



Transforming Biological Science Research Through AI-Enabled Tools: A Comparative Analysis of Data Interpretation, Experimental Design, and Research Productivity

Souvik Chakraborty ^{1*}, Dr. Harikrishnan M ²

¹ Research Scholar, School of Education, Sanskriti University, Mathura (U.P.), India

² Assistant Professor, School of Education, Sanskriti University, Mathura (U.P.), India

* Corresponding Author: Souvik Chakraborty

Article Info

P-ISSN: 3051-3383

E-ISSN: 3051-3391

Volume: 07

Issue: 02

Received: 08-07-2026

Accepted: 06-08-2026

Published: 04-09-2026

Page No: 73-83

Abstract

While various AI tools still have room to grow, as of now, they provide computational tools that contain research domain knowledge. By exploring the use of various tools, this study analyzes how AI tools influence data interpretation, experimental design, workflows, research and/or analytical work, and productivity. An illustrative dataset was created by the researcher using 400 biologically credible researcher profiles and was not compiled from surveyed or institutional datasets. Descriptive statistics, correlation, Cronbach's alpha, t-tests, ANOVA, regression, multiple and hierarchical regression, and mediation analysis via bootstrapping were performed on the multiple-item constructs. AI positively influenced data interpretation and the design of experiments and productivity. Integrated records led to better outcomes in the main metrics, and using responsible AI did not yield a significant gender difference. Regression models indicated that the variables associated with the research process and the workflow efficiency accounted for a significant portion of the outcome, and all variables did not need to be included. The workflow efficiency variable fully mediated the relationship of use and productivity. Based on the results, AI can assist biological research in the current state, as long as it is used to further the thinking and rationalizes the structure of the scientific framework, and is verifiable, reproducible, and communicated to the researcher.

DOI: <https://doi.org/10.54660/IJAIET.2026.7.2.73-83>

Keywords: artificial intelligence, biological science, bioinformatics, experimental design, research productivity, data interpretation, research workflow, responsible AI

1. Introduction

Integrating instruments, structures, and computational methods with proteomics and microscopy is where modern biology is heading. Innovative approaches to planning, documenting literature gaps, and predictions, as well as self-modifying code, are getting simpler to implement thanks to advancements in machine learning and computational biology (Chicco *et al.*, 2020; Li *et al.*, 2020; Bhardwaj *et al.*, 2022) ^[4, 1]. Solutions based on AI answer the needs of bioinformatics and structural biology (Jumper *et al.*, 2021; Varadi *et al.*, 2022) ^[12, 28]. In this context, what role do you think AI should have in forming observations and designing and executing the experiments that yield the results?

1.1 AI in Biological Science

In biological science, AI is necessary for predictive modeling and pattern recognition, molecular and image design, representation and language modeling, and the development of project support systems for decision making, together with genomics, proteomics, and customized medicine, target identification, and other similar activities (Leite *et al.*, 2021) ^[14]. Geneformer demonstrated the use of big multi-omics data to learn transcripts for the prediction of network biology and related problems in single-cell transcriptomics data (Theodoris *et al.*, 2023) ^[24]. More recently, the logic of Geneformer has been

extended

to a bigger model foundation for working with different omics data (Cui *et al.*, 2024; Hao *et al.*, 2024)^[5, 7]. AI helps in biology and related fields to select and prioritize problems and to generate new hypotheses.

1.2 AI-Enabled Research Tools

AI can help researchers with math and stats, bioinformatics, protein structure prediction, reading and interpreting images and text, coding, and using LLMs and generative AI. People have started using ChatGPT to analyze bibliomedical texts, although trust scores and (Chen *et al.*, 2023; Wang *et al.*, 2024)^[3, 30] trust scores are highly questionable. By trust, they do not mean computational chattiness and interactivity, but rather how biologically meaningful the technology is. Some research article authors think that knowledge graphs and retrieval can help biomedical problem solving with reasoning and understanding (Matsumoto *et al.*, 2022; Soman *et al.*, 2022).

1.3 AI and Biological Data Interpretation

AI can overcome the existing approaches, limitations and challenges with regard to data interpretation in the areas of images and molecular data. In this context, deep learning can discover intricate, non-trivial, and non-linear relationships and interactions within and across various biological domains and networks and the integrated omics level (Jin *et al.*, 2021; Li *et al.*, 2022)^[11]. Currently, AI and explainability are the focus. It is possible to improve AI and its predictability at the expense of explainability and understanding (Karim *et al.*, 2022)^[13].

1.4 AI and Bioinformatics

In the future, advanced computational algorithms in bioinformatics will be designed using AI. These algorithms will help analyze and integrate different types of omics data (i.e. genomics, transcriptomics, and proteomics data). (Li *et al.*, 2020; Bhardwaj *et al.*, 2022)^[1]. With the help of foundation models, the first drafts of intelligence for specific tasks will require even less labeled data. (Ma *et al.*, 2024) Even if the validation and verification of advanced AI systems becomes a barrier, there will not stop the progression of such systems. As a result of the rapidly available poor quality data, confidence and certainty with which AI systems will provide wrong answers will only increase.

1.5 AI and Experimental Design

AI will help automate and improve the way scientists experiment by changing the number of assay conditions needed to determine the operating bounds of autonomous biological assays. Current research using deep reinforcement learning and active learning has shown a reduction of the number of required conditions within experiments and in the design of mammalian cell cultures. (Treloar *et al.*, 2022; Hashizume *et al.*, 2023)^[27, 8]. These systems advise users within the context of the current system and help users achieve their goals. In the absence of significant bias in data and measurement, there will be a significant improvement in the efficiency of the systems.

1.6 AI and Research Workflow Automation

Closed-loop experiments will be one of the research tasks performed by self-driving laboratories. Most steps in the research workflow will be integrated and automated,

meaning data will be cleaned and formatted automatically, as will analysis and visualization. Additional research steps that will be automated include literature searches, documentation, and reproducibility. Automation of these steps will mean that systems will have to cooperate, and metadata will need to be standardized (Sanders *et al.*, 2023)^[21]. Although use of automation will allow researchers to perform programming tasks involving low-level skill with language models, references will still need to be checked (Lubiana *et al.*, 2023)^[18].

1.7 AI and Research Productivity

Researchers will benefit from a substantial freeing up of time caused by the reduction of analysis and literature screening. Increased productivity will also be apparent in research reporting and coding, as well as optimization and re-ordering of experiments. Positive signs of a rapidly expanding area are seen in the growing interest in the AI-related activities in various regions of the world, specifically the life sciences (Schmallenbach *et al.*, 2024)^[22]. Though productivity should not be equated to increased publications, research will need to retain its quality if it is to maintain its scholarly evidence.

