timely responses to technical problems and to facilitate out-of-class communication between teachers and students. At the end of the project, each group was required to integrate results from each stage into a final, research-style presentation and written report. This culminating task further enhanced students' research logic and academic expression abilities, and helped form a complete teaching loop from knowledge input and guided practice to independent application and capability output.

Outcomes of the Teaching Reform

The teaching reform has significantly improved students' professional application skills, learning experience, and research literacy. Overall, students not only completed the required experimental tasks but also showed a stronger capacity to transfer what they had learned to new problems and independent projects.

In terms of professional application skills, students have gradually mastered the full workflow of bioinformatics analysis, including data acquisition, sequence alignment, functional prediction, and omics data processing. They are able to choose appropriate tools according to the characteristics of the data and the nature of the problem, rather than relying mechanically on fixed procedures. In project practice, most students can independently design basic analysis pipelines, adjust parameters based on intermediate results, and provide reasonable biological explanations for their findings. This indicates a clear shift from "operating tools" to "applying knowledge", and from passive execution to active problem solving. Some students further applied these skills in their graduation projects or faculty-led research, taking responsibility for data processing and preliminary result interpretation.

In terms of learning experience, the teaching reform has greatly increased student participation and sense of achievement. Classroom observations and course evaluations show that students are more willing to ask questions, share experiences, and discuss different analysis strategies. Feedback from students indicates that they find the course "rich in content", "highly practical", and "very rewarding", with many suggesting the introduction of advanced follow-up modules focusing on more complex datasets or disease models. Under the flipped classroom and group collaboration mechanisms, students experienced clear role division and effective teamwork, such as taking turns acting as data manager, method designer, or result presenter. Their awareness of self-directed learning has significantly increased, as reflected in the time they spent exploring additional tools and reading background literature beyond the minimum course requirements. A number of students continued to use the methods learned in the course to assist with experimental data processing or participate in faculty research after the course ended, which demonstrates solid and sustainable knowledge transfer to practice.

Regarding research literacy, the course has established a clear pathway from classroom learning to research-oriented practice, effectively enhancing students' data literacy and academic communication skills. Through repeated training in problem formulation, method selection, and result interpretation, students learned to structure their analysis around scientific questions rather than isolated operations. In project reports and presentations, many students demonstrated improved abilities in organizing logical arguments, using figures and tables to support claims, and clearly explaining methodological limitations. Several students showed outstanding performance in research projects and innovation training programs, being able to complete bioinformatics analysis tasks with minimal supervision and to engage in meaningful discussion of biological implications with supervisors. Some student teams won awards in provincial competitions such as the "Challenge Cup", where their work was commended for the rational design of analytical pipelines and the clarity of data interpretation. These outcomes fully demonstrate the practical effectiveness of the course reform in cultivating research application and innovation capabilities, and suggest that the PBL-based model has strong potential for supporting students' long-term academic and professional development.

Conclusions

This study, based on the PBL model, constructed a reform framework for bioinformatics experimental teaching centered on the "Influenza Virus Analysis" project, emphasizing the cultivation of students' applied abilities. Through project-driven and problem-oriented teaching design, knowledge transfer, skill training, and

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industry. In the future, with further advancements in agricultural technology and increasing consumer attention to food safety, we should strengthen the innovation and application of yam cultivation techniques. Particularly, breakthroughs are needed in areas such as intelligent management, precision fertilization, and green pest control to drive the yam industry toward higher levels of development. Meanwhile, we should also enhance exchanges and cooperation with other countries and regions to jointly promote the prosperity and development of the global yam industry.

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research thinking were organically integrated, driving a shift in the curriculum from basic tool operation to comprehensive practical ability development. Teaching practice has demonstrated that this model effectively enhances students' bioinformatics analysis skills and practical application capabilities, showing strong adaptability and potential for wider implementation in local universities. Going forward, the teaching team will continue to refine its focus on applied competencies, diversify course content, and enhance teaching methods. The ultimate goal is to establish a sustainable and replicable teaching model for local universities to cultivate bioinformatics talents with comprehensive applied capabilities.

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