

A network epidemic model with preventive behaviour

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Based on joint work with Frank Ball (Nottingham);
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Motivation

- Mathematically tractable epidemic models are valuable tools for understanding, predicting, mitigating, planning, ... in the context of infectious diseases.
- Classical models include several assumptions of homogeneity, many of which are unrealistic.
- A popular/common/useful/interesting departure from homogeneous mixing of homogeneous individuals is to incorporate structure through networks, modelled with random graphs, to (hopefully) capture population structures like social networks in human/animal populations, network connectivity of computers.
- Such models typically involve an epidemic spreading on a static network. We investigate a simple model where the network changes in response to the epidemic.

Outline

- SIR epidemics on a network/graph, in particular a *configuration model* random graph.
- Preventive behaviour during the epidemic: Individuals can ‘drop’ edges and possibly ‘rewire’ too.
 - Without rewiring: results on the mean and variance of the temporal evolution and final outcome of the epidemic.
 - With rewiring: not nearly that much detail, but some interesting qualitative results.

Ball, Britton, Leung and Sirl (2019). A stochastic SIR network epidemic model with preventive dropping of edges. *J. Math. Biol.* 78:1875–1951.

Leung, Ball, Sirl and Britton (2018). Individual preventive social distancing during an epidemic may have negative population-level outcomes. *J. R. Soc. Interface* 15:20180296.

Stochastic SIR epidemic on a network

Given a graph G (undirected), identify nodes with individuals and edges with 'friendships' and define an epidemic model:

- SIR (susceptible \rightarrow infectious \rightarrow removed) progression.
- Initially 1 infectious (chosen UAR) and $N - 1$ susceptible.
- Infectious individuals remain so for a random time distributed as I , then become removed.
- Infectious individuals make contacts with each neighbour in G at the points of Poisson Processes of rate $\lambda > 0$; if neighbour is susceptible it becomes infectious.
- Infectious periods and PPs mutually independent.
- Continue until no infectious individuals remain.

Classical model has $G = K_N$, $\lambda^{(N)} = \lambda/N$. Another simple-ish case is $G = G(N, p)$. Analysis is typically as $N \rightarrow \infty$.

Configuration model and SIR epidemics

- A random graph model with specified degree distribution.
- Two versions
 - Molloy-Reed: prescribed degrees $\mathbf{d}^{(N)} = (d_i^{(N)})_{i=1}^N$.
 - Newman-Strogatz-Watts: IID degrees $D_i \sim D$.

Both have the key feature that, asymptotically as $N \rightarrow \infty$, the degree of a uniformly chosen node is distributed as some random variable D . (MR/NSW: same mean, different variability.)

- Construction (NSW): Given $N \in \mathbb{Z}_+$ and $\{p_k\}_{k=0}^{\infty} \sim D$,
 - Assign $D_i \stackrel{\text{iid}}{\sim} D$ stubs / half-edges to node $i = 1, 2, \dots, N$,
 - Pair half-edges UAR to form edges in a graph.
- Run an SIR epidemic on the graph.

(Possible imperfections; no clustering, no assortativity, ...)

SIR epidemics on networks: methods/results

- Early stages & Final outcome
 - Generation-based (GW) or real-time (CMJ) branching process approximations for early stages: threshold results and chance of a large outbreak with few initial infectives.
 - Susceptibility sets, generation based approach for investigating final outcome: mean (and variance) of final size.
- Full temporal behaviour
 - Usually deterministic: mean-field models, pair approximations, moment closure,
 - Varying degrees of rigour and interpretation of 'approximate'.
- For the CM-SIR epidemic, quite a bit known in the former category but in the latter category known results are in the Markov case and address the mean but not the variability.

Our model: CM-SIR with preventive measures

- CM network model, SIR progression as before but Markov (so $I \sim \exp(\gamma)$).
- Also let each susceptible neighbour of an infective drop their connection to the infective at rate $\omega \geq 0$.

So infectives

- infect each neighbour at rate λ ,
- recover at rate γ ,
- 'inform' each neighbour at rate ω ,

Later:

- With probability α , a susceptible that drops an edge replaces it with an edge to an individual chosen uniformly from the population.

