Variant interpretation training for the genomics era: Learning outcomes to inform professional competencies and education

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Clear professional competencies and career pathways in variant interpretation (VI) are lacking. We co-developed learning outcomes in VI and describe how these can inform education and competencies across professions and can assist credentialing and career benchmarking. A case study illustrates its use in continuing education, which has been proven effective at developing entry-level proficiency.

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Variant interpretation training for the genomics era: Learning outcomes to inform professional competencies and education

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Summary

Genomic medicine is increasingly being integrated into healthcare systems worldwide, requiring a skilled genomic workforce. Variant interpretation (VI) is crucial to genomic testing, yet there are no agreed professional competencies in VI, career pathways are ill-defined for some professions, and there is limited literature on educational needs and programs. We referenced education theory and curricula from nascent local VI training activities to co-develop learning outcomes in VI with content experts that informed scalable continuing education activities, evaluated using longitudinal cross-sectional surveys. We defined 16 learning outcomes in VI covering fundamental genetics and bioinformatics theory and the stages of variant identification, curation, and classification. The education program included options for self-directed online learning or blended learning (online pre-reading plus workshops). Program reach was 951 individuals (49.2% scientists and 27.8% clinicians). At completion, the majority reported increased understanding of learning outcomes (96.1%, 171/178) and increased confidence in the processes of VI (93.3%, 166/178). The majority (91.7%, 231/252) indicated that the learnings would impact their professional role. Our education program was effective at developing entry-level proficiency in VI across different professions. The learning outcomes can inform multiple aspects of VI education and training programs, including defining the desired level of mastery and program content and aligning evaluation measures. They also provide a basis for an educational framework to inform competencies in VI across multiple professions and for career benchmarking more broadly.

Introduction

Genomic medicine has arrived. With next-generation sequencing delivering reductions in test costs and turnaround times and the evidence base for its utility for real-time diagnostics and treatment, countries across the world have established programs to implement genomics into healthcare systems.[1] Translating genomic testing from research into routine healthcare requires skilled clinical, diagnostic, and data science workforces, with professionals who can perform the key step of determining the biological and clinical significance of variants, that is, variant interpretation (VI).[2–4] Scientists working in diagnostic laboratories are known as "clinical scientists," "healthcare scientists," or "medical scientists." Scientists specializing in VI for diagnostic or research purposes are known variously as "variant curators," "variant analysts," "variant scientists," or "biocurators."[3–5]

Standards exist for enabling consistent pathogenicity assessment of variants,[6] but the same efforts have not been undertaken to ensure consistent competency in VI. While the knowledge and skills required for VI are similar across clinical diagnostics and research settings,[7] there is a lack of consensus within and between professions, regions, laboratories, and health services regarding who should complete which tasks and to what level of proficiency.[8,9] "Competencies" can be used to define effective performance of tasks to an agreed standard, e.g., the knowledge, skills, and attitudes required for safe clinical VI practice.[10] Professional competencies can be defined at local, national, or international levels and can inform education at any scale—from local initiatives to national strategies.[11] Ideally, education and training initiatives should have clearly defined goals (learning objectives) and measurable learning outcomes[10] that align with relevant competencies and inform assessment measures. However, while competencies are emerging for clinical genomics and bioinformatics, there are still no published competencies in diagnostic genomics relating to VI.[12]

There is an emerging literature describing education and training initiatives for VI across a range of settings. Individual research organizations and health services are developing bespoke, local programs.[4,13] Genetic counselor qualifications are incorporating VI content in

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courses and practical rotations, with some reports of learning objectives in VI for this profession,[7,14,15] and NHS England developed Master's and massive open online courses for clinical and diagnostic staff that include some modules on VI.[13,16] There is one report of leveraging large language models to explain concepts and classification criteria to provide accessible training, particularly for learners in low-resource settings.[17] However, there are no comprehensive descriptions of learning objectives or outcomes for VI that would enable more consistent approaches to education and training[18] and inform the development of role- or profession-specific competencies. Most evaluations of VI education reported to date have focused on quality improvement and/or measuring implementation (reach, engagement, and satisfaction) and short-term outcomes (gain in knowledge, skills, and confidence),[4,13,15] with one report of resultant change in practice at individual and departmental levels.[16]

Here we present learning outcomes for VI targeted primarily at professionals working in or with diagnostic laboratories. The learning outcomes then informed the development, design, and evaluation of a VI education program to meet the needs of a nascent diagnostic genomics workforce in Victoria, Australia. As part of the Melbourne Genomics change program, we defined learning outcomes for VI both to inform our education program and its evaluation and as a basis for considering competency in VI across and within professions involved in genomic testing.

