

HerbAgent: Leveraging LLM Agents to Automate and Accelerate Scalable Network Pharmacology

Wanchen Cao^{1,*}
yuhengchen@bucm.edu.cn

Kai Zhao^{2,*}
manuelkaizhao@gmail.com

Yi Zhao^{1,†}
biozy@ict.ac.cn

¹Beijing University of Chinese Medicine

²Technical University of Darmstadt

*These authors contributed equally to this work.

†Corresponding author.

Abstract

Network pharmacology has become essential for understanding the complex mechanisms of Traditional Chinese Medicine (TCM), yet conventional workflows remain labor-intensive and prone to human error. We introduce HerbAgent, an AI-powered framework that leverages Large Language Models and multi-agent collaboration to automate network pharmacology research. The system features a modular architecture that automates analytical tasks from target identification to protein-protein interaction analysis, while ensuring user-friendly interaction and comprehensive reporting. Our evaluation demonstrates that HerbAgent significantly reduces manual effort while maintaining analytical rigor and scalability. The work highlights the potential of AI-driven methodologies to reshape network pharmacology, paving the way for accelerated, large-scale analysis and discovery in herbal medicine research and drug discovery. Our code demo is available at: <https://anonymous.4open.science/r/research-7CCD/>

1 Introduction

Network pharmacology, an emerging discipline at the intersection of systems biology, computational science, and pharmacology, has revolutionized the way researchers conceptualize the effects of multi-component herbal medicines (WANG et al., 2021). Over the past decade, multiple studies have demonstrated the potential of network pharmacology to better characterize therapeutic mechanisms, identify new drug targets, and optimize the design of multi-component therapies. Nonetheless, despite its promise and continuous advances in computational tools, as shown in Figure 1, the network pharmacology workflow remains non-trivial: researchers must aggregate and curate heterogeneous data from numerous public databases (LI and ZHANG, 2013), perform complex analyses

such as target prediction and network construction (Zhang et al., 2019; Chen, 2011), and interpret multi-layered results that cut across molecular, cellular, and physiological levels, requiring a high level of interdisciplinary expertise (Chandran et al., 2016; Noor et al., 2022; Li et al., 2014).

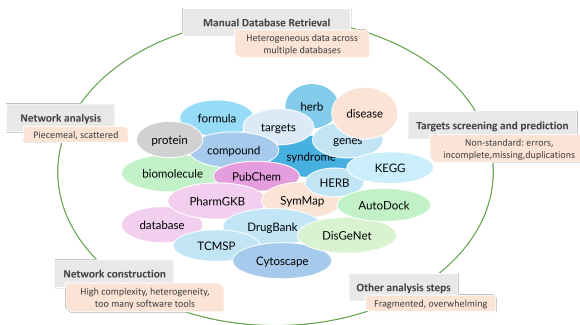


Figure 1: Key challenges in network pharmacology workflows. The diagram highlights the complex integration of diverse databases, fragmented analytical tools, and the need for significant interdisciplinary expertise in data retrieval, screening, and network analysis.

In recent years, a variety of databases (e.g., TCMSP (Ru et al., 2014), DisGeNet (Piñero et al., 2019, 2016), DrugBank (Knox et al., 2023; Wishart et al., 2017, 2007)) and tools (e.g., Cytoscape (Smoot et al., 2010), AutoDock (Forli et al., 2016), and pathway enrichment analysis platforms (Zhou et al., 2017)) have advanced network pharmacology research. However, significant manual effort and domain expertise are still required to link heterogeneous data sources, and issues such as data inconsistency and repetitive tasks hinder efficiency. As molecular and clinical data repositories grow, integrating and interpreting such large-scale information remains a major challenge for traditional workflows.

Recent advancements in Large Language Models (LLMs) (Chang et al., 2024; Teubner et al., 2023) have enabled automation of complex, data-intensive tasks. LLM Agents—built on GPT-like

models—can perform multi-step operations such as information retrieval, iterative analysis, and result interpretation (Ge et al., 2023; Alberts et al., 2023). With strong natural language capabilities (Huang et al., 2024), they support tasks like automated literature review, unstructured data extraction, and tool orchestration (Li et al., 2024; Wu et al., 2023), significantly reducing the manual effort and fragmentation in network pharmacology workflows (Qiu et al., 2024).

As shown in Figure 2, we propose HerbAgent—a specialized LLM Agent designed to automate the end-to-end network pharmacology workflow for traditional Chinese medicine (TCM) (Ren et al., 2024; Thirunavukarasu et al., 2023). HerbAgent leverages LLMs to tackle key challenges such as inconsistent data curation, complex multi-step analyses, and large-scale data integration. By combining domain-specific ontologies, curated databases, and AI-driven reasoning, it aims to streamline research, enhance reproducibility, and support natural language interaction. The system enables efficient exploration of herbal mechanisms, even for users without network pharmacology expertise.

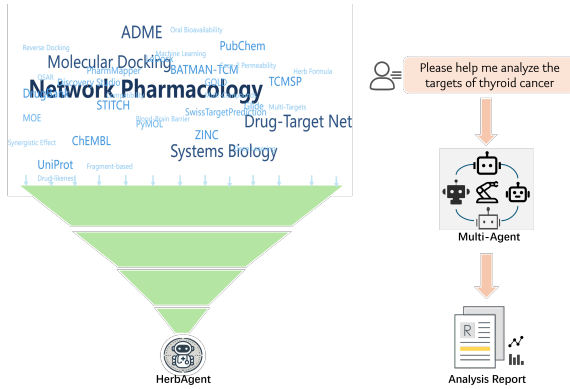


Figure 2: **Left:** The funnel diagram illustrates how HerbAgent integrates diverse network pharmacology processes, tools and databases into a unified workflow. **Right:** A demonstration of HerbAgent’s multi-agent system architecture that efficiently processes natural language queries and rapidly generates comprehensive analysis reports.

