Continuous-Time Relationship Prediction in Dynamic Heterogeneous Information Networks

Sina Sajadmanesh #1, Sogol Bazargani #2, Jiawei Zhang *3, Hamid R. Rabiee #4

Department of Computer Engineering, Sharif University of Technology

Tehran, Iran

1 sajadmanesh@ce.sharif.edu
2 bazargani@dml.ir
3 rabiee@sharif.edu

* Department of Computer Science, Florida State University

Tallahassee, FL, USA
2 jzhang@cs.fsu.edu

Abstract—Online social networks, World Wide Web, media and technological networks, and other types of so-called information networks are ubiquitous nowadays. These information networks are inherently heterogeneous and dynamic. They are heterogeneous as they consist of multi-typed objects and relations, and they are dynamic as they are constantly evolving over time. One of the challenging issues in such heterogeneous and dynamic environments, is to forecast those relationships in the network that will appear in the future. In this paper, we try to solve the problem of continuous-time relationship prediction in dynamic and heterogeneous information networks. This implies predicting the time it takes for a relationship to appear in the future, given its features that have been extracted by considering both the heterogeneity and the temporal dynamics of the underlying network. To this end, we first introduce a meta-path-based feature extraction framework to effectively extract features suitable for relationship prediction regarding the heterogeneity and dynamicity of the network. Next, we propose a supervised nonparametric approach, called Non-Parametric Generalized Linear Model (NP-GLM), which infers the hidden underlying probability distribution of the relationship building time given its features. We then present a learning algorithm to train NP-GLM and an inference method to answer time-related queries. Extensive experiments conducted on both synthetic dataset and real-world DBLP bibliographic citation network dataset demonstrate the effectiveness of NP-GLM in solving continuous-time relationship prediction problem vis-à-vis alternative baselines.

I. Introduction

Link prediction is the problem of prognosticating a certain relationship, like interaction or collaboration, between two entities in a networked system that are not connected already [1]. Due to the popularity and ubiquity of networked systems in real world, such as social, economical, or biological networks, this problem has attracted a considerable attention in recent years and has found its applications in various interdisciplinary domains, such as viral marketing, bioinformatics, recommender systems, and social network analysis [2]. For example, suggesting new friends in an online social network [3] or predicting drug-target interactions in a biological network [4] are two quite different problems, but can both cast as the prediction task of friendship links and drug-target links respectively.

The problem of link prediction has a long literature and is studied extensively in the last decade. Initial works on link prediction problem mostly concentrated on homogeneous networks, which are composed of single type of nodes connected by links of the same type [3], [5], [6]. However, many of the today's networks, such as online social networks or bibliographic networks, are inherently *heterogeneous*, in which multiple types of nodes are interconnected using multiple types of links [7], [8]. For example, a bibliographic network may contain author, paper, venue, etc. as different node types; and write, publish, cite, and so on as diverse link types that bind nodes of different types to each other. In these heterogeneous networks, the concept of a link can be generalized to a relationship, which can be constructed by combining different links with different types. For instance, author-citepaper relationship can be defined in a bibliographic network as a combination of author-write-paper and paper-cite-paper links. Analogously, one can generalize the link prediction to relationship prediction in heterogeneous networks which tries to predict complex relationships instead of links [9].

While most of the studies on the link/relationship prediction in heterogeneous networks utilize a static snapshot of the underlying network, many of these networks are *dynamic* in nature, which means that new nodes and linkages are continually added to the network, and some existing nodes and links may be removed from the network over time. For example, in online social networks such as Facebook, new users are joining in the network every day, and new friendship links are being added to the network, gradually. This dynamic characteristic causes the structure of the network to change and evolve over time, and taking these changes into account can significantly boost the quality of link prediction task [10].

In recent years, newer studies have shifted from traditional link prediction on static and homogeneous networks toward newer domains, considering heterogeneity and dynamicity of the networks [11], [12], [13], [14], [15]. However, most of these works merely focus on one of these aspects, disregarding the other. Although there are quite a few studies that address both the challenges of heterogeneity and dynamicity [16], [17],

to the best of our knowledge, all of them have ultimately formulated the link prediction problem as a binary classification task, i.e. predicting whether a link will appear in the network in the future. However, in dynamic networks, new links are continually appearing over time. So a much more interesting problem, which we call it continuous-time link prediction in this paper, is to predict when a link will emerge or appear between two nodes in the network. Examples of this problem include predicting the time at which two individuals become friends in a social network, or the time when two authors collaborate on writing a paper in a bibliographic network [9]. Inferring the link formation time in advance can be very useful in many concrete applications. For example, if a social network recommender system could predict the relationship building time between two people, then it can issue a friendship suggestion close to that time since it will have a relatively higher chance to be accepted. Good continuous-time link prediction results will lead to denser connections among users, and can greatly improve users' engagement that is the ultimate goal of online social networks [18].

In this paper, we aim to solve the problem of continuoustime relationship prediction, in which we forecast the relationship building time between two nodes in a dynamic and heterogeneous environment. This problem is very challenging from the technical perspective, and cannot be solved trivially for three main reasons. First, the formulation of continuous-time relationship prediction is quite different from conventional link prediction due to the involvement of temporal dynamics of the network and the necessity of considering network evolution time-line. Second, we only know the building time of those relationships that are already present at the network and for the rest of them that are yet to happen, which are excessive in number versus the existing ones, we lack such information. Finally, as opposed to the works concerning the binary link prediction, there are very rare works in the literature on continuous-time link prediction that attempt to answer the "when" question. As far as we know, the only work that has studied the continuous-time relationship prediction problem so far, is proposed by Sun et al. [9]. They infer a probability distribution over time for each pair of nodes given their features, and answer time-related queries about the relationship building time between the two nodes using the inferred distribution. However, the drawback of their method, not to mention neglecting the temporal dynamics of the network, is that it mainly relies on the assumption that relationship building times are coming from a certain probability distribution which must be fixed beforehand. This assumption though simplifying is very restrictive because, in real applications, this distribution is unknown and considering any specific one as a priori could be far from reality or limit the solution generality.

In order to address the above challenges, we propose a supervised non-parametric method to solve the problem of continuous-time relationship prediction. To this end, we first formally define the continuous-time relationship prediction problem and formulate the approach to solve it generally.

Then, we introduce our meta-path-based feature extraction framework which leverages both heterogeneity and dynamicity of information networks, well-suited for relationship prediction task. Next, we present Non-Parametric Generalized Linear Model (NP-GLM) which models the distribution of relationship building time given the features extracted before. The strength of this non-parametric model is that it is capable of learning the underlying distribution of the relationship building time, as well as the amount of contribution of each extracted feature in the network. Inferring such probability distribution, we propose an inference algorithm to answer queries, like the most probable time by which a relationship will appear between two nodes, or the probability of relationship creation between them during a specific period. Finally, we conduct comprehensive experiments over a synthetic dataset to verify the correctness of NP-GLM's learning algorithm, and on a realworld DBLP bibliographic network dataset to demonstrate the effectiveness of the proposed method in predicting the relationship building time versus the relevant baselines. As a summary, we can enumerate our major contributions as follows:

- The proposed meta-path-based feature extraction framework can utilize heterogeneity of the data as well as capturing the temporal dynamics of the network.
- Our non-parametric model takes a unique approach toward learning the underlying distribution of relationship building time without imposing any significant assumption on the problem.
- Extensive evaluations over both synthetic data and DBLP real-world bibliographic network is performed to indicate the effectiveness of the proposed method.
- To the best of our knowledge, this paper is the first one which studies the continuous-time relationship prediction problem in both dynamic and heterogeneous network configuration.

The rest of this paper is organized as follows. In Section II, we provide introductory backgrounds on the concept and formally define the problem of continuous-time relationship prediction. Then in Section III, we introduce our meta-path-based feature extraction framework. Next, we go through the details of our proposed NP-GLM method in Section IV, explaining its learning method and how it answers inference queries. Experimental results are described in Section V. Section VI discusses the related works and finally in Section VII, we conclude the paper.

II. PROBLEM FORMULATION

In this section, we introduce some important concepts and definitions used throughout the paper and formally define the problem of continuous-time relationship prediction.

