Introduction

- Network models are an important class of models in epidemiology, which can produce realistic predictions on disease systems, for the case of heterogeneous populations.

Then we have (Volz 2007b) for all $k \geq 0$, $\frac{3}{2} + 2\phi_k = \phi_{k+1}$, so that the proportion of nodes of degree $k$ gets “depleted” at rate $\phi_k$, i.e. it times faster than nodes of degree $1$. It can also be shown that $S_t = g(S)$, where $g$ is the p.g.f. of $K_t$. If we now denote $K^*_t$ as the degree of a random infected, then the number of new cases arising from this individual at time $t$ is Binomial $N(S_t\frac{\beta}{\alpha}\theta S_0(\theta_1)$. Since, on average, only a fraction $S_t$ of its contacts will still be susceptible. From this, we can derive the epidemics factor $X_t$, i.e. the number of secondary cases from an infected individual, which has mean and variance $E(X_t) = nS_0(\theta)g(\theta)$ and $Var(X_t) = nS_0(\theta)g(\theta) - 1 - nS_0(\theta)g(\theta')$.

Observation model and approximate likelihood calculation

- For true counts, we have $k_{ij} = \sum_j x_{ij} \sim N(n\alpha, \sigma^2 S_0)$, where $\mu_0$ and $\sigma^2$ are $E(X_t)$ and $Var(X_t)$, respectively.
- Assume that we observe counts $Y_{ij}$, $\sim N(n\alpha, \psi^2\theta S_0)$, where $\psi$ is an overdispersion factor as in Ionides et al. (2006).
- Assume also that given the observed counts, the true are $E(Y_{ij}) = \mu_0Y$ and $Var(Y_{ij}) = \psi^2\theta S_0$.

Under these assumptions we can show that $E(Y_{ij}) = \mu Y$ and $Var(Y_{ij}) = \psi^2\theta S_0$.

- Given data $y_{ij}, t = 0, \ldots, T$ on the number of doctor’s visits for each discrete time period, we can compute the likelihood for parameter set $\theta$ as $f(y|\theta) = \prod_{t=0}^{T} f(y_{ij}|\theta) = \prod_{t=0}^{T} N(n\alpha, \sigma^2 S_0)$.

We still need an estimate of $S_0^*$ (note that $S_0 = S_0^* + \psi$). We estimate this at each step as $S_{t+1}^* = S_t^* - \frac{\beta}{\alpha} + (1 - S_t^*)\frac{\beta}{\alpha}$, where $K$ is the number of visits per week if everyone in the population (with degree at least one) were infected.

Network degree distributions

- The methodology presented above works for any degree distribution. In practice, a few distributions have received special attention. The Poisson degree distribution with mean $\lambda$, with
  $$P(K_0 = k) = \frac{e^{-\lambda} \lambda^k}{k!}, \quad k \geq 0$$

- The discrete Exponential distribution with mean $\lambda$
  $$P(K_0 = k) = (1 - e^{-\lambda} - k\lambda^k), \quad k \geq 0$$

- The power law (scale-free) distribution with an upper cutoff
  $$P(K_0 = k) \propto k^{-\gamma}, \quad k = 1, 2, \ldots, k_{max}$$

- For some distributions, calculations simplify and we can specify an appropriate distribution for the expansion factor $\theta$
  - For the Poisson distribution, $X_t \sim \text{Poisson}(\theta n S_0)$
  - For the Exponential distribution, $X_t \sim \text{NegBin}(\theta' = 2, \frac{\theta}{2})$

- In the scale-free case, there are no simplifications, and so we use
  $$g(\theta) \sum_{k=0}^{\infty} (k+1)^{-\gamma+1} P(\theta) = \theta$$

and invert this function numerically to obtain $\theta = g^{-1}(\theta)$.

Main Objectives

1. Build a prediction model for hospital visits in the next week given influenza count data
2. Inference for epidemic network models from set in a discrete time SIRS framework, with the following simplify degree distribution of the nodes, contacts are then established at random according to the configuration model (Molloy and Reed 1995). The underlying population is assumed to be part of a network constructed according to the configuration model (Molloy and Reed (1998)). One key feature of this network model is that given the degree distribution of the nodes, contacts are then established at random.

Materials and Methods

- Assume the pre-existing contact network, the spread of disease is set in a discrete time SIRS framework, with the following simplifying assumptions, specific to influenza:
  - The step is one week (to match the data collection frequency).
  - Incubation and infectious periods are fixed, and cumulatively last one week.
  - Following infection, the individual is temporarily immune to the whole spectrum of ILI strains, with length of immunity distributed as Exponential with rate $\psi$.

Define: $K_0$ is the degree of a random susceptible at time $t$; $P_k$ is the proportion of nodes of degree $k$ in the entire population at time $t$; $S_t$ is the fraction of the susceptible population, and $S_0^*$ is the fraction of the susceptible population with at least one connection.

- **Main Objectives**
  - Define:
    - $K_0$ is the degree of a random susceptible at time $t$;
    - $P_k$ is the proportion of nodes of degree $k$ in the entire population at time $t$;
    - $S_t$ is the fraction of the susceptible population, and
    - $S_0^*$ is the fraction of the susceptible population with at least one connection.
  - **Ongoing Work and Future Research**
    1. The likelihood function is found to be rugged, with ridges, peaks and local minima. This prevents standard errors to be estimated for the parameter m.l.e.’s in the usual way. We plan to simulate time series starting from the best fit parameters, to obtain a sampling distribution for the m.l.e.’s.
    2. A uniform reporting rate for the entire population is not realistic. Some age groups have more visits per infection than others. We can use the detailed CDC data to estimate a different degree distribution for each age group.

**References**


**Acknowledgements**

This research was supported by the OMAF and MRA-U of G Partnership.