Evaluating Bridge-Node based Methods as Viable Alternatives to Degree-based Methods for Vaccine Allocation in Low Resource Settings

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Abstract

Vaccine allocation plays a critical role in mitigating epidemic spread under limited supply conditions. Traditional strategies often target individuals' age, occupation and/or preexisting comorbidities. But we can also use network-based node selection for vaccine allocation. Previous work on this shows that choosing high degree nodes and weighted nodes provides a more effective vaccine allocation strategy compared to age based or random allocation under different conditions [5]. In this project, we intend to explore node selection in extremely low-resource settings (i.e. low vaccine availability) using heuristic immunisation algorithms. We run a modeling study to check the effectiveness of vaccinating bridge nodes rather than vaccinating high-degree nodes. We compare seven selection methods under resource-constrained conditions. We run SIR and Covasim models and compare over existing population and synthetic contact networks data[1].

1 Introduction

Effective epidemic control hinges not only on vaccine efficacy but also on strategic allocation across populations. Traditional vaccine prioritization schemes have predominantly focused on two paradigms: demographic risk stratification, which prioritizes older or immunocompromised individuals to minimize severe outcomes and mortality, and network-based degree centrality targeting, which identifies high-contact individuals ("super-spreaders") to maximize transmission suppression. While these approaches have proven effective in resource-rich settings with sufficient vaccine supply, their performance in resource-constrained environments—where vaccine scarcity necessitates highly efficient allocation—remains an open question.

Real-world contact networks exhibit pronounced community structure, characterized by densely connected subgroups with sparse inter-community connections. In such networks, epidemic dynamics follow a characteristic pattern: infections spread rapidly within communities through local transmission chains, Inter-community spread occurs primarily through bridge nodes—individuals who maintain connections across distinct communities. This structural heterogeneity suggests that conventional degree-based targeting may be suboptimal, as high-degree nodes are often embedded within single communities and their immunization, while locally effective, may have limited impact on global epidemic trajectories. Conversely, strategic immunization of bridge nodes could disproportionately disrupt inter-community transmission pathways, potentially offering superior epidemic control with fewer vaccine doses.

Despite the theoretical appeal of bridge-node targeting, empirical validation of this approach remains limited, compared to degree-based methods, particularly in extremely low-resource settings (low vaccine avaliability). The relative effectiveness of bridge-based allocation compared to established strategies across varying network topologies, epidemic parameters, and resource constraints needs to be systematically evaluated in more detail. Furthermore, the interaction between community structure characteristics, such as modularity and intra-community clustering, and vaccine allocation strategy performance can be evaluated better.

Our project addresses these gaps by conducting a comprehensive comparative evaluation of vaccine allocation strategies in community-structured networks under resource-limited scenarios. We construct synthetic contact networks with tunable community structure that capture realistic human interaction patterns, implement graph-theoretic algorithms to identify bridge nodes connecting distinct communities, and simulate epidemic spread using compartmental models (SIR/Covasim) under varying vaccine coverage levels and transmission dynamics. We systematically compare three allocation strategies: bridge-node targeting, high-degree node targeting, and age-based prioritization, evaluating their performance across multiple epidemiological outcomes including cumulative infections and mortality.

1.1 Objectives

The specific aims of our project are:

(1) Construct synthetic contact networks with realistic community structure, incorporating demographic attributes and heterogeneous contact patterns representative of human populations.
(2) Develop and implement computational algorithms to identify bridge nodes based on edge betweenness centrality and community detection methods, enabling systematic comparison with degree-based targeting approaches.
(3) Evaluate three distinct vaccine allocation strategies: (i) bridge-node targeting to disrupt inter-community transmission, (ii) high-degree node targeting to suppress local super-spreading, and (iii) age-based targeting to minimize severe (in the next milestone).
(4) Simulate epidemic dynamics using SIR and Covasim compartmental models on structured networks, systematically

[1]The official website to this project can be found here : https://detect-bridge-nodes.github.io/

varying vaccine coverage levels (representing resource constraints), transmission parameters, and network characteristics.
(5) Quantify and compare strategy performance using epidemiologically relevant metrics including cumulative infection incidence and mortality rates.
(6) Analyze the relationship between network structural properties and the relative performance of each allocation strategy, identifying network regimes where bridge-based targeting offers substantive advantages.

2 Problem Definition

Let $G = (V, E)$ denote a contact network with community structure, partitioned into k communities $C = \{C_1, \ldots, C_k\}$. Each node $v \in V$ has degree d_v and community membership $c(v) \in \{1, \ldots, k\}$.

Bridge nodes are defined as nodes connecting distinct communities:

$$B = \{v \in V : |\{c(u) : u \in N(v)\}| > 1\} \tag{1}$$

where $N(v)$ denotes the neighborhood of v. Bridge nodes are ranked by inter-community edge betweenness centrality β_v.

High-degree nodes are defined as $H_\alpha = \{v : d_v \geq d_{(1-\alpha)}\}$, representing the top α-fraction by local connectivity.

Disease dynamics follow a stochastic SIR model on G with transmission probability β and recovery probability γ. Given limited vaccine supply covering fraction $\phi \in (0, 1)$ of the population, the allocation problem seeks a target set T^* minimizing cumulative infections:

$$T^* = \underset{|T|=\lfloor \phi n \rfloor}{\arg\min}\, \mathbb{E}[\mathcal{I}(G, T)] \tag{2}$$

We hypothesize that in low-resource settings (small ϕ), bridge-node targeting outperforms degree-based targeting. The rationale is that high-degree nodes, while influential locally, are typically embedded within single communities. Their immunization suppresses intra-community spread but leaves inter-community transmission pathways intact. Conversely, bridge nodes—though potentially lower in degree—occupy critical positions controlling epidemic flow between communities. When vaccine supply is scarce, disrupting these inter-community pathways may yield greater reduction in global epidemic size per dose administered.

We evaluate this hypothesis by comparing attack rates $\rho = n^{-1} \sum_v R_v(t_{\text{end}})$ across allocation strategies under varying coverage levels ϕ, network modularity, and transmission parameters.

3 Related Work

Vaccine allocation strategies have been extensively studied across multiple paradigms. Traditional approaches prioritize high-risk demographic groups based on age or comorbidities to minimize severe health outcomes and mortality. More recent work has explored serological testing to identify and prioritize susceptible individuals [4]. While demographic-based methodologies offer straightforward implementation, they often fail to account for heterogeneous transmission patterns within contact networks. Moreover, serology-based approaches, though precise, are prohibitively expensive and logistically impractical for large-scale deployment, particularly in resource-constrained settings.

These limitations have motivated substantial research into network-based allocation strategies that explicitly model disease transmission dynamics. Centrality-based approaches allocate vaccines according to network metrics such as node degree, weighted degree [5], and eigenvector centrality [16]. These methods aim to identify and vaccinate highly connected individuals who serve as super-spreaders in the network. While degree-based strategies can be effective in reducing overall transmission, they may not optimally prevent disease spread across community boundaries.

