

Genomics-Oriented Human Resource Development and AI-Assisted Genomic Analytics Adoption: A PLS-SEM Model of Bioinformatics Self-Efficacy and Knowledge Sharing Characterization

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Abstract

This study examines how genomics-oriented human resource development (GOHRD) relates to adoption of AI-assisted genomic analytics (AIGAA) through bioinformatics self-efficacy (BSE) and knowledge sharing (KS). A four-construct, 20-indicator reflective PLS-SEM model was analyzed in IIISR SEM Lab using 200 complete records and 5,000 bootstrap samples. GOHRD was associated with BSE ($\beta = .469$, $p < .001$), BSE with KS ($\beta = .567$, $p < .001$), and KS with AIGAA ($\beta = .495$, $p < .001$). The specific serial indirect path GOHRD $\rightarrow$ BSE $\rightarrow$ KS $\rightarrow$ AIGAA was positive (effect = .132, 95% CI [.079, .200]); the direct GOHRD $\rightarrow$ AIGAA path was not statistically distinguishable from zero ($\beta = .021$, $p = .755$). The model explained 28.4% of the variance in AIGAA. These results suggest an association between development opportunities, task confidence, knowledge exchange and tool use. The work provides an explicitly domain-specific measurement proposal and a testable account of how organizational learning may be linked to genomic analytics adoption.

Keywords: bioinformatics; genomic analytics; human resource development; self-efficacy; knowledge sharing; PLS-SEM; AI adoption.

Introduction

on

Artificial intelligence (AI) can support parts of genomic data processing and interpretation, yet organizational use cannot be understood solely as the availability of software. The employees expected to integrate analytical technologies into research workflows must acquire relevant capabilities, develop confidence in performing tasks, and work with colleagues to exchange analytical knowledge. This study considers the organizational and social components of AI-assisted genomic analytics adoption rather than treating it as a purely technical procurement decision. Its outcome variable concerns reported use and integration of AI tools into genomic analysis activities, not accuracy of an algorithm or clinical benefit. (Mahmud & Banerjee, 2026; Duong & Solomon, 2025).

Human resource development (HRD) includes organized opportunities for skill acquisition and workplace learning. Research on employees' perceptions of HR practices warns that the experience and interpretation of development opportunities may matter alongside formally announced policies (Beijer et al., 2021). Workplace learning research similarly treats competence development as activity embedded in day-to-day work (Decius et al., 2019). In genomics, training may help employees understand analytical pipelines, distinguish plausible outputs from errors, and identify when specialist input is needed. Whether such development translates into use of AI-assisted tools, however, depends on more than exposure to training: employees must believe they can accomplish specific technical tasks and be able to obtain and share knowledge relevant to those tasks. (Lukhele et al., 2025; Brooksbank et al., 2024).

Computer self-efficacy concerns perceived capability to carry out computer-related activities (Compeau & Higgins, 1995). The present study specializes this construct to bioinformatics, where confidence pertains to computational analysis, interpretation, acquiring unfamiliar analytical skills, and troubleshooting. Knowledge sharing captures interpersonal exchange of experience, practices and useful information. Work on knowledge donating and

collecting provides a basis for distinguishing the social transmission of expertise from an individual's confidence in possessing it (van den Hooff & de Ridder, 2004). The technology-acceptance literature likewise distinguishes drivers of use from use itself (Venkatesh et al., 2003). (Lukhele et al., 2025; Rony et al., 2024).

The research problem is therefore not simply whether genomic professionals receive training or use AI tools, but how organizational development, task confidence and collective knowledge processes appear together in a model of adoption. The study assesses six direct and three specified indirect hypotheses, including a serial route from GOHRD through BSE and KS to AIGAA. Its conceptual contribution is to join HRD, efficacy, knowledge-sharing and technology-use constructs in one genomics-oriented framework. Its empirical contribution is to evaluate the proposed structural and measurement relationships within a genomics-oriented PLS-SEM framework. (Lanfranchi et al., 2026; Mahmud & Banerjee, 2026).

