

# Associating Healthcare Teamwork with Patient Outcomes for Predictive Analysis

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## Abstract

Cancer treatment outcomes are influenced not only by clinical and demographic factors but also by the collaboration of healthcare teams. However, prior work has largely overlooked the potential role of human collaboration in shaping patient survival. This paper presents an applied AI approach to uncovering the impact of healthcare professionals' (HCPs) collaboration—captured through electronic health record (EHR) systems—on cancer patient outcomes. We model EHR-mediated HCP interactions as networks and apply machine learning techniques to detect predictive signals of patient survival embedded in these collaborations. Our models are cross validated to ensure generalizability, and we explain the predictions by identifying key network traits associated with improved outcomes. Importantly, clinical experts and literature validate the relevance of the identified crucial collaboration traits, reinforcing their potential for real-world applications. This work contributes to a practical workflow for leveraging digital traces of collaboration and AI to assess and improve team-based healthcare. The approach is potentially transferable to other domains involving complex collaboration and offers actionable insights to support data-informed interventions in healthcare delivery.

## 1 Introduction

Cancer outcomes are influenced by a complex interplay of clinical, demographic, and organizational factors. While considerable research has focused on patient-level variables such as age, disease stage, and comorbidities (Søgaard et al. 2013; Brandt et al. 2015), less attention has been paid to the role of human collaboration—particularly how healthcare professionals (HCPs) work together to coordinate and deliver care. Yet, effective collaboration is increasingly recognized as a critical determinant of care quality and patient outcomes in oncology and other complex medical domains (Gurses and Xiao 2006; Smits et al. 2010; Bagnasco et al. 2013; Verhaegh et al. 2017).

Electronic Health Records (EHRs) play a central role in modern healthcare coordination, serving not only as repositories of patient information but also as platforms through which clinicians communicate, document, and implicitly collaborate (Blumenthal and Tavenner 2010; Horwitz and Detsky 2011; Wu et al. 2011). These digital traces of interaction offer a rich, but currently underutilized source of data

for understanding how care teams function and how their collaboration may influence patient trajectories.

In this study, we propose a novel, data-driven workflow to evaluating team-based cancer care by modeling HCP collaboration patterns as networks derived from EHR interactions. We then apply machine learning techniques to these networks to identify predictive signals associated with patient survival. This approach allows us to move beyond static clinical indicators (i.e., cancer stage) and uncover human factors that associate with patient outcomes. By using cross-validation and explainable AI techniques, we ensure that our findings are both generalizable and actionable.

Feedback from medical experts indicated that our findings aligned with a long-standing hypothesis: involving general practitioners in coordinating cancer treatment can positively affect patient outcomes. A review of prior literature (Smith et al. 2017; Perfors et al. 2019; Goderis et al. 2010) confirmed that this hypothesis had been proposed but lacked empirical validation using real-world cancer treatment data. Our results provide the first data-driven evidence supporting it, reinforcing the practical relevance and credibility of our approach.

Our contributions are threefold: (1) we introduce a transferable framework for extracting and modeling EHR-mediated collaboration networks; (2) we show how medical collaboration data should be analyzed to avoid introducing spurious signals and demonstrate how machine learning can be applied to these networks to predict patient survival; and (3) we provide evidence that the learned features offer actionable insights for improving care delivery. More broadly, this work showcases how leveraging digital traces of collaboration and AI can potentially support the assessment and optimization of team-based care in oncology, with potential applications across other high-stakes clinical domains.

## 2 Related Works

Cancer outcome prediction has traditionally focused on patient-level variables such as age, cancer stage, comorbidities, and treatment history (Piccirillo et al. 2004; Søgaard et al. 2013; Brandt et al. 2015; Nixon et al. 1994). These models have achieved varying levels of success in forecasting survival, but they often treat patients as isolated entities and overlook the broader context of care delivery and team-based coordination.

