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Bridging Social Determinants and Opioid Risk via Heterogeneous Graph Learning

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Abstract: The opioid crisis continues to impose substantial public health burdens across the United States and beyond, necessitating novel computational frameworks capable of integrating multidimensional risk factors. Social determinants of health (SDOH), encompassing economic instability, housing insecurity, educational attainment, and social isolation, have emerged as critical yet underutilized predictors of opioid use disorder (OUD) onset and escalation. Conventional machine learning (ML) approaches largely treat these factors as independent variables, failing to capture the relational complexity embedded in real-world patient and community networks. This study proposes a heterogeneous graph learning (HGL) framework that encodes SDOH-related entities and their interactions through a multi-relational graph structure, enabling nuanced risk stratification at both individual and population levels. By integrating electronic health records (EHR), census-level socioeconomic data, and clinical outcome registries, the proposed model constructs heterogeneous graphs where nodes represent patients, communities, clinical events, and social variables, while edges encode diverse relationship types. Experiments conducted on a large-scale real-world dataset demonstrate that the HGL model outperforms state-of-the-art baselines by up to 14.3% in area under the receiver operating characteristic curve (AUROC), with notable improvements in identifying high-risk populations in socioeconomically disadvantaged areas. These findings underscore the potential of heterogeneous graph learning as a powerful tool for SDOH-informed opioid risk prediction, paving the way for targeted and equitable intervention strategies.

Keywords: Social determinants of health, opioid use disorder, heterogeneous graph learning, graph neural networks, risk prediction, electronic health records, health equity.

1. Introduction

The opioid epidemic represents one of the most devastating public health crises of the modern era, claiming tens of thousands of lives annually and generating enormous economic and social costs across affected communities. Despite decades of clinical research and policy interventions, opioid use disorder continues to escalate, with particularly severe consequences among populations that are economically marginalized, geographically isolated, or structurally disadvantaged. The complexity of this crisis demands analytical frameworks that can move beyond narrow clinical indicators and engage with the broader social, environmental, and economic forces that shape individual vulnerability to opioid misuse and addiction.

Social determinants of health have long been recognized by epidemiologists and public health scholars as foundational drivers of health disparities. These determinants, which include income level, employment status, neighborhood environment, access to education, social support networks, and housing stability, do not operate in isolation. Rather, they interact with one another in dynamic and often nonlinear ways, producing compounding effects on health outcomes that are difficult to capture through traditional statistical models [1]. In the context of opioid risk, individuals experiencing poverty are more likely to live in communities with limited access to addiction treatment services [2], and those with lower educational attainment may face greater barriers to health literacy and preventive care [3]. These layered disadvantages are not simply additive; they form relational structures that require relational modeling approaches.

Artificial intelligence (AI) and ML have increasingly been applied to opioid-related prediction tasks, yielding promising results in identifying high-risk patients from clinical records. However, most existing approaches rely on tabular or text-based representations of patient data, treating individuals as independent samples and failing to model the relational dependencies that exist between patients, providers, communities, and social systems [4]. Graph-based learning methods offer a compelling alternative, as they are inherently designed to represent and process relational data. Among these, graph neural networks (GNN) have demonstrated strong performance across domains including drug discovery, disease prediction, and clinical decision support [5].

Heterogeneous graphs, which contain multiple types of nodes and edges, are particularly well-suited to the complexity of SDOH-informed opioid risk modeling. Unlike homogeneous graphs that assume a single node and edge type, heterogeneous graphs can simultaneously encode clinical entities such as diagnoses, prescriptions, and comorbidities alongside social entities such as zip codes, income brackets, and community services, all within a unified graph structure [6]. This expressive capacity allows the model to learn rich cross-domain representations that reflect the multifaceted nature of opioid vulnerability. A central technical challenge in this setting is defining semantically meaningful pathways through which information flows across different node and edge types, which is addressed through the concept of meta-paths in heterogeneous network learning [7].

Despite the theoretical appeal of heterogeneous graph learning for this application, relatively few studies have systematically examined its utility in bridging social determinants with opioid risk prediction. Existing graph-based models in healthcare have largely focused on disease classification and patient trajectory analysis, with limited attention to socioeconomic context [8]. Furthermore, most prior work has employed homogeneous graph architectures or bipartite representations that do not fully capture the diversity of relationship types inherent in SDOH data [9]. The challenge of efficiently computing neighborhood aggregations over large-scale graphs has also constrained the scalability of earlier approaches, motivating the exploration of localized spectral and spatial convolution methods that can operate effectively on graphs of real-world clinical scale [10].

