



GraphRAG for Relationship-Oriented Biomedical Knowledge Integration and Retrieval



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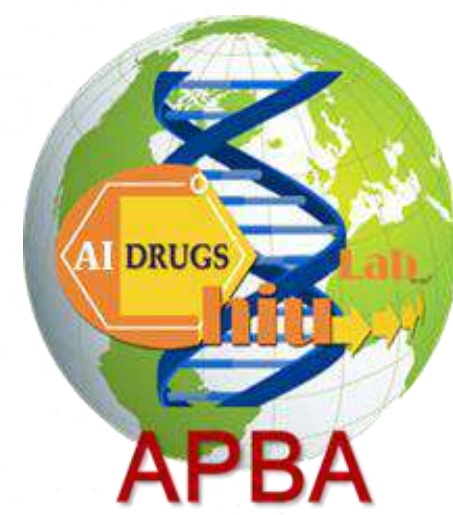


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Abstract

Biomedical knowledge requires integrating scattered evidence across multiple databases. Traditional endpoint-centric APIs rely on linear queries, struggling to capture complex biomedical relationships. To address this, our study upgrades to relationship-oriented structured retrieval, leveraging GraphRAG to integrate cross-entity biomedical knowledge networks. Performance evaluations indicate that traditional APIs require extensive manual cross-endpoint alignment and are highly vulnerable to workflow interruption caused by missing intermediate results. Conversely, GraphRAG executes continuous analyses from a single natural language prompt. By integrating Ontologies and well-performed databases (e.g. CELLxGENE datasets) for standardized data and utilizing a knowledge graph for robust fault tolerance via alternative path traversal, Taiwan BT&D² Team utilizes GraphRAG to effectively synthesize quantitative evidence and scientific summaries. This approach successfully reduces repeated manual data integration during query execution and drastically accelerates biomedical knowledge discovery.

Introduction

The GraphRAG system advances biomedical data integration by shifting from traditional, linear database queries toward a relationship-oriented knowledge network. By integrating Knowledge Graphs with Large Language Models (LLMs), it enables a more automated and context-aware workflow for biomedical research.