1.8 Traditional vs AI-Integrated Research Workflows

AI-integrated research workflows enable each phase of the research process to be completed by the researcher or in some cases, by the AI. Some models can perform analysis, outlier detection, prioritize factors, conduct a literature search, and even suggest literary sources. These models tend to be quite broad and fast, but they ultimately increase the risk of bias. Automation bias is when a user of a system develops a preference and reliance on specific recommendations made by a model. Certain tasks, for example, determining the cause, limits, and consequences of a system, or other ethical considerations, should still be done by humans.

2. Literature Review and Theoretical/Conceptual Foundation

The literature shows the complementarity between AI and humans. AI uses pattern recognition, computational thinking, and search, while humans rely on domain knowledge, causal reasoning, and judgment. When assessing drug design, the most important aspect is to interrogate the results of algorithms in relation to existing science and problems rather than to make unsubstantiated claims (Walters & Barzilay, 2021)^[29]. In the Life Sciences, there are certain measures for the reproducibility of machine learning, which refer to more openness and greater transparency in the sequence of data processing and analysis, the publication of code, and the publication of results (Heil *et al.*, 2021)^[9]. Similarly, as with machine learning, systems-level modeling also relies on computational modeling (Tiwari *et al.*, 2021)^[26]. Incorporating AI is aimed at integrating research infrastructures and research outputs in the creative workflow of the researcher and AI literacy.

2.1. Research Gap

While many AI systems have been studied and analyzed at different levels, the majority of these papers only analyze AI systems in isolation, at most, data and productivity of research frameworks and approaches integrating statistical methods. This research aims to fill this gap with a unified framework of science and AI literacy.

2.2 Aim, Objectives, Research Questions and Hypotheses

This study aimed to understand how AI practices affect different steps of the biological-scientific research process and how these practices assist in analyzing experimental data and designing experiments. The study also aimed to examine how these practices alter the quality and the quantity of research. AI practices can potentially separate research teams. They can also amplify incremental predictions based on the AI literacy level of the researcher. The main questions were around the impact of extensive AI use on the interpretation of data and the design of subsequent experiments. One hypothesis stated that the use of AI would increase productivity over the background control. The other hypothesis stated that AI would improve the design of experiments and would improve the research and the workflow.

3 Materials and Methods

A research demonstration was conducted in a quantitative manner utilizing an analytical dataset that the researcher developed. This research did not use participants, contain any surveys, interviews, or evaluations. There were no institutional datasets used; therefore, there were also no ethical issues. This meant that there was no need to prepare anything to ensure approval was granted or to include a statement for consent or a participant recruitment form.

3.1 Research Design and Dataset Structure

I collected 400 records, each of a construct, built from hypothetical biological researchers' profiles. Each record contained information about age, gender, research and education years, the domain of biological sciences, the type and level of AI, frequency of AI tool use, and responses to multiple items. The domain of Biological Sciences included biotechnology, molecular biology, microbiology, genetics, biochemistry, bioinformatics, environmental biology, and biomedical sciences. I classified the level of AI integration, placing lower and traditional AI tools in one category and more advanced tools in the other category; since ANOVA needed a minimum of three levels in the construct of AI use, I created a separate three-level construct.

3.2 Variables and Measurement

Each of the sub-components of the Artificial Intelligence for Technical University (AITU) measured nine elements: (i) statistics, (ii) literature, (iii) bioinformatics, (iv) visualization, (v) modeling, (vi) design of experiments, (vii) programming, (viii) scientific writing, and (ix) interpretation of images and data. Each of AI Research Literacy (AIRL), Research Workflow Efficiency (RWE), Data Interpretation Efficiency (DIE), Experimental Design Efficiency (EDE), Perceived Research Quality (PRQ), Responsible AI Use (RAIU), and Research Productivity (RP) was measured by four elements. Three constructs measured Analytical Accuracy (AA). Greater values of the constructs were considered to be higher.

3.3 Statistical Analysis

Characteristics of distributions are described through descriptive statistics. Reliability was assessed through Cronbach's Alpha. Construct association was assessed through Pearson's correlations. Welch's t tests were used to determine the 95% confidence interval for the comparison of the integration groups, and Cohen's d was used to analyze the result. One-way ANOVA and Tukey HSD test were used to analyze productivity across groups with low, moderate and high AI use. Three multiple regressions were used to predict DIE, EDE and RP. Hierarchical regression was used with age, experience, education level and AI training as block one, AI tutoring as block two, and AIRL and RWE as block three. Multicollinearity was assessed using variance inflation factor (VIF). The indirect AITU-RWE-RP pathway was estimated using 5000 sample bootstrap. Two-sided $p < .05$ was considered statistically significant.

4. Results

Our sample of 400 respondents has an average age of 31.77 years (SD = 6.43) and an average total years of research experience of 6.96 years (SD = 3.94). These two metrics show substantial similarity. More than a third, (36.75%), of our respondents have PhDs. Half (56.25%) of our respondents have some experience with AI. The three largest domains that participants operate in are molecular biology, biotechnology, and bioinformatics respectively. The mean AITU was 3.44 (SD = 0.94) as well as the mean scores for the other components, which range from 3.26 to 3.57.

Table 1: Demographic and Research Characteristics

Characteristic	Category/Statistic	Value
Age (years)	Mean $\pm$ SD	31.77 $\pm$ 6.43
Research experience (years)	Mean $\pm$ SD	6.96 $\pm$ 3.94
Gender	Male	211 (52.75%)
Gender	Female	180 (45.00%)
Gender	Other/Prefer not to say	9 (2.25%)
Academic level	Doctoral Researcher	147 (36.75%)
Academic level	Postgraduate Researcher	89 (22.25%)
Academic level	Postdoctoral/Early-career Scientist	60 (15.00%)
Academic level	Research Assistant	58 (14.50%)
Academic level	Laboratory Researcher	46 (11.50%)
Biological science domain	Molecular Biology	61 (15.25%)
Biological science domain	Biotechnology	59 (14.75%)
Biological science domain	Bioinformatics	58 (14.50%)
Biological science domain	Microbiology	51 (12.75%)
Biological science domain	Biomedical Sciences	50 (12.50%)
Biological science domain	Genetics	42 (10.50%)
Biological science domain	Environmental Biology	41 (10.25%)
Biological science domain	Biochemistry	38 (9.50%)

Table 2: AI Tool Usage Characteristics

Variable	Category	n	Percent
AI training status	Yes	225	56.25
AI training status	No	175	43.75
AI tool use frequency	Low	73	18.25
AI tool use frequency	Moderate	98	24.50
AI tool use frequency	High	112	28.00
AI tool use frequency	Very High	117	29.25
AI integration group	Higher AI Integration	202	50.50
AI integration group	Lower/Traditional AI Integration	198	49.50

Table 3: Descriptive Statistics of Major Study Constructs

Construct	Mean	SD	Minimum	Maximum	Median	Skewness
AITU	3.438	0.943	1.222	5.000	3.556	-0.274
DIE	3.368	1.107	1.000	5.000	3.500	-0.197
EDE	3.394	1.065	1.000	5.000	3.500	-0.346
RWE	3.381	1.033	1.000	5.000	3.500	-0.260
AA	3.325	1.105	1.000	5.000	3.333	-0.298
RP	3.471	1.134	1.000	5.000	3.600	-0.425
AIRL	3.570	1.005	1.000	5.000	3.750	-0.372
PRQ	3.413	1.082	1.000	5.000	3.500	-0.393
RAIU	3.264	1.038	1.000	5.000	3.250	-0.188

4.1 Descriptive Statistics and Reliability

Lengths of composite scores reviewed and average lengths of the sections of their composite score components were optimal. The composite scores reviewed had the following Cronbach's Alphas: AITU (.905), DIE (.878), EDE (.829),

RWE (.812), RP (.883), AIRL (.812), PRQ (.823), RAIU (.797), and RP (.767). The results confirmed the absence of redundancy and the use of composite scores.

