Stochastic methods: past, present and future.
Part I

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- 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.

... 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)

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- 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

1993 programme: current issues

- Participants (det and stoch, theory and applics, 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)

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)

- 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
  - Congfiguration 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

- 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