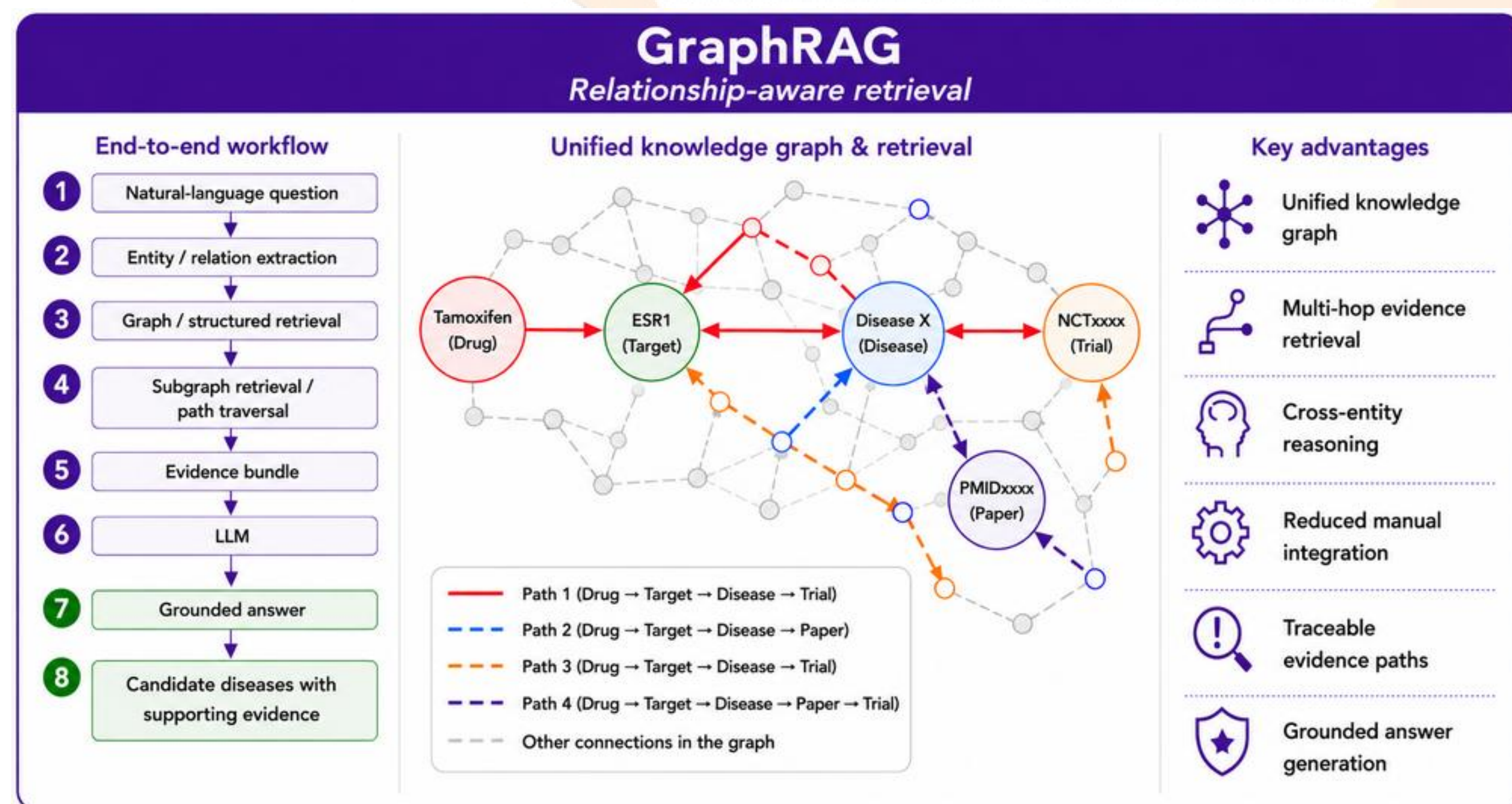
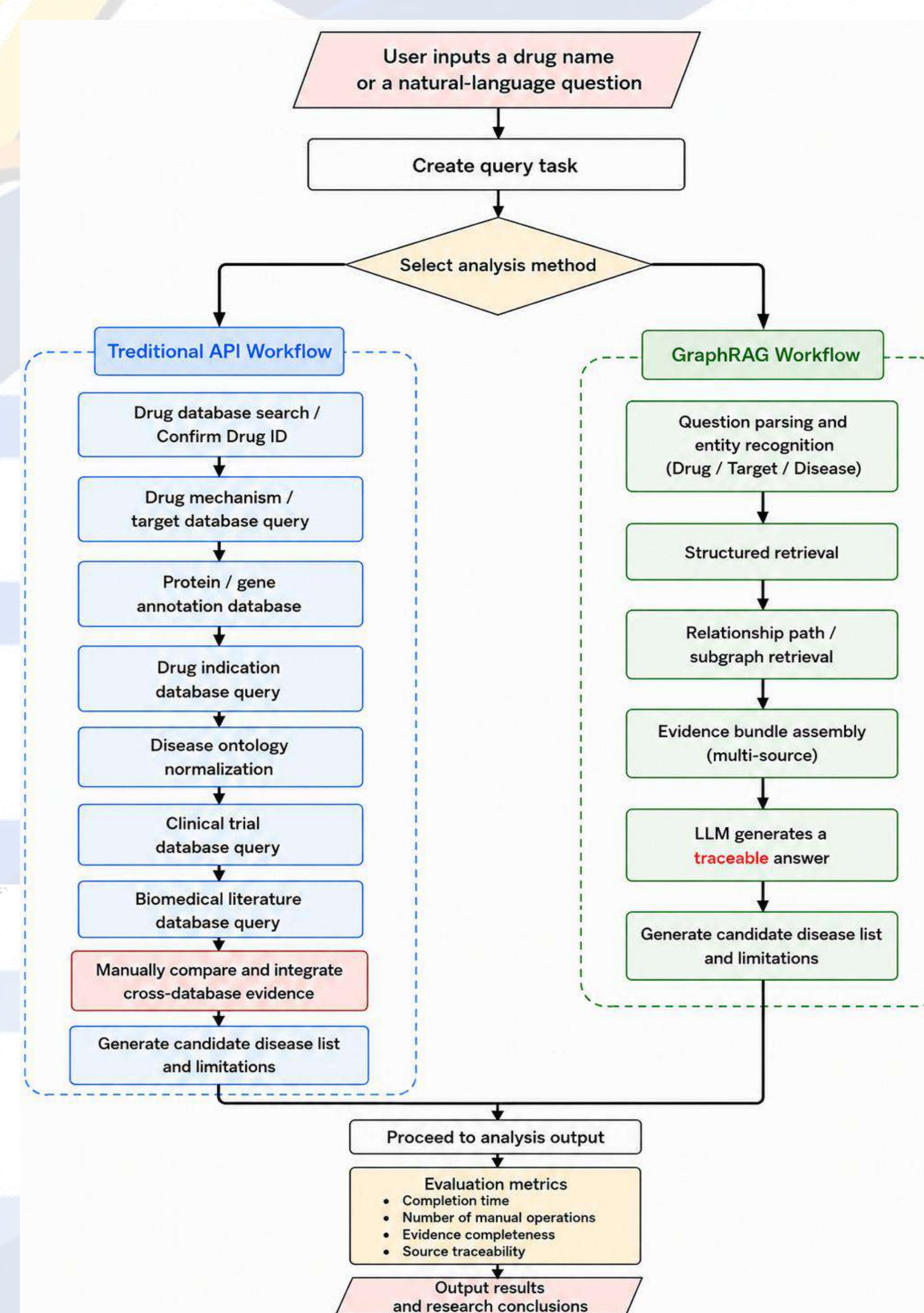


