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Incorporating Genome Projects and Comparative Genomics into Problem-Based Learning for Future Biomedical Scientists

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ABSTRACT

Problem-based learning (PBL) offers a student-centered framework for cultivating critical thinking, collaboration, and inquiry in biomedical education. Integrating genome projects and comparative genomics into PBL enhances learning by providing authentic, data-rich scenarios that bridge theory and practice. Flagship initiatives such as the Human Genome Project, the 1000 Genomes Project, and the UK Biobank offer extensive datasets for exploring genetic variation, evolutionary conservation, and cross-species analyses. These resources allow students to formulate hypotheses, evaluate evidence, and engage in data-driven reasoning, while reinforcing ethical, legal, and social considerations surrounding genomic data. Incorporating real-world genomic datasets into case-based scenarios promotes analytical literacy, computational competence, and understanding of biomedical research. Such integration prepares future biomedical scientists to navigate genomics-informed research, clinical applications, and data stewardship, equipping them with the skills and frameworks needed for the evolving landscape of precision medicine and genomics-based inquiry.

Keywords: *problem-based learning, PBL, genome projects, comparative genomics, biomedical education, Human Genome Project, 1000 Genomes Project, UK Biobank, data literacy, critical thinking, ethics in genomics, cross-species analysis, case-based learning.*

INTRODUCTION

Problem-based learning (PBL) is a student-centered pedagogy that emphasizes inquiry, collaboration, and real-world problem solving (D. Shaffer et al., 2010). Cases are guided by significant instructor prompts that initiate an investigative process and invite students to join a discourse involving fundamental concepts

(Pucker et al., 2019). PBL cultivates awareness of a wider skill set that must be acquired upon graduation and the connections among them. Through genome-informed scenarios, students can apply critical thinking beyond problems that strictly adhere to a particular discipline or a knowledge taxonomy. By enforcing compliance with data access policies and providing mechanisms for transparent attribution, educators can guide students in the responsible use of publicly available genomic datasets. Selected genome projects and comparative genomics concepts align well with the PBL framework and contribute to evidence-based classification of variants in genomic, transcriptomic, and proteomic analyses.

Foundations of problem-based learning in biomedical education

Problem-based learning (PBL) emphasizes student-centered inquiry through realistic problems instead of predetermined hierarchical learning objectives. PBL groups investigate diverse scenarios at varying depths of content knowledge, fostering critical thinking, self-directed study, team collaboration, and adult learning approaches (Gair et al., 2018). Examination and diagrammatic representation of the problem ground the inquiry, shaping knowledge acquisition and guiding the generation of pertinent follow-up questions. A facilitator engages PBL groups through a series of strategic vignettes that throttle the inquiry, maintaining productivity without confounding autonomy. The educator's dual role as both teaching instructor and learning resource is paramount during the PBL process (Pérez-Losada et al., 2020).

Two foundational learning theories further endorse the integration of genome projects and comparative genomics into PBL tasks: social learning theory and cognitive load theory. Social learning emphasises learning from others through observation and interaction, stressing the influence of peers, instructors, and societal factors on knowledge assimilation. Cross-institutional collaboration with experts and improved rehearsal of teacher-student interactions thus foster pedagogical competency and deepen understanding of educational content and practices, creating a positive cycle of knowledge transfer that students find stimulating, motivating, and relevant.

Genome projects: scope, data resources, and educational relevance

The first publication in the Human Genome Project (HGP), a twenty-five-year international scientific endeavor aimed at determining the sequence of the human genome, appeared in 1990. The agglomeration of ongoing genome sequencing efforts, whether termed “genome projects,” “genome sequencing endeavors,” or simply “genomics,” has attracted intensifying public and scientific interest. The incorporation of genome projects into educational contexts is made valid by their widespread values: novel datasets and queries to enable evidence evaluation, challenging biological concepts to investigate, essential biomedical domain relevance, and the demand for effective reasoning to accommodate intricate, dispersed information while scrutinizing the burgeoning trove. The accessibility and ubiquity of genomic data continue to flourish, fostering the hasty adoption of training programs to cultivate topical skills in the increasing number of domains fed by genomic data: discovery of novel immunity genes, the affirmation of homologies, the in-silico inference of transmutation or transfer events, and cross-species study of the gametophytic pathway. Such information illustrates the pioneering, ruling relevance of genome projects to educational configurations at diverse stages.

