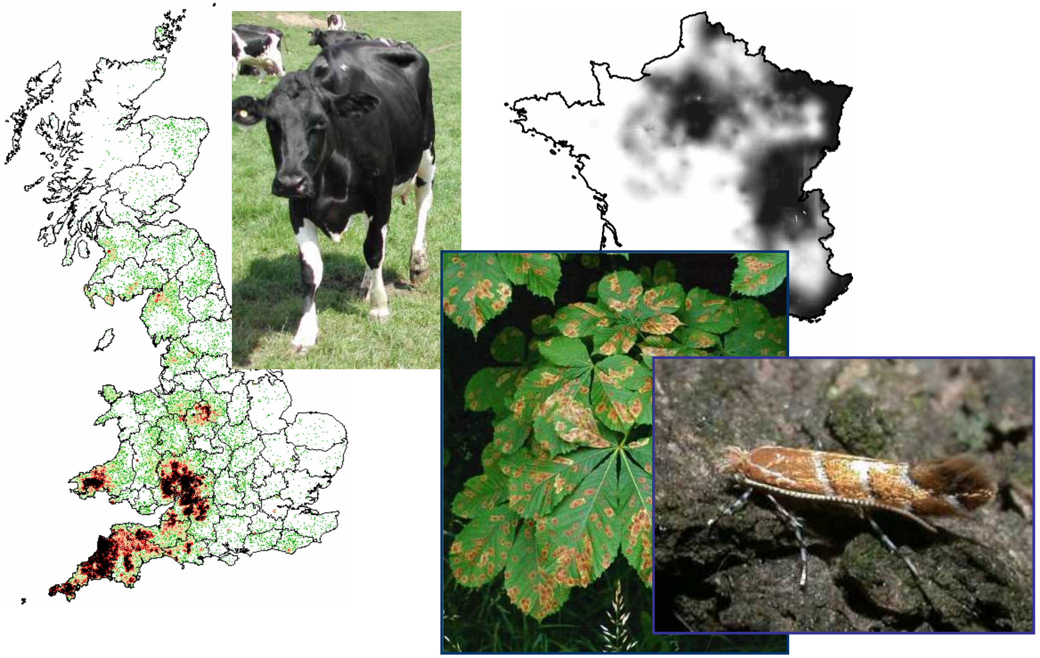
Modelling the spread of invading organisms: accounting for long-distance dispersal and landscape heterogeneity



Dr Marius Gilbert

Lutte biologique et Ecologie spatiale (LUBIES)

Université Libre de Bruxelles

Biological invasion models: Skellam's model

- Skellam (1951) introduced the diffusion of individuals in a random Brownian motion into the Malthusian (unlimited) population growth model.

$$\frac{\partial n}{\partial t} = D\left(\frac{\partial^2 n}{\partial x^2} + \frac{\partial^2 n}{\partial y^2}\right) + rn$$