Figure 1. GraphRAG retrieves relevant entities and relationships from the knowledge graph, constructing a task-specific subgraph, and using the LLM to synthesize the retrieved evidence into a grounded response.

Experimental Design



We compared a traditional API-based reasoning pipeline with a GraphRAG-based approach for biomedical knowledge synthesis.

The API workflow uses sequential database queries, while GraphRAG retrieves relevant subgraphs from natural language queries and synthesizes evidence with an LLM. Both approaches are evaluated using the same biomedical questions.

To compare the results, we performed evaluations based on four parts: completion time, number of manual operations, evidence completeness and source traceability to determine our final

Figure 2. Traditional API vs. GraphRAG workflow output results.

Results

	Completion Time	Number of Manual Operations	Evidence Completeness	Source Traceability
Traditional API	80 s	8 steps		
GraphRAG	30 s	3 steps		

Figure 3. (Left Panel) Four Performance Comparison Matrix between Traditional API and GraphRAG Workflows.

Figure 4. (Right Panel) The Biomedical KG-enhanced GraphRAG framework demonstrates exceptional source traceability. By linking multi-dimensional entities via structured paths, the system synthesizes fragmented evidence to deliver rigorous, highly credible, and well-supported inferences.

Discussion & Conclusion

- Clearer and Evidence-Grounded Responses: Evaluation across completion time, manual operations, evidence completeness, and source traceability showed that GraphRAG produced clearer and better-supported biomedical answers than the traditional API workflow.
- Relationship-Oriented Integration: By organizing evidence through explicit relationships rather than isolated database queries, GraphRAG enables more coherent synthesis of information from multiple biomedical sources.
- Future Expansion: Future development will extend the knowledge graph to capture more complex biomedical relationships and integrate additional drug discovery and pharmaceutical service modules, enabling broader end-to-end biomedical applications.



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