Methods

Context

In Australia, after obtaining an undergraduate degree, medical scientists typically gain employment and then specialize, e.g., in genetics, microbiology, anatomical pathology, hematology, etc. Within genetics, subspecialties traditionally include cytogenetics, biochemical genetics, and molecular diagnostics. Specialty training is usually provided through workplace learning or continuing education, where available. Professional accreditation of medical scientists in genetics is overseen by the Human Genetics Society of Australasia and requires a relevant combination of tertiary qualifications, diagnostic laboratory experience, and written case reports, benchmarked against a curriculum that is also applicable to training for more senior scientists and pathologists through the Royal College of Pathologists of Australasia.[19] However, the curriculum was developed in 2017, with VI only added as an elective component in 2024, and does not specifically recognize VI as a required skill set.

Melbourne Genomics was a consortium of health services and academic organizations formed to demonstrate if and how genomic medicine could be delivered at scale within the existing Victorian health system.[20] When Melbourne Genomics commenced in 2013, genomic medicine was in its infancy in Australia. Australian pathology services were yet to offer accredited exome or genome testing for clinical care, few professionals were skilled in clinical or diagnostic genomics, and there were no standardized approaches to VI across research or diagnostic laboratories and no relevant continuing professional development or university award offerings. (In 2026, three Australian universities now offer award degrees that include subjects that teach VI at an appropriate level for medical scientists: Master of Genomics & Health, the University of Melbourne, Victoria; Master of Genome Analytics, Monash University, Victoria; and Master of Diagnostic Genomics, Queensland University of Technology, Queensland.) The first priority of the education program was therefore upskilling professionals central to delivering genomic testing in pathology services within the Melbourne Genomics member organizations, through in-person workshops (2015–2019) and laboratory cross-training experiences (2016–2019). Initial insights from these activities revealed a need for defined learning outcomes in VI to inform the development of scalable, multimodal education in VI for graduate students and other professionals who may need to understand and/or perform VI.

Theoretical frameworks, education program development, and delivery

We used a real-world, outcomes-based learning approach to design an education program for different professionals who may wish to perform VI.[10] Authors with educational and subject matter expertise (scientific, bioinformatic, and/or clinical) (J.H., D.L., L.G., N.T., and A.N.) reviewed individual learning objectives from our previous cross-training program and workshops to draft an initial set of desired knowledge and skills in VI.[21] The learning outcomes were iteratively reviewed and refined over a series of 11 meetings.

We then used a program logic approach to design, deliver, and evaluate a continuing education program based on the learning outcomes,[22] described in this publication with reference to RISE2 Genomics standards (Figure S1).[23] We first applied the revised version of Bloom's taxonomy[24] to create course-specific learning objectives, selecting verbs from a spectrum of *remember*, *understand*, *apply*, and *analyze*, through to *evaluate* and *create*. Experience with previous cross-training and workshops informed the development of a program that offered online courses for use as either self-directed online learning or blended learning (online pre-reading followed by in-person workshops; Figure 1). Learning designs within each initiative aligned with the course objectives and were informed by theories of education (experiential learning and adult learning), behavior change, and implementation science, to ensure that the content and activities provided engaging learning experiences that were relevant to professional practice.[16,25]

Initially, these courses were promoted through internal communications to Melbourne Genomics member organizations. From 2023, blended learning courses were advertised for open enrollment on the Melbourne Genomics website. Learners provided basic demographic data at registration (role, location, career stage, and experience with VI) for triaging into introductory and/or advanced courses and to inform advertising strategies. There were no prerequisite knowledge or skills required for introductory courses, and learners could apply for either or both courses. Those applying for advanced courses were required to have either completed the introductory course or self-reported sufficient experience in performing VI at registration (response options are shown in Table S1). Individuals applying for the advanced course who had not completed an introductory course or did not have sufficient experience (i.e., selected "I've heard the