A. Heterogeneous Information Networks

An information network is *heterogeneous* if it contains multiple kinds of nodes and links. Formally, it is defined as a directed graph G = (V, E) where $V = \bigcup_i V_i$ is the set of nodes comprising the union of all the node sets V_i of type

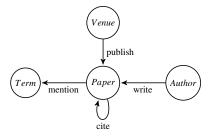


Fig. 1. Schema for DBLP bibliographic citation network.

i. Similarly, $E = \bigcup_j E_j$ is the set of links constituted by the union of all the link sets E_j of type j. Now we bring the definition of the *network schema* [19] which is used to describe a heterogeneous information network at a meta-level:

Definition 1. (Network Schema) The schema of a heterogeneous network G is a graph $S_G = (V, \mathcal{E})$ where V is the set of different node types and \mathcal{E} is the set of different link types in G.

In this paper, we focus on the bibliographic network, where $V = \{Author, Paper, Venue, Term\}$ is the set of different node types, and $\mathcal{E} = \{write, publish, mention, cite\}$ is the set of different link types. The schema of this network has been depicted in Fig. 1.

As we mentioned in the Introduction section about heterogeneous networks, the concept of a link can be generalized to a relationship. In this case, a relationship could be either a single link, or a composite relation constituted by concatenation of multiple links that together has a particular semantic meaning. For example, the co-authorship relation in a bibliographic network with the schema shown in Fig. 1, can be defined as the combination of two Author-write-Paper links, making Author-write-Paper-write-Author relation. When dealing with the link or relationship prediction in heterogeneous networks, we must exactly specify what a kind of link or relationship we are going to predict. This is called the Target Relation [9]. In this paper, we aim to predict if and when an author in a bibliographic network will cite a paper from another certain author. Thus the target relation in this case would be Authorwrite-Paper-cite-Paper-write-Author.

B. Dynamic Information Networks

An information network is *dynamic* when its nodes and linkage structure could change over time. That is, in a dynamic information network, all nodes and links are associated with a birth and death time, which denotes the time range when they exist in the network. More formally, a dynamic network between time t_0 and t_1 is defined as $G^{t_0,t_1} = (V^{t_0,t_1}, E^{t_0,t_1})$ where V^{t_0,t_1} and E^{t_0,t_1} are the set of nodes and the set of links between time t_0 and t_1 , respectively, which are defined as follows:

$$V^{t_0,t_1} = \{ v : v \in V \land t_0 < t_b(v) \le t_1 < t_d(v) \}$$

$$E^{t_0,t_1} = \{e : e \in E \land t_0 < t_b(e) \le t_1 < t_d(e)\}\$$

where V and E are accordingly the set of all nodes and links ever appeared or removed during the time interval $(t_0, t_1]$, and $t_b(x)$ and $t_d(x)$ denotes the birth and death time of a network entity x (which can be node or link), respectively. For the sake of simplicity, we assume that each network entity have only a single birth and death time, and we do not consider the cases of reoccurring or multiple links.

In this paper, we consider the case that an information network is both dynamic and heterogeneous. This means that all network entities are associated with a type, and they also have their birth and death times, regardless of their types. The bibliographic network is an example of both dynamic and heterogeneous network. Whenever a new paper is published, a new *Paper* node will be added to the network, alongside with the corresponding new *Author*, *Term*, and *Venue* nodes (if they don't exist yet). New links will be formed among these newly added nodes to indicate the *write*, *publish* and *mention* relationships. Some linkages might also form between the existing nodes and the new ones, like new *cite* links connecting the new paper with the existing papers in its reference list.

C. Continuous-Time Relationship Prediction

Suppose that we are given a dynamic and heterogeneous information network as G^{t_0,t_1} , observed between the timestamps t_0 and t_1 , together with its network schema S_G . Now, given the target relation R, the aim of continuous-time relationship prediction is to continuously forecast the building time $t \ge t_1$ of R for node pairs from G^{t_0,t_1} provided in the query.

To solve this problem, we first introduce a feature extraction framework to cope with both the dynamicity and heterogeneity of the network, and then propose a non-parametric model which utilizes the extracted features to perform predictions about the building time of the target relationship.

III. FEATURE EXTRACTION FRAMEWORK

In this section, we present our framework to extract features which is designed to have three major characteristics: First, it effectively considers different type of nodes and links available in a heterogeneous information network and regard their impact on the building time of the target relationship. Second, it takes the temporal dynamics of the network into account and leverage the network evolution history instead of simply aggregating it into a single snapshot. Finally, the extracted features are suitable for not only the link prediction problem, but also the generalized *relationship prediction*. We will incorporate these features in the proposed non-parametric model in Section IV to solve the continuous-time relationship prediction problem.

A. Data Preparation For Feature Extraction

To solve the problem of continuous-time relationship prediction in dynamic networks, we need to pay attention to the temporal history of the network data from two different point of views. First, we have to mind the evolution history of the network for the feature extraction, so that the extracted features reflect the changes made in the network over time. Second, we have to specify the exact relationship building time for each pair of nodes, because our goal is to propose a supervised method to predict a continuous variable, which in this case is the relationship building time. Hence, for each sample pair of nodes, we need a feature vector \mathbf{x} , associated with a target variable t which indicates the building time of the target relationship between them.

Suppose that we have a dynamic network G^{t_0,t_1} which has been recorded in the interval $(t_0,t_1]$. According to Fig 2, we split this interval into two parts: the first part for extracting the feature \mathbf{x} , and the second for determining the target variable t. We refer to the first interval as *Feature Extraction Window* whose length is denoted by Φ , and the second as *Observation Window* whose length is denoted by Ω . Now, based on the existence state of target relationships in Observation Window, we categorize them into the following three different groups:

- Relationships that are already formed before beginning of Observation Window (formed in the Feature Extraction Window).
- 2) Relationships that will be built in the Observation Window for the first time (not existing before).
- Relationships that will not form at all (neither in Feature Extraction Window nor Observation Window).

Those pair of nodes that act as the starting and ending nodes of the relationships in the 2nd and 3rd categories constitute our data samples, and will be used in the learning procedure. For such pairs, we extract their feature vector \mathbf{x} using the history available in Feature Extraction Window. For each node pair in the 2nd category, we have seen that the target relationship between them is created at a time like $t_r \in (t_0 + \Phi, t_1]$. So we set $t = t_r - (t_0 + \Phi)$ as the time it takes for the relationship to form since the beginning of the Observation Window. For these samples, we also set an auxiliary variable y = 1 which indicates that we have observed their exact building time. On the other hand, For node pairs in the 3rd category, we haven't seen their exact building time, but we know the it is definitely after t_1 . For such samples, which we call them censored ones, we set $t = t_1 - (t_0 + \Phi)$ which is equal to the length of the Observation Window Ω , and set y = 0 to indicate that the true relationship building time is in fact beyond the recorded time. These type of samples though look useless, are also of interest because their features will give us some information about their time falling after t_1 . As a result, each final sample is associated with a triple $(\mathbf{x}, \mathbf{y}, t)$ representing its feature vector, observation status, and the time it takes for the target relationship to form, respectively.

B. Meta-Path-based Dynamic Feature Extraction

In this part, we describe how to utilize the temporal history of the network in the Feature Extraction Window in order to extract features for continuous-time relationship prediction problem. We extend the feature set proposed in [9] for heterogeneous information networks, by including the capability to exploit the temporal dynamics of the network as well. Hereby, we begin by defining the concept of meta-path [19]:

TABLE I Similarity Meta-Paths Used for Feature Extraction [9]

Meta-Path	Semantic Meaning		
$A \rightarrow P \leftarrow A$ $A \rightarrow P \rightarrow A \leftarrow P \leftarrow A$ $A \rightarrow P \rightarrow V \leftarrow P \leftarrow A$ $A \rightarrow P \rightarrow T \leftarrow P \leftarrow A$ $A \rightarrow P \rightarrow P \leftarrow P \leftarrow A$ $A \rightarrow P \leftarrow P \rightarrow P \leftarrow A$	Authors co-write a paper Authors have common co-authors Authors publish in the same venues Authors use the same terms Authors cite the same papers Authors are cited by the same papers		

Definition 2 (Meta-Path). In a heterogeneous information network, a meta-path is a directed path following the graph of the network schema to describe the general relations that can be derived from the network. Formally speaking, given a network schema $S_G = (V, \mathcal{E})$, the sequence $v_1 \xrightarrow{\varepsilon_1} v_2 \xrightarrow{\varepsilon_2} \dots v_{k-1} \xrightarrow{\varepsilon_{k-1}} v_k$ is a meta-path defined on S_G where $v_i \in V$ and $\varepsilon_i \in \mathcal{E}$.