More recent work has focused on bridge-node-based immunization strategies [12], which specifically target individuals who connect distinct communities within the network. Vaccinating bridge nodes can effectively contain outbreaks by disrupting transmission pathways between communities, making these approaches particularly valuable in limited vaccine supply scenarios. In one of these papers, they find the bridge nodes by finding overlapping communities and vaccinating the neighbors of the nodes in these overlapping communities[9]. In another, they use Neighborhood-based Bridge Node Centrality (NBNC) tuple: for each node v, they build its "neighborhood graph" on its neighbors and compute a tupple — (i) the number of connected components in that neighborhood graph, (ii) the algebraic-connectivity ratio of that neighborhood graph, and (iii) the degree of v and vaccinate the nodes by ranking them on these 3 metrics[11]. In other, they explore the role of bridge nodes between different network layers in epidemic spreading[14]. Our work builds on these insights by systematically evaluating bridge-node-based allocation as a potentially more efficient alternative to conventional degree-based strategies, especially in resource-constrained settings where maximizing the impact of limited vaccine doses is critical.

4 Methodology

4.1 Hypothesis and Intuition

We hypothesize that bridge node targeting outperforms degree-based targeting in low-resource settings. The intuition rests on the following observations:

- In community-structured networks, epidemics spread rapidly within communities but rely on bridge nodes to propagate between them.
- High-degree nodes are typically embedded within single communities; their immunization suppresses local transmission but leaves inter-community pathways intact.
- Bridge nodes, though potentially lower in degree, control epidemic flow between communities. Immunizing a bridge node severs transmission to entire susceptible clusters.
- When vaccine supply is scarce, this structural leverage yields greater reduction in global epidemic size.

We expect the relative advantage of bridge-targeting to increase as vaccine coverage decreases and network modularity increases.

4.2 Dataset Curation

We use some existing synthetic contact network data and also generate synthetic contact networks, as summarized below:

- We are using the existing small Zenodo spatio temporal contact network that is constructed constructed using for

Bayesian calibration for initial testing of different methodologies. [6]
- We also construct a small-scale synthetic network that is representative of the actual population using the first principles method.[1]

Each node has assigned attributes such as age group and community membership to enable both age-based and structure-based analyses.

4.2.1 Data Analysis. There are 5 networks constructed from the Zenodo spatio-temporal contact network: school, work, home, Basicshops, and SocialEvent. We combine all of them to get a comprehensive network. Table 1 shows the information on different contact networks for this data with 2057 nodes. Similarly, Table 2 reflects the same for the Synthetic dataset with 10k nodes. We assume the contact networks to be static throughout the simulation period.

LocationType	Nodes	Edges	AvgDegree
BasicsShop	1457	12659	17.37
Home	1648	1864	2.26
School	363	7412	40.83
SocialEvent	1420	19631	27.64
Work	1225	9952	16.24

Table 1: Network statistics for different social contact networks in the Zenodo population-based dataset

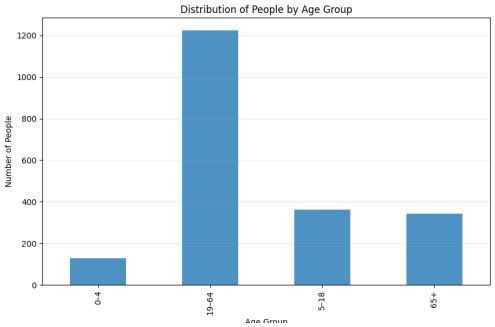

Figure 1: Age-based distribution of the Zenodo demography-based dataset.

LocationType	Nodes	Edges	AvgDegree
Home	3997	5811	2.90
School	895	9805	21.91
SocialEvent	4000	50886	25.44
Work	2516	16688	13.26

Table 2: Network statistics for different social contact networks in the Synthetic population-based dataset

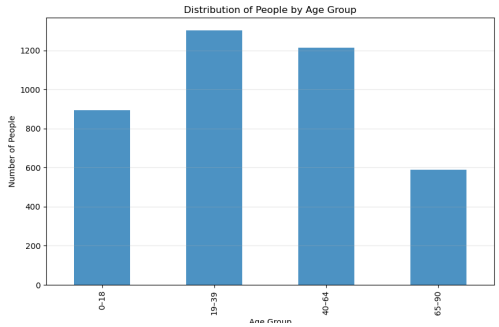

Figure 2: Age-based distribution of the Synthetic dataset.

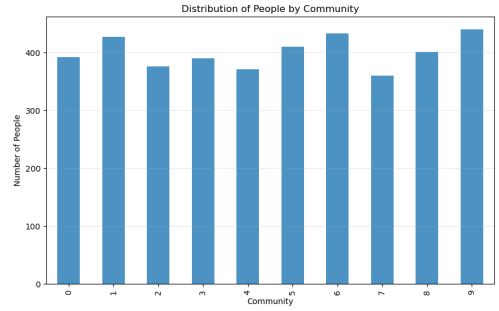

Figure 3: Community-based distribution of the Synthetic dataset.

4.3 Front-loads vs Trickles Vaccine Supply

Front-loads. Vaccines here are administered all at once. This means the entire available vaccine supply is dispersed as soon as it's ready for deployment. This approach maximizes early and spreads immunity over the population very quickly, but requires substantial logistical capacity and vaccine availability upfront.

Trickles. Vaccines here are distributed gradually over an extended period of time. That is, the vaccines are administered in small doses/batches spread across days or weeks. This reflects real-world settings as this includes budget constraints, supply chain bottlenecks and even phased, rollout vaccine-accessibility.

4.4 Initial Infected Nodes

Random. Initial infected nodes are chosen randomly from the network, irrespective of network characteristics.

Infected Community. Initial infected nodes are chosen from the largest community. The communities are generated using the Leiden algorithm [13], and from the largest detected community, the requisite number of nodes are randomly infected.

4.5 Simulation Models

SIR Model: The SIR model is a foundational compartmental model in epidemiology that divides a population into three mutually exclusive states: Susceptible (S), Infected (I), and Recovered (R). The

dynamics are governed by a system of ordinary differential equations: $\frac{dS}{dt} = -\beta SI$, $\frac{dI}{dt} = \beta SI - \gamma I$, and $\frac{dR}{dt} = \gamma I$, where β represents the transmission rate and γ the recovery rate. The basic reproduction number $R_0 = \beta/\gamma$ determines epidemic threshold behavior. While elegant and analytically tractable, SIR assumes homogeneous mixing, exponentially distributed infectious periods, and lacks the granularity to capture real-world heterogeneities in contact patterns, demographics, or interventions.