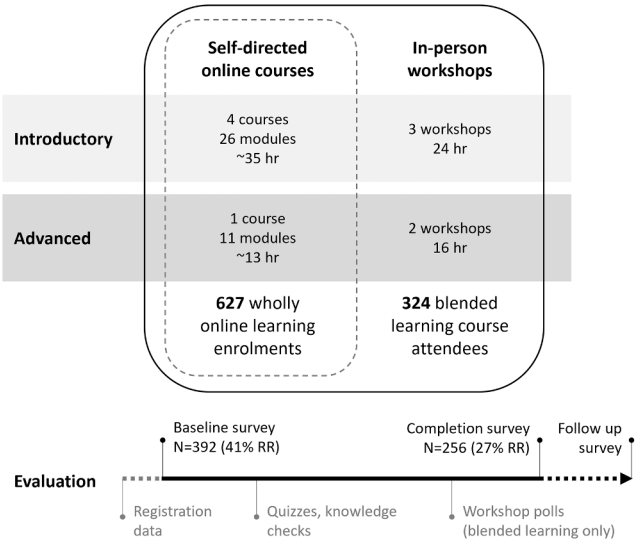

Figure 1. Melbourne Genomics' multimodal education program in variant interpretation, showing overlap in content/delivery modes between wholly self-directed online and blended learning

Longitudinal evaluation is shown at the bottom. Data for instruments in gray are not reported here. RR, response rate.

term but that's about it!" or "I've dabbled but don't know much about the underlying concepts or processes") were directed to complete the introductory course first. Online learning was accessed through an instance of Androgogic's Totara Learn learning management system. All blended learning workshops were conducted in person in Melbourne, Victoria, facilitated by subject-matter experts from partner organizations (some of whom were previous cross-training program alumni); participants brought their own laptops to practice VI processes under supervision. Maximum attendance for each workshop was dictated by room capacity, additionally complying with COVID-19 social distancing safety measures.

Education program evaluation

Evaluation was informed by the Kirkpatrick model of transferring learning to behavior across four levels: (1) reactions, (2) learner changes, (3) learner behavior, and (4) system impact.[26] Both wholly self-directed online and blended learning courses were evaluated longitudinally (Figure 1), with results interpreted using both the Kirkpatrick model and an evaluation framework for genomics education.[27] This paper reports the evaluation of the education program delivered from 2022 onwards to determine program reach and impact.

We deployed online surveys at baseline, completion, and 12 months after completion (2022 learners only). Measures included demographic data (role, location, career stage, experience with VI, and reasons and goals for completing VI education); perceived importance of VI processes to role; engagement with and usefulness of content (Kirkpatrick level 1); and self-reported understanding of VI course-specific learning objectives and confidence in VI processes and tools (level 2), behavior change (level 3), and system impact (level 4). Reference data on the age/gender/ethnicity of Australian medical scientists are not available, so these data were not collected. Questions were developed by authors with expertise in evaluation (M.M. and A.N.) and VI (N.T.). Questions were a mix of categorical, Likert scale, and

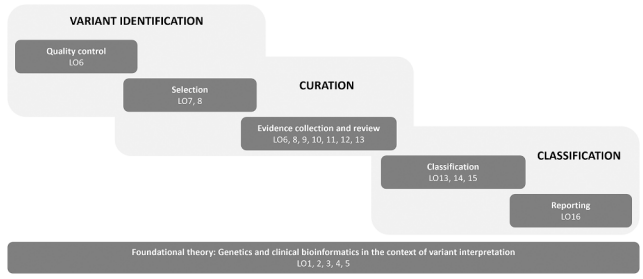

Figure 2. Framework for learning outcomes, showing the three main stages of variant interpretation—identification, curation, and classification—underpinned by the foundational theory of genetics and clinical bioinformatics in the context of variant interpretation

LO, learning outcome.

open text. Response options for self-reported understanding of VI and level required for the role were based on the revised Bloom's taxonomy.[24] The sample size for the follow-up survey was insufficient to power statistical analyses, so only qualitative data are reported.

Ethics approval for the evaluation was granted by the University of Melbourne (HREC/13/MH/326). Informed consent was obtained from all survey respondents. Surveys were hosted on a REDCap instance hosted at the Murdoch Children's Research Institute.[28] Data were cleaned to remove duplicate or incomplete responses; surveys were included in analyses if the demographics section was complete. Sample sizes differ due to missing data for some questions and the evolution of curricula and questions over time. Statistical analyses were performed using STATA/BE 17.0 and Microsoft Excel and included descriptive statistics (unpaired *t* test; significance set at 0.05). Qualitative data (open-text survey responses) were reviewed for common themes and illustrative quotes by A.N.,[29] with data managed in Excel.

