BioMARS: A Multi-Agent Robotic System for Autonomous Biological Experiments

Anonymous authors
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Abstract

Large language models (LLMs) and vision-language models (VLMs) have the potential to transform biological research by enabling autonomous experimentation. Yet, their application remains constrained by rigid protocol design, limited adaptability to dynamic lab conditions, inadequate error handling, and high operational complexity. Here we introduce BioMARS (Biological Multi-Agent Robotic System), an intelligent platform that integrates LLMs, VLMs, and modular robotics to autonomously design, plan, and execute biological experiments. BioMARS uses a hierarchical architecture: the Biologist Agent synthesizes protocols via retrieval-augmented generation; the Technician Agent translates them into executable robotic pseudo-code; and the Inspector Agent ensures procedural integrity through multimodal perception and anomaly detection. The system autonomously conducts cell passaging and culture tasks, matching or exceeding manual performance in viability, consistency, and morphological integrity. It also supports context-aware optimization, outperforming conventional strategies in differentiating retinal pigment epithelial cells. A web interface enables real-time human-AI collaboration, while a modular backend allows scalable integration with laboratory hardware. These results highlight the feasibility of generalizable, AI-driven laboratory automation and the transformative role of language-based reasoning in biological research.

1 Introduction

The convergence of robotic automation and artificial intelligence is reshaping experimental biology, promising greater reproducibility, throughput, and independence from human variability Holland & Davies (2020). However, the complexity of biological protocols—which demand adaptive decision-making, multi-stage coordination, and interpretation of nuanced environmental feedback—has hindered the realization of fully autonomous systems. Existing automation solutions, ranging from specialized liquid handling robots Dettinger et al. (2022); Novak et al. (2020); Taguchi et al. (2023), to modular single-arm platforms for cell culture automation Hamm et al. (2024); Tristan et al. (2021), and dual-arm platforms enabling automated cell production Königer et al. (2024); Yachie & Natsume (2017); Ochiai et al. (2021), often require extensive manual oversight and lack the flexibility to navigate unanticipated procedural deviations. Early systems focused on streamlining specific tasks, including biofoundries Chao et al. (2017), IoT-enabled experimental platforms Miles & Lee (2018), and clinical sample preparation Müller et al. (2020), but these non-robotic arm systems still faced hardware limitations that prompted the development of robotic arm solutions.

Concurrently, large language models (LLMs) and vision–language models (VLMs) are transforming scientific problem-solving by enabling machines to parse literature, synthesize knowledge, and execute multi-modal reasoning across diverse domains Vaswani et al. (2017); Wang et al. (2024); Luu & Buehler (2024); Zhang et al. (2025). Recent efforts leveraging LLMs in chemical experimentation Boiko et al. (2023); Darvish et al. (2025); Cooper et al. (2025) and biological protocol generation O'Donoghue et al. (2023); Huang et al. (2024) signal a paradigm shift toward AI-native experimentation. Yet, their integration with physical robotic systems for biological execution remains underexplored.

Here we introduce BioMARS (Biological Multi-Agent Robotic System), a dual-arm robotic platform orchestrated by LLMs and VLMs Zhu et al. (2023); Zhang et al. (2024) for fully autonomous

execution of biological experiments. BioMARS performs end-to-end protocol design, environmental coordination, and robotic manipulation through adaptive multimodal reasoning. By converting research literature into actionable procedures and coupling them with error-aware execution strategies, the system ensures both flexibility and robustness in complex biological tasks.

We demonstrate BioMARS across five experimental capabilities: (1) efficiently searching and analyzing online research documentation to design experimental protocols for diverse cell types under varying conditions; (2) accurately translating and executing these protocols using a dual-arm biological laboratory; (3) detecting experimental errors via keyframe analysis; (4) performing end-to-end cell culturing; and (5) resolving optimization issues through the analysis of historical experimental data.

2 Related Work

2.1 Automation in Life Science Research Laboratory

In recent years, laboratory automation technology has rapidly advanced in the life sciences, with its core objectives being to enhance experimental efficiency and reproducibility through standardized operational workflows and reduced human intervention. Initial studies have explored various systems without robotic arms: the biofoundry system proposed by Chao et al. Chao et al. (2017) for synthetic biology automation, the IoT-enabled closed-loop experimental platform developed by Miles and Lee Miles & Lee (2018) which integrates real-time data feedback, and Müller's team Müller et al. (2020) that demonstrated automated clinical sample preparation. Additionally, Dettinger's team Dettinger et al. (2022) developed an open-source pipetting robot featuring customizable liquid-handling protocols. These systems laid down essential workflows that boosted experimental efficiency while also highlighting limitations in hardware adaptability.

To address these constraints, researchers shifted focus to robotic-arm systems. Initial efforts centered on single-arm platforms: Li et al. Li et al. (2023) pioneered a robotic-arm-based 3D bioprinting system for tissue engineering. Precision in these systems was further refined through innovations like Zhang et al.'s Zhang et al. (2023) vision-assisted pipetting method, which dynamically adjusted for container deformation. Hamm et al. Hamm et al. (2024) extended single-arm capabilities through modular designs optimized for automated cell culture workflows.

Nevertheless, inherent limitations in single-arm flexibility for multi-step coordination drove exploration of dual-arm systems. Koniger's team Königer et al. (2024) achieved a breakthrough with their dual-arm platform enabling uninterrupted 3D epithelial tissue production through synchronized mechanical manipulation and fluidic control. Ochiai et al. Ochiai et al. (2021) advanced this paradigm by developing a variable-scheduling system capable of parallel maintenance for eight mammalian cell lines through dynamic task prioritization. These developments collectively signify a paradigm shift in laboratory automation, transitioning from discrete single-function devices to integrated systems capable of executing complex experimental protocols through coordinated multi-arm operations.

