VI Southern-Summer School on Mathematical Biology

# Mathematical Theory of Biological Invasions Part II

Sergei Petrovskii

Department of Mathematics, University of Leicester, UK http://www.math.le.ac.uk/PEOPLE/sp237

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### Plan of the course

- Introduction & a glance at field data
- Overview of mathematical tools
- Diffusion-reaction systems
  - Single-species system: traveling waves, the problem of critical domain, effects of environmental heterogeneity
  - Predator-prey system and the problem of biological control: traveling waves and pattern formation
  - Beyond the traveling waves: patchy invasion
- Lattice models
- Kernel-based models (integro-difference equations): fat-tailed kernels, "superspread", pattern formation
- Extensions, discussion, conclusions

### Plan of the course – Part II

### • Lattice models

- Kernel-based models (integro-difference equations): fat-tailed kernels, "superspread", pattern formation
- Extensions, discussion, conclusions



# Lattice models of biological invasion

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### How essential is the choice of the model?

Specific questions:

- Is the patchy spread an artifact of the diffusion-reaction system?
- Concerns: Time-discrete framework may be more appropriate, at least in some cases (e.g. for species with clearly different life stages)
- In order to take into account also the environment heterogeneity, we now consider a system that is discrete both in space and time

### Ecological example: metapopulation



(by Katrin Körner & Florian Jeltsch, University of Potsdam)

### In a more formal way:



(by Victoria Sork, UCLA)

A possible mathematical framework: discrete space, continuous time (Keitt et al., 2001)

### Coupled Map Lattice: single species

Continuous space (x, y) changes into a discrete 'lattice'  $(x_m, y_n)$  where k = 1, ..., M and n = 1, ..., N.

Population numbers are defined only in the lattice nodes:



Each discrete step from t to t + 1 consists of distinctly different dispersal stage and the 'reaction' stage.

The dispersal stage includes emigration and immigration:

$$N'_{x,y,t} = (1-\mu)N_{x,y,t} + \sum_{(a,b)\in V_{x,y}} \frac{\mu}{4}N_{a,b,t} ,$$

where  $\mu$  is the population fraction that emigrates from the site.

The choice of  $V_{x,y}$  can be different, for instance

$$V_{x,y} = \{(x-1,y), (x+1,y), (x,y-1), (x,y+1)\},\$$

which corresponds to a certain 'dispersal stencil':



The reaction stage is  $N_{x,y,t+1} = f(N'_{x,y,t})$ .

We assume that the population growth is hampered by the strong Allee effect.

In particular, we consider

$$N_{t+1} = f(N_t) = \frac{\alpha \left(N_t\right)^2}{1 + \beta^2 \left(N_t\right)^2}.$$

This function f(N) has two steady states,  $N_1^*$  and  $N_2^*$ .

We also consider its approximation with a simpler function:

$$f(N)\approx \tilde{f}(N)=N_2^*H(N-N_1^*)$$

where H(z) is the Heaviside step function.

### Population growth in discrete time



### Consider a single-site species introduction:



Questions to be answered:

- Under what conditions this introduction will lead to successful establishment (and, possibly, spread)?
- What can be the rate of spread?
- What can be the pattern of spread?

### Establishment

The species will persist at the site p of initial introduction iff its size after dispersal does not fall below the Allee threshold:

$$N'_{p} = (1 - \mu)N_{2}^{*} > N_{1}^{*}$$

that is, for

$$\mu < 1 - \kappa$$
 where  $\kappa = N_1^*/N_2^*$ . (1)

The spread into a neighboring site q will be successful iff the density after dispersal exceeds the Allee threshold:

$$N'_q = rac{\mu}{4}N_2^* > N_1^*$$

that is, for

$$\mu > 4\kappa.$$
 (2)

Conditions for establishment and spread are now not the same!

### Extinction-invasion diagram



Domain I - establishment & spread, Domain III - establishment without spread (invasion pinning), Domain II - spread with pattern formation in the wake, Domain IV - extinction

### Spread

For the step-like growth function, the rate of spread is exactly 1 (one site per generation).



The shape of the envelope is an artefact of the dispersal stencil.

### Spread

But with a little bit of environmental heterogeneity...



Now the shape of the envelope looks much more realistic!

