Disease challenges of the 21st Century: challenges for modelling

Neil Ferguson

MRC Centre for Outbreak Analysis and Modelling
Faculty of Medicine
Imperial College

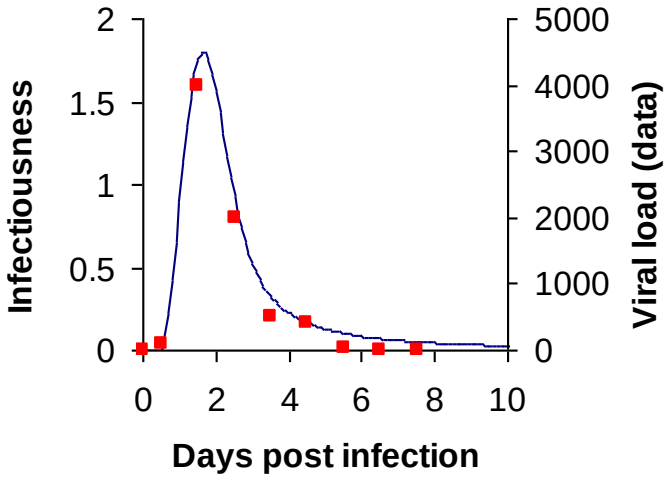
Issues

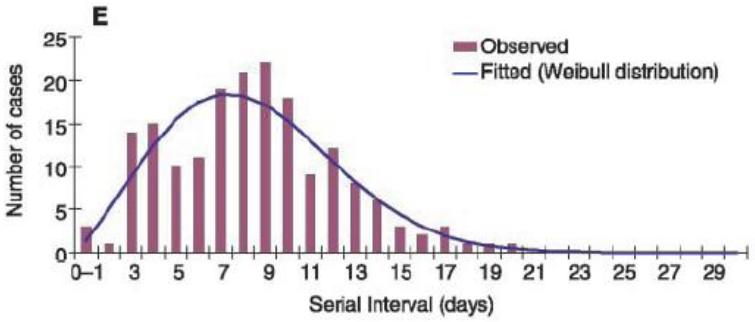
- **Technical**:
  - ➢ Better natural history / transmission models.
  - ➢ Quantifying and validating proxy measures of ‘infectious contact’ patterns.
  - ➢ Integration of model scales.
  - ➢ Inference methods
  - ➢ Data needs.
  - ➢ Maintaining simplicity.

- **General:**
  - ➢ Motivations for modelling – where’s the (public health) beef?
  - ➢ Conflicting priorities – emerging infections vs the big 3, rich vs poor.

Natural history models

- People do not have constant infectiousness…
- …or exponentially distributed infectious periods.
- Critically important issue if considering ‘case-centred’ interventions with delays.
- Need to estimate infectiousness over time from epidemiological data…
- …perhaps informed by shedding data.
- Or at least estimate true generation time distribution (eg Wallinga & Lipsitch).
- Variability between individuals potentially important – by age, or intrinsic (‘superspreading’).
- Modellers need to cite primary data!