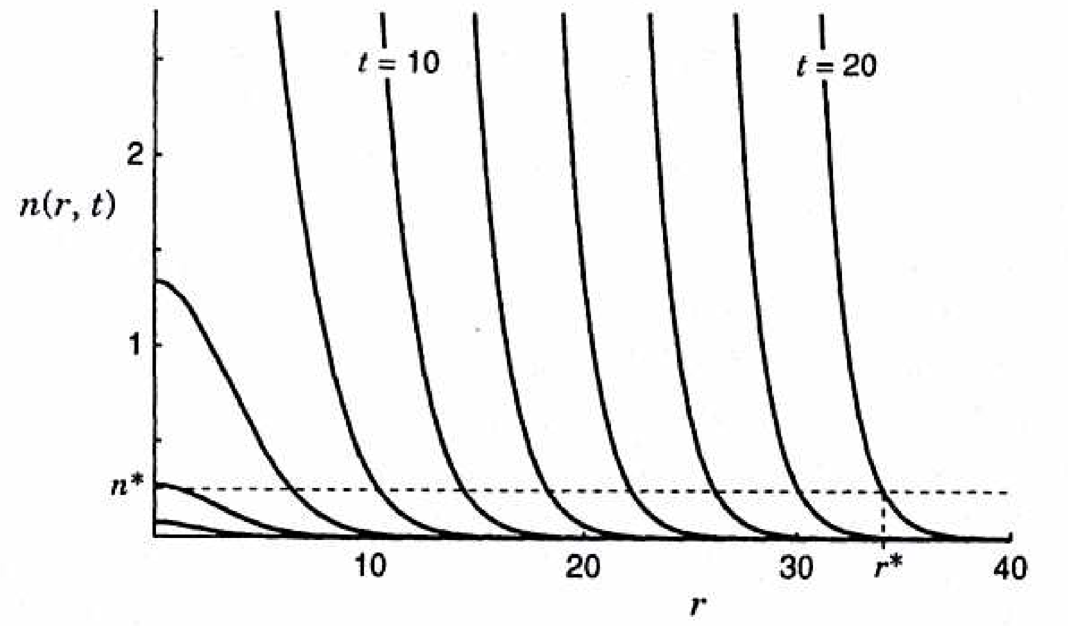
- Mathematical solution

$$n_{(x,y,t)} = \frac{n_{(0,0,0)}}{4\pi Dt}\exp\left(rt - \frac{x^2 + y^2}{4Dt}\right)$$

Biological invasion models: Skellam's model

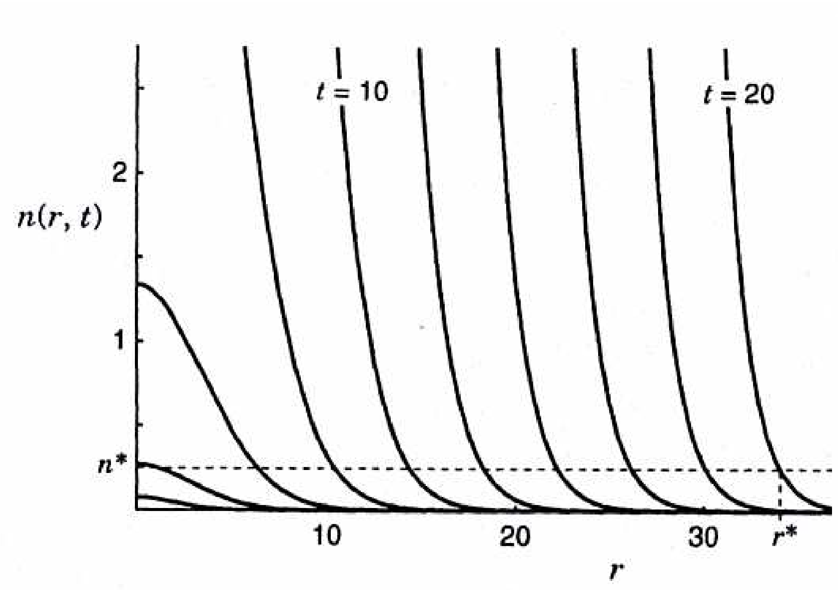
$$n_{(x,y,t)} = \frac{n_{(0,0,0)}}{4\pi Dt}\exp(rt - \frac{x^2+y^2}{4Dt})$$