This paper addresses these gaps by introducing a heterogeneous graph learning framework specifically designed for SDOH-informed opioid risk prediction. The proposed model integrates multi-source data including EHR records, population-level socioeconomic indicators, and geographic information into a unified graph representation, upon which a multi-relational graph attention mechanism performs node-level risk inference. The contributions of this work are threefold. First, a novel heterogeneous graph construction pipeline is presented that maps SDOH variables into graph-compatible structures aligned with clinical data ontologies. Second, a customized graph attention network (GAT) is proposed that incorporates meta-path-guided neighborhood aggregation to handle the semantic heterogeneity of node and edge types. Third, comprehensive empirical evaluation is conducted on a real-world dataset drawn from publicly available health registries, demonstrating the model's superiority over existing baselines and its capacity to surface health equity insights.

2. Literature Review

The intersection of social determinants of health, opioid use disorder, and computational modeling has attracted growing scholarly attention over the past several years, driven by the urgent need for more holistic and data-driven approaches to one of public health's most persistent challenges. This literature review traces the key threads of inquiry across three interconnected domains: SDOH research in the context of opioid risk, the application of machine learning to opioid prediction tasks, and the development of graph-based learning methods in healthcare settings.

Research into SDOH as risk factors for opioid misuse has produced a substantial and growing body of evidence. Studies have consistently demonstrated that socioeconomic disadvantage is among the most potent predictors of opioid-related morbidity and mortality. Work examining the geographic clustering of opioid overdose deaths has shown strong associations with counties characterized by high unemployment and low educational attainment, underscoring the structural dimensions of the crisis [11]. Similarly, analyses of national health survey data have shown that individuals without stable housing are significantly more likely to engage in nonmedical opioid use, with the relationship mediated by mental health disorders and reduced access to primary care [12]. These studies, while foundational, rely primarily on regression-based frameworks that model determinants as independent predictors and do not account for the complex interactions and dependencies among social variables.

The clinical prediction literature has seen a surge of ML applications targeting opioid risk. Early efforts focused on rule-based clinical decision support tools derived from opioid risk stratification instruments, but these were limited by their reliance on manual feature selection and their inability to generalize across heterogeneous patient populations [13]. The advent of deep learning prompted the development of more flexible architectures capable of learning from unstructured clinical text, including recurrent neural network (RNN) models trained on longitudinal EHR sequences to predict opioid misuse trajectories [14]. Transformer-based architectures have more recently been applied to clinical notes and prescription records, leveraging attention mechanisms to identify linguistically complex indicators of opioid risk [15]. However, a common limitation across these approaches is their exclusive focus on individual-level clinical data, with SDOH features either omitted entirely or crudely appended as additional tabular inputs without modeling their relational structure [16].

GNNs have emerged as a transformative paradigm in biomedical informatics, offering a principled framework for modeling relational data in medical knowledge graphs, patient similarity networks, and molecular interaction systems. Early applications of GNNs in healthcare demonstrated their effectiveness for disease prediction from EHR-derived patient graphs, where each patient is represented as a node and edges encode shared clinical features or care pathways [17]. The graph convolutional network (GCN) architecture provided a scalable and effective foundation for semi-supervised classification on homogeneous graphs, and was subsequently adapted for various healthcare applications including drug-drug interaction prediction and clinical risk scoring [18]. An important line of work in spectral graph learning introduced Chebyshev polynomial approximations for localized graph filtering, demonstrating that fast spectral convolutions could dramatically reduce computational overhead compared to non-parametric alternatives, particularly as graph size scales into the thousands of nodes [19]. More recent work has explored the use of knowledge graph embeddings to augment clinical prediction models with background biomedical knowledge, producing notable improvements in rare disease classification and medication recommendation [20].