Flagship genome projects-namely, the Human Genome Project, the 1,000 Genomes Project, and the Cancer Genome Atlas-satisfy the preceding scrutiny. The number of species (ninety-eight), sequences available, queries permitted, and varied inquiries proffered further complement the educational significance of the Genomic Encyclopedia of Bacteria and Archaea project. A genomic dataset encompassed, for example, the complete nucleotide sequence of a human sample produced by the 1,000 Genomes Project. Access to raw sequences deposited into the International Nucleotide Sequence Database Collaboration remains unrestricted, with detailed conditions and appropriate attributions delineated; provenance and versioning information appear readily and continually updated. The seventh edition from eighteen genome sequences, comprising specified individuals and populations, tempts systematic exploration of variant data

accumulated over the years. Genome project families impart especially powerful insights into the field of comparative genomics—a didactic foundation that nourishes the genesis of educational scenarios. Genomics-borne concepts such as orthology, conservation, and synteny emerge as vital underpinning notions, alongside the observable consideration of the standing data; the inspection may reside within phylogenetic scrutiny, permeating cross-species examination that stimulates informed conjectures regarding attributes or events common to organisms examined (D. Shaffer et al., 2010) [table 1].

Table 1: Genome Projects and Comparative Genomics in Biomedical Education

Concept / Project	Key Features	Educational Relevance / Applications
Human Genome Project (HGP)	Reference sequence of human genome; annotations; mitochondrial genome; ongoing refinements	Provides datasets for variant analysis, functional annotation, and evidence-based problem-solving
1000 Genomes Project (1000GP)	Focus on human genomic variation; population structure; variant calls	Enables cross-population studies, genotype-phenotype association analysis, and PBL exercises on diversity
UK Biobank (UKBB)	Genomic, phenotypic, environmental, and EHR-linked data on 500,000 volunteers	Case studies in genome-informed medicine; supports bioinformatics workflows and critical thinking
Comparative Genomics	Orthology, paralogy, sequence conservation, synteny; cross-species comparisons	Facilitates hypothesis generation, critical reasoning, evolutionary insights, and PBL scenarios
Data Resources & Access	International Nucleotide Sequence Database Collaboration; provenance and versioning information; open-access sequences	Teaches responsible data use, reproducibility, and ethical data handling

Major genome projects and their pedagogical implications

Three genome projects - the Human Genome Project (HGP), the 1000 Genomes Project (1000GP), and the UK Biobank (UKBB) - exemplify contemporary datasets and illustrate several pedagogical implications. The HGP, supervised by the US Department of Energy and the National Institutes of Health, generated a reference sequence of the human genome and extensive processing tools. Although the initial version dates to April 2003, the project continues to refine and augment materials (D. Shaffer et al., 2010). The Human Genome Assembly and Annotation Hub provides sequences, annotations, and variant data for multiple genomes, alongside a sequence of the human mitochondrial genome. The 1000GP focused on human genomic variation. Sequencing data, variant calls, and related data on population structure and history are available. The UKBB offers extensive genomic, phenotypic, environmental, and linked electronic health record data on 500,000 volunteers, released under a system that classifies data sensitivity according to planned analysis. Large-scale genomic investigation of traits, diseases, common genetic variation, and gene function is actively ongoing. Such projects hold educational relevance, including for problem-based learning curricula. Extensive genome-wide association study data helps students generate and evaluate scientific arguments regarding genotype–phenotype associations based on open-access data. Further pedagogical aspects include policies governing data access, resource versioning, and provenance.