Meta-paths are commonly used in heterogeneous information networks to describe multi-typed relations which have concrete semantic meanings. For example, in the bibliographic network whose schema were show in Fig 1, we can define the co-authorship relation with the following meta-path:

$$Author \xrightarrow{write} Paper \xleftarrow{write} Author$$

or simply by $A \to P \leftarrow A$. Also, the author citation relation which is used as the target relation in this paper, can be specified as:

Author
$$\xrightarrow{\text{write}}$$
 Paper $\xrightarrow{\text{cite}}$ Paper $\xleftarrow{\text{write}}$ Author

or abbreviated as $A \rightarrow P \rightarrow P \leftarrow A$.

Among the possible meta-paths that can be defined on a network schema, there are some that capture the similarity between two nodes. For example, $A \rightarrow P \leftarrow A$ which is the co-authorship relation between two authors in a bibliographic network, creates a sense of similarity between two *Author* nodes. These type of meta-paths, called *similarity meta-paths*, are widely used to define topological features for link prediction problem in heterogeneous networks [20], [21], [13]. Some examples of similarity meta-paths that capture the topological similarity between two *Author* nodes in the bibliographic network, are available in Table I.

The concept of similarity meta-paths can be extended to define topological features suitable for relationship prediction problem, where we have a target relation. Here we follow the same approach as in [9] which suggests the following three meta-path-based blocks to describe features for relationship prediction problem, given a target relation between two nodes of type *A* and *B*:

similarity target
1)
$$A \sim A \sim B$$
target similarity

2) $A \sim B \sim A$

relation relation 3) $A \sim \sim \sim C \sim \sim B$

where \rightsquigarrow denotes a meta-path, with labels *similarity* and *target* denoting a similarity meta-path and the target relationship,

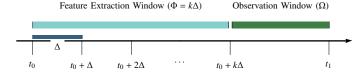


Fig. 2. The evolutionary timeline of the network data.

respectively. The *relation* label denotes an arbitrary meta-path relating two nodes of possibly different types. The first block tells that there are some nodes of type A similar to a single node of the same type that has made the target relationship with a node of type B. Therefore, those similar nodes may also form the target relation with the type B node. An analogous intuition is behind the second block. For the third, it says that some nodes of type A are in relation with some type C nodes, which are themselves in relation with some nodes of type B. Hence, it is likely that type A nodes form some relationships, such as the target relationship, with type B nodes.

For our case study with the bibliographic network, for the target relation we use $A \to P \to P \leftarrow A$ as meta-path denoting the author citation relation. In Addition, Paper-cite-Author $(P \to P \to A)$ and Author-cite-Paper $(A \to P \to P)$ are also used as the arbitrary relations, and the similarity meta-paths of Table I to define the features for author citation relationship prediction.

After specifying the suitable meta-paths, we need a method to quantify them as features. Here, due to the dynamicity of the network, different links are emerging and vanishing from the network over time. Therefore, the quantifying method must handle this dynamicity. Here, we formally define *Time-Aware Meta-Path-based Features*:

Definition 3 (Time-Aware Meta-Path-based Feature). Suppose that we are given a dynamic heterogeneous network G^{t_0,t_1} along with its network schema $S_G = (V, \mathcal{E})$, and a target Relation $A \rightsquigarrow B$. For a given pair of nodes $a \in A$ and $b \in B$, and a meta-path $\Psi = v_1 \stackrel{\mathcal{E}_1}{\longrightarrow} v_2 \stackrel{\mathcal{E}_2}{\longrightarrow} \dots v_{k-1} \stackrel{\mathcal{E}_{k-1}}{\longrightarrow} v_k$ defined on S_G , the time-aware meta-path-based feature in the time interval (t_p, t_q) is calculated as:

$$f_{a,b}^{\Psi}(t_{p}, t_{q}) = I(a, A)I(b, B)$$

$$\sum_{n_{1} \in \nu_{1}, n_{2} \in \nu_{2}, \dots, n_{k} \in \nu_{k}} \prod_{i=1}^{k-1} I((n_{i}, n_{i+1}), \varepsilon_{i})I((n_{i}, n_{i+1}), t_{p}, t_{q})$$
(1)

where:

$$I(u, \mathcal{U}) = \begin{cases} 1 & \text{if } u \in \mathcal{U} \\ 0 & \text{otherwise} \end{cases}$$

checks whether a network entity (node or link) u belongs to type U, and:

$$I(e, t_p, t_q) = \begin{cases} 1 & \text{if } t_p < t_b(e) \le t_q < t_d(e) \\ 0 & \text{otherwise} \end{cases}$$

checks whether a link exists in the interval (t_p, t_q) .

By using the above definition, we will be able to quantify the number of instances of a particular meta-path in a specific time period. If we set this time period equal to the Feature Extraction Window, it is as though we are aggregating the network into a single snapshot observed at time $t_0+\Phi$. In order to avoid such an aggregation, we divide the Feature Extraction Window into a sequence of k contiguous intervals of a constant size Δ , as shown in Fig. 2. By doing this discretization, we intend to extract time-aware features in each sub-window, and then weigh them in a way that decay exponentially with the time, giving the recent features a higher weight. With this in mind, we define *Dynamic Meta-Path-based Features* as follows:

Definition 4 (Dynamic Meta-Path-based Feature). Suppose that we are given a dynamic heterogeneous network G^{t_0,t_1} with a Feature Extraction Window of size Φ , along with its network schema $S_G = (V, \mathcal{E})$ and a target Relation $A \rightsquigarrow B$. Also suppose that the Feature Extraction Window is divided into k fragments of size Δ . For a given pair of nodes $a \in A$ and $b \in B$ in $G^{t_0,t_0+\Phi}$, and a meta-path Ψ defined on S_G , the dynamic meta-path-based feature of (a,b) is calculated as:

$$x_{a,b} = \sum_{i=0}^{k-1} f_{a,b}^{\Psi} \left(t_0 + i\Delta, t_0 + (i+1)\Delta \right) \exp\{-\mu_{\Psi} i\Delta\}$$
 (2)

where $\mu_{\Psi} \geq 0$ is the rate parameter for the meta-path Ψ which controls the decay of $f_{a,b}^{\Psi}$ over time.

With the rate parameter μ_{Ψ} , we can adjust the decay rate of time-aware features over time. As $\mu_{\Psi} \to 0$, the dynamic metapath-based feature will give the same weight to all Δ -sized windows so we would again end up in the case of a single static snapshot observed at the end of the Feature Extraction Window. On the contrary, as $\mu_{\Psi} \to \infty$ only the very recent Δ -sized window will take part in the feature extraction and the rest of them will be ignored. With different rate parameters for different meta-paths we can exactly tune the weight of each feature over time.

IV. PROPOSED NON-PARAMETRIC MODEL

In this section we introduce our proposed model, called Non-Parametric Generalized Linear Model, to solve the problem of continuous-time relationship prediction based on the extracted features. Since the relationship building time is treated as a continuous random variable, we attempt to model the probability distribution of this time, given the features of the target relationship. Thus, if we denote the target relationship building time by t and its features by \mathbf{x} , our aim is to model the probability distribution $f_T(t \mid \mathbf{x})$. A conventional approach to modeling this distribution is to fix a parametric distribution for t (e.g. Exponential distribution) and then relate x to t using a Generalized Linear Model [9]. The major drawback of this approach is that we need to know the exact distribution of the relationship building time, or at least, we could guess the best one that fits. The alternative way that we follow is to learn the shape of $f_T(t \mid \mathbf{x})$ from the data using a non-parametric solution.

TABLE II
CHARACTERISTICS OF SOME PROBABILITY DISTRIBUTIONS USED FOR EVENT-TIME MODELING

Distribution	Density function $f_T(t)$	Reliability function $S(t)$	Intensity function $\lambda(t)$	Cumulative intensity $\Lambda(t)$
Exponential	$\alpha \exp(-\alpha t)$	$\exp(-\alpha t)$	α	αt
Rayleigh	$\frac{t}{\sigma^2}\exp(-\frac{t^2}{2\sigma^2})$	$\exp(-\frac{t^2}{2\sigma^2})$	$\frac{t}{\sigma^2}$	$\frac{t^2}{2\sigma^2}$
Gompertz	$\alpha e^t \exp\left\{-\alpha(e^t - 1)\right\}$	$\exp\left\{-\alpha(e^t-1)\right\}$	$lpha e^t$	$lpha e^t$

In the rest of this section, we first bring the necessary theoretical backgrounds related to the concept, then we go through the details of the proposed model. At the end, we explain the learning and inference algorithms of Np-GLM.