2 System Design

HerbAgent is a modular framework built to automate and streamline network pharmacology studies, particularly in the field of traditional Chinese medicine. It harnesses large language models (LLMs) within a multi-agent architecture for flex-

ibility, scalability, and robustness. We employed Langchain (Team, 2025) as the agent orchestration framework and integrated Qwen-Max (Ahmed et al.) through API calls as the core LLM, though researchers can readily substitute other models like GPT-4 (OpenAI et al., 2024) based on their preferences and requirements. Together, these components provide the robust natural language capabilities essential for handling network pharmacology analyses. The HerbAgent framework is composed of several key modules, each targeting a distinct component of the workflow, from data extraction and target prediction to network construction and result interpretation.

2.1 Collaborative Workflow

HerbAgent employs a hierarchical multi-agent design to automate network pharmacology tasks, particularly for Chinese herbal medicine (CHM). At the top level, as shown in Figure 3 an Input-ProcessingAgent extracts and organizes entities (herbs, syndromes, diseases) from user inputs, then dispatches them to four domain-specific agents: HerbTargetAnalysisAgent, SyndromeTargetAnalysisAgent, DiseaseTargetAnalysisAgent, and Drug-TargetAnalysisAgent. Each of these agents leverages a specialized tool to map entities to relevant molecular targets and pharmacological information. Their outputs feed into an AnalysisInteractionAgent, which coordinates user-driven decisions—such as proceeding with protein-protein interaction (Phizicky and Fields, 1995; Rao et al., 2014; Jones and Thornton, 1996) or random walk analyses (Valdeolivas et al., 2018)—through two specialized agents (PPIPipelineAgent and RandomWalkAnalysisAgent). Finally, PPIReportAgent and RandomWalkReportAgent compile and summarize analytical results, highlighting critical findings in a concise manner.

Our architecture consists of 10 agents and 6 dedicated tools, unified by a **HerbAnalysisCoordinator** implemented in LangChain. This coordinator optimizes interactions between agents and tools, ensuring a seamless workflow that covers data ingestion, target identification, network analysis, and result reporting. By pairing each agent with a specialized tool or function, we maintain clear responsibilities and enable flexible integration of new capabilities.

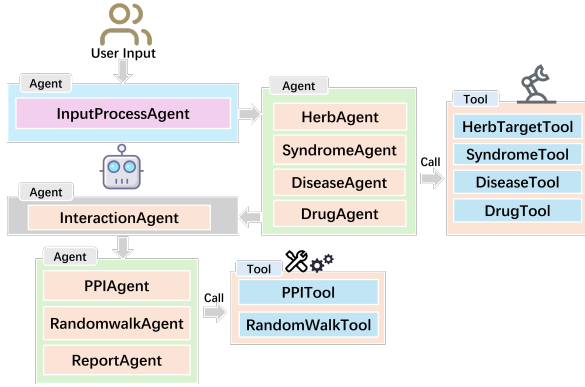


Figure 3: The system begins with user input processing, branches into specialized agents (Herb, Syndrome, Disease, and Drug) that utilize corresponding analysis tools, and culminates in interaction analysis through PPI and random walk pathways, with dedicated agents for result reporting.

2.2 Multi-Agent Roles

HerbAgent’s multi-agent architecture begins with the InputProcessingAgent, which extracts and preprocesses user input to clarify intent and prepare data. As shown in Figure 4, a set of specialized analysis agents then handle key tasks:

HerbTargetAnalysisAgent (with HerbTargetTool, using HERB (Fang et al., 2020)) maps herbs to molecular targets; SyndromeTargetAnalysisAgent (with SyndromeTool, using SymMap (Wu et al., 2018)) explores TCM syndromes; DiseaseTargetAnalysisAgent (with DiseaseTool, leveraging DisGeNet (Piñero et al., 2015), GeneCards (Safran et al., 2021), and UMLS (Campbell et al., 1998; Bodenreider, 2004)) identifies disease targets; DrugTargetAnalysisAgent (with DrugTool, accessing DrugBank (Klinger et al., 2024)) investigates drug-target links.

Downstream, the PPIPipelineAgent and RandomWalkAnalysisAgent build and refine PPI networks using restart random walk algorithms. Final outputs are handled by PPIReportAgent and RandomWalkReportAgent, each generating task-specific reports for modularity and clarity. The AnalysisInteractionAgent manages user interaction post-analysis, coordinating follow-up tasks or ending sessions to ensure a smooth, adaptable workflow.

2.3 Tool Design

Tool development in HerbAgent addresses two key goals: ensuring task-specific precision and en-

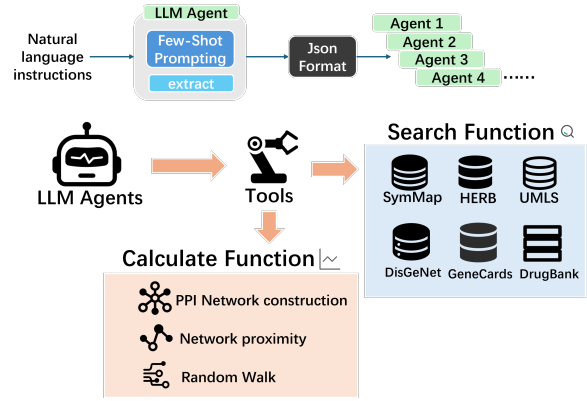


Figure 4: The system processes natural language instructions through few-shot prompting to coordinate multiple specialized agents. These agents interact with various tools to perform search functions across biological databases (including SymMap, HERB, GeneCards, DrugBank, UMLS, and DisGeNet) and calculate functions such as PPI network construction, network proximity, and random walk analysis.

abling smooth coordination across agents. Each agent is paired one-to-one with a dedicated tool, treating the LLM as the “brain” and tools as “digital appendages.” This design maintains modularity while supporting complex interactions.

The HerbTargetTool, SyndromeTool, DiseaseTool, and DrugTool handle target mapping from herbs, syndromes, diseases, and drugs respectively. For network-level tasks, the PPITool explores protein-protein interactions using integrated datasets, while the RandomWalkTool applies restart random walk for refinement. Features like bilingual queries and multi-database integration ensure each tool contributes reliable, structured outputs to downstream agents, minimizing errors and enhancing overall workflow robustness.