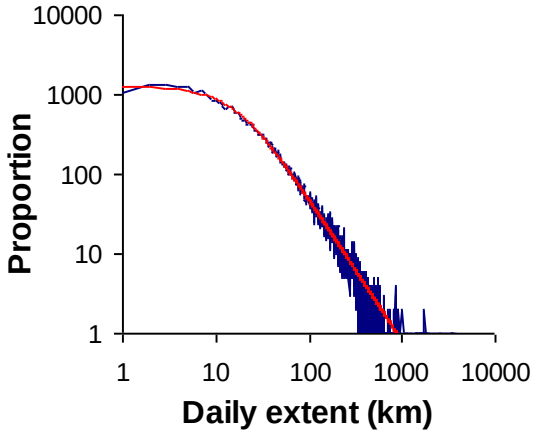
Transmission models

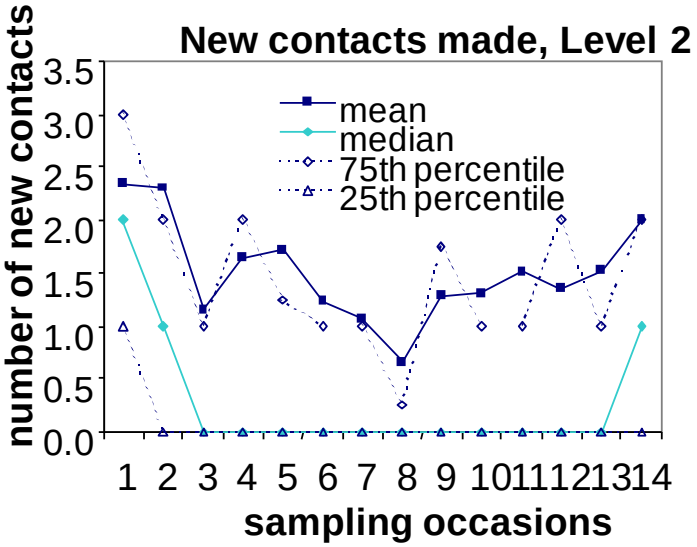
- How does infectiousness partition between contacts?
- … and scale with number of contacts? - probably not Reed-Frost.
- - acts vs partnerships issue.
- Makes a huge difference – esp with (absurd) scale-free networks.

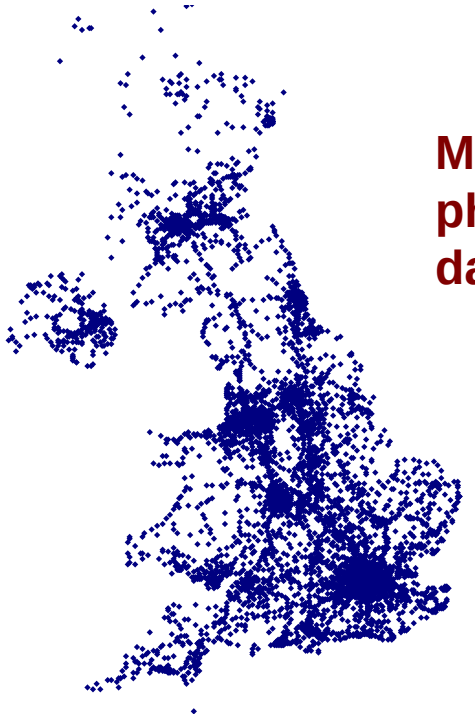
- Need better mechanistic models of transmission.
- … and data.

Contact/movement patterns

- Need data on local network structure and dynamics and on large-scale (spatial) structure of interactions.
- Travel/interaction data key to building this new generation of realistic socio-spatial models.
- Need to validate models against disease data…but how?