A. Background

Here we define some essential concepts that are necessary to study before we proceed to the proposed model. Generally, the formation of a relationship between two nodes in the network can simply be considered as an event with its occurring time as a random variable T coming from a density function $f_T(t)$. Regarding this, we can have the following definitions:

Definition 5 (Survival Function). Given the density $f_T(t)$, the survival function denoted by S(t), is the probability that an event occurs after a certain value of t, which means:

$$S(t) = P(T > t) = \int_{t}^{\infty} f_{T}(t)dt$$
 (3)

Definition 6 (Intensity Function). The intensity function (or failure rate function), denoted by $\lambda(t)$, is the instantaneous rate of event occurring at any time t given the fact that the event has not occurred yet:

$$\lambda(t) = \lim_{\Delta t \to 0} \frac{P(t \le T \le t + \Delta t \mid T \ge t)}{\Delta t} \tag{4}$$

Definition 7 (Cumulative Intensity Function). The cumulative intensity function, denoted by $\Lambda(t)$, is the area under the intensity function up to a point t:

$$\Lambda(t) = \int_0^t \lambda(t)dt \tag{5}$$

The relations between density, survival, and intensity functions come directly from their definitions as follows:

$$\lambda(t) = \frac{f_T(t)}{S(t)} \tag{6}$$

$$S(t) = \exp(-\Lambda(t)dt) \tag{7}$$

$$f_T(t) = \lambda(t) \exp(-\Lambda(t))$$
 (8)

Table II shows the density, reliability, intensity, and cumulative intensity functions of some widely-used distributions for event time modeling.

B. Model Description

Looking at the Eq. 6, we see that the density function can be specified uniquely with its intensity function. Since the intensity function often has a simpler form than the density itself, if we learn the shape of the intensity function, then we can infer the entire distribution eventually. Therefore, we focus on learning the shape of the conditional intensity function $\lambda(t \mid \mathbf{x})$ from the data, and then accordingly infer the conditional density function $f_T(t \mid \mathbf{x})$ based on the learned intensity. In order to reduce the hypothesis space of the problem and avoid the curse of dimensionality, we assume that $\lambda(t \mid \mathbf{x})$, which is a function of both t and t, can be factorized into two separate positive functions as the following:

$$\lambda(t \mid \mathbf{x}) = g(\mathbf{w}^T \mathbf{x}) h(t) \tag{9}$$

where g is a function of \mathbf{x} which captures the effect of features via a linear transformation using coefficient vector \mathbf{w} independent of t, and h is a function of t which captures the effect of time independent from x. This assumption, referred to as proportional hazards condition [22], holds in GLM formulations of many event-time modeling distributions, such as the ones shown in Table II. Our goal is now to fix the function g and then learn both the coefficient vector \mathbf{w} and the function h from the training data. In order to do so, we begin with the likelihood function of the data which can be written as follows:

$$\prod_{i=1}^{N} f_{T}(t_{i} \mid \mathbf{x}_{i})^{y_{i}} P(T \ge t_{i} \mid \mathbf{x}_{i})^{1-y_{i}}$$
(10)

The likelihood consists of the product of two parts: The first part is the contribution of those samples for which we have seen their exact building time, in terms of their density function. The second part on the other hand, is the contribution of the censored samples. For these samples, we use the probability of the building time being greater than the recorded one. Applying the Eq. 6, 7, and 9, the likelihood function becomes:

$$\prod_{i=1}^{N} \left[g(\mathbf{w}^{T} \mathbf{x}_{i}) h(t_{i}) \right]^{y_{i}} \exp\{-g(\mathbf{w}^{T} \mathbf{x}_{i}) \int_{0}^{t_{i}} h(t) dt \}$$
 (11)

Since we don't know the form of h(t), we cannot directly calculate the integral appeared in the likelihood function. To deal with this problem, we treat h(t) as a non-parametric function by approximating it with a piecewise constant function

that changes just in t_i s. Therefore, the integral over h(t), denoted by H(t), becomes a series:

$$H(t_i) = \int_0^{t_i} h(t)dt \simeq \sum_{i=1}^i h(t_i)(t_i - t_{i-1})$$
 (12)

assuming samples are sorted by t in increasing order, without loss of generality. The function H(t) defined above plays an important role in both learning and inference phases. In fact, both the learning and inference phases rely on H(t) instead of h(t), which we will see later in this paper. Replacing the above series in the likelihood and taking the logarithm, we end up with the following log-likelihood function:

$$\log \mathcal{L} = \sum_{i=1}^{N} \left\{ y_i \left[\log g(\mathbf{w}^T \mathbf{x}_i) + \log h(t_i) \right] - g(\mathbf{w}^T \mathbf{x}_i) \sum_{i=1}^{i} h(t_i)(t_i - t_{j-1}) \right\}$$
(13)

The log-likelihood function depends on the vector \mathbf{w} and the function h(t). In the next part, we explain an iterative learning algorithm to learn both \mathbf{w} and h(t) collectively.

C. Learning Algorithm

Maximizing the log-likelihood function (Eq. 13) rely on the choice of the function g. There are no particular limits on the choice of g except that it must be a non-negative function. For example, both quadratic and exponential functions of $\mathbf{w}^T\mathbf{x}$ will do the trick. Here, we proceed with $g(\mathbf{w}^T\mathbf{x}) = \exp(\mathbf{w}^T\mathbf{x})$ since it makes the log-likelihood a convex function with respect to \mathbf{w} . Subsequent equations can be derived for other choices of g analogously.

Setting the log-likelihood derivative with respect to $h(t_k)$ to zero yields a closed form solution for $h(t_k)$:

$$h(t_k) = \frac{y_k}{(t_k - t_{k-1}) \sum_{i=k}^{N} \exp(\mathbf{w}^T \mathbf{x}_i)}$$
(14)

Applying Eq. 12, we get the following for $H(t_i)$:

$$H(t_i) = \sum_{j=1}^{i} \frac{y_j}{\sum_{k=j}^{N} \exp(\mathbf{w}^T \mathbf{x}_k)}$$
(15)

which depends on the vector \mathbf{w} . On the other hand, we cannot obtain a closed form solution for \mathbf{w} from the log-likelihood function. Therefore, we turn to use Gradient-based optimization methods to find the optimal value of \mathbf{w} . The negative log-likelihood function with respect to \mathbf{w} , denoted by $NL(\mathbf{w})$ is as follows:

$$NL(\mathbf{w}) = \sum_{i=1}^{N} \left\{ \exp(\mathbf{w}^{T} \mathbf{x}_{i}) H(t_{i}) - y_{i} \mathbf{w}^{T} \mathbf{x}_{i} \right\}$$
(16)

which depends on the function H. As the learning of both \mathbf{w} and H depends on each other, they should be learned collectively. Here, we use an iterative algorithm to learn \mathbf{w} and H alternatively. We begin with a random vector $\mathbf{w}^{(0)}$. Then in

Algorithm 1: The learning algorithm of Np-GLM

```
Input: \mathbf{X}_{N\times d} = (\mathbf{x}_1, \dots \mathbf{x}_N)^T as d-dimensional feature vectors,
             \mathbf{y}_{N\times 1} as observation states, and \mathbf{t}_{N\times 1} as recorded times.
Output: Learned parameters \mathbf{w}_{d\times 1} and \mathbf{H}_{N\times 1}.
converged \leftarrow False;
threshold \leftarrow 10^{-4};
\tau \leftarrow 0:
\log \mathcal{L}^{(\tau)} = -\infty;
Initialize \mathbf{w}^{(\tau)} with random values;
while Not converged do
       \tau \leftarrow \tau + 1;
       Use Eq. 15 to obtain \mathbf{H}^{(\tau)} using \mathbf{w}^{(\tau-1)};
       Optimize Eq. 16 to obtain \mathbf{w}^{(\tau)} using \mathbf{H}^{(\tau)};
       Use Eq. 13 to obtain \log \mathcal{L}^{(\tau)} using \mathbf{w}^{(\tau)} and \mathbf{H}^{(\tau)};
       if \|\log \mathcal{L}^{(\tau)} - \log \mathcal{L}^{(\tau-1)}\| < threshold then
        " converged ← True;
       end
end
\mathbf{w} \leftarrow \mathbf{w}^{(\tau)}:
\mathbf{H} \leftarrow \mathbf{H}^{(\tau)};
```

each iteration τ , we first update $H^{(\tau)}$ via Eq. 15 using $w^{(\tau-1)}$. Next, we optimize Eq. 16 using the values of $H^{(\tau)}(t_i)$ to obtain $\mathbf{w}^{(\tau)}$. We continue this routine until convergence. The pseudo code of the learning procedure is available in Algorithm 1.

