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NHOS™ Clinical Interaction Network™ (CIN™): A Multi-Layer Architecture for Drug–Medication, Drug–Herb, and Polypharmacy Interaction Intelligence

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ABSTRACT

Objectives: To describe the NHOS Clinical Interaction Network™ (CIN™), a network-oriented clinical informatics architecture designed to represent medication and natural-product interaction intelligence beyond conventional pairwise lookup.

Materials and Methods: The architecture integrates structured medication and natural-product entities with interaction relationships, pharmacological mechanisms, biological pathways, evidence provenance, edge-type classification, and research-stage polypharmacy scoring. Relationships are classified as Documented, Mechanistically Inferred, Class-Associated, or Computationally Derived. The implementation uses local-first processing and structured evidence traceability.

Results: The August 2026 implementation snapshot contains approximately 650+ documented interaction relationships, 250+ pharmacological mechanisms, and 19 biological pathway mappings within a broader health-knowledge environment containing 1,450+ herbal profiles, 440+ medication profiles, 13,000+ symptom mappings, 1,500+ academic citations, and 155+ clinical guidelines. The architecture also includes internal 0–40 Polypharmacy and 0–10 Severity scoring constructs.

Discussion: CIN™ represents interaction intelligence as a multi-layer relationship network in which direct interaction findings can be interpreted alongside mechanisms, pathways, therapeutic classes, evidence provenance, and contextual risk factors. Explicit edge provenance is designed to reduce conflation of established evidence with mechanistic or computational inference.

Conclusion: CIN™ provides a research-stage architecture for evidence-linked network analysis of medication safety and polypharmacy. The scoring constructs, interaction coverage, and clinical utility require independent validation before clinical deployment.

LAY SUMMARY

Medication and supplement interactions can become difficult to interpret when several substances are used at the same time. The NHOS Clinical Interaction Network™ is a research-stage clinical informatics architecture that organizes interaction information as connected relationships among substances, mechanisms, biological pathways, therapeutic classes, and evidence sources. It also records whether a relationship is documented or computationally derived. The architecture is intended to make the context and provenance of an interaction more visible, not to replace established clinical references. The system has not undergone independent clinical validation and is not intended to diagnose, prescribe, or replace professional clinical judgment.

BACKGROUND AND SIGNIFICANCE

Medication safety is a major patient-safety concern, and the World Health Organization has identified polypharmacy, high-risk situations, and transitions of care as important domains for medication-safety action.[1,2] At the same time, medication-related interaction intelligence may involve prescription medicines, over-the-counter medicines, dietary supplements, and natural products. The evidence base for herb–drug interactions is heterogeneous; some relationships are supported by clinical studies, whereas others may be hypothetical, mechanistically inferred, or based on indirect experimental evidence.[3] Regulatory and monographic resources provide

additional structured evidence about herbal medicinal products and their safe or traditional uses.[4,5]

Conventional interaction lookup frequently represents an interaction as a pair, such as Drug A–Drug B or Herb A–Drug B. Pairwise representation is useful for direct lookup but can make it difficult to represent the broader context in which an interaction occurs. In polypharmacy, the relevant context may include multiple concurrent substances, therapeutic-class duplication, narrow-therapeutic-index medications, shared pharmacological mechanisms, convergent biological pathways, and differences in evidence provenance.

The NHOS Clinical Interaction Network™ (CIN™) was developed within the NHOS Intelligence Matrix Engine™ (NIME™) as a network-oriented representation of medication and natural-product interaction intelligence. The design objective is not to replace established interaction references, but to provide a machine-readable and inspectable structure in which entities, relationships, mechanisms, pathways, evidence, and computational derivations can be linked and traced. The architecture is documented in a versioned NHOS Research Series record.[6]

OBJECTIVES

1. Define a machine-readable network representation for medication and natural-product interaction intelligence.
2. Connect interaction relationships with pharmacological mechanisms and biological pathways.
3. Distinguish documented evidence from mechanistically inferred, class-associated, and computationally derived relationships.

4. Provide transparent research-stage constructs for polypharmacy and interaction-severity scoring.
5. Preserve evidence provenance and support privacy-conscious local processing.

MATERIALS AND METHODS

Architecture and knowledge representation

CIN™ is implemented within NIME™, using a structured entity registry covering medications, herbs and natural products, symptoms, conditions, therapeutic classes, mechanisms, pathways, and evidence sources. The architecture supports normalization, alias resolution, entity linking, relationship retrieval, mechanism expansion, pathway expansion, network construction, provenance classification, evidence association, network analysis, research-stage risk scoring, and human-readable output.

The network representation is organized as a sequence of linked information layers: entities, interactions, mechanisms, pathways, network context, polypharmacy risk constructs, and evidence-traceable output. This organization permits a direct interaction to be examined within its surrounding relationships rather than as an isolated lookup result.