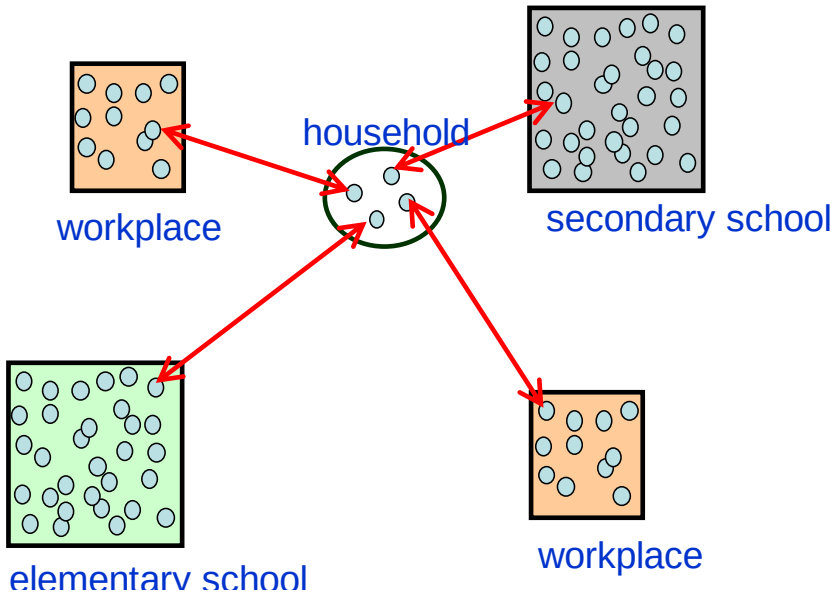


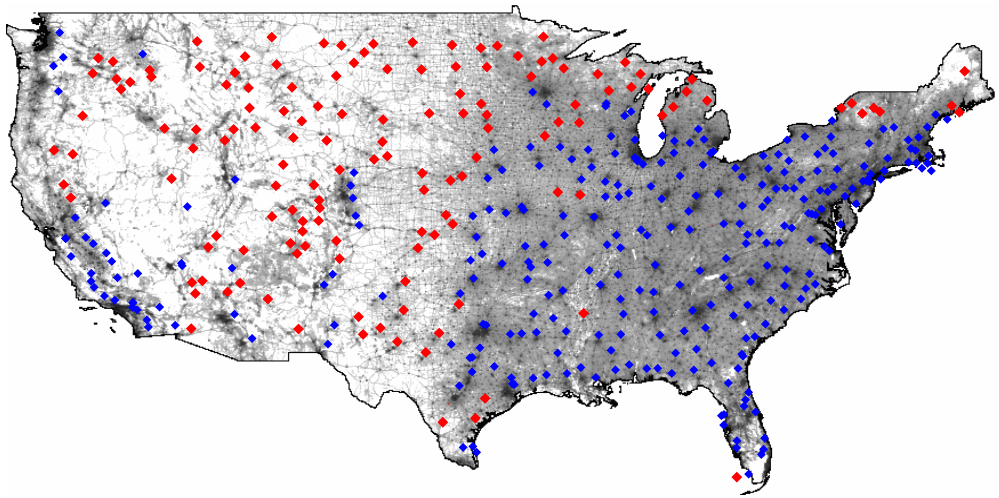


Mobile phone data

Integration of scales

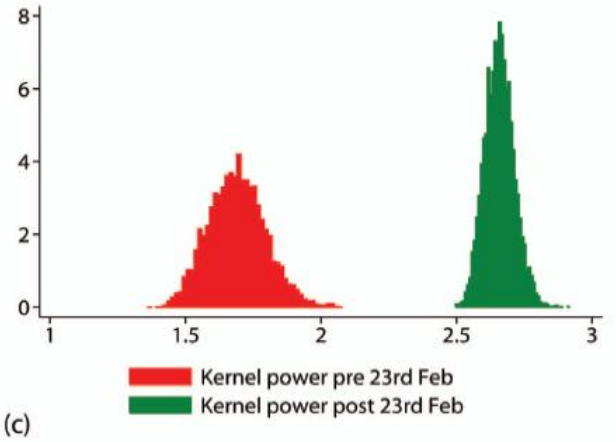
- Network paradigm useful conceptually, but often too fuzzy for practical use.
- Assumption of constant link strength particularly problematic.
- Multiple levels of mixing arguably a more satisfactory way of representing persistent contacts.
- … but then how do we represent casual contacts.
- End up partitioning transmission rather arbitrarily – and introducing a component of localised mass-action.