2.2 Large Model based Multi-agent Systems

With breakthroughs in cross-modal reasoning and task planning capabilities of large language models (LLMs) Achiam et al. (2023), researchers have begun exploring their application paradigms in multi-agent collaboration. Early foundational concepts of agent coordination and communication were proposed by Wooldridge and Jennings Wooldridge & Jennings (1995), while the emergence of powerful LLMs has injected new vitality into this field. Brown et al. demonstrated the potential of LLMs in simulating human dialogues, which can be applied to inter-agent communication Brown et al. (2020). In terms of architectural design, Patil et al. Patil et al. (2025) proposed connecting multiple functional APIs via LLMs for task decomposition, while Cai et al. Cai et al. (2023) validated LLMs' potential as "tool generators" capable of dynamically creating specialized agents. For multi-robot collaboration scenarios, Chen et al. Chen et al. (2024) compared the performance boundaries of centralized versus distributed multi-robot systems, and the RoCo framework developed by Mandi et al. Mandi et al. (2024) enables semantic-level conversational planning among multiple robots through LLMs. Zheng et al. Zheng et al. (2023) utilized multi-agent LLMs to optimize material crystal structures, Hua et al. Hua et al. (2023) constructed a war simulation multi-agent system, and

Aher et al. Aher et al. (2023) explored LLMs' applications in replicating psychological experiments. These interdisciplinary advancements highlight the universal advantages of LLM-based multi-agent systems in complex decision-making scenarios.

2.3 LLMs and VLMs as Robot Planners

In the field of robotic task planning, LLMs demonstrate value through two complementary pathways: (1) Semantic reasoning-based high-level instruction decomposition, exemplified by Song et al. Song et al. (2023) with their few-shot planning framework, and Silver et al. Silver et al. (2024) who leverage GPT-4 to generate PDDL domain models. (2) Direct generation of executable control code, as seen in Liang et al. Liang et al. (2023)'s "code-as-policies" paradigm, Huang et al. Huang et al. (2023)'s 3D value map synthesis method, and Wu et al. Wu et al. (2023)'s implementation of personalized household robots.

To address the physical perception limitations of pure language modalities, vision-language models (VLMs) have been integrated into planning pipelines: Hu et al. Hu et al. (2023) developed a visual foresight mechanism that significantly reduces physical interaction error rates, while Shirai et al. Shirai et al. (2024) created a vision-language interpreter for dynamic task sequence adjustment. Mei et al. Mei et al. (2024) further enhanced this through their ReplanVLM system, achieving real-time plan corrections via multimodal feedback.

These advancements collectively improve robotic adaptability in dynamic environments. Notably, Gao et al. Gao et al. (2024) proposed a physically-grounded model that simultaneously processes visual signals and manipulation constraints, while Wake et al. Wake et al. (2024) validated GPT-4V's multimodal planning capabilities in imitation learning scenarios.

3 Architecture of BioMARS system

BioMARS (Biological Multi-Agent Robotic System) enables end-to-end autonomous execution of biological experiments through a network of specialized LLM- and VLM-based agents (Fig. 1a). Built on an enhanced Agentic Retrieval-Augmented Generation (RAG) framework with modular error correction Singh et al. (2025), BioMARS decomposes complex protocols, interprets unstructured literature, and dynamically synthesizes findings into executable procedures.

The Biologist Agent ingests diverse open-access research documents, generates executable protocol steps by leveraging biological domain knowledge to create structured, constraint-aware queries. By incorporating constraints such as container type (e.g., petri dishes, flasks) and platform capacity, it tailors each protocol to the laboratory's operational environment. The Technician Agent transforms high-level plans into fine-grained control primitives for robotic execution. These primitives are allocated across dual robotic arms and coordinated with environmental modules such as incubator and centrifuge.

To ensure execution robustness, the Inspector Agent—powered by ViTs and VLMs—performs rapid anomaly detection. It identifies procedural deviations including geometric misalignments (e.g., unattached pipette tips, misaligned petri dishes) and mechanical failures, prompting replanning or user notification. This tri-agent system mirrors the modularity and task specialization seen in other autonomous platforms Boiko et al. (2023); M. Bran et al. (2024), enabling BioMARS to operate adaptively under changing experimental conditions.

The platform supports natural language prompts (e.g., "How to passage HeLa cells") via a web interface. Users can initiate, monitor, and modify experiments interactively. Critically, BioMARS's modular architecture allows seamless integration of new hardware and protocol domains through programmable function modules, facilitating extensibility across diverse biological workflows.

3.1 Protocol Synthesis under Environmental Constraints

Reliable generation of biological protocols from literature poses challenges due to procedural complexity, heterogeneous experimental conditions, instrumentation constraints, and output formatting requirements. BioMARS addresses this through a multi-agent reasoning framework that integrates