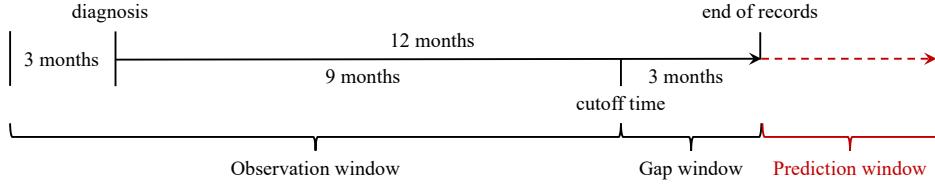


Figure 1: The key milestones in the data collection and processing timeframe are as follows. We divide collected data at the nine-month post-diagnosis mark into an observation window for training and a gap window for preventing data leakage.

In parallel, there is growing recognition that collaboration among healthcare professionals can affect patient outcomes. Existing approaches include analyzing communication pathways and assessing the composition and roles of care teams (Gurses and Xiao 2006; Smits et al. 2010; Bagnasco et al. 2013; Verhaegh et al. 2017). Despite this growing body of work, the role of team collaboration is still rarely integrated into predictive modeling pipelines.

Electronic health records (EHRs) offer a promising avenue for capturing these collaborative practices. Now pervasive in modern healthcare, EHRs serve as the primary platform for documenting, coordinating, and delivering care. Unlike surveys or observational studies, EHRs provide fine-grained, time-stamped logs that capture how healthcare professionals interact around patient care. While most research has focused on patient-level physiological data within EHRs (Huang et al. 2017; Amirahmadi, Ohlsson, and Etminani 2023; Nelson, Butte, and Baranzini 2019), fewer studies have explored the metadata generated through system usage—such as access logs, shared documentation, or co-signatures—as signals of clinical collaboration. These underutilized digital traces can provide a nuanced and scalable view of how care teams function in real-world settings.

Machine learning has been increasingly applied to healthcare problems, including disease prediction, treatment recommendation, and patient risk stratification (Uddin et al. 2019; Atan, Jordon, and Van der Schaar 2018; Ballinger et al. 2018; Rath et al. 2022). Some efforts have introduced explainability techniques to improve model transparency in clinical contexts (Mienye and Jere 2024; Alsaleh et al. 2023). However, most of these works have focused on patient-level signals, with limited attention to modeling human factors such as collaboration among care providers. In our work, we apply machine learning to model EHR-mediated collaboration and address the unique challenges posed by this setting—such as the risk of spurious associations. Our approach emphasizes careful data modeling to ensure predictive validity and generalizability, offering a framework that can extend to other domains involving complex, team-based decision-making.

### 3 Methodology

#### 3.1 Data: collaboration among HCPs through EHR

**Data overview.** Our raw data consists of EHR digital traces from 505 patients diagnosed with Stage 2 or 3 breast, lung, and colorectal cancers, with approval from the IRB for data

use. For each patient, the dataset includes their *basic information* and *access logs* of their EHR data. Basic information encompasses demographics (e.g., age and gender), treatments, comorbidities, and survival outcome (alive/dead). EHR access logs contain timestamped events spanning three months before to one year after the diagnosis date. A timestamped EHR access event involves a healthcare professional (HCP) accessing (reviewing or writing) a document, such as a note or a message, on the EHR system. Since HCPs typically record a patient’s medical conditions in notes, while messages often lack context, we include only the access events involving notes in our analysis. To focus on assessing the interactions within core teams, following the recommendations of our medical doctor collaborators, we include only HCPs with the titles MD, NP, PA, RN, Pharmacy Technician, Pharmacist, and Case Manager.

This data captures the flow of information among HCPs, allowing us to track which HCP authored a note and who subsequently read it. Those who read the note may then write additional notes, further disseminating the acquired information. We extract these collaborative interactions that enable information transfer. To ensure a consistent collaboration timeframe, we exclude patients who passed away within a year of diagnosis.

**Data processing and categorization.** To extract the collaboration surrounding a patient, we identify all notes related to the patient and the HCPs who have reviewed, written, or edited these notes using EHR access logs. Each note is further characterized by three variables: the category of the note’s intent, the category of its content, and a label indicating whether it was created during an inpatient period. There are five intent categories, including *Orders* and *Patient Clinical Information*, and 32 content categories, such as *Order Canceled* and *Note Signed*. For each HCP, we provide context into their role in the collaboration using four variables: title, type, specialty, and a label indicating whether they are a resident. There are seven titles (e.g., *MD* or *RN*), 12 types (e.g., *Physician Faculty* or *Physician Fellow*), and 71 specialties (e.g., *Cardiology* or *Dermatology*).