3 Demonstration

To evaluate HerbAgent in real-world scenarios, we conducted end-to-end testing and compared its outputs with manual results based on the 2022 Chinese Thyroid Cancer Diagnosis Guidelines (Ying and Ruochuan, 2024), focusing on the syndrome Han Tan Zheng and the TCM formula Yang He Tang combined with Ban Xia Xiao Luo Wan.

As shown in Figure 5, when given a natural language prompt containing herbs, syndrome, and disease details, HerbAgent accurately parsed and extracted all relevant medical entities within seconds. This demonstrates its ability to automate semantic recognition and information extraction using

LLM-driven workflows.

After processing the input, the system guided the user to select further analysis options: PPI Network Proximity or Restart Random Walk, completing a full automated research cycle from input to actionable insight.

HerbAgent: AI Herbal Target Analysis System

Welcome to HerbAgent Traditional Chinese Medicine Target Analysis System! I'm HerbAgent, a professional network pharmacology analysis assistant, how can I help you?

Please enter the formula, herb, syndrome, and disease you want to analyze:

>

Please analyze the pattern of Han Tan, Yang He Tang He Ban Xia Xiao Lai Wan Jia Jian shuifang, rougui, baijixi, pojiang, gancuo, mahuang, banxia, xuanshen, zhebiru, as well as key information about the disease Thyroid Neoplasms/Thyroid carcinoma/Thyroid Cancer.

We have completed the following analyses: - Herb analysis: Yanghe Decoction combined with Banxia Xiaoluo Pills, with modifications - Syndrome analysis: Cold Phlegm - Disease analysis: Drug analysis Would you like to proceed with any of the following additional analyses? 1. PPI network proximity analysis 2. Restart random walk analysis 3. Exit system Please let me know your choice.

Please enter your choice >

Enter your message... Send

Figure 5: Interface of HerbAgent, showcasing an input query for analyzing the formula, herbs and syndrome in relation to a disease.

We have completed the following analyses: - Herb analysis: Yanghe Decoction combined with Banxia Xiaoluo Pills, with modifications - Syndrome analysis: Cold Phlegm - Disease analysis: Drug analysis Would you like to proceed with any of the following additional analyses? 1. PPI network proximity analysis 2. Restart random walk analysis 3. Exit system Please let me know your choice.

Please enter your choice >

Restart random walk analysis

Restart random walk analysis report generated

Analysis Report on Network Pharmacology of Traditional Chinese Medicine Formula: Yanghe Decoction Combined with Banxia Xiaoluo Pill
1. Core Chemical Component Analysis and Its Core Flavor Analysis in Formulas "Identification and Explanation of the Most Important Core Chemical Components and Core Flavors": "Ephedra (Ephedra)" (HERB003658)*. --Total Score** 0.033594873235869. --Top Ingredient Count*: 4. --Top Ingredients*: Coumarin, Geraniol, Herbacetin-3-beta-D-(2-O-beta-D-glucopyranosidogluco-pyranoside)-8-beta-D-glucopyranoside, Methyl-7-epigallocatecatechol-3-O-gallate, "Core Flavors": Bitter, Pungent, Warm. --白芥子 (White Mustard Seed) (HERB002225)*. --Total Score** 0.026953384232885. --Top Ingredient Count*: 1. --Top Ingredients*: Mustard oil. --Core Flavors*: Pungent, Hot. --白芷 (Bulb of Thunberg Fritillary) (HERB006950)*. --Total Score** 0.026288319300138. --Top Ingredient Count*: 2. --Top Ingredients*: Adenine nucleoside, Adenosine. --Core Flavors*: Bitter, Sweet, Cold. --枳实 (Cassia Bark) (HERB004694)*. --Total Score** 0.007596169993066. --Top Ingredient Count*: 2. --Top Ingredients*: 2-deoxy-D-ribose-1,4-lactone, Coumarin. --Core Flavors*: Pungent, Sweet, Hot. --玄参 (Figwort Root) (HERB006280)*. --Total Score** 0.0064345447817959. --Top Ingredient Count*: 2. --Top Ingredients*: Adenosine, Cis-oleic acid. --Core Flavors*: Salty, Bitter, Cold. --半夏 (Tuber of Pinellia) (HERB00330)*. --Total Score** 0.0046250576740654. --Top Ingredient Count*: 1. --Top Ingredients*: Adenosine. --Core Flavors*: Pungent, Warm. --归根 (Root of Ural Licorice) (HERB001779)*. --Total Score** 0.004333702223461. --Top Ingredient Count*: 1. --Top Ingredients*: Artonin E. --Core Flavors*: Sweet, Neutral. --Analysis of the Relationship Between Them*: "Coumarin" is a common component in both 枳实 and 归根, indicating its potential importance in the formula. --Adenosine is present in 玄参, 玄参, and 半夏, suggesting it plays a significant role in the pharmacological effects of the formula. --Pungent and Bitter Flavors* are predominant, which may contribute to the formula's ability to disperse cold, promote circulation, and clear heat. ### 2. Feature Analysis "Overall Characteristics of Core Chemical Components and Their Formulas": The formula contains a mix of pungent, bitter, and sweet flavors, which are balanced to achieve the desired therapeutic effects. --Coumarin* and --Adenosine* are the most frequently occurring chemical components, indicating their central roles in the formula. The presence of "Mustard oil" in 白芥子 suggests a strong warming and dispersing effect, which is consistent with the formula's goal of treating cold conditions. --Key Information*: The formula is designed to balance yin and yang, warm the body, and resolve phlegm. The combination of herbs with different flavors and properties ensures a comprehensive

Figure 6: HerbAgent returned the target search results for Herb, Syndrome, Disease, and Drug, and asked the user for the next operation: PPI network proximity analysis; Restart random walk analysis; Exit system. If the user choose to excute Restart random walk analysis, the report will be automatically generated.

Due to the large number of targets, the PPI network analysis module requires significant computational resources. For testing purposes, we limited the input to 30 targets to ensure smooth end-to-end execution. As a result, the analysis may not yield statistically significant outcomes, which is expected. Future users can utilize more computational resources (e.g., GPUs) to perform full-scale analyses.