Results

Learning outcomes in variant interpretation

Learning outcomes were defined to reflect VI as a process from variant identification, through curation, then classification, underpinned by foundational theory to ensure all learners have the language and basic concepts on which to build knowledge of VI principles and processes (Figures 2 and 3). Foundational genetics and bioinformatics outcomes are defined in the context of VI, including nomenclature, test types, clinical information and gene lists, and research versus clinical applications of bioinformatics pipelines. Variant identification includes quality assessment and filtering, prioritizing, and selecting variants. Variant curation includes assessing relevance; using databases, prediction tools, and conservation and constraint approaches; variant effects and prevalence; and collecting evidence. Variant classification includes applying the ACMG scheme[6] to classify variants and preparing reports. The learning outcomes relating to each stage of VI and each step are shown in Figures 2 and 3; some relate to multiple steps, reflecting that VI is an iterative process.

		Remember	Understand	Apply	Analyze	Evaluate	Create
Foundational theory	1. Genetic concepts and nomenclature used in the context of variant interpretation		Understand				
	2. Variant interpretation for different types of genomic tests		Understand				
	3. Importance of clinical information in variant interpretation, including gathering patient phenotype information, and how gene lists are developed and updated		Understand				
	4. Differences between research and clinical bioinformatics		Understand				
	5. Clinical bioinformatics pipelines, including key stages, inputs and outputs, types of variants detected by different pipelines, and limitations		Understand				
Variant interpretation: identification, curation, classification	6. Principles and processes of sample and variant quality assessment			Apply	●		
	7. Variant annotation sources and software for filtering, prioritizing, and selecting variants for curation based on phenotype matching and gene lists			Use	●		
	8. Relevance of variants against phenotypic data, suspected mode of inheritance, variant population frequency, and transcripts			Assess	●		
	9. Concepts and features of population and disease variant databases, including limitations of each			Apply	●		
	10. Concepts and features of *in silico* prediction tools, and conservation and constraint approaches, including limitations of each			Apply	●		
	11. Effect of a variant on protein function, including functional models and disease mechanisms			Assess	●		
	12. Prevalence of variants in individuals with the disease phenotype – literature searches and co-segregation analyses			Assess	●		
	13. Evidence required to classify a variant using ACMG guidelines, multidisciplinary review, and preparing a genomic test report			Collect	●		
	14. Concepts and limitations of the ACMG variant classification scheme, including evidence required to reach a classification			Apply	●		
	15. Variant interpretation principles and processes to classify variants			Apply	●		
	16. Guidelines, principles, and components of genomic test reporting			Apply	●		

Figure 3. Learning outcomes in variant interpretation
Bloom's taxonomy can be used to define the desired level of proficiency when designing education to meet the needs of different audiences. Shaded cells reflect an introductory level of proficiency, showing the verbs used for our introductory courses; dots show how these can be extended to a more advanced level.

We restricted the scope to interpreting highly penetrant variants in patients with suspected rare monogenic germline disorders, as our programs primarily aimed to provide introductory-level genomic literacy relating to VI. Figure 3 also shows how the learning outcomes can be adapted for other types of education and training programs by using Bloom's taxonomy[24] to select appropriate verbs that align with the target audience's needs and program goals. The shaded cells reflect the suggested knowledge or level of proficiency required for entry-level medical scientists to, for example, *apply* principles of quality assessment (learning outcome 6) or assess the effect of a variant on protein function (learning outcome 11). While all audiences would be expected to *understand* foundational theory, the dots in Figure 3 represent how learning outcomes for VI principles and processes can be extended to *analyze*, informing curricula with more complex content for advanced audiences.

Education program structure, content, and attendance

We used the learning outcomes to inform learning objectives and curricula for introductory and advanced courses (Figures 1 and 3). Within each topic (be it an online module or workshop session), learning is scaffolded, beginning with summaries to prepare learners for the depth and complexity of content. Theoretical content is presented, then simple monogenic examples, practical exercises, and worked cases, followed by more complex examples. "Signposts" highlight concepts or examples that are revisited in more complexity in subsequent courses. For example, learning outcome 11 relates to the effects of variants on protein function. The introductory course curricula include straightforward examples, exercises, and cases using a well-known dominant missense loss-of-function variant, then a well-characterized recessive variant, before introducing truncations with less well-known effects, such as nonsense-mediated decay. In the advanced course, this same learning outcome underpins content on variants associated with variable penetrance or splicing, requiring more sophisticated knowledge and skills to curate and classify.

Self-directed online learning consisted of four sequential introductory courses and one advanced course (Figure S2 lists the topics). Each online course begins with course-specific learning objectives, with optional learner reflections for these at baseline and again at completion to self-assess progress (Figure S3). Modules include knowledge checks and quizzes throughout for learners to self-assess progress, with an online discussion board for queries.