**Bipartite network construction.** After identifying all participants in the collaboration surrounding a patient (notes and HCPs), we define the information flow among these entities. This flow is represented as a directed bipartite network, where notes and HCPs serve as network nodes, and edges capture the reviewing and writing events recorded in the EHR system. For example, if  $HCP_A$  reviews  $Note_B$ , an edge is established from  $Note_B$  to  $HCP_A$ , indicating that the information from  $Note_B$  flows toward  $HCP_A$ . The bipartite

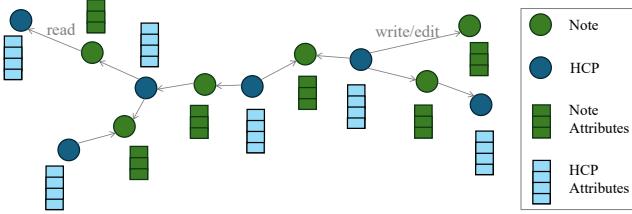


Figure 2: The illustration of the attributed bipartite collaboration network.

nature of this collaboration network ensures that edges only form between a note and an HCP, but not between two notes or two HCPs. This reflects the fact that interactions among HCPs within the EHR are always mediated through notes rather than direct communication. Finally, the variables extracted to characterize each note and HCP are assigned as node attributes. The constructed collaboration networks are illustrated in Fig. 2.

### 3.2 Prediction using Graph Neural Network

**Prediction variables and time windows.** Our goal is to prove that beyond the severity of a patient’s medical condition, how HCPs collaborate also influences patient survival outcomes. Therefore, we train a machine learning model to predict a patient’s survival outcome based on the traits of their collaboration network.

We define three time windows to prevent data leakage in our predictive analysis. As shown in Fig. 1, the EHR log collection period spans from three months before to twelve months after a patient’s diagnosis. We divide this period at the nine-month post-diagnosis mark into an observation window and a gap window. The EHR records from the observation window are used to train our prediction model, while those from the gap window are excluded. The decision to exclude the last three months of records aligns with the rationale for incorporating the three months preceding diagnosis, as this duration is considered significant in cancer treatment. Excluding the records from the gap window reduces the risk of information leakage, as later records may encode treatment decisions or clinical notes reflecting the patient’s imminent survival status, which could confound the true patterns of collaboration we aim to study. Additionally, using only earlier data for prediction enables timely identification of underperforming collaborations, allowing for necessary interventions. It is important to note that all patients are still alive at the end of the recorded timeframe (i.e., twelve months post-diagnosis). The final survival outcome is determined at varying points after this period, depending on the patient. As a result, the length of the prediction window is not fixed due to the nature of this data. However, we ensure a consistent analysis timeframe for the observation and gap windows.

**Model architecture.** Based on the defined time window configuration, we train a graph neural network (GNN) to learn from collaboration networks using only records from the observation window to predict patient survival outcomes. We use GraphSAGE (Hamilton, Ying, and Leskovec 2017)

to aggregate information from neighboring nodes in the collaboration network, leveraging their inductive capability to enhance the model’s generalizability to unseen patient collaborations in the future. As shown in Fig. 3, the model architecture comprises four GraphSAGE layers followed by a fully connected prediction layer. The hidden outputs from each GraphSAGE layer are concatenated to form the final node embeddings, which are then max-pooled (i.e., aggregated by taking the maximum value of each dimension) across all nodes in the network to generate a graph embedding. This graph embedding is passed through the fully connected layer to produce the predicted probability of patient survival.

Our GNN model captures the network traits shaped by both the collaboration topology and the node attributes, such as HCP specialty and note content, as detailed in Sec. 3.1. The four-layer GraphSAGE architecture enables the model to capture collaboration patterns within four hops of information propagation, exemplified by paths such as HCP-note-HCP-note-HCP or note-HCP-note-HCP-note.