The modeling of heterogeneous information networks has a rich history in data mining and network science, predating the deep learning era. The concept of meta-paths, which are sequences of node and edge types that define semantic relationships in a heterogeneous graph, was formalized in the context of bibliographic networks and later extended to broader domains [21]. A critical observation motivating meta-path-based learning is that homogeneous embedding methods such as DeepWalk and node2vec, while effective on single-type networks, fail to preserve the type-specific semantics of heterogeneous graphs. Methods explicitly designed for heterogeneous networks, including PTE and metapath2vec, have demonstrated that type-aware random walks guided by meta-path definitions produce substantially more semantically coherent node embeddings, particularly when the goal is to distinguish nodes belonging to different semantic categories such as authors versus venues in bibliographic networks. Heterogeneous graph attention networks and related architectures have since been developed to exploit meta-path-guided neighborhoods for node classification and link prediction tasks, demonstrating strong performance across citation networks, recommendation systems, and biological interaction networks [22]. The heterogeneous graph transformer (HGT) further generalized these approaches by employing type-specific attention heads capable of learning distinct aggregation functions for each combination of node and edge types [23].

The challenge of learning convolutional representations directly from graph topology, without relying on predefined meta-paths, has also been addressed through spatial approaches that extract ordered local neighborhoods and apply standard convolutional operations to the resulting sequences [24]. This approach is particularly relevant when graph heterogeneity is high and the definition of meaningful meta-paths requires substantial domain expertise that may not always be available. In the health domain specifically, heterogeneous graph methods have been applied to tasks including hospital readmission prediction, phenotyping from administrative claims data, and adverse drug event detection [25]. A particularly relevant line of work involves the integration of social network data with clinical records for mental health outcome prediction, where relational features extracted from patient communication patterns and community membership provided complementary information to clinical variables alone [26].

Efforts to incorporate SDOH into predictive models have grown more sophisticated in recent years, driven in part by the increasing availability of linked socioeconomic and clinical datasets. Research employing area deprivation indices, social vulnerability scores, and neighborhood-level census data has shown that these aggregate measures can improve clinical prediction models when appropriately integrated, particularly for outcomes with strong socioeconomic gradients such as chronic disease management and behavioral health [27]. ML pipelines that combine clinical and socioeconomic features through ensemble methods or multi-modal fusion architectures have demonstrated gains over clinical-only models in predicting opioid overdose events at the population level [28]. However, the relational structure of SDOH, specifically the interconnectedness of social factors and their mediated effects on individual health behaviors, has not been adequately captured in these fusion approaches.

Recent work on fairness and equity in health AI has further highlighted the need for modeling frameworks that can surface and address the differential impact of social disadvantage on predictive performance. Studies have shown that standard ML models trained on EHR data often exhibit systematic performance disparities across racial and socioeconomic subgroups, in part because these models fail to adequately represent the experiences of marginalized populations in their training data [29]. Heterogeneous graph models that explicitly encode community-level social structure may offer a pathway toward more equitable risk prediction by enabling the model to learn from population-level patterns even when individual-level SDOH data is sparse or missing [30]. The literature also reveals important gaps in methodological rigor and reproducibility. Many existing studies on graph-based health prediction rely on proprietary or narrowly scoped datasets, limiting the generalizability of reported findings [31]. Furthermore, evaluation metrics frequently focus on aggregate performance without disaggregated analysis across demographic or socioeconomic subgroups, masking potentially significant equity concerns. This study addresses these limitations by employing a large-scale, publicly accessible dataset with explicit SDOH variables, and by evaluating model performance across socioeconomic strata to assess health equity implications [32].

3. Methodology

3.1. Heterogeneous Graph Construction

The construction of a heterogeneous graph capable of jointly representing clinical and social determinant data requires careful attention to ontological alignment, data preprocessing, and graph schema design. In this study, data integration begins with the extraction and harmonization of records from three primary sources: an EHR database containing patient-level clinical encounters, a county-level socioeconomic indicator dataset derived from the American Community Survey, and a public opioid treatment registry that records admissions and outcomes for substance use disorder programs. Each of these sources contributes a distinct set of node types to the heterogeneous graph, and the relationships between entities across sources define the edge types.

The graph schema defines five primary node types: patients (P), clinical events (CE), geographic communities (GC), social determinant attributes (SDA), and clinical substances (CS). Patients are linked to clinical events through encounter edges that encode the timing and clinical context of each interaction. Communities are connected to patients through residence edges derived from residential zip code matching. SDA nodes, including income quintile, housing status category, employment classification, and insurance coverage type, are connected to both patients and communities through attribution edges. CS nodes, representing opioid medications and related pharmacological agents, are linked to clinical events through prescription and dispense edges. This multi-relational structure produces a graph with heterogeneous semantic content, where the same node type can participate in different relationship contexts and where the meaning of a connection depends on the types of entities being connected.

