
GRAPH NEURAL NETWORKS FOR SOURCE DETECTION: A REVIEW AND BENCHMARK STUDY

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ABSTRACT

The source detection problem arises when an epidemic process unfolds over a contact network, and the objective is to identify its point of origin, i.e., the source node. Research on this problem began with the seminal work of Shah and Zaman in 2010, who formally defined it and introduced the notion of *rumor centrality*. With the emergence of Graph Neural Networks (GNNs), several studies have proposed GNN-based approaches to source detection. However, some of these works lack methodological clarity and/or are hard to reproduce. As a result, it remains unclear (to us, at least) whether GNNs truly outperform more traditional source detection methods across comparable settings. In this paper, we first review existing GNN-based methods for source detection, clearly outlining the specific settings each addresses and the models they employ. Building on this research, we propose a principled GNN architecture tailored to the source detection task. We also systematically investigate key questions surrounding this problem. Most importantly, we aim to provide a definitive assessment of how GNNs perform relative to other source detection methods. Our experiments show that GNNs substantially outperform all other methods we test across a variety of network types. Although we initially set out to challenge the notion of GNNs as a solution to source detection, our results instead demonstrate their remarkable effectiveness for this task. We discuss possible reasons for this strong performance. To ensure full reproducibility, we release all code and data on GitHub. Finally, we argue that epidemic source detection should serve as a benchmark task for evaluating GNN architectures.

Keywords Graph Neural Networks · Epidemic Source Detection · Single-Source Problems · Multi-Source Problems

1 Introduction

Epidemic processes are ubiquitous and extend far beyond biological pathogens such as SARS-CoV-2 in the human domain or the foot-and-mouth disease in the animal domain. With the rise of the internet and social media, the spread of rumors and misinformation has become an acute problem. On a more positive note, the technological revolution

based on the introduction of the internet has also contributed to making data about the contact network underlying such epidemic processes more available. For example, RFID sensors and the Bluetooth technology allow collecting human face-to-face contacts [1, 2], industrial animal movements can be collected from farmers or transport companies [3, 4], often using digital reporting tools, and online contact network data can be scraped from the internet [5, 6], or are sometimes provided to the public by social media or other companies [7, 8, 9]. The availability of such data has prompted many interesting research questions, one of them being the problem of source detection, famously introduced by Shah and Zaman [10].

The aim of source detection is to identify one or multiple source nodes of an epidemic process, given the underlying network of contacts and some observed state about the process (e.g., the current epidemic state of some or all nodes in the network). This is generally a hard problem for which closed-form solutions only exist for simplified problem settings [10]. After a plethora of solutions have been proposed in the years following the seminal introduction of the source detection problem by Shah and Zaman in 2010 [10], Dong et al. [11] and, a bit later, Shah et al. [12] were the first to propose the use of Graph Neural Networks (GNNs) for the source detection problem. The fundamental idea is that a GNN is trained on a static network of contacts using a large number of simulated epidemic outcomes as training data (learning step). The trained GNN can then be used to predict the source for a new epidemic outcome on this network (inference step). As Dong et al. [11] point out, GNNs seem to be well suited to tackle the source detection problem as the node embeddings resulting from a GNN aggregate neighborhood information which contains the key information to determine whether a node is a likely source or not: a source node would have many infected nodes in the close neighborhood, but a decreasing density of infected nodes in further out neighborhoods. If the embeddings, learned by the GNN, can encode this information in a meaningful way, then GNNs should be a sensible approach to source detection.

While research on GNNs in the context of epidemics is currently a very active research area [13], the problem of using GNNs for source detection is rather understudied. We counted a total of (at least) seven papers proposing GNN-based source detection methods [11, 12, 14, 15, 16, 17, 18] at the time of writing this paper. The seven papers address varied problem settings: while some consider the *single-source* problem [12, 15, 16, 18], others focus on *multi-source* problems [11, 17], and one paper covers both problems [14]. Or, as another example, Ru et al. [18] assume a temporal contact network while all other works assume static contact networks. This makes it hard or even impossible to compare the different approaches. Another issue with the proposed works is that they are difficult to reproduce for two reasons: first, some of the papers lack the exact details of their GNN architectures (e.g., number of layers), and second, only few authors [14, 17] provide the code for their methods and experiments. Finally, some papers lack precision and rigor in the presentation of their method and/or make claims that are incorrect or at least questionable. For example, several papers [11, 12, 15, 16, 18] claim that, unlike more conventional methods, GNN-based source detection is independent of the spreading model and its parameters or even model-agnostic and fail to acknowledge that all GNN-based approaches are trained on simulated spreading scenarios for which, at least implicitly, strong assumptions about the spreading process are made.

This paper attempts to bring order to the understudied area of using GNNs for source detection. After an exposition of the general problem setting to be studied (Section 2), we critically review prior research in this subfield (Section 3) and provide a formal description of the different GNN architectures that have been proposed for source detection (Section 4). We then propose a GNN architecture informed by insights from related work and the broader GNN literature (Section 5). Using this architecture, we aim to address several important questions that, in our view, remain unresolved (Section 6). The central question we examine is whether GNN-based source detectors truly outperform conventional source detection methods. In addition, we investigate how source detectability changes over time, how detection performance scales with increasing training set sizes, and how critical it is to know the exact time elapsed between the start of the epidemic and the observation of the snapshot of node states. Section 7 briefly elaborates on the computational complexity of the GNN-based approach and some of the benchmarks. Before we conclude in Section 9, we present a real-world use case in which apply a learned GNN to an observed snapshot of the 2009 H1N1 pandemic (Section 8).

2 Problem Formulation

In this section, we first present the necessary preliminaries on network representations and epidemic processes. We then formalize the specific problem setting considered in this work. Finally, we discuss the distinction between the single-source and multi-source variants of the problem.

2.1 Preliminaries

In this paper, we focus on the source detection problem on *static* networks, as do all the related papers except for Ru et al. [18]. We denote such networks as $G(V, E)$ with V being the set of nodes and E the set of edges. The network

contains a total of $N = |V|$ nodes. We write an edge as $(v, u) \in E$, with $v, u \in V$. Note that edges can be directed or undirected, but, in line with related work, we focus on the case of undirected edges. The network's adjacency matrix is denoted by $\mathbf{A} \in \mathbb{R}^{N \times N}$, where $A_{ij} = 1$ if $(i, j) \in E$ and $A_{ij} = 0$ otherwise. For each node v , we denote by $\mathcal{N}(v)$ the set of its immediate neighbors.

The observed epidemic state of each node is the result of an underlying (stochastic) propagation model that evolves in continuous time. At any time t , a node $v \in V$ is in some epidemic state that we denote as $X_v(t)$. The most prominent such propagation model, and therefore the one we will focus on here, is the *Susceptible-Infectious-Recovered* (SIR) model in which any node $v \in V$ is in one of three possible states, i.e., $X_v(t) \in \{S, I, R\}$. In the most straightforward version of the SIR model, there are two possible state transitions, both following a Poisson process, and all events are independent of each other [19]. The state transitions are (i) a susceptible node becoming infected at a rate $k\beta$ for k infected neighbors, and (ii) an infected node recovering at a constant rate μ .

2.2 Our Problem Setting

We assume that the described SIR process originates at some time t_0 from a single initially infected node in the network (*single-source* problem). At time $t_1 = t_0 + T$, we observe a complete snapshot of the epidemic, i.e., the states of all nodes in the network. Formally, we represent this snapshot (i.e., the observed *evidence*) as $E_{t_1} = \{(v, x_v(t_1)) : v \in V\}$. The majority of the related work assumes a similar observation process. An important decision in setting up the precise problem is whether the start of the epidemic, t_0 , and, by implication, its duration at the time of observation, T , are assumed to be known. Throughout this work, we primarily assume that T is known. Nonetheless, we also include results that examine how the detection performance is affected when T is not precisely known.

The task is to infer the source node v^* , given the network $G(V, E)$ and the observed snapshot of the epidemic E_{t_1} at time t_1 . $G(V, E)$ and E_{t_1} form an attributed graph in which each node is assigned its epidemic state at t_1 . Our objective is to develop a model that takes this attributed graph as input and outputs a prediction of the source node. Consequently, the task can be framed as a *graph prediction* problem, specifically as a multi-class classification problem with N possible classes, one for each node in the network.

A natural way to approach this problem using GNNs is to treat it as a supervised learning task, where a large set of simulated epidemic scenarios is used as training and validation data. Each training instance consists of the adjacency matrix \mathbf{A} , the observed snapshot which is typically encoded as a node feature matrix $\mathbf{X} \in \mathbb{R}^{N \times 3}$ containing the one-hot encoded node states at time t_1 , and the corresponding label (true source node). Crucially, the reliance on simulated data implies that some knowledge of the underlying spreading process is available.

Figure 1 schematically illustrates the overall source inference process once the model has been trained.

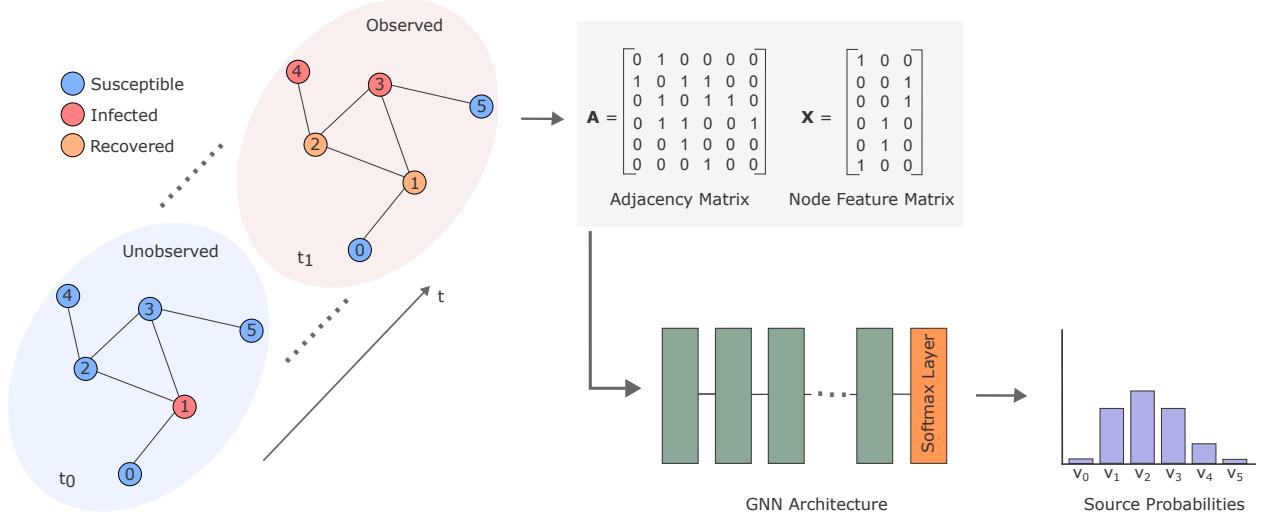


Figure 1: Schematic representation of the source detection problem. An epidemic originates from node 1 and evolves over time. At observation time t_1 , a full snapshot of node states is available, but the identity of the source is unknown. The GNN receives as input the graph adjacency matrix and a node feature matrix containing the one-hot encoded epidemic states, and outputs a probability distribution over nodes indicating the most likely source.

2.3 Single-Source vs. Multi-Source Problem

As stated above, this paper focuses on the single-source problem. Some related work, however, considers the multi-source setting, which has important implications for the design of the GNN’s output layer and the corresponding loss function.

For the single-source case, the output layer typically uses a softmax activation together with the cross-entropy loss, defined as

$$E_m(\Theta) = - \sum_{v \in V} y_{v,m} \cdot \ln(\hat{y}_{v,m}(\Theta)) \quad (1)$$

where $y_{v,m} = 1$ if node v is the true source in the m -th training instance and $y_{v,m} = 0$ otherwise. The term $\hat{y}_{v,m}$ denotes the softmax output of the model for node v in instance m , and Θ represents all learnable model parameters.

In contrast, the multi-source problem can be formulated as a multi-label binary classification task, where the GNN predicts, for each node, whether it belongs to the set of sources. This formulation implicitly assumes independence among source nodes. Instead of a softmax activation, each output neuron applies a sigmoid function, and training is performed using the multi-label binary cross-entropy loss:

$$E_m(\Theta) = - \sum_{v \in V} y_{v,m} \cdot \ln(\hat{y}_{v,m}(\Theta)) + (1 - y_{v,m}) \cdot \ln(1 - \hat{y}_{v,m}(\Theta)), \quad (2)$$

where $y_{v,m} = 1$ for each node v that is a true source in instance m and $y_{v,m} = 0$ otherwise, and $\hat{y}_{v,m}$ denotes the sigmoid output of the model for node v .

In the following section, we discuss the related work in greater detail, highlighting how the corresponding problem formulations differ from the one adopted in this paper.

3 Related Work

In this section, we first introduce traditional approaches to (single-) source detection grounded in physics- and statistics-based methods. We then discuss recent studies that employ GNNs for source detection.

3.1 Traditional Source Detection Methods

The field of source detection on networks was coined by Shah and Zaman in 2010 [10] who proposed a maximum likelihood source estimator (called *rumor center*). Their analysis focused on a simplified setting involving undirected regular tree graphs and a *Susceptible-Infectious* (SI) spreading model, and they proposed an approximate solution based on breadth-first search (BFS) trees for general networks. Zhu and Ying [20] later proposed an estimator applicable to SIR processes, called *Jordan center*, which identifies the source as the node minimizing the maximum distance to any node in the infected subgraph. Pinto et al. [21] examined a different problem setting in which a subset of nodes acts as observers that record infection arrival times. On tree graphs, the source can then be estimated under a distributional assumption on propagation delays, while for general networks a BFS-based heuristic is applied. Paluch et al. [22] improved the computational efficiency of Pinto et al.’s method, and Xu et al. [23] proposed a simpler correlation-based estimator that selects the node maximizing the correlation between infection arrival times and shortest-path distances from the candidate source to the observers.