### 3.3 Simplifications for explaining GNN predictions

Our HCP collaboration networks pose unique challenges for explainability due to their complexity—particularly their bipartite and directed structure—on which existing explainable GNN methods (Ying et al. 2019; Luo et al. 2020; Yuan et al. 2020) have not been directly evaluated or demonstrated consistent behavior. To address this, we disentangle and examine the two distinct sources of predictive signals separately: node attributes and network topology.

**Node attributes.** To assess the influence of node attributes on patient survival, we apply a max-pooling layer directly to the input attributes, bypassing the GraphSAGE and concatenation layers (see Fig. 3). The pooled attributes are then fed into the fully connected prediction layer. This simplified architecture relies exclusively on node attributes for prediction, thereby eliminating interference from topological information.

**Network topology.** To isolate predictive signals arising from topology, we simplify the collaboration networks to contain only HCPs or only notes, while removing all node attributes. In this case, predictions depend solely on structural relationships. For instance, as illustrated in Fig. 4, a simplified edge is drawn from  $HCP_A$  to  $HCP_B$  if at least one note conveys information between them. The GNN is then trained on these reduced networks to learn exclusively from topological traits.

By constraining each model to a single source of information—either attributes or topology—we approximate and explain the behavior of the full GNN. This separation allows us to attribute predictive power more precisely, enhancing interpretability.

### 3.4 Understanding predictions using explainable GNN methods

To help users interpret the GNN explanations, we leverage visual analytics techniques that enable interactive expl-

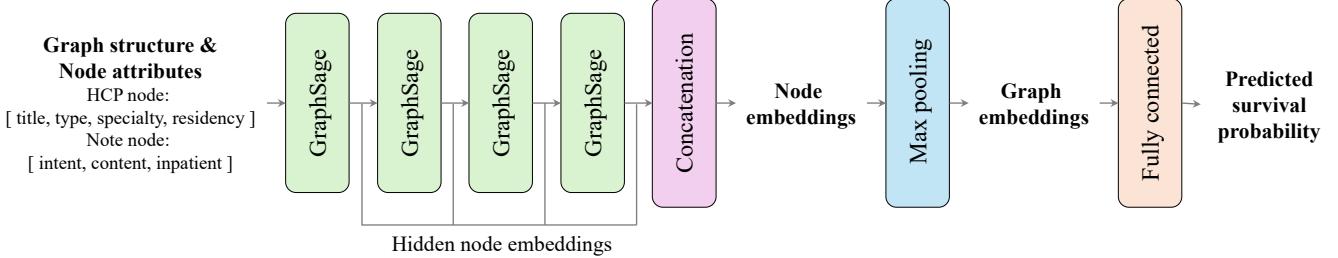


Figure 3: Our prediction model uses GraphSAGE layers to aggregate information from neighboring nodes and generate graph embeddings. A fully connected layer is then applied to these embeddings to predict patient survival.

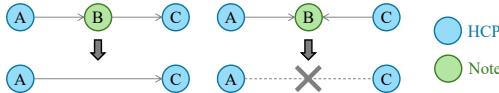


Figure 4: The illustration depicts the simplification of the collaboration network from a bipartite structure to an all-HCP collaboration network. The same edge-rerouting procedure is also applied when simplifying from the bipartite structure to the all-notes network.

ration of the model’s findings. For predictive signals originating from node attributes, we use NetworkCV (Lu et al. 2024a), which is specifically designed to explain neural network predictions on attribute-rich, multivariate networks, aligning with our simplified model architecture that focuses solely on node attributes. NetworkCV computes SHapley Additive exPlanations (SHAP) value (Lundberg and Lee 2017) as a metric for quantifying the influence from a node attribute to the patient survival. To interpret the role of topological traits in the original collaboration networks, we employ GNNAnatomy (Lu et al. 2024b) to explain the GNN predictions made by using the simplified collaboration networks (i.e., excluding all node attributes). This tool allows us to pinpoint the topological signals contributing to the patient survival outcome predictions.