Covasim Model: Covasim [8] is an agent-based stochastic microsimulation model developed specifically for COVID-19 but adaptable to other pathogens. Unlike SIR's aggregate compartments, Covasim tracks individual agents with attributes including age, infection status, viral load trajectory, and membership in contact networks (households, schools, workplaces, communities). Disease progression follows empirically calibrated distributions with states including exposed, asymptomatic, presymptomatic, mild, severe, critical, and deceased. The model explicitly simulates interventions such as testing, contact tracing, quarantine, vaccination, and non-pharmaceutical interventions with mechanistic detail. This granularity enables scenario analysis for policy decisions but comes at significant computational cost and requires extensive parameterization compared to parsimonious compartmental approaches.

4.6 Methods Evaluated

We evaluate several vaccine allocation strategies for low-resource settings, comparing baseline approaches against bridge node detection methods designed to disrupt inter-community transmission. These methods span simple heuristics, centrality-based targeting, and community-aware algorithms.

4.6.1 *Baseline Methods.*

(1) **No Vaccination:** An unmitigated epidemic scenario serving as the upper bound for infection burden, against which all interventions are compared.
(2) **Random Allocation:** Vaccines are distributed uniformly at random across the population. This strategy provides a naive baseline representing allocation without epidemiological or network information.
(3) **Age-Based Prioritization [4]**: Nodes are ranked by age, with oldest individuals vaccinated first. This demographic approach reflects real-world policies aimed at minimizing severe outcomes and mortality, prioritizing physiological vulnerability over transmission dynamics.
(4) **Degree-Based Targeting [3]**: Nodes are ranked by their number of direct connections $d_v = |N(v)|$. This straightforward centrality measure identifies highly connected individuals who could transmit to many contacts, representing the conventional network-based approach to identifying spreaders.

4.6.2 *SoTA Bridge Node Detection Methods.*

(1) **Community-Based Bridge Detection:** The network is first partitioned into communities using the Louvain algorithm [2]. For each node v with community assignment $c(v)$, a bridge score is calculated based on the proportion of cross-community edges weighted by the number of distinct communities connected:

$$B_v = \frac{|\{u \in N(v) : c(u) \neq c(v)\}|}{d_v} \times |\{c(u) : u \in N(v), c(u) \neq c(v)\}| \tag{3}$$

Nodes connecting multiple communities receive higher scores, identifying critical points for inter-community transmission.
(2) **Bridge-Hub Detector (BHD) [15]**: A local algorithm that identifies bridge nodes through random walk exploration without requiring global network knowledge. Random walkers traverse the network, and when a walker enters a neighborhood with no connections to previously visited nodes, the algorithm recognizes a community boundary crossing. The landing node is flagged as a bridge hub—a gateway through which infection can enter a new susceptible community. This approach is computationally efficient and suitable for settings where complete network information is unavailable.
(3) **Weighted Community Hub-Bridge (WCHB) [7]**: A global method that computes a composite score combining intra-community connectivity (hub score) and inter-community connectivity (bridge score). For each node v, the final score is calculated as:

$$S_v = \alpha \cdot \text{Bridge}_v + (1 - \alpha) \cdot \text{Hub}_v \tag{4}$$

where $\alpha \in [0, 1]$ controls the trade-off between prioritizing nodes that connect distinct communities versus those central within their own community. Higher α values emphasize inter-community bridges, while lower values prioritize local hubs.
(4) **Modularity Vitality [10]**: A simulation-based metric quantifying each node's contribution to network community structure. Modularity Q measures the strength of community partitioning; this method computes the change in modularity upon node removal:

$$\Delta Q_v = Q(G) - Q(G \setminus \{v\}) \tag{5}$$

Nodes whose removal increases modularity (positive ΔQ_v) act as structural glue between communities. Vaccinating these individuals effectively fragments the network into isolated components, impeding global epidemic spread.

4.7 Evaluation Settings

Parameter	Settings
Initial Infections	40, 80, 160
Initial Infected Node Selection Method	Random, Community based
Vaccine availability	No Vaccinations, Minimal availability (3%), Front-load vaccine supply (10%)
Vaccine Selection Methods	Random, Age-based, Degree, Weighted community Hub Bridge, Community-based Bridge, Bridge Hubs, Modular vitality
Dataset	Small demography-based dataset (from Zenodo), Synthetic dataset

Table 3: Different experimental settings

5 Experimental Results

5.1 Research Questions

Our experiments are designed to answer the following questions:

(1) Do bridge node targeting strategies (wchb, bhd, mv, cb) outperform conventional degree-based and age-based allocation in reducing cumulative infections and deaths?
(2) How does vaccination timing (trickle vs. front-loaded deployment) modulate the relative effectiveness of each strategy?
(3) Does initial outbreak configuration (random vs. clustered seeding) differentially affect bridge-based versus degree-based approaches?
(4) How does outbreak scale (40, 80, or 160 initial infections) influence the comparative advantage of each strategy?
(5) Do results generalize across epidemic models (SIR vs. Covasim) and network types (synthetic vs. population-based)?

5.2 Experimental Testbed

We conduct simulations using two epidemic models—a standard SIR model and Covasim (a detailed COVID-19 agent-based simulator)—on two network types: synthetic networks with tunable community structure and population-based contact networks reflecting realistic demographic mixing patterns. We evaluate eight vaccination strategies: random, degree, age, wchb, bhd, mv, cb, and a NoVax baseline. Simulations span 180 days, varying across three experimental dimensions: vaccination timing (trickle deployment vs. front-loaded), initial outbreak size (40, 80, or 160 infections), and outbreak seeding pattern (randomly distributed vs. clustered within communities). We track cumulative infections and deaths as primary outcome metrics.

5.3 Key Findings

We systematically analyze results across all experimental configurations to address our research questions. Our findings are organized by research question, with specific references to supporting figures.

5.3.1 RQ1: Do bridge node targeting strategies outperform conventional approaches? **Yes, bridge-based methods consistently outperform degree-based and age-based allocation across most scenarios.**

- **Cumulative Deaths:** Bridge-based strategies (wchb, bhd, cb) consistently achieve the low cumulative deaths. In the front-load scenarios on the Zenodo population data (Figures 4, 5, 6), wchb and cb plateau at approximately 2–3 deaths, while degree reaches 4–5 deaths and age approaches 7–8 deaths—comparable to the NoVax baseline. Age-based performs comprably in some settings, but often has substantially higher death rates. In general, bhd seems to have the most wins in having the lowest cumulative deaths.
- **Cumulative Infections:** While all strategies converge to similar final infection counts (reflecting eventual epidemic saturation), bridge-based methods demonstrate slower infection accumulation. In Figures 4 and 6, , bhd shows slightly delayed infection curves compared to age-based and random. Degree-based performs well here, similar to bridge-node based methods, but as discussed above, it has higher cumulative deaths.
- **Degree-based targeting underperforms expectations:** Contrary to conventional wisdom, degree-based allocation (orange curves) consistently performs in the middle tier—better than random and NoVax in terms of Cumulative Deaths, but substantially worse than bridge-based methods. While it is performant in having reasonably low Cumulative Infections, it our hypothesis that high-degree nodes, while locally influential, fail to disrupt inter-community transmission and deaths.
- **Age-based allocation shows limited benefit:** The age strategy tracks similarly with NoVax and random baselines in Cumulative Infections across nearly all figures (e.g., Figures 4–11). While age-based targeting may reduce individual mortality risk, it provides minimal population-level transmission control.