D. Inference Queries

In this part, we explain how to answer the common inference queries based on the inferred distribution $f_T(t \mid \mathbf{x})$. Suppose that we have learned the vector \mathbf{w} and the function H using the training samples (\mathbf{x}_i, y_i, t_i) , i = 1...N following Algorithm 1. Afterwards, for a testing relationship R associated with a feature vector \mathbf{x}_R , the following queries can be answered:

Ranged Probability. What is the probability for the relationship R to be formed between time t_{α} and t_{β} ? This is equivalent to calculating $P(t_{\alpha} \le T \le t_{\beta} \mid \mathbf{x}_{R})$, which by definition is:

$$P(t_{\alpha} \leq T \leq t_{\beta} \mid \mathbf{x}_{R}) = S(t_{\alpha} \mid \mathbf{x}_{R}) - S(t_{\beta} \mid \mathbf{x}_{R})$$

= $\exp\{-g(\mathbf{w}^{T}\mathbf{x}_{R})H(t_{\alpha})\} - \exp\{-g(\mathbf{w}^{T}\mathbf{x}_{R})H(t_{\beta})\}$ (17)

The problem here is to obtain the values of $H(t_{\alpha})$ and $H(t_{\beta})$, as t_{α} and t_{β} may not be among t_{i} s of the training samples, for which H is estimated. To calculate $H(t_{\alpha})$, we find $k \in \{1, 2, ..., N\}$ such that $t_{k} \leq t_{\alpha} < t_{k+1}$. Due to the piecewise constant assumption for the function h, we get:

$$h(t_{\alpha}) = \frac{H(t_{\alpha}) - H(t_k)}{t_{\alpha} - t_k}$$
 (18)

On the other hand, since h only changes in t_i s, we have:

$$h(t_{\alpha}) = h(t_{k+1}) = \frac{H(t_{k+1}) - H(t_k)}{t_{k+1} - t_k}$$
(19)

Combining Eq. 18 and 19, we get:

$$H(t_{\alpha}) = H(t_k) + (t_{\alpha} - t_k) \frac{H(t_{k+1}) - H(t_k)}{t_{k+1} - t_k}$$
(20)

Following the similar approach, we can calculate $H(t_{\beta})$, and then answer the query using Eq. 17. The dominating operation here is to find the value of k. Since we have t_i s sorted beforehand, this operation can be done using a binary search with $O(\log N)$ time complexity.

Quantile. By how long the target relationship R will be formed with probability α ? This question is equivalent to find the time t_{α} such that $P(T \le t_{\alpha} \mid x_R) = \alpha$. By definition, we have:

$$1 - P(T \le t_{\alpha} \mid \mathbf{x}_R) = S(t_{\alpha} \mid \mathbf{x}_R) = \exp\{-g(\mathbf{w}^T \mathbf{x}_R)H(t_{\alpha})\} = 1 - \alpha$$

Taking logarithm of both sides and rearranging, we get:

$$H(t_{\alpha}) = -\frac{\log(1 - \alpha)}{g(\mathbf{w}^T \mathbf{x}_R)}$$
 (21)

To find t_{α} , we first find k such that $H(t_k) \leq H(t_{\alpha}) < H(t_{k+1})$. We eventually have $t_k \leq t_{\alpha} < t_{k+1}$ since H is a non-decreasing function due to non-negativity of the function h. Therefore, we again end up with Eq. 20, which by rearranging we get:

$$t_{\alpha} = (t_{k+1} - t_k) \frac{H(t_{\alpha}) - H(t_k)}{H(t_{k+1}) - H(t_k)} + t_k$$
 (22)

By combining the Eq. 21 and 22, we can obtain the value of t_{α} which is the answer to the quantile query. It worth mentioning that if $\alpha = 0.5$ then t_{α} becomes the median of the distribution $f_T(t \mid \mathbf{x}_R)$. Here again the dominant operation is to find the value of k, which due to the non-decreasing property of the function H can be found using a binary search with $O(\log N)$ time complexity.

V. Experiments

We have conducted extensive experiments on both synthetic and real-world datasets to assess the effectiveness of Np-Glm.

A. Experiments on synthetic data

We use synthetic data to verify the correctness of NP-GLM and its learning algorithm. Since NP-GLM is a non-parametric method, we generate synthetic data using various parametric models with previously known random parameters, and evaluate how well NP-GLM can learn the parameters and the underlying distribution of the generated data.

Experiment Setup. We consider generalized linear models of two widely used distributions for event-time modeling, Rayleigh and Gompertz, as the ground truth models for generating synthetic data. Algorithm 2 is used to generate a total of N data samples with d-dimensional feature vectors, consisting N_o non-censored (observed) samples and remaining $N_c = N - N_o$ censored ones. For all synthetic experiments, we generate 10-dimensional feature vectors (d = 10) and set $g(\mathbf{w}^T\mathbf{x}) = \exp(\mathbf{w}^T\mathbf{x})$. We repeat every experiment 100 times and report the average.

Experiment Results. Since NP-GLM's learning is done in an iterative manner, we first analyzed whether this algorithm converges as the number of iterations increase. We recorded the log-likelihood of NP-GLM, averaged over the number

Algorithm 2: Synthetic dataset generation algorithm.

Input: The number of observed samples N_a , the number of

```
censored samples N_c, the dimension of the feature
          vectors d, and the desired distribution dist
Output: Synthetically generated data \mathbf{X}_{N\times d}, \mathbf{y}_{N\times 1}, and \mathbf{t}_{N\times 1}.
N \leftarrow N_o + N_c;
Draw a weight vector \mathbf{w} \sim \mathcal{N}(0, \mathbf{I}_d), where \mathbf{I}_d is the
 d-dimensional identity matrix;
Draw scalar intercept b \sim \mathcal{N}(0, 1);
for i \leftarrow 1 to N do
      Draw feature vector \mathbf{x}_i \sim \mathcal{N}(0, \mathbf{I}_d);
      Set distribution parameter \alpha_i \leftarrow \exp(\mathbf{w}^T \mathbf{x}_i + b);
      if dist == Rayleigh then
            Draw t_i \sim \alpha_i t \exp\{-0.5\alpha_i t^2\};
      else if dist == Gompertz then
           Draw t_i \sim \alpha_i e^t \exp\{-\alpha_i(e^t - 1)\};
end
Sort pairs (\mathbf{x}_i, t_i) by t_i in ascending order;
for i \leftarrow 1 to N_o do
y_i \leftarrow 1;
for i \leftarrow (N_o + 1) to N do
y_i \leftarrow 0;
```

of training samples N in each iteration. We repeated this experiment for $N \in \{1000, 2000, 3000\}$ with a fixed censoring ratio of 0.5, which means half of the samples are censored. The result is depicted in Fig. 3. We can see that the algorithm successfully converges with a rate depending on the underlying distribution. For the case of Rayleigh, it requires about 100 iterations to converge but for Gompertz, this reduces to about 30. Also, we see that using more training data results in achieving more log-likelihood as expected.

In Fig. 4, we fixed N=1000 and performed the same experiment this time using different censoring ratios. According to the figure, we see that by increasing the censoring ratio, the convergence rate increases. This is because Np-Glm infers the values of H(t) for all t in the observation window. Therefore, as the censoring ratio increases, the observation window is decreased, so Np-Glm has to infer a fewer number of parameters, leading to a faster convergence. Note that as opposed to Fig. 3, here a higher log-likelihood doesn't necessarily indicate a better fit, due to the likelihood marginalization we get by the censored samples.

Next, we analyzed the performance of Np-GLM in terms of the achieved log-likelihood on a separate test dataset by gradually increasing the number of training samples under different censoring ratios. We put away a number of 100K synthetically generated test data samples and trained Np-GLM with a training dataset of size ranging from 100 to 900. In each step, we calculated the average log-likelihood of the trained model on the test. We repeated this experiment using different censoring ratios. The result is depicted in Fig. 5. According to the figure, the log-likelihood achieved on the test dataset gradually rises with the increase in the number of training samples. That is because using more training samples could result in a better estimate of the parameters by which the test

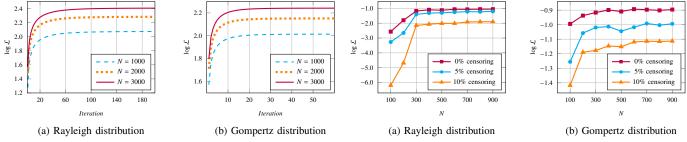


Fig. 3. Convergence of Np-GLM's average log-likelihood (log \mathcal{L}) for different number of training samples (N). Censoring ratio has been set to 0.5.