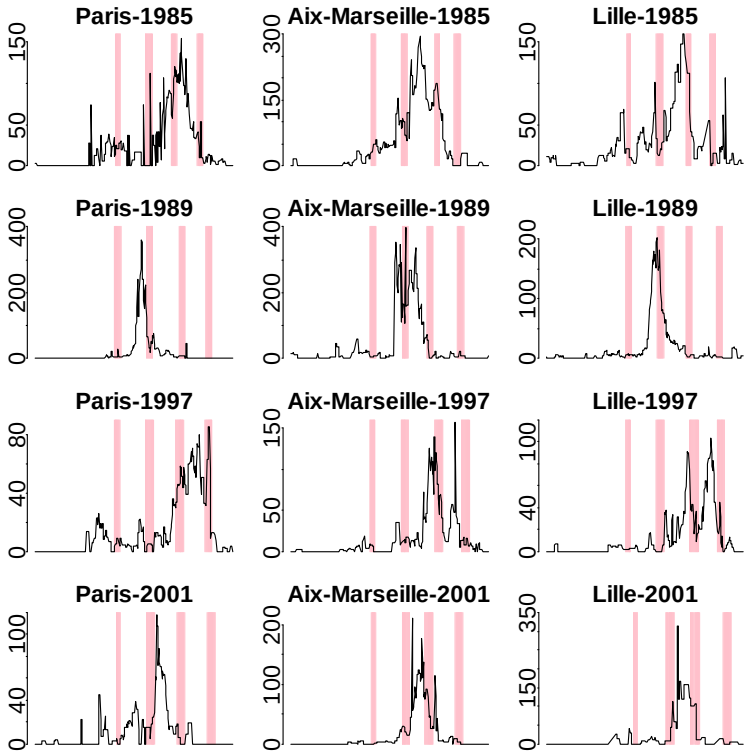




Inference

- As modelling expected to be ever more predictive, parameter estimation ever more critical.
- Optimally would like to estimate parameters from epidemic (and study) data using the same model used for prediction.
- MCMC fine for moderate scale closed epidemics (e.g. FMD, SARS).
- … but what about fitting national flu surveillance data to a model with households and schools?
- Need new approaches to make inference computationally tractable (e.g. constrained simulation/importance sampling/EM approaches).



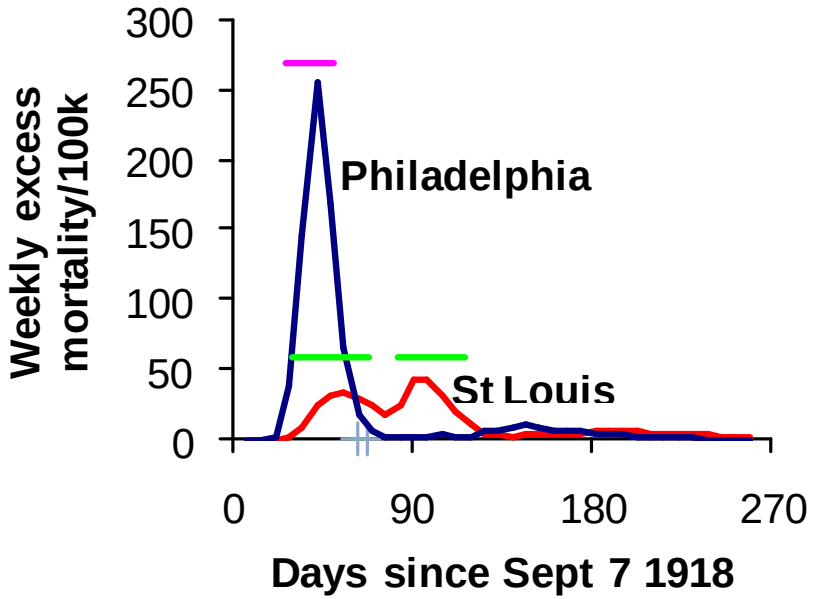


Data needs

• Data needs to be collected with modelling in mind – can only happen via collaboration with public health agencies and ID clinicians.

• Need data (from studies or historical analysis) on:

- ➢ spontaneous behavioural responses to epidemics (e.g. HIV, SARS, 1918 flu).
- ➢ effectiveness of 'behavioural modification' methods – i.e. social distancing/NPIs.
- ➢ transmission mechanisms and rates of transmission in different contexts.
- ➢ spatial/seasonal heterogeneity in transmission…
- ➢ etc…



Maintaining simplicity

• Default position should be to leave out population structure, unless:

- ➢ data exist to parameterise transmission.
- ➢ or controls are likely to target that structure (e.g. households, schools, geographic areas).

• Similarly with disease biology – though to non-modellers, exponentially distributed infectious periods are not ‘simple’.

• Need to be honest about data limitations.

• Many problems with current pandemic models in this regard (e.g. Elveback & Fox, Longini and Germann model, Glass model, EpiSims…).

• Leads, for instance, to unsupportable predictions about school closure/social distancing.

• Similar problem for animal diseases (e.g. EpiMan).