2. Literature Review and Hypothesis Development

2.1 Theoretical perspective and construct positioning

A social-cognitive account suggests that people's judgments about their ability to perform tasks can shape their willingness to undertake demanding activities (Compeau & Higgins, 1995). In parallel, organizational learning creates conditions for skill acquisition, experimentation and exchange. Neither perspective implies that training automatically produces tool use. Rather, a staged explanation is plausible: development opportunities relate to confidence; confidence relates to interactions with colleagues; and sharing usable information relates to implementation of analytical tools. The present model tests these links as associations and does not infer temporal or causal direction from a single estimated structural model. (Brooksbank et al., 2024; Lukhele et al., 2025).

GOHRD denotes reported organizational provision of genomics, bioinformatics and AI-related skill development. BSE denotes confidence in performing genomics-related computational tasks. KS denotes the sharing of genomic methods, insights, and troubleshooting knowledge with colleagues. AIGAA denotes reported integration of AI-assisted genomic analysis tools into current tasks. AIGAA is defined here as actual self-reported use, not behavioral intention; consequently, the constructs should not be interpreted as measuring the same phenomenon. (Mahmud & Banerjee, 2026; Hu et al., 2025).

2.2 Human resource development, efficacy and knowledge exchange

Training and development can expose employees to specialist terminology, workflows and practical exercises that may strengthen task-specific confidence. Compeau and Higgins (1995) characterize efficacy as a judgment about one's ability, rather than a simple measure of years of experience. In genomic analytics, repeated practice may give staff a basis for judging whether they can process datasets, interpret machine-generated outputs or learn a new analytical platform. Thus, H1: GOHRD positively relates to BSE. (Lukhele et al., 2025; Brooksbank et al., 2024).

Development activities may also create opportunities for staff to circulate procedures, demonstrate new tools and discuss problems. Yet the presence of training is not identical to the presence of a sharing culture. Organizational support may relate to KS directly, or its association may operate primarily through employees who feel capable of explaining their work. Thus, H2: GOHRD positively relates to KS. Confidence may in turn enable employees to contribute solutions and describe methods more readily, although knowledge exchange may also depend on team norms and perceived incentives. Thus, H3: BSE positively relates to KS. (Hu et al., 2025; Lukhele et al., 2025).

2.3 Efficacy, sharing and analytics adoption

When employees consider themselves able to operate bioinformatics software and interpret outputs, they may be more inclined to incorporate those tools in their work. This reasoning distinguishes perceived capability from actual reported integration of the technology. Thus, H4: BSE positively relates to AIGAA. Knowledge sharing may spread practical demonstrations, quality-control routines, analytical shortcuts and experiences with specific

applications, making it easier to embed AI-assisted tools into routine genomic tasks. Thus, H5: KS positively relates to AIGAA. HRD itself may also be associated with uptake when structured development directly improves understanding of tool functionality and appropriate use. Thus, H6: GOHRD positively relates to AIGAA. (Rony et al., 2024; Lanfranchi et al., 2026; Hu et al., 2025).

2.4 Mediation hypotheses

Three indirect routes are considered. First, development may be associated with adoption because it builds capability beliefs; thus H7: BSE mediates the association between GOHRD and AIGAA. Second, training can furnish transferable methods and shared understanding; thus H8: KS mediates the association between GOHRD and AIGAA. Third, an ordered account proposes that GOHRD relates to BSE, BSE relates to KS, and KS relates to AIGAA. Thus H9: BSE and KS serially mediate the GOHRD-AIGAA association. These are statistical mediation hypotheses; a demonstrated indirect coefficient alone does not establish temporal ordering or causality. (Hu et al., 2025; Lukhele et al., 2025).