Comparative genomics as a pedagogical tool

Genomic sequence data and processing tools generated by large-scale sequencing projects provide accessible entry points and exemplary materials for implementing problem-based learning (PBL) within undergraduate biomedical education. Genome sequencing initiatives have produced extensive and readily shareable datasets, allowing for tasks grounded in authentic research questions and encompassing key life sciences disciplines. Furthermore, pedagogy informed by genome projects engages anticipated competencies in critical thinking, data literacy, and analytical reasoning, which are essential for professional proficiency in the biomedical sciences and expected by regulatory agencies in higher education.

The scope of genome sequencing initiatives is therefore considered, together with the types of data they yield and specific educational opportunities that arise. Major genome-sequencing projects classify into three broad tiers: flagship projects that integrate sequencing and assembly of whole genomes, organism-centric projects that generate sequence information or reference genomes within particular taxonomic groups, and single-species studies that substantively advance the state of knowledge for previously sequenced species. Of universal relevance across case studies based on different organismal groups, concepts and terminology associated with comparative genomics constitute an additional PBL asset. The distinction between orthologous and paralogous genes, evolutionary pressure manifested in sequence conservation, synteny conservation, and analytical approaches exploiting these ideas, readily lend themselves to the formulation of learning scenarios. Such principles guide the design of tasks that require students to conduct cross-species analyses, support hypothesis generation, practise critical reasoning, and construct evidence-based arguments. (Prost et al., 2020)

Alignment of genome data with problem-based learning objectives

Biomedicine is data-centric, knowledge-driven, and collaborative. Biomedical education should cultivate higher-order reasoning while embedding the discipline's fundamental concepts and practices. Classroom-centred approaches often fall short of these targets. Problem-based learning, student-centered inquiry where case studies anchor learning, profoundly reorients educational experiences toward these ideals. Integration of genome projects and comparative genomics into PBL enhances the educational experience for present and future biomedical scientists in several ways.

Critical thinking and data literacy should permeate genomics education. Although the broad definition of critical thinking encompasses diverse skills, the analytic dimension—"the ability to discern, clarify, and evaluate evidence"—is particularly relevant (Lynn Petrie & Xie, 2021). Derived from a refined hierarchy of evidence types and uncertainty handling (Pérez-Losada et al., 2020), a set of cognate tasks can anchor learning in PBL. Inquiring into variant data stored in public databases, for example, and gauging evidence for their involvement in human disease aligns with both the formal agenda and the theme of genome-informed education [table 2].

Table 2: Problem-Based Learning (PBL) Frameworks in Genomics Education

PBL Aspect	Description	Implementation / Pedagogical Benefits
Student-Centered Inquiry	Students tackle real-world, ill-structured genomic problems	Develops critical thinking, self-directed learning, and collaborative problem-solving
Critical Thinking & Data Literacy	Evaluating evidence, analyzing genome data, identifying conserved regions	Enhances analytical reasoning, hypothesis formulation, and cross-species comparison skills
Ethical, Legal, and Social Implications (ELSI)	Privacy, consent, data-sharing, societal attitudes toward genomics	Prepares students for responsible research practices and professional decision-making

PBL Models	1) Facilitated Case Study 2) Inquiry-Driven 3) Team-Based	Supports iterative learning, collaboration, independent exploration, and scaffolded guidance
Integration of Real-World Datasets	Use of genome-scale data for case studies	Connects theory to authentic scientific problems; reinforces bioinformatics, statistical, and reasoning skills
Curriculum Design	Modular cases aligned with research, data analysis workflows, and cross-species genomics	Prepares biomedical students for research, clinical, or industry roles; fosters constructivist learning

Real-world datasets can elevate the relevance of case-based scenarios while grounding reasoning in available evidence. A sequence-variant fly case that interrogates both phenotypic outcomes and candidate mechanism illustrates the richness of genome data and the capacity of cross-species analysis to support hypothesis generation. Such scenarios deepen exposure to the accompanying analytical challenges. The ethical, legal, and social implications (ELSI) associated with genome data represent an equally vital aspect of genomics literacy across diverse educational stages. Educational material can frame human privacy, consent, and data-sharing considerations within a genome-informed context. In the light of genome projects, comparative genomics emerges not only as a research area in its own right, but also as a crucial educational tool for guiding the development of genome-informed PBL cases. Three core concepts—orthology, conservation, and synteny—map directly onto learning objectives articulated in the pedagogical blueprint.