Analysis of model with dropping

- Model proposed by Britton *et al.*¹, with SEIR dynamics.
- Britton *et al.* analyse the early stages (reproduction number R_0 and Malthusian/exponential growth rate r).
 - Branching process approximation.
 - Pair approximation (deterministic ODEs for the number of singletons, pairs, triples, ... of individuals in the various disease states); system of 10 ODEs (7 for SIR).
 - Amongst other things, they show that rewiring can make the epidemic worse (in terms of R_0 and r) in the SEIR case.
Explanation: E-I links rewire to E-S, which become I-S after the latent period, facilitating more infection than without rewiring.
- We investigate, for the SIR model,
 - temporal and final size behaviour without rewiring, and
 - some final size properties with rewiring.

¹Britton, Juher & Saldaña (2016).

Results I

- Construct the network and the epidemic at the same time; using an effective degree approach².
- Theory of *density dependent* Markov chains³ yields LLNs and CLTs for many quantities of interest.
- Example 1: Final size Z satisfies, for large outbreaks in large populations of size N ,

$$Z \stackrel{D}{\approx} N \cdot z + \sqrt{N} \cdot N(0, \sigma^2)$$

with $z \in (0, 1)$ and $\sigma^2 > 0$ available theoretically and numerically.

²Ball and Neal (2008).

³Ethier & Kurtz (1986, Chapter 11).

Results II

- Example 2: The number of infectives $I(t)$ ($t \geq 0$) satisfies

$$I(t) \stackrel{D}{\approx} N \cdot x(t) + \sqrt{N} \cdot G(t),$$

with $x(\cdot)$ solving a system of ODEs and $G(\cdot)$ a zero-mean Gaussian process with covariance function computable numerically at the same time as $x(\cdot)$.

- ICs involve starting with a positive fraction of infectives.
- Total of $(2M + 4)(2M + 3)$ ODEs if allowing degrees $\leq M$.
- The system of ODEs underlying $x(\cdot)$ reduces to a single driving ODE⁴.

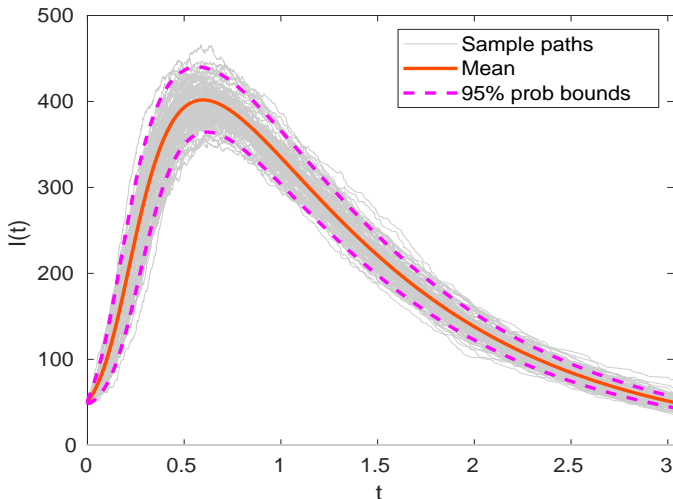
⁴cf. Volz (2008); Miller, Slim & Volz (2012) when $\omega = 0$

Some numerical illustration

- Use $D \sim \text{Geo}(1/6)$; has $\mu_D = 5$, $\sigma_D \approx 5.5$.

(Has unbounded degrees, even though theory 'requires' a maximum degree M .)

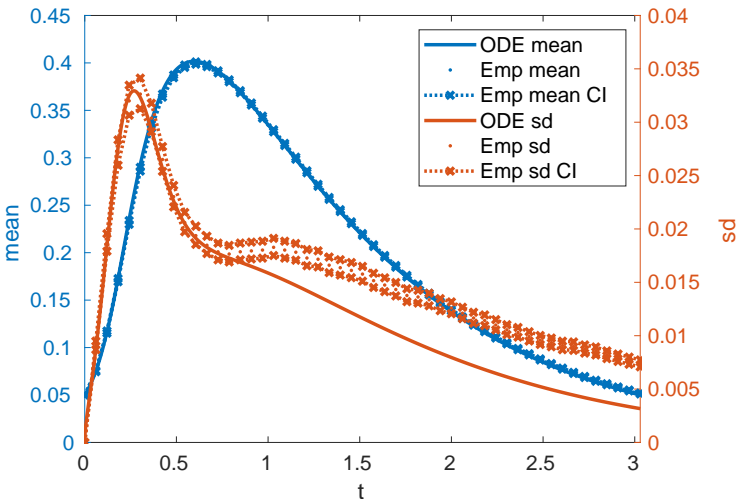
Temporal CLT



100 simulated trajectories of $I(t)$ and CLT predictions.