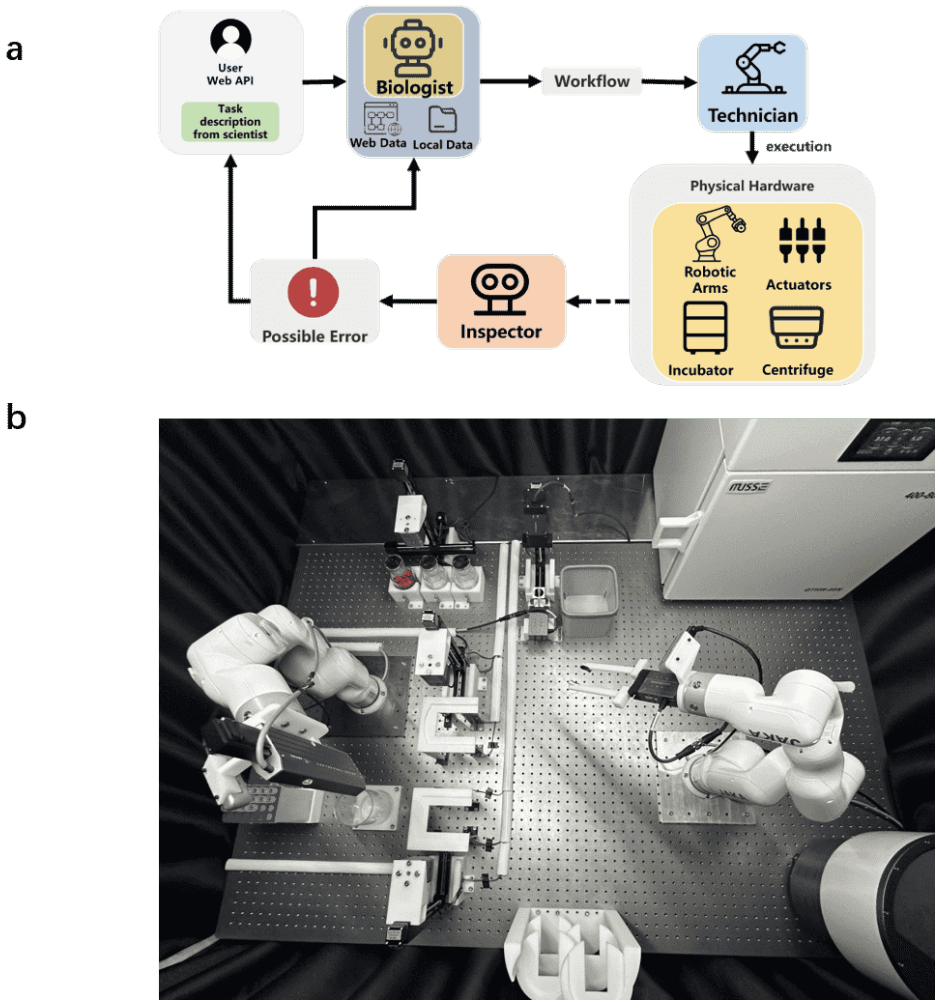

Figure 1: **System architecture and robotic setup. a,** Multi-agent workflow of BioMARS, comprising Biologist, Technician, and Inspector agents. **b,** Dual-arm robotic platform configured for autonomous biological experimentation.

LLM-based planning with vector-based retrieval and verification mechanisms to generate biologically accurate, context-aware procedures.

At the center of this system is the Biologist Agent, which operates within an enhanced Agentic Retrieval-Augmented Generation (RAG) architecture (Fig. 2a). The agent retrieves relevant knowledge using online query APIs (Google and Bing), extracting three PDFs and three high-relevance web snippets per query. Full paragraphs associated with each snippet are selected to preserve semantic context. These passages, along with the embedded user query (using OpenAI's Ada model), undergo vector similarity ranking. The top five text chunks are used as context for downstream protocol generation.

Protocol construction is distributed across three sub-agents: the Knowledge Checker (KC), which filters domain-inconsistent content; the Workflow Generator (WG), which formulates stepwise procedures; and the Workflow Checker (WC), which iteratively refines outputs for logical coherence. The system accounts for laboratory constraints, such as limited stock of specific containers (e.g. 10 cm culture dishes), pipette tip volume (10 ml), and robotic station limits, ensuring that all outputs are executable on the BioMARS platform.

System performance was evaluated using a 70-query benchmark comprising 10 procedural categories across seven cell lines, ranging from routine tasks (e.g., cell passaging, thawing) to complex

