Controlling Epidemic Spread using Probabilistic Diffusion Models on Networks

The MinInfEdge Problem

- We are given a social contact network in the form of a graph G = (V, E) with weights $c_e \ge 0$ for all $e \in E$, and a vertex $s \in V$. For notational convenience, let n = |V|.
- An infectious disease starts from s and spreads through the edges.
- We assume an SIR model of disease spread which is equivalent to the following percolation process: Consider a random subgraph $G(\vec{p}) = (V, E(\vec{p}))$ obtained by retaining each edge $e \in E$ independently with probability p_e . Vertices that are connected to s in $G(\vec{p})$ will get infected. The vector \vec{p} is assumed to be known.
- **Idea:** Mitigate the spread by removing edges. This corresponds to a social distancing strategy.
- If we remove a cut $F \subseteq E$ from the graph, we denote by $inf(V, E \setminus F, s)$ the number of vertices that are in the same connected component as s in the *residual* graph $G_F = (V, E \setminus F)$. The expected number of infected vertices in the percolation process is then $\mathbb{E}_{G(\vec{p})}[inf(V, E(\vec{p}) \setminus F, s)].$
- Goal: Choose $F \subseteq E$ such that: $\mathbf{O}(F) \leq B$ for some given budget B. **2** $\mathbb{E}_{G(\vec{p})}[inf(V, E(\vec{p}) \setminus F, s)]$ is minimized.

Further Comments

- An SIR process like the one above is a common way of modeling the spread of a disease.
- Rigorous results for this problem are only known for when $p_{u,v} = 1$ for all $(u, v) \in E$ [1, 4, 3, 6], i.e., the case of highly contagious diseases

(α, β) -approximation

We say that $F \subseteq E$ is an (α, β) -approximation if $c(F) \leq \alpha B$, and $\mathbb{E}_{G(\vec{p})}[inf(V, E(\vec{p}) \setminus F, s)] \leq \beta \cdot$ $\mathbb{E}_{G(\vec{p})}[inf(V, E(\vec{p}) \setminus F^*, s)],$ where F^* is an optimal solution for the given instance.

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A Warm-Up Result for a Special Case of MinInfEdge

- Here we assume that all edge costs c_e are equal to 1 and that the transmission probabilities are uniform, i.e., $p_e = p$ for all $e \in E$ and some $p \in [0, 1].$
- Furthermore, let c_{min} be the size of the minimum cut in G and assume that $p \cdot c_{min} = \Omega(\log n).$
- Using the previous assumptions and a cut sparsification result from [5], we give an (O(1), O(1))-approximation for MININFEDGE.

A Path-Counting SAA Approach

- Here we use the Sample Average Approximation (SAA) technique, where we sample a polynomial number of graphs from $G(\vec{p})$.
- We proceed by an LP-based approach, where we formulate an "empirical" LP on the set of sampled graphs.
- Finally, we develop a randomized rounding scheme for the fractional solution of the above LP, which returns a solution $F_0 \subseteq E$.
- Let Γ the expected number of simple paths in a graph drawn from $G(\vec{p})$.
- Main Result: For any chosen constants $\epsilon > 0$ and $\gamma > 1$, the following hold: 1 With probability at least $1 - O(n^{-\gamma})$, we have
- $c(F_0) \leq O(\frac{\gamma}{\epsilon}) \log n \cdot B$ **2** When $\Gamma \leq \operatorname{poly}(n)$, we have $\mathbb{E}[inf(V, E(\vec{p}) \setminus F_0, s)] \le (1 + O(\epsilon) + O(1/n))OPT$
- The randomness in the above statement can be of three distinct types:
- **1** Type 1: This randomness is over the random choice, if any, of our network G = (V, E) (randomness resulting from a random-graph model for G). If the network G is deterministic, Type 1 is vacuous: there is no such randomness.
- **2** Type 2: This randomness arises from the choices of our randomized rounding algorithm.
- **3 Type 3:** This type of randomness refers to the random percolation/diffusion of the disease, governed by \vec{p} .

The Chung-Lu [2] Random-Graph Model

• In this model, we have a set of vertices V, and a weight w_v for every node $v \in V$ that denotes its expected degree in the graph. The edges E of the graph are determined via the following random process. For every $u, v \in V$, the probability of having the (u, v) edge in E is

 $q_{u,v} = \frac{w_u w_v}{\sum_{r \in V} w_r},$

- where these edges are present independently and self-loops are allowed. A common instantiation of this model is with a power law, in which n_i , the number of nodes of weight i, satisfies $n_i = \Theta(n/i^{\beta})$, with $\beta > 2$ being a model parameter.
- The random graphs captured by the Chung-Lu model are more realistic in terms of a social contact network.
- We refer to MININFEDGE when the graph G = (V, E) is from the Chung-Lu model as MININF-CL.
- The random process for constructing the graph G = (V, E) in this model should not be confused with the percolation process occurring on G during the spread of the disease. The whole situation can be viewed as happening in two steps. At first, G is chosen randomly according to the Chung-Lu model. Afterwards, the disease starts its diffusion in the chosen network according to the probability vector \vec{p} .

Counting Paths in the Chung-Lu Model

- We show that when $\beta > 3$ we have $\Gamma = \text{poly}(n)$. This result combined with our SAA approach gives a bicriteria algorithm for MININF-CL that works with high probability.
- We show that when $\beta < 3$, Γ is no longer polynomial in n.

- 1999.

A Different Deterministic Rounding SAA Approach

• Instead of the randomized rounding mentioned earlier, we apply a simple deterministic rounding scheme. The advantage of the latter is that the success probability of the algorithm no longer relies on the value Γ . However, this comes at the expense of much worse bicriteria factors.

• Main result: With high probability, we compute a solution that is an $(O(n^{2/3}), O(n^{2/3}))$ -approximation for MININFEDGE.

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