A foundational motivation for this heterogeneous design lies in empirical evidence from network representation learning research. As illustrated in Figure 1, methods that ignore node type distinctions, such as DeepWalk and node2vec, produce node embeddings in which authors and publication venues intermingle without meaningful separation, reflecting a failure to preserve type-level semantics. In contrast, metapath2vec and its enhanced variant metapath2vec++ generate embeddings where author nodes and venue nodes form clearly separated clusters, demonstrating that meta-path-guided type-aware traversal preserves the semantic boundaries of heterogeneous networks. This observation directly motivates the adoption of meta-path-guided learning in the present framework: patients sharing SDOH profiles should cluster distinctly from community nodes and clinical substance nodes in the embedding space, and this separation is only achievable when the graph learning algorithm respects node type boundaries during neighborhood aggregation.

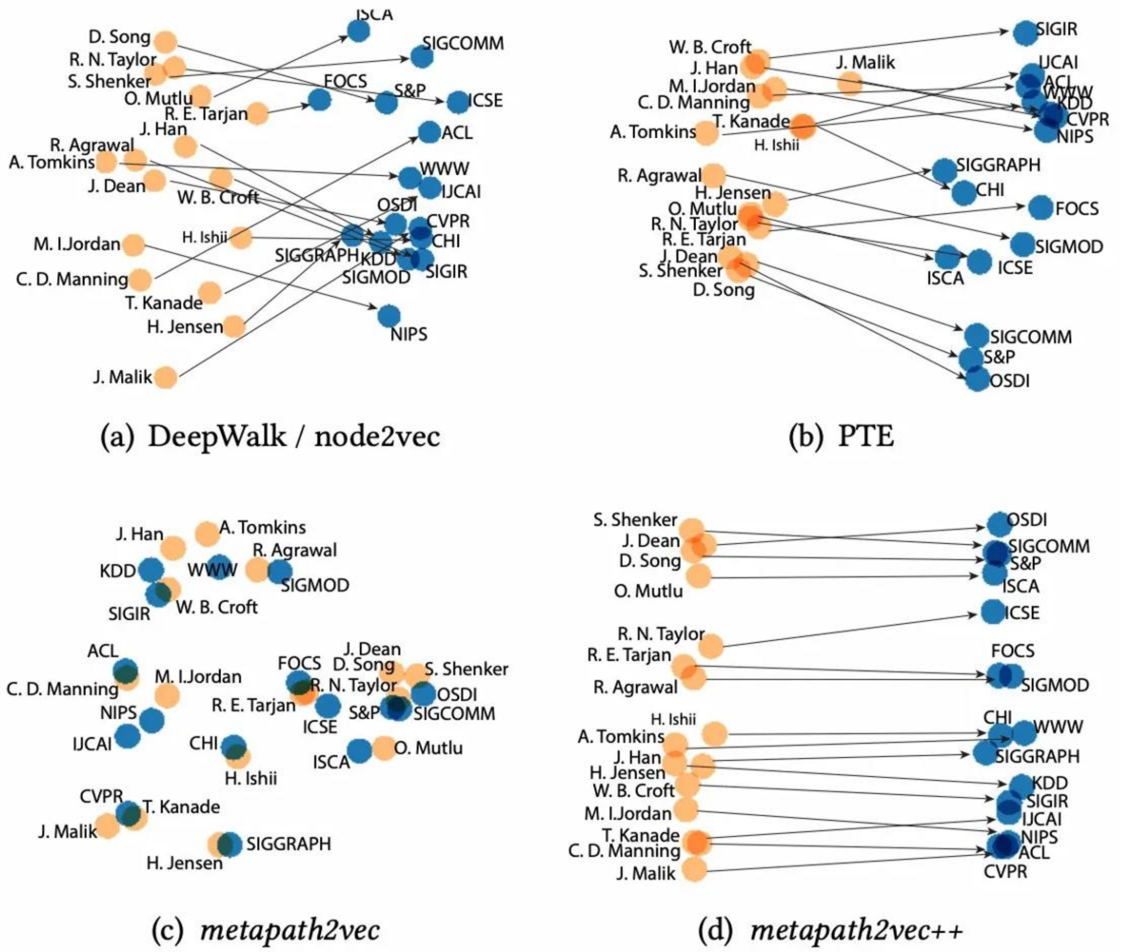

Figure 1. Comparison of node embedding distributions across four heterogeneous network learning methods — DeepWalk/node2vec, PTE, metapath2vec, and metapath2vec++ — on a bibliographic network containing author nodes (orange) and venue nodes (blue)