Since closed-form solutions only exist for simplified problem settings, a substantial portion of the literature on source detection uses Monte-Carlo simulations of epidemic processes. Beginning with the work by Agaskar and Lu [24] who sample arrival times which they use to determine the most likely source, simulation-based approaches have also been used by Antulov-Fantulin et al. [25], Dutta et al. [26], and Sterchi et al. [27]. Both Antulov-Fantulin et al. and Dutta et al. compare simulated outcomes with the observed epidemic snapshot to infer source likelihoods. Sterchi et al., in contrast, use simulations to estimate node-state probabilities conditional on each possible source, from which a (factorized) likelihood is derived under a node independence assumption. A related line of research [28, 29] replaces stochastic simulations with deterministic update equations to compute node-state probabilities, again relying on independence assumptions. Another probabilistically motivated approach by Braunstein and Ingrosso [30] employs loopy belief propagation to approximate the posterior distribution of infection times for all nodes, identifying the source as the node with the highest marginal probability of initial infection. Their approach, however, is computationally rather expensive, with a single (parallel) run on a realistic network taking up to 11 minutes.

A topological perspective on source detection is offered by Brockmann and Helbing [31] and Rozenstein et al. [32]. Brockmann and Helbing address a metapopulation problem setting and introduce the concept of *effective distance*, derived from fluxes between subpopulations. Their source estimate corresponds to the node producing the most

Table 1: The problem settings addressed in related work. The contributions are listed in chronological order. All abbreviations are introduced in the main text.

Authors	Model	Network	Epidemics	Single/Multi	Snapshot
Dong et al. [11]	GCNSI	Undirected, static	SI, SIR, SIS, IC, LT	Multi	Full
Shah et al. [12]	-	Undirected, static	SIR, SEIR	Single	Full
Shu et al. [15]	MCGNN	Undirected, static	Heterogeneous SI	Single	Full
Guo et al. [16]	IGCN	Undirected, static	SI, SIR, IC	Single	Full
Sha et al. [14]	SD-STGCN	Undirected, static	SIR, SEIR, delay SIR	Both	Multiple full
Had. and Fig. [17]	-	Undirected, static	SI	Multi	Full
Ru et al. [18]	BN	Directed/undir., temporal	SIR	Single	Full

concentric infection pattern in terms of shortest distances between infected nodes (using the effective distances). Rozenshtein et al. [32] proposed a truly model-agnostic formulation, identifying the source as the node that minimizes the cost of a Steiner tree spanning all infected nodes.

3.2 GNN-based Source Detection Methods

In this subsection, we review the related work that employs GNN architectures for the source detection problem. We begin with the two multi-source approaches, one of which represents the earliest known GNN-based source detector, and then proceed to single-source contributions. Our discussion is limited to studies that consider the spread of biological pathogens as a representative use case. A number of related works instead focus uniquely on rumor propagation, which entails a somewhat different problem formulation; these works are briefly summarized at the end of this subsection. Moreover, we note that Li et al. [33] also propose a GCN-based framework for source detection. However, due to several technical and methodological issues, we do not include this work in our detailed discussion. Finally, we conclude with a short summary highlighting the open questions that emerge from the reviewed literature.

3.2.1 Multi-Source Approaches

To the best of our knowledge, Dong et al. [11] were the first to apply GNNs to the source detection problem on networks. Specifically, they address a multi-source setting on static networks, assuming that a full snapshot of all node states is observed at some time after the outbreak and that the number of sources is known *a priori*. Their approach, termed *Graph Convolutional Networks based Source Identification* (GCNSI), is motivated by rumor spreading in social networks and guided by two principles: *source prominence*, the notion that true sources tend to be surrounded by many infected nodes, and *rumor centrality*, the idea that distant nodes are less likely to be infected. These principles align naturally with the message-passing paradigm of GNNs, in which nodes learn representations based on information exchanged with their neighbors.

Methodologically, Dong et al. [11] first apply a label-propagation method [34] to augment initial node representations beyond simple one-hot encoded epidemic states. However, the benefit of this feature augmentation remains unclear, as GNNs inherently learn higher-order node representations. The study does not include a quantitative analysis of its effect. Moreover, the approach is benchmarked only against two earlier multi-source methods [35, 34] and is evaluated in simplified epidemic scenarios, where each node is either infected or not. While such a binary assumption may be reasonable for rumor propagation, it is overly simplistic for disease-spreading contexts that typically include additional states such as *exposed* or *recovered*. Some of the reported results also raise concerns, for instance, the model’s performance appears to improve with larger numbers of true sources, which, presumably, is an artifact of the evaluation metric. Finally, although the authors describe GCNSI as model-agnostic (meaning it does not require explicit prior knowledge of the spreading dynamics), the approach nonetheless relies on specifying a spreading model to generate the training data. This notion of spreading model agnosticism is a recurring yet misleading claim found throughout much of the subsequent literature. Table 1 summarizes the problem settings addressed by Dong et al. [11] and the other studies reviewed in this subsection.

Haddad and Figueiredo [17] investigate the same multi-source detection problem as Dong et al. [11], but differ in two key aspects. First, they employ the GraphSAGE architecture instead of the GCN architecture used in [11]. Second, they design additional node features to enrich each node v ’s initial representation: (i) the fraction of infected nodes within its k -hop neighborhood, and (ii) the fraction of infected nodes among the neighbors of v at distance k , for $k = 1, \dots, K$, where K is a hyperparameter.

In contrast to related work, Haddad and Figueiredo train and test their models on potentially different networks which is an unusual choice that contradicts the standard assumption in source detection that the underlying network is fully known and fixed during inference. As in [11], the number of true sources is assumed to be known a priori, a simplification that makes the task more tractable.

3.2.2 Single-Source Approaches

In contrast to the previous two contributions, Shah et al. [12] address the single-source detection problem. The general setting remains similar, assuming a full snapshot of node states is available at inference time t_1 . Unlike Dong et al. [11] and Haddad and Figueiredo [17], Shah et al. do not augment the initial node features and instead use only one-hot encoded node states as input. The training data are generated from large numbers of simulated epidemic realizations using SIR (or SEIR) dynamics. Shah et al. evaluate several GNN architectures, including variants of Graph Convolutional Networks (GCNs) and Graph Attention Networks (GATs), but find no substantial performance differences between them. While their approach clearly outperforms the benchmark method of Lokhov et al. [28], the exceptionally long inference times reported for the benchmark method raise some doubts regarding the robustness of the results.

Shu et al. [15] propose a *Multi-Channel GNN* (MCGNN) framework. The overall setting is similar to that in [12], except that they consider a heterogeneous SI model in which transmission probabilities may vary across edges. As the name suggests, their model comprises two channels: the first applies GCN layers to process node features, while the second constructs a line graph and computes various node properties within that graph. This second channel is intended to enhance performance by incorporating edge-level information, which the authors identify as the main improvement over prior methods. The outputs of both channels are concatenated and fed into the model's output layer. As in related work [11, 17], feature augmentation plays a central role. In both channels, several network-based measures (primarily centrality metrics) are computed for each node and used as input features. Additionally, the first (node) channel is enriched with established source detection indicators such as rumor centrality [10] and Jordan centrality [20].

A key issue with their approach lies in the incorrect formulation of the learning objective. The authors erroneously treat the single-source problem as a multi-label classification task. Consequently, their output layer contains N sigmoid-activated units trained using independent binary cross-entropy losses. However, the single-source problem requires a probability distribution over all nodes, which is appropriately modeled using a softmax output and categorical cross-entropy loss.

Guo et al. [16] address the same problem setting as Shah et al. [12] but propose a distinct architecture, the *Infected Graph Convolutional Network* (IGCN). After an initial GCN layer, the model applies three lightweight neighborhood aggregation layers containing only four trainable weights. These weights depend on the epidemic states of the focal node and its neighbors and are used during message aggregation. Since the authors consider only two possible states (infected vs. not infected), there are four state combinations per node pair, requiring exactly four parameters. Notably, the authors account for uncertainty in the underlying spreading dynamics by simulating the training data from three different spreading models with varying parameter settings.

Sha et al. [14] attempt to address some of the critiques raised during the review process of Shah et al. [12] on OpenReview [36], and accordingly modify their problem setting. However, this modification appears to stem from a misunderstanding of one reviewer's comment. The reviewer questioned the feasibility of a learning-based approach (apparently unaware that training data can be generated through simulations) by noting that "we only have access to one snapshot for a given graph and learning is impossible" [36]. Sha et al. interpret this remark as motivation to modify the problem setting so that, instead of a single full snapshot, multiple full snapshots of the epidemic at different time steps are available for inference.

In addition to this revised observation model, the authors adopt more realistic epidemic dynamics, including SEIR and delayed SIR models with non-exponential distributions of the infectious periods, and they evaluate their method on a broader range of both synthetic and empirical networks. Because multiple snapshots are observed, the node feature input becomes a three-dimensional tensor, with the third dimension representing time. To process such data, Sha et al. propose a *Spatio-Temporal GCN architecture for Source Detection* (SD-STGCN), originally developed for traffic forecasting [37]. Each block of the SD-STGCN consists of a Convolutional Neural Network (CNN) layer applied along the temporal dimension, a GCN layer aggregating neighborhood information, and another CNN layer for temporal refinement. Overall, the paper presents a thorough evaluation, including comparisons with baseline GCNs, experiments on different observation schemes (randomly sampled vs. consecutive snapshots), and training across varying epidemic parameters to account for uncertainty in the underlying dynamics.

While all previously discussed studies assume static networks, Ru et al. [18] address the single-source detection problem on temporal networks, which they conceptualize as sequences of static snapshots. As in prior work, a full snapshot

of a SIR epidemic is assumed to be available at inference time. Ru et al. explicitly incorporate uncertainty about the epidemic’s start time t_0 and duration T : their method requires an additional input specifying a time interval within which the outbreak is assumed to have begun, which is used during the simulation of training data.

The core idea of their approach, termed the *Backtracking Network* (BN), is to represent the network as static by including all edges that appeared across time, but to incorporate temporality through edge features. Specifically, the model takes as input both the one-hot encoded epidemic states of nodes and an edge feature matrix encoding the temporal activity patterns of the edges. It employs two interdependent convolution-style update equations: one for computing edge embeddings and another for computing node embeddings. They then compare their BN approach to several baselines, including Antulov-Fantulin et al.’s soft margin estimator (SME) [25]. However, the description of the SME in their paper is inaccurate, and the implementation relies on only 200 simulations per source node, which makes the comparison quantitatively unreliable and biased in favor of BN.

3.2.3 Other Works

Cheng et al. [38] address a multi-source problem setting that is heavily focused on the information spreading use case. As a consequence, they assume that for a fraction of the nodes the node states, but also the times when nodes received the information, and potentially the propagating nodes are observed. Their method is then a mix of feature augmentation based on a spectral decomposition of the infected subgraph Laplacian and a simple attention mechanism similar to GAT. Another work focused on information spreading is that of Ling et al. [39], who apply a Variational Autoencoder to the problem of multi-source detection. Their problem setting differs from ours in that they observe, for each node, a probability indicating whether the information has reached it. Given these probabilities and the underlying graph, they aim to infer both the number and the identities of the source nodes.

3.2.4 Summary

Our review of the GNN-based source detection literature reveals several open questions and directions for improvement. First, we argue that these approaches should not be described as model-agnostic, since in all cases the training data are simulated under explicit assumptions about the underlying spreading dynamics, and the learned models inevitably encode those assumptions. Second, although prior work does compare GNN-based methods against baselines, important benchmark models, such as the SME by Antulov-Fantulin et al. [25], are often omitted or implemented incorrectly. Consequently, the true potential of GNN-based approaches relative to classical methods remains uncertain. Third, while several studies emphasize feature augmentation, few provide a quantitative analysis of its actual effect on model performance. Fourth, the influence of training set size is rarely discussed. Given that training data are generated through simulations, it remains unclear whether systematic scaling laws exist, i.e., how model performance improves with increasing training data. Finally, only a small number of works relax the assumption that the duration T between the outbreak and the observed snapshot is known, even though this parameter is typically uncertain in realistic scenarios.

4 GNN Architectures for Source Detection

In this section, we offer a more formal exposition of the GNN architectures proposed for the source detection problem. For each method, we outline the node-level update equations, detail any specific processing steps applied to the input features, and describe the structure of the output layer together with the corresponding loss function.

4.1 Graph Convolutional Network (GCN)

The most commonly employed architecture for source detection is the Graph Convolutional Network (GCN) [11, 12, 15]. Dong et al. [11] adopt the standard GCN formulation proposed by Kipf and Welling [40]. Each node v is initialized with its feature vector $\mathbf{h}_v^{(0)} = \mathbf{x}_v \in \mathbb{R}^m$, where m denotes the number of node features. The layer-wise update rule is given by

$$\mathbf{h}_v^{(l)} = \text{ReLU} \left(\mathbf{W}_l \sum_{u \in \{\mathcal{N}(v) \cup \{v\}\}} \frac{\mathbf{h}_u^{(l-1)}}{\sqrt{\tilde{d}_v \tilde{d}_u}} \right), \quad l = 1, \dots, L, \quad (3)$$

where \tilde{d}_v denotes the degree of node v augmented by one. The symmetric normalization applied here has been shown to perform well in practice [40]. The neighborhood aggregation includes the node itself, and $\mathbf{W}_l \in \mathbb{R}^{s_l \times s_{l-1}}$ projects the embeddings to dimension s_l , followed by a ReLU activation. Typically, after the first layer projects the input features to the hidden dimension, the number of hidden units is kept constant, i.e., $s_{l-1} = s_l$ for all $l \geq 2$.

Table 2: Overview of design choices and learning configurations used by the different contributions. A dash (-) indicates that no information has been reported. Note that the method by Sha et al. [14] is conceptually quite different to the others and hyperparameter settings should thus not be directly compared.