We explicitly disentangle the explanations for node attributes and for network topology to improve both interpretability and specificity. In contrast, most explainable GNN methods such as GNNExplainer (Ying et al. 2019) use a generative model to jointly identify the most influential topology together with the attributes. However, this joint modeling does not quantify the relative importance of topology versus attributes, which can lead to ambiguous or inconsistent interpretations. Moreover, the influential subgraph identified by such methods reflects importance only within a particular graph instance, and its relevance may not generalize to other collaboration graphs.

## 4 Experiments

### 4.1 The importance of topological traits in collaborations among HCPs

Our goal is to prove that the human factor—specifically, how HCPs collaborate—has an association with patient survival outcomes. However, other factors may implicitly influence

the prediction. For instance, if a patient is more severely ill, HCPs may collaborate in a distinct manner. In this case, the true determinant of survival may not be the collaboration pattern itself but rather the patient’s level of sickness. To isolate the effect of HCP collaboration on patient survival and rule out as many confounding factors as possible, we use three different sets of data to conduct predictive analyses, supplemented by additional correlation analyses.

**Predictive analyses.** A common approach to assessing a patient’s general level of sickness is through comorbidities. Our comorbidity dataset includes 39 diseases, each represented by a binary label indicating whether the patient has been diagnosed with this condition. These 39 binary labels form a 39-dimensional comorbidity vector, which we use as a representation of patient sickness.

We conduct three predictive analyses: one using only the comorbidity vector, one using only the collaboration, and one combining both. The model architecture described in 3.2 corresponds to the *collaboration-only* approach. The *comorbidity-only* model consists of a single fully connected layer followed by a nonlinear activation function. The *combined* model follows the *collaboration-only* architecture before the fully connected layer. The comorbidity vector is concatenated with the graph embedding before passed to the fully connected layer for final prediction.

Additionally, we separate the collaboration networks based on the patient’s cancer type: breast cancer, lung cancer, and colorectal cancer. Since the teamwork patterns and the specialties of HCPs involved in treatment are expected to differ across cancer types, this separation ensures that the prediction model captures the unique collaboration patterns within each cancer type which influence patient survival. We also partition the data into separate training and testing sets for each cancer type, ensuring that the model learns generalizable characteristics rather than overfitting to previously seen data.

As shown in Table 1, the numbers of survived and deceased patients are listed alongside the counts of correctly predicted cases for each model. While the distribution is notably skewed for breast cancer and colorectal cancer, all models achieve strong overall prediction accuracy (above 80%). Notably, the *collaboration-only* model outperforms all others across all three cancer datasets, followed by the *combined* model, while the *comorbidity-only* model demonstrates the lowest accuracy. These results suggest that while

	Female Breast Cancer Patients			Lung Cancer Patients			Colorectal Cancer Patients		
	survived count (correct/all)	dead count (correct/all)	accuracy = # correct / # all	survived count (correct/all)	dead count (correct/all)	accuracy = # correct / # all	survived count (correct/all)	dead count (correct/all)	accuracy = # correct / # all
comorbidity-only	171/184	23/26	0.9238	67/89	48/61	0.8000	109/119	19/24	0.8951
<b>collaboration-only</b>	<b>179/184</b>	23/26	<b>0.9619</b>	86/89	61/61	<b>0.9800</b>	119/119	20/24	<b>0.9720</b>
<b>combined</b>	<b>177/184</b>	21/26	<b>0.9429</b>	74/89	58/61	<b>0.8800</b>	119/119	15/24	<b>0.9371</b>

Table 1: The prediction results using three different models on collaboration networks for each cancer type are presented. Bold text highlights the highest prediction accuracy, while red text marks the second-best performer. The results demonstrate that our *collaboration-only* model consistently achieves the best patient survival prediction across all three cancer types.

the comorbidity vector—representing a patient’s level of sickness—provides a reasonable indication of survival, it does not generalize well across all patients with the same cancer type. In contrast, the collaboration encodes more nuanced signals that contribute to more accurate predictions across different patients.

Interestingly, the *combined* model does not outperform the *collaboration-only* model, indicating that the signals extracted from comorbidity and collaboration are not well-aligned. This misalignment likely causes the *combined* model to struggle in determining which signals to prioritize for prediction. Nevertheless, since the *combined* model still outperforms the *comorbidity-only* model, and the *collaboration-only* model achieves the highest accuracy, these findings highlight the dominant role of HCP collaboration in predicting patient survival.