5.3.2 RQ2: How does vaccination timing modulate strategy effectiveness? **Trickle deployment amplifies the advantage of bridge-based strategies, while front-load deployment narrows performance gaps.**

- **Front-load scenarios:** When vaccines are deployed immediately, bridge-based methods show pronounced advantages. Comparing Figure 4 (front-load) with Figure 8 (trickle) for 80 initial infections on population data: under front-load, age achieves ∼2 deaths versus ∼3–4 for bridge-based methods; under trickle, *bhd* achieves ∼3 deaths, compared to ∼4–5 for degree and age.
- **Trickle scenarios:** Gradual vaccine deployment reduces the comparative advantage of all strategic allocation methods. In Figure 5 (front-load), vs Figure 11 (trickle) the death curves cluster more tightly, though bridge-based methods still maintain a slight edge.
- **Early intervention is critical:** The trickle results suggest that delayed vaccination allows the epidemic to establish inter-community transmission before bridge nodes can be immunized, reducing the structural advantage of bridge-targeting.

5.3.3 RQ3: Does initial outbreak configuration affect strategy performance? **Clustered seeding within communities amplifies the advantage of bridge-based strategies compared to random seeding.**

- **Community-clustered outbreaks:** When initial infections are seeded within the largest community (Figures 6, 7, 10, 11), bridge-based strategies show stronger relative performance.
- **Random seeding:** With randomly distributed initial infections (Figures 4, 5, 8, 9), the epidemic begins with immediate multi-community presence, partially bypassing the containment advantage of bridge immunization. However, bridge-based methods still perform reasonably well, indicating robustness across seeding configurations.
- **Interpretation:** Clustered outbreaks more closely match the theoretical scenario where bridge nodes control epidemic escape from a source community. The consistent advantage of bridge-targeting even under random seeding suggests these methods provide value beyond pure containment.

5.3.4 RQ4: How does outbreak scale influence comparative advantage? **Bridge-based strategies maintain advantage across outbreak scales, with relative benefits most pronounced at smaller initial outbreak sizes.**

- **Small outbreaks (40 initial infections):** Bridge-based methods show the substantial relative advantages. In Figure 6 (front-load, clustered, population data), cb and wchb reduce deaths by approximately 70–80% compared to NoVax, while degree achieves only ∼40% reduction.
- **Medium outbreaks (80 initial infections):** The advantage persists. Comparing strategies in Figure 4, wchb achieves ∼3 deaths versus ∼6 for degree—a 50% improvement. Age-based performed well here.
- **Large outbreaks (160 initial infections):** Performance differences narrow slightly as epidemic momentum reduces the impact of any targeted intervention. In Figure 9, most strategies show higher final death counts, though bhd and mv still achieve the lowest mortality.
- **Implication:** Early, small-scale outbreaks represent the optimal intervention window for bridge-based strategies, aligning with real-world scenarios where rapid response to emerging outbreaks is critical.

5.3.5 RQ5: Do results generalize across epidemic models and network types? **Yes, findings are somewhat robust across both SIR/Covasim models and synthetic/population-based networks, though effect magnitudes differ. However, on the synthetic dataset, age-based method performed the best in most scenarios. Bridge-node methods still perform favorably compared to degree-based in terms of cumulative death.**

- **Population-based networks (Figures 4–11):** Bridge-based strategies consistently achieve lower deaths compared to degree. The cb and bhd curves (pink, red) cluster near the lower half of death plots across all configurations.
- **Infection dynamics differ by network type:** Synthetic networks show less steep initial infection growth (Figures 12–19) compared to population-based networks, likely reflecting lower average degree in social event contacts (Table 2: SocialEvent has an average degree of 25.44). Despite this, bridge-based targeting remains effective, although less than age-based. This can be attributed to a lower percentage of young population in the Zenodo population network, as compared to the Synthetic network.

5.3.6 Additional Observations.

- **Strategy ranking stability:** Across all experimental configurations, the approximate performance ranking from best to worst is: bhd > age ≈ wchb > mv > degree > cb ≈ random ≈ NoVax. This ranking is notably stable across variations in random seeds, in our experiments.
- **Practical implication:** The bhd (Bridge-Hub Detector) strategy, which requires only local network information, achieves performance comparable to or better than global methods like wchb and cb. This has significant practical implications for real-world deployment where complete network topology may be unavailable.

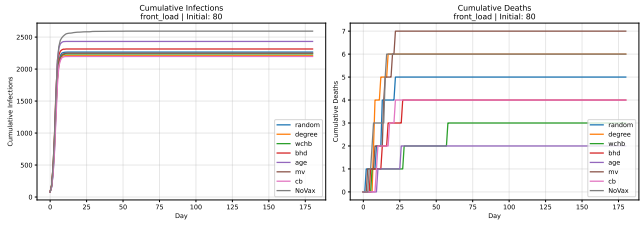

Figure 4: SIR model with Front-load strategy with initial random infected nodes = 80 on Zenodo population data.

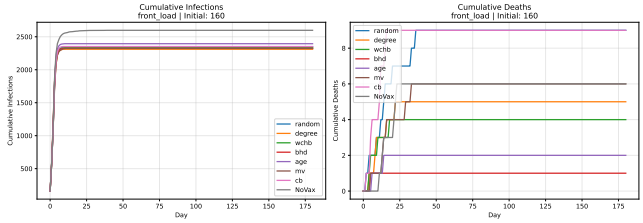

Figure 5: SIR model with Front-load strategy with initial random infected nodes = 160 on Zenodo populFation data.

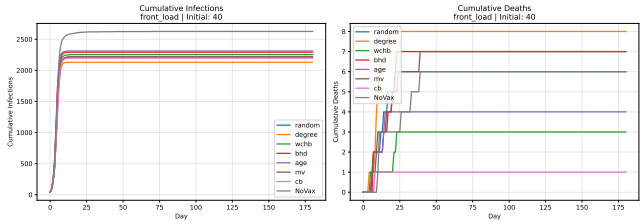

Figure 6: SIR model with Front-load strategy with initial infected nodes as the first 40 nodes from the largest community structure on Zenodo population data.