Authors	# Layers	# Hidden Units	Learning Rate	Dropout Rate	# Epochs	Optim.
Dong et al. [11]	5–10	512 or 1024	0.001–0.005	0.1 or 0.3	900–4000	ADAM
Shah et al. [12]	10 (GAT: 5)	128	0.003 (GAT: 0.004)	0.265	150	ADAM
Shu et al. [15]	-	-	-	-	-	-
Sha et al. [14]	2–4	36	0.001	-	3	RMSProp
Guo et al. [16]	3 (+1 GCN)	512	0.001	0.1	50	ADAM
Had. and Fig. [17]	3	128	0.001	0.1	500 (early stop.)	ADAM
Ru et al. [18]	1–7	-	0.001	-	200	ADAM

For the output layer, consistent with the multi-label nature of the multi-source problem, a dense layer with sigmoid activation is used:

$$\hat{y}_v = \sigma(\mathbf{w}^\top \mathbf{h}_v^{(L)}), \quad (4)$$

where $\mathbf{w} \in \mathbb{R}^{s_L}$. The model is trained using binary cross-entropy loss with L2 regularization. Table 2 summarizes the hyperparameter choices and training details for this and the other approaches discussed below.

Shah et al. [12] use an architecture similar to that of Dong et al. [11], with several notable modifications. Before applying the GCN layers, the node feature vectors are linearly projected to match the hidden layer dimension,

$$\mathbf{h}_v^{(0)} = \mathbf{U}\mathbf{x}_v \in \mathbb{R}^{s_0}, \quad \mathbf{U} \in \mathbb{R}^{s_0 \times m}. \quad (5)$$

The authors introduce three main architectural differences: (i) inclusion of a bias term $\mathbf{b}_l \in \mathbb{R}^{s_l}$, (ii) residual connections between layers instead of self-inclusion in the aggregation, and (iii) the use of batch normalization (BatchNorm). The resulting layer update is given by

$$\mathbf{h}_v^{(l)} = \mathbf{h}_v^{(l-1)} + \text{LeakyReLU} \left(\text{BatchNorm} \left(\mathbf{W}_l \sum_{u \in \mathcal{N}(v)} \frac{\mathbf{h}_u^{(l-1)}}{\sqrt{d_v d_u}} + \mathbf{b}_l \right) \right), \quad l = 1, \dots, L. \quad (6)$$

Although alternative aggregation schemes were tested, the results were largely invariant to this choice. Their output layer is defined as

$$\hat{y}_v = \mathbf{p}^\top \text{ReLU}(\mathbf{Q}\mathbf{h}_v^{(L)}), \quad (7)$$

where $\mathbf{Q} \in \mathbb{R}^{s_L \times s_L}$ and $\mathbf{p} \in \mathbb{R}^{s_L}$ transform the final node embedding into the model prediction. The authors do not appear to apply a softmax activation in the output layer, despite the fact that the task is single-source detection. Moreover, no information regarding the loss function is provided.

Shu et al. [15] also build on a GCN backbone similar to Dong et al. [11], with the addition of a bias term in the layer update:

$$\mathbf{h}_v^{(l)} = \sigma \left(\mathbf{W}_l \sum_{u \in \{\mathcal{N}(v) \cup \{v\}\}} \frac{\mathbf{h}_u^{(l-1)}}{\sqrt{d_v d_u}} + \mathbf{b}_l \right), \quad l = 1, \dots, L. \quad (8)$$

The final GCN embedding $\mathbf{h}_v^{(L)}$ is concatenated with f additional node-level features derived from a line graph; a dense layer followed by a sigmoid activation yields the model output \hat{y}_v . Training is performed with binary cross-entropy and L2 regularization. The authors do not report hyperparameter settings. We note, however, that using a sigmoid output and independent binary cross-entropy losses is inappropriate for the single-source formulation considered in the paper. The single-source problem requires a valid probability distribution over all candidate nodes (i.e., mutually exclusive classes), which is correctly modeled with a softmax output and a categorical (multi-class) cross-entropy loss rather than independent sigmoids.

4.2 GraphSAGE

Haddad and Figueiredo [17] employ the GraphSAGE architecture [41] instead of a GCN. Their model consists of $L = 3$ GraphSAGE layers that use element-wise max. pooling to aggregate neighbor embeddings:

$$\mathbf{h}_v^{(l)} = \text{ReLU} \left(\mathbf{W}_l \left[\mathbf{h}_v^{(l-1)} \parallel \text{MAX} \left(\{\mathbf{h}_u^{(l-1)} : u \in \mathcal{N}(v)\} \right) \right] + \mathbf{b}_l \right), \quad l = 1, \dots, L, \quad (9)$$

where \parallel denotes vector concatenation. The first two layers use ReLU activations, while the third layer serves directly as the output layer, with dimensions of \mathbf{W}_3 and \mathbf{b}_3 chosen such that $\mathbf{h}_v^{(3)}$ is a scalar.

Since Haddad and Figueiredo address the multi-source problem, they apply a sigmoid activation in the final layer to obtain the probability that node v is a source. Training is based on a weighted binary cross-entropy loss, where source nodes are upweighted to address class imbalance.

4.3 Graph Attention Network (GAT)

Besides several GCN variants, Shah et al. [12] also evaluate a Graph Attention Network (GAT) [42]. The node update equation is given by

$$\mathbf{h}_v^{(l)} = \sigma \left(\mathbf{W}_l \sum_{u \in \{\mathcal{N}(v) \cup \{v\}\}} a_{vu} \mathbf{h}_u^{(l-1)} + \mathbf{b}_l \right), \quad l = 1, \dots, L, \quad (10)$$

where a_{vu} denotes the learned attention coefficient between node v and its neighbor u .

The attention mechanism is computed in two steps. First, an unnormalized attention weight is obtained as

$$e_{vu} = \text{LeakyReLU} \left(\mathbf{a}^\top \left[\mathbf{W}_l \mathbf{h}_v^{(l-1)} \parallel \mathbf{W}_l \mathbf{h}_u^{(l-1)} \right] \right), \quad (11)$$

where $\mathbf{a} \in \mathbb{R}^{2s_l}$ ensures that e_{vu} is a scalar. These attention scores are then normalized across all neighbors using a softmax:

$$a_{vu} = \frac{\exp(e_{vu})}{\sum_{w \in \{\mathcal{N}(v) \cup \{v\}\}} \exp(e_{vw})}. \quad (12)$$

In practice, attention mechanisms are often used in a *multi-head* setting, with several attention functions computed in parallel to stabilize training and improve expressiveness. Shah et al. [12], for instance, use $K = 4$ attention heads, combining their outputs via element-wise averaging or summing in the final layer.

4.4 Infected Graph Convolutional Network (IGCN)

Guo et al. [16] first augment the node feature vectors with additional topological descriptors such as betweenness centrality and subsequently normalize all features. This input layer is followed by a standard GCN layer using LeakyReLU activation. The core innovation lies in a sequence of IGCN layers, each defined as

$$\mathbf{h}_v^{(l)} = \sigma \left(\sum_{u \in \{\mathcal{N}(v) \cup \{v\}\}} w(x_v(t_1), x_u(t_1)) \mathbf{h}_u^{(l-1)} \right), \quad l = 1, \dots, L, \quad (13)$$

where

$$w(x_v(t_1), x_u(t_1)) = \begin{cases} w_{S,S}, & \text{if } x_v(t_1) = S, x_u(t_1) = S, \\ w_{S,I}, & \text{if } x_v(t_1) = S, x_u(t_1) = I, \\ w_{I,S}, & \text{if } x_v(t_1) = I, x_u(t_1) = S, \\ w_{I,I}, & \text{if } x_v(t_1) = I, x_u(t_1) = I, \end{cases} \quad (14)$$

represent four learnable weights used to modulate the aggregation based on the epidemic states of nodes v and u . No other parameters are learned within these layers. The architecture concludes with a fully connected layer and a softmax activation, producing a probability distribution over all nodes. Model training uses the cross-entropy loss with an additional regularization term.

4.5 Source Detection Spatial-Temporal Graph Convolutional Network (SD-STGCN)

Sha et al. [14] extend the spatio-temporal GCN architecture originally proposed by Yu et al. [37] to address the source detection problem with multiple epidemic snapshots. Their model consists of two *spatio-temporal convolution blocks*, each containing a GCN layer sandwiched between two temporal convolution (CNN-based) layers.

The model takes as input the adjacency matrix \mathbf{A} and a node feature tensor $\mathbf{X} \in \mathbb{R}^{k \times N \times m}$, where k is the number of epidemic snapshots observed at different times. The temporal layers are implemented as 1-D CNNs followed by Gated Linear Units (GLUs). A total of 36 CNN kernels with sizes $K_t \in \{2, 3, 4\}$ are used, applied without padding, thereby reducing the temporal dimension by $K_t - 1$ at each step.

Within each block, the spatial dependency among nodes is captured by the GCN layer, implemented either as the standard GCN [40] (using 2–4 layers) or the precursor based on the Chebyshev polynomials approximation [43], both followed by a ReLU activation. In the output layer, a final CNN reduces the temporal dimension to one, after which a dense layer and a softmax activation produce a probability vector $\hat{\mathbf{y}} \in \mathbb{R}^N$ over all nodes.

4.6 Backtracking Network (BN)

As noted earlier, Ru et al. [18] are the only ones to address the single-source problem on *temporal networks*, which they model as a sequence of static graphs G_0, \dots, G_T . Their GNN takes as input the (one-hot encoded) node states $\mathbf{x}_v \in \mathbb{R}^m$, which are first linearly projected, the adjacency matrix of the aggregated network \tilde{G} containing all edges that appear in any time slice, $\mathbf{A}_{\tilde{G}}$, and edge feature vectors $\mathbf{x}_{(v,u)} \in \mathbb{R}^{T-1}$ that indicate, for each time step, whether edge (v, u) is active or not.

To incorporate temporal edge information, the model alternates between updating *edge* and *node* embeddings. First, edge embeddings are updated as

$$\mathbf{e}_{(v,u)}^{(l)} = \text{ReLU}\left(\mathbf{W}_l^1 \left[\mathbf{e}_{(v,u)}^{(l-1)} \| \mathbf{h}_u^{(l-1)} \right]\right), \quad l = 1, \dots, L, \quad (15)$$

followed by node embedding updates:

$$\mathbf{h}_v^{(l)} = \text{ReLU}\left(\mathbf{W}_l^2 \mathbf{h}_v^{(l-1)}\right) + \sum_{u \in \mathcal{N}(v)} \mathbf{e}_{(v,u)}^{(l)}. \quad (16)$$

A final dense layer maps each node embedding to a scalar, and a softmax activation yields a probability distribution over all nodes, representing the likelihood of each being the source. Accordingly, the model is trained using the multi-class cross-entropy loss.

5 Proposed Architecture

In this section, we introduce the GNN architecture proposed for the single-source detection problem on static networks with SIR dynamics. The design of our model is primarily informed by (i) the GNN design space analysis of You et al. [44] and (ii) the related GNN-based source detection approaches discussed in Sections 3 and 4. The architecture consists of four main components: a set of preprocessing layers, a sequence of message-passing layers, a set of postprocessing layers, and a final output layer. We begin by outlining the model design, then describe the network datasets and SIR process used to train the model, and finally present the results of our hyperparameter tuning. This section is intentionally comprehensive to ensure that our method and training process can be readily reproduced. All source code is publicly available on GitHub (<https://github.com/anon-author123/source-detection>).

5.1 Design

5.1.1 Pre- and Postpressing Layers

The inclusion of preprocessing and postprocessing layers in GNN architectures was advocated by You et al. [44]. Both types of layers apply a linear transformation followed by batch normalization (BN) and a parametric ReLU (PReLU) activation. The consistent use of PReLU and BN has been shown to be beneficial across various GNN tasks [44], motivating their use throughout our architecture. Formally, these layers are defined as:

$$\mathbf{h}_v^{(l)} = \text{PReLU}\left(\text{BN}\left(\mathbf{W}^{(l)} \mathbf{h}_v^{(l-1)} + \mathbf{b}^{(l)}\right)\right). \quad (17)$$

Below, we tune both the *number* of pre- and postprocessing layers (ranging from 0 to 2) and the embedding dimensionality of the preprocessing layers. The postprocessing layers adopt the embedding size of the final message-passing layer.

5.1.2 Message-Passing Layers

Between the preprocessing and postprocessing layers, we include a stack of message-passing (GNN) layers. We adopt the general graph convolution formulation introduced by Morris et al. [45], defined as:

$$\mathbf{h}_v^{(l)} = \text{PReLU}\left(\text{BN}\left(\mathbf{W}_1^{(l)} \mathbf{h}_v^{(l-1)} + \mathbf{W}_2^{(l)} \text{AGG}\left(\{\mathbf{h}_u^{(l-1)} : u \in \mathcal{N}(v)\}\right) + \mathbf{b}^{(l)}\right)\right). \quad (18)$$

Table 3: Overview of empirical networks. The middle part of the table reports the number of nodes, the number of edges, the average degree, the average shortest path length, the diameter, and the average local clustering coefficient for each network. The right part lists the infection rate β and the duration T until the snapshot was observed. Note that the Workplace and Highschool networks are originally temporal networks and we simply use their static projections.

Name	$ V $	$ E $	$\langle k \rangle$	$\langle l \rangle$	$\text{diam}(G)$	C	β	T
Karate [46]	34	77	4.53	2.42	5	0.54	1.300	0.85
Iceland [47]	75	114	3.04	3.20	6	0.29	5.100	0.34
Dolphin [48]	62	159	5.13	3.36	8	0.26	0.900	2.20
Fraternity [49, 14]	58	967	33.34	1.42	3	0.75	0.073	3.50
Workplace [50]	92	755	16.41	1.96	3	0.43	0.165	3.50
Highschool [51]	327	5818	35.58	2.16	4	0.50	0.065	7.50

Key design choices for this stage of the architecture include the number of message-passing layers, their embedding dimensionality, and the choice of aggregation function. We fix the aggregation function to *summation*, as prior work shows that it consistently outperforms alternatives such as *max* and *mean* [44]. Both the number of layers and embedding dimensionality are treated as tunable hyperparameters due to their strong dependence on graph structure and dataset characteristics. In particular, using too many layers can lead to oversmoothing, making node representations indistinguishable, while too few layers may limit the receptive field. You et al. [44] and the related work (Table 2) provide no definitive guidance on the optimal depth, further motivating our empirical exploration.

