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MULTI-AGENT AI IN GENETICS AND MOLECULAR BIOLOGY: A REVIEW OF EMERGING ARCHITECTURES, APPLICATIONS AND FUTURE DIRECTIONS

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ABSTRACT

Advancements in Artificial Intelligence (AI) particularly Large Language Models (LLMs), have accelerated the development of Multi-Agent Artificial Intelligence (MAAI) systems in biomedical research. In contrast to the traditional single-agent systems multi-agent system consists of multiple specialized agents which perform reasoning, tool usage, data retrieval, hypothesis generation, workflow orchestration and validation in a collaborative manner. This review analyses developments of multi-agent AI use in genetics and molecular biology with focus on genomics, transcriptomics, bioinformatics, drug discovery, plant biology and biomedical scientific discovery. Different important frameworks like Robin, OpenBioLLM, GenomAgent, Coated-LLM, PhenoAssistant and oncology-focused genomic systems are analyzed to understand their architectures, functionalities, advantages, and limitations. Existing studies demonstrate how multi-agent systems helps to improve genomic reasoning, to automate bioinformatics workflows, to enhance biological data interpretation and also helps for scientific hypothesis generation. The review also highlights the growing integration of LLMs with retrieval systems, biological databases and multi-omics platforms. Though the results are encouraging, still there are challenges which includes limited biological validation, lack of standardized benchmarks, explainability concerns, reproducibility issues, computational cost and insufficient real-world deployment. Evidence advocates that multi-agent AI has potential to transform genetics and molecular biology by enabling autonomous scientific assistants, adaptive reasoning systems, and intelligent bioinformatics platforms. Future research should move on the direction of on trustworthy AI, clinically validated systems, multi-omics reasoning, standardized evaluation protocols and safer autonomous scientific workflows.

KEYWORDS: Multi-Agent Artificial Intelligence (MAAI); Large Language Models (LLMs); Genetics; Molecular Biology; Bioinformatics.

INTRODUCTION

The growth of genomic, transcriptomic, proteomic and multi-omics datasets has created major computational and analytical challenges in modern biology and medicine. Traditional bioinformatics pipelines often require substantial human intervention, domain expertise and complex software integration. With development of the Large Language Models (LLMs) and autonomous AI systems researchers have explored Multi-Agent Artificial Intelligence (MAAI) as a solution for automating scientific reasoning and biological analysis.

Multi-agent systems consist of multiple specialized intelligent agents to perform complex tasks in the same specialization and then collaborate. Unlike Single Agent AI, MAAI divide the whole workflows into modular components such as data retrieval, hypothesis generation, reasoning, validation, and tool execution. This collaborative structure improves scalability, interpretability, adaptability and robustness. In genetics and molecular biology, these systems are now being applied to genomic question answering, RNA-seq analysis, transcriptomics, drug discovery, phenotype analysis, multi-omics integration and autonomous scientific discovery.

Developments in Large Language Models (LLMs), reinforcement learning, and agentic AI architectures have accelerated the development of intelligent multi-agent systems which is capable of adaptive reasoning and orchestration [5, 9, 16]. Also Multi-Agent Artificial Intelligence (MAAI) systems extend traditional AI by enabling multiple autonomous agents to collaborate, communicate, negotiate, coordinate and make decentralized decisions in real time [2, 15,17,19,20]. The researchers like [3,12] established the success of Multi-Agent AI systems in other domains like pharmaceutical sales prediction and business management. Also Workflow optimization in healthcare, emergency response coordination, hospital resource allocation and intelligent healthcare management systems are important application areas for MAAI [4,22]. This has encouraged exploration of use of the same in genetics and molecular biology. Some past studies established Multi Agent system in a collaborative manner could outperform traditional single-agent methods in complex forecasting and decision-making tasks with multiple interacting variables. These developments motivated researchers to investigate whether similar multi-agent architectures could also be helpful for better biological reasoning, genomic analysis, therapeutic discovery, and scientific workflow automation.

This review analyses developments in multi-agent AI use in genetics and molecular biology. The review first discusses general multi-agent architectures and their integration with LLMs. Then it explores applications in genomics and bioinformatics, biological discovery systems, plant biology, biomedical hypothesis generation and oncology-related genomic systems. Also the review analyses research gaps, limitations and future scopes for autonomous AI-driven molecular biology research.

Multi-Agent Architectures in Bioinformatics and Genomics

Some studies reveal that multi-agent systems are establishing their importance in genomics and bioinformatics. In their study [6] the authors proposed that the future of bioinformatics will depend on the integration of biological foundation models, multi-agent AI systems and automated validation frameworks. Their review discussed foundation models like scGPT, EpiAgent and Nicheformer, which support transcriptomics, epigenomics, and spatial omics analysis. The authors also suggsted that future bioinformatics systems will move from simple predictive AI toward agentic AI capable of reasoning, planning, iterative hypothesis generation, and tool utilization.