Table 4: Reliability Analysis of Study Constructs

Construct	Items	Cronbach alpha	Interpretation
AI-Enabled Tool Utilization	9	0.905	Strong
Data Interpretation Effectiveness	4	0.878	Strong
Experimental Design Effectiveness	4	0.829	Strong
Research Workflow Efficiency	4	0.812	Strong
Research Productivity	5	0.883	Strong
AI Research Literacy	4	0.812	Strong
Perceived Research Quality	4	0.823	Strong
Responsible AI Use	4	0.797	Acceptable
Analytical Accuracy	3	0.767	Acceptable

4.2 Correlation and Comparative Analysis

As predicted, AITU was positively correlated with DIE ($r = .528$, $p < .001$), EDE ($r = .356$, $p < .001$), and RP ($r = .523$, $p < .001$). Thus, H1-H3 were confirmed. In higher-integration records, mean DIE was higher ($M = 3.80$, $SD = 1.01$), as compared to lower/traditional ($M = 2.92$, $SD = 1.03$). As

such, $t(397.27) = 8.62$, $p < .001$, $d = 0.86$. EDE was also higher (3.62 versus 3.17), $t(396.40) = 4.30$, $p < .001$, $d = 0.43$, confirming H4-H5. There was also a large effect in productivity (3.97 versus 2.96), $t(386.79) = 9.95$, $p < .001$, $d = 1.00$. A secondary gender comparison for responsible AI use was non-significant, $t(380.72) = -0.57$, $p = .567$.

Table 5: Pearson Correlation Matrix

Construct	AITU	DIE	EDE	RWE	RP	AIRL	PRQ
AITU	1.000						
DIE	0.528***	1.000					
EDE	0.356***	0.304***	1.000				
RWE	0.478***	0.461***	0.239***	1.000			
RP	0.523***	0.457***	0.368***	0.512***	1.000		
AIRL	0.402***	0.439***	0.350***	0.409***	0.393***	1.000	
PRQ	0.376***	0.342***	0.306***	0.429***	0.364***	0.353***	1.000

Note. *** $p < .001$; ** $p < .01$; * $p < .05$.

Table 6: Comparison of Research Outcomes by AI Integration Level

Outcome	Lower M (SD)	Higher M (SD)	Mean diff.	t	df	p	Cohen d	95% CI
DIE	2.92 (1.03)	3.80 (1.01)	0.878	8.62	397.27	<.001	0.86	[0.678, 1.078]
EDE	3.17 (1.06)	3.62 (1.02)	0.448	4.30	396.40	<.001	0.43	[0.243, 0.653]
RWE	3.04 (1.01)	3.71 (0.94)	0.667	6.81	394.58	<.001	0.68	[0.475, 0.860]
AA	2.91 (1.07)	3.73 (0.98)	0.820	7.98	393.58	<.001	0.80	[0.618, 1.022]
RP	2.96 (1.09)	3.97 (0.94)	1.013	9.95	386.79	<.001	1.00	[0.813, 1.213]
PRQ	3.10 (1.08)	3.72 (1.00)	0.623	6.00	394.12	<.001	0.60	[0.419, 0.827]
RAIU	3.11 (1.10)	3.42 (0.95)	0.313	3.05	388.25	0.002	0.30	[0.111, 0.516]

Note. Lower/traditional n = 198; higher integration n = 202. Welch tests were used. A secondary female-versus-male comparison for RAIU was non-significant, $t(380.72) = -0.57$, $p = .567$.

4.3 ANOVA

There were three levels of AI use as defined above: low, moderate and high. Productivity levels differed for these levels of AI use, $F(2,397) = 60.85$, $p < .001$, eta squared = .235. Productivity increased for low use (mean = 2.66, SD = 1.06),

moderate use (mean = 3.39, SD = 1.02) and high use (mean = 4.02, SD = 0.93) groups, respectively. Comparisons using Tukey's tests showed that differences among all levels were significant.

Table 7: ANOVA of Research Productivity by AI Tool Utilization Category

Source	SS	df	MS	F	p	Eta squared
Between groups	120.466	2	60.233	60.853	0.002	0.235
Within groups	392.957	397	0.990			
Total	513.424	399				

Table 7A: Tukey HSD Post-hoc Comparisons

group1	group2	meandiff	p-adj	lower	upper	reject
High	Low	-1.363	0.000	-1.656	-1.071	True
High	Moderate	-0.635	0.000	-0.909	-0.360	True
Low	Moderate	0.729	0.000	0.418	1.039	True

4.4 Multiple and Hierarchical Regression

The DIE model accounted for 38.5 % of the total variance. The exceptions, in the order of significance, were AI training, AITU, AIRL, experience and RWE (adjusted R squared = .377, $F(5, 394) = 49.36$, $p < .001$). The EDE model contributed 18.4 % of the total variance, explaining 18.4 % of the total variance. The exceptions in the order of significance were AITU, AIRL, RAIU, training, and experience (adjusted R squared = .174, $F(5, 394) = 17.78$, p

<.001). In the RP model, the exception of AIRL, AITU, DIE, EDE and RWE, explained 40.9 % variations. The model has an adjusted R squared value of .402 and $F(5, 394) = 54.58$, $p < .001$. After the proximal process variables, including controls, we explained 3.5 % variations, and the adjusted R squared value is .377. Together with AITU, AIRL ($B = 0.146$, $p = .006$) and RWE (adjusted R squared = .097), and supported H6.

Table 8: Multiple Regression Predicting Data Interpretation Effectiveness

Predictor	B	SE	Beta	t	p	95% CI	VIF
AITU	0.396	0.055	0.338	7.245	<.001	[0.289, 0.504]	1.392
AIRL	0.223	0.051	0.203	4.396	<.001	[0.123, 0.323]	1.362
Research experience	0.031	0.011	0.109	2.749	0.006	[0.009, 0.053]	1.016
AI training	0.080	0.092	0.036	0.870	0.385	[-0.101, 0.261]	1.095
RWE	0.214	0.050	0.200	4.260	<.001	[0.115, 0.313]	1.406

Note. Model $R^2 = 0.385$; adjusted $R^2 = 0.377$; $F(5,394) = 49.36$, $p < .001$.