5.1.3 Output Layer

The output layer follows the same structure as the pre- and postprocessing layers (equation 17). Its weight matrix is shaped such that, for each node v , a linear transformation of the preceding embeddings yields a scalar value representing the predicted likelihood of node v being the epidemic source. A final log-softmax activation produces a normalized probability distribution across all nodes in the graph. Unlike in other graph-level prediction tasks, we do not apply global pooling operations, since any aggregation across nodes would eliminate the rich, node-specific information necessary for source detection.

Additionally, we include an optional skip connection from the input layer directly to the output layer. The original node features are concatenated with the final node embeddings before the last linear transformation. You et al. [44] report that such concatenation-based skip connections offer slight yet consistent performance gains over alternative types of skip connections. The complete architecture is illustrated schematically in Figure 2.

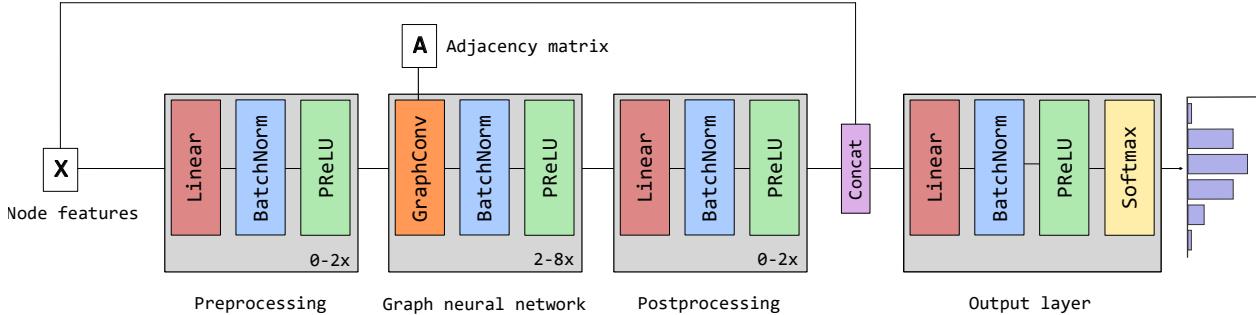


Figure 2: Proposed GNN model architecture. The four main components are enclosed in grey boxes. The numbers of preprocessing, message-passing, and postprocessing layers are tunable and may vary across datasets.

5.2 Network Data and SIR Process

We train our model on six static networks, most of which are well established in the network science literature. Their key structural characteristics, along with the epidemic parameters used in our experiments, are summarized in Table 3.

Without loss of generality, we fix the recovery rate to $\mu = 1$. The infection rate β is chosen such that the basic reproduction number $R_0 \approx 2$, ensuring comparable epidemic intensity across networks. The duration until the snapshot is observed, T , is selected such that, on average, roughly 40% of nodes are infected at the observation time.

Table 4: Dimensions of the design space. The left column lists the architecture and training hyperparameters. The middle column indicates the range of explored values. If only a single value is shown, the corresponding hyperparameter was held fixed at that value (e.g., batch normalization). The right columns report, for each network, the best-performing configuration. A dash (–) indicates non-applicability (e.g., when preprocessing layers were omitted). For the number of epochs, we report the epoch count at which early stopping was triggered.

Hyperparameter	Value(s) tested	Karate	Iceland	Dolphin	Frat.	Workpl.	Highschool
General architecture							
Number of preproc. layers	0–2	1	2	0	1	0	1
Embedding dim. (preproc.)	16, 32, 64	16	32	–	16	–	16
Number of postproc. layers	0–2	0	0	0	0	2	1
Skip connection	True, False	True	True	False	True	True	True
Batch normalization	True			— True —			
Activation	PReLU			— PReLU —			
Message-passing design							
Number of layers	2–8	3	6	5	2	8	3
Aggregation	Sum			— Sum —			
Embedding dim.	16, 32, 64, 128	16	32	64	128	128	64
Training hyperparameter							
Dropout rate	0.0, 0.1, 0.2, 0.3	0.1	0.1	0.1	0.2	0.0	0.1
Batch size	128			— 128 —			
Learning rate	0.001			— 0.001 —			
Weight decay	0.0005			— 0.0005 —			
Optimizer	ADAM			— ADAM —			
Number of epochs	500 (early stop.)	68	42	42	63	45	23

5.3 Hyperparameter Tuning

To identify the optimal hyperparameters, we perform a hyperparameter optimization using the well-known Optuna library [52]. As summarized in Table 4, we consider six tunable hyperparameters and one tunable training parameter, namely the dropout rate. While You et al. [44] recommend omitting dropout, we find that introducing a small amount improves training stability, therefore, we include it as a tunable variable.

Other training-related parameters are kept fixed, as the related work (Table 2) shows broad consensus regarding their choice. Specifically, we set the learning rate to 0.001, employ the ADAM optimizer with a small weight decay of 0.0005, and use a batch size of 128 to ensure stable gradient updates given our relatively small graphs. The maximum number of training epochs is set to 500, but we apply early stopping with a patience of five epochs. The loss function is the negative log-likelihood loss, which aligns with the log-softmax output activation.

For each of the six networks in Table 3, we run 50 trials within the Optuna framework. For each trial, epidemic realizations are simulated using the SIR model and parameters specified in Table 3. We generate 500 simulated outbreaks per potential source node, thus ensuring a balanced dataset. The resulting data are split in a stratified manner into 70% training and 30% validation data. Early stopping is based on the validation loss, and model performance for each hyperparameter configuration is measured as the average of the last five validation losses prior to termination.

The tuning results in Table 4 and Figure A.1 reveal several consistent patterns. Postprocessing layers offer little benefit in this setting, while a moderate amount of preprocessing can be beneficial. A skip connection and modest dropout values clearly improve performance. The right panels of Figure A.1 suggest a U-shaped relationship between dropout rate and validation loss, suggesting that optimal performance occurs for dropout rates between 0.1 and 0.2.

As expected, networks with relatively small diameters and short average path lengths achieve the best performance with 2–3 message-passing layers, whereas networks with larger diameters (Iceland and Dolphin) benefit from deeper architectures with five or more layers. One exception to this trend is the Workplace network, however, the corresponding plot in Figure A.1 indicates that the performance differences between two and eight layers are minor and may be attributable to random variation. Interestingly, the optimal embedding dimensionality for the message-passing layers varies substantially across networks, suggesting that the required level of expressiveness is problem-dependent. Overall, Figure A.1 also shows that the differences in average validation loss across hyperparameter settings for a given network are relatively small, implying that the GNN performance is fairly robust to suboptimal architectural choices.

6 Experiments

In this section, we present the results that address our core research questions. We begin by examining how detectability evolves as the time between outbreak and observation of the snapshot increases. We then turn to our central question: the actual potential of GNN-based source detection compared with a number of heuristic and probabilistic benchmarks. Finally, we analyze how performance scales with training set size for three approaches (including our GNN) and assess the importance of knowing the precise time interval between the outbreak and the observed snapshot.

We evaluate all results using top-5 accuracy, defined as the proportion of experiments in which the true source appears among the five highest-ranked nodes returned by a method. In the subsection comparing GNNs with heuristic and probabilistic benchmarks, we additionally report alternative evaluation metrics, highlighting that the choice of performance measure for source detection is itself a nontrivial consideration.

6.1 Detectability of Source

The detectability of the epidemic source has previously been examined by Shah and Zaman [10], who analyzed their rumor-source estimator on tree graphs. They showed theoretically that, for nontrivial graph structures and the SI model, the probability of correctly identifying the source does not converge to zero as time progresses. Instead, it approaches a strictly positive limit. Antulov-Fantulin et al. [25] studied detectability from a different angle by computing the normalized Shannon entropy of their source-probability estimates. Their results on lattice graphs suggest that higher infection probabilities, *ceteris paribus*, lead to greater detectability because outbreak patterns become more distinct across candidate sources, an effect that only manifests when the network is sufficiently large to avoid constraining the spread.

Some GNN-based related works touch on detectability as well, though in indirect ways. For instance, Dong et al. [11] perform inference after 30% of nodes have become infected, while Haddad and Figueiredo [17] do so after 20%. The underlying idea is to choose an epidemic duration that yields non-trivial but not overly extensive outbreaks that may severely hamper detectability. Consistent with this intuition, we set T such that, on average, roughly 40% of nodes are infected, striking a balance between complexity of the outbreaks and detectability.

To complement prior work, we conduct experiments on our six empirical networks. Keeping R_0 fixed (as specified in Table 3), we evaluate the detection performance of our GNN and a simple baseline across increasing values of T (Figure 3). The resulting outbreak dynamics differ markedly across the networks despite identical R_0 calibration. For example, in the relatively sparse Iceland network (Figure 3b), achieving $R_0 \approx 2$ requires a high infection rate, causing outbreaks to propagate quickly and ultimately infect about 75% of the nodes, on average.

In line with the second law of thermodynamics and prior empirical findings, we expect detectability to deteriorate as T increases. Moreover, Antulov-Fantulin et al. [25] note, that increasing T , combined with the modest size of our networks, reduces the distinctiveness of outbreak patterns, making sources harder to distinguish. This expectation is confirmed by the results in Figure 3: top-5 accuracy decreases with T for both the GNN and the baseline. More importantly, the GNN consistently converges to a higher accuracy than the baseline across all networks, indicating that the GNN can still yield benefits even when inference is performed relatively late in the outbreak. Finally, the fact that the GNN’s accuracy does not collapse to the random baseline may reflect the theoretical result of Shah and Zaman [10], who showed that detectability remains bounded away from zero at later times.

6.2 Comparison with Benchmarks

In this subsection, we address the central question of this paper: do GNNs truly outperform traditional source-detection methods? The suitability of GNNs for this task has been questioned [36], and the existing literature remains inconclusive regarding their true potential in source detection. A major reason is that prior work (focused on the single-source setting) has primarily compared GNNs with heuristic approaches (e.g., the Jordan center) or with the dynamic message passing (DMP) method introduced by Lokhov et al. [28]. Only one study [18] incorporates the soft margin estimator (SME), a notable contribution by Antulov-Fantulin et al. [25].

Moreover, broader concerns persist regarding the feasibility of learning-based approaches for this problem [36], particularly in light of their potentially high training and inference costs. Our objective in this subsection is therefore to provide results that enable a more definitive assessment of the suitability of GNN-based methods for source detection. To this end, we compare GNN models against a diverse set of established benchmarks and design our evaluation to be as transparent and reproducible as possible.

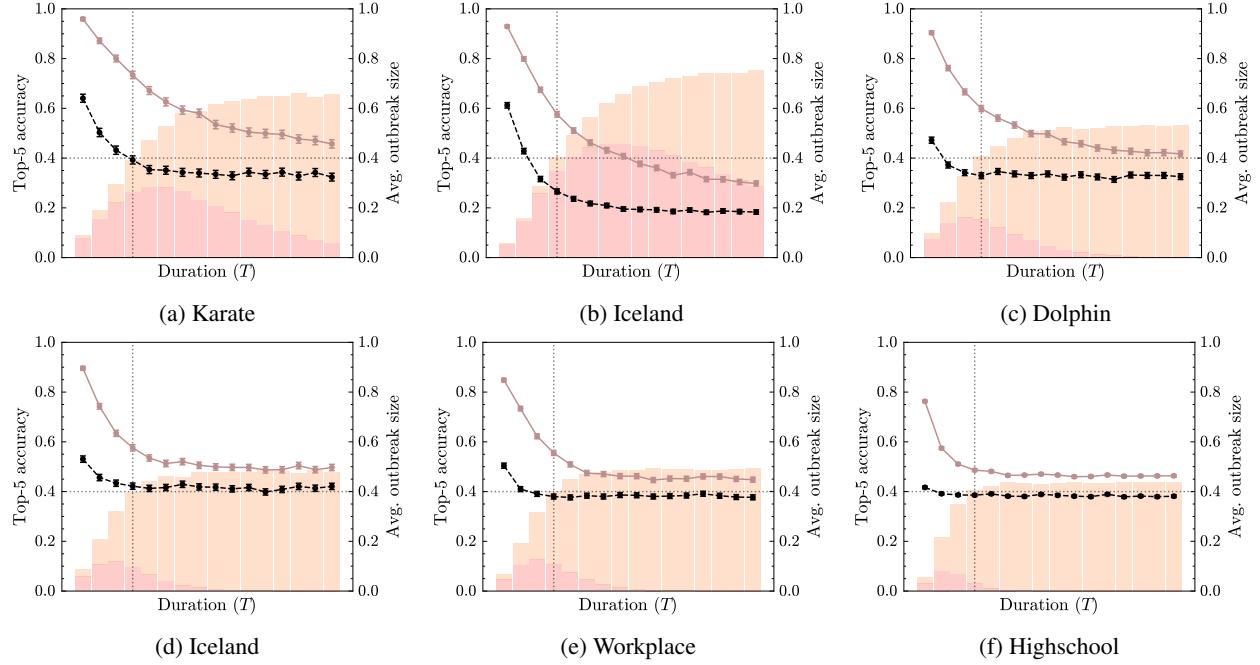


Figure 3: Source detection performance across outbreak durations T . Each plot reports top-5 accuracy for our GNN architecture and for a baseline that selects the source uniformly at random from the infected subgraph. Bars indicate the average proportion of infectious and recovered nodes at each duration (secondary y-axis). In each plot, the fourth bar (marked by dotted lines) corresponds to the value of T at which approximately 40% of all nodes are infected. Units of time are omitted, as the absolute values of durations are not relevant.