Mindful of the capacity gaps prevalent across the target audience, attention to data stewardship, reproducibility, and ethical use emerges as a likely common ground for the integration of any new pedagogical materials. The framing of genome-informed cases can thus encompass these topics in their own right.

Critical thinking and data literacy in genomics

Advancements in interdisciplinary fields reveal the importance of critical assessment, prioritization, and pattern recognition. A learner oriented towards biomedical science may pursue a diverse array of subjects; nonetheless, genomic information is now used in discussions related to nutrition, addiction, population migrations, physical or psychological health determinants, and ancestry. This raises fundamental questions: what causal impacts do such substances exert on genome, transcriptome, and proteome responses? Which mechanisms prompt reversed or diverging responses upon repeated exposures, and how is prior exposure recorded? Addressing such inquiries necessitates knowledge of fundamental biology concepts throughout the individual's education, wherein genomic projects constitute a vital information source. Proficiency in genome analysis facilitates formulation of plausible hypotheses and critiques of other explanatory models. Yet students find genomic data daunting. Reinforcement of critical assessment emerges as an educational proponent; only via comprehensive knowledge can information assimilation proceed.

The preceding section identified principal genomic acquisition processes. Investigating class-set genomes, students can explore these procurement modalities and their underlying motivations. Genome scale, modification and analytical convenience, sample collection feasibility, derivation from established repositories, and harmonization with species transcending the human domain render the human genome a pedagogically favorable target. The Internet-disseminated bacteriophage T7 prompt similarly emerges. Students may assess the respective illustrative roles, evaluation of integrated technical literature, and the precision of individual comprehension, subsequently determining the availability of conserved genome regions across class-set organisms. Anticipated variations in annotated explanatory documentation, and

consultation of distinct nomenclature on independent repos, emphasize annotation source influence on information compilation. (S Boguski et al., 2013)

Integrating real-world datasets into case-based scenarios

Problem-based learning encourages inquiry-based learning by presenting students with real-world cases and problems to solve. It promotes independent thinking, motivates students by connecting disciplines to society's needs, and develops key skills for research and careers. Researchers from the Faculty of Medicine at Imperial College London developed curriculum modules based on this approach to improve biomedical education, starting with a project on genome-scale datasets. Genome-wide projects and comparative genomics facilitate practical case-based learning in the life sciences. Curriculum aligns case studies with the wider research landscape, supporting modular bioinformatic workflows that lower the entry barrier to digital genomics. Earlier biochemistry feedback indicates that such cases stimulate intelligent and relevant scientific discussion (Victoria Schneider & C. Jimenez, 2012).

Ethical, legal, and social implications in genomics education

The rise of personal genomics raises complex ethical, legal, and social implications, which should also form an integral component of undergraduate education in genomics (S Boguski et al., 2013). Such issues include questions of privacy, informed consent, and data sharing, all of which may strongly influence attitudes towards the incorporation of personal genome or similar data in biomedical sciences curricula. As prospective biomedical scientists, students need to examine these implications for their eventual professional practice. To facilitate this discussion, instructors could pose questions regarding the implications of retrieving human sequences through large-scale genome analysis, the desirability of incorporating such data into genomics course content, and the ethical dilemmas surrounding the use of data generated from students' own sequences.

Curriculum design and instructional strategies

Curricula characterised by problem-based learning (PBL) succeed in promoting scientific inquiry and developing analytical skills that are essential for the field of genomics. Three models of PBL - facilitated, inquiry-driven, and team-based – provide complementary conceptual tools for PBL design. A facilitated case study model invites students to explore genome sequences from various bacterial species for clues about genome reduction after life-cycle transition (Pérez-Losada et al., 2020) ; an inquiry-driven flavour engages students in comparative genomics from the outset (Martins et al., 2020) ; and a team-driven variant shifts the focus to collaborative multi-institutional genome analysis (Mierdel & X. Bogner, 2020). Each model corresponds to the PBL pedagogical framework of ill-structured problems that lack unique solutions; genome-informed scenarios meet the criteria.