**Correlation analyses.** To further ensure the effect of HCP collaboration on patient survival and minimize the influence of confounding factors, we examine four additional variables identified by our medical doctor collaborators as potentially correlated with patient survival: gender, cancer stage (Stage 2 or 3), age, and insurance type (private or public). We assess the alignment between each variable’s distribution and patient survival using both Spearman and Pearson correlation coefficients, along with their corresponding *p*-values. As shown in Table 2, the results from both correlation measures are highly consistent, providing nearly identical indications of the strength of association between these variables and patient survival.

Additionally, the highest correlation is observed between cancer stage and patient survival within the lung cancer dataset. However, even this highest correlation remains below 0.3, indicating little to no meaningful association between the two variables. Furthermore, the relatively high *p*-values (some exceeding 0.6) suggest that any weak correlation detected is likely due to chance rather than a true relationship. Thus, the likelihood of these four variables being primary drivers of patient survival is minimal. Based on this, we conclude that the association between HCP collaboration and patient survival is both evident and valid.

## 4.2 The collaboration patterns affecting patient survival outcome

To understand the predictive signals captured by our GNN model, we use GNNAnatomy to explain the topological traits and NetworkCV to identify contributing node attributes, as introduced in Sec. 3.4. GNNAnatomy (Lu et al.

2024b), found that there are no dominant topology underlying the information flows among healthcare providers and clinical notes that directly contribute to patient survival. In contrast, NetworkCV (Lu et al. 2024a) highlighted several non-trivial node attributes that point to meaningful collaboration patterns.

In lung cancer, we observed that some NetworkCV-identified contributing HCP attributes are subtle indicators of comorbidities—such as the involvement of cardiologists or other specialists. Additionally, some important Note attributes suggest that patients whose providers infrequently accessed clinical notes tended to have poorer outcomes. Importantly, the range of SHAP values for these node attributes are comparable, implying that the model is not overly reliant on one trait to make predictions, but rather incorporates a diverse set of behavioral signals.

For breast and colorectal cancers, the most influential HCP attribute is the involvement of general practitioners (GPs). The presence of a GP in the care team was consistently associated with improved patient outcomes. Notably, the SHAP value for GP involvement exceeded those of the subtle comorbidity signals—such as involvement of emergency medicine or cardiology. This highlights a particularly strong impact of GP participation. Additionally, this pattern holds across multiple cancer types, further suggesting that GP involvement may reflect a more holistic, coordinated care process that benefits patient survival. These findings offer evidence reinforcing the clinical hypothesis that generalist physicians play a critical role in cancer care.

As shown in Fig. 5, when comparing two breast cancer patients with different survival outcomes, we observe that the GP played a central role in coordinating across the main clusters of collaboration for the patient who survived. In contrast, the collaboration network without a GP was largely confined to a small group of HCPs, with limited reach to other potentially helpful providers. This limited connectivity may reflect a lack of treatment coordination stemming from the absence of GP involvement.

## 4.3 Evaluations and broader impact

In this study, we sought to isolate collaboration patterns associated with cancer survival while minimizing confounding factors (Table 2). To test robustness, we performed five-fold cross-validation, reporting average metrics across folds (Table 1). This design reduces overfitting and shows that the learned predictive signals generalize to unseen patients, with consistent performance supporting the model’s stability.

Correlation between patient survival and	Female Breast Cancer Patients				Lung Cancer Patients				Colorectal Cancer Patients			
	Pearson corr.		Spearman corr.		Pearson corr.		Spearman corr.		Pearson corr.		Spearman corr.	
gender	-	-	-	-	0.1554	0.0576	0.1554	0.0576	0.0850	0.3128	0.0850	0.3128
stage	0.0858	0.2156	0.0858	0.2156	0.2996	0.0002	0.2996	0.0002	0.1225	0.1450	0.1225	0.1450
age	0.2607	0.0001	0.2574	0.0002	0.1018	0.2149	0.0975	0.2353	0.2401	0.0039	0.2350	0.0047
payer	0.2522	0.0002	0.2529	0.0002	-0.0449	0.5853	0.0426	0.6051	0.2293	0.0059	0.2129	0.0107

Table 2: The correlation analyses examine four additional confounding factors that might be associated with patient survival. The results indicate that these factors exhibit little to no correlation with patient survival, as evidenced by correlation coefficients lower than 0.3. Therefore, the likelihood of these factors being the primary drivers influencing patient survival is minimal.