6.2.1 Benchmark Methods

Our simplest baseline, referred to as Random, selects an estimated source uniformly at random from all nodes in the infected subgraph. We then consider two purely topological heuristics: the Jordan center [20] and the node with the highest betweenness centrality within the infected subgraph (Betweenness). Although we also evaluated degree- and closeness-based heuristics, betweenness centrality consistently yielded the strongest performance among them.

To incorporate probabilistic methods into the comparison, we evaluate the soft margin estimator (SME) [25] as well as the Monte Carlo mean field (MCMF) approach [27] (see Appendix for details). The SME has the appealing property that, as the number of simulations per potential source increases, it converges to direct Monte Carlo estimation and should, in principle, recover the true likelihood of each source node eventually. In practice, however, achieving this regime is computationally infeasible except for very small graphs. MCMF is conceptually similar to dynamic message passing (DMP) [28] but can be more computationally efficient, mitigating some of the scalability limitations reported for DMP [12]. With a sufficiently large number of simulations, MCMF also tends to yield more accurate estimates of node state probabilities than DMP. Importantly, SME and MCMF are both computed using the same set of simulated outbreaks that serve as training data for the GNNs, ensuring that all methods operate on the same data substrate.

6.2.2 Data Augmentation

Several related works [11, 17, 38] emphasize the potential importance of data (feature) augmentation. However, empirical evidence assessing its impact on source detection is largely lacking, particularly in [11, 17]. Furthermore, it is not obvious whether data augmentation is necessary in this setting at all, given that GNNs are typically capable of learning rich representations of local node neighborhoods.

In this work, we evaluate a simple form of augmentation: each node is augmented with its degree, betweenness centrality, closeness centrality, and the local clustering coefficient. Thus, the feature vector for every node consists of the one-hot encoded observed epidemic state together with these four additional measures. We report GNN performance both with and without this augmentation.

6.2.3 Results

We adopt the same experimental setup as described in Section 5. To evaluate the different source detection methods, we simulate an additional 100 outbreak scenarios per node, using the same epidemic parameters as those used for generating the training data. Several performance metrics are available for assessing the methods. Given our fully balanced experimental design, accuracy-based metrics commonly used in related work [12, 14, 16, 18] are appropriate. Specifically, we report the previously introduced top-5 accuracy. In addition, we compute the average error distance [15], which measures the mean shortest-path distance between the true and the estimated MAP source. As a third metric, we use the average reciprocal rank [14], where the reciprocal of the true source’s rank ensures that higher values correspond to better performance. Our fourth metric, the average 90% credible set size [53], applies only to methods that output probability distributions and quantifies the sharpness of those distributions by measuring the number of nodes required to accumulate at least 90% posterior probability mass. Finally, we evaluate performance using the Resistance score, a novel proper scoring rule for distributions on graphs that balances rewarding accuracy with avoiding overconfidence and generally encourages an honest uncertainty quantification (lower values indicate better performance) [54]. For each network, we trained the optimally calibrated GNN three times, using different random seeds for both the training data and weight initialization. The results reported in Table 5 are averaged over these three runs.

The most striking finding is that GNNs substantially outperform all other methods across all relevant evaluation measures, with the exception of the average error distance. More generally, probabilistic approaches (including GNNs) consistently outperform heuristic baselines and the random baseline. The results also show no clear benefit from data augmentation. However, because we tested only a small set of simple features, more extensive feature engineering may still yield improvements.

The findings further underscore the limitations of methods such as MCMF, which rely on strong independence assumptions when computing source likelihoods. Although MCMF achieves competitive detection accuracy and typically trails only the GNN, its probability mass tends to be overly concentrated on a small subset of nodes, as reflected by its small 90% credible set sizes. As a consequence, when MCMF is wrong, it often assigns very little or no probability to the true region of the network. This weakness is also evident in the Resistance scores, where MCMF consistently underperforms the GNN. SME, by contrast, may be limited by the relatively small sample size used here (500 simulations per node), as it is expected to surpass mean-field-based approaches when sufficiently large samples are available.

Finally, the values reported in Table 5 reflect aggregated performances across a wide range of outbreak scenarios. This is further illustrated in Figure 4, which plots the top-5 accuracy of all methods for varying outbreak sizes on the Karate network. Notably, the GNN attains its largest performance gains in medium to large outbreak scenarios that are far from trivial.

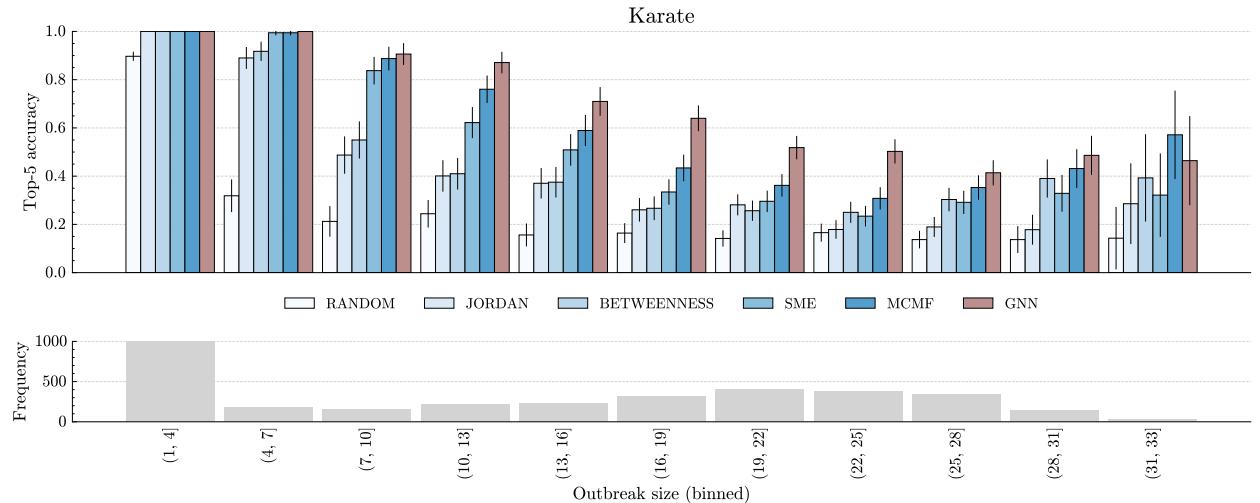


Figure 4: Detection performance by outbreak size for the Karate network. The upper plot reports the top-5 accuracy of the different source detection methods across outbreak categories, defined by outbreak size. Error bars denote 95% confidence intervals. The lower plot depicts the absolute frequency of outbreaks within each category. The total number of outbreaks is 3,400.

Table 5: Performance of different source detection methods across six network datasets. Test sets are generated by simulating 100 outbreaks from each node in the network. All performance measures are averaged over three runs, each using a different random seed. The 95% confidence intervals shown in parentheses reflect the uncertainty across these runs. For each metric (except CSS), the best-performing method is highlighted in bold. The performance of the GNN and the GNN with data augmentation (DA) is highlighted in red.

Dataset	Model	Top-5 accuracy	Error dist.	Rec. rank	90% CSS	Resistance
Karate	Random	39.15% ($\pm 0.41\%$)	1.33 (± 0.0049)	0.35 (± 0.0017)	-	-
	Jordan	52.48% ($\pm 0.46\%$)	1.08 (± 0.0038)	0.40 (± 0.0000)	-	-
	Betweenness	55.40% ($\pm 0.11\%$)	0.91 (± 0.0007)	0.43 (± 0.0000)	-	-
	SME	60.20% ($\pm 0.65\%$)	1.07 (± 0.0108)	0.48 (± 0.0028)	6.13 (± 0.12)	0.2980 (± 0.0042)
	MCMF	65.45% ($\pm 0.17\%$)	0.90 (± 0.0089)	0.51 (± 0.0020)	3.61 (± 0.05)	0.2490 (± 0.0011)
	GNN	73.31% ($\pm 0.27\%$)	0.95 (± 0.0167)	0.55 (± 0.0016)	9.42 (± 0.15)	0.2155 (± 0.0002)
	GNN (DA)	73.28% ($\pm 0.11\%$)	0.94 (± 0.0217)	0.55 (± 0.0010)	9.35 (± 0.12)	0.2154 (± 0.0004)
Iceland	Random	26.56% ($\pm 0.34\%$)	1.95 (± 0.0133)	0.24 (± 0.0001)	-	-
	Jordan	35.72% ($\pm 0.16\%$)	1.44 (± 0.0042)	0.28 (± 0.0000)	-	-
	Betweenness	37.47% ($\pm 0.25\%$)	1.25 (± 0.0007)	0.30 (± 0.0000)	-	-
	SME	45.75% ($\pm 0.14\%$)	1.51 (± 0.0047)	0.37 (± 0.0013)	13.73 (± 0.15)	0.6741 (± 0.0028)
	MCMF	50.92% ($\pm 0.11\%$)	1.37 (± 0.0053)	0.40 (± 0.0011)	4.96 (± 0.07)	0.6067 (± 0.0012)
	GNN	57.82% ($\pm 0.06\%$)	1.45 (± 0.0454)	0.43 (± 0.0019)	18.50 (± 0.56)	0.5265 (± 0.0002)
	GNN (DA)	58.21% ($\pm 0.25\%$)	1.34 (± 0.0124)	0.44 (± 0.0008)	18.00 (± 0.15)	0.5268 (± 0.0011)
Dolphin	Random	33.09% ($\pm 0.12\%$)	1.76 (± 0.0091)	0.31 (± 0.0013)	-	-
	Jordan	41.29% ($\pm 0.27\%$)	1.44 (± 0.0037)	0.35 (± 0.0000)	-	-
	Betweenness	43.11% ($\pm 0.03\%$)	1.39 (± 0.0015)	0.37 (± 0.0000)	-	-
	SME	45.39% ($\pm 0.31\%$)	1.48 (± 0.0062)	0.39 (± 0.0011)	13.03 (± 0.27)	0.2820 (± 0.0004)
	MCMF	51.31% ($\pm 0.40\%$)	1.22 (± 0.0095)	0.43 (± 0.0022)	5.11 (± 0.07)	0.2710 (± 0.0013)
	GNN	60.31% ($\pm 0.51\%$)	1.20 (± 0.0757)	0.48 (± 0.0028)	14.79 (± 0.44)	0.2124 (± 0.0006)
	GNN (DA)	60.63% ($\pm 0.50\%$)	1.15 (± 0.0077)	0.48 (± 0.0016)	15.49 (± 0.52)	0.2131 (± 0.0008)
Fraternity	Random	42.15% ($\pm 0.06\%$)	0.81 (± 0.0036)	0.40 (± 0.0011)	-	-
	Jordan	50.56% ($\pm 0.55\%$)	0.77 (± 0.0033)	0.42 (± 0.0000)	-	-
	Betweenness	51.94% ($\pm 0.05\%$)	0.66 (± 0.0006)	0.45 (± 0.0000)	-	-
	SME	51.47% ($\pm 0.11\%$)	0.77 (± 0.0006)	0.46 (± 0.0021)	6.51 (± 0.22)	0.0291 (± 0.0002)
	MCMF	54.51% ($\pm 0.18\%$)	0.69 (± 0.0031)	0.48 (± 0.0018)	6.35 (± 0.14)	0.0240 (± 0.0002)
	GNN	57.14% ($\pm 0.57\%$)	0.77 (± 0.0598)	0.50 (± 0.0006)	16.66 (± 0.17)	0.0199 (± 0.0000)
	GNN (DA)	57.05% ($\pm 0.22\%$)	0.81 (± 0.0354)	0.50 (± 0.0027)	16.56 (± 0.24)	0.0199 (± 0.0001)
Workplace	Random	37.84% ($\pm 0.10\%$)	1.16 (± 0.0008)	0.37 (± 0.0014)	-	-
	Jordan	45.28% ($\pm 0.04\%$)	1.02 (± 0.0020)	0.40 (± 0.0000)	-	-
	Betweenness	46.21% ($\pm 0.04\%$)	0.93 (± 0.0006)	0.41 (± 0.0000)	-	-
	SME	46.16% ($\pm 0.22\%$)	1.11 (± 0.0020)	0.42 (± 0.0013)	6.16 (± 0.18)	0.0685 (± 0.0005)
	MCMF	49.56% ($\pm 0.09\%$)	0.93 (± 0.0055)	0.45 (± 0.0011)	3.93 (± 0.43)	0.0583 (± 0.0011)
	GNN	54.90% ($\pm 0.76\%$)	1.00 (± 0.0982)	0.48 (± 0.0044)	22.30 (± 1.71)	0.0465 (± 0.0001)
	GNN (DA)	54.65% ($\pm 0.19\%$)	1.00 (± 0.0793)	0.47 (± 0.0040)	22.68 (± 1.28)	0.0472 (± 0.0006)
Highschool	Random	38.48% ($\pm 0.08\%$)	1.22 (± 0.0023)	0.38 (± 0.0007)	-	-
	Jordan	46.42% ($\pm 0.01\%$)	1.19 (± 0.0012)	0.41 (± 0.0000)	-	-
	Betweenness	46.66% ($\pm 0.01\%$)	1.02 (± 0.0007)	0.42 (± 0.0000)	-	-
	SME	46.64% ($\pm 0.02\%$)	1.19 (± 0.0003)	0.43 (± 0.0003)	26.05 (± 5.99)	0.0265 (± 0.0007)
	MCMF	46.92% ($\pm 0.06\%$)	1.03 (± 0.0176)	0.43 (± 0.0006)	1.66 (± 0.33)	0.0281 (± 0.0009)
	GNN	48.67% ($\pm 0.20\%$)	1.11 (± 0.0553)	0.45 (± 0.0019)	95.00 (± 1.66)	0.0199 (± 0.0000)
	GNN (DA)	48.61% ($\pm 0.27\%$)	1.12 (± 0.0890)	0.44 (± 0.0026)	96.89 (± 3.14)	0.0199 (± 0.0000)

6.2.4 Single Scenarios

To gain deeper insight into the detection quality of the GNN and its comparison to MCMF and SME, we examine two specific outbreak scenarios: one on the Karate network (Figure 5) and another on the Iceland network (Figure 6).