Parameters are $N = 1000$, $\lambda = 3/2$, $\gamma = 1$, $\omega = 1$, $i_0 = 0.05N$.

Temporal CLT 2

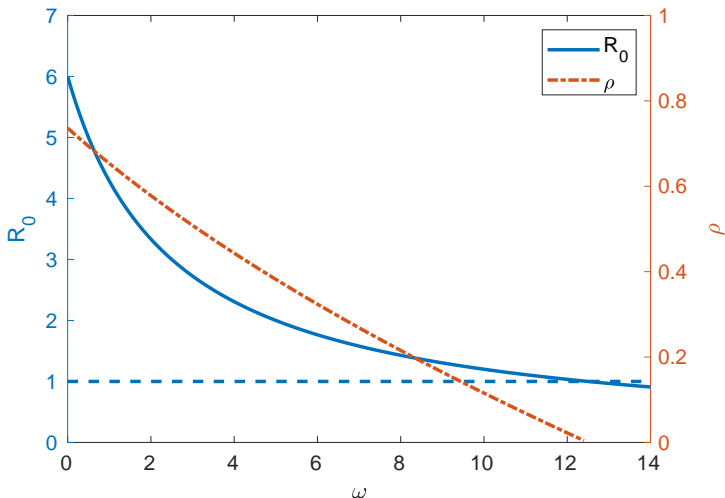


Mean and sd of 1000 simulated trajectories of $I(t)$ and CLT predictions. Parameters are $N = 1000$, $\lambda = 3/2$, $\gamma = 1$, $\omega = 1$, $i_0 = 0.05N$.

Exploring the model

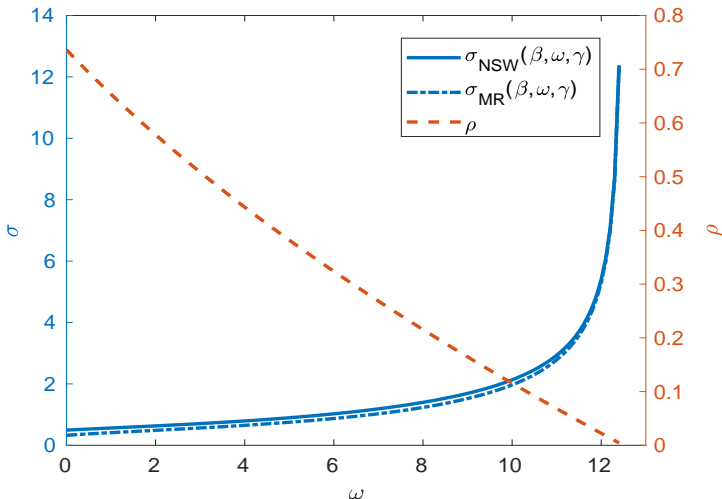
- The asymptotic results provide good approximations to quantities of interest for finite populations.
- So (with only minor caveats) we can explore the behaviour of the asymptotics to learn about the properties of our model in finite populations with N in the hundreds (or larger).