All-day, in-person workshops for blended learning courses were spaced a month apart to allow time for participants to work through online content assigned as pre-reading before each workshop. There were three introductory workshops and two advanced workshops, each with specific learning objectives. Learning designs for online courses and workshops included a mix of passive and active learning through theory, demonstrations, practical exercises, and cases,[25] with links to relevant VI software and databases to practice real-world simulations of VI processes in a safe learning environment (Figures S3 and S4). Workshop facilitators incorporated optional, anonymous polls to assess learner progress in real time.

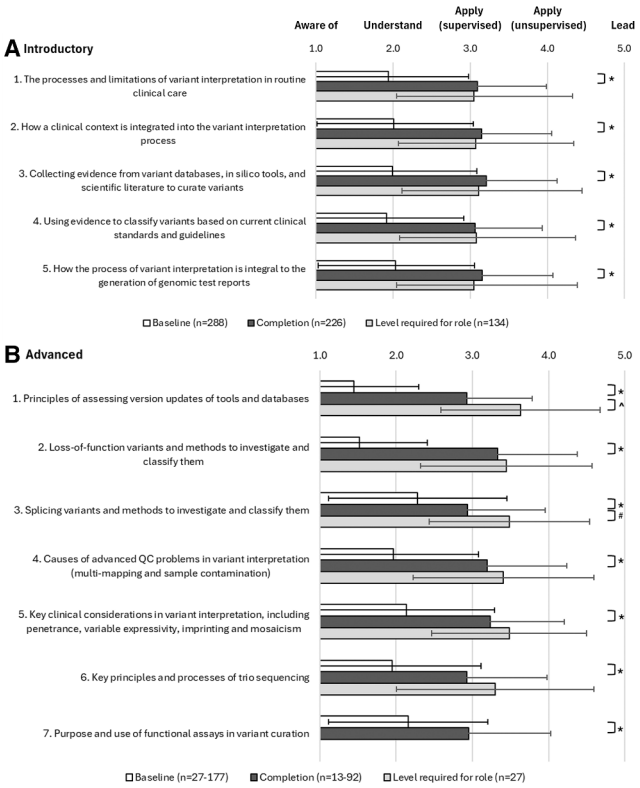

Figure 4. Mean self-reported level of understanding of course learning objectives at baseline and course completion, plus perceived level of understanding required for professional role

(A) Iintroductory.

(B) Advanced.

Sample sizes for advanced learning objectives vary, as curricula expanded. Perceived level of understanding required for role was not asked for the seventh advanced learning objective. $^{*}p < 0.001$, $^{\wedge}p < 0.041$, and $^{\#}p < 0.023$. Error bars show one standard deviation.

Of the 951 learners who completed courses from 2022 to 2024, 627 enrolled in wholly self-directed online learning, and 324 attended blended learning courses (average of 46 attendees per workshop; range of 31–68).

Education program evaluation and impact

Learners completed 392 baseline surveys (41.2% response rate [RR]) and 256 completion surveys (26.9% RR; Figure 1). Characteristics of baseline survey respondents are shown in Table S1 and Figure S5. Overall, the majority were medical scientists (49.2%) or clinicians (27.8%, including 12.0% non-genetic physicians), plus bioinformaticians/data scientists (5.4%) and graduate students (5.1%). Half (49.2%) had less than 5 years' professional experience, and 10.5% reported more than 20 years' experience. Nearly two-thirds (64.2%) had no or limited knowledge of the concepts and processes of VI, 25.0% had some experience, and 10.8% were performing VI independently or supervising others. A higher proportion of scientists completed self-directed or advanced learning, and, conversely, more clinicians completed blended or introductory learning. More bioinformaticians, data scientists, and graduate students completed advanced courses. A higher proportion of genetic counselors and clinical geneticists attended introductory courses than advanced, with the opposite true for non-genetic physicians.

Course satisfaction (Kirkpatrick level 1) was high, with 79.5% (202/254) of completion survey respondents rating the course they completed as "very good" or "excellent," 99.4% (180/181) gaining what they had hoped to, and 80.3% (143/178) reporting that the course revealed unexpected gaps in their knowledge or additional benefits. Learners engaged with all components of the online courses; over 80.0% of respondents reported accessing or completing all learning objective reflections, theory modules, and quizzes (Figure S6). Open-text comments revealed that learners also intended to use the online content as an ongoing resource: "SO [sic] much useful information – I will definitely be referring back to these modules" (medical scientist, completion survey).