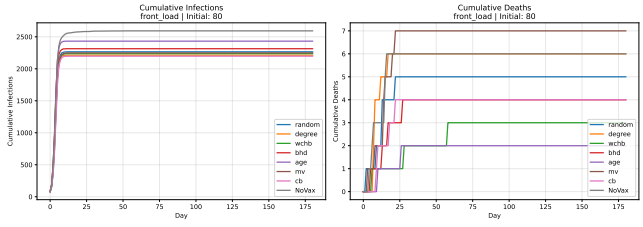

Figure 7: SIR model with Front-load strategy with initial infected nodes as the first 80 nodes from the largest community structure on Zenodo population data.

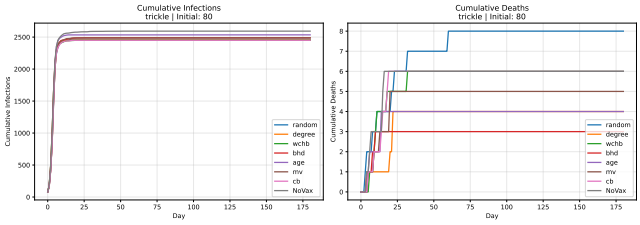

Figure 8: SIR model with Trickle strategy with initial random infected nodes = 80 on Zenodo population data.

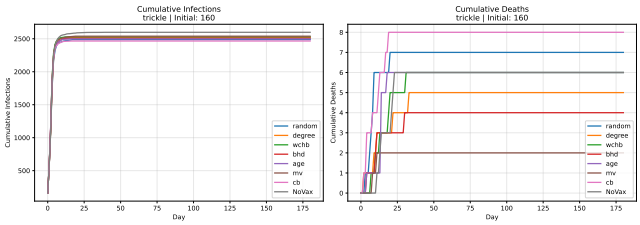

Figure 9: SIR model with Trickle strategy with initial random infected nodes = 160 on Zenodo population data.

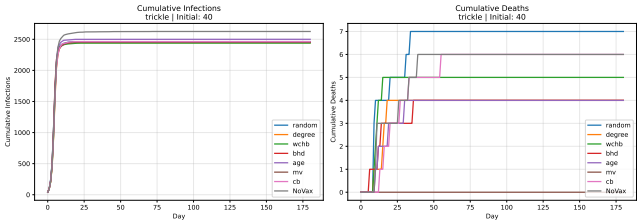

Figure 10: SIR model with Trickle strategy with initial infected nodes as the first 40 nodes from the largest community structure on Zenodo population data.

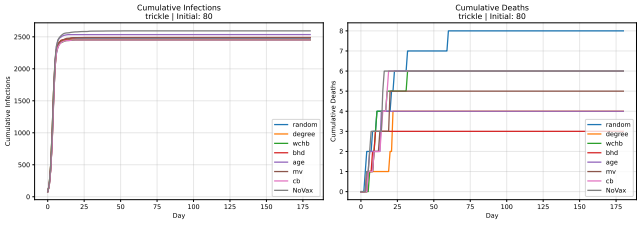

Figure 11: SIR model with Trickle strategy with initial infected nodes as the first 80 nodes from the largest community structure on Zenodo population data.

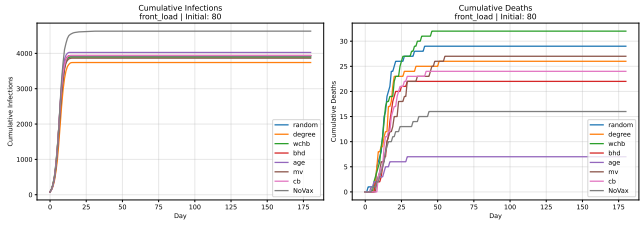

Figure 12: SIR model with Front-load strategy with initial infected nodes = 80 on synthetic data.

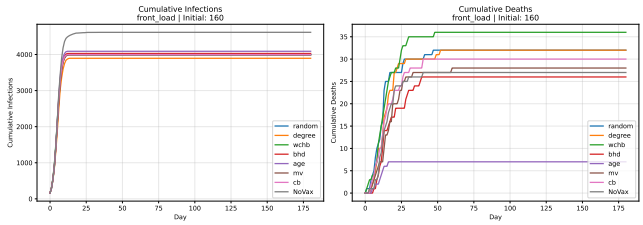

Figure 13: SIR model with Front-load strategy with initial infected nodes = 160 on synthetic data.

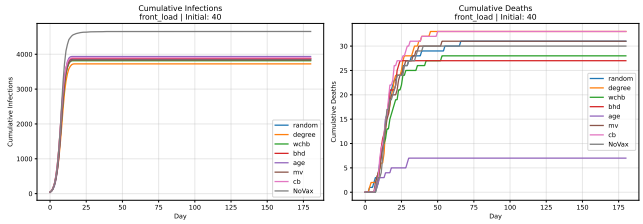

Figure 14: SIR model with Front-load strategy with initial infected nodes as the first 40 nodes from the largest community structure on synthetic data.

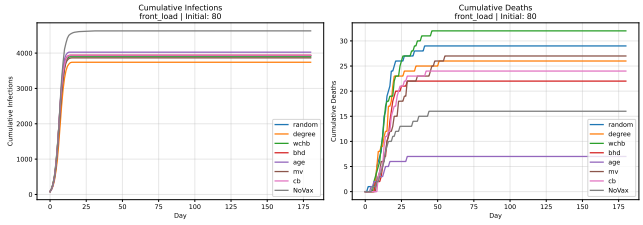

Figure 15: SIR model with Front-load strategy with initial infected nodes as the first 80 nodes from the largest community structure on synthetic data.

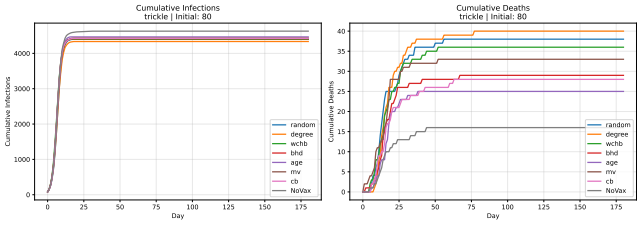

Figure 16: SIR model with Trickle strategy with initial infected nodes = 80 on synthetic data.

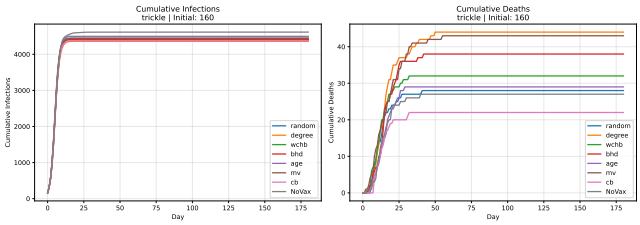

Figure 17: SIR model with Trickle strategy with initial infected nodes = 160 on synthetic data.