Table 9: Multiple Regression Predicting Experimental Design Effectiveness

Predictor	B	SE	Beta	t	p	95% CI	VIF
AITU	0.283	0.057	0.251	4.999	<.001	[0.172, 0.394]	1.215
AIRL	0.242	0.055	0.228	4.404	<.001	[0.134, 0.349]	1.295
Research experience	0.015	0.012	0.054	1.174	0.241	[-0.010, 0.039]	1.010
AI training	0.121	0.102	0.056	1.182	0.238	[-0.080, 0.322]	1.100
RAIU	0.003	0.048	0.003	0.065	0.948	[-0.092, 0.098]	1.071

Note. Model $R^2 = 0.184$; adjusted $R^2 = 0.174$; $F(5,394) = 17.78$, $p < .001$.

Table 10: Multiple Regression Predicting Research Productivity

Predictor	B	SE	Beta	t	p	95% CI	VIF
AITU	0.293	0.059	0.243	4.923	<.001	[0.176, 0.410]	1.631
DIE	0.127	0.050	0.124	2.526	0.012	[0.028, 0.226]	1.602
EDE	0.162	0.046	0.152	3.548	<.001	[0.072, 0.252]	1.225
RWE	0.298	0.051	0.272	5.791	<.001	[0.197, 0.399]	1.467
AIRL	0.086	0.052	0.076	1.653	0.099	[-0.016, 0.189]	1.421

Note. Model $R^2 = 0.409$; adjusted $R^2 = 0.402$; $F(5,394) = 54.58$, $p < .001$. VIF values provide multicollinearity diagnostics.

Table 11: Hierarchical Regression Predicting Research Productivity

Step	Variables Entered	R squared	Adjusted R squared	Delta R squared	F change	p for change
1	Controls	0.035	0.026	0.035	3.627	0.006
2	+ AITU	0.283	0.274	0.247	135.864	<.001
3	+ AIRL and RWE	0.380	0.369	0.097	30.692	<.001

Note. Final step AIRL $B = 0.146$, $p = 0.006$. Mediation: indirect $AITU \rightarrow RWE \rightarrow RP$ effect = 0.195, 95% bootstrap CI [0.134, 0.260], 5,000 samples.

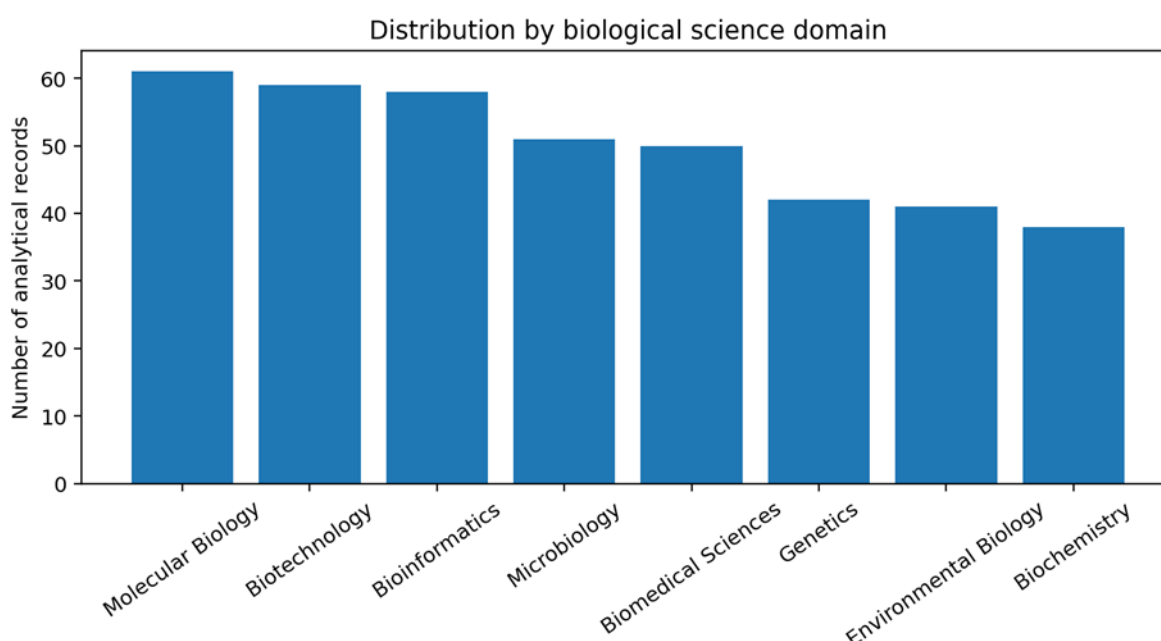
4.5 Multicollinearity, Mediation, and Hypothesis Testing

Three main regressions had VIF values from 1.01 to 1.63. RWE predicted PRQ ($B = 0.450$, $t = 9.48$, $p < .001$, R squared = .184). This provides support to H7. The total AITU effect on RP was mediated and the value was $B = 0.629$. After RWE was added the value for the direct effect was $B = 0.434$ and

for the indirect effect was $B = 0.195$, and the 95% bootstrap interval (0.134, 0.260) was entirely outside of zero. Therefore, we can say that workflow efficiency was part of the relationship between utilization and productivity. This indicates that all 7 hypotheses were supported.

Table 12: Hypothesis Testing Summary

Hypothesis	Statement	Test	Key Statistic	p-value	Decision
H1	AITU positively associated with DIE	Pearson correlation	$r = 0.528$	<.001	Supported
H2	AITU positively associated with EDE	Pearson correlation	$r = 0.356$	<.001	Supported
H3	AITU positively associated with RP	Pearson correlation	$r = 0.523$	<.001	Supported
H4	Higher AI integration has greater DIE	Welch t test	$t = 8.62$	<.001	Supported
H5	Higher AI integration has greater EDE	Welch t test	$t = 4.30$	<.001	Supported
H6	AIRL predicts RP beyond background controls	Hierarchical regression	$B = 0.146$	0.006	Supported
H7	RWE positively predicts PRQ	Linear regression	$B = 0.450$	<.001	Supported