Interaction and edge-type model

Each interaction relationship can carry an explicit provenance state: Documented, Mechanistically Inferred, Class-Associated, or Computationally Derived. A Documented edge is associated with an identified evidence source. A Mechanistically Inferred edge is derived from represented pharmacological mechanism relationships. A Class-Associated edge is generated from therapeutic or entity-class relationships. A Computationally Derived edge is produced

through computational relationship logic. These categories are deliberately separated because computational availability of a relationship is not treated as equivalent to direct clinical evidence.

Relationships may additionally carry evidence tiers, severity categories, mechanisms, and available source citations. The provenance model is therefore intended to make uncertainty structurally visible and to support later evaluation of whether an edge is adequately supported for a particular use. The four provenance categories and their interpretation are summarized in Table 2.

Mechanism and pathway layers

The network expands direct relationships through a mechanism layer and a biological pathway layer. The documented implementation contains more than 250 pharmacological mechanisms and 19 biological pathway mappings. The resulting representation permits analysis of direct relationships, shared mechanisms, pathway convergence, and related risk clusters.

Polypharmacy scoring constructs

The research implementation includes an internal Polypharmacy Score on a 0–40 scale. The documented calculation incorporates active medication count, duplication of therapeutic classes, weighting for narrow-therapeutic-index medications, and interaction contributions adjusted by severity and edge-type weighting. A separate Severity Score uses values of 9 for MAJOR, 5 for MODERATE, and 2 for MINOR interactions. These are architectural and methodological constructs rather than clinically validated predictive models and are not presented as estimates of patient outcome risk. The research-stage scoring constructs and their current status are summarized in Table 3.

Retrieval, network construction, and output

The broader NIME™ implementation provides natural-language query handling, alias resolution, fuzzy matching, contextual retrieval, and structured citation generation. Within the CIN™ workflow, user terms are resolved to canonical entities; relevant relationships are retrieved; mechanisms and pathways are expanded; a relevant subgraph is constructed; edge provenance is classified; evidence is associated; network relationships are analyzed; and a human-readable result is generated with citations, uncertainty indicators, safety flags, and professional-review recommendations.

Privacy and local processing

The architecture emphasizes offline-first operation, local processing, and local storage mechanisms. The stated design objective is to reduce unnecessary transmission of sensitive medication or health information. These are architectural properties rather than claims of independent security certification or formal security validation.

Evaluation framework

The source research program defines a future validation framework spanning entity resolution, interaction detection, edge-type classification, mechanism mapping, pathway mapping, network construction, evidence classification, risk-score correlation, explainability, privacy, and computational performance. Proposed evaluation resources include expert-labeled datasets, reference interaction datasets, authoritative pathway sources, independent curation, expert review, benchmark testing, reviewer studies, and security assessment. These evaluations have not yet established clinical validity or clinical utility.

RESULTS

The documented August 2026 implementation snapshot reports 1,450+ herbal profiles, 440+ medication profiles, 13,000+ symptom mappings, 650+ categories, 1,500+ academic citations, 155+ clinical guidelines, 650+ documented interaction relationships, 250+ pharmacological mechanisms, 19 biological pathways, 160+ natural-language processing patterns, and 130+ vocabulary terms. These counts describe a versioned implementation snapshot and are not intended to represent exhaustive clinical coverage.[6]

The implemented interaction workflow comprises entity recognition, normalization, linking, relationship retrieval, mechanism expansion, pathway expansion, network construction, edge-type classification, evidence association and weighting, network analysis, research-stage risk scoring, and human-readable output. The documented implementation snapshot is summarized in Table 1. The architecture therefore documents an implemented computational workflow while retaining explicit boundaries around validation and clinical use.

Table 1. Documented implementation snapshot.

Component	Documented scale
Herbal profiles	1,450+
Medication profiles	440+
Symptom mappings	13,000+
Academic citations	1,500+
Clinical guidelines	155+
Documented interaction relationships	650+
Pharmacological mechanisms	250+
Biological pathways	19

Table 2. Interaction relationship provenance.

Edge type	Interpretation
Documented	Supported by an identified evidence source
Mechanistically Inferred	Derived from represented pharmacological mechanism relationships
Class-Associated	Associated through therapeutic or entity-class relationships
Computationally Derived	Generated through computational relationship logic

Table 3. Research-stage scoring constructs.

Construct	Scale	Status
Polypharmacy Score	0–40	Internal research framework; not clinically validated
Severity Score	0–10	Internal research classification; not clinically validated
Risk-level classification	Low to Critical	Methodological categorization requiring validation

DISCUSSION

The principal architectural contribution of CIN™ is the explicit representation of interaction intelligence as a multi-layer relationship network. The model places direct interaction findings within a wider structure of mechanisms, pathways, evidence, therapeutic classes, and contextual factors. For clinical informatics research, this provides a basis for studying how interaction evidence can be represented, retrieved, traced, and analyzed without implicitly treating every computational relationship as an established clinical fact.