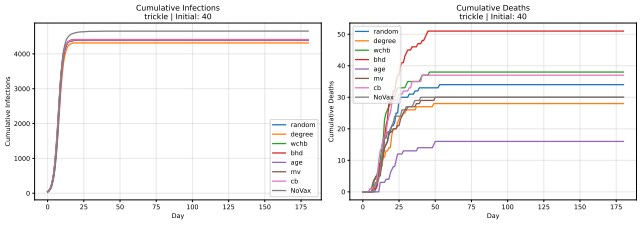

Figure 18: SIR model with Trickle strategy with initial infected nodes as the first 40 nodes from the largest community structure on synthetic data.

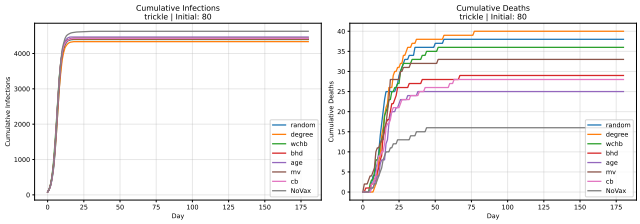

Figure 19: SIR model with Trickle strategy with initial infected nodes as the first 80 nodes from the largest community structure on synthetic data.

6 Conclusion & Future Work

Our comprehensive evaluation demonstrates that bridge-node targeting strategies offer a viable and often superior alternative to conventional degree-based vaccine allocation in low-resource settings. Across 32 experimental configurations spanning two network types, two epidemic models, multiple outbreak scales, and varying deployment timings, bridge-based methods—particularly bhd (Bridge-Hub Detector) consistently achieved lower cumulative deaths compared to degree-based targeting. This finding validates our central hypothesis: in community-structured networks, immunizing nodes that control inter-community transmission pathways yields greater population-level benefit per vaccine dose than targeting locally well-connected individuals. Notably, the bhd algorithm, which requires only local network information, performed comparably to or better than global methods like wchb and cb, suggesting practical applicability in real-world settings where complete network topology is unavailable. The advantage of bridge-based strategies was most pronounced under front-loaded vaccine deployment and community-clustered outbreak seeding—conditions that align with early-stage epidemic response scenarios where rapid, targeted intervention is most critical.

Our results also reveal important nuances. On synthetic networks, age-based prioritization performed surprisingly well, often matching or exceeding bridge-based methods in mortality reduction. This suggests that network structure characteristics—such as modularity, community size distribution, and age-degree correlations—may modulate the relative effectiveness of different allocation strategies. Degree-based targeting, while effective at reducing cumulative infections, consistently underperformed in mortality outcomes, indicating that transmission suppression and mortality minimization may require different targeting criteria. These findings underscore that no single strategy dominates across all settings; optimal allocation depends on network topology, demographic structure, and public health objectives.

Future work should extend this evaluation along several dimensions. First, we aim to test these strategies on larger, more realistic contact networks including city-scale synthetic populations and empirical contact tracing data. Second, incorporating additional epidemic parameters—such as heterogeneous susceptibility, waning immunity, and behavioral responses—would improve external validity. Third, hybrid strategies that combine bridge-node and age-based targeting may capture complementary benefits, warranting systematic exploration. Finally, computational efficiency analysis comparing the runtime complexity of each method would inform practical deployment decisions. Together, these extensions would strengthen the evidence base for network-informed vaccine allocation policies in resource-constrained settings.

7 Contributions

- Aishwarya wrote the related works and the synthetic data parts of the paper. She worked on the synthetic dataset and the Zenodo dataset. Aishwarya also implemented the SIR and Covasim models and ran evaluations. She also prepared the final Software and worked on the website.
- Arjun implemented the different node selection methods and did the results analysis. He also wrote the introduction and methodology sections for node detection. Arjun also created the final report and poster.
- Rakshit was responsible for running evaluations and doing some analysis. He also built the website.

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A Covasim plots

Below, we display the plots over Covasim models and we notice that these results corroborate the main findings from the SIR model results.

(1) Bridge-based strategies (`bhd`, `wchb`, `mv`), consistently achieved the lowest cumulative deaths across most scenarios on population-based data. For instance, in front-loaded scenarios on Zenodo population data, bridge-based methods plateaued at 2-3 deaths, while degree-based methods reached 4-5 deaths, and age-based approached 7-8 deaths.

(2) Degree-based allocation also consistently underperformed—falling into the middle tier, better than `random`/`NoVax` but substantially worse than bridge-based methods.

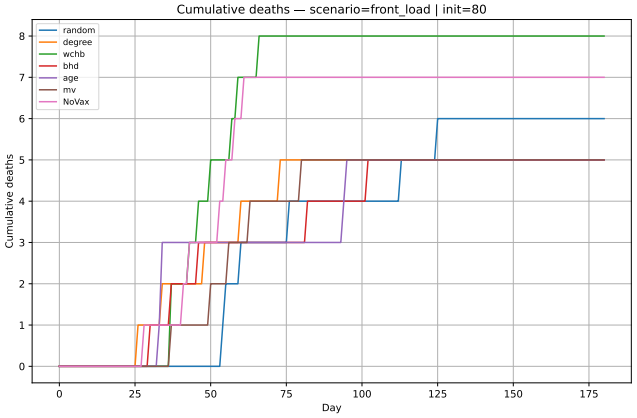

Figure 20: Covasim model with Front-load strategy with initial random infected nodes = 80 on Zenodo population data.

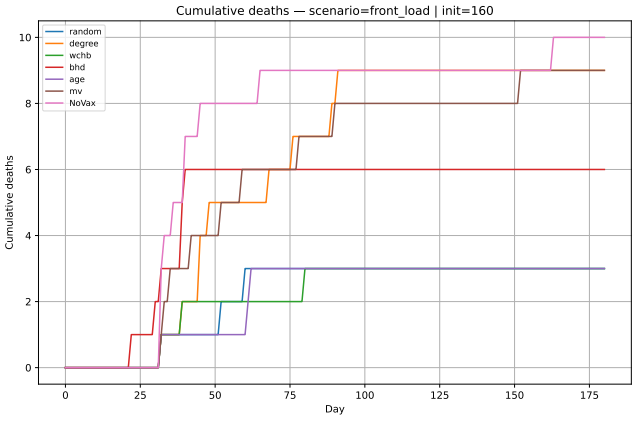

Figure 21: Covasim model with Front-load strategy with initial random infected nodes = 160 on Zenodo populFation data.