**Fig 1:** Distribution of analytical records by biological science domain.

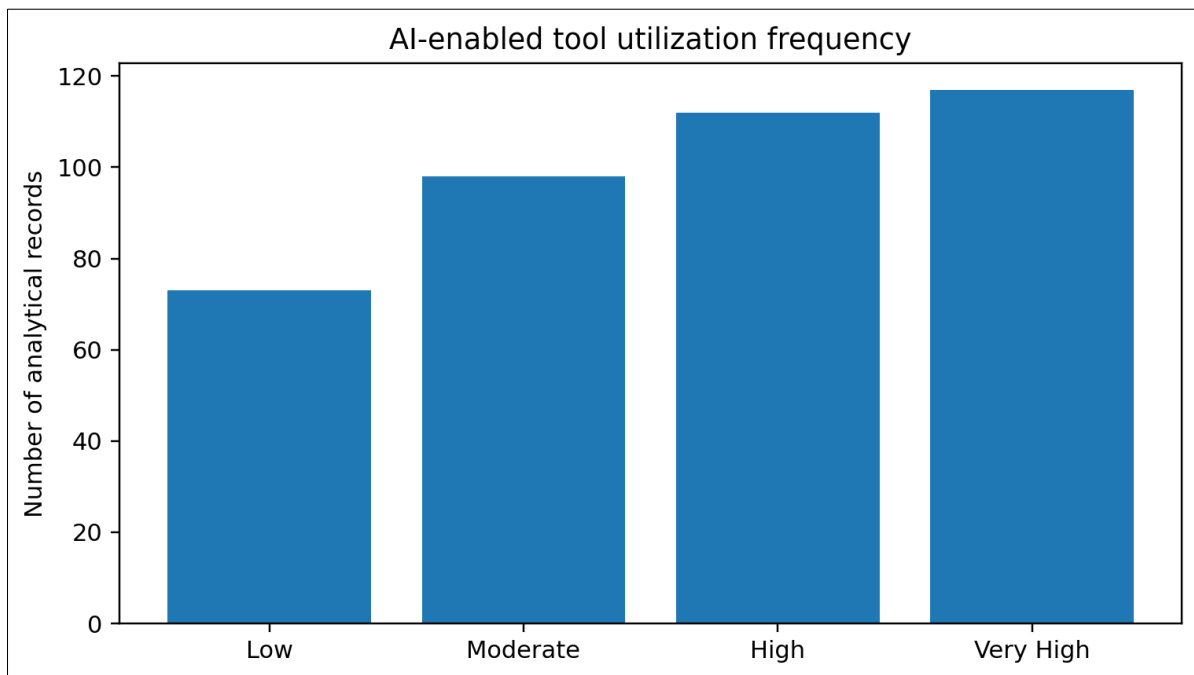


Fig 2: Frequency distribution of AI-enabled tool utilization.

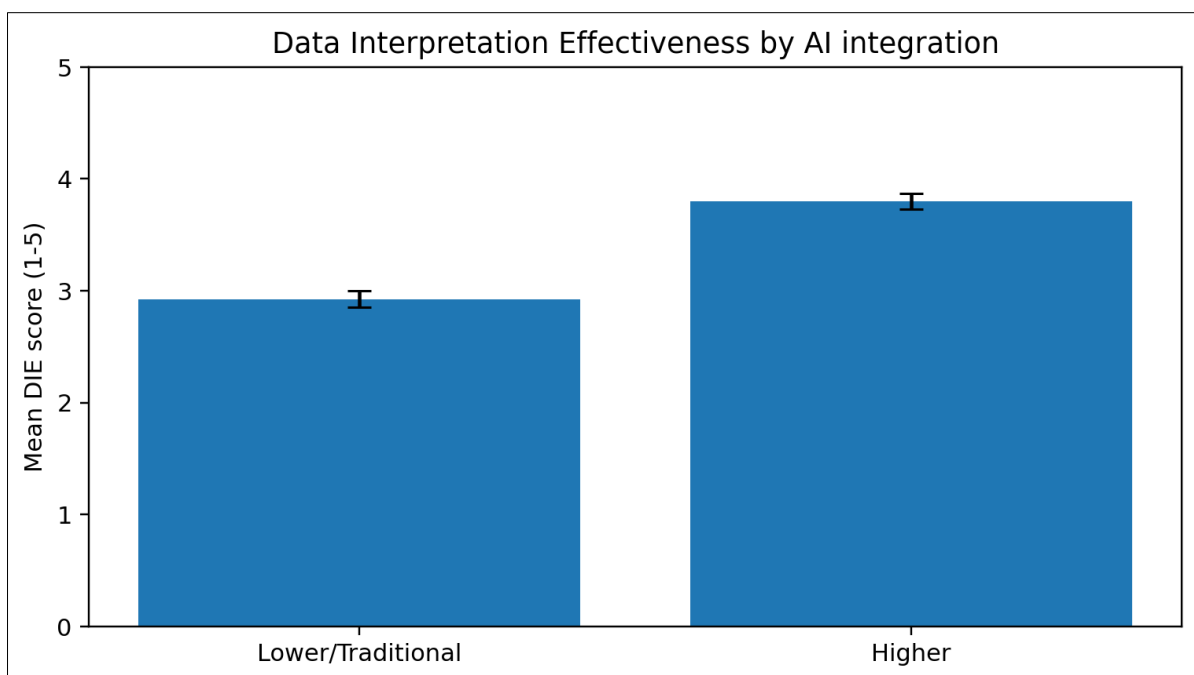


Fig 3: Mean Data Interpretation Effectiveness by AI integration group.

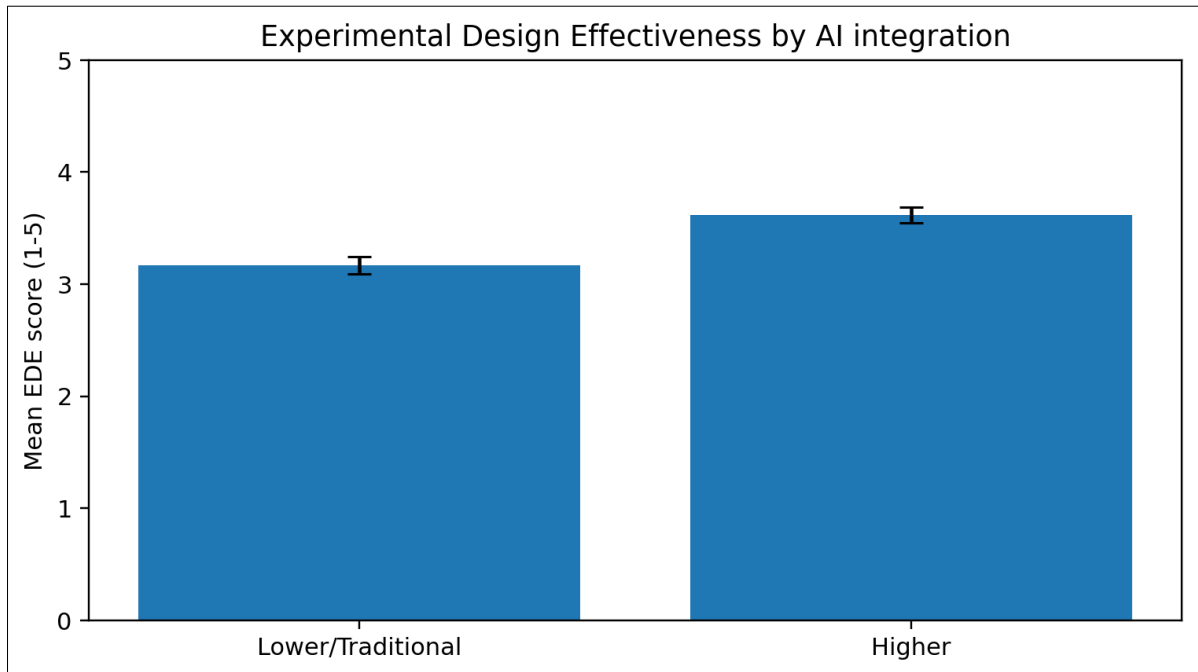


Fig 4: Mean Experimental Design Effectiveness by AI integration group.