1.8

1.6

1.2

1.0

0.8

0.6

7 1.4 9 1.2

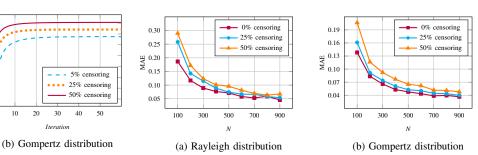


Fig. 4. Convergence of Np-GLM's average log-likelihood (log \mathcal{L}) for different censoring ratios with 1K samples.

5% censoring

25% censoring

50% censoring

NP-GLM's mean absolute error (MAE) vs the number of training samples (N) for different censoring ratios.

Fig. 5. Np-GLM's achieved average log-likelihood on the separate test data

vs the number of training samples (N) with different censoring ratios.

data samples are generated.

30 50

Iteration

(a) Rayleigh distribution

2.0

1.0

<u>0.0</u>

-2.0

In another experiment, we evaluated how good Np-GLM can infer the parameters used to generate the synthetic data. To this end, we varied the number of training samples N and measured the mean absolute error (MAE) between the learned weight vector $\hat{\mathbf{w}}$ and the ground truth. Fig. 6 illustrates the result for different censoring ratios. It can be seen that as the number of training samples increases, the MAE gradually decreases. The other point to notice is that more censoring ratio results in higher error due to the information loss we get by censoring.

Finally, we investigated whether censored samples are informative or not. For this purpose, we fixed the number of observed samples N_o and changed the number of censored samples from 0 to 200. We measure the MAE between the learned w and the ground truth for $N_o \in \{200, 300, 400\}$. The result is shown in Fig. 7. It clearly demonstrates that adding more censored samples causes the MAE to dwindle up to an extent, after which we get no substantial improvement. This threshold is dependent on the underlying distribution. In this case, for Rayleigh and Gompertz it is about 80 and 120, respectively.

B. Experiments on real data

We apply NP-GLM with the proposed feature set on realworld dataset to evaluate its effectiveness and compare its performance in predicting the time of link creation vis-à-vis different parametric models.

Dataset. We have used DBLP bibliographic citation network, provided by [23], as the real-world dataset which has both attributes of dynamicity and heterogeneity. Based on the publication venue of the papers, we extracted two networks,

named dblp-db and dblp-th, from the original DBLP dataset. The dblp-db is composed of papers which are published in conferences or journals related to Database, Data Mining, Machine Learning, and Artificial Intelligence. Moreover, those papers that are published in venues relative to the theoretical computer science, constitute the dblp-th network. The demographic statistics of both networks is presented in Table III.

Experiment Setup. We confined the dataset to the papers which has been published between the years 1995 and 2016, and selected the authors who had published more than 5 papers in the Feature Extraction Window of each experiment. Following the method described for feature extraction in Section III, we extracted 19 dynamic meta-path-based features. The rate parameter of features were determines using a separate validation set to get the best results. As NP-GLM needs the data samples sorted by their corresponding time variables, the samples were sorted according to their recorded time. Finally, since the features extracted for different meta-paths have different scales, we normalized the data using Z-Score. In all experiments, the author citation relation $(A \to P \to P \leftarrow A)$ were chosen as the target relation.

To challenge the performance of Np-Glm, we use the generalized linear model-based framework proposed in [9] with Exponential, Rayleigh, and Gompertz as distributions with different shapes, denoted as Exp-GLM, RAY-GLM, and GOM-GLM, respectively. We use 10-fold cross-validation and report the average results for all the experiments in this section.

Experiment Results. In the first set of experiments, we evaluated the prediction power of different models using different feature sets, and assessed how well they generalize

TABLE III
PROPERTIES OF DBLP BIBLIOGRAPHIC NETWORK

		Network		
	Property	dblp-db	dblp-th	
	Author	51,486	29,542	
# NT 1	Paper	79,069	64,333	
# Nodes	Venue	19	40	
	Term	22,567	18,578	
	write	123,343	77,783	
# D 1 .:	publish	39,965	30,732	
# Relations	cite	217,037	141,215	
	mention	278,257	206,735	

in different configurations for the feature extraction window and the observation window. Under each configuration, we considered the median of the distribution $f_T(t \mid \mathbf{x}_{test})$ as the predicted time for that sample and then compared it to the ground truth time t_{test} . Mean Absolute Error (MAE) and Mean Relative Error (MRE) are used to measure the accuracy of the predicted values. To examine the effect of considering the dynamicity of the network on the performance of the models, we evaluated each one with two different feature sets: dynamic and static. Dynamic feature set is our proposed features which captures the dynamicity of the network. On the contrary, static feature set only uses the very last snapshot of the network just before the beginning of the observation window, failing to reflect the temporal dynamics of the network.

In Table IV, we set $\Phi=10$ and varied Ω within the set $\{3,6,9\}$. The MAE and MRE of all models under both dblpdb and dblp-th networks, and using both dynamic and static feature sets has been recored. We see that in both networks, NP-GLM using the dynamic features is superior to the other models. For instance, when $\Omega=3$, our model NP-GLM can obtain an MAE of 0.21 for the dblp-db dataset, which is 28.5% lower than the MAE obtained by its closest competitor, Exp-GLM. As of MRE, NP-GLM achieves 0.16 on dblp-db, which is 25% lower than Exp-GLM. On dblp-th, NP-GLM reduces the MAE and MRE by 36% and 11%, respectively, relative to Exp-GLM. Comparable results hold for other values of Ω as well. Moreover, in this table it is evident that using the dynamic features has a positive impact on the performance of all models and decreases their prediction error.

Table V compares the MAE and MRE of different models when we set $\Omega=6$ and selected Φ from the set $\{5,10,15\}$. Again the results of all models have been obtained under both dblp-db and dblp-th networks, and using both static and dynamic feature sets. It is clear that NP-GLM has performed better than other baselines, even when it uses static features. When $\Phi=15$ for example, NP-GLM achieved an MAE of 0.62 and an MRE of 0.35 on the dblp-db dataset, which are respectively 22% and 14% lower than Exp-GLM's. On dblp-th, NP-GLM caused a 7% cut in MAE and a 30% cut in MRE compared to Exp-GLM's results. Here, the obtained results also show that leveraging more historical data to extract features could lead to more accurate predictions and lower error rates.

In the final experiment, we investigated for what fraction of

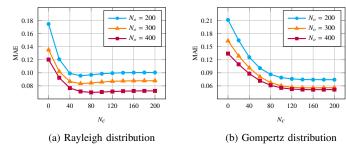


Fig. 7. Np-GLM's mean absolute error (MAE) vs the number of censored samples (N_c) for different number of observed samples (N_o).

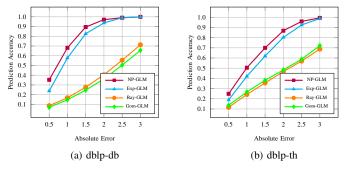


Fig. 8. Prediction accuracy of different methods vs the maximum tolerated absolute error with $\Phi=10$ and $\Omega=6.$

test samples a model can have a lower prediction error than a threshold. In other words, to evaluate the prediction accuracy of a model, we record the fraction of test samples for which the difference between their true times and the predicted ones are lower than a given threshold, called *tolerated error*. To this end, we again used the median as the predicted value by all models that were trained using our dynamic features. The feature extraction and observation windows were set to 10 and 6, respectively, and the results for different tolerated errors in range {0.5, 1.0, ..., 3.0} were plotted in Fig 8. The result demonstrates that Np-GLM can achieve a higher accuracy in all cases relative to other baselines, especially when dealing with lower tolerated errors.