In this demonstration, the restart random walk analysis module was executed first, as shown in Figure 6, followed by the PPI network analysis, to validate whether the system can seamlessly integrate multiple analytical methods within a complete workflow, as shown in Figure 7. After performing each step of analysis, HerbAgent automat-

Would you like to proceed with the PPI network proximity analysis? You can type "exit" at any time to end the session.

Please enter your choice >

PPI network proximity analysis

Analysis report generation completed:

Analysis Report: PPI Network Analysis of Drug-Disease Associations ##### 1. Statistical Overview **Summary of Statistical Indicators**: --Z-Value**: The Z-Values in the dataset range from -4.1602 to 0.2775. A Z-Value indicates how many standard deviations an element is from the mean. In this context, a negative Z-Value suggests that the observed association is lower than expected by chance, while a positive Z-Value suggests it is higher. --P-Value**: The P-Values range from 0.0000 to 0.9600. A P-Value is a measure of the evidence against a null hypothesis. A lower P-Value (typically < 0.05) indicates stronger evidence against the null hypothesis, suggesting a statistically significant association. --Distribution Characteristics**: --Most Z-Values are negative, indicating that the observed associations are generally lower than expected. - The P-Values are mostly above 0.05, suggesting that most associations are not statistically significant at the conventional 0.05 threshold. - The most extreme Z-Value and the lowest P-Value are associated with the drug "阳和汤合半夏消瘿丸加减" (Yanghe Tang combined with Banxia Xiaoluo Wan). ##### 2. Significance Analysis **Significant Associations**: --Drug: 阳和汤合半夏消瘿丸加减, Disease: disease*. --Z-Value: -4.1602. --P-Value: 0.0000. - This association is highly significant, as the P-Value is 0.0000, indicating very strong evidence against the null hypothesis. --Drug: 阳和汤合半夏消瘿丸加减, Disease: syndrome 27*. --Z-Value: -3.0318. --P-Value: 0.0030. - This association is also significant, with a P-Value below the 0.05 threshold. --Other Notable Associations*: --Drug: DB00997, Disease: disease*. --Z-Value: -2.1701. --P-Value: 0.1080. - Although the P-Value is slightly above 0.05, the Z-Value is relatively low, suggesting a potentially meaningful association that may warrant further investigation. ##### 3. Biological Significance **Key Node Identification**: --阳和汤合半夏消瘿丸加减 (Yanghe Tang combined with Banxia Xiaoluo Wan). **This traditional Chinese medicine (TCM) formula appears to be a key node in the network, showing significant associations with both the general disease category and a specific syndrome (syndrome 27). This suggests that this TCM formula may have a broad and significant impact on the disease and its related syndromes. --Potential Biological Pathways*: - The significant associations with "阳和汤合半夏消瘿丸加减" suggest that this TCM formula may influence multiple biological pathways. Given its traditional use in treating various conditions, it is likely that it affects inflammatory, immune, and metabolic pathways. - Further pathway analysis and experimental validation would be needed to identify the specific mechanisms involved. --Possible Mechanisms of Action*: --Anti-inflammatory and Immune Modulation*: Traditional Chinese medicines often have anti-inflammatory and immune-modulating properties. The significant associations with the disease and syndrome suggest that these properties may play a crucial role. --Metabolic Regulation*: TCMs can also influence metabolic processes, which might be relevant for the observed associations. ##### 4.

Figure 7: After the execution of the Restart Random Walk Analysis, HerbAgent prompted the user to either proceed with the PPI Network Proximity Analysis or exit the system. The user chose to continue, and HerbAgent eventually provided an interpretation report of the PPI network analysis results.

ically generates an analysis report based on the analysis results.

4 Result and Evaluation

The results in Figure 8 demonstrate that HerbAgent not only achieves high consistency with manual annotations but also significantly expands the scope, particularly in the disease category, demonstrating its comprehensive coverage capabilities.

As shown in Table 1, the results obtained through HerbAgent's Restart Random Walk Analysis fully encompass the findings from manual analysis, demonstrating the algorithm's comprehensive coverage. Furthermore, HerbAgent effectively identified and output a significantly larger set of core herbs and their corresponding chemical components, addressing the limitations of manual analysis which often suffers from incompleteness and missing critical herb-component relationships, to standardize and automate the analysis process.

4.1 Generated Report of Restart Random Walk Analysis

The report (Figure 6) summarizes herb rankings from the Restart Random Walk analysis. Ephedra scored highest (0.0336), followed by White Mustard Seed (0.0270) and Bulb of Thunberg Fritillary (0.0263); others ranged from 0.0080 to 0.0044. Key bioactive compounds, such as coumarin and adenosine, appeared across multiple herbs, indicating their central pharmacological roles.

The report also analyzes flavor profiles (e.g., pungent, bitter, sweet) and herb interactions, noting shared compounds like coumarin (Ephedra, Cassia Bark) and adenosine (three herbs). These findings

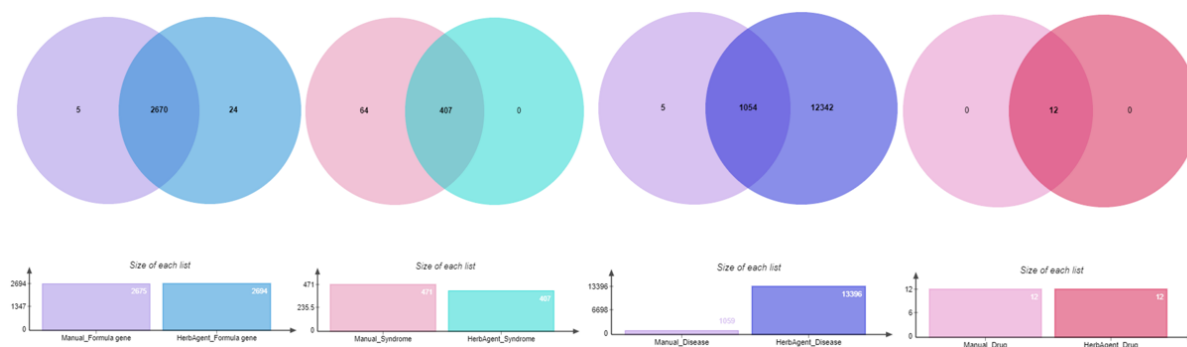


Figure 8: The figure presents overlaps between manually curated targets and those identified by HerbAgent across: (1) formula-related gene targets, (2) syndrome-related targets, (3) disease-related targets, and (4) drug counts.