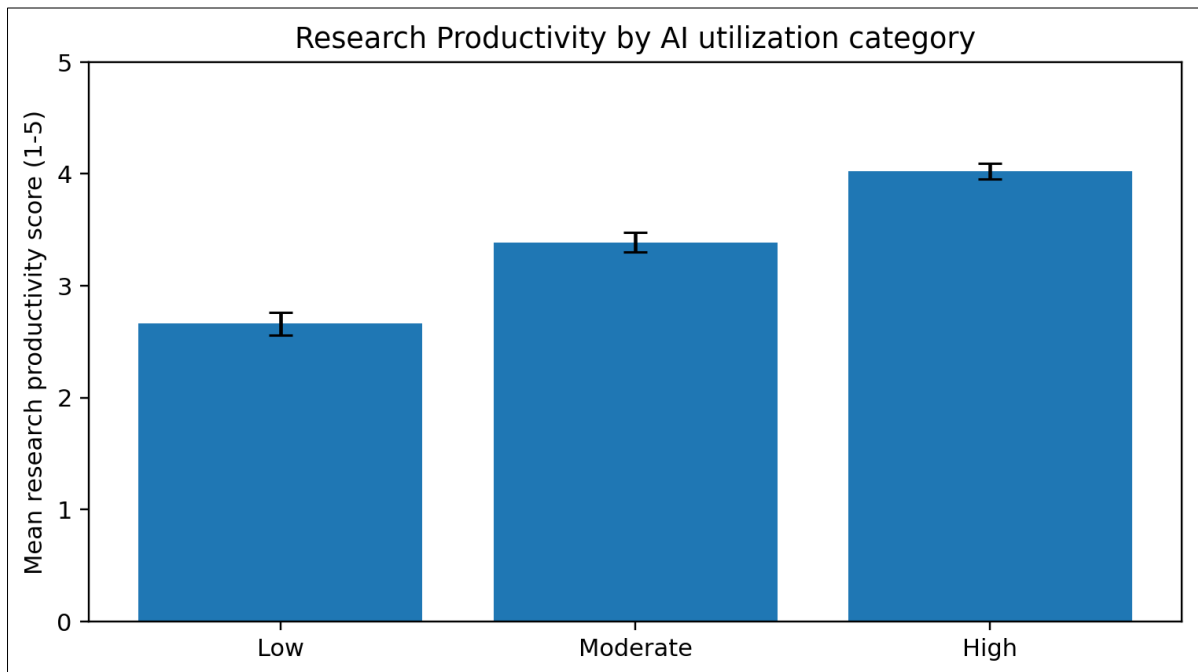


Fig 5: Mean Research Productivity by AI utilization category.

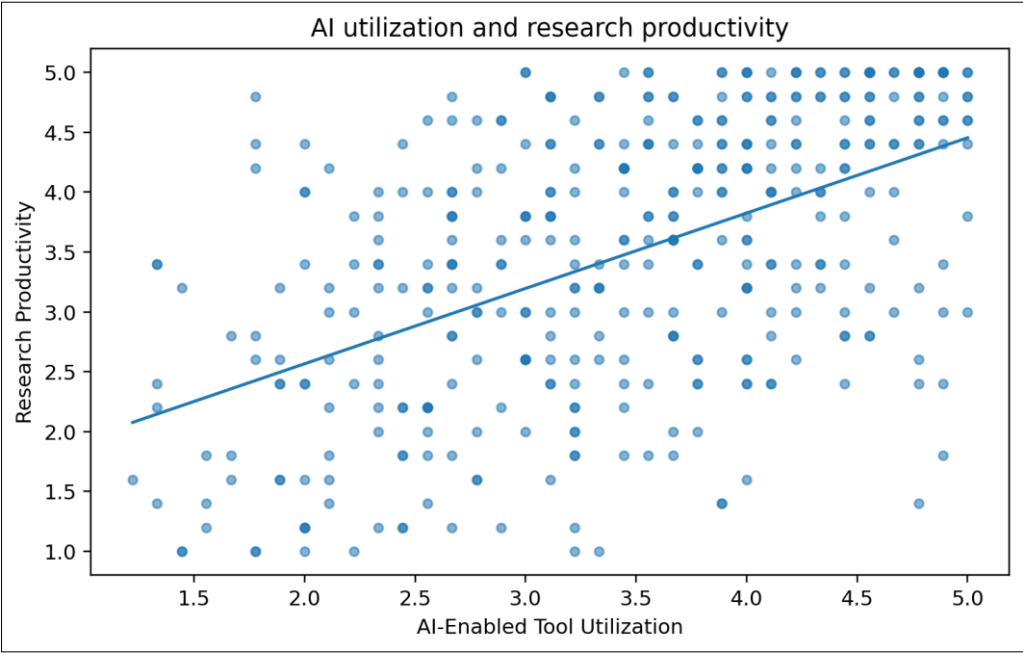


Fig 6: Scatter plot of AI-Enabled Tool Utilization and Research Productivity with fitted linear trend.

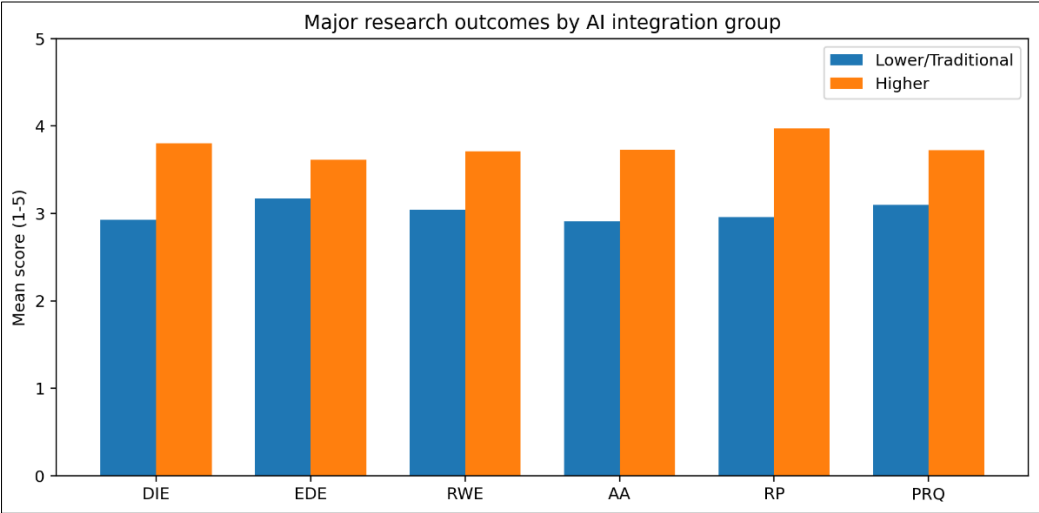


Fig 7: Comparison of major research outcomes between lower/traditional and higher AI integration groups.