Learning analytics can monitor PBL emergence under academic freedom, shaping an indicative roadmap for progression and institutional programme maturation. Genomic literacy and problem-solving skills are reflective of the biomedical sciences readiness domain; provisional measures by completion year and discipline track advancement into research, clinical, or industry sectors. Quantification of multiple facets enables dashboards for individual or aggregate assessment.

Frameworks for problem-based learning in genomics

Various frameworks have been proposed for implementing problem-based learning in the genomics context. The PBL literature distinguishes between different models. The five-phase facilitative PBL model, described by Savin-Baden (Pérez-Losada et al., 2020) , comprises the phases of clarifying the problem, exploring and researching the problem, synthesising findings, and evaluating the problem-solving process. In inquiry-driven PBL, as characterised by Huda et al. (2021), groups encounter an ill-structured problem, select questions to explore, conduct investigations to seek answers, and engage in cyclic reporting and discussions. Though flexible, these inquiry-driven frameworks may be cumbersome to apply. By contrast,

the team-based learning model (Martins et al., 2020) emphasises peer-to-peer interaction and team preparation over traditional instructor-led facilitation; team readiness assurance testing occurs via individual and group readiness assurance tests; and content delivery follows only after readiness assurance to ensure students engage with materials independently in advance. These models could structure both entirely genomics-focused case studies and cases revolving around genome-related material.

Although individual work is often preferred in PBL, the incorporation of genomic data-rich team assignments could promote critical analytical skills and constructivist approaches and create an authentic, accessible starting point for adopting PBL. Several approaches could further assist instructors in applied STEM domains. Cross-group feedback sessions enable diverse perspectives, and instructors can guide remaining queries across multiple discussion rounds to bolster the iterative generation of coherent proposals. In situations lacking both manufacturing methodologies and in-depth analytical training, colleagues with objective expertise could offer support. Individual visualisation could allow learners to explore and validate their work prior to collective presentation, sustaining the dual, iterative nature of exploration and articulation.

Learning analytics and assessment in genome-informed PBL

Developing a genome-informed problem-based learning (PBL) curriculum entails assessing learning outcomes, integrating formative assessments and rubrics, and mapping curricular milestones to track student progress. Evidence suggests that educational rigor and expectations are frequently misaligned, contributing to elevated dropout rates and delays in degree completion (Jean Lim et al., 2009). Formative assessments, which gauge progress without contributing to final grades, afford opportunities for pedagogical refinement and curriculum optimization, supporting the data-driven enhancement of teaching practice. Accordingly, learning analytics and assessment-formative, summative, and included as a curricular commitment, constitute a logical progression following the establishment of a PBL curriculum featuring genome projects and comparative genomics.

Resource considerations and equitable access

Comprehensive genome data accompany nearly every problem to be addressed in biomedical education; therefore, outright equitable access to these resources is essential to implementing genome-informed problem-based learning. Approaching genome-informed problem-based learning requires accommodations that address factors influencing resource availability and subsequent efforts to integrate these data into learning materials.

Four major resources should be made widely available to all students: genome datasets from major genome projects, software tools for analyzing these data, laboratory access to automate genome sequence reading, and high-performance computing facility access to process these datasets in a reasonable time frame. Institutions may provide genome data with varying degrees of support. When software dependence on a single operating system restricts compatibility with institutional computing resources, platforms such as Anaconda or Docker can supply cross-platform solutions to disseminate software tools consistently across institutions. To guarantee equitable access, institutions can deploy common genome datasets through centralized servers, thereby maximizing potential engagement with genome-derived observations during investigations (Ziyaev, A. A., et al).

Laboratory experiences and computational workflows

Lab experiences with genome projects and comparative genomics motivate the integration of practical activities in both wet-lab and in-silico environments into PBL curricula. Although large-scale sequencing projects-such as those to elucidate the evolution of genomes and the knowledge-based identification of variation-are taught as standard subjects at the pre-university level, the contents do not connect as seamlessly to the biomedical curriculum as the proposed teaching materials, and the programming aspects may exceed the understanding of school students. Consequently, the focus at this stage is on genome

educational components that introduce relevant ancestors, establish broad study objectives, and support cross-programme collaboration (Azimova, S., et al).