Similarly in another study [14] performed a systematic review of agentic AI systems in genomics and transcriptomics domains. The review analyzed applications including CRISPR guide design, biomarker discovery, transcriptomics, Mendelian randomization and workflow automation. The study concluded that multi-agent systems are specially important for uncertain biological tasks involving interpretation and reasoning where deterministic workflows may still be effectively handled by single-agent systems.

The authors [13] presented one of the most comprehensive reviews of multi-agent genomic systems between 2022 and 2025. The researchers analyzed twenty-five genomic and oncology-focused systems according to architectural style, execution strategy, automation level, agent typology and LLM integration. The authors found that more than 60% of genomic systems already integrate LLMs and that general genomics systems are more mature and automated than oncology-specific systems. Their work also categorized agents as reasoning agents, orchestration agents, conversational agents, multi-omics agents and tool-based agents, demonstrating the growing complexity of multi-agent genomic ecosystems.

Another study [18] examined multi-agent systems for biological and clinical data analysis. The study emphasised orchestration frameworks like CrewAI, LangGraph and MCP, which support coordination among multiple specialized agents. Applications included genomics, drug discovery, bioinformatics and clinical decision support. The review concluded that multi-agent systems improve workflow automation and reasoning quality but still face challenges related to scalability, safety, computational cost, and real-world deployment.

Together, these studies establish that multi-agent AI is evolving into a foundational paradigm for future bioinformatics and molecular biology research.

Multi-Agent AI for Genomic Question Answering and Bioinformatics

One of the most important direct applications of multi-agent AI in genetics is genomic question answering and biological database interaction. The study [8] proposed OpenBioLLM, an open-source multi-agent architecture developed as an improvement over GeneGPT. The system employs multiple specialized agents for routing, query generation, retrieval, BLAST analysis, evaluation and generation of final response. Experimental evaluation on GeneTuring and GeneHop benchmarks demonstrated that OpenBioLLM could match or outperform GeneGPT while reducing computational latency.

Similarly [1] proposed GenomAgent, a multi-agent extension of GeneGPT for genomic question answering. GenomAgent introduced specialized agents responsible for task identification, API coordination, response extraction, and decision synthesis. The study reported around 12% performance improvement and also lower computational cost compared to the original GeneGPT architecture. These studies establish that specialized collaborative agents can be able to improve genomic reasoning, interpretability and biological information retrieval.

A major advantage of these systems is their ability to interact in an autonomous manner with biological databases like NCBI APIs and BLAST tools. Instead of relying on a single or monolithic model different agents perform complementary functions including sequence alignment, genomic retrieval, validation of evidence and generation of answer. Such modularity improves scalability and transparency in genomic workflows.

Still there are limitations. Both OpenBioLLM and GenomAgent are heavily dependent on external biological databases and failures occur because of incomplete data or incorrect API parameter generation. Additionally most evaluations remain restricted to benchmark datasets rather than real-world biological experimentation or clinical applications.

Multi-Agent AI for Scientific Discovery and Biomedical Hypothesis Generation

Apart from answering the questions, Multi-agent AI systems are being used in autonomous scientific discoveries. Ghareeb and Chang presented Robin, a multi-agent system for automating steps in experimental biology discovery. Robin combines literature-mining agents with data-analysis agents, to create hypotheses, suggest experiments, analyse RNA-seq data, and iteratively enhance scientific reasoning. Using dry age-related macular degeneration as a case study, Robin discovered prospective treatment techniques and molecular targets including ABCA1.

Robin is a key step towards semi-autonomous biological research combining literature retrieval, experimental reasoning, and transcriptome analysis in a coordinated multi-agent context. But the framework still requires a lot of human interference in the design of the experiments, implementation in the lab and validation.

Another major approach called Coated-LLM was proposed by [21] for biomedical hypothesis generating in drug combination research. The system used three types of agents (Researcher, Reviewer and Moderator) to collectively produce and validate biomedical hypotheses for Alzheimer's disease treatment. The research revealed that the multi-agent collaboration increased the quality of reasoning and reduced hallucinations compared to previous approaches. Importantly, one of the AI-predicted medication combinations was confirmed in vitro.

