# Piecewise-Velocity Model for Learning Continuous-time Dynamic Node Representations

Keywords: social networks, link prediction, dynamic networks, embeddings, visualization

## **Extended Abstract**

In numerous domains, networks (or graphs) have become essential and pervasive elements for modeling the relationships among various entities. For instance, social networks illustrate friendships among individuals, while some biological networks are employed to show protein-protein interactions [4]. Recent years have seen a significant rise in Graph Representation Learning (GRL) methods to extract noteworthy information from these structures and to perform some downstream tasks, such as missing link prediction. Although networks evolve over time, most existing methods address only static networks (i.e., a snapshot of networks at a specific time). Current limitations in effectively modeling continuous-time dynamic networks while explicitly considering network features like homophily and transitivity [5, 2] hinder accurate network characterization and visualization [3]. In this regard, we propose the PIecewise-VElocity Model (PIVEM) for the representation of continuous-time dynamic networks.

The interactions (or links/edges) among nodes do not necessarily exhibit any recurring characteristics; instead, they vary over time in many real networks. Therefore, we suppose the number of links between a pair of nodes  $(i, j) \in \mathcal{V}^2$  follows a Nonhomogeneous Poisson Point Process with intensity  $\lambda_{ij}(t)$ . Then, we write the log-likelihood function as

$$\mathcal{L}(\Omega) := \log p(\mathcal{G}|\Omega) = \sum_{i < j} \left( \sum_{e_{ij} \in \mathcal{E}_{ij}} \log \lambda_{ij}(e_{ij}) - \int_0^T \lambda_{ij}(t) dt \right)$$
 (1)

where  $\mathcal{E}_{i,j}$  is the set of links of node pair (i,j) on the timeline [0,T], and  $\Omega$  is model hyperparameters. The intensity function is defined as  $\lambda_{ij}(t) := \exp(\beta_i + \beta_j - ||\mathbf{r}_i(t) - \mathbf{r}_j(t)||^2)$  where  $\mathbf{r}_i(t) \in \mathbb{R}^D$  and  $\beta_i \in \mathbb{R}$  denote the embedding vector at time t and the bias term of node i. Since our primary purpose is to learn continuous-time node representations in a latent space, we express the representation of node i at time t based on a linear model by  $\mathbf{r}_i(t) := \mathbf{x}_i^{(0)} + \Delta_B \mathbf{v}_i^{(1)} + \Delta_B \mathbf{v}_i^{(2)} + \cdots + (t \mod(\Delta_B)) \mathbf{v}_i^{(\lfloor t/\Delta_B \rfloor + 1)}$ . Here,  $\mathbf{x}_i^{(0)}$  can be considered as the initial position and  $\mathbf{v}_i$  the velocity of the corresponding node. It can be seen that increasing the number of bins can enhance the accuracy of tracking nodes' trajectories in the latent space. We also employ a Gaussian Process prior over the initial position  $\mathbf{x}^{(0)}$  and velocity vectors  $\mathbf{v}$  in order to control the smoothness of the motion in the latent space.

#### **Experiments**

We rigorously assess the performance of the proposed approach compared to prominent benchmarks in challenging tasks across various social interaction datasets [1]. In the *network reconstruction* task, our goal is to see how accurately a model can learn the interaction patterns and produce embeddings showing their temporal relationships in a latent space. The performance of the models in terms of the AUC scores is reported in Table 1a. When we compare the performance of PIVEM with the baselines, we notice that it provides favorable performance for all

Table 1: The performance evaluation of the proposed method (PIVEM) over various datasets.