VI. RELATED WORKS

The problem of link prediction has been studied extensively in recent years and many approaches have been proposed to solve this problem [24], [25]. Previous works on time-aware link prediction have mostly considered temporality in analyzing the long-term network trend over time [26]. Authors in [10] have shown that temporal metrics are an extremely valuable new contribution to link prediction, and should be used in future applications. Dunlavy *et al.* focused on the problem of periodic temporal link prediction [27]. They focused on bipartite graphs that evolve over time and also considered weighted matrix that contained multilayer data and tensor-based methods for predicting future links. Oyama *et al.* solved the problem of cross-temporal link prediction, in which the links among nodes in different time frames are inferred [28]. They mapped data objects in different

TABLE IV Performance Comparison of Different Methods Under Different Lengths for Observation Window when $\Phi=10$

		Model	$\Omega = 3$		$\Omega = 6$		$\Omega = 9$	
Dataset	Feature		MAE	MRE	MAE	MRE	MAE	MRE
dblp-db	Dynamic	NP-GLM EXP-GLM RAY-GLM GOM-GLM	$0.21 \pm 0.02 \\ 0.27 \pm 0.09 \\ 0.40 \pm 0.04 \\ 0.38 \pm 0.09$	0.16 ± 0.07 0.20 ± 0.02 0.32 ± 0.05 0.32 ± 0.09	0.76 ± 0.05 0.83 ± 0.09 1.90 ± 0.06 1.89 ± 0.07	0.34 ± 0.03 0.43 ± 0.06 1.00 ± 0.09 1.23 ± 0.02	1.10 ± 0.09 1.39 ± 0.04 2.56 ± 0.01 3.30 ± 0.07	0.43 ± 0.02 0.66 ± 0.01 1.60 ± 0.02 2.03 ± 0.01
иотр-ио	RAY-GLM	Np-Glm Exp-Glm Ray-Glm Gom-Glm	0.27 ± 0.01 0.33 ± 0.01 0.48 ± 0.02 0.48 ± 0.01	0.20 ± 0.01 0.24 ± 0.01 0.37 ± 0.02 0.36 ± 0.01	0.85 ± 0.03 0.93 ± 0.03 2.16 ± 0.06 2.28 ± 0.02	0.45 ± 0.02 0.51 ± 0.02 1.30 ± 0.04 1.37 ± 0.03	1.32 ± 0.07 1.54 ± 0.06 3.37 ± 0.12 4.24 ± 0.10	0.56 ± 0.02 0.74 ± 0.05 1.84 ± 0.11 2.28 ± 0.06
dblp-th	Dynamic	NP-GLM EXP-GLM RAY-GLM GOM-GLM	0.22 ± 0.03 0.30 ± 0.03 0.41 ± 0.01 0.38 ± 0.06	0.17 ± 0.08 0.19 ± 0.07 0.34 ± 0.01 0.30 ± 0.09	$0.75 \pm 0.09 \\ 0.75 \pm 0.09 \\ 1.83 \pm 0.06 \\ 1.88 \pm 0.05$	0.36 ± 0.02 0.43 ± 0.06 1.11 ± 0.02 1.23 ± 0.02	1.06 ± 0.09 1.37 ± 0.03 3.01 ± 0.07 3.97 ± 0.06	0.47 ± 0.08 0.60 ± 0.02 1.56 ± 0.04 2.14 ± 0.02
	Static	NP-GLM Exp-GLM Ray-GLM Gom-GLM	0.28 ± 0.01 0.34 ± 0.02 0.50 ± 0.03 0.50 ± 0.01	0.21 ± 0.01 0.25 ± 0.02 0.39 ± 0.02 0.38 ± 0.02	0.89 ± 0.04 0.98 ± 0.03 2.26 ± 0.07 2.38 ± 0.06	0.47 ± 0.02 0.54 ± 0.02 1.36 ± 0.05 1.43 ± 0.07	1.37 ± 0.07 1.59 ± 0.07 3.54 ± 0.13 4.41 ± 0.14	0.57 ± 0.03 0.77 ± 0.04 1.92 ± 0.08 2.40 ± 0.07

time frames into a common low-dimensional latent feature space, and identified the links on the basis of the distance between the data objects. Özcan *et al.* proposed a novel link prediction method for evolving networks based on NARX neural network [29]. They take the correlation between the quasi-local similarity measures and temporal evolutions of link occurrences information into account by using NARX for multivariate time series forecasting. Yu *et al.* developed a novel temporal matrix factorization model to explicitly represent the network as a function of time [30]. They provided results for link prediction as an specific example and showed that their model performs better than the state-of-the-art techniques.

The most relevant works to this study are available in [14], [16], [17], [9]. The Authors in [14] approaches the problem of time series link prediction by extracting simple temporal features from the time series, such as mean, (weighted) moving average, and exponential smoothing besides some topological features like common neighbor and adamic-adar. But their method is designed for homogeneous networks and fail to consider the heterogeneity of the modern networks. Aggarwal et al. [16] tackle the link prediction problem in both dynamic and heterogeneous information networks using a dynamic clustering approach alongside with content-based and structural models. However they aim to solve the conventional link prediction problem, not the continuous-time relationship prediction problem studied in this paper. In [17], the authors proposed a feature set, called TMLP, well suited for link prediction in dynamic and heterogeneous information networks. Although their proposed feature set cope with both dynamicity and heterogeneity of the network, it cannot be extended for the generalized problem of relationship prediction and is only designed for solving the simpler link prediction problem.

Most of the aforementioned works answered the question of *whether* a link will appear in the network. To the best of our knowledge, the only work that has focused on the continuous-time relationship prediction problem is proposed by Sun *et al.* [9], in which a generalized linear model based

framework is suggested to model the relationship building time. They consider the building time of links as independent random variables coming from a pre-specified distribution and model the expectation as a function of a linear predictor of the extracted topological features. A shortcoming of this model is that we need to exactly specify the underlying distribution of times. We came over this problem by learning the distribution from the data using a non-parametric solution. Furthermore, we considered the temporal dynamics of the network which has been entirely ignored in their work.

VII. Conclusion

In this paper, we studied the problem of continuous-time relationship prediction in both dynamic and heterogeneous information networks. To effectively tackle this problem, we first introduced a meta-path based feature extraction framework to systematically extract features suitable for solving the continuous-time relationship problem which takes both the temporal dynamics and heterogeneous characteristics of the network into account. We then proposed a supervised non-parametric model, called NP-GLM, which exploits the extracted features to predict the relationship building time in information networks. The strength of our model is that it does not impose any significant assumption on the underlying distribution of the relationship building time given its features, but tries to infer it from the data via a non-parametric approach. Extensive experiments conducted on both synthetic dataset and real-world DBLP bibliographic network demonstrated the correctness of our method and its effectiveness in predicting the relationship building time.

References

- L. Lü and T. Zhou, "Link prediction in complex networks: A survey," *Physica A: Statistical Mechanics and its Applications*, vol. 390, no. 6, pp. 1150–1170, 2011.
- [2] S. Wasserman and K. Faust, Social network analysis: Methods and applications. Cambridge university press, 1994, vol. 8.

TABLE V Performance Comparison of Different Methods Under Different Lengths for Feature Extraction Window when $\Omega=6$

			Φ = 5		$\Phi = 10$		Φ = 15	
Dataset	Feature	Model	MAE	MRE	MAE	MRE	MAE	MRE
dblp-db	Dynamic	NP-GLM EXP-GLM RAY-GLM GOM-GLM	0.78 ± 0.01 0.83 ± 0.02 1.65 ± 0.08 2.05 ± 0.06	0.37 ± 0.01 0.41 ± 0.05 1.00 ± 0.03 1.12 ± 0.06	0.76 ± 0.05 0.83 ± 0.09 1.90 ± 0.06 1.89 ± 0.07	0.34 ± 0.03 0.43 ± 0.06 1.00 ± 0.09 1.23 ± 0.02	0.62 ± 0.07 0.76 ± 0.07 1.84 ± 0.04 1.95 ± 0.01	$\begin{array}{c} \textbf{0.35} \pm \textbf{0.03} \\ 0.40 \pm 0.03 \\ 1.00 \pm 0.02 \\ 1.17 \pm 0.08 \end{array}$
do.p do	Static	NP-GLM EXP-GLM RAY-GLM GOM-GLM	0.86 ± 0.02 0.94 ± 0.03 2.17 ± 0.05 2.28 ± 0.03	0.44 ± 0.01 0.50 ± 0.02 1.29 ± 0.04 1.35 ± 0.02	0.85 ± 0.03 0.93 ± 0.03 2.16 ± 0.04 2.28 ± 0.06	0.44 ± 0.02 0.51 ± 0.02 1.29 ± 0.03 1.36 ± 0.04	0.81 ± 0.05 0.93 ± 0.04 2.12 ± 0.07 2.22 ± 0.08	0.41 ± 0.02 0.51 ± 0.03 1.28 ± 0.05 1.34 ± 0.07
dblp-th	Dynamic	NP-GLM EXP-GLM RAY-GLM GOM-GLM	0.77 ± 0.01 0.85 ± 0.06 1.77 ± 0.05 2.10 ± 0.06	$0.40 \pm 0.01 \\ 0.40 \pm 0.09 \\ 1.15 \pm 0.09 \\ 1.07 \pm 0.03$	0.75 ± 0.09 0.75 ± 0.09 1.83 ± 0.06 1.88 ± 0.05	0.36 ± 0.02 0.43 ± 0.06 1.11 ± 0.02 1.23 ± 0.02	0.70 ± 0.04 0.75 ± 0.08 1.95 ± 0.08 1.76 ± 0.04	0.36 ± 0.09 0.47 ± 0.02 1.10 ± 0.06 1.08 ± 0.05
	Static	NP-GLM EXP-GLM RAY-GLM GOM-GLM	0.90 ± 0.03 0.98 ± 0.03 2.33 ± 0.07 2.42 ± 0.04	0.46 ± 0.01 0.52 ± 0.03 1.32 ± 0.04 1.41 ± 0.06	0.89 ± 0.04 0.97 ± 0.03 2.29 ± 0.04 2.40 ± 0.08	0.45 ± 0.01 0.53 ± 0.03 1.36 ± 0.04 1.41 ± 0.06	0.85 ± 0.04 0.98 ± 0.04 2.21 ± 0.12 2.31 ± 0.08	0.43 ± 0.03 0.54 ± 0.03 1.34 ± 0.08 1.40 ± 0.07