• Large scale not necessarily complex though.

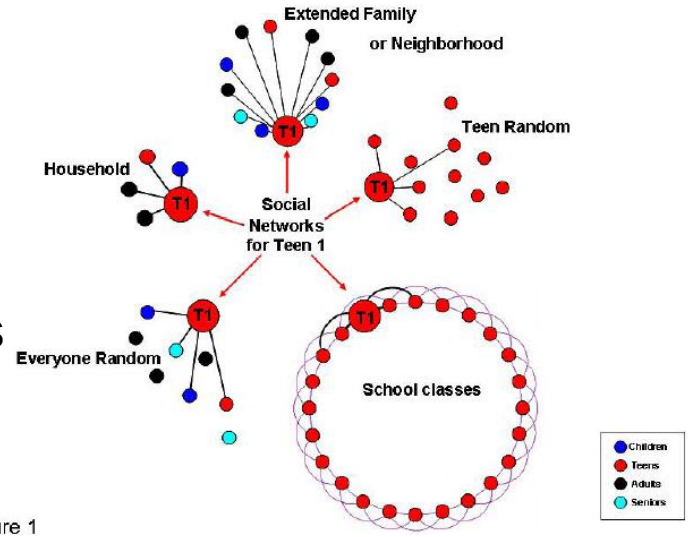


Figure 1

Why do we model?

- *Maths*: Because epidemics are interesting examples of branching processes.
- *Ecology*: Because epidemics are interesting ecological systems with interspecific non-linear interactions.
- *Public health*: Because understanding and modelling epidemics will inform clinical and public health practice and policy-making.

• Nearly everyone argues the public health case when raising money, writing high-profile papers…

•… but how much has your work actually done to improve outbreak response, clinical practice, surveillance, etc?

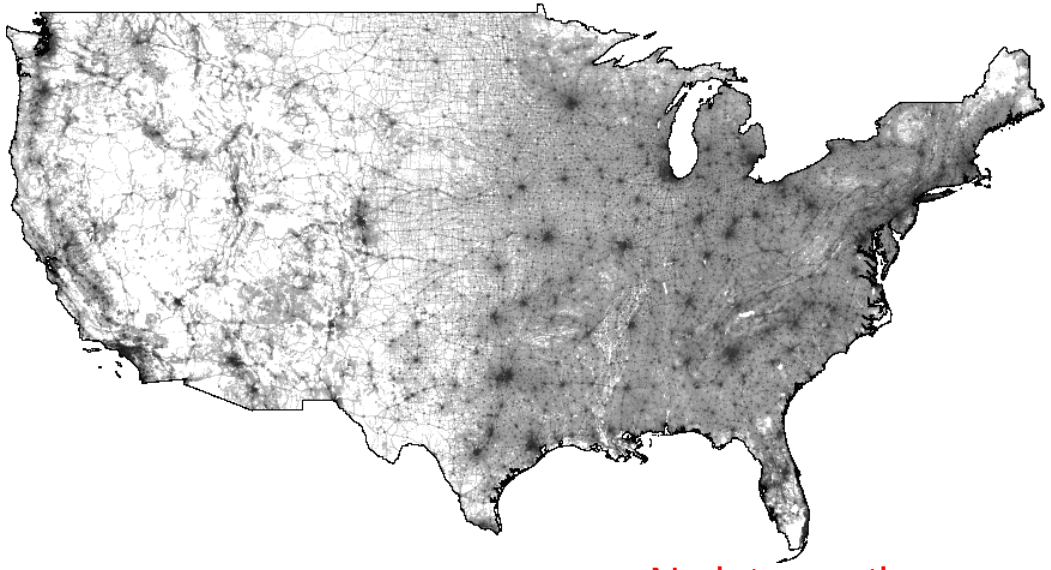
• We need to make much more effort to ensure our work gets translated into real public benefit – funders will expect it and monitor this in future.

• Needs real engagement with medics, vets, public health people, govt.