In Figure 5, we observe a relatively large outbreak on the Karate network (23 infected nodes). The true source node (0) is centrally located and has already recovered, making it a likely source candidate. Accordingly, both the GNN and MCMF assign it high probability, with MCMF concentrating a large portion of its probability mass on this node, reflecting the fact that the product of node state probabilities computed for node 0 is maximal. However, other plausible source candidates, such as nodes 11, 17, and 21, are assigned virtually no probability by MCMF. Their lower centrality

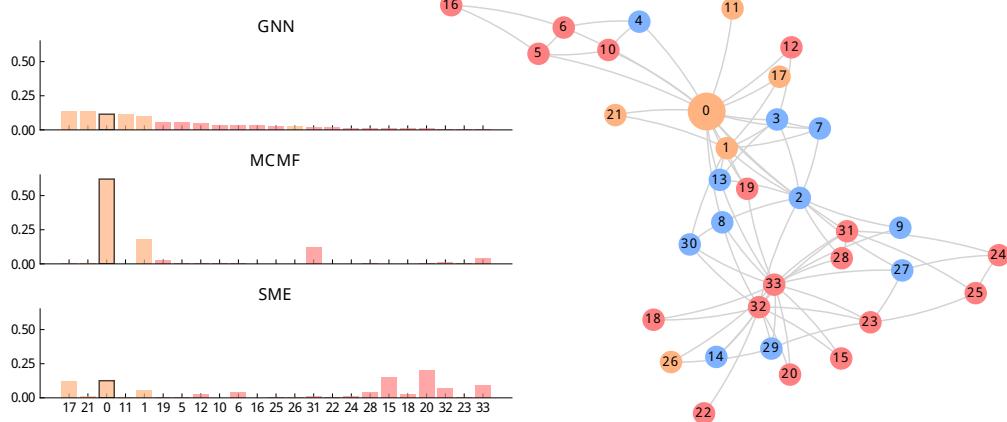


Figure 5: Example outbreak scenario on the Karate network. The plot on the right depicts the network, with node colors indicating epidemic states (blue: susceptible, red: infectious, orange: recovered). The true source node (0) is emphasized by a larger size. The three bar plots on the left show the source predictions of the GNN (top), MCMF (middle), and SME (bottom). Nodes on the x-axis are ordered by descending GNN probabilities, and the true source is highlighted with a dark frame. Susceptible nodes are not included in the distributions.

results in state probability products that are orders of magnitude smaller than those of more central nodes such as 0, 1, 31, and 33. By contrast, the GNN distributes probability mass more smoothly across nodes in the infected subgraph, favoring recovered nodes while accounting for the local density of infectious and recovered neighbors. For example, although node 26 has recovered, it is surrounded by infectious and susceptible nodes only, leading the GNN to assign it lower probability. The output of SME is less clear and may reflect instabilities due to the small sample size and the convergence condition (see Appendix).

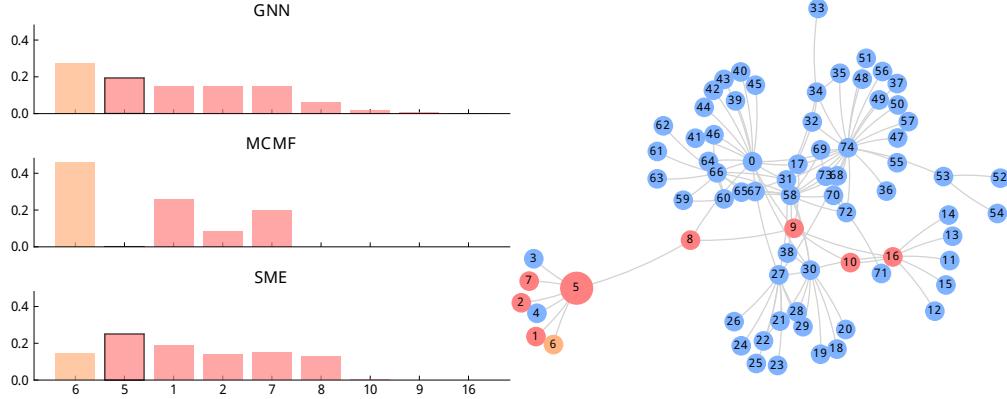


Figure 6: Example outbreak scenario on the Iceland network. The description provided for Figure 5 applies here as well.

In Figure 6, we consider a small outbreak on the Iceland network (9 infected nodes). Here, the GNN ranks the true source node (5) as the second most likely source, while MCMF assigns it negligible probability mass. The direct connection of node 5 to the susceptible nodes 3 and 4 makes the product of node state probabilities comparatively small. Interestingly, the GNN correctly assigns equal probability to nodes 1, 2, and 7, which are topologically indistinguishable relative to the rest of the network. MCMF, however, assigns different probabilities to these nodes, likely reflecting small variations in the estimated node state probabilities due to Monte Carlo sampling. SME exhibits a similar discrepancy among nodes 1, 2, and 7, but, unlike MCMF, successfully identifies node 5 as the true source.

6.3 Training Data

In this final subsection, we examine two aspects related to the generation of training data, which affects not only the GNN but also MCMF and SME. First, we investigate how the detection performance of these three methods scales with the number of simulations per source node. To the best of our knowledge, no prior work has explored this question.

Second, we relax the assumption that the exact time between the outbreak and the observation of the snapshot (denoted by T) is known, and we assess how uncertainty in T influences detection performance.

6.3.1 Scaling the Training Data

The size of the training (and validation) data, i.e., the number of simulated outbreak scenarios, has received relatively little attention in related work on GNN-based source detection and has often been treated as a negligible hyperparameter. In several studies, the training set size is not reported at all [11, 17], while others adopt widely varying dataset sizes, ranging from 1,000 [15] to 20,000 [12, 18] simulated scenarios. Typically, these works further withhold a subset of the simulations for validation and testing. Crucially, however, all prior studies appear to choose the training set size independently of the underlying graph size. In this paper, we argue that training data size should be determined on a per-node basis. Throughout most of our analysis, we therefore use a training/validation set size of 500 simulated scenarios per (source) node. For example, a graph with 50 nodes leads to a total of 25,000 training (and validation) samples, already exceeding the dataset sizes commonly used in related work.

Figure 7 reports the top-5 accuracy across the six networks as the number of simulations per node increases by an order of magnitude (followed by a final doubling) starting from 50 simulations per node. Overall, detection performance improves as the sample size grows. For both GNN and MCMF, the most substantial gains are observed when increasing the number of simulations from 50 to 500 per node. In contrast, the trend for SME is less pronounced. In principle, however, SME should (at least for SI dynamics) converge to the true likelihood of each candidate source node as the number of simulations grows large, a regime not reached in our experiments because we were not able to choose n large enough and because we consider SIR dynamics. Most importantly, the results indicate that increasing the number of simulations beyond 500 per node yields only marginal improvements in detection performance, suggesting that the associated computational cost cannot be justified.

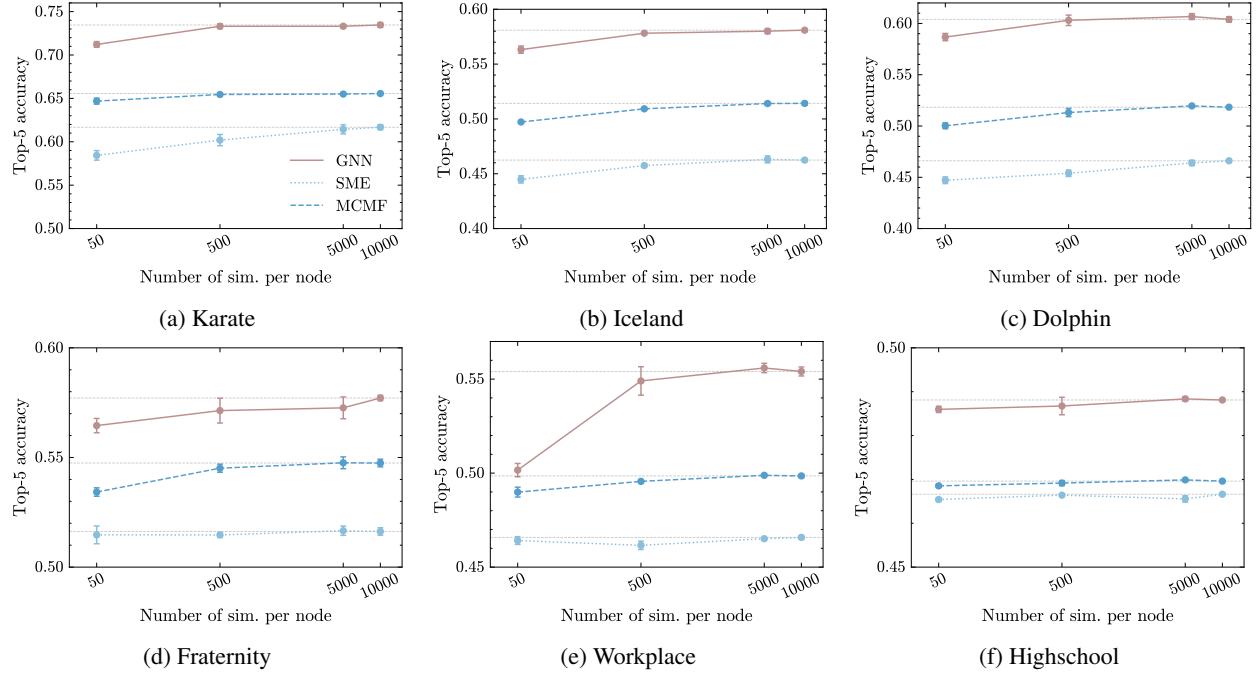


Figure 7: Detection performance, measured by top-5 accuracy, across all six networks for the three methods GNN, SME, and MCMF. All performance measures are averaged over three runs, each using a different random seed. Results are shown for four sample sizes, corresponding to the number of simulations per node. Horizontal dashed lines indicate the performance achieved with the largest sample size. Error bars denote 95% confidence intervals, reflecting uncertainty across runs.

6.3.2 Uncertainty in Time until Snapshot Observation

Another factor that receives little attention in related work is the assumption that the starting time of the outbreak (t_0), or, equivalently, the time between the outbreak and the observed snapshot (T), is known. This assumption allows us

to simulate training data for the same period of time as for the test outbreaks. In practice, however, it is unrealistic: typically only rough estimates of how long a disease has been spreading are available.

A notable exception is the work by Ru et al. [18], who investigate uncertainty in the knowledge of t_0 . Their method requires specifying an interval within which the outbreak is assumed to have started, and simulations are generated using a uniformly sampled starting time from this interval. However, their study does not quantify the effect of relaxing the known- t_0 assumption on model performance.

In our analysis, we relax this assumption as follows: for each training and validation instance, we sample a value of T uniformly from the interval $(0, 4T^*]$, where T^* is the true elapsed time used when generating test instances. This setup mimics a scenario in which knowledge of T and t_0 is noisy at best. Moreover, it even introduces systematic bias as the sampled values of T have mean $2T^*$. Figure 8 presents the results. As expected, this uncertainty and bias in T leads to reduced performance across all networks and nearly all methods. SME, however, seems to be less affected by the relaxation of this assumption than the GNN and MCMF. Notably, the GNN performance remains above the benchmark levels even under this relaxation.

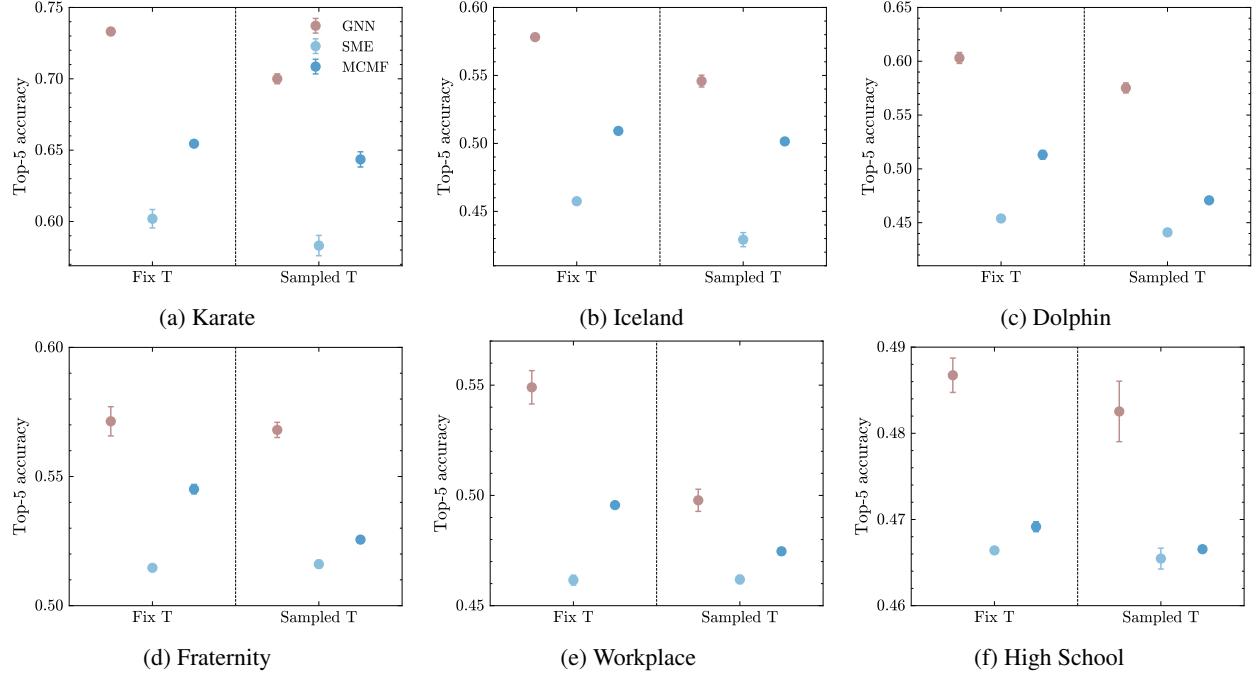


Figure 8: Detection performance, measured by top-5 accuracy, across all six networks and for the three methods GNN, SME, and MCMF. All performance measures are averaged over three runs, each using a different random seed. Performance is shown for a fix, known duration T until the snapshot is observed (left) and an uncertain, sampled duration T until the snapshot is observed (right). Error bars represent 95% confidence intervals, reflecting uncertainty across runs.