	College	Contacts	Email	Forum	Hypertext		College	Contacts	Email	Forum	Hypertext
LDM	.951	.860	.954	.909	.818	LDM	.931	.836	.948	.863	.761
Node2Vec	.655	.756	.828	.619	.696	Node2Vec	.685	.787	.818	.635	.596
CTDNE	.661	.787	.854	.657	.725	CTDNE	.601	.752	.831	.568	.554
HTNE	.721	.846	.871	.723	.775	HTNE	.673	.792	.853	.596	.602
MMDNE	.725	.844	.867	.737	.778	MMDNE	.677	.819	.844	.596	.587
PIVEM	.948	.938	.978	.907	.830	PIVEM	.935	.873	.951	.879	.770

a) Network reconstruction.

networks. This emphasizes the significance and capacity of PIVEM in detecting and accounting for structure in a continuous time frame. The *network completion* experiment is relatively more complicated than the reconstruction task. Since we conceal 10% of the network links, the dyads containing events are also viewed as non-link pairs, causing the temporal models to position these nodes far apart in the embedding space. Table 1b once again demonstrates a notable superiority of PIVEM over the baselines, which reaffirms the significance of utilizing time-evolving representations for modeling and tracking temporal networks.

**Visualization**. From a human perspective, visualizing the latent node representations is highly significant as it allows us to comprehend the intricate interactions among entities. Although GRL methods are effective in downstream tasks, they often require high-dimensional spaces, so a postprocessing step is needed for visualization. The experiments show that PIVEM is capable of learning embeddings and offers the ability to animate network evolution over time, which makes it an essential tool for capturing the underlying network characteristics. Figure 1 compares the ground-truth and the animation generated by PIVEM for an artificial network.

#### Conclusion

We have proposed a continuous-time dynamic network representation learning method. We evaluated the performance in network reconstruction and completion tasks over various social networks. The experimental results indicated that PIVEM could precisely embed nodes into a two-dimensional space with high performance in downstream tasks such as network completion and reconstruction. Therefore, it can be directly utilized to animate the embeddings to gain insights into networks' underlying characteristics specifying their evolution through time.

### References

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b) Network completion.

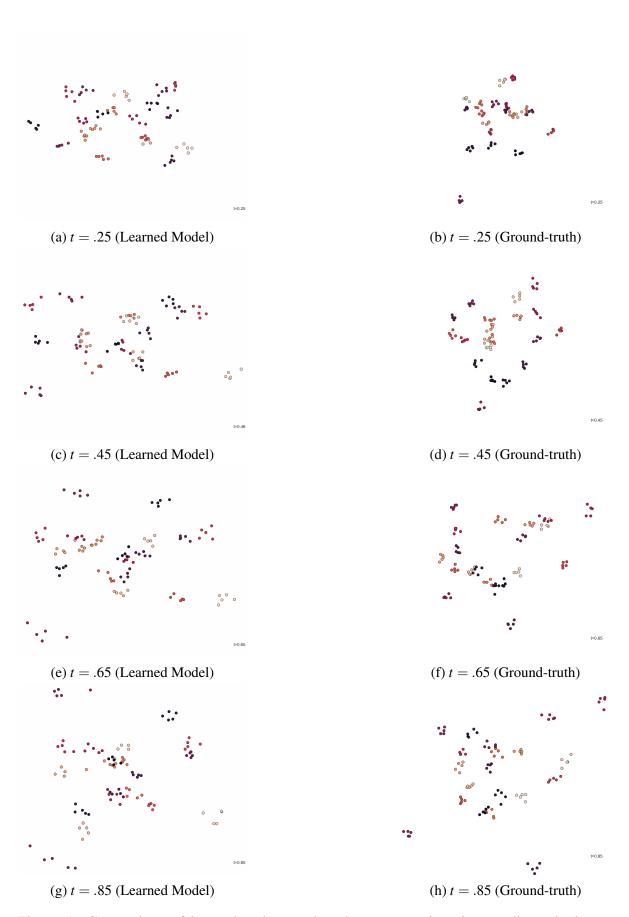


Figure 1: Comparison of learned and ground-truth representations in two-dimensinal space for various time points. The full version of the animation and more details can be found at https://tinyurl.com/pivem.