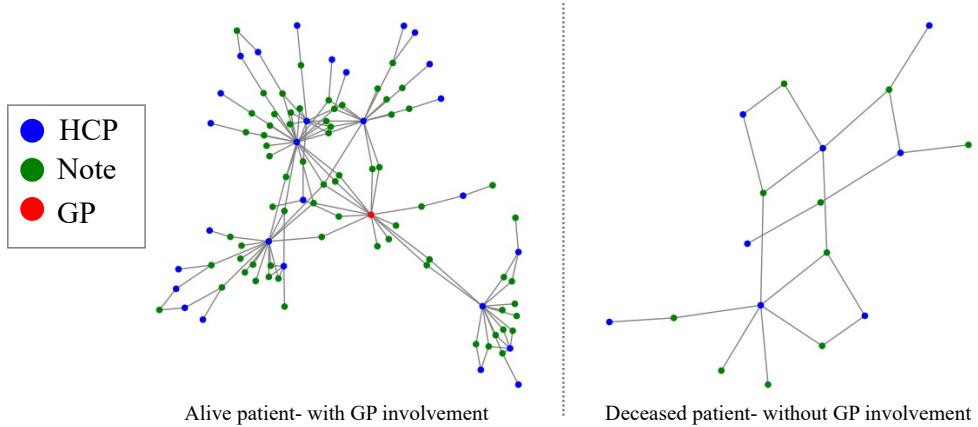


Figure 5: The comparison between two breast cancer patients with different outcomes.

To assess the clinical relevance of our findings, we presented key model insights to domain experts in oncology and primary care. Experts confirmed that the involvement of general practitioners (GPs) in cancer care aligns with their hypothesis that GPs play a central role in coordinating treatment plans across multiple providers. This feedback echoes the broader hypothesis of shared care, where collaboration between primary care and specialist providers is known to improve the management of long-term and complex conditions. While this model of care has been advocated in prior literature (Smith et al. 2017; Perfors et al. 2019; Goderis et al. 2010; Smith et al. 2008; Scherpbier-de Haan et al. 2013; Holm et al. 2002; Dey et al. 2002; Byng et al. 2004), especially for chronic diseases, its application in cancer care has not been validated using real-world data. Our study offers the first empirical support for the effectiveness of shared care in oncology, providing evidence that involving general practitioners should be more formally considered in efforts to improve cancer treatment delivery and patient outcomes.

## 5 Discussion

**Validation in Real Practice.** While our findings align with prior literature and expert feedback, they require validation in clinical settings. In particular, the association between collaboration patterns—such as GP involvement—and patient outcomes should be assessed by medical professionals before guiding interventions. Future work includes implementing trials to evaluate their causal impact on patient care

and survival.

**Time Window Length Exploration.** There is no standard for defining observation and prediction windows in HCP collaboration studies. Our chosen windows were guided by data availability and cancer treatment practices, making them effective for this context but not necessarily generalizable. They should be seen as empirically motivated design choices, not benchmarks. Future work should explore how varying window configurations affect the stability and interpretability of collaboration patterns.

## 6 Conclusion

This paper presents a data-driven framework for modeling and analyzing healthcare professional collaboration using electronic health record (EHR) data to predict cancer patient survival. Our approach demonstrates robust and generalizable predictive performance through careful experimental design and evaluation, while also providing clinically meaningful insights supported by expert feedback and extensive prior literature. Notably, our findings offer the first empirical evidence for a long-standing hypothesis: the involvement of general practitioners plays a beneficial role in cancer care coordination and patient survival outcomes. By leveraging real-world data and machine learning, our work contributes a methodology for identifying actionable intervention targeting human factors in complex care collaborations, with potential applications beyond oncology.

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