Stochastic methods: past, present and future.
Part I

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Isaac Newton Institute, Cambridge, 19 August 2013
Programme on Infectious Disease Dynamics
19 August - 13 September 2013
Stochastic methods: past, present and future

- Stochastic methods: *generic stochastic modelling* where focus is on representing and understanding a *process*
  excl. model-data interactions, model fitting, models for specific applications
- Past: just before 1993
- Present: 1993–2013
- Future: 2013 onwards

*Historical perspective and scene setting for later sessions.*
In the beginning ...

... was the word and the word was $R_0$ (more later).

- Extension of basic SIR compartmental model to range of human, animal and plant infections
- Control issues paramount, thresholds determined for different scenarios
- Processes described in stochastic terms but often analysed deterministically
  - densities in large populations, discrete counts ignored
  - pitfalls not always appreciated e.g., the attofox (DM91)
  - easy numerical solution, possibility to incorporate realistic details
- (Better) approximations to full stochastic model e.g., moment closure methods being explored, limiting Gaussian diffusions (Whittle 57; Kurtz, Barbour...70s)
The proposal 1990-91

- 1990 Idea of proposal to newly-formed INI hatched at Skokloster workshop on stochastic modelling and data analysis
- Two fundamental problem areas identified:
  - Dependence of the rate of spread on population heterogeneity and connectivity of the contact structure
  - Determining the basic parameters that drive complex models, and the sensitivity of the dynamics to the way in which these are incorporated into the model
- Integration of deterministic and stochastic approaches was needed, and comparison of basic properties such as dynamics and thresholds
- Examples included spatial models and comparison of chaotic and time series modelling of childhood diseases, then a topical issue
- Useful approximations to solutions of stochastic models, and conceptual counterparts in stochastic models to the qualitative results involving bifurcation and thresholds in deterministic models also needed
Participants (det and stoch, theory and apps, maths and life sci) included Norman Bailey, Henry Daniels, John Jacquez

$R_0$ featured prominently, now on a firm (deterministic) footing (JAPH92). The term ‘reproduction rate’ was outlawed

Three one week workshops: scene setting; animal infections; human infections

- **Scene setting**: Papers on generic stochastic models covered model structure (DM), coupling methods (FGB), the final outcome (L&P), thresholds (IN) and spatial (lattice) epidemic models (RD)
- **Applications**: Many deterministic analyses (allowing for random variability of parameters over the population) — numerical progress without resorting to stochastic simulation (more a computational deterrent then)

One day workshop on network models including random graph models (DM)

Judgement day: short contributions from long-term participants including space (DM), structured models (FGB), model approximations (VI) and SIS models (IN)
RSS discussion meeting

Key challenges (all of relevance to stoch modelling):

- **heterogeneity** (population and mixing)
- **thresholds and persistence** - effects of pop size, fade-out, edge effects
- **nonstationarity** - weather, behaviour, demography, evolution
- **control** - effects of interventions, optimal strategies

Topics included

- det-stoch comparison, stoch counterparts to det nonlinear phenomena, randomness vs det chaos, approximations via moment closure, model parameterisation

Discussion contributions included:

- coupling (FGB, WSK), preliminary results announced for household model (BMS-T97); understanding $R_0$ in structured populations; hybrid models and perturbation approximations (IN); immunoepidemiology (KD); interacting particle systems (AB)
• **Metapopulations** (surrogates for spatial structure): coupling and branching process approximations - thresholds for spread, final size distributions (Ball and many collaborators)

• Generalisation to **overlapping** groups of hosts (Ball & Neal)

• Host heterogeneity: **multitype** epidemics (Ball & Lyne)

• Extensions: vaccination and isolation, infector and exposure-dependent severities (Ball & Britton +)

• Variations: **SIS**

• **Movement** of hosts between locations

• Groups with underlying **network** structure (Ball, Sirl & Trapman)
1993–2013: Approximations