### Coupled Maps Lattice: predator-prey system

Now we have, for the dispersal stage

$$\begin{split} N_{x,y,t}' &= (1 - \mu_N) N_{x,y,t} + \sum_{(a,b) \in V_{x,y}} \frac{\mu_N}{4} N_{a,b,t} ,\\ P_{x,y,t}' &= (1 - \mu_P) P_{x,y,t} + \sum_{(a,b) \in V_{x,y}} \frac{\mu_P}{4} P_{a,b,t} , \end{split}$$

and for the reaction stage

$$N_{x,y,t+1} = f\left(N'_{x,y,t}, P'_{x,y,t}\right),$$
$$P_{x,y,t+1} = g\left(N'_{x,y,t}, P'_{x,y,t}\right).$$

### Predator-prey on a lattice

Specifically, we choose the reaction term as follows

$$N_{x,y,t+1} = \frac{r(N_{x,y,t})^{2}}{1 + b(N_{x,y,t})^{2}} \cdot \exp(-P_{x,y,t}),$$

and

$$P_{x,y,t+1} = N_{x,y,t}P_{x,y,t}.$$

(in dimensionless variables) where N is prey and P is predator.

This system shows a very complicated dynamical behavior including traveling waves, regular spatial patterns and spatiotemporal chaos.





This patchy invasion occurs in the parameter range where the nonspatial system goes extinct





# Chapter VI

# Kernel-based (integral-difference) models of biological invasion

### Kernel-based models

Consider an insect population, e.g. moth, in a continuous space but with separated growth and dispersal stages:

$$U_t(x) \rightarrow \tilde{U}_t = f(U_t(x)) \rightarrow \mathcal{L}(\tilde{U}) = U_{t+1}(x)$$

adult moth	laid eggs,	adult moth,
settling down	larvae etc.	new generation

where  $\mathcal{L}$  is a spatial operator describing dispersal.

For simplicity, we consider dispersal at the infinite space.

Let k(x, y) is the probability distribution that a moth released at x will lay eggs at the position y, then

$$U_{t+1}(x) = \int_{-\infty}^{\infty} k(x,y) \tilde{U}_t(y) dy$$
.

### Kernel-based models

Assume that space is homogeneous,  $k(x, y) \rightarrow k(x - y)$ .

We therefore obtain the following equation:

$$U_{t+1}(x) = \int_{-\infty}^{\infty} k(x-y) f(U_t(y)) dy ,$$

where k(z) is also called the dispersal kernel.

Questions:

- How much different the kernel-based framework is from diffusion-reaction equations?
- If it is different, what can be the rate of spread?

The answer depends on the properties of the dispersal kernel.

### Examples of dispersal kernel



Intuitively, the faster the rate of decay of k(z) at large *z*, the lower the rate of spread.

The properties of the kernel can be quantified by the behavior of its moments. (e.g. see Kot et al., 1996)

The moment of the *n*th order:

$$m_n = \int_{-\infty}^{\infty} z^n k(z) dz, \quad m_0 = 1, \quad m_1 = .$$

For almost any k(z),  $m_n$  is an increasing function of n.

However, a lot depends on how fast is the rate of increase.

**Case 1**. All moments exist and the asymptotical rate of increase of  $m_n$  is not faster than the factorial of n, i.e. at most

 $m_n \sim n!$ 

which means that k(z) is exponentially bounded.

In this case, the kernel-based equation with compact initial conditions describes a traveling front propagating with a constant speed (Lui 1983; Kot 1992)

# The kernel-based model appears to be equivalent to the diffusion-reaction equation

(Petrovskii & Li, 2006, Section 2.2; Lewis et al., 2016, Section 2.4)

**Case 2**. For a k(z) with a fatter tail (rate of decay lower than exponential), the model has solutions of a new type: accelerating traveling waves.

The difference between the corresponding kernels can be expressed in terms of the moment-generating function:

$$M(s) = \int_{-\infty}^{\infty} e^{sz} k(z) dz$$

(Kot et al. 1996), that is:

- Constant-speed traveling waves if M(s) exists
- Accelerating traveling waves if *M*(*s*) does not exist (the integral diverges for any *s* ≠ 0)

Accelerating waves do not exist if the population growth is dumped by the strong Allee effect

### Patterns in the wake

Interestingly, pattern formation in the wake of the traveling front appears possible even in a single-species kernel-based model:



(Andersen, 1991)

### Questions arising

What can be the effect of other species?

How it may change the pattern of spread?