Effect of dropping



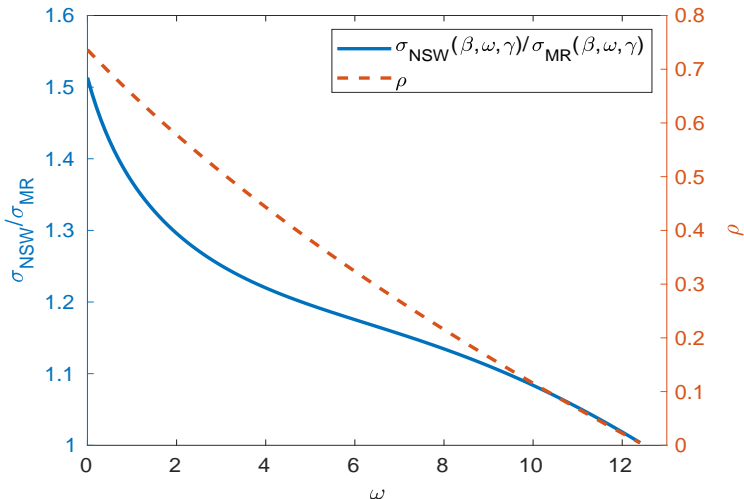
Impact of increasing the dropping rate ω from zero.
Baseline model has $\lambda = 3/2$, $\gamma = 1$, $i_0/N \downarrow 0$.

Effect of graph type



Comparison of final size variability for NSW and MR graphs as dropping rate increases. Baseline model has $\lambda = 3/2$, $\gamma = 1$, $i_0/N = 0$.

Effect of graph type 2



Comparison of final size variability for NSW and MR graphs as dropping rate increases. Baseline model has $\lambda = 3/2$, $\gamma = 1$, $i_0/N = 0$.

Some observations/comments

- DD theory assumes a positive initial fraction infected; we let this fraction go to zero with initial infectives being chosen UAR, not as those infected by an emerging outbreak⁵.
- DD theory applies only when there is a maximum degree.
 - Bounded degree sufficient for most practical purposes.
 - Would like to extend to unbounded degree
(\exists LLNs for $\omega = 0$ and a CLT for $\gamma = \omega = 0$ with moment assumptions on D).
 - Numerical results support the conjectured extensions.
- Extend to non-Markov case?
- Extend to more complex population structures?

⁵Ball & House (2017).

Our model: CM-SIR with preventive measures

- CM network model, Markov SIR epidemic (so $I \sim \exp(\gamma)$).
- Also let each susceptible neighbour of an infective drop their connection to the infective at rate $\omega \geq 0$.

So infectives

- infect each neighbour at rate λ ,
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Additionally:

- With probability α , a susceptible that drops an edge replaces it with an edge to an individual chosen uniformly from the population.

Social distancing is beneficial...

- Suppose that I'm susceptible and my neighbour 'informs' me that they are infectious; so I drop the edge.
- What can happen next?
 - No rewiring.
 - Rewire to a removed individual.
 - Rewire to a susceptible individual.
 - Rewire to an infectious individual.

⇒ I might be better off; and I cannot be worse off.

- But is the population as a whole necessarily better off?

Some networks

We study this model on:

- The standard CM network.
- A CM network with cliques.
 - In the CM network model, partition the population into groups/cliques of 3 individuals. In addition to CM connections, connect individuals in the same clique.
- Empirical networks.
 - arXiv General Relativity collaboration network and Facebook social circles network⁶.
 - 2 'Infectious sociopatterns' networks, SG1 and SG2⁷.

⁶Leskovec & Krevl (2014).

⁷SocioPatterns collaboration (2011).

Results

- With CM network structure:
 - Threshold parameter R_0 decreases with ω .
 - The mean final size of a large outbreak can increase with ω .
- With CM network + clique structure:
 - A threshold parameter R_* (clique-to-clique reproduction number) can increase with ω ; possibly from below to above threshold.
 - But R_* always decreases with ω for sufficiently large ω .
 - The mean final size of a large outbreak can increase with ω (even when R_* doesn't).
- On the empirical networks:
 - We 'usually' observe straightforward 'social distancing helps', but
 - we also observe all possible combinations of these behaviours, for some plausible values of other parameters.

Some observations/comments II

- A variety of behaviours of final size properties as dropping is introduced/increased.
- Final size increasing with dropping rate ω is more likely when
 - the 'baseline' epidemic is well above criticality,
 - the network has many individuals of low degree,
 - the network has many components,
 - the rewiring probability α is higher.

Summary & future

- Temporal and final size LLN and CLT for a SIR-CM epidemic with dropping of edges.
- Some interesting behaviour when rewiring is allowed too.
- Further work on the model with rewiring.
- Obvious extensions like households, the non-Markov case, vaccination,

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