Those who attended workshops as part of blended learning courses perceived all workshop components as useful (Figure S7):

"The team delivered a wonderfully structured course, increasing in difficulty and yet leaving us all feeling empowered as we left the practical component of the course." (Medical scientist, completion survey).

Figure 4 shows self-reported levels of understanding at baseline and completion for course-specific learning objectives, developed from the learning outcomes. The courses positively impacted learner understanding and confidence (Kirkpatrick level 2). 96.1% (171/178) reported their overall understanding of the processes of VI had improved, with no difference found between those completing self-directed online (14/14, 100%) versus blended learning (156/163, 95.7%; $p = 0.430$). Significant gains were seen for all course learning objectives from baseline to completion (Figure 4, $p < 0.001$ for all outcomes). Introductory learners achieved the perceived required level of understanding required for their professional role (Figure 4A), and advanced learners achieved this for four of the six objectives evaluated (Figure 4B), indicating further workplace learning is required to achieve proficiency in some advanced principles and processes.

"[What we need most is] practice with the workflows that arise around specific curation platforms." (Medical scientist, follow-up survey.)

"As someone who trains/assesses competency of curators, you and your team gave me an insight as to how I can modify my approach to training." (Pathologist, completion survey)

The majority (93.3%, 166/178) of respondents reported their confidence in the processes of VI improved after completing a course, with, again, no difference found between those completing self-directed online (13/14, 92.9%) versus blended learning (152/163, 93.3%; $p = 0.954$). The majority of learners also reported improved

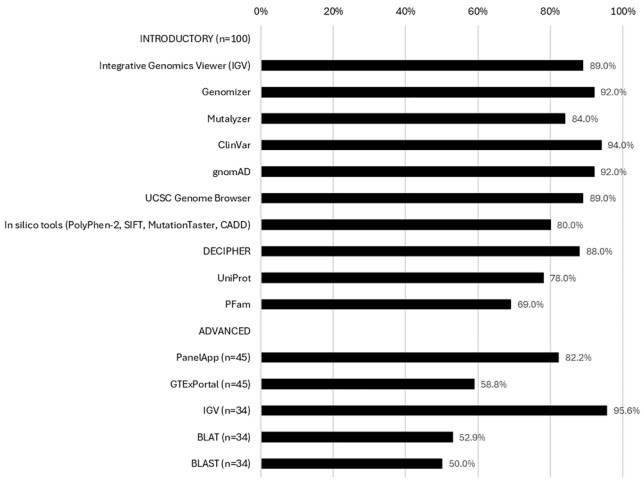

Figure 5. Self-reported gain in confidence in using tools for VI after completing courses

Sample sizes vary per question due to the evolution of content/surveys over time.

confidence in using specific VI tools and databases (Figure 5), particularly ClinVar (94.0%, 94/100), Genomizer (92.0%; 92/100), gnomAD (92.0%; 92/100), and Integrated Genomics Viewer (IGV; 89.0% [89/100] introductory learners and 95.6% [43/45] advanced learners).

One respondent commented "When learning on the job, so many details get missed (i.e. search functions in databases). Going over the basics and consolidating foundations was so useful for me for confidence in professional practice." (Medical scientist, follow-up survey.)

Encouragingly, at completion, the majority (91.7%; 231/252) anticipated their learning impacting their professional role (Kirkpatrick level 3):

"[The course] allowed me to move confidently into a new role." (Medical scientist, follow-up survey.)

Discussion

We developed learning outcomes in VI to inform continuing education courses for the existing and emerging diagnostic genomic workforce in Victoria, Australia, using a program logic approach to ensure curricula, learning designs, and evaluation aligned.[22] Over 3 years, our continuing education courses reached nearly a thousand scientists, clinicians, bioinformaticians, and students, contrasting with existing international VI training programs that are either unimodal (wholly online, laboratory rotations, or curated case exercises), small (e.g., blended learning delivered within one organization), targeted to one profession (e.g., genetic counselors), and/or teach VI as just one component of a larger course.[4,7,13,15–17] Using an outcomes-focused approach to co-design and evaluate VI education resulted in a program that met an identified local need across a range of professions and career stages,[30] with understanding exceeding that required for their role for most introductory course learning objectives. Our program positively impacted understanding and confidence in performing VI for both the current and emerging workforces, moving toward a workforce capable of meeting the increasing demand for genomic testing in Australia. Efforts continue to embed the curricula in professional training and graduate programs, including pathways for different professions to specialize in VI.