Method	Herbs	Chemical Components
Manual	Ma Huang	coumarin, methyl-7-epigano derate, geraniol
	Bai Jie zi	mustard oil
	Zhe Beimu	none
HerbAgent	Ma Huang	coumarin, geraniol, herbacetin-3-beta-d-(2-o-beta-d-glucopyranosidogluco-pyranoside)-8-beta-d-glucopyranoside, methyl-7-epiganoderate
	Bei Jiezi	mustard oil
	Zhe Beimu	adeninenucleoside, adenosine
	Rou Gui	2-deoxy-d-ribono-1,4-lactone, coumarin
	Xuan Shen	adenosine, cis-oleic acid
	Ban Xia	adenosine
	Gan Cao	Artonin E

Table 1: Comparison of core herbs and their core chemical components identified by Restart Random Walk Analysis.

support the formula’s therapeutic goals—balancing yin and yang, warming the body, and resolving phlegm. In particular, mustard oil from White Mustard Seed is highlighted for its warming, dispersing effects aligned with treating cold-related conditions.

4.2 Generated Report of PPI Network Analysis

After completing the random walk analysis, the user triggered the PPI network module to evaluate associations between Thyroid Cancer and candidate drugs. The system generated a report (Figure 7) summarizing key statistical and biological findings.

The report explains Z-values (-4.1602 to 0.2775) and P-values (0.0000 to 0.9600), noting that most Z-values are negative and most P-values exceed 0.05, suggesting weak associations in general. However, strong significance was observed for *Yanghe Tang + Banxia Xiaoluo Wan*, showing the lowest Z-value (-4.1602) and a P-value of 0.0000. This formula also

showed a significant link to syndrome_27: Han Tan ($Z = -2.0018$, $P = 0.0280$). A potential association was noted for DB00997, though its P-value (0.1080) exceeds the standard threshold.

Biological interpretation suggests that the highlighted formula may influence inflammatory, immune, and metabolic pathways, aligning with traditional use. Possible mechanisms include anti-inflammatory and immune-modulating effects, warranting further experimental validation.

4.2.1 Result Evaluation

HerbAgent’s report generation capability demonstrates exceptional proficiency in transforming complex statistical data into meaningful research insights. Employing a two-stage approach—first executing statistical analysis to obtain quantitative data, then deploying a language model agent to generate interpretive reports—the system effectively bridges the gap between computational methods and medicine research.

The report generation process exhibits three key

strengths: first, the system faithfully represents original data (including statistical values to four decimal places) while providing accurate contextual interpretations; second, the reports demonstrate domain integration capability, correlating modern pharmacological compounds with traditional property theories, while connecting quantitative network data with biological mechanism explanations; third, the multi-level analytical approach—from individual herbs to cross-pattern relationships to formula-level interpretations, or from statistical overviews to significance analyses to biological implications—creates a logical structure that mirrors human research approaches. This report generation capability significantly enhances HerbAgent’s utility as a research acceleration tool, reducing what would typically be days or weeks of expert analysis to seconds, while maintaining scientific accuracy and relevance to TCM research, providing actionable insights for researchers across all levels of expertise.

5 Conclusion

Our end-to-end experiments demonstrate that the proposed system effectively integrates user input, extracts key medical concepts, and connects PPI and random walk analyses into a coherent workflow. The multi-dimensional outputs—combining statistical indicators and core active components—support rapid drug and target identification in complex formula–disease relationships. These results validate the feasibility of a multi-agent system powered by LLMs in optimizing network pharmacology workflows and highlight its potential for large-scale drug discovery applications.

6 Discussion

This study presents HerbAgent, an AI-powered framework that combines Large Language Models (LLMs) with a modular multi-agent architecture to automate and scale network pharmacology research in herbal medicine. By integrating automated data processing, advanced network analysis (e.g., PPI and RWR), and intuitive user interfaces, HerbAgent streamlines complex workflows and improves research efficiency.

Key contributions include: End-to-end automation of data retrieval, analysis, and interpretation; Modular agent design enabling flexibility and scalability; Robust analytical tools for deeper pharma-

cological insights; User-centric interaction, producing accessible, comprehensive reports. The framework’s extensible design allows easy adaptation to other medical domains or integration with modern drug discovery pipelines. Future directions involve enabling adaptive learning from updated databases and user feedback, and optimizing computational performance for broader accessibility. Expanding to other biomedical applications could further enhance its impact.

In summary, HerbAgent bridges traditional herbal knowledge with AI-driven analysis, offering a scalable, automated, and user-friendly approach that holds promise for accelerating network pharmacology and advancing personalized medicine.

7 Limitations

Despite its strengths, HerbAgent has limitations. Its performance relies on the quality and consistency of external databases, which require ongoing maintenance. Integration challenges may arise due to differing data standards. While LLMs support advanced analysis, interpretability remains limited, necessitating expert oversight. Some modules, such as PPI and random walk analysis, are computationally demanding. Overall, the system augments but does not replace human expertise.

Future work should focus on improving data integration, model explainability, computational efficiency, and real-world validation.

References

- Imtiaz Ahmed, Sadman Islam, Partha Protim Datta, Imran Kabir, Naseef Ur Rahman Chowdhury, and Ahshanul Haque. [Qwen 2.5: A comprehensive review of the leading resource-efficient llm with potential to surpass all competitors.](#)
- Ian L Alberts, Lorenzo Mercolli, Thomas Pyka, George Prenosil, Kuangyu Shi, Axel Rominger, and Ali Afshar-Oromieh. 2023. [Large language models \(llm\) and chatgpt: what will the impact on nuclear medicine be?](#) *European journal of nuclear medicine and molecular imaging*, 50(6):1549–1552.
- Olivier Bodenreider. 2004. [The unified medical language system \(umls\): integrating biomedical terminology.](#) *Nucleic Acids Research*, 32(suppl_1) : D267 – – D270.
- Keith E. Campbell, Diane E. Oliver, Kent A. Spackman, and Edward H. Shortliffe. 1998. [Representing thoughts, words, and things in the umls.](#) *Journal of the American Medical Informatics Association*, 5(5):421–431.