Consider a predator-prey system:

$$u_{t+1}(\mathbf{r}) = \int_{\Omega} k^{(u)} (|\mathbf{r} - \mathbf{r}'|) f(u_t(\mathbf{r}'), v_t(\mathbf{r}')) d\mathbf{r}',$$
  
$$v_{t+1}(\mathbf{r}) = \int_{\Omega} k^{(v)} (|\mathbf{r} - \mathbf{r}'|) g(u_t(\mathbf{r}'), v_t(\mathbf{r}')) d\mathbf{r}',$$

Local demography: predator-prey system

$$u_{t+1}(\mathbf{r}) = \frac{r (u_t(\mathbf{r}))^2}{1 + b (u_t(\mathbf{r}))^2} \cdot \exp(-v_t(\mathbf{r})),$$
  
$$v_{t+1}(\mathbf{r}) = u_t(\mathbf{r})v_t(\mathbf{r}).$$

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Dispersal kernel: the "reference case"

$$k_G\left(|\mathbf{r}-\mathbf{r}'|\right) = \frac{1}{2\pi\alpha_i^2} \exp\left(-\frac{|\mathbf{r}-\mathbf{r}'|^2}{2\alpha_i^2}\right)$$

Dispersal with the Gaussian kernel is known to be equivalent (in some sense) to diffusion.



### Fat-tailed kernels in 1D

Long-distance asymptotics for the Gaussian kernel:

 $k(x) \sim e^{-ax^2}.$ 

Fat tailed kernel - power-law decay:

$$k(x) \sim x^{-\mu}$$
 (1 <  $\mu$  < 3)

In case  $\mu = 2$ , the stable distribution is available in a closed form known as Cauchy distribution:

$$k_C(x) = rac{eta}{\pi(eta^2 + x^2)} \sim x^{-2}.$$

### Fat-tailed kernels in 2D

Long-distance asymptotics:  $k(\mathbf{r}) \sim r^{-(\mu+1)}$  (1 <  $\mu$  < 3)

Explicit form of the stable distribution is not available, hence extension onto the 2D case is ambiguous.

Cauchy kernels Type I:

$$k_{C_l}({f r},{f r}') = rac{eta_l^2}{\pi(eta_l+|{f r}-{f r}'|)^3} ~\sim ~ |{f r}-{f r}'|^{-3} ~,$$

Cauchy kernels Type II:

$$k_{C_{ll}}(\mathbf{r},\mathbf{r}') = rac{\gamma_i}{2\pi \left(\gamma_i^2 + |\mathbf{r} - \mathbf{r}'|^2
ight)^{3/2}} ~\sim~ |\mathbf{r} - \mathbf{r}'|^{-3}$$

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(Rodrigues et al., 2015)

### Fat-tailed kernels

Cauchy kernel has significantly different properties compared to the Gaussian kernel: the variance does not exist,  $< r^2 >= \infty$ .

- The fact that < r<sup>2</sup> >= ∞ is sometimes interpreted as the infinite correlation length
- Invasive species can spread with an accelerating speed (Kot et al. 1996)

Questions arising:

- Can patchy spread occur for the fat-tailed dispersal?
- How the rate of spread may differ between different kernels?

### Simulations, kernel Type I



### Simulations, kernel Type II



How can we compare the results for different dispersal kernels, i.e. Gaussian, Cauchy Type I and Cauchy Type II ?

Standard approach (equating the variances) does not work as the variance does not exist – "scale-free" process

### Conditions of equivalence

Consider radius  $\epsilon$  within which the probability of finding an individual after dispersal is 1/2:

$$P_{\epsilon} = \int \int_{|\mathbf{r}| \leq \epsilon} d\mathbf{r} = \int_{0}^{2\pi} \int_{0}^{\epsilon} k_{i}(\mathbf{r}, \theta) \mathbf{r} d\mathbf{r} d\theta = \frac{1}{2}.$$

For the Gaussian kernel, we obtain  $\epsilon = \alpha \sqrt{2 \ln 2}$ .

For Cauchy kernel Type I:

$$\beta = \epsilon(\sqrt{2} - 1) = \alpha(2 - \sqrt{2})\sqrt{\ln 2} \approx 0.4877\alpha.$$

For Cauchy kernel Type II:

$$\gamma = \frac{\epsilon}{\sqrt{3}} = \alpha \sqrt{\frac{2}{3} \ln 2} \approx 0.6798 \alpha.$$

### Radius of invaded area vs time



Cauchy Type I

Cauchy Type II

Invasion rates are related by the above equivalence condition.

#### There is no accelerated spread.

Invasion rates obtained for the Cauchy kernels are between 1-10 km/year, hence in excellent agreement with field data.

(Rodrigues et al., 2015)

# This is the end of the course...

### This is **the end** of the course...

But certainly not the end of the story

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# Good luck with your research!