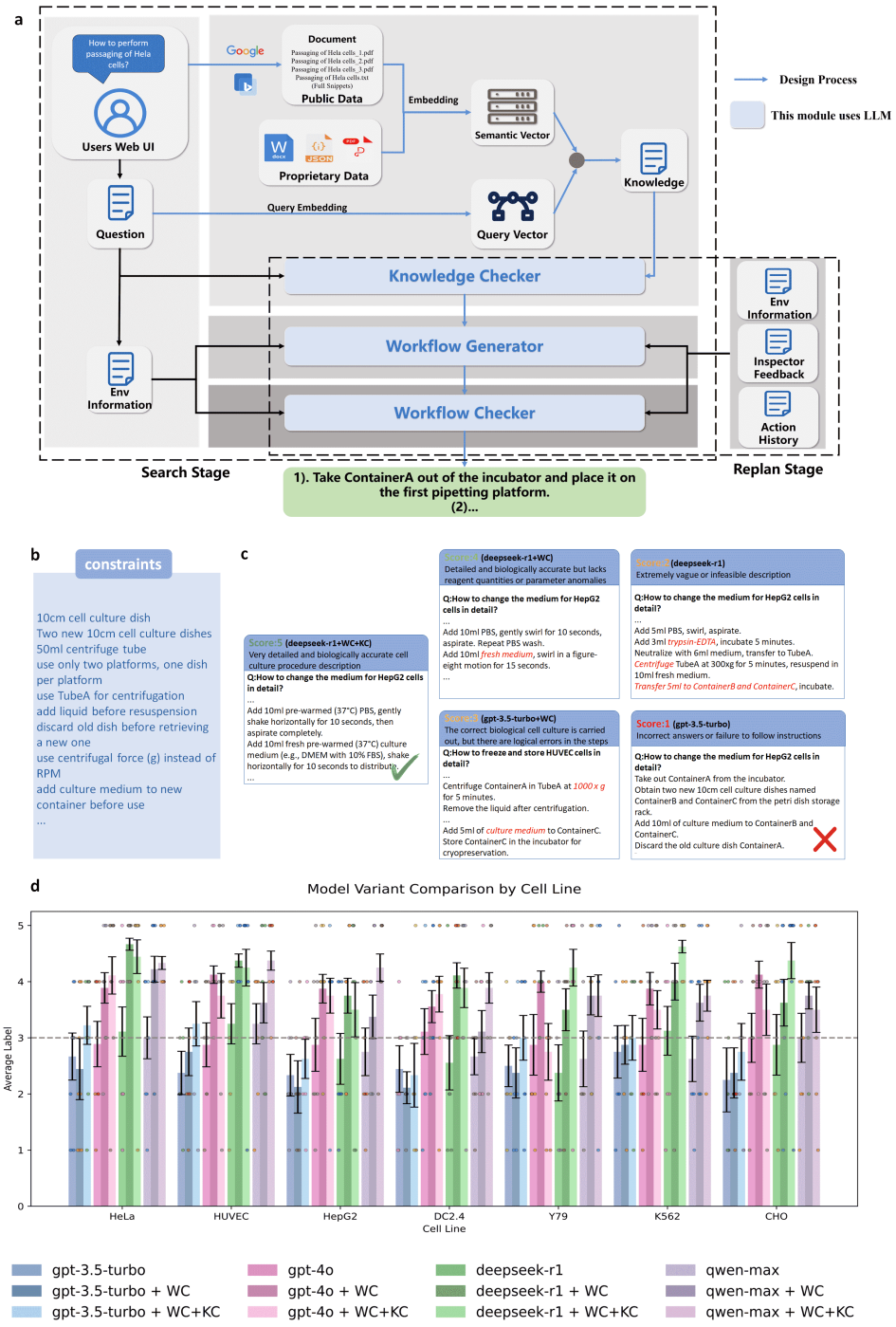

Figure 2: **Biologist Agent architecture and evaluation.** **a,** Biologist agent pipeline integrating document retrieval, semantic matching, and workflow refinement under constraints. **b,** Representative experimental constraints. **c,** Example protocol outputs with scores and errors. **d,** Performance comparison of four models (GPT-3.5-Turbo, GPT-4o, Deepseek-R1, Qwen-Max) and their variants on seven cell lines.

protocols (e.g., 3D culture, apoptosis analysis). Following Boiko et al. Boiko et al. (2023), model outputs were scored on a 5-point scale: 5 for fully detailed and accurate procedures; 4 for biologically sound steps with minor omissions; 3 for logically flawed but conceptually plausible outputs; 2 for vague or infeasible workflows; and 1 for incorrect or non-compliant procedures. Outputs below a score of 3 were considered task failures. Fig. 2c presents representative outputs with annotations.

Without WC or KC modules, base models—including GPT-4o, Qwen-Max, and DeepSeek-R1—did not exceed a mean score of 3. GPT-3.5 Turbo consistently underperformed; in one instance, it misinterpreted "How to change the HepG2 culture medium" by suggesting disposal of viable dishes and initiating culture from scratch (score: 1). DeepSeek-R1 proposed cell redistribution via trypsinization (score: 2), demonstrating procedural confusion.

Incorporation of the WC module significantly improved structural logic. For example, DeepSeek-R1+WC successfully outlined PBS rinsing and medium replacement steps but omitted critical conditions (temperature, CO_2 levels), yielding a score of 4. Further integration with the KC module provided domain-specific validations: in the cryopreservation task for HUVECs, KC-corrected protocols mitigated centrifugation errors and ensured cryostorage in liquid nitrogen.

The best-performing configuration—DeepSeek-R1+WC+KC—achieved consistent scores of 5. Its output for HepG2 medium replacement detailed exact reagent volumes, environmental settings (37°C, 5% CO_2), and handling protocols (PBS rinse with horizontal agitation), aligning closely with expert protocols. These results affirm the critical role of domain validation (KC) and procedural refinement (WC) in transforming LLM outputs into executable, high-fidelity biological protocols (Fig. 2c,d).