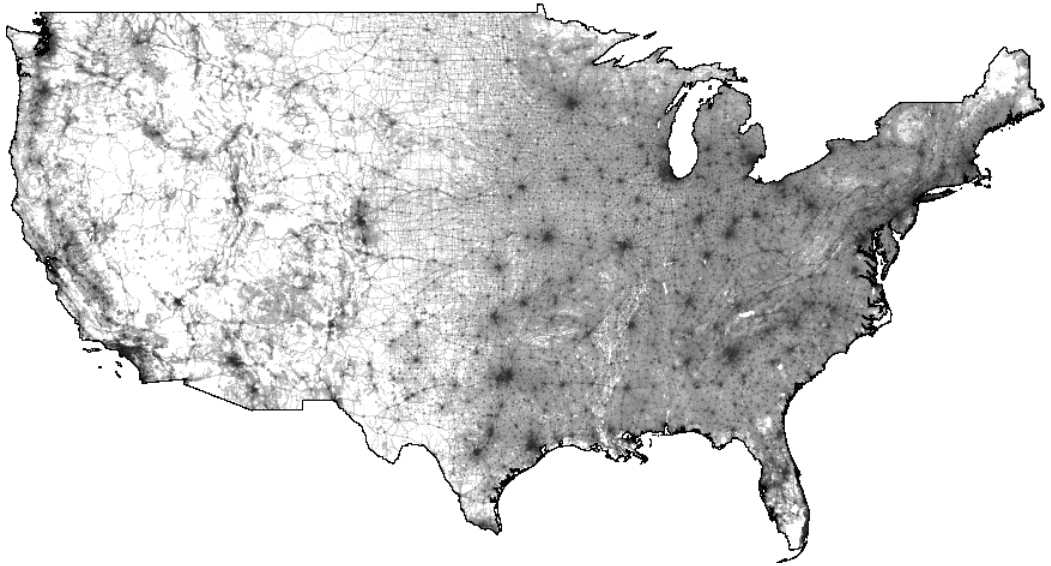
Wider political issues

- 9-11/SARS/H5N1 has focussed short-term attention/money on novel disease outbreaks.
- How do we sustain preparedness, once ‘bird-flu’ has dropped off the media agenda?
- How do we balance preparing for lethal pandemics, against immediate demands - HIV, malaria, TB etc?
- How do we make surveillance and response systems multi-purpose (e.g. to detect other zoonoses, to benefit general healthcare)?
- Should modellers be development advocates, or optimise response within externally defined constraints?
- How do we engage/build capacity in key developing regions (China, India, Africa)?

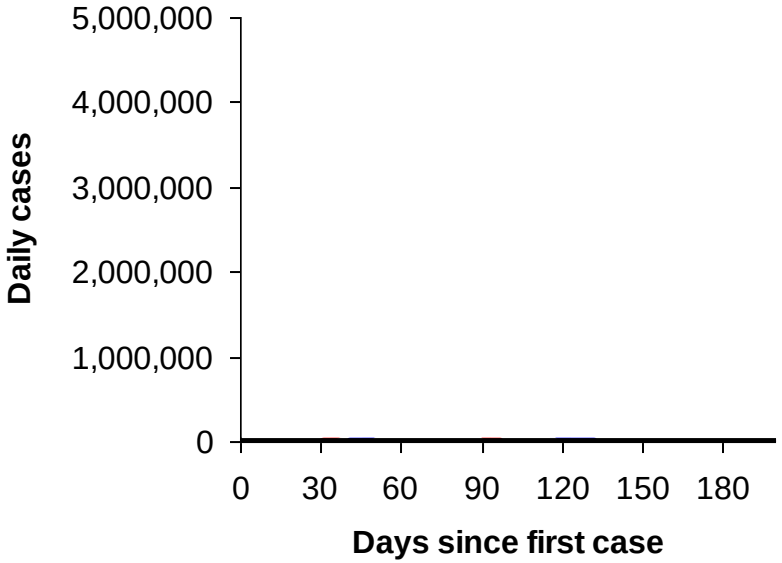
The movie moment!



No intervention



With intervention



Intervention : next-day treatment of 90% of cases with anti-virals, reactive school closure, 50% household quarantine.