7 Computational Complexity

The time complexity of source detection methods can be divided into three main components: (i) the generation of training data through simulation, (ii) the model training (only applicable to GNNs), and (iii) inference, i.e., applying one of the methods to detect the source.

7.1 Simulation of Training Data

This step is required by GNNs, SME, and MCMF, all of which rely on a set of simulated outbreak scenarios. In the worst case, generating these simulations has time complexity $\mathcal{O}(nN\bar{r})$, where n denotes the number of simulations per source node and \bar{r} is the worst-case runtime of a single simulation. In our paper, we employ the static-network variant of the fast (event-driven) simulation algorithm proposed by Holme [55] (see Appendix). Its worst-case complexity, derived from [55], is $\mathcal{O}(N^2 \log N)$: $\mathcal{O}(N \log N)$ arises from operating the priority queue for the algorithm, while

Table 6: Average run times in seconds. For the simulations, the reported values correspond to the average run time per simulation. GNN training times are reported on a per-batch basis. Inference times represent the average time per test instance. For reference, all experiments were conducted on a machine equipped with an AMD Ryzen Threadripper PRO (24 cores), 128 GB of RAM, and a single RTX 5080 GPU with 16 GB of VRAM.

Network	Simulations	GNN		SME	MCMF
		Training	Inference	Inference	Inference
Karate	0.000001	0.0037	0.0028	0.0026	0.0017
Iceland	0.000003	0.0122	0.0049	0.0933	0.0140
Dolphin	0.000003	0.0044	0.0044	0.0530	0.0140
Fraternity	0.000005	0.0034	0.0046	0.0568	0.0144
Workplace	0.000006	0.0080	0.0069	0.1337	0.0156
Highschool	0.000039	0.0259	0.0297	0.2207	0.0784

an additional factor of N accounts for the worst-case cost of iterating over all neighbors of each node in the queue. Consequently, constructing the full training dataset incurs a worst-case time complexity of $\mathcal{O}(nN^3 \log N)$.

7.2 Model Training

To simplify the complexity analysis, and because hyperparameter tuning showed that pre- and post-processing layers are used infrequently, we focus on the message-passing layers of the GNN. Using a convolutional message-passing architecture, we adapt the complexity analysis of Wu et al. [56]. The (worst-case) cost of a full forward pass over all L layers is $\mathcal{O}(L \cdot (N^2 s + 2Ns^2))$, where s denotes the embedding dimension. The first term in the sum captures the neighborhood aggregation, while the second term accounts for the two linear transformations in the update equation (see equation 18). Following Bajaj et al. [57], we approximate the cost of a combined forward and backward pass as a multiplicative factor $(1 + \eta)$ of the forward-pass cost. The total training cost must be further scaled by the batch size B (since each pass processes B identical graphs), the number of batches, and the number of training epochs.

7.3 Inference

The inference complexity for a single outbreak snapshot varies by method. For GNNs, inference consists of a single forward pass, as described above. For MCMF, inference requires summing (logarithmic) node state probabilities over all nodes for each potential source node, yielding a complexity of order $\mathcal{O}(N^2)$. This, however, assumes that these node state probabilities are already computed: obtaining them incurs an additional (one-time) cost of order $\mathcal{O}(N^2)$. For SME, the bottleneck lies in computing the Jaccard distance between the observed outbreak and each simulated outbreak, resulting in a complexity of order $\mathcal{O}(nN)$ (see Supplemental Material of [25]).

7.4 Empirical Results

Table 6 reports the average run times for the outbreak simulations, GNN training, and inference for the GNN, MCMF, and SME. The empirical cost of generating the simulations is negligible across all networks. As expected, however, these run times generally increase with the network size N , with the notable exception of the relatively small Fraternity network, whose comparatively high computational cost is likely due to its high density.

Although all three methods incur the cost of generating simulated training data, only the GNN requires an additional, typically substantial, computational cost for model training. Table 6 shows that the average per-batch training time for the Highschool network is considerably higher than for the other networks. Owing to differences in the chosen model architectures, however, these training times are not directly comparable across networks.

Finally, the theoretical analysis above indicates that the dominant inference cost for the GNN and MCMF scales as $\mathcal{O}(N^2)$, whereas for SME it scales as $\mathcal{O}(nN)$. Table 6 shows that, with the exception of the Karate network, the GNN exhibits the lowest inference time among the three methods, largely due to highly optimized forward-pass operations. Moreover, since $n > N$ for all networks in our experimental setting, SME incurs a substantially higher empirical inference cost than MCMF.

8 Real-World Case

As a real-world demonstration, we consider the global spread of the 2009 H1N1 (“swine flu”) pandemic. It is well established that the outbreak originated in Mexico [31]. The observed snapshot can be created by considering the arrival times of the virus in 91 countries obtained from Table S4 of Brockmann and Helbing [31]. We re-centered these reported arrival times such that Mexico has arrival time zero, and all other countries’ values represent the number of weeks after initial detection in Mexico.

8.1 Network

To construct a data-driven mobility network, we used the global airline transportation network derived from OpenFlights data (<https://openflights.org/data>) from 2014. Although data for 2009 were unavailable, we assume that large-scale global airline connectivity patterns did not change in ways that would invalidate the present analysis. We aggregated the airline data at the country level, yielding a network in which nodes correspond to countries. Following [31], we treated all connections as undirected and defined the weight of an edge as the total number of airline connections between the corresponding pair of countries. The strongest connection in the network is between Spain and the United Kingdom, with 1030 daily flights. The resulting network is undirected and weighted, comprising 225 nodes and 2317 edges. It is fully connected, with an average degree of 20.60, a diameter of 5, an average shortest-path length of 2.33, and an average clustering coefficient of 0.65.

8.2 Epidemic Model

Instead of employing a metapopulation framework as is common in such use cases [58, 31], we generated synthetic training data using a simple SI model with no recovery. The base infection rate was set to 1 and was, for each edge, adjusted proportional to the edge weight. For each potential source node, we simulated 500 outbreak realizations and the duration of the simulated outbreaks was chosen such that approximately 45 countries (roughly half of the 92 countries reported to have been affected during the actual pandemic) were infected, on average.

8.3 Results

We trained a GNN using the hyperparameters identified in Subsection 5.3: a dropout rate of 10%, five message-passing layers with embedding dimension 64, and a skip connection. After training, the GNN was applied to epidemic snapshots at multiple stages of the spreading process. For comparison, we also computed source probability distributions using SME and MCMF, applied to the same simulation data as the GNN. The results are presented in Figure 9.

Figure 9b shows the inferred rank of Mexico in the source distribution over time. The GNN assigns Mexico lower ranks than the other two methods for up to 19 weeks after the outbreak, after which SME achieves a better performance. Figure 9c displays the full source distributions at week 12. Across all three methods, probability mass concentrates on a small set of countries: Costa Rica, El Salvador, Mexico, and Cuba. Inspection of the airline network (Figure 9a) suggests two plausible source clusters, one in Central America and the other in Western Europe. Notably, all three methods assign overwhelmingly higher probability to the Central American cluster.

9 Conclusions

This study set out (i) to review existing work on the use of GNNs for epidemic source detection and (ii) to assess their effectiveness for this task. Our analysis reveals several limitations in the related literature. In particular, comparisons with classical methods are often incomplete and, in some cases, methodologically flawed. Against this backdrop, our empirical results demonstrate that GNNs perform remarkably well at detecting the source of an epidemic across a diverse set of network topologies. In all considered settings, the main contenders MCMF and SME are clearly outperformed. For MCMF, the underlying independence assumption results in source distributions that fail to adequately capture uncertainty across candidate sources. For SME, achieving competitive performance requires a prohibitively large number of simulated outbreaks, rendering the method computationally inefficient in practice. Moreover, our scaling experiments indicate that GNN performance saturates after a moderate number of simulations per node, suggesting that further increases in simulation effort yield diminishing returns. Finally, while we provide some general findings on the optimal GNN architecture, our results indicate that performance is not overly sensitive to specific architectural choices.

We hope that the present work provides useful guidance for future research on epidemic source detection. First, we caution against describing GNN-based source detection methods as (spreading-) model-agnostic. Instead, we advocate for systematic investigations of robustness to model misspecification in order to meaningfully assess sensitivity to

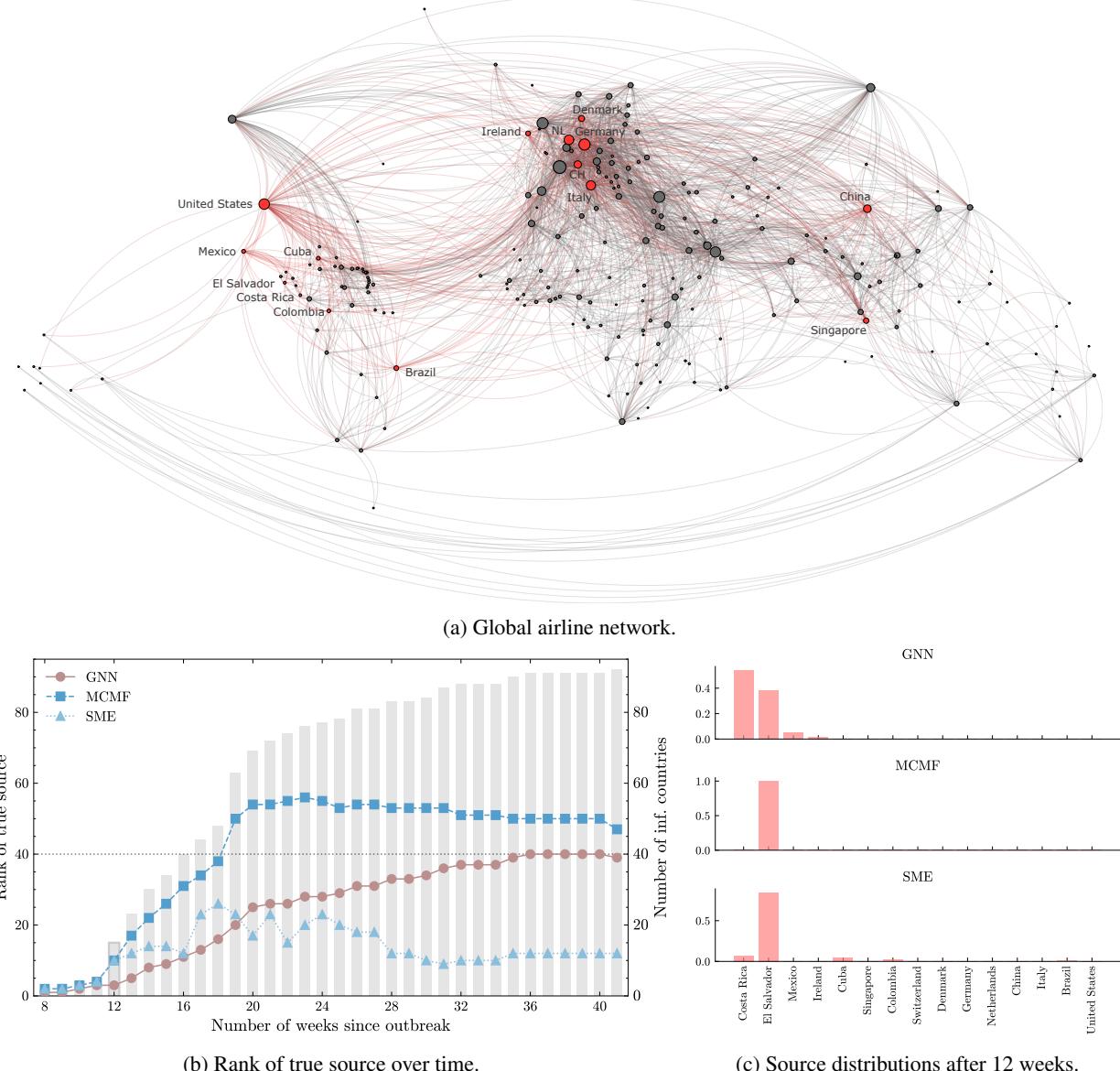


Figure 9: Source detection results for the 2009 H1N1 (swine flu) pandemic. (a) Global airline transportation network (in 2014), aggregated at the country level. Mexico is the known origin of the outbreak. The 15 countries shown in red (and labeled) correspond to those reported as infected 12 weeks after the initial detection in Mexico. (b) Rank of the true source (Mexico) over the course of the pandemic for the three source-detection methods considered. Bars (right y-axis) denote the number of infected countries at each point in time. (c) Source probability distributions inferred by the GNN, MCMF, and SME at week 12, corresponding to the set of 15 infected countries highlighted in panel (a). Countries along the x-axis are sorted in decreasing order of GNN source probabilities.

incorrect spreading dynamics or parameters. Second, our results suggest that the number of simulated outbreaks should be determined on a per-node basis rather than globally, as this choice has important implications for both performance and computational cost and should take the graph size into account. Finally, we argue that epidemic source detection constitutes an interesting benchmark task for evaluating GNN architectures. In its single-source formulation, the problem naturally corresponds to a multi-class graph prediction task. An attractive feature of this task is that training and test data can be generated synthetically and efficiently for common spreading models such as SI, SIR, or SEIR, allowing precise control over data scale and structure. While we currently release code and network data, future work will focus on providing additional resources and evaluation protocols to further establish epidemic source detection as a benchmark task.