Basing learning outcomes in Bloom's revised taxonomy of learning provides a basis for educational frameworks and competencies in VI that can be applied across the genomic workforce. We selected verbs for each learning outcome to reflect the knowledge required for entry to practice, as that was the initial target of our education program. The learning outcomes also informed our advanced course for those wishing to move to the next level. Achieving higher levels of proficiency requires continued study or experiential workplace learning. Verbs that could be used to define the knowledge required across the different career stages of a variant curator are shown in Figure 6. For example, a graduate student would be expected to *remember* an outcome, while new or inexperienced staff would be expected to *understand* with close supervision. Working variant curators would be expected to know how to *apply* and then increasingly *analyze* each learning outcome as they progressed from supervised to independent work. Senior staff would be expected to be able to *evaluate* each outcome, with service leads *creating* new knowledge or processes related to VI.

Identifying differing required levels of factual, conceptual, and procedural knowledge[10,24] for novice through advanced learning enables adaptation for different forms of education, such as formal award study, continuing education, or structured workplace learning.[25] For example, content from introductory online courses informed curriculum development of two graduate specialist VI award subjects (170 h total), delivered through a Master of Genomics and Health at the University of Melbourne; abridged content also informed subjects in the Master of Genetic Counseling. Many alumni went on to supplement their introductory learning by completing an advanced course. The content could be further simplified for secondary school subjects to create awareness of genomics as an option for further study or careers. The Australasian Society of Diagnostic Genomics approached us to license the online courses for members to access self-directed continuing education, in conjunction with supervised experiential workplace learning to practice and extend competency relevant to their local context.

A lack of clear requirements for credentialing of medical scientists as "variant curators" impacts employers' ability to hire suitably experienced staff and curators' ability to see career pathways with clear benchmarking to progress to more senior positions.[3] A recent US study revealed varied prerequisites to gain employment performing VI (e.g., graduate study versus work experience), differing job titles, ill-defined career pathways, and limited visibility of

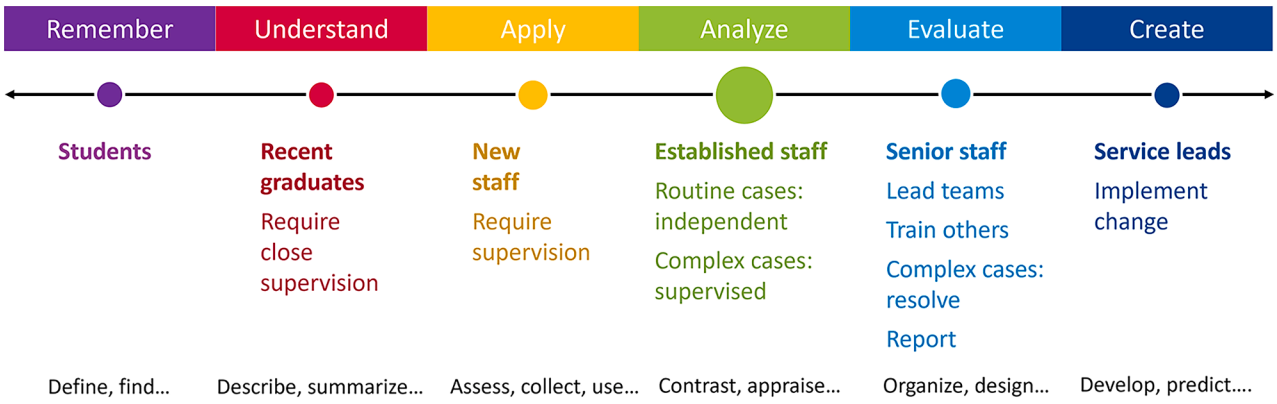

Figure 6. The revised Bloom's taxonomy of learning applied to the different career stages of a variant curator

the profession.[3] Australian medical scientists wishing to achieve competency in VI face the same challenges. The learning outcomes proposed here can serve as a basis to consider the level of competency required at different stages of a variant curator's career, or across the professions involved in diagnostic genomic testing, relevant to local service delivery models or other settings, such as the use of multidisciplinary team approaches.[31] The verbs and descriptors shown in Figure 6 could be applied for each learning outcome to set benchmarks for variant curators to perform at consistent levels within each career stage and more clearly delineate requirements to progress careers in VI. The majority of staff may follow these requirements, with some individuals self-identifying as "champions," choosing to extend into specialized learning in some areas.[32] Professional bodies can also build on these outcomes to update, develop, and/or accredit discipline-specific professional competencies, which can be used to benchmark career progression on a national level. Our program evaluation involved self-reported understanding of course learning objectives. To address the challenge of authentically assessing proficiency in VI within education settings,[13] the learning outcomes could also inform objective, standardized measures, such as audited case log books, practical tasks, competency-based assessments, or entrustable professional activities that could be used for accreditation.[21]