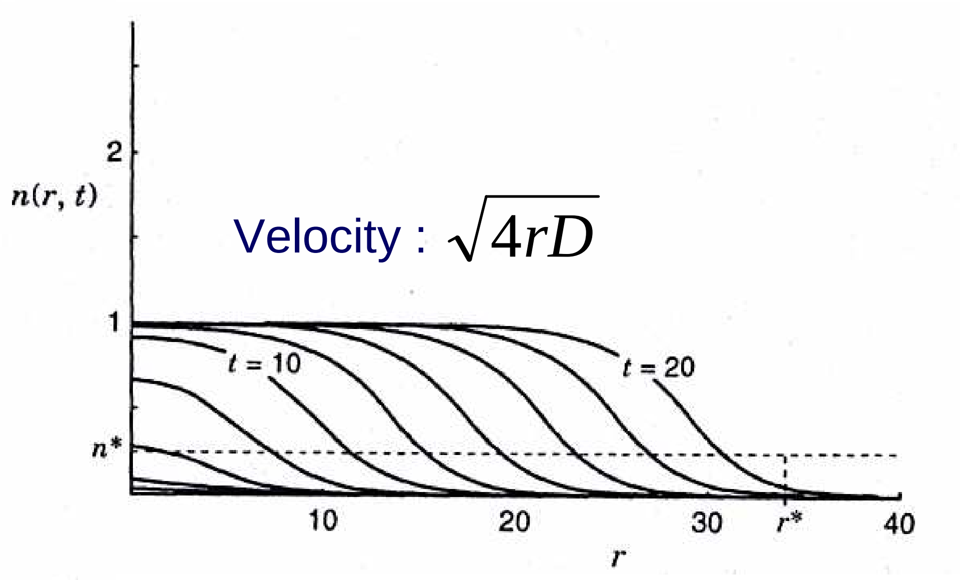
Velocity : $\sqrt{4rD}$



Biological invasion models: Fisher's model

Fisher's model $$\frac{\partial n}{\partial t} = D\left(\frac{\partial^2 n}{\partial x^2} + \frac{\partial^2 n}{\partial y^2}\right) + \varepsilon\left(1 - \frac{n}{K}\right)n$$





Biological invasion models: some practical limitations

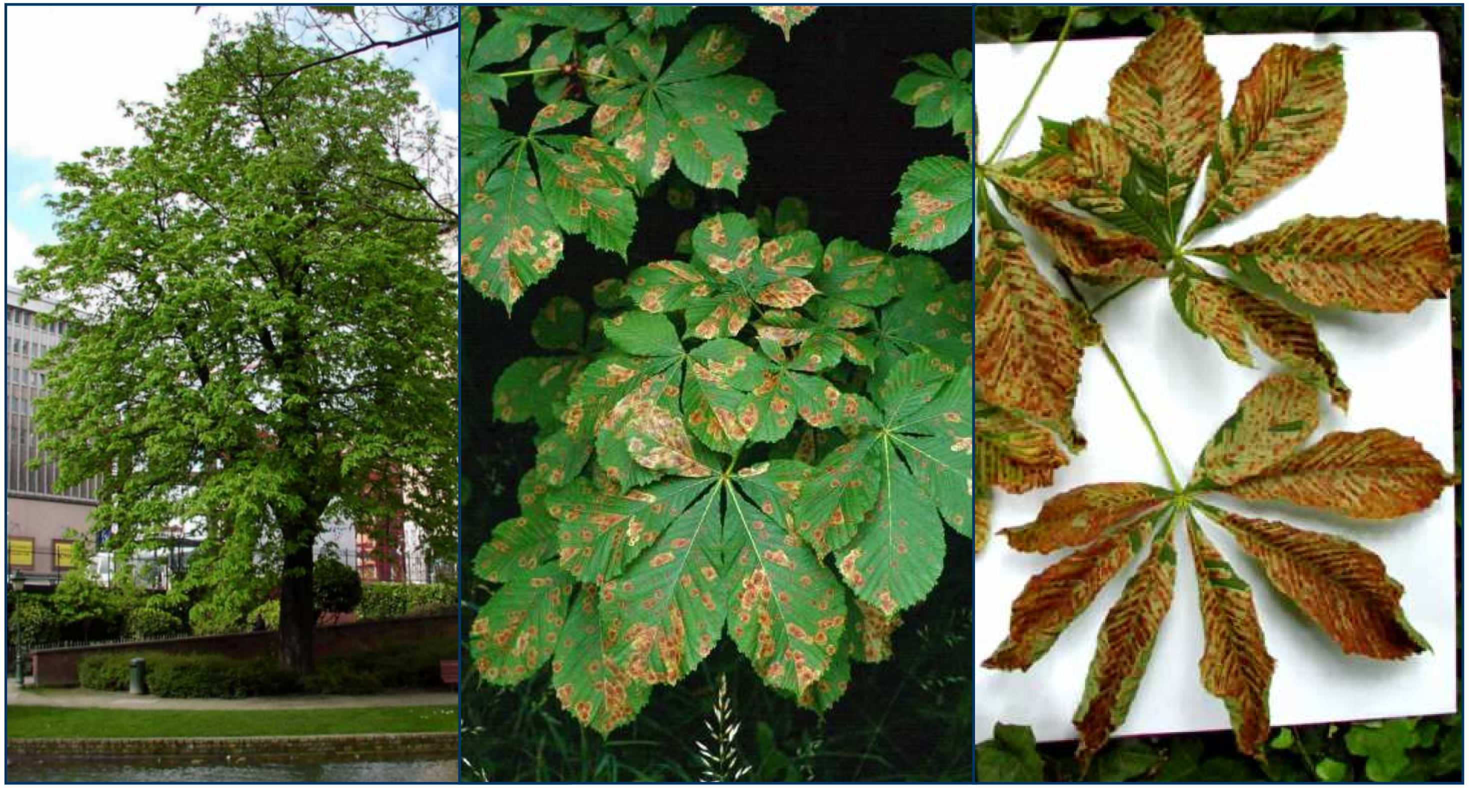
- Random walk *vs*. correlated random walk