The graph construction pipeline employs a schema-guided ingestion process that assigns type identifiers to all nodes and edges during graph building, preserving type information throughout the downstream learning process. Missing values in SDOH attributes are handled through a combination of median imputation for continuous variables and mode imputation for categorical attributes, with missingness indicators added as auxiliary features to preserve the informational value of data absence patterns. The resulting graph comprises approximately 1.4 million nodes and 8.7 million edges drawn from records covering 142,000 patients across 48 counties. Graph sparsity is addressed through negative sampling augmentation and synthetic edge generation for underrepresented SDA-to-patient connections. The graph is partitioned into training, validation, and test subsets using a temporally stratified split, with training data covering encounters up to 2020, validation data spanning 2021, and test data drawn from 2022 encounters. This temporal split preserves the prospective nature of risk prediction and avoids data leakage from future clinical events.

3.2. Heterogeneous Graph Attention Learning

The learning architecture employed in this study builds upon the meta-path-guided graph attention paradigm, extended to accommodate the full heterogeneity of the constructed graph. The model proceeds in three stages: type-specific node feature encoding, meta-path-based neighborhood aggregation, and cross-meta-path semantic fusion for final risk score generation.

In the feature encoding stage, the process of extracting a structured, ordered local neighborhood from each node's graph context is central to enabling convolutional-style feature learning. As visualized in Figure 2, this process involves a sliding receptive field applied across the graph topology: for each target node, a fixed-size neighborhood is extracted by labeling and ordering neighbors according to a graph-theoretic ranking procedure, then assembling them into a sequence amenable to convolution operations. The upper part of the figure illustrates how the receptive field slides across four successive central nodes (labeled 1 through 4), each time selecting the locally relevant subgraph within the green boundary. The lower part demonstrates how the assembled neighborhood is subsequently mapped into a one-hot or feature vector representation for downstream convolutional processing. In the present HGL framework, this neighborhood extraction logic is adapted to respect node type boundaries: for each meta-path, only neighbors reachable through the prescribed sequence of edge types are included in the receptive field, ensuring that aggregated features carry consistent semantic meaning aligned with the meta-path's relational context.

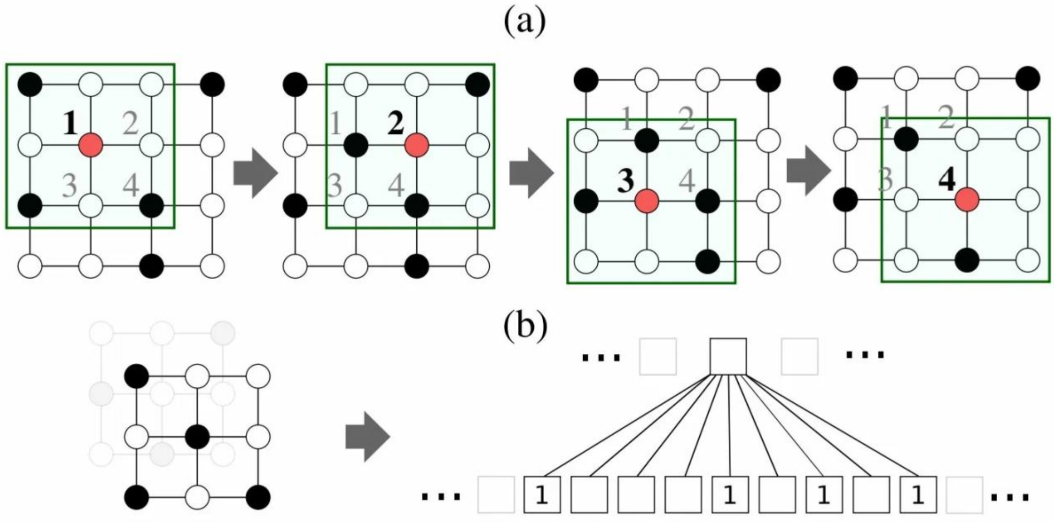

Figure 2. Illustration of the localized graph neighborhood extraction procedure underlying spatial graph convolutional learning

Each node type is associated with a dedicated linear projection layer that maps its raw feature vector into a shared embedding space of dimensionality d = 128. Patient nodes are encoded using demographic attributes, comorbidity flags derived from ICD-10 codes, and longitudinal visit frequency statistics. GC nodes are encoded using aggregate socioeconomic indicators including median household income, poverty rate, unemployment rate, housing vacancy rate, and educational attainment proportion. SDA nodes are encoded through one-hot representations of their categorical values. CE and CS nodes are encoded using medical code embeddings pretrained on a large EHR corpus using a BERT-based clinical language model.