3 Methodology

This study adopted a quantitative, cross-sectional design and employed Partial Least Squares Structural Equation Modeling (PLS-SEM) using IIISR SEM Lab v2.0.5 to examine the relationships among Genomics-Oriented Human Resource Development (GOHRD), Bioinformatics Self-Efficacy (BSE), Knowledge Sharing (KS), and AI-Assisted Genomic Analytics Adoption (AIGAA). The dataset comprised 200 complete observations with no dropped cases or missing values across the 20 indicators. Each construct was modeled reflectively using five items measured on a five-point response scale. GOHRD items captured organizational training, AI-related development, participation in relevant courses, continuous learning, and application of newly acquired skills, drawing conceptually on Beijer et al. (2021) and Decius et al. (2019). BSE was adapted from the computer self-efficacy framework of Compeau and Higgins (1995), while KS was informed by van den Hooff and de Ridder (2004). AIGAA was conceptually grounded in the technology-use perspective of Venkatesh et al. (2003). The item wording was contextually adapted and did not reproduce the original scales verbatim. The reflective measurement model was assessed using standardized indicator loadings, Cronbach's alpha, composite reliability, and average variance extracted (AVE). The structural model was evaluated through standardized path coefficients, bootstrap standard errors, t statistics, p values, confidence intervals, and coefficients of determination (R^2). Statistical significance was assessed through non-parametric bootstrapping with 5,000 requested and successfully completed resamples. Specific indirect effects were also examined using bootstrap-based confidence intervals and p values.

4. Results

4.1 Measurement model

All 20 displayed outer loadings were positive and ranged from .774 (BSE5) to .860 (GOHRD5), consistent with substantial indicator-construct association in the estimated model. The reported internal consistency and extracted variance statistics are summarized in Table 1. All four AVE values exceeded .50, and each construct's Cronbach alpha and composite reliability exceeded .88. These descriptive assessments do not substitute for verification that the proposed adapted items adequately cover the four domains.

Table 1. Internal consistency and extracted variance statistics

Construct	α	Composite reliability	AVE	Loading range
GOHRD	.893	.921	.700	.825-.860
BSE	.882	.914	.679	.774-.856

KS	.891	.920	.697	.817-.844
AIGAA	.887	.917	.689	.797-.857

4.2 Structural relationships

The structural relationship is presented in the structural model (figure 1). The direct-path results in Table 2 indicate positive associations from GOHRD to BSE, BSE to KS and KS to AIGAA.

