

Stochastic methods: past, present and future Part II

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What is our goal?

Two extreme types of modellers

- People who want to study nice probability theory and need inspiration for models (or a real-life applications for funding)
 - Bias towards critical systems
 - “Physicist's proofs” are not good enough
- People who want to provide some contribution to public health
 - Bias towards super-critical systems
 - interest in some quantitative results

Some directions of future research

- Population dynamics and leaving the SIR framework
- Spatial epidemics and percolation
- Behavior change
- Phylogenetics and epidemics
- Useful parameterizations (not discussed here)

Static population and demographic turnover

Consider an SIR epidemic in your favorite structured population
Allow for individuals to be replaced by susceptibles

- Model close to SIRS model
- No longer possible to ignore time
- Even on a line this model is not trivial

Open problem

- Markov SIRS epidemic on square lattice
- Given recovery and “regaining susceptibility” rate

It is not known whether

- Probability of a large outbreak is non-decreasing in the infection rate
- It is possible to define a critical infection rate, below which an epidemic is not possible and above which it is?

Dynamic populations

- Assume that in a household population individuals can die and newcomers can come in. Furthermore, individuals can migrate between households
- Assume that in a network population individuals can die (and so connections disappear) and newcomers can come in, acquiring new relations. Furthermore, relationships can be broken and new relationships can be formed.

Households

- If households are all large, multi-type populations can be analyzed
- If households are of moderate size, troubles appear
 - Even in static household models, probabilities for final sizes in SIR models have terrifying expressions (although elegant algorithmic representations)
 - We have to keep track of real time dynamics: How long does an epidemic restricted to a household last?
- Question: Is it possible to create inter-household dynamics for which we have “friendly” expressions to do further computations with?

Dynamic networks

- The network itself need to be studied
 - Asymptotic quantities
 - How sensitive to details of the model formulation
- Epidemic is influenced, because of new connections to susceptibles
- Some modeling possible in Markovian models in which network size grows to infinity (See work by Britton, Turova and co-authors)

Interlude: What is R_0 ?

- in uniformly mixing population n individuals are represented by n vertices
- An edge is drawn from the vertex representing the initially infectious individual to every individual it contacts during its infectious period
- From the vertices at graph distance k of the origin, edges are drawn to all vertices that
 - 1 they contact during their infectious period
 - 2 are not within graph distance $k - 1$ of the origin

- The start of an epidemic in a large population, is well approximated by a Galton-Watson branching process
- Initial infective is generation 0 individual
- Neighbors (in graphical representation) of generation k individuals, that are not in generation 1 up to k , are in generation $k + 1$
- The basic reproduction number R_0 is the expected number of generation 1 individuals, i.e. the offspring mean in the approximating branching process (i.e. the number of individuals at graph distance 1 of the initial infective in the graphical representation)

- Let $Z^{(k)}$ be the size of k -th generation of branching process
- Let $|\mathcal{B}_k| := \sum_{i=0}^k Z^{(i)}$ be the number of individuals in the first k generations of the branching process.
- From branching process theory we know that if $R_0 > 1$, then $(R_0)^{-k} |\mathcal{B}_k| \rightarrow W$ a.s., with W a non-trivial random variable
- For epidemics: we will use a variant of R_0 :

$$R_0 := \lim_{k \rightarrow \infty} \lim_{n \rightarrow \infty} (\mathbb{E}(|\mathcal{B}_k|))^{1/k}$$

where n is the number of individuals in the population

- This definition makes also sense for network and multi-type epidemics

Back to space

- Consider square lattice
- Contacts are only possible between individuals within distance M of each other
- $|\mathcal{B}_k| \leq (2kM + 1)^2$ and therefore
 $(\mathbb{E}(|\mathcal{B}_k|))^{1/k} \leq (2kM + 1)^{2/k} \rightarrow 1$ as $k \rightarrow \infty$
- In general R_0 does not make sense/is useless in spatially organized population
- Long-range percolation can be used

(Nearest-neighbor) percolation

What is percolation?

- Consider \mathbb{Z}^d with nearest neighbor edges
- For each edge flip a (biased) coin. If heads (with probability p) keep the edge, if tails (with probability $1 - p$) delete the edge
- Let $\theta(p)$ be the probability that the origin is part of an infinite cluster

Questions of interest:

- Will there be an infinite cluster?
- Is there a critical $0 < p_c < 1$ such that
 - $\theta(p) = 0$ for $p < p_c$
 - $\theta(p) > 0$ for $p > p_c$?

(Answer: Yes, for $d \geq 2$)

- If there is an infinite cluster, will it be unique and will it have positive density?(Answer: Yes)
- What happens at p_c ?(Answer: Physicists know and mathematicians believe: no infinite cluster)
- What is the value of p_c ?(In general: Nobody knows)

But ...



In 1980 a paper by Harry Kesten appeared, with the title:
“The critical probability of bond percolation on the square lattice
equals $1/2$ ”

And abstract: “We prove the statement in the title of the paper”

Long-range percolation

Construct a random graph:

- vertex set \mathbb{Z}^d
- an undirected edge between vertices x and y is present with probability $p(x, y) = p(\|x - y\|) = 1 - e^{-\lambda(\|x - y\|)}$
- The presence or absence of an edge is independent of the presence or absence of other edges

Interesting from mathematical perspective even in super-critical regime (work by Biskup, Berger, Newman and others)

How fast epidemic can grow depends on $\lambda(r)$

What to do next?

- What if population is not a lattice or homogeneous Poisson process?
- What do real populations and networks look like?
- What if our estimates for R_0 are close to 1?
- Can we do anything with *SIS* dynamics?

Behavior change

- If we have a new frightening disease around, people or governments will take measures, which will lead to changing parameters (real time dynamics/ duration of epidemic is important)
- It becomes harder/more interesting if people take measures depending on what they observe in their neighborhood (ring vaccination for animal diseases)
- For network epidemics: Does information spread along same channels as disease? Is there a relation with competing disease models or re-infection models?

Phylogenetics and epidemics

A lot of discussion coming up in Oberwolfach, November 2013