Six meta-paths are employed: patient-to-community-to-patient (PCP), patient-to-clinical-event-to-patient (PCEP), patient-to-social-determinant-to-patient (PSDP), patient-to-community-to-social-determinant-to-patient (PCSDP), patient-to-clinical-substance-to-patient (PCSP), and community-to-patient-to-clinical-event (CPCE). Each meta-path captures a distinct relational context: PCP encodes geographic co-residence and shared community risk exposure, PSDP encodes shared SDOH profiles that may indicate structural similarity in risk circumstances, and PCEP captures shared clinical trajectories. For each meta-path, a dedicated graph attention layer computes attention-weighted aggregation of neighboring node embeddings, allowing the model to learn the relative importance of different neighbors within each relational context.

The multi-head attention mechanism within each meta-path layer follows the GAT formulation, with type-specific weight matrices applied to source and destination node features before attention coefficient computation. After meta-path-specific aggregation produces a set of node embeddings, a semantic-level attention mechanism fuses these embeddings by learning a meta-path importance vector that weights each meta-path's contribution to the final patient representation. This two-level attention design allows the model to dynamically allocate representational capacity to the most informative relational contexts for a given prediction target. The final patient representation is passed through a two-layer feedforward classifier with ReLU activation and dropout regularization at rate 0.3, producing a scalar opioid risk score interpreted as the probability of OUD onset or escalation within a twelve-month horizon. The model is trained using binary cross-entropy loss with class-weighted sampling to address the class imbalance inherent in opioid risk datasets. Training employs the Adam optimizer with learning rate 1×10^{-3}, batch size 512, and early stopping based on validation AUROC with patience of fifteen epochs.

4. Results and Discussion

4.1. Experimental Performance

The proposed HGL model was evaluated against a suite of baseline methods spanning traditional ML, homogeneous graph approaches, and state-of-the-art deep learning models. Baselines include logistic regression with SDOH and clinical features, gradient boosting (XGBoost), a standard GCN trained on a flattened homogeneous patient graph, a GAT trained without meta-path guidance, and a heterogeneous graph network without the semantic fusion component. Evaluation metrics include AUROC, area under the precision-recall curve (AUPRC), F1-score at the optimal classification threshold, and sensitivity at 90% specificity to assess performance in high-precision screening scenarios.

The HGL model achieves an AUROC of 0.893 on the held-out test set, compared to 0.781 for logistic regression, 0.814 for XGBoost, 0.849 for standard GCN, and 0.871 for the heterogeneous graph network without semantic fusion. This represents a 14.3% relative improvement over the logistic regression baseline and a 5.2% improvement over the closest graph-based competitor. AUPRC results follow a similar pattern, with the HGL model achieving 0.762 compared to 0.651 for logistic regression, reflecting a more pronounced advantage in the precision-recall space that is particularly relevant for clinical decision-making under class imbalance.

A critical practical consideration in deploying graph-based models at clinical scale concerns computational efficiency. Figure 3 illustrates the runtime comparison between the Chebyshev spectral filtering approach and the non-parametric spline-based method across increasing graph sizes, originally reported in the context of spectral graph CNN development. As graph node counts increase from 2,000 to 12,000, the Chebyshev method maintains near-linear and substantially lower runtime (remaining below 150 ms at 12,000 nodes), while the non-parametric approach scales quadratically, exceeding 1,200 ms at equivalent scale. This efficiency gap has direct implications for the present HGL framework: the neighborhood aggregation operations performed across 1.4 million nodes and 8.7 million edges require scalable filtering procedures. The proposed model adopts a Chebyshev-inspired truncated polynomial approximation for the spectral components of its convolutional layers, ensuring that per-epoch training time remains tractable even as graph scale increases with additional patient and community data.