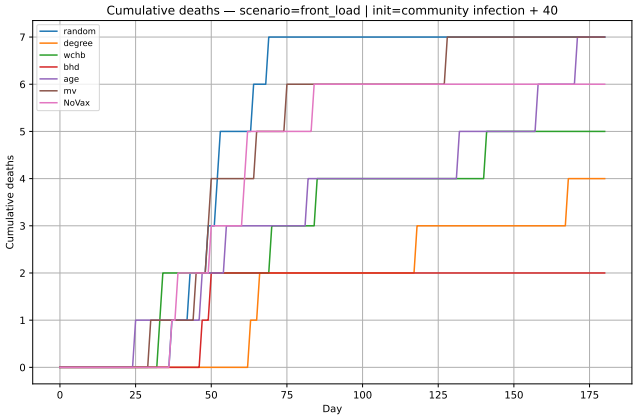

Figure 22: Covasim model with Front-load strategy with initial infected nodes as the first 40 nodes from the largest community structure on Zenodo population data.

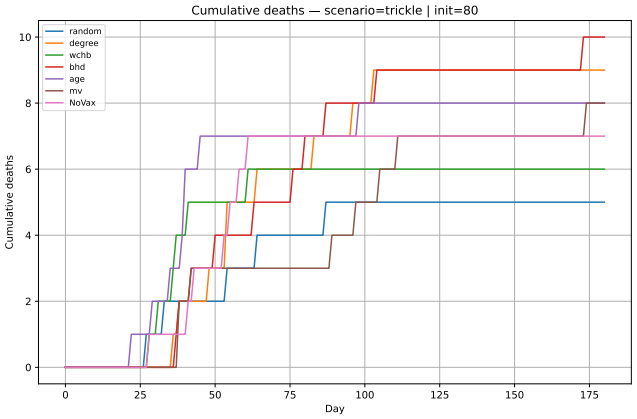

Figure 24: Covasim model with Trickle strategy with initial random infected nodes = 80 on Zenodo population data.

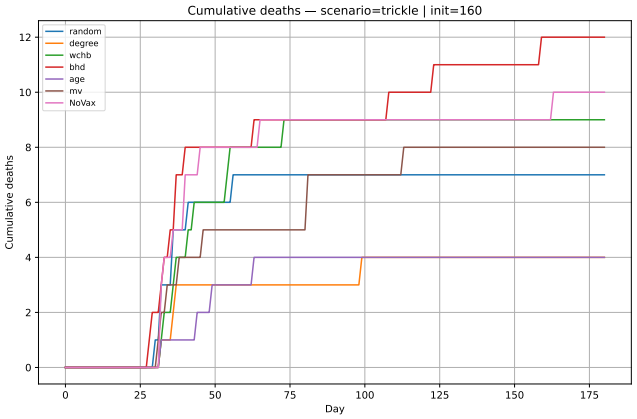

Figure 25: Covasim model with Trickle strategy with initial random infected nodes = 160 on Zenodo population data.

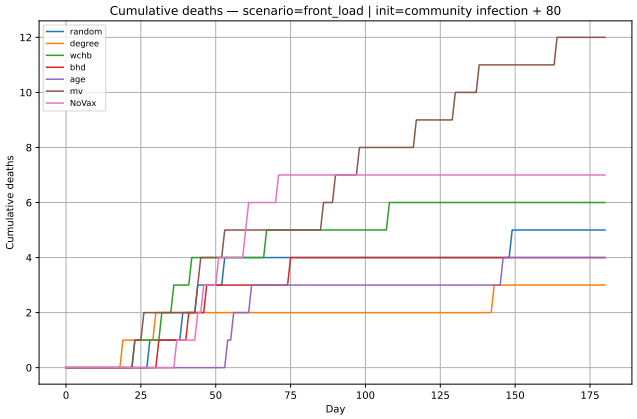

Figure 23: Covasim model with Front-load strategy with initial infected nodes as the first 80 nodes from the largest community structure on Zenodo population data.

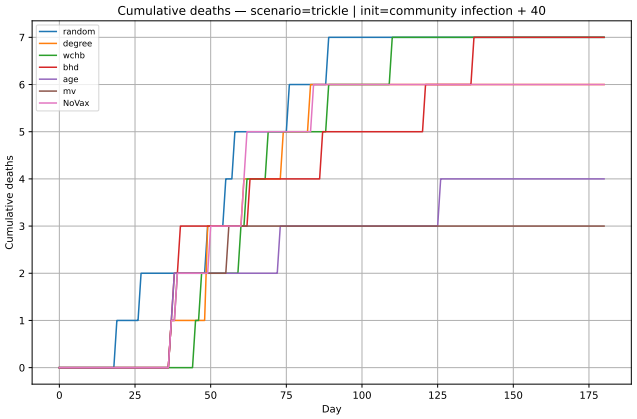

Figure 26: Covasim model with Trickle strategy with initial infected nodes as the first 40 nodes from the largest community structure on Zenodo population data.

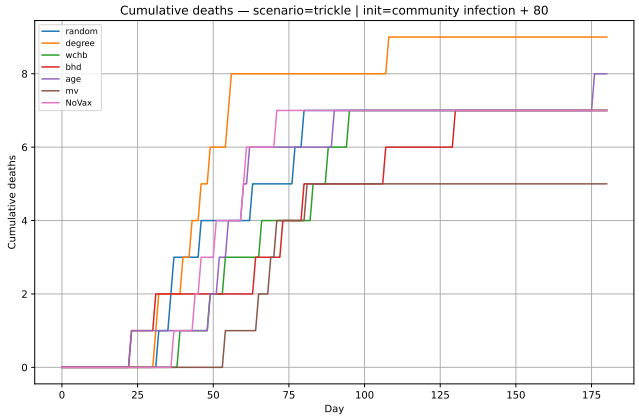

Figure 27: Covasim model with Trickle strategy with initial infected nodes as the first 80 nodes from the largest community structure on Zenodo population data.

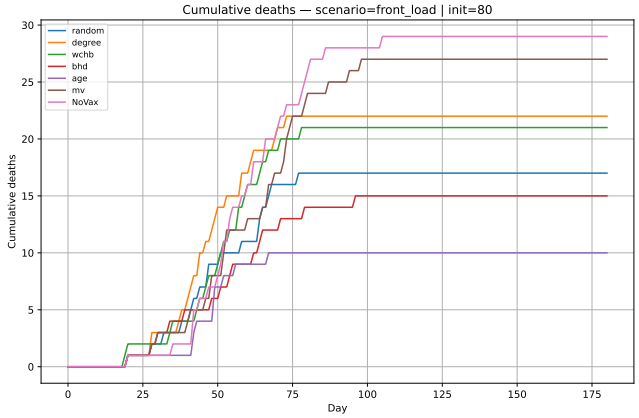

Figure 28: Covasim model with Front-load strategy with initial infected nodes = 80 on synthetic data.