Another eye catching development in biomedical multi-agent systems was presented by the researcher in the study [23] through the "Virtual Biotech" framework. The system was designed to match the structure of a biotechnology company using coordinated specialized AI agents supervised by a Chief Scientific Officer (CSO) agent. Individual agents handled genetics, genomics, pathway biology, pharmacology, toxicology and clinical research tasks along with integrating evidence from GWAS, QTLs, transcriptomics, pathway analysis, protein interactions, and clinical trial databases. The framework analyzed more than 55,000 clinical trials and identified relationships between cell-type-specific genes and therapeutic success rates. It also generated mechanistic insights for lung cancer and ulcerative colitis therapies. This study demonstrated how multi-agent AI systems support translational therapeutic discovery by integrating genetics, molecular biology and clinical evidence within a collaborative reasoning framework.

These papers demonstrate how multi-agent AI can assist in biomedical thinking, drug development and experimental planning. Still contemporary systems suffer from tiny data sets, insufficient biological validation and domain-specific implementations.

Applications in Plant Biology and Phenotyping

Multi-agent systems are also being developed in plant biology and in phenotyping studies. [7] developed PhenoAssistant, an AI system which is conversational and multi-agent, designed to automate plant phenotyping. The framework consists of various dedicated agents for image analysis, phenotypic extraction, statistical analysis, visualization, literature search and model training.

PhenoAssistant showed good performance on several plant datasets, e.g. Arabidopsis and winter wheat. The approach reduced computational hurdles to plant scientists by allowing natural-language interface with biological activities. Importantly, the research underscored that multi-agent systems could democratize the processing of biological data and enhance reproducibility.

The system is very important to biology but only indirectly related to genetics as the main focus is on phenotypic analysis rather than genomic sequencing or gene regulation. However, as phenotypes are the result of the interaction of genetics and environment, systems such as this are still useful to wider studies in molecular biology.

Emerging Autonomous Biomedical AI Agents

The recent literature has highlighted the shift from traditional machine learning to autonomous AI scientists. Gao et al. examined the future of AI agents in biomedical research, offering concepts such as brainstorming agents, debate agents, self-driving laboratories and autonomous scientific helpers. Their work offered several levels of AI autonomy from simple helpers to completely autonomous AI scientists that can perform experimental reasoning and collaborate.

The authors believe that multi-agent systems can change genomics, virtual cell modeling, drug discovery, protein interaction analysis and molecular simulation. But they also highlighted several major issues including hallucinations, inconsistent reasoning, ethical dangers, the deficiency of multimodal datasets and inadequate generalization ability.

Many of the papers evaluated share these issues. Most systems today remain semi-autonomous and require significant human control. Further, there is a need for the development of established evaluation benchmarks, explainability mechanisms, and clinical validation frameworks.

Comparative Analysis of Current Multi-Agent Systems

The analyzed papers collectively reveal a number of repeating architectural trends. Most systems use specialized agents for retrieval, reasoning, validation, orchestration and tool execution. We are seeing more hybrid execution models that combine sequential and parallel processing, notably in genomic workflows.

Another big trend is the growing incorporation of LLMs into biological AI systems. These days, genomic analysis platforms are frequently using models like GPT-4, Llama, Gemini, DeepSeek, Claude, and Qwen. LLMs improve natural-language interaction, reasoning, workflow automation and biological interpretation.

However, critical issues persist and are unresolved. And first, many systems still suffer from hallucinations and inaccurate thinking. Second, the majority of studies do not provide prospective validation of biological or clinical data. Third, reproducibility remains a challenge due to reliance on varied biological datasets and developing APIs. Fourth, the computational cost and the complexity of orchestration increase significantly with the number of agents.

Also missing in the field are defined benchmarks that may evaluate end-to-end biological discovery, quality of agent collaboration, interpretability, and long-term reproducibility. Therefore, it is difficult to compare the systems directly.

CONCLUSIONS

Multi-agent Artificial Intelligence is quickly becoming a breakthrough paradigm in genetics and molecular biology. Research has shown that collaborative AI agents can improve genomic reasoning, automate bioinformatics procedures, facilitate biological hypothesis development, and accelerate scientific discovery. Applications today include genomics, transcriptomics, drug discovery, RNA-seq analysis, plant phenotyping, precision oncology and multi-omics integration.

The experiments covered here show that multi-agent architectures have considerable advantages over monolithic AI systems, especially for complicated biological activities requiring reasoning, coordination and interface with external tools and databases. OpenBioLLM, GenomAgent, Robin, Coated-LLM, and PhenoAssistant are examples of the increasing maturity and diversity of multi-agent biological AI platforms.

But the field is still in an early stage of development. Most systems still require human oversight, are not validated in real-world clinical settings, and are challenged by explainability, scalability, reproducibility, safety, and regulatory compliance.

Future efforts should be directed toward developing trustworthy and interpretable AI systems that can robustly reason across multi omics, autonomously design experiments and provide clinically verified decision support.