- Poisson approximations (Ball & Neal)
- Quasi-stationary distributions *e.g.*, SIS (Clancy & Pollett)
- Piecing together the epidemic curve - forward and backward branching processes (Barbour & Reinert)
• Models for random networks and their properties (e.g., Bollobás, Chung & Lu, Durrett):
  • Generalisations of Erdös-Rényi: node-dept edge probs
  • Configuration graphs, scale-free graphs
  • Random geometric graphs (Penrose; clustering and correlation)
  • Rewiring algorithms

• Epidemics on networks
  • Effect of network structure on dynamics
  • Empirical observations that clustering plays a big role in limiting spread
  • Formal confirmation (Ball, Britton & Sirl) of this and that spread increases with correlation just above threshold, but decreases when well above the threshold
  • Role of the spectral radius of the network (Draief, Ganesh & Massoulié)
Macroparasites: Expansion of state space (part of parasite life-cycle external to host, load increases through re-infection) - parasite stages per host, immune responses, parasite genotypes, gender (mating)

- Model simplification - focus on particular aspects of physical process, reduce/eliminate nonlinearities
  - Remove feedback loop e.g., early-season helminths in sheep, a high degree of spatial clustering can lead to a dramatically enhanced rate of invasion by drug-resistant strains (Cornell, I. & Grenfell)
  - Remove immune reaction (Herbert & I.; retain parasite-induced host mortality)
  - Hybrid models e.g., competition and coexistence of multispecies infections (Bottomley, I. & Basáñez)
  - Branching process approximations - use of promiscuous G-W metapopulation model to show stoch fluctuations can enhance the chance of spread (Cornell & I.)
  - Moment closure approximations (Grenfell, I. +)
But nonlinearities are important and simulation can be a last(?) resort e.g., for helminths...
  - when rare, spread of infection can be more likely and more severe in small host populations

Many challenges for further work ...

Immunoepidemiology for microparasites?
• The theory of percolation may be used for modelling SIR epidemics where infectious periods are not random
• Excellent book written by Grimmett
• Since 2000 most work in direction of 2 dimensional percolation and the critical behavior through Schramm-Loewner evolution (scaling limit; led to fields medals for Werner and for Smirnov)
• Work by Miller, Kenah and Meester & Trapman led to extensions where infectious periods are random
The contact process is the Markov SIS epidemic. For overview see book by Liggett. Interesting behavior even on the 1 dimensional line, where individuals can only infect their nearest neighbors. On networks represented by regular trees there are three regimes:

- extinction
- weak survival: Epidemic goes on forever, but everybody will get infected only finitely many times (and some not at all)
- strong survival: Epidemic goes on forever and everybody will be infected infinitely many times

Durrett and Jung showed difference between weak and strong survival on (a variant of) small-world networks. Chatterjee and Durrett showed that there is no subcritical regime for SIS epidemics on power-law (configuration model) random graphs, not even if the power is above 3 (in contrast to claims of Vespignani and Pastor-Satorras).
If individuals are located in some (metric) space and contact rates between individuals depend on their distance, then long-range percolation is useful to model SIR epidemics.

It was introduced in the 80’s by Schulman and Newman, with main focus on phase transition: (at criticality there is an infinite cluster in a natural 1 dimensional model).

In this century Berger, Biskup, Schramm and others looked at super-critical long-range percolation, mainly at diameter of percolation graph if restricted to large component in a large box.

Dawson and co-authors and Koval, Meester & Trapman looked at long-range percolation in hierarchically structured populations.

Overview in 2011 paper of Biskup.
2013 onwards: Networks

- Threshold equivalents of $R_0$, final size results and dependence on network topology. Role of spectral radius of network
- Blend local and global scales to create flexible yet parsimonious models of dynamic networks
- Time-evolving network models: creation and annihilation of nodes as well as edges
- Dynamic evolution of processes on networks that alter the underlying network structure
- Movement of nodes in spatial case - cf mobile networks, virus spread via on board vehicle navigation systems etc