PBL students bring different skills and knowledge sets to discussions on the scientific methodologies of genome projects. Before meeting in PBL sessions, they can conduct safe wet-lab experiments at home which derive from genome topics, do on-line demonstrations, or submit individual demonstrations covering selected genome projects, comparative genome concepts, and related PBL scenarios. Illustrative cases from the same or different fields can also help enrich the students' grasp of genome and PBL content. After the sequencing of a representative genome, drawing upon such information and data suitably adapted remains a possibility. Several interactive computational experiences available guide learners through genomic analysis of a specified variant or throughout complete software workflows on languages unsuitable for novices. Consequently, adaptable analyses with human or model organisms, even via spreadsheets, constitute additional complementary tasks enriching biomedical education. (Pucker et al., 2019)

Wet-lab concepts through genome projects

The advent of genome projects should play a central role in a first biomedical sciences laboratory course; they provide an opportunity for students to engage with scientific problems through inquiry-based experimentation and computational modelling. The lack of genome-level questions and data analyses in undergraduate curriculums has been identified as a notable gap in education programs world-wide, and genome sequencing projects are sometimes referred to as the greatest scientific endeavour in history (Sasmakov, S. A., et al). The Human Genome Project (HGP) alone has yielded exponential growth of biological knowledge, techniques and technology; comparable in impact to the periodic table of the elements or newtonian physics; and it has been claimed that the genomic sciences have the capacity to revolutionize all of the life sciences, creating a more profound change than the change from chemistry to the life sciences and opening an entirely new scientific era. The genome remains the largest single repository of information for the life sciences, yet no substantial laboratory or computer-based instruction on genome-level problems is offered (Pucker et al., 2019).

In silico analyses and bioinformatics workflows for learners

Problem-based learning can target experimental design using creative genome topics like CRISPR–Cas9 target screening and variants affecting transcription or splicing. By shifting digital tasks from suppliers to learners, educators promote autonomy and adapt work to diverse career aspirations. The wealth of freely available datasets supports broad access to genome research and flexibility in the illustration of diverse principles such as orthology and synteny. Access to genotyping, variant evaluation, and expression data further enriches the discussion of data curation and epidemiological, pharmacogenomic, and population-genomic trends (Pucker et al., 2019).

Clear pedagogical objectives guide integration of programming and bioinformatics into projects like genome annotation and CRISPR screening analysis using publicly available genomes and sequencing data. Genome-scale data integration cultivates an evolving spectrum of genomic literacy-from experimental design and data acquisition via NCBI and ENA to quality validation and interpretation of variant pathogenicity using guidelines and databases like SIFT, PolyPhen, and ClinVar (Martins et al., 2020). Genotype-to-phenotype workflow based on these principles enhances comprehension of relevant pressures, conservation, phylogenomic relationships, data sharing, privacy, and ethical handling (Salakhova E., et al).

Interdisciplinary collaboration and research culture

Collaboration between classrooms, laboratories, and data repositories enhances research-integrated curricula. Teacher–researcher partnerships can involve collaborative teaching, student access to real-world data, coordination of access to field sites and specimens, and sharing of equipment and software. Data-sharing agreements can establish terms for deposit and analysis of project datasets before general release (D. Shaffer et al., 2010). Such arrangements enable mutually beneficial exchanges of ideas and insights

between research and teaching domains. Students also develop skills in communicating science as they engage in writing, presentation, and teamwork activities. Regular peer and instructor feedback helps learners evaluate their work transparently before formal submission. These communication tasks nurture collaborative research mindsets in preparation for future careers (Sasmakov, S. A., et al).