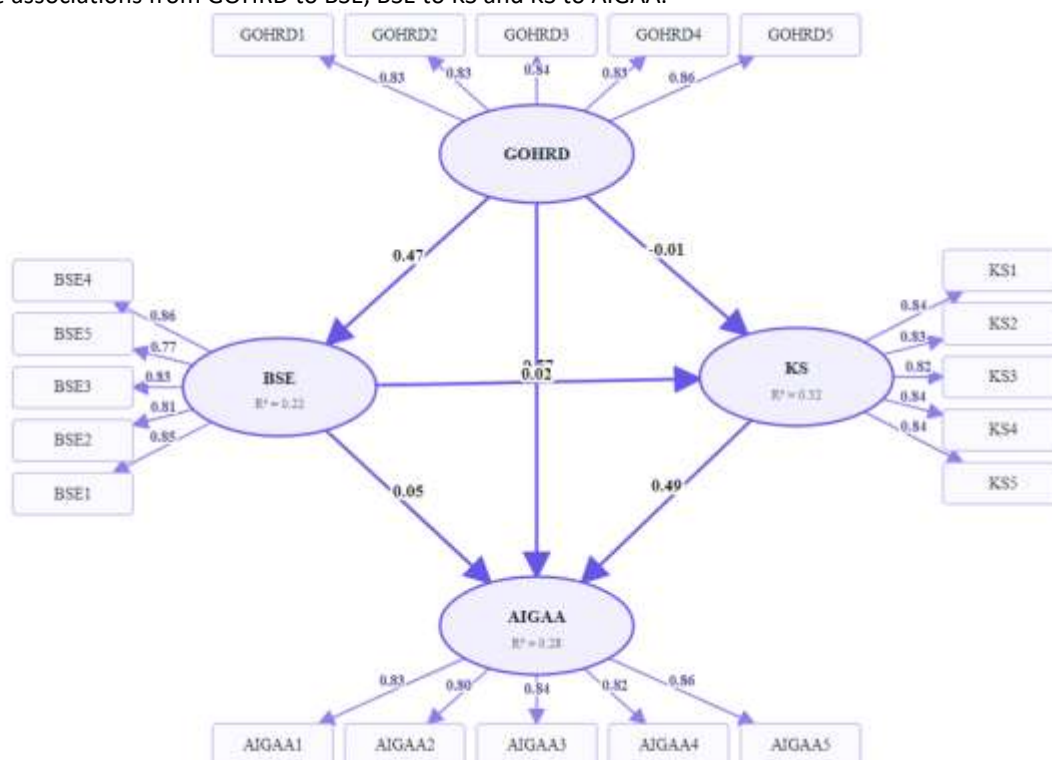


Figure 1: Structural model

The positive direct coefficients for GOHRD → AIGAA and BSE → AIGAA were small and statistically nonsignificant, while GOHRD → KS was close to zero and slightly negative. Hypotheses H1, H3 and H5 were supported in the estimated model; H2, H4 and H6 were not. A nonsignificant coefficient is not evidence that the true effect is exactly zero, and the directions should not be interpreted as established causal effects.

Table 2. Reported bootstrap direct effects

Hypothesis and path	β	t	p	95% CI	Result
H1 GOHRD → BSE	.469	8.659	< .001	[.358, .574]	Supported
H2 GOHRD → KS	-.009	-.121	.903	[-.146, .136]	Not supported
H3 BSE → KS	.567	9.535	< .001	[.449, .682]	Supported
H4 BSE → AIGAA	.053	.622	.534	[-.106, .222]	Not supported
H5 KS → AIGAA	.495	7.096	< .001	[.358, .628]	Supported
H6 GOHRD → AIGAA	.021	.312	.755	[-.115, .158]	Not supported

Explained variance (R^2) was .220 for BSE (adjusted .216), .317 for KS (adjusted .311), and .284 for AIGAA (adjusted .273). These results indicate that the specified predecessors accounted for 22.0%, 31.7% and 28.4% of the corresponding construct-score variance. The analysis additionally lists Q^2_{predict} values of .197 for BSE, .298 for KS and .256 for AIGAA.

4.3 Specific indirect effects

The sequential GOHRD → BSE → KS → AIGAA effect was positive, and its 95% bootstrap confidence interval excluded zero (effect = .132, $p < .001$, CI [.079, .200]). This is consistent with H9 in the fitted model. Neither the GOHRD → BSE → AIGAA route nor the GOHRD → KS → AIGAA route had a confidence interval excluding zero; hence H7 and H8 were not supported by these specific indirect-effect tests. The software additionally estimated GOHRD → BSE → KS (effect = .266, $p < .001$, CI [.186, .362]) and BSE → KS → AIGAA (effect = .281, $p < .001$, CI [.183, .400]); these are supplementary indirect associations, not substitutes for the prespecified AIGAA-focused hypotheses.

Table 3. Reported bootstrap indirect effects.

Indirect path	Effect	p	95% CI	Interpretation
H7 GOHRD → BSE → AIGAA	.025	.545	[-.051, .110]	Not supported
H8 GOHRD → KS → AIGAA	-.004	.904	[-.076, .064]	Not supported
H9 GOHRD → BSE → KS → AIGAA	.132	< .001	[.079, .200]	Supported
GOHRD → BSE → KS	.266	< .001	[.186, .362]	Additional path
BSE → KS → AIGAA	.281	< .001	[.183, .400]	Additional path

5. Discussion

The fitted model provides a differentiated picture of development-related analytics use. Organizational genomics-related development is strongly associated with employees' perceived ability to perform bioinformatics tasks, but is not directly associated with analytics adoption after the modeled intermediates are included. Bioinformatics self-efficacy, in turn, is associated with knowledge sharing rather than showing an independent direct association with adoption. Knowledge sharing exhibits the clearest direct association with reported analytics use among the immediate predecessors of AIGAA. The pattern is compatible with an explanation in which capability becomes relevant to technology use through the communication of methods, practical experiences and troubleshooting knowledge.