- Dispersal of invasive species results from the combination of short-distance (autonomous) and long-distance (anthropogenic) dispersal: stratified dispersal.

- Some invasions show an accelerating velocity, that deviates from the predictions of Skellam and Fisher models.

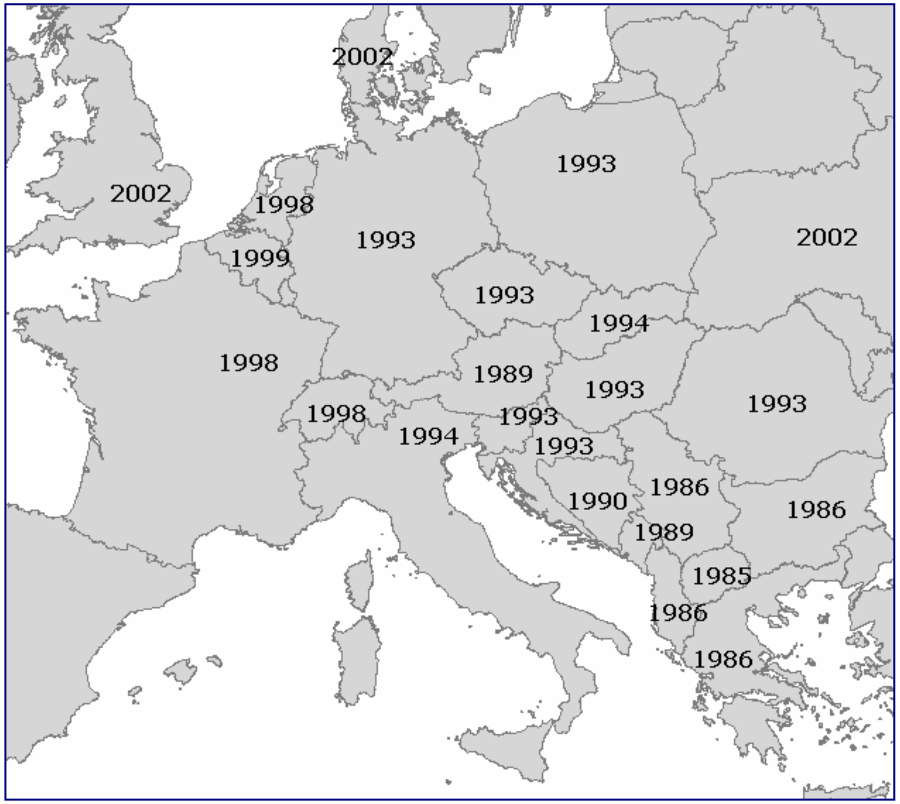
- Invasion models assume homogeneous environment

The horse chestnut leafminer *Cameraria ohridella*



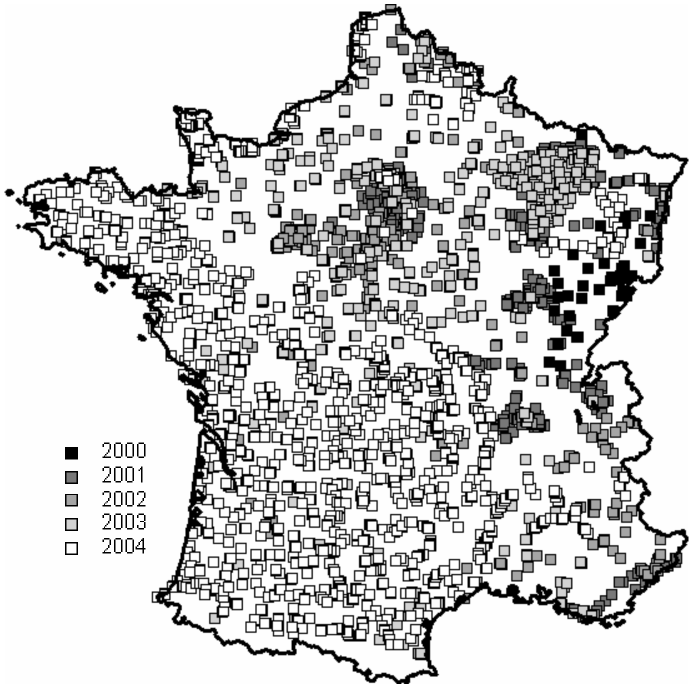
The horse chestnut leafminer *Cameraria ohridella*

