Large Markovian Population Processes

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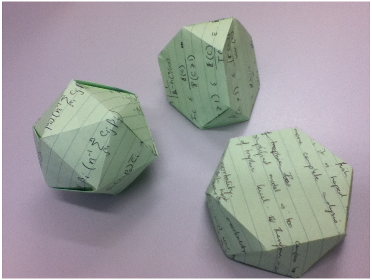
About me

- PhD from QUT a very long time ago.
- Currently at UQ supervised by Phil Pollett.
- Mathematical hobbies — juggling and origami.



Overview of research

Overall aim: To understand the effects of spatial structure and individual variation in large population models.

Three areas of applications

- Metapopulations: Habitat patches at distinct spatial locations which may support a local population of some species. Aim is to determine conditions under which the metapopulation persists.
- Epidemics: Similar to metapopulations. Aim is to determine when the disease dies out.
- Parasitology: Aim to understand factors affecting the distribution of parasite burden in hosts.

Some details

We model a metapopulation with n patches as a continuous time Markov chain on $\{0,1\}^n$ with transition rates

$$\begin{aligned} &(\textit{colonise}) \quad X_i \to 1 \quad \text{at rate} \quad (1-X_i)\sum_{j=1}^{n} a(z_j)c(z_i,z_j)X_j(t);\\ &(\textit{go extinct}) \quad X_i \to 0 \quad \text{at rate} \quad e(z_i)X_i. \end{aligned}$$

where z is patch location, a is patch area, e is extinction rate and $c(\cdot,\cdot)$ is connectivity.

Similar models are used to model spatial disease spread.

Some results – joint with Barbour and Pollett

Suppose the patch locations of the metapopulations are independently distributed.

Define the measures

$$\bar{X}_t(A) := n^{-1} \sum_{i=1}^{n} X_i(t)\mathbb{I}(z_i \in A), \quad \bar{p}_t := n^{-1} \sum_{i=1}^{n} p_i(t)\mathbb{I}(z_i \in A),$$

where

$$\frac{dp_i(t)}{dt} = (1 - p_i(t)) \left(\sum_{j=1}^{n} a(z_j)c(z_i, z_j)p_j(t) \right) - e(z_i)p_i(t)$$

and $A \in \mathcal{A}$, a class of sets with bounded VC dimension. Then with high probability

$$\sup_{t\in[0,T]} \sup_{A\in\mathcal{A}} \left| \bar{X}_T(A) - \bar{p}_t(A) \right| \leq c_1 n^{-1/2} e^{c_2 T}.$$

Some results – joint with Barbour and Pollett

Since $X(t)$ is well approximated by $p(t)$, we hope that the equilibrium of $p(t)$ might reflect the asymptotic behaviour $(t \to \infty)$ of $X(t)$. Unfortunately, the equilibrium of $p(t)$ is not available in closed form.

In work near completion, we show that with high probability the equilibrium of $p(t)$ is approximately

$$1 - \frac{e(z_i)}{\sum_j a(z_j)c(z_i, z_j)}.$$

provided $c(\cdot, \cdot)$ is sufficiently localised.

Open problems

(i) How to perform fast simulation of the metapopulation model when n is large? Can we incorporate ideas from tau-leaping?

(ii) Is the equilibrium of the a metapopulation with dynamic landscape always unique? This seems to be related to the following problem:

Let P and Q be two $(m \times m)$ stochastic matrices and let π and ω be their respective invariant distributions.

For a partition $\{A, B\}$ of $\{1, 2, \ldots, m\}$ suppose the following conditions hold:

- for all $i \in A$ and $j \in B$, $P_{ij} \geq Q_{ij}$.
- for all $i, j \in A$, $P_{ij} \leq Q_{ij}$.
- for all $i \in B$ and $j \in \{1, 2, \ldots, m\}$, $P_{ij} = Q_{ij}$.

Is it true that for all $i \in A$ $\pi_i \leq \omega_i$ and for all $i \in B$ $\pi_i \geq \omega_i$?