3.2 Protocol-to-Code Translation for Robotics

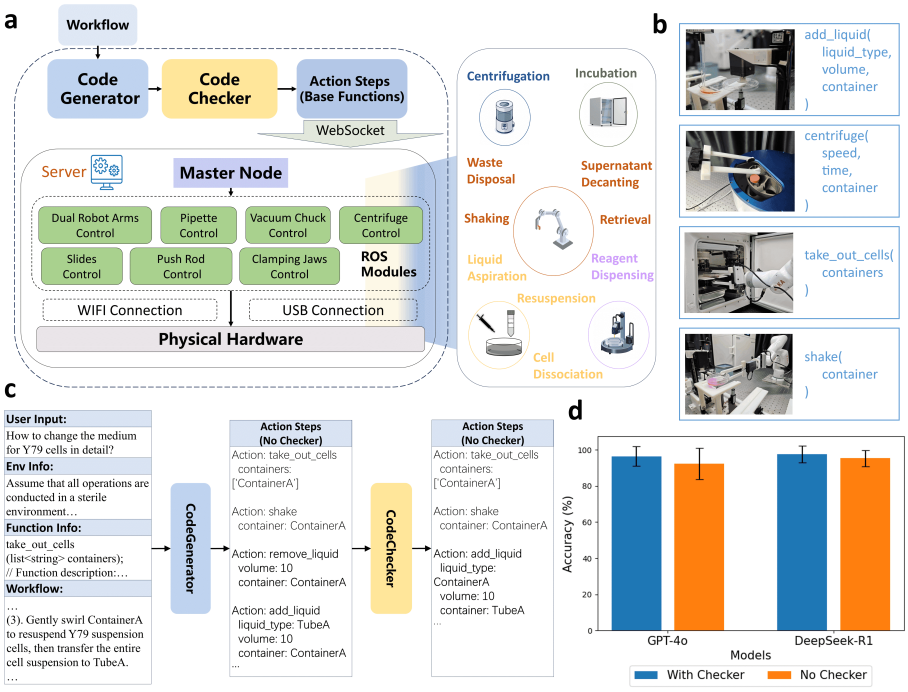

Figure 3: **Technician Agent architecture and performance of protocol translation and execution framework.** **a,** System workflow of Technician Agent, including CodeGenerator, CodeChecker, ROS node and the corresponding hardware module. **b,** Example pseudo-code instructions and corresponding robotic actions. **c,** The specific workflow of Technician Agent. **d,** Instruction accuracy comparison with and without CodeChecker for GPT-4o and DeepSeek-R1.

Translating free-text experimental protocols into executable robotic commands remains a central bottleneck in laboratory automation. Existing systems typically rely on rigid, manually curated command sequences Kanda et al. (2022); Köniğer et al. (2024), which limits their adaptability to diverse and unstructured inputs. To address this constraint, we developed the Technician Agent—a dual-module system that autonomously interprets natural language protocols and converts them into validated robotic instructions.

The Technician Agent operates through a cooperative pipeline comprising a CodeGenerator and a CodeChecker module (Fig. 3a). The CodeGenerator, powered by an LLM, maps protocol descriptions into pseudo-code composed of primitive robotic operations such as `add_liquid`, `centrifuge`, and `shake` (Fig. 3b). The CodeChecker subsequently performs rule-based validation, enforcing functional correctness and environmental compatibility based on the predefined specification set.

The pipeline structure is illustrated in Fig. 3c. Given a protocol input, the CodeGenerator produces candidate instructions tailored to the lab environment. These instructions are then parsed by the CodeChecker, which applies logical and semantic checks including parameter validation, function relevance, and argument structure. This ensures that all generated commands adhere to the operational and safety constraints of the BioMARS platform.

To assess performance, we benchmarked the Technician Agent across 300 experimental protocol steps. As shown in Fig. 3d, the full pipeline (CodeGenerator + CodeChecker, GPT-4o) achieved a 96.4% instruction-matching accuracy, outperforming a single-module baseline (92.4%). The impact of the CodeChecker module is particularly evident in complex procedural constructs. For example, when parsing the instruction "resuspend the cell pellet in 10 mL fresh complete growth medium," the baseline failed to recognize the prerequisite transfer step. In contrast, the Technician Agent inserted an implicit `add_liquid` operation before resuspension, preserving procedural logic.

Beyond resolving implicit steps, the CodeChecker module also corrects parameter mismatches, enforces range constraints, and eliminates superfluous instructions. For instance, it detects and corrects overfilled volumes relative to container capacity and replaces invalid data types in function arguments. This systematic refinement substantially improves the robustness of the robotic instruction set.

By converting ambiguous natural language into explicit, verifiable pseudo-code, the Technician Agent enhances experimental reproducibility, reduces human error, and simplifies execution on robotic platforms. This capability shifts the experimental burden away from manual coding, enabling researchers to focus on scientific inquiry rather than operational encoding.

3.3 Hierarchical VLM-Based Error Detection

Biological experimentation demands strict precision, where minor procedural errors can compromise outcomes. Conventional automation platforms typically rely on basic object detection without semantic context awareness, limiting their robustness in dynamic laboratory environments Jiang et al. (2022). To address this, we developed the Inspector Agent—a hierarchical visual monitoring system integrating vision–language models (VLMs) and vision transformers (ViTs) Han et al. (2022) for multi-stage perception and error detection (Fig. 4a).

The first stage performs visual segmentation of experimental scenes using few-shot prompting with a VLM. Key objects—such as pipette tips, culture plates, and tubes—are segmented from raw RGB inputs. To enhance spatial resolution and minimize background interference, the bounding boxes generated by the VLM are manually refined. These cropped subregions are converted to grayscale, preserving structural cues like pipette orientation and tube angles while reducing color-based noise.

In the second stage, a ViT-based keyframe detection module encodes 23 visually discriminative actions (selected from 11 control primitives) into a reference embedding library. This module enables sub-second recognition of procedural steps. In benchmark tests, ViT achieved a mean inference latency of 0.3066 s - 91. 9% faster than GPT-4o (3.7960 s) - with lower temporal variability (coefficient of variation: 13.08% vs. 42.80%; Fig. 4d). In real-world experimental settings, the ViT achieved an F1 score of 88.7% and a recall of 94.0%, demonstrating high temporal stability and operational fidelity (Fig. 4c).