- Uma Chandran, Neelay Mehendale, Saniya Patil, Rathnam Chaguturu, and Bhushan Patwardhan. 2016. [Network pharmacology](#). *Innovative approaches in drug discovery*, page 127.
- Yupeng Chang, Xu Wang, Jindong Wang, Yuan Wu, Linyi Yang, Kaijie Zhu, Hao Chen, Xiaoyuan Yi, Cunxiang Wang, Yidong Wang, Wei Ye, Yue Zhang, Yi Chang, Philip S. Yu, Qiang Yang, and Xing Xie. 2024. [A survey on evaluation of large language models](#). *ACM Trans. Intell. Syst. Technol.*, 15(3).
- Calvin Yu-Chian Chen. 2011. [Tcm database@ taiwan: the world's largest traditional chinese medicine database for drug screening in silico](#). *PloS one*, 6(1):e15939.
- ShuangSang Fang, Lei Dong, Liu Liu, JinCheng Guo, LianHe Zhao, JiaYuan Zhang, DeChao Bu, XinKui Liu, PeiPei Huo, WanChen Cao, QiongYe Dong, JiaRui Wu, Xiaoxi Zeng, Yang Wu, and Yi Zhao. 2020. [Herb: a high-throughput experiment- and reference-guided database of traditional chinese medicine](#). *Nucleic Acids Research*, 49(D1):D1197–D1206.
- Stefano Forli, Ruth Huey, Michael E Pique, Michel F Sanner, David S Goodsell, and Arthur J Olson. 2016. [Computational protein–ligand docking and virtual drug screening with the autodock suite](#). *Nature protocols*, 11(5):905–919.
- Yingqiang Ge, Wenyue Hua, Kai Mei, jianchao ji, Juntao Tan, Shuyuan Xu, Zelong Li, and Yongfeng Zhang. 2023. [Openagi: When llm meets domain experts](#). In *Advances in Neural Information Processing Systems*, volume 36, pages 5539–5568. Curran Associates, Inc.
- Xu Huang, Weiwen Liu, Xiaolong Chen, Xingmei Wang, Hao Wang, Defu Lian, Yasheng Wang, Ruiming Tang, and Enhong Chen. 2024. [Understanding the planning of llm agents: A survey](#). *arXiv preprint arXiv:2402.02716*.
- Susan Jones and Janet M Thornton. 1996. [Principles of protein-protein interactions](#). *Proceedings of the National Academy of Sciences*, 93(1):13–20.
- Christen M Klinger, Jordan Cox, Denise So, Teira Staath, Michael Wilson, Alex Wilson, and Craig Knox. 2024. [Drugbank online: A how-to guide](#). *Open Access Databases and Datasets for Drug Discovery*, pages 67–99.
- Craig Knox, Mike Wilson, Christen M Klinger, Mark Franklin, Eponine Oler, Alex Wilson, Allison Pon, Jordan Cox, Na Eun (Lucy) Chin, Seth A Strawbridge, Marysol Garcia-Patino, Ray Kruger, Aadhavya Sivakumaran, Selena Sanford, Rahil Doshi, Nitya Khetarpal, Omolola Fatokun, Daphnee Doucet, Ashley Zubkowski, Dorsa Yahya Rayat, Hayley Jackson, Karxena Harford, Afia Anjum, Mahi Zakir, Fei Wang, Siyang Tian, Brian Lee, Jaanus Liigand, Harrison Peters, Ruo Qi (Rachel) Wang, Tue Nguyen, Denise So, Matthew Sharp, Rodolfo da Silva, Cyrella Gabriel, Joshua Scantlebury, Marissa Jasinski, David Ackerman, Timothy Jewison, Tanvir Sajed, Vasuk Gautam, and David S Wishart. 2023. [Drugbank 6.0: the drugbank knowledgebase for 2024](#). *Nucleic Acids Research*, 52(D1):D1265–D1275.
- Shao Li, Tai-Ping Fan, Wei Jia, Aiping Lu, and Weidong Zhang. 2014. [Network pharmacology in traditional chinese medicine](#). *Evidence-based complementary and alternative medicine: eCAM*, 2014.
- Shao LI and Bo ZHANG. 2013. [Traditional chinese medicine network pharmacology: theory, methodology and application](#). *Chinese Journal of Natural Medicines*, 11(2):110–120.
- Xinyi Li, Sai Wang, Siqi Zeng, Yu Wu, and Yi Yang. 2024. [A survey on llm-based multi-agent systems: workflow, infrastructure, and challenges](#). *Vicinagearth*, 1(1):9.
- Fatima Noor, Muhammad Tahir ul Qamar, Usman Ali Ashfaq, Aqel Albutti, Ameen S. S. Alwashmi, and Mohammad Abdullah Aljasir. 2022. [Network pharmacology approach for medicinal plants: Review and assessment](#). *Pharmaceuticals*, 15(5).
- OpenAI, Josh Achiam, Steven Adler, Sandhini Agarwal, Lama Ahmad, Ilge Akkaya, Florencia Leoni Aleman, Diogo Almeida, Janko Altschmidt, Sam Altman, Shyamal Anadkat, Red Avila, Igor Babuschkin, Suchir Balaji, Valerie Balcom, Paul Baltescu, Haiming Bao, Mohammad Bavarian, Jeff Belgum, Irwan Bello, Jake Berdine, Gabriel Bernadett-Shapiro, Christopher Berner, Lenny Bogdonoff, Oleg Boiko, Madeleine Boyd, Anna-Luisa Brakman, Greg Brockman, Tim Brooks, Miles Brundage, Kevin Button, Trevor Cai, Rosie Campbell, Andrew Cann, Brittany Carey, Chelsea Carlson, Rory Carmichael, Brooke Chan, Che Chang, Fotis Chantzis, Derek Chen, Sully Chen, Ruby Chen, Jason Chen, Mark Chen, Ben Chess, Chester Cho, Casey Chu, Hyung Won Chung, Dave Cummings, Jeremiah Currier, Yunxing Dai, Cory Decareaux, Thomas Degry, Noah Deutsch, Damien Deville, Arka Dhar, David Dohan, Steve Dowling, Sheila Dunning, Adrien Ecoffet, Atty Eleti, Tyna Eloundou, David Farhi, Liam Fedus, Niko Felix, Simón Posada Fishman, Juston Forte, Isabella Fulford, Leo Gao, Elie Georges, Christian Gibson, Vik Goel, Tarun Gogineni, Gabriel Goh, Rapha Gontijo-Lopes, Jonathan Gordon, Morgan Grafstein, Scott Gray, Ryan Greene, Joshua Gross, Shixiang Shane Gu, Yufei Guo, Chris Hallacy, Jesse Han, Jeff Harris, Yuchen He, Mike Heaton, Johannes Heidecke, Chris Hesse, Alan Hickey, Wade Hickey, Peter Hoeschele, Brandon Houghton, Kenny Hsu, Shengli Hu, Xin Hu, Joost Huizinga, Shantanu Jain, Shawn Jain, Joanne Jang, Angela Jiang, Roger Jiang, Haozhun Jin, Denny Jin, Shino Jomoto, Billie Jonn, Heewoo Jun, Tomer Kaftan, Łukasz Kaiser, Ali Kamali, Ingmar Kanitscheider, Nitish Shirish Keskar, Tabarak Khan, Logan Kilpatrick, Jong Wook Kim, Christina Kim, Yongjik Kim, Jan Hendrik Kirchner, Jamie Kiros, Matt Knight, Daniel Kokotajlo, Łukasz Kondraciuk, Andrew Kondrich, Aris Konstantinidis, Kyle Kosic, Gretchen Krueger, Vishal Kuo, Michael Lampe, Ikai Lan, Teddy Lee, Jan Leike, Jade Leung, Daniel Levy, Chak Ming Li, Rachel Lim, Molly Lin, Stephanie Lin, Mateusz Litwin, Theresa Lopez, Ryan Lowe, Patricia Lue, Anna Makanju, Kim Malfacini, Sam Manning, Todor Markov, Yaniv Markovski, Bianca Martin, Katie Mayer, Andrew Mayne, Bob McGrew, Scott Mayer McKinney, Christine McLeavey, Paul McMillan, Jake McNeil, David