- [3] D. Liben-Nowell and J. Kleinberg, "The link prediction problem for social networks," journal of the Association for Information Science and Technology, vol. 58, no. 7, pp. 1019–1031, 2007.
- [4] X. Chen, M.-X. Liu, and G.-Y. Yan, "Drug-target interaction prediction by random walk on the heterogeneous network," *Molecular BioSystems*, vol. 8, no. 7, pp. 1970–1978, 2012.
- [5] C. Wang, V. Satuluri, and S. Parthasarathy, "Local probabilistic models for link prediction," in *Data Mining*, 2007. ICDM 2007. Seventh IEEE International Conference on. IEEE, 2007, pp. 322–331.
- [6] R. N. Lichtenwalter, J. T. Lussier, and N. V. Chawla, "New perspectives and methods in link prediction," in *Proceedings of the 16th ACM SIGKDD international conference on Knowledge discovery and data mining*. ACM, 2010, pp. 243–252.
- [7] B. Taskar, M.-F. Wong, P. Abbeel, and D. Koller, "Link prediction in relational data," in *Advances in neural information processing systems*, 2004, pp. 659–666.
- [8] C. Shi, Y. Li, J. Zhang, Y. Sun, and S. Y. Philip, "A survey of heterogeneous information network analysis," *IEEE Transactions on Knowledge and Data Engineering*, vol. 29, no. 1, pp. 17–37, 2017.
- [9] Y. Sun, J. Han, C. C. Aggarwal, and N. V. Chawla, "When will it happen?: Relationship prediction in heterogeneous information networks," in *Proceedings of the Fifth ACM International Conference on Web Search and Data Mining*, ser. WSDM '12. New York, NY, USA: ACM, 2012, pp. 663–672.
- [10] A. Potgieter, K. A. April, R. J. Cooke, and I. O. Osunmakinde, "Temporality in link prediction: Understanding social complexity," *Emergence: Complexity and Organization*, vol. 11, no. 1, p. 69, 2009.
- [11] Y. Dong, J. Tang, S. Wu, J. Tian, N. V. Chawla, J. Rao, and H. Cao, "Link prediction and recommendation across heterogeneous social networks," in *Data Mining (ICDM)*, 2012 IEEE 12th International Conference on. IEEE, 2012, pp. 181–190.
- [12] D. Davis, R. Lichtenwalter, and N. V. Chawla, "Multi-relational link prediction in heterogeneous information networks," in *Advances in Social Networks Analysis and Mining (ASONAM)*, 2011 International Conference on. IEEE, 2011, pp. 281–288.
- [13] S. Sajadmanesh, H. R. Rabiee, and A. Khodadadi, "Predicting anchor links between heterogeneous social networks," in 2016 IEEE/ACM International Conference on Advances in Social Networks Analysis and Mining (ASONAM), Aug 2016, pp. 158–163.
- [14] A. Hajibagheri, G. Sukthankar, and K. Lakkaraju, "Leveraging network dynamics for improved link prediction," in Social, Cultural, and Behavioral Modeling: 9th International Conference, SBP-BRiMS 2016, Washington, DC, USA, June 28-July 1, 2016, Proceedings 9. Springer, 2016, pp. 142–151.
- [15] B. Moradabadi and M. R. Meybodi, "A novel time series link prediction method: Learning automata approach," *Physica A: Statistical Mechanics and its Applications*, vol. 482, pp. 422–432, 2017.
 [16] C. Aggarwal, Y. Xie, and P. S. Yu, "On dynamic link inference in
- [16] C. Aggarwal, Y. Xie, and P. S. Yu, "On dynamic link inference in heterogeneous networks," in *Proceedings of the 2012 SIAM International Conference on Data Mining*. SIAM, 2012, pp. 415–426.

- [17] N. Sett, S. Basu, S. Nandi, and S. R. Singh, "Temporal link prediction in multi-relational network," World Wide Web, pp. 1–25, 2017.
- [18] H. Kwak, C. Lee, H. Park, and S. Moon, "What is twitter, a social network or a news media?" in *Proceedings of the 19th international* conference on World wide web. ACM, 2010, pp. 591–600.
- [19] Y. Sun, J. Han, X. Yan, P. S. Yu, and T. Wu, "Pathsim: Meta path-based top-k similarity search in heterogeneous information networks," *Proceedings of the VLDB Endowment*, vol. 4, no. 11, pp. 992–1003, 2011.
- [20] Y. Sun, R. Barber, M. Gupta, C. C. Aggarwal, and J. Han, "Co-author relationship prediction in heterogeneous bibliographic networks," in *Advances in Social Networks Analysis and Mining (ASONAM)*, 2011 International Conference on. IEEE, 2011, pp. 121–128.
- [21] J. Zhang, P. S. Yu, and Z.-H. Zhou, "Meta-path based multi-network collective link prediction," in *Proceedings of the 20th ACM SIGKDD* international conference on Knowledge discovery and data mining. ACM, 2014, pp. 1286–1295.
- [22] N. E. Breslow, "Analysis of survival data under the proportional hazards model," *International Statistical Review / Revue Internationale de Statistique*, vol. 43, no. 1, pp. 45–57, 1975.
- [23] J. Tang, J. Zhang, L. Yao, J. Li, L. Zhang, and Z. Su, "Arnetminer: Extraction and mining of academic social networks," in *Proceedings* of the 14th ACM SIGKDD International Conference on Knowledge Discovery and Data Mining, ser. KDD '08. New York, NY, USA: ACM, 2008, pp. 990–998.
- [24] P. Wang, B. Xu, Y. Wu, and X. Zhou, "Link prediction in social networks: the state-of-the-art," *Science China Information Sciences*, vol. 58, no. 1, pp. 1–38, 2015.
- [25] T. Wang and G. Liao, "A review of link prediction in social networks," in Management of e-Commerce and e-Government (ICMeCG), 2014 International Conference on. IEEE, 2014, pp. 147–150.
- [26] Y. Dhote, N. Mishra, and S. Sharma, "Survey and analysis of temporal link prediction in online social networks," in Advances in Computing, Communications and Informatics (ICACCI), 2013 International Conference on. IEEE, 2013, pp. 1178–1183.
- [27] D. M. Dunlavy, T. G. Kolda, and E. Acar, "Temporal link prediction using matrix and tensor factorizations," ACM Transactions on Knowledge Discovery from Data (TKDD), vol. 5, no. 2, p. 10, 2011.
- [28] S. Oyama, K. Hayashi, and H. Kashima, "Cross-temporal link prediction," in *Data Mining (ICDM)*, 2011 IEEE 11th International Conference on. IEEE, 2011, pp. 1188–1193.
- [29] A. Özcan and Ş. G. Öğüdücü, "Temporal link prediction using time series of quasi-local node similarity measures," in *Machine Learning* and Applications (ICMLA), 2016 15th IEEE International Conference on. IEEE, 2016, pp. 381–386.
- [30] W. Yu, C. C. Aggarwal, and W. Wang, "Temporally factorized network modeling for evolutionary network analysis," in *Proceedings of the Tenth ACM International Conference on Web Search and Data Mining*. ACM, 2017, pp. 455–464.