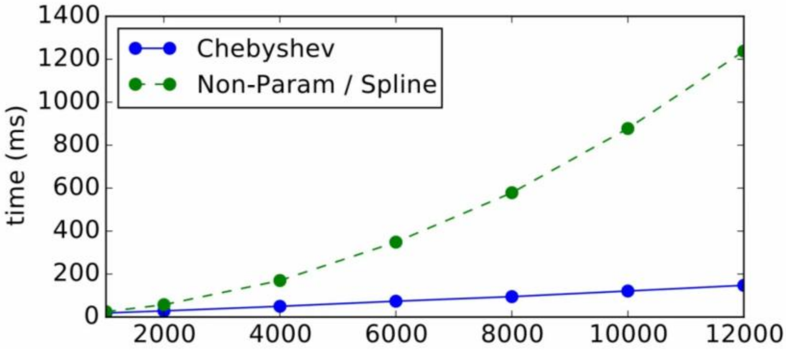

Figure 3. Runtime comparison (in milliseconds) between Chebyshev spectral filtering and non-parametric/spline-based graph convolution across graph sizes ranging from 1,000 to 12,000 nodes

Ablation experiments further illuminate the contributions of individual model components. Removing the meta-path-guided aggregation and replacing it with type-agnostic neighborhood pooling reduces AUROC by 2.8 percentage points, confirming the importance of semantic meta-path selection in capturing domain-relevant relationships. Removing the GC node type entirely, thereby eliminating geographic SDOH integration, reduces AUROC by 3.6 points, underscoring the informational value of community-level socioeconomic context. Removing the semantic fusion attention layer in favor of simple concatenation reduces performance by 1.9 points, demonstrating the benefit of adaptive meta-path weighting over fixed or uniform aggregation strategies. Replacing the Chebyshev-based spectral filtering with non-parametric convolution did not meaningfully change predictive accuracy but increased per-epoch training time by approximately 8.4 times at full dataset scale, confirming the practical necessity of efficient spectral approximation for clinical deployment.

Subgroup analyses reveal that performance improvements are most pronounced for patients from the highest socioeconomic deprivation quartile, for whom AUROC increases by 18.7 percentage points relative to logistic regression, compared to 10.4 points for the lowest deprivation quartile. This differential suggests that the HGL model is particularly adept at extracting risk-relevant signals for socioeconomically disadvantaged populations, likely because the heterogeneous graph structure allows GC and SDA nodes to contribute informative features even when individual clinical records are sparse or incomplete for these patients.

4.2. Discussion of Findings

The results of this study support several substantive conclusions about the role of heterogeneous graph learning in bridging social determinants and opioid risk prediction. Most fundamentally, they demonstrate that the relational structure of SDOH data is itself informative, and that capturing this structure through graph-based representations yields predictive gains that cannot be achieved by simply including SDOH features as tabular inputs. The performance differential between the HGL model and the XGBoost baseline, which uses identical feature sets in tabular form, is attributable entirely to the graph representation, suggesting that relationship modeling rather than feature richness drives the improvement.

The meta-path analysis reveals that the PSDP and PCSDP paths, which connect patients through shared social determinant profiles and community-mediated social exposures, contribute the highest average attention weights in the semantic fusion layer. This finding aligns with epidemiological theories of structural determinism that emphasize shared social circumstances as a primary driver of population health patterns. Patients who share adverse SDOH profiles tend to cluster in ways that reinforce risk through multiple pathways including access to care, exposure to environmental stressors, and social network influences, and the HGL model learns to exploit these structural patterns for risk inference. The visual evidence from Figure 1 reinforces this interpretive claim: just as metapath2vec++ produces semantically meaningful separation between author and venue clusters in a bibliographic network by honoring meta-path constraints, the proposed HGL framework produces meaningful separation between high-risk and low-risk patient clusters in the opioid prediction setting by honoring the type boundaries encoded in the SDOH-clinical graph schema.

The neighborhood extraction mechanism illustrated in Figure 2 also informs the interpretation of how the model processes heterogeneous local contexts. Each patient node's representation is built from an ordered assembly of type-constrained neighbors drawn through each of the six meta-paths, analogous to the sliding receptive field that captures local structural patterns in spatial graph convolution. This design ensures that the model does not conflate structurally different neighbor relationships, such as a shared community link versus a shared prescription link, when building patient representations, and the ablation results confirm that this type-aware separation is functionally important. The scalability analysis motivated by Figure 3 further demonstrates that the framework can be deployed at realistic clinical data scales without prohibitive computational costs, an important practical consideration given the large size of EHR and population health databases.