- Medina, Aalok Mehta, Jacob Menick, Luke Metz, Andrey Mishchenko, Pamela Mishkin, Vinnie Monaco, Evan Morikawa, Daniel Mossing, Tong Mu, Mira Murati, Oleg Murk, David Mély, Ashvin Nair, Reiichiro Nakano, Rajeev Nayak, Arvind Neelakantan, Richard Ngo, Hyeonwoo Noh, Long Ouyang, Cullen O’Keefe, Jakub Pachocki, Alex Paino, Joe Palermo, Ashley Pantuliano, Giambattista Parascandolo, Joel Parish, Emy Parparita, Alex Passos, Mikhail Pavlov, Andrew Peng, Adam Perelman, Filipe de Avila Belbute Peres, Michael Petrov, Henrique Ponde de Oliveira Pinto, Michael, Pokorny, Michelle Pokrass, Vitchyr H. Pong, Tolly Powell, Alethea Power, Boris Power, Elizabeth Proehl, Raul Puri, Alec Radford, Jack Rae, Aditya Ramesh, Cameron Raymond, Francis Real, Kendra Rim-bach, Carl Ross, Bob Rotsted, Henri Roussez, Nick Ryder, Mario Saltarelli, Ted Sanders, Shibani San-turkar, Girish Sastry, Heather Schmidt, David Schnurr, John Schulman, Daniel Selsam, Kyla Sheppard, Toki Sherbakov, Jessica Shieh, Sarah Shoker, Pranav Shyam, Szymon Sidor, Eric Sigler, Maddie Simens, Jordan Sitkin, Katarina Slama, Ian Sohl, Benjamin Sokolowsky, Yang Song, Natalie Staudacher, Felipe Petroski Such, Natalie Summers, Ilya Sutskever, Jie Tang, Nikolas Tezak, Madeleine B. Thompson, Phil Tillet, Amin Tootoonchian, Elizabeth Tseng, Preston Tuggle, Nick Turley, Jerry Tworek, Juan Felipe Cerón Uribe, An-drea Vallone, Arun Vijayvergiya, Chelsea Voss, Carroll Wainwright, Justin Jay Wang, Alvin Wang, Ben Wang, Jonathan Ward, Jason Wei, CJ Weinmann, Akila Welihinda, Peter Welinder, Jiayi Weng, Lilian Weng, Matt Wiethoff, Dave Willner, Clemens Winter, Samuel Wol-rich, Hannah Wong, Lauren Workman, Sherwin Wu, Jeff Wu, Michael Wu, Kai Xiao, Tao Xu, Sarah Yoo, Kevin Yu, Qiming Yuan, Wojciech Zaremba, Rowan Zellers, Chong Zhang, Marvin Zhang, Shengjia Zhao, Tianhao Zheng, Juntang Zhuang, William Zhuk, and Barret Zoph. 2024. [Gpt-4 technical report](#). *Preprint*, arXiv:2303.08774.
- E M Phizicky and S Fields. 1995. [Protein-protein interactions: methods for detection and analysis](#). *Microbiological Reviews*, 59(1):94–123.
- Janet Piñero, Àlex Bravo, Núria Queralt-Rosinach, Alba Gutiérrez-Sacristán, Jordi Deu-Pons, Emilio Centeno, Javier García-García, Ferran Sanz, and Laura I. Furlong. 2016. [Disgenet: a comprehensive platform integrating information on human disease-associated genes and variants](#). *Nucleic Acids Research*, 45(D1):D833–D839.
- Janet Piñero, Núria Queralt-Rosinach, Àlex Bravo, Jordi Deu-Pons, Anna Bauer-Mehren, Martin Baron, Ferran Sanz, and Laura I. Furlong. 2015. [Disgenet: a discovery platform for the dynamical exploration of human diseases and their genes](#). *Database*, 2015:bav028.
- Janet Piñero, Juan Manuel Ramírez-Angueta, Josep Saüch-Pitarch, Francesco Ronzano, Emilio Centeno, Ferran Sanz, and Laura I Furlong. 2019. [The disgenet knowledge platform for disease genomics: 2019 update](#). *Nucleic Acids Research*, 48(D1):D845–D855.
- Jianing Qiu, Kyle Lam, Guohao Li, Amish Acharya, Tien Yin Wong, Ara Darzi, Wu Yuan, and Eric J Topol. 2024. [Llm-based agentic systems in medicine and healthcare](#). *Nature Machine Intelligence*, 6(12):1418–1420.
- V Srinivasa Rao, K Srinivas, GN Sujini, and GN Sunand Kumar. 2014. [Protein-protein interaction detection: methods and analysis](#). *International journal of proteomics*, 2014(1):147648.
- Yaxuan Ren, Xufei Luo, Ye Wang, Haodong Li, Hairong Zhang, Zeming Li, Honghao Lai, Xuanlin Li, Long Ge, Janne Estill, et al. 2024. [Large language models in traditional chinese medicine: A scoping review](#). *Journal of Evidence-Based Medicine*, page e12658.
- Jinlong Ru, Peng Li, Jinan Wang, Wei Zhou, Bohui Li, Chao Huang, Pidong Li, Zihu Guo, Weiyang Tao, Yin-feng Yang, et al. 2014. [Tcmsp: a database of systems pharmacology for drug discovery from herbal medicines](#). *Journal of cheminformatics*, 6:1–6.
- Marilyn Safran, Naomi Rosen, Michal Twik, Ruth BarShir, Tsippi Iny Stein, Dvir Dahary, Simon Fishilevich, and Doron Lancet. 2021. The genecards suite. *Practical guide to life science databases*, pages 27–56.
- Michael E. Smoot, Keiichiro Ono, Johannes Ruscheinski, Peng-Liang Wang, and Trey Ideker. 2010. [Cytoscape 2.8: new features for data integration and network visualization](#). *Bioinformatics*, 27(3):431–432.
- LangChain Team. 2025. [Introduction | LangChain](#). LangChain.
- Timm Teubner, Christoph M Flath, Christof Weinhardt, Wil van der Aalst, and Oliver Hinz. 2023. [Welcome to the era of chatgpt et al. the prospects of large language models](#). *Business & Information Systems Engineering*, 65(2):95–101.
- Arun James Thirunavukarasu, Darren Shu Jeng Ting, Ka-bilan Elangovan, Laura Gutierrez, Ting Fang Tan, and Daniel Shu Wei Ting. 2023. [Large language models in medicine](#). *Nature medicine*, 29(8):1930–1940.
- Alberto Valdeolivas, Laurent Tichit, Claire Navarro, Sophie Perrin, Gaëlle Odelin, Nicolas Levy, Pierre Cau, Elisabeth Remy, and Anaïs Baudot. 2018. [Random walk with restart on multiplex and heterogeneous biological networks](#). *Bioinformatics*, 35(3):497–505.
- Xin WANG, Zi-Yi WANG, Jia-Hui ZHENG, and Shao LI. 2021. [Tcm network pharmacology: A new trend towards combining computational, experimental and clinical approaches](#). *Chinese Journal of Natural Medicines*, 19(1):1–11.
- David S Wishart, Yannick D Feunang, An C Guo, Elvis J Lo, Ana Marcu, Jason R Grant, Tanvir Sajed, Daniel Johnson, Carin Li, Zinat Sayeeda, Nazanin Assempour, Ithayavani Iynkkaran, Yifeng Liu, Adam Maciejewski, Nicola Gale, Alex Wilson, Lucy Chin, Ryan Cum-mings, Diana Le, Allison Pon, Craig Knox, and Michael Wilson. 2017. [Drugbank 5.0: a major update to the drugbank database for 2018](#). *Nucleic Acids Research*, 46(D1):D1074–D1082.