Partnerships between classrooms, laboratories, and data repositories

Problem-based learning (PBL) courses in the biomedical sciences can integrate contemporary genomic sequencing efforts by providing easily accessible data sets from significant projects such as the Genome 10K Project, the Earth BioGenome Project, and the Genome in a Bottle Consortium. These projects generate data on the genomes of vertebrates, eukaryotes, and human variation, respectively, and their outputs closely align with selected instructional Los (Azimova, S., et al). Moreover, second-generation comparative genomics remains a leading bioinformatics approach in genome analyses and elucidates key concepts such as homology, orthology, synteny, and phylogeography. Resources such as GenBank, Ensembl, and the University of California, Santa Cruz Genome Browser have made available the data needed to construct cases that challenge students to reason across taxa and generate genomics-based hypotheses. Such activities foster core PBL skills—querying databases, evaluating variant evidence, and managing uncertainty—while adhering to the original aim of applying genomic sequence, structure, and evolution knowledge for the broader training of future biomedical professionals. Because a major goal of biomedical education is to equip students with computational and data-analytic skills that transcend modules, these components can be seamlessly integrated into PBL scenarios centred on genome sequencing. (D. Shaffer et al., 2010)

Cultivating scientific communication and collaboration skills

Scientific communication and interdisciplinary collaboration comprise essential competencies for future biomedical scientists (Pucker et al., 2019). Within the proposed genome-centered educational approach, fostering these skills can take on various formats for writing, oral presentations, and teamwork. For example, an initial sequence of assigned writing tasks can culminate in an extended report on an individual topic. Teams may also prepare presentations for major projects; during these sessions, peer review may substitute or supplement traditional instructor feedback (Sasmakov, S. A., et al). While guidance on scientific writing enhances the effectiveness of these exercises, an emphasis on effective scientific communication warrants their inclusion across the curriculum. Transparent sharing of research objectives, approaches, preliminary results, and planned next steps, in both written and oral formats, assists students in progressively clarifying the focus of their investigations. Such communication opportunities reflect professional practice in research and help prepare students for a seamless transition to a research-intensive career or graduate training.

Simple co-creation of collaborative online resources provides additional opportunities to hone communication and collaboration skills. For instance, contacting large consortia to obtain materials for large-scale surveys can illustrate the interplay of life cycle constraints on scientific endeavour in a real-world context. Writing a joint manuscript following a team-based project on genome function or similar topic is another option. Such encouragement of professional exchange across disciplines complements the socio-constructivist principles underpinning the proposed curriculum.

Evaluation of learning outcomes and impact

Reliable assessment of educational outcomes is crucial for both course evaluation and continual program enhancement. Incorporating genome projects and comparative genomics into problem-based learning (PBL) offers an opportunity to engage biomedical students with genomics and bioinformatics in ways that align with course objectives and increase analytical proficiency. The proposed approaches impart valuable skills, knowledge, and awareness beyond the immediate PBL context, notably critical thinking, data literacy, habit formation, and the ethical, legal, and social implications of genomics and data science within modern biomedical sciences (Khalikova R., et al).

Two sets of proposed evaluative measures target both specific genomic content and PBL-related objectives. One addresses indicators for genomic literacy and competencies in problem-solving. Three additional dimensions of competency-knowledge of the nature of science, information literacy, and an understanding of the role of science within societal development-have been found to meaningfully enrich overall professional preparation for biomedical students; an additional track for these advanced objectives is therefore proposed to augment the analysis of PBL initiatives. A longitudinal strategy for gauging readiness for research, clinical, or industrial mathematics-based biomedicine further contributes to the formative assessment of PBL content by tracking information who pursue mathematics- or bioinformatics-rich endeavors post-graduation.

Metrics for genomic literacy and problem-solving proficiency

The acquired competencies include the capacity to access databases, formulate queries, acquire the location of DNA variants in sequences, interpret data associated with the variations, evaluate evidences for pathogen risky or safeguarding role in the host, and model approaches to use genomic data in practice (Pérez-Losada et al., 2020). Genomic competencies are denoted as knowledge and capacity demonstrated by individuals to use genomic data in an informed and responsible way (Martins et al., 2020). The above noted skillset may be tracked through formative assessments (e.g. question banks and templates), exemplified pre-and post-evaluations or definition of individual learning dashboards going through the lines of the. Another educational perspective is the analysis of occupation and scholarly trajectory through participation in the problem-solving tasks, activity classes or research projects related to genome data. The Professional Life Trajectories refer to the process and associated events individuals experience towards the achievement of their aspirations on occupation or research scholar-this could be further assessed in six domains: between scholar and research, between scholar and applied, within scholar, within applied, and inert participation. Genomic pedagogical suggestions are anchored within the articulation of Genomic-Problem Solving Competencies and Professional Life Trajectories as elementary to comprehend when the students are graduated (Omonov Q., et al).