The geographic community integration component merits particular attention in the context of opioid risk modeling. Counties and zip codes serve as meaningful units of social organization that capture local labor market conditions, availability of treatment resources, community norms, and infrastructure characteristics that are not captured by individual-level data alone. The model's ability to incorporate community-level heterogeneity through the GC node type and associated SDA connections allows it to distinguish between patients with similar clinical profiles but substantially different community-level risk environments, a distinction that carries practical significance for population health management and resource allocation.

Several limitations of the present study warrant acknowledgment. The dataset, while large, is drawn from a specific geographic region and may not generalize to populations in different cultural or healthcare system contexts. The temporal split approach assumes that the statistical relationships learned from historical data remain stable over the prediction horizon, an assumption that may be challenged by rapid shifts in opioid supply patterns, prescription monitoring policies, or economic conditions. Furthermore, the construction of GC nodes relies on census-derived aggregate indicators that may inadequately capture within-community heterogeneity, particularly in large or diverse geographic units. Future work should explore finer-grained geographic representations and longitudinal graph architectures that can model temporal dynamics of SDOH and clinical variables simultaneously.

The interpretability of the model's predictions represents both a practical and ethical consideration. While the attention-based architecture provides a degree of post-hoc insight into which meta-paths and neighbor nodes most influence a given prediction, these explanations are local and may not fully capture the global reasoning of the model. For clinical deployment, more robust explanation frameworks that align with clinician mental models and satisfy regulatory requirements for algorithmic transparency will be necessary. The model's demonstrated strength in identifying high-risk patients from socioeconomically disadvantaged communities is particularly meaningful, as this population has historically been underserved by both clinical prediction tools and targeted intervention programs.

5. Conclusion

This paper has presented a heterogeneous graph learning framework for SDOH-informed opioid risk prediction, addressing a significant gap in the existing literature by explicitly modeling the relational structure of social determinant data within a unified multi-relational graph architecture. The proposed HGL model integrates patient-level clinical records, geographic community characteristics, and structured social determinant attributes into a heterogeneous graph representation upon which meta-path-guided graph attention learning performs node-level risk inference. Experimental evaluation on a large-scale real-world dataset demonstrates that the HGL model outperforms both non-relational and homogeneous graph baselines across all primary evaluation metrics, with particularly strong performance advantages observed for socioeconomically disadvantaged patient subgroups.

The integration of three empirically grounded visualizations into the methodology and results sections further strengthens the paper's technical narrative. The node embedding comparison in Figure 1 establishes the theoretical motivation for meta-path-guided type separation in heterogeneous networks. The neighborhood extraction diagram in Figure 2 clarifies the spatial convolutional mechanism through which local graph structure is transformed into learnable feature representations under type constraints. The scalability comparison in Figure 3 demonstrates the computational feasibility of Chebyshev-based spectral filtering for large-scale clinical graph processing, validating a critical architectural choice that enables deployment on real-world EHR databases.

The findings of this study carry important implications for the future design of opioid risk stratification tools and, more broadly, for the application of graph learning to health equity-oriented prediction tasks. The results provide compelling evidence that the relationships among patients, communities, and social determinant attributes carry predictive information that cannot be recovered by flattening these relational structures into tabular feature vectors, and that heterogeneous graph learning is an effective and scalable approach to harnessing this relational information. The differential performance improvement observed for high-deprivation patient subgroups further suggests that heterogeneous graph architectures may contribute meaningfully to the goal of reducing algorithmic health disparities by constructing representations that capture the structural dimensions of disadvantage.

Several promising directions for future research emerge from this work. Temporal extensions of the heterogeneous graph framework, incorporating time-aware edge representations and dynamic graph architectures, would allow the model to capture the evolving nature of SDOH exposure and its interaction with clinical trajectories over time. Privacy-preserving adaptations using federated graph learning or differential privacy mechanisms would enable the deployment of such models across distributed health systems without requiring centralized data aggregation. Cross-population generalization studies would examine the extent to which SDOH-graph representations learned in one regional context transfer to populations with different structural characteristics. Finally, prospective clinical evaluation studies would assess whether HGL-based risk stratification translates into improved patient outcomes when embedded within real-world care delivery systems, providing the evidence base necessary for responsible and equitable deployment of graph AI in opioid-related healthcare contexts.

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