The majority of survey respondents in our program reported that the learnings would impact their professional role. Over a quarter were clinicians, with the largest group of these being physicians not trained in genetics, followed by genetic counselors and clinical geneticists. This reflects the breadth of professionals increasingly wishing to upskill in VI.[13,18] More genetic counsellors and clinical geneticists attended our introductory courses than advanced courses, with the opposite seen for non-genetic physicians. This possibly reflects a greater exposure to workplace learning in VI afforded by working in genetics services, e.g., through variant prioritization and review meetings. However, increasing implementation efforts in genomic medicine worldwide will gradually afford more workplace learning opportunities for professionals not trained in genetics.[33] In the UK, a self-directed "massive open online course" upskilled NHS England healthcare professionals in VI.[13] Program evaluation highlighted that mastery required more than foundational online learning and that educational programs should be adapted to the needs of different professions, particularly those not trained in genetics. In contrast, our online courses moved beyond theory to include practical exercises and cases for a range of learners to practice increasingly complex VI skills in a safe learning environment, either self-directed or facilitated by experts. In some countries, genetic counselors are moving into laboratory positions and performing VI, requiring both foundational learning and experiential learning to gain proficiency.[7,18] Our proposed learning outcomes can be applied to design different forms of education and training, from award programs through structured workplace learning, to meet the needs of diverse professions. Figure S8 illustrates how different professions may require more or less competency for different learning outcomes. For example, clinical bioinformaticians could be expected to have sufficient knowledge and skills to *evaluate* and *create* clinical bioinformatics pipelines (LO3), while the majority of pathologists could be expected to *analyze*, and medical scientists to *apply* these in their professional practice. Clinical geneticists and genetic counsellors could be expected to *understand* the principles behind clinical bioinformatics pipelines. Conversely, while medical scientists and pathologists could be expected to be able to *analyze* or *evaluate* the effect of a variant on protein function (LO11), a clinical bioinformatician or geneticist may need to *apply* the principle. Non-genetic physicians may only need to *remember* or be *aware* of both principles.

The proposed learning outcomes were initially designed for introductory learning of VI for inherited, monogenic conditions by medical scientists working in diagnostic laboratories in Australia. They are not intended to be applied to predictive testing or screening and need to be modified to somatic VI. These learning outcomes can be used to inform education and training in varied

contexts by reflecting on the levels of proficiency required by different professions across local health service delivery models.[22] Our courses and curricula developed from these learning outcomes have been run in two other countries, with different health systems, resulting in similar positive impacts on understanding and confidence in VI (data not shown). Needs assessments could be conducted to inform tailored learning outcomes for these different settings and professions. The outcomes align with two of four genomic data science core skills and competency domains: "technical skills" and "biological and domain knowledge."[34] Of the remaining two domains, "data management and governance" is beyond the current remit of a variant curator, but "soft skills and interdisciplinary collaboration" are central to the everyday practice of a variant curator, for example, translating and communicating complex information during multidisciplinary team meetings to prioritize or classify variants.

The learning outcomes can also be adapted to inform more advanced topics as the highly complex field of VI evolves, for example, to accommodate updates to ACMG guidelines for more complex concepts (such as varying expressivity, multifactorial, or polygenic conditions) or new clinical applications with more professions performing VI. Institutions, services, and professional organizations can build on the learning outcomes to inform education programs, employment practices, and professional competencies in VI to support burgeoning local diagnostic genomic workforces.

Data and code availability

Survey data are available upon reasonable request.

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Author contributions

Conceptualization, A.N., M.M., C.L.G., and N.T.; investigation, A.N., D.L., and N.T.; methodology, A.N., M.M., C.L.G., and N.T.; resources, A.N., D.L., L.G., C.C., M.M., J.H., N.L.B., V.B., M.F.-F., A.P.F., S.L., D.G.P., A.R., Z.S., T.Y.T., B.T., and N.T.; data curation, A.N.; validation, A.N., M.M., and N.T.; formal analysis, A.N.; writing – original draft, A.N.; writing – review & editing, A.N., D.L., L.G., C.C., M.M., J.H., S.L., Z.S., T.Y.T., B.T., C.L.G., and N.T.; visualization, A.N.; project administration, A.N. and D.L.; supervision, M.M., C.L.G., and N.T.; funding acquisition, C.L.G.

Declaration of interests

The authors declare no competing interests.

Supplemental information

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