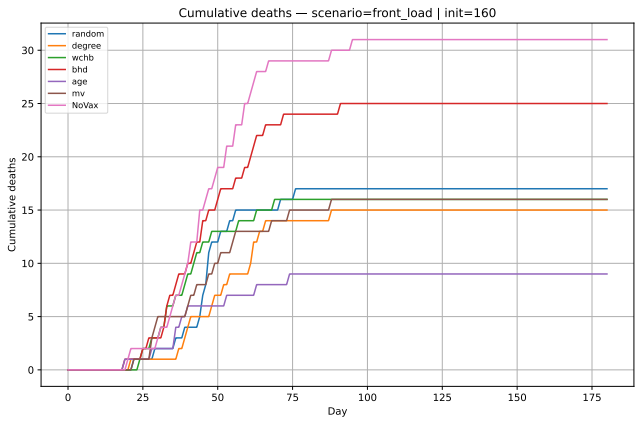

Figure 29: Covasim model with Front-load strategy with initial infected nodes = 160 on synthetic data.

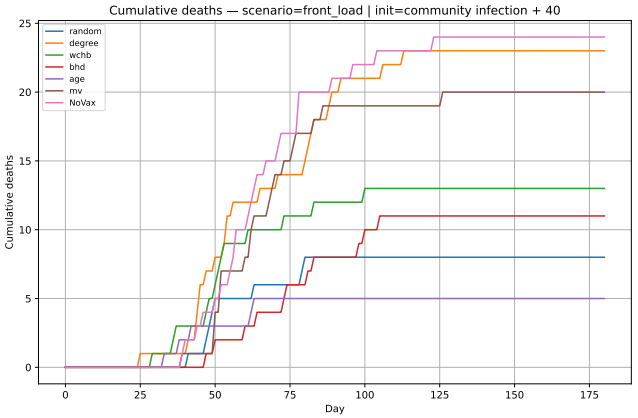

Figure 30: Covasim model with Front-load strategy with initial infected nodes as the first 40 nodes from the largest community structure on synthetic data.

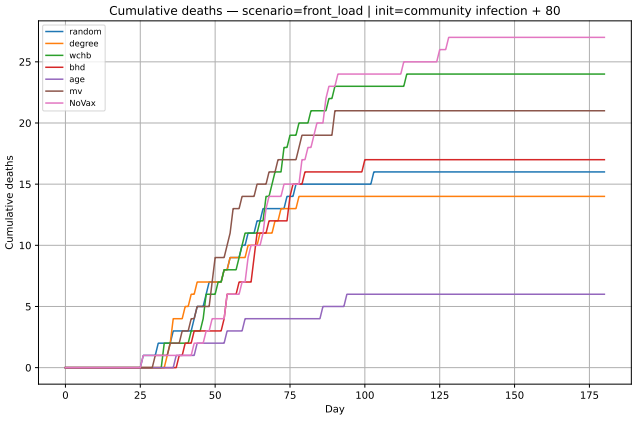

Figure 31: Covasim model with Front-load strategy with initial infected nodes as the first 80 nodes from the largest community structure on synthetic data.

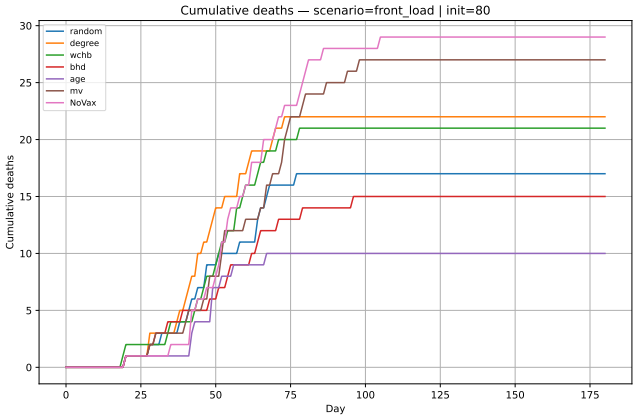

Figure 32: Covasim model with Trickle strategy with initial infected nodes = 80 on synthetic data.

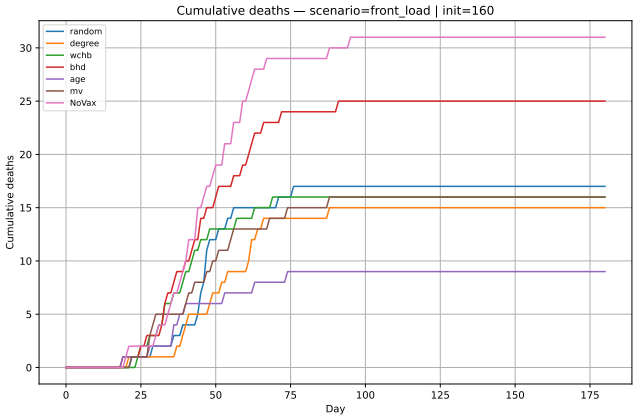

Figure 33: Covasim model with Trickle strategy with initial infected nodes = 160 on synthetic data.

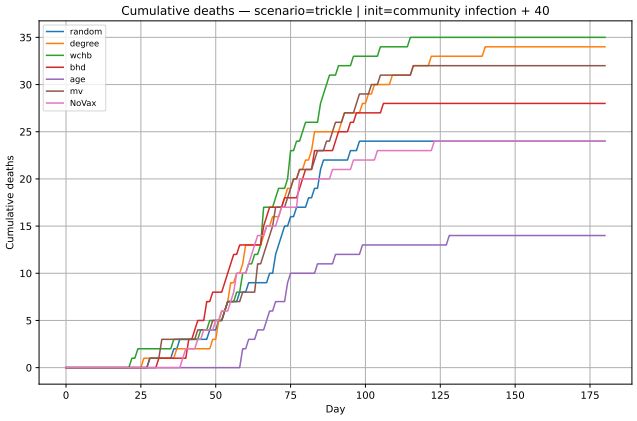

Figure 34: Covasim model with Trickle strategy with initial infected nodes as the first 40 nodes from the largest community structure on synthetic data.

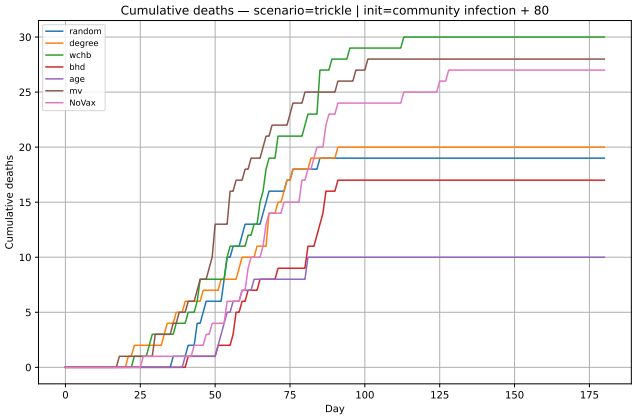

Figure 35: Covasim model with Trickle strategy with initial infected nodes as the first 80 nodes from the largest community structure on synthetic data.