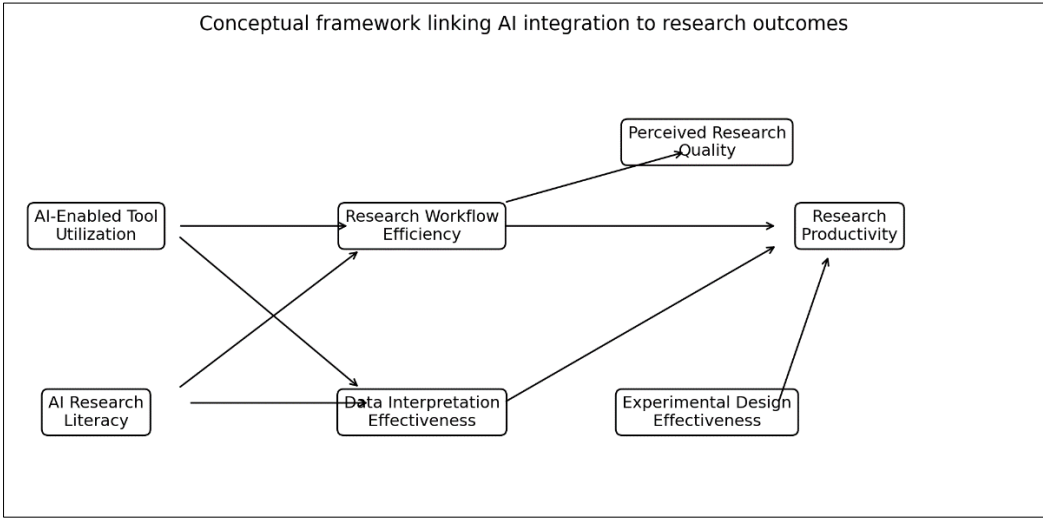


Fig 8: Conceptual Framework Linking AI Integration to Research Outcomes.

5. Discussion

The results indicate that AI alongside tool integration should be treated as a procedural component rather than a tool in research. The strongest associations were found for skills of data analysis and effectiveness. This is consistent with the use of AI for research in omics, biological networks, computational investigations, and structural predictions (Jumper *et al.*, 2021; Li *et al.* 2022; Theodoris *et al.*, 2023)^[12, 24]. The correlation with experimental design was less pronounced since the quality of design is impacted by multiple factors of the biological situation, for example, articulation of the problem, the reliability and the feasibility of the measurement. Once the boundaries of the problem and the goal are known, model-driven selection of experiments can help reduce the complexity of the problem (Elder *et al.*, 2021; Hashizume *et al.*, 2023)^[6, 8].

5.1 Consequences for Biological Science Investigation

Artificial intelligence (AI) will redefine scientific inquiry in several ways. When AI is used in scientific inquiry, it is important to view the process of creating a training AI as learning how to do scientific research rather than as programming. Leakage and the ambiguity of prompts and their interpretations pose additional challenges. The use of AI will likely change the nature of scientific research by changing the tasks and the processes of scientific research. The incorporation of AI should be viewed as a drastic change to scientific research. Issues should be addressed when AI and large language models (LLMs) are used as well as prediction systems that rely on official data and biological data (Cui *et al.*, 2024; Lu *et al.*, 2024)^[5].

5.2 Ethical and Responsible Artificial Intelligence Considerations

AI has a host of problems that range from the production of untrustworthy information to violations of privacy and security. Systems might also produce contracts that are based on discriminatory information. AI can make irreversible changes to systems. Text processing systems may have some reliability issues, but systems that divide biomedical text into smaller semantic units have larger issues. Given the existing problems and the prevailing research integrity standards, we urge authors to cite other works and explain their observed discrepancies using empirical data rather than the data used in the current study (Blau *et al.*, 2024)^[2]. There are still problems of transparency and the ability to replicate models. Models should not be used in fundamental research at all costs, but most especially in research that might produce effects or outcomes that will lead to highly risky or highly irreversible interventions (Heil *et al.*, 2021; Karim *et al.*, 2023)^[9, 13].

5.3 Constraints and Prospective Research Avenues

The case studies presented here help to clarify ideas. They do not help to draft dimensions, occurrences, or casual connections for a trait. It could be useful to a certain extent to leverage Likert composites to help to simplify some of the complicated nuances found in biological research, in the context of AI. In this research, I want to integrate the synthesis of exposure to AI, with specific AI technologies. Important research gaps need to be filled. Currently, researchers are tasked to undertake prospective, multicenter collaborative studies. Furthermore, for their current research, they need to incorporate engagement metrics, activity logs,

and methods to enhance blinding and quality evaluation. Assessment of decision quality and the consistency of errors is justified. In the end, the quality of tasks performed by machines has to be evaluated.

6. Summary

Research with artificial intelligence (AI) can mimic and automate biological research to a significant extent. Use of AI could assist in streamlining the process of research and developing more intelligent research frameworks. Based on existing research, the use of AI has generally had a positive impact on biological research. Artificial intelligence models (including a number of variables) suggested the combination of understanding, analysis, design, and research workflow elements will have the greatest overall positive impact. The models suggested that there is not necessarily one key element of AI. The type of modeling in which complementarities dominate (rather than substitutability) suggests that AI will have the greatest potential to positively impact biological research as an integrated system rather than a replacement for the work of a researcher.