The H1 estimate aligns with the concept that development activities can strengthen beliefs about task capability, a domain-specific extension of computer self-efficacy (Compeau & Higgins, 1995). The H3 estimate suggests that employees who report higher task confidence also report greater sharing of bioinformatics knowledge. However, the nonsignificant H2 coefficient indicates that GOHRD has no identifiable direct association with KS after BSE is accounted for in this model. One possible interpretation is that perceived training benefits are translated into collective exchange largely through acquired confidence; another is that unmeasured team norms, workflow arrangements, or access to colleagues explain the residual sharing behavior. The current records cannot distinguish these explanations. (Lukhele et al., 2025; Brooksbank et al., 2024).

The contrast between H4 and H5 is substantively important. Feeling able to perform technical tasks was not separately associated with analytics uptake at the chosen inference level, whereas sharing expertise was. Practical tool adoption may require interpersonal transfer of tacit knowledge—how to interpret unusual outputs, resolve software problems or adapt an unfamiliar procedure to a particular dataset. This interpretation is consistent with the distinction between individual competence beliefs and the social exchange processes discussed by van den Hooff and de Ridder (2004), although the data do not test whether particular kinds of knowledge, organizational structures or software characteristics account for this difference. (Hu et al., 2025; Lanfranchi et al., 2026).

The serial indirect effect is the primary model-specific finding. Development shows a positive indirect association

with adoption through the ordered product of BSE and KS coefficients, even when the direct GOHRD-AIGAA path and both simpler adoption-focused indirect routes are not significant. A significant product can occur when an intermediate relationship is relatively strong although one or more direct paths are weak; it does not demonstrate that participants actually moved through successive stages over time. The single-model estimates are therefore best understood as a theoretically organized association pattern, not as evidence that introducing a training programme would necessarily cause increased AI adoption. (Hu et al., 2025; Lukhele et al., 2025).

Theoretical implications follow from separating the four constructs rather than merging them into one generalized readiness index. The findings underscore the possibility that task-specific efficacy and social knowledge exchange have different positions in an analytics-adoption framework. The distinction also refines the application of technology-use research: AIGAA was defined as existing use and workflow integration, not willingness or intention, which would be conceptually different outcomes under technology-acceptance models such as UTAUT (Venkatesh et al., 2003). Additionally, the domain-adapted indicators illustrate how general HR, efficacy and sharing constructs can be operationalized for genomic analytical work, subject to further content and construct validation. (Mahmud & Banerjee, 2026; Lanfranchi et al., 2026).

For organizational practice, the association pattern suggests a testable proposition that HR development may be paired with peer demonstrations, accessible analytical documentation, collaborative problem-solving and opportunities to explain new procedures to colleagues. These are possible interventions for future evaluation, not proven effects of the present model. Separately, confident employees should not automatically be assumed to use a tool: software availability, approved workflows, dataset suitability and organizational constraints may all matter. Decisions about deploying AI in genomic work also require independent technical verification, information governance and expert oversight, none of which are assessed by the four constructs. (Brooksbank et al., 2024; Lukhele et al., 2025).

Future research can recruit verified genomic and bioinformatics professionals, document institutional and geographic settings, use temporally separated measures and investigate how organizational sharing culture or software access conditions alter the proposed paths. Triangulating self-reported use with approved audit logs, workflow records or task-based measures would strengthen outcome validity. Comparing different professional roles and types of genomic analytical tools could show whether the present construct relations remain stable beyond a single measurement context. (Lanfranchi et al., 2026; Duong & Solomon, 2025).

6. Conclusion

This study organizes genomics-oriented HR development, bioinformatics self-efficacy, knowledge sharing and AI-assisted genomic analytics adoption within one PLS-SEM framework. In the sample of 200 respondents, GOHRD was positively associated with BSE, BSE with KS, and KS with AIGAA. The serial GOHRD → BSE → KS → AIGAA indirect effect was positive and statistically distinguishable from zero, whereas the direct GOHRD → AIGAA effect and the two simpler adoption-focused indirect effects were not. The modeled predictors accounted for 28.4% of AIGAA variance. These findings motivate further attention to the social exchange of technical knowledge alongside individual skill development.

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