Longitudinal assessment of career readiness in biomedical sciences

Careers in the biomedical sciences span a wide spectrum. Graduates often pursue research-oriented roles, working as technicians, assistants, or trainees in laboratories at academic, government, or industrial institutions. Others take a more clinical route, becoming physicians, dentists, veterinarians, or pharmacists. Alternate paths lead into non-bench roles such as project management, regulatory affairs, or scientific writing in the biomedical industry, or into the informatics space, as data science or data science roles. Graduates also continue education in graduate school, pursuing advanced study in areas including molecular biology, biochemistry, systems biology, biophysics, or bioengineering. Tracking cohort progression into these roles can help gauge student career readiness (Sasmakov, S. A., et al).

Longitudinal tracking of career readiness can establish benchmarks reflective of the broad spectrum of biomedical career trajectories. Data concerning the immediate post-graduation destinations of cohort members can be collected routinely and made accessible by updating a high-frequency, low-burden tracking instrument. Such tracking can also indicate new opportunities graduating cohorts explore, helping appraise the continual evolution of the career landscape as well as the ongoing relevance of the program. Any adjustment of the aggregation mechanism can facilitate reporting on training progression and career readiness (Pucker et al., 2019) ; Pérez-Losada et al., 2020).

Challenges, limitations, and opportunities for future work

Future integration of genome projects and comparative genomics into problem-based learning (PBL) for biomedical teaching faces several challenges. For institutions lacking PBL cycles, obstacles to case development include time constraints, absence of prior experience, and lack of suitable problems (Prost et al., 2020). Many genome resources (assemblies, annotations, variation datasets) remain underexploited by educators and deliver their greatest pedagogical impact when students formulate cases based on their own

observations (Pucker et al., 2019). The need for supplementary “by-design” PBL genomes thus persists. Such projects probe the production and application of genome data, providing decision support on species selection, generation of diverse datasets, and connections to policy questions. Scaling to additional topics with comparable data types and student challenges expands pedagogical reach beyond genomic content.

Multiple levels of genome data access, metadata granularity, reproducibility, and provenance influence the feasibility of deploying genome datasets on campus. Multiple equally valuable genome datasets exist for many species. The pedagogical benefits of genome-informed tasks resonate with PBL’s emphasis on student autonomy, growth beyond prescribed curricula, and application of academic knowledge to realistic or authentic contexts. Nevertheless, developing supplementary resources, dataset suites, and support for genome-centered PBL remains a viable pathway toward innovative, mission-aligned teaching initiatives (Jabborova D., et al).

Conclusion

Genome projects and comparative genomics undergird extensive, valuable data resources capable of enriching problem-based learning for tomorrow’s biomedical scientists. Across disciplines and applications, broad-scale projects such as the human genome project, the earth bio-genome project, and brahmaputra genomics initiative establish catalyzing questions for investigating critical pangenome shifts; supplementary projects focusing on particular species (the zebrafish, for instance) also support rigorous PBL inquiry. Comparative genomics complements these considerable datasets. Through orthology definitions, conservation assessments, and synteny examinations, comparative data stimulate hypothesis generation and critical reasoning across species as well as reveal the impact of genome duplication, horizontal gene transfer, and genome-scale variation on pertinent case questions. Carefully crafted, genome-informed problems enhance prospective analysis, evaluation, and reasoning for beginner-level genome projects. In turn, genome analysis promotes query formulation, variant interpretation, dataset assessment, information hierarchy, uncertainty characterisation, and synthesis-core analytical undertakings in the contemporary research landscape, analogous to pre-modern data generation with far-reaching impact (Pucker et al., 2019).

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