Several directions for future research remain open. A more comprehensive understanding of how training set size affects GNN performance, as well as that of competing methods, is still needed. Recent work on scaling laws, largely motivated by the success of large language models [59], suggests that jointly increasing training data and model capacity can lead to substantial performance improvements. While our study explores the effects of scaling the training data alone, we leave a systematic investigation of simultaneous architectural scaling for future work. In addition, source detection performance should be studied as a function of graph size and structural properties, potentially using synthetic graph models to disentangle these effects. Finally, the more challenging multi-source detection problem remains underexplored, with open questions ranging from the inference of the number of sources to the development of appropriate evaluation metrics.

While the present study is primarily academic in nature, our application to a real-world case study yields promising and practically relevant results. We therefore view this work as a step toward making GNN-based epidemic source detection methods applicable in real-world settings and intend to continue pursuing this direction in future research.

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A Benchmark Methods

A.1 Monte Carlo Simulations of SIR on Static Networks

We employ a fast, event-driven simulation method for static networks in continuous time, implemented in C by Holme [60]. An extension of this algorithm to temporal networks is described in detail in a paper [55].

The key idea of the algorithm is to manage infection events using a priority queue (implemented in practice as a binary heap). The core simulation loop proceeds by removing the node v associated with the earliest scheduled event from the priority queue and sampling its recovery time. Subsequently, for each neighbor of v , a potential infection time is sampled. Recovery and infection times are drawn from exponential distributions with rates μ and β , respectively. If a sampled infection time occurs before the recovery of v and before any previously scheduled infection event involving the neighbor, the corresponding infection event is inserted into the priority queue. The queue is then reordered, and the algorithm continues by processing the next event at the top of the queue.

A.2 Soft Margin Estimator (SME)

The Soft Margin Estimator (SME) was introduced by Antulov-Fantulin et al. [25] in 2015. Its core idea is to compare the n simulated outbreaks $r_{q,i}$ generated from a candidate source q with the observed snapshot, denoted here by r_* . The closer the simulated outbreaks are to the observed one, the higher the likelihood of the corresponding source q .

Antulov-Fantulin et al. propose measuring similarity between the observed and simulated outbreaks using the Jaccard similarity $\varphi(r_*, r_{q,i})$. Treating $\varphi(r_*, r_{q,i})$ as a random variable, its empirical probability density function is given by

$$\hat{f}_q(x) = \frac{1}{n} \sum_{i=1}^n \delta(x - \varphi(r_*, r_{q,i})), \quad (\text{A.1})$$

where $\delta(\cdot)$ denotes the Dirac delta function. Using this empirical density together with a Gaussian weighting function $w_a(x) = \exp(-(x-1)^2/a^2)$, the likelihood is estimated as

$$\begin{aligned} \hat{P}(r_* | q) &= \int_0^1 w_a(x) \hat{f}_q(x) dx \\ &= \int_0^1 w_a(x) \frac{1}{n} \sum_{i=1}^n \delta(x - \varphi(r_*, r_{q,i})) dx \\ &= \frac{1}{n} \sum_{i=1}^n \int_0^1 w_a(x) \delta(x - \varphi(r_*, r_{q,i})) dx \\ &= \frac{1}{n} \sum_{i=1}^n w_a(\varphi(r_*, r_{q,i})) \\ &= \frac{1}{n} \sum_{i=1}^n \exp(-(\varphi(r_*, r_{q,i}) - 1)^2/a^2). \end{aligned} \quad (\text{A.2})$$

The convergence parameter a controls the extent to which the estimator approaches direct Monte Carlo estimation, where only exact matches between r_* and $r_{q,i}$ contribute to the likelihood. In the limit $a \rightarrow 0$, the weighting function satisfies $w_{a \rightarrow 0}(x) = 0$ for $x \neq 1$ and $w_{a \rightarrow 0}(1) = 1$. Following the procedure described in the Supplemental Material of [25], we determine the optimal value of a as the smallest value that satisfies the convergence criterion

$$\left| \hat{P}_a^n(q_{\text{MAP}} | r_*) - \hat{P}_a^{2n}(q_{\text{MAP}} | r_*) \right| \leq 0.05. \quad (\text{A.3})$$

Here, only the most probable source candidate q_{MAP} is considered when assessing convergence. The quantity $\hat{P}_a^{2n}(q_{\text{MAP}} | r_*)$ is estimated via bootstrap resampling of the n simulated outbreaks.

Finally, we note that for the SIR model, SME based on Jaccard similarity does not distinguish between infectious and recovered nodes. This limitation may place it at a disadvantage relative to methods that fully exploit the available node state information.

A.3 Monte Carlo Mean Field (MCMF)

The Monte Carlo Mean Field (MCMF) method builds on prior work by Sterchi et al. [27] and proceeds in two stages. In the first stage, we estimate conditional node-state probabilities $P(X_v(t_1) | q)$ for every node v and each candidate source node q at the inference time t_1 using the Monte Carlo simulations. For the SIR model, these probabilities are obtained by computing, for each source q , the fraction of simulation runs in which node v is in the susceptible, infectious, or recovered state at time t_1 .

In the second stage, we compute the likelihood of each candidate source q given the observed node states E_{t_1} (which, for SME, we denote as r_*). To make this computation tractable, we adopt a strong mean-field-like assumption of conditional independence across nodes, which yields the factorized likelihood

$$\hat{P}(E_{t_1} | q) = \prod_{v, x_v(t_1) \in E_{t_1}} P(X_v(t_1) = x_v(t_1) | q). \quad (\text{A.4})$$

In practice, we evaluate the log-likelihood, thereby converting the product of node-state probabilities into a sum of their logarithms. When a normalized posterior over source nodes is required, we employ the standard log-sum-exp trick for numerical stability.

Finally, when the number of Monte Carlo simulations is small, some estimated node-state probabilities may be zero for a given source q , potentially resulting in a zero likelihood even if the source is a plausible candidate. To mitigate this issue, we apply add-one smoothing to the estimated probabilities, while enforcing that a source node q cannot have a nonzero probability of being susceptible at the inference time.

B Further Results

This appendix contains further results that were not included in the main text.

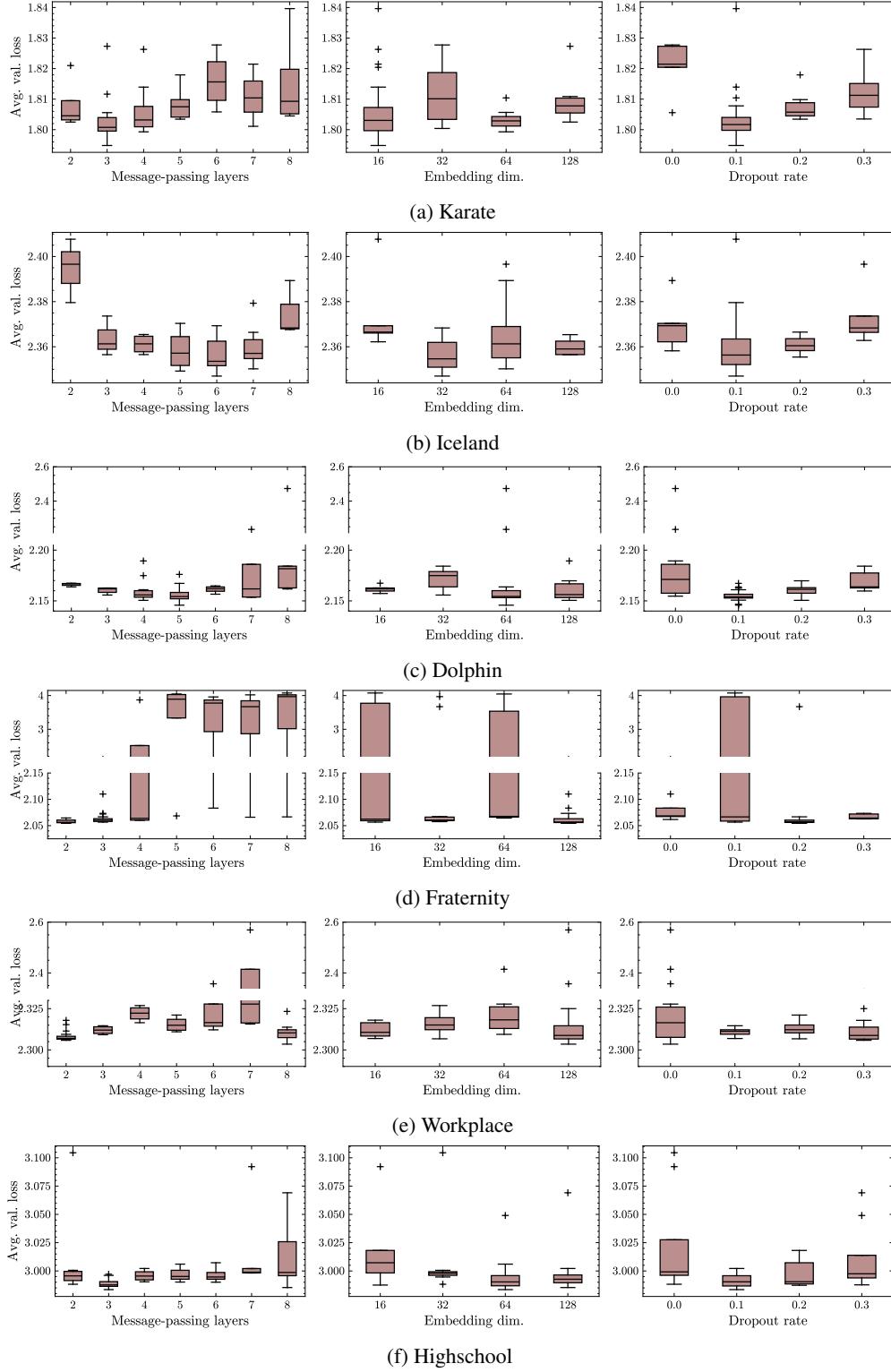


Figure A.1: Hyperparameter tuning results for the number of message-passing layers (left), embedding dimensionality (middle), and dropout rate (right). Each plot shows the distribution of average validation losses (computed over the last five epochs) for each tested hyperparameter value. For the networks in (c) – (e), the y-axis is split to enhance visibility of smaller differences.

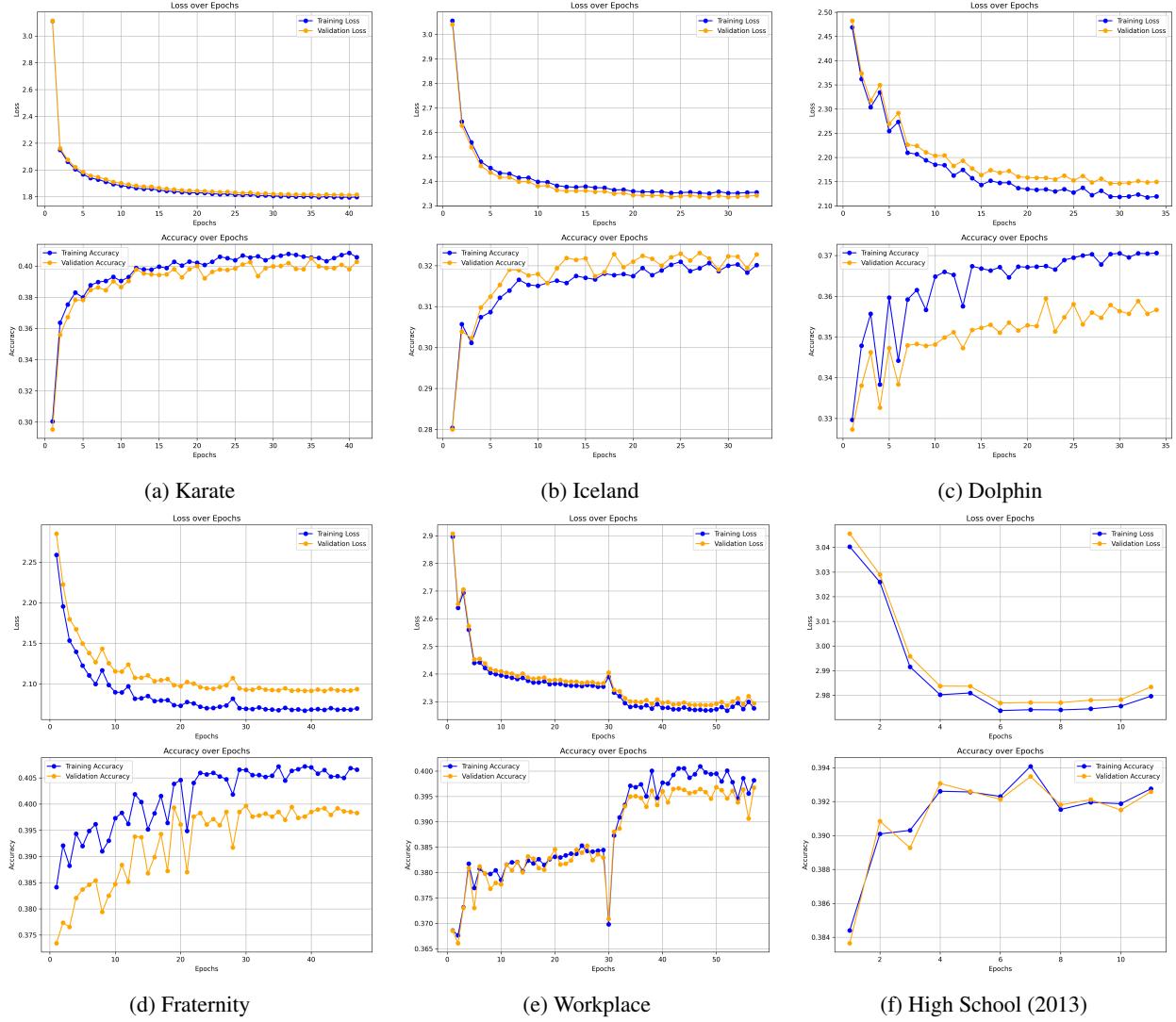


Figure A.2: Learning curves for the six empirical networks. For each network, the top panel reports the training and validation loss across epochs, and the bottom panel shows the corresponding training and validation top-1 accuracy. The curves shown correspond to one representative run from the three independent trials conducted for the benchmark analysis (see Subsection 6.2).