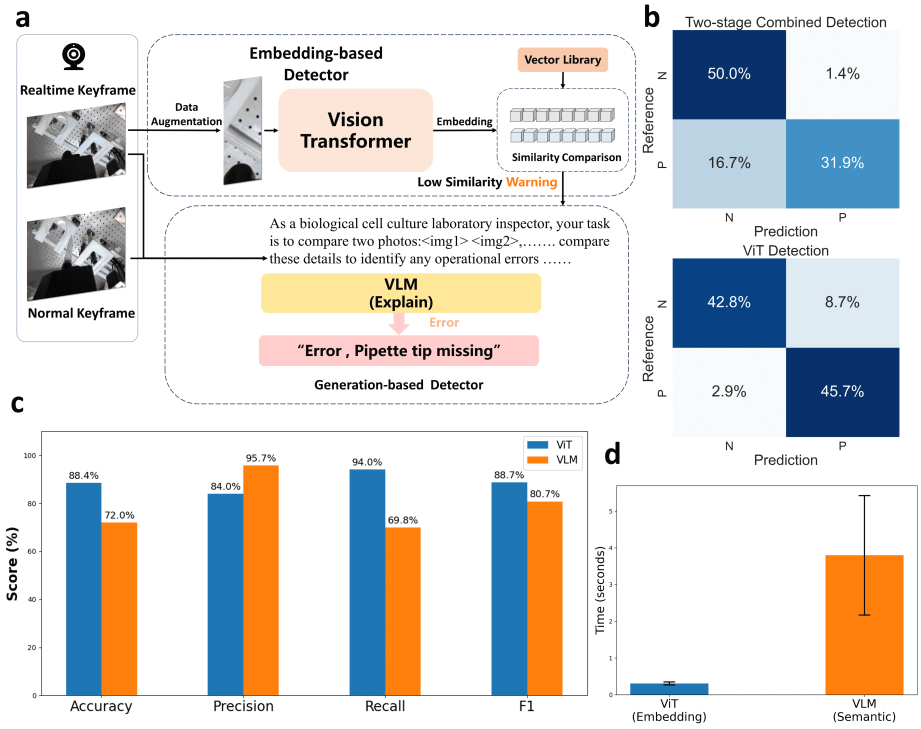

Figure 4: **Inspector Agent Overview and Performance Metrics.** **a,** Workflow diagram of the Technician Agent. **b,** Confusion matrix of two-stage combined detection and ViT detection. **c,** Performance of ViT and VLM on four evaluation metrics. **d,** The time performance of the two detection methods, ViT and VLM.

A final stage introduces zero-shot semantic validation using the VLM. When the ViT flags anomalies, frames are semantically compared with idealized keyframes using language-guided prompts (e.g., "attach pipette tip"). This semantic differential analysis enables detection of contextual errors beyond geometry alone. In validation, this mechanism achieved 95.7% precision and 80.7% F1 score(Fig. 4c), reducing the false positives rate from 8.7% to 1.4%—an 83% improvement (Fig. 4b). For example, detecting a detached pipette tip without a visible pipette is correctly flagged as an action violation. Upon confirmation, robotic operations are automatically paused and visual alerts issued.

By integrating geometric and semantic vision processing, the Inspector Agent ensures procedural robustness, accelerates feedback response times, and significantly reduces downstream execution failures.

4 Biological Experiment Design

4.1 Integrated Biological Experiment Design

To evaluate the biological reliability and operational efficiency of BioMARS, we conducted a comparative study between automated and manual cell passaging protocols across three representative cell types: HeLa (adherent), Y79 (suspension), and DC2.4 (semi-adherent/suspension). Experimental evaluation included metabolic viability, survival consistency, morphological preservation, and coefficient of variation (CV) analysis. All workflows adhered to established protocols, with BioMARS dynamically adapting process parameters to each cell line.

Cells were cultured in standard media: HeLa in DMEM with 10% FBS and 1% penicillin–streptomycin, Y79 in RPMI-1640 with 20% FBS and DC2.4 in RPMI-1640 with 10% FBS - under 5% CO2 at 37 ° C. Media changes were performed every 2–3 days. For passaging, adherent cells were detached with 0.25% trypsin–EDTA. The BioMARS system adjusted enzymatic digestion time and centrifugation based on cell type: 6 minutes for HeLa and 3 minutes for Y79, ensuring optimal yield and viability.

Metabolic viability was assessed 48 hours post-passaging using the CCK-8 assay. Optical density (OD) measurements showed no significant difference between BioMARS and manual protocols across all three cell types (Fig. 5d), indicating that automated processing maintained normal cellular proliferation. CV analysis revealed enhanced reproducibility in the BioMARS group: HeLa and Y79 samples exhibited 12–18% lower variability compared to manual handling (Fig. 5e).

Live/dead staining confirmed high post-passaging viability, with over 92% concordance between automated and manual groups (Fig. 5a,b). Green fluorescence indicated dominant live-cell populations, with clear contrast to the red-stained positive control. Morphological evaluation (Fig. 5c) showed no detectable structural abnormalities, further confirming the BioMARS system's ability to preserve cell integrity.

In addition to biological fidelity, BioMARS markedly improved operational efficiency. Manual passaging required approximately 60 minutes per cell line, whereas the BioMARS system reduced hands-on time to 5–8 minutes—representing a 90% reduction. This time savings translates into higher throughput and improved standardization, minimizing human error and procedural variability.

Collectively, these results establish that BioMARS performs comparably or superior to manual protocols in biological outcome metrics while offering significant gains in consistency, reproducibility, and efficiency.

4.2 Biological Optimizing Capability

Beyond static protocol generation, the Biologist Agent was evaluated for its capacity to perform biological optimization—an advanced task requiring iterative reasoning, mechanistic understanding, and strategic parameter adjustment. We assessed this capability using a publicly available dataset for optimizing differentiation efficiency of induced pluripotent stem cell-derived retinal pigment epithelial (iPSC-RPE) cells Kanda et al. (2022), which defines a high-dimensional experimental space grounded in biological constraints.