References

1. Bhardwaj A, Kishore S, Pandey DK. Artificial intelligence in biological sciences. *Life*. 2022;12(9):1430. doi:10.3390/life12091430.
2. Blau W, Cerf VG, Enriquez J, *et al.* Protecting scientific integrity in an age of generative AI. *Proc Natl Acad Sci U S A*. 2024;121(22):e2407886121. doi:10.1073/pnas.2407886121.
3. Chen Q, Sun H, Liu H, Jiang Y, Ran T, Jin X, *et al.* An extensive benchmark study on biomedical text generation and mining with ChatGPT. *Bioinformatics*. 2023;39(9):btad557. doi:10.1093/bioinformatics/btad557.
4. Chicco D, Heider D, Facchiano A. Editorial: Artificial Intelligence Bioinformatics: Development and Application of Tools for Omics and Inter-Omics Studies. *Front Genet*. 2020;11:309. doi:10.3389/fgene.2020.00309.
5. Cui H, Wang C, Maan H, Pang K, Luo F, Duan N, *et al.* scGPT: toward building a foundation model for single-cell multi-omics using generative AI. *Nat Methods*. 2024;21(8):1470-1480. doi:10.1038/s41592-024-02201-0.
6. Elder S, Klumpp-Thomas C, Yasgar A, *et al.* Cross-Platform Bayesian Optimization System for Autonomous Biological Assay Development. *SLAS Technol*. 2021;26(6):579-590. doi:10.1177/24726303211053782.
7. Hao M, Gong J, Zeng X, Liu C, Guo Y, Cheng X, *et al.* Large-scale foundation model on single-cell transcriptomics. *Nat Methods*. 2024;21(8):1481-1491. doi:10.1038/s41592-024-02305-7.
8. Hashizume T, Ozawa Y, Ying BW. Employing active learning in the optimization of culture medium for mammalian cells. *NPJ Syst Biol Appl*. 2023;9:20. doi:10.1038/s41540-023-00284-7.
9. Heil BJ, Hoffman MM, Markowitz F, Lee SI, Greene CS, Hicks SC. Reproducibility standards for machine learning in the life sciences. *Nat Methods*. 2021;18(10):1132-1135. doi:10.1038/s41592-021-01256-7.

10. Jiménez-Luna J, Grisoni F, Weskamp N, Schneider G. Artificial intelligence in drug discovery: Recent advances and future perspectives. *Expert Opin Drug Discov.* 2021;16(9):949-959. doi:10.1080/17460441.2021.1909567.
11. Jin S, Zeng X, Xia F, Huang W, Liu X. Application of deep learning methods in biological networks. *Brief Bioinform.* 2021;22(2):1902-1917. doi:10.1093/bib/bbaa043.
12. Jumper J, Evans R, Pritzel A, *et al.* Highly accurate protein structure prediction with AlphaFold. *Nature.* 2021;596:583-589. doi:10.1038/s41586-021-03819-2.
13. Karim MR, Islam T, Shajalal M, Beyan O, Lange C, Cochez M, *et al.* Explainable AI for bioinformatics: Methods, tools and applications. *Brief Bioinform.* 2023;24(5):bbad236. doi:10.1093/bib/bbad236.
14. Leite ML, Costa LSL, Cunha VA, Kreniski V, Braga Filho MO, Cunha NB, *et al.* Artificial intelligence and the future of life sciences. *Drug Discov Today.* 2021;26(11):2515-2526. doi:10.1016/j.drudis.2021.07.002.
15. Li H, Tian S, Li Y, Fang Q, Tan R, Pan Y, *et al.* Modern deep learning in bioinformatics. *J Mol Cell Biol.* 2020;12(11):823-827. doi:10.1093/jmcb/mjaa030.
16. Li R, Li L, Xu Y, Yang J. Machine learning meets omics: Applications and perspectives. *Brief Bioinform.* 2022;23(1):bbab460. doi:10.1093/bib/bbab460.
17. Lu Z, Peng Y, Cohen T, Ghassemi M, Weng C, Tian S. Large language models in biomedicine and health: Current research landscape and future directions. *J Am Med Inform Assoc.* 2024;31(9):1801-1811. doi:10.1093/jamia/ocae202.
18. Lubiana T, Lopes R, Medeiros P, Silva JC, Goncalves ANA, Maracaja-Coutinho V, *et al.* Ten quick tips for harnessing the power of ChatGPT in computational biology. *PLoS Comput Biol.* 2023;19(8):e1011319. doi:10.1371/journal.pcbi.1011319.
19. Ma Q, Jiang Y, Cheng H, Xu D. Harnessing the deep learning power of foundation models in single-cell omics. *Nat Rev Mol Cell Biol.* 2024;25(8):593-594. doi:10.1038/s41580-024-00756-6.
20. Matsumoto N, Moran J, Choi H, Hernandez ME, Venkatesan M, Wang P, *et al.* KRAGEN: A knowledge graph-enhanced RAG framework for biomedical problem solving using large language models. *Bioinformatics.* 2024;40(6):btae353. doi:10.1093/bioinformatics/btae353.
21. Sanders LM, Scott RT, Yang JH, *et al.* Biological research and self-driving labs in deep space supported by artificial intelligence. *Nat Mach Intell.* 2023;5:208-219. doi:10.1038/s42256-023-00618-4.
22. Schmallenbach L, Bärnighausen TW, Lerchenmueller MJ. The global geography of artificial intelligence in life science research. *Nat Commun.* 2024;15:7527. doi:10.1038/s41467-024-51714-x.
23. Soman K, Rose PW, Morris JH, *et al.* Biomedical knowledge graph-optimized prompt generation for large language models. *Bioinformatics.* 2024;40(9):btae560. doi:10.1093/bioinformatics/btae560.
24. Theodoris CV, Xiao L, Chopra A, *et al.* Transfer learning enables predictions in network biology. *Nature.* 2023;618:616-624. doi:10.1038/s41586-023-06139-9.
25. Tian S, Jin Q, Yeganova L, Lai PT, Zhu Q, Chen X, *et al.* Opportunities and challenges for ChatGPT and large language models in biomedicine and health. *Brief Bioinform.* 2024;25(1):bbad493. doi:10.1093/bib/bbad493.
26. Tiwari K, Kananathan S, Roberts MG, *et al.* Reproducibility in systems biology modelling. *Mol Syst Biol.* 2021;17(2):e9982. doi:10.15252/msb.20209982.
27. Treloar NJ, Braniff N, Ingalls BP. Deep reinforcement learning for optimal experimental design in biology. *PLoS Comput Biol.* 2022;18(11):e1010695. doi:10.1371/journal.pcbi.1010695.
28. Varadi M, Anyango S, Deshpande M, *et al.* AlphaFold Protein Structure Database: Massively expanding the structural coverage of protein-sequence space with high-accuracy models. *Nucleic Acids Res.* 2022;50(D1):D439-D444. doi:10.1093/nar/gkab1061.
29. Walters WP, Barzilay R. Critical assessment of AI in drug discovery. *Expert Opin Drug Discov.* 2021;16(9):937-947. doi:10.1080/17460441.2021.1915982.
30. Wang J, Cheng Z, Yao Q, Liu L, Xu D, Hu G. Bioinformatics and biomedical informatics with ChatGPT: Year one review. *Quant Biol.* 2024;12(4):345-359. doi:10.1002/qub.2.67.

How to Cite This Article

Chakraborty S, Harikrishnan M. Transforming biological science research through AI-enabled tools: a comparative analysis of data interpretation, experimental design, and research productivity. *Int J Artif Intell Eng Transform.* 2026;7(2):73-83. doi:10.54660/IJALET.2026.7.2.73-83.

Creative Commons (CC) License

This is an open access journal, and articles are distributed under the terms of the Creative Commons Attribution NonCommercial-ShareAlike 4.0 International (CC BY-NC-SA 4.0) License, which allows others to remix, tweak, and build upon the work noncommercially, as long as appropriate credit is given and the new creations are licensed under the identical terms.