A second contribution is the explicit edge-type provenance model. By separating documented relationships from mechanistic, class-associated, and computationally derived relationships, the architecture makes uncertainty visible in the data model. This distinction is particularly relevant to herb–drug interaction intelligence, where authoritative sources note that some interaction concerns remain uncertain, indirect, or incompletely studied.[3] It also creates a potential basis for evaluating not only whether an edge exists, but why the system represents it and what evidence supports that representation.

The network formulation also provides a computational framing for polypharmacy. Rather than considering only the number of pairwise interactions, the architecture can represent medication count, therapeutic-class duplication, narrow-therapeutic-index status, interaction

severity, shared mechanisms, and pathway convergence. The current scoring system, however, is explicitly a research construct. It should not be interpreted as a validated estimate of patient risk or as a clinical decision rule.

The architecture is intentionally broader than herb–medication interaction lookup. Its representation can be extended to other relationship types, including drug–drug, drug–food, drug–laboratory, drug–genotype, and related clinical interaction domains. Such extensions would require domain-specific evidence models, terminology normalization, validation datasets, and independent evaluation.

LIMITATIONS

- The architecture has not undergone independent clinical validation or prospective clinical utility assessment.
- The Polypharmacy Score and Severity Score have not been validated as predictors of adverse drug events or patient outcomes.
- Knowledge-base counts represent a versioned implementation snapshot and do not establish exhaustive clinical coverage.
- Some network relationships are explicitly inferred or computationally derived and therefore should not be interpreted as equivalent to documented evidence.
- The proposed validation framework has not yet supplied the expert-labeled datasets, independent curation, benchmark testing, security assessment, or reviewer studies required to establish performance.
- The current implementation is an architecture and health-information research system rather than a clinically validated diagnostic, prescribing, or treatment-decision system.

FUTURE RESEARCH

Future work should prioritize independent validation of entity resolution, interaction detection, edge-type classification, mechanism and pathway mapping, evidence classification, explainability, privacy properties, and computational performance. Additional work should determine whether network-derived features add measurable value beyond conventional pairwise interaction lookup and whether the research-stage scoring constructs correlate with independently defined reference outcomes.

A particularly important evaluation question is whether explicit provenance improves reviewer calibration and reduces inappropriate interpretation of inferred relationships. Independent expert annotation, blinded comparison with established interaction references, and prospective or simulated workflow studies could test this proposition. Future research should also examine how the architecture performs when evidence is conflicting, incomplete, outdated, or available only through indirect mechanisms.

CONCLUSION

The NHOS Clinical Interaction Network™ provides a research-stage, evidence-informed architecture for representing medication and natural-product interaction intelligence as a connected network of entities, relationships, mechanisms, pathways, evidence, and contextual risk factors. Its explicit provenance model separates documented evidence from inferred and computationally derived relationships. The architecture establishes a foundation for future validation studies in clinical informatics, medication safety, knowledge representation, polypharmacy analysis, and privacy-conscious digital health.

DATA AVAILABILITY

The technical architecture is documented in the NHOS Research Series and is publicly archived as a Zenodo record (DOI: 10.5281/zenodo.22312651).[6] The current manuscript describes the architecture and documented implementation snapshot. Underlying datasets and executable source code are not presented as a publicly released clinical dataset in this manuscript; release of additional artifacts should be evaluated separately according to privacy, licensing, and reproducibility requirements.

ETHICS STATEMENT

Not applicable. This manuscript describes a software architecture and versioned research implementation and does not report research involving human participants, interventions, identifiable patient records, or patient-level clinical outcomes.

FUNDING

No external funding was received for this work. The architecture was developed independently by NHOS Labs, Inc.

COMPETING INTERESTS

Adedapo Ogundiran is Founder and Lead Architect of NHOS Labs, Inc., the organization responsible for developing the NHOS platform and the architecture described in this manuscript. This institutional relationship is disclosed because the manuscript reports on an architecture developed by the author. No other competing interests are declared.

AUTHOR CONTRIBUTIONS

Adedapo Ogundiran: conceptualization; architecture design; methodology; implementation framework; analysis; documentation; and manuscript preparation.

CLINICAL USE AND SAFETY STATEMENT

CIN™ is an educational and research-stage health-information architecture. It is not a clinically validated diagnostic, prescribing, or treatment-decision system. The Polypharmacy Score and Severity Score are internal research constructs and should not be used independently to make clinical decisions. Interaction information represented by the architecture should be interpreted against appropriate authoritative sources and by qualified professionals when clinical decisions are involved.

AI ASSISTANCE DISCLOSURE

Generative AI tools were used to assist with manuscript organization and language editing. The underlying technical claims, architecture, implementation description, research-stage limitations, and responsibility for the final manuscript remain with the author and NHOS Labs, Inc.

RELATED PUBLICATION AND VERSION RECORD

The manuscript is derived from the NHOS Clinical Interaction Network™ technical white paper, Version 3.0 (Final Research Version), deposited in the NHOS Research Series with DOI 10.5281/zenodo.22312651.[6] The journal manuscript is intended as a focused scholarly presentation of the architecture and its research-stage implementation, not as a claim of independent clinical validation.

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