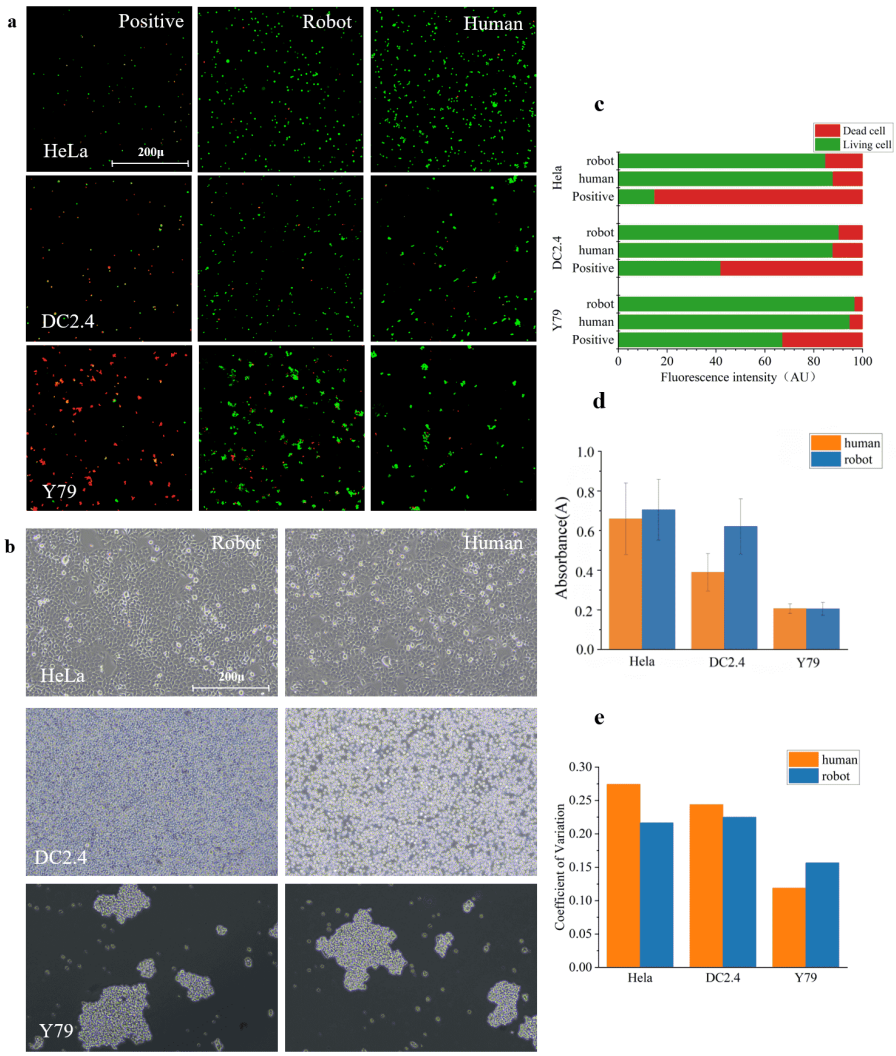

Figure 5: **Comparison of automated vs. manual cell passaging outcomes. a,** Fluorescence images of live/dead-stained cells (automated vs. manual) at 48 h post-passaging. **b,** Bright-field images of cell morphology post-passaging. **c,** Live/dead cell ratio comparison after passaging. **d,** Cell viability comparison between methods. **e,** CV of CCK-8 viability across repeats (reproducibility).

The optimization target was the pigment score, a key phenotypic marker of iPSC-RPE maturation. Seven tunable parameters were considered across preconditioning, detachment, and differentiation stages: FGFRi concentration (PC: 0–505 nM) and exposure duration (PP: 1–6 days); trypsin incubation time (DP: 5–23 min), pipetting strength (DS: 10–100 mm / s) and pipetting length (DL: short/long); KSR withdrawal schedule (KP: 1–19 days); and three-supplement exposure duration (3P: 3–19 days). This setup presents a biologically grounded, combinatorially complex optimization challenge.

To simulate realistic experimental conditions, optimization was constrained to 20 iterations, initialized from 10 randomly selected low-performing conditions (pigment score ¡ 0.6). Parameter selection used KDTree-based nearest-neighbor interpolation Friedman et al. (1977), with outputs formatted in structured JSON for reproducibility. We compared three strategies: DeepSeek-R1, GPT-4o, and Bayesian optimization under identical initialization settings.