Multi-agent AI may potentially offer autonomous scientific assistants capable of expediting discoveries in genetics, molecular biology, and precision medicine as LLMs, foundation models, and orchestration frameworks continue to advance.

REFERENCES:

1. Abedini K, Shami F and Silvello G (2026). From single to multi-agent reasoning: advancing GeneGPT for genomics QA. In: European Conference on Information Retrieval. Springer Nature Switzerland, Cham, pp. 577-585.
2. Allmendinger S, Bonenberger L, Endres K, Fetzer D, Gimpel H and Kühl N (2026). Multi-agent AI. Electron. Mark. 36.
3. Battapothu V (2024). Multi-Agent AI architectures for automated customer experience management platforms. Int. J. Res. Appl. Innov. 7: 11929-11946.
4. Borkowski AA and Ben-Ari A (2025). Multiagent AI systems in health care: envisioning next-generation intelligence. Fed. Pract. 42: 188
5. Borghoff UM, Bottoni P and Pareschi R (2025). An organizational theory for multi-agent interactions integrating human agents, LLMs, and specialized AI. Discov. Comput. 28: 138.
6. Branda F, Ahmed MM, Ciccozzi M, Guzzi PH and Scarpa F (2026). The next paradigm in bioinformatics: a review of multi-agent systems and foundational models for end-to-end scientific discovery. Brief. Bioinform. 27: bbag245.
7. Chen F, Stogiannidis I, Wood A, Bueno D, Williams D, Macfarlane F, et al. (2026). A conversational multi-agent AI system for automated plant phenotyping. Nat. Commun.
8. Chen H, Zuccon G and Leelanupab T (2025). Beyond GeneGPT: a multi-agent architecture with open-source LLMs for enhanced genomic question answering. In: Proceedings of the Annual International ACM SIGIR Conference on Research and Development in Information Retrieval in the Asia Pacific Region, pp. 143-152.
9. Gabler V and Wollherr D (2024). Decentralized multi-agent reinforcement learning based on best-response policies. Front. Robot. AI 11: 1229026.
10. Gao S, Fang A, Huang Y, Giunchiglia V, Noori A, Schwarz JR, et al. (2024). Empowering biomedical discovery with AI agents. Cell 187: 6125-6151.
11. Ghareeb AE, Chang B, Mitchener L, Yiu A, Szostkiewicz CJ, Shved D, et al. (2026). A multi-agent system for automating scientific discovery. Nature: 1-3.
12. Kanungo SS, Samarpita S and Biswal R (2026). A multi-agent prediction framework for weekly pharmaceutical demand forecasting. Int. J. Drug Deliv. Technol. 16: 774-778.
13. Mannai Z, Omheni N and Mahmoudi R. Innovative multi-agent architectures propelling genomic analysis in general and oncology domains.
14. Rozen I, Omar M, Barash Y, Kruskal JB, Brook OR, Klang E and Gorenshtein A (2026). Emerging use of agentic AI systems across genomics and transcriptomics domains: a systematic review.
15. Safir N, Albezuirat MK and Ahmed N (2024). Multi-agent systems: a review. Int. J. Eng. Artif. Intell. 5: 48-55.

16. Sapkota R, Roumeliotis KI and Karkee M (2025). AI agents vs. agentic AI: a conceptual taxonomy, applications and challenges. Inf. Fusion: 103599.
17. Singh M (2025). Multi-agent systems: the future of distributed AI platforms for complex task management. World J. Adv. Res. Rev. 26: 48-55.
18. Spieser J, Balapour A, Meller J, Patra KC and Shamsaei B (2026). A review of multi-agent AI systems for biological and clinical data analysis. Methods Protoc. 9: 33.
19. Talasila D (2026). Agentic AI in multi-agent systems: exploring the coordination, negotiation, and cooperation of autonomous artificial agents in competitive and collaborative digital ecosystems. J. Integr. Sci. Soc. Impact 2: 64-71.
20. Wooldridge M (2009). An Introduction to Multiagent Systems. John Wiley & Sons.
21. Xu Q, Soto C, Shahnawaz M, Liu X, Jiang X and Kim Y (2025). Multi agent large language models for biomedical hypothesis generation in drug combination discovery. iScience 28.
22. Walji Z, Badhwar R, Dave P, Choi D, Virani S and Park J (2026). Multi-Agent System for Emergent Care (MAS-EC): focused on workload, efficiency, and user experience. Hum. Factors Healthc. 100133.
23. Zhang HG, Eckmann P, Miao J, Mahon AB and Zou J (2026). The Virtual Biotech: a multi-agent AI framework for therapeutic discovery and development. bioRxiv 2026-02.