- David S. Wishart, Craig Knox, An Chi Guo, Dean Cheng, Savita Shrivastava, Dan Tzur, Bijaya Gautam, and Murtaza Hassanali. 2007. [Drugbank: a knowledgebase for drugs, drug actions and drug targets](#). *Nucleic Acids Research*, 36(suppl₁) : D901 – –D906.
- Qingyun Wu, Gagan Bansal, Jieyu Zhang, Yiran Wu, Shaokun Zhang, Erkang Zhu, Beibin Li, Li Jiang, Xiaoyun Zhang, and Chi Wang. 2023. [Autogen: Enabling next-gen llm applications via multi-agent conversation framework](#). *arXiv preprint arXiv:2308.08155*.
- Yang Wu, Feilong Zhang, Kuo Yang, Shuangfang Fang, Dechao Bu, Hui Li, Liang Sun, Hairuo Hu, Kuo Gao, Wei Wang, Xuezhong Zhou, Yi Zhao, and Jianxin Chen. 2018. [Symmap: an integrative database of traditional chinese medicine enhanced by symptom mapping](#). *Nucleic Acids Research*, 47(D1):D1110–D1117.
- Peng Ying and Cheng Ruochuan. 2024. [Interpretation of the chinese 'caca thyroid cancer diagnosis and treatment guidelines \(2022 edition\)' from a surgical perspective](#). *Journal of Xi'an Jiaotong University (Medical Sciences)*, 45(1).
- Runzhi Zhang, Xue Zhu, Hong Bai, and Kang Ning. 2019. [Network pharmacology databases for traditional chinese medicine: review and assessment](#). *Frontiers in pharmacology*, 10:123.
- Tao Zhou, Jun Yao, and Zhanjiang Liu. 2017. [Gene ontology, enrichment analysis, and pathway analysis](#). *Bioinformatics in aquaculture: Principles and methods*, pages 150–168.