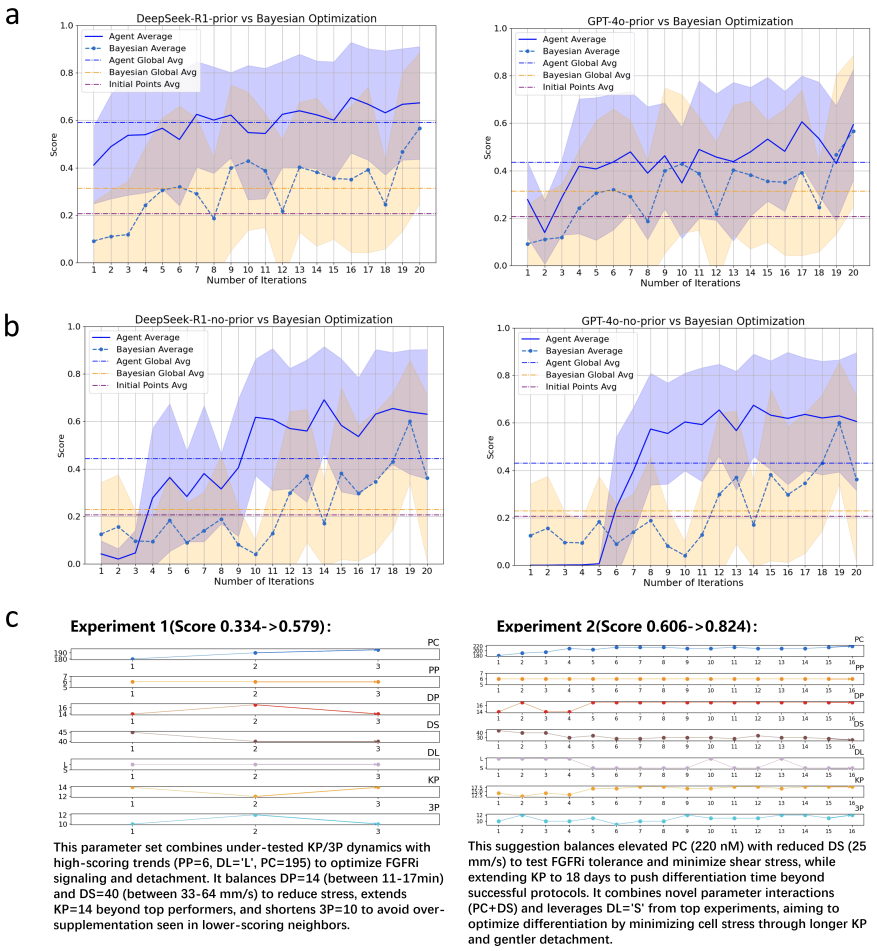

Figure 6: **Results of the iPSC-RPE optimization experiments. a,** Performance comparison between DeepSeek-R1 and GPT-4o models versus Bayesian Optimization using 10 prior experimental data points. **b,** Comparative analysis of DeepSeek-R1 and GPT-4o against Bayesian Optimization without leveraging prior experimental knowledge. **c,** Parameter recommendations from LLM-based optimizers across selected iteration rounds.

In the prior-informed setting (Fig. 6a), DeepSeek-R1 consistently outperformed baselines, reaching a final pigment score of 0.5913—surpassing GPT-4o (0.4344; +15.8%) and Bayesian optimization (0.3130; +28.5%). By iteration 7, it achieved 0.6252 and continued steady improvement. GPT-4o plateaued at 0.606, while Bayesian optimization peaked early at 0.5671. DeepSeek-R1's advantage stems from its ability to encode mechanistic constraints; for instance, in one high-scoring trial (Fig. 6c), it selected PC = 220 nM (balancing efficacy and toxicity), DS = 25 mm/s (minimizing shear stress), and KP = 18 days (prolonging Wnt signaling), reflecting domain-consistent reasoning.

GPT-4o occasionally produced viable configurations but lacked consistent convergence, likely due to reliance on pretrained heuristics. Bayesian optimization, devoid of biological priors, frequently proposed implausible combinations (e.g., PC = 405.17 nM; KP = 2 days), resulting in limited progress.

In the no-prior setting (Fig. 6b), DeepSeek-R1 again demonstrated robust generalization, reaching performance comparable to the prior-informed case. GPT-4o improved after iteration 8, ultimately reaching a moderate score of 0.6303. Bayesian optimization showed minimal learning, with scores remaining near baseline. DeepSeek-R1 also exhibited superior balance between exploration and

exploitation, as evidenced by a lower standard deviation in output scores (0.2366 vs. 0.2447 for GPT-4o and 0.2785 for Bayesian optimization), enabling more stable convergence.

These results validate the potential of knowledge-integrated LLMs to optimize complex biological systems under data-sparse conditions. By combining contextual reasoning with structured decision-making, such agents reduce dependency on manual tuning and offer scalable solutions for experimental design. Future directions include reinforcement learning frameworks to further enhance adaptive feedback integration in regenerative biology workflows.

5 DISCUSSION

This study introduces BioMARS, an intelligent agent system driven by LLMs and VLMs, capable of autonomously designing, planning and executing biological experiments. By integrating language-driven reasoning with multimodal perception and robotic control, BioMARS addresses the procedural complexity of biological workflows and generates reproducible, high-quality outcomes. These capabilities are enabled by granting LLMs and VLMs access to essential research tools, including scientific literature, programming environments and robotic execution platforms. The development of such integrated AI systems holds substantial promise for accelerating discovery in the life sciences.

While BioMARS demonstrates robust performance in standard cell culture tasks, several challenges remain. Its operation under atypical or highly customized experimental conditions is limited, with occasional human oversight required for critical steps such as pipetting volumes and centrifugation parameters. Furthermore , although BioMARS integrates multimodal reasoning to interpret and execute experimental protocols, its dependence on existing online procedures limits its capacity for adaptive parameter tuning across diverse laboratory contexts. Its responsiveness to unexpected experimental deviations is also limited, as real-time judgment remains an open challenge. Ongoing efforts focus on enhancing the system's adaptability and fault tolerance using advanced learning algorithms, with preliminary improvements observed.

BioMARS represents a substantial step toward scalable, reproducible automation in biological research. By addressing key barriers in protocol interpretation and execution, it lays the groundwork for more reliable, flexible and scalable research practices. Its ability to ensure consistent procedural replication enhances reproducibility and quality control, both of which are critical in applications such as drug discovery and cell model production. In parallel , automation reduces operational burden, with notable gains in time, material efficiency and labor reduction. Given that labor constitutes a major cost component in biological production, deployment of BioMARS offers the potential to significantly lower operational expenses. This economic benefit is expected to increase proportionally with production scale.

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