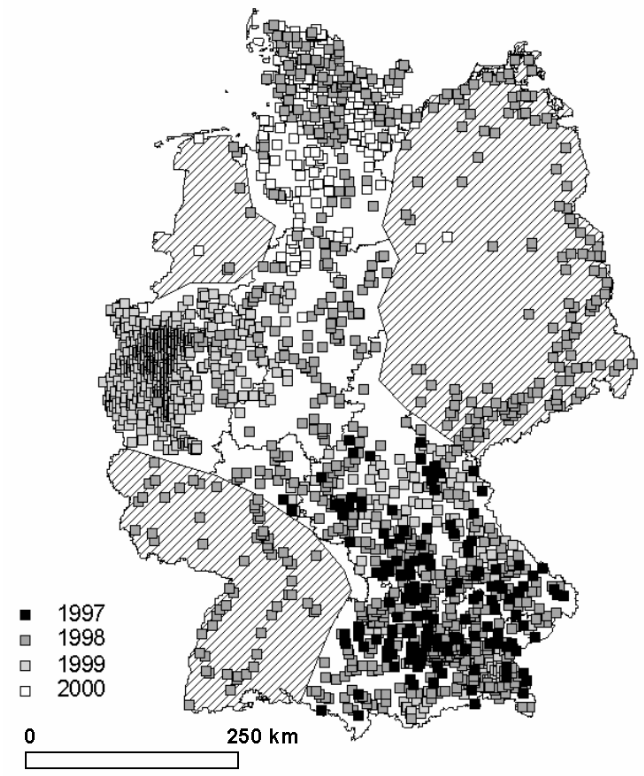
A fast invasion…



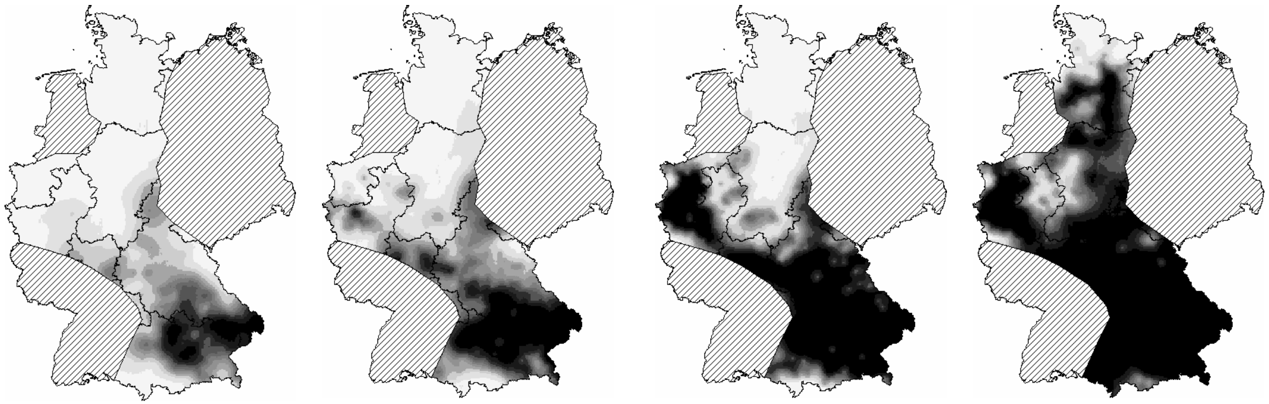
- ➢Unknown origin and first observed in the Balkans (lake Ohrid)
- ➢Very few natural enemies, with very little impact (parasitoids, ants, birds, spiders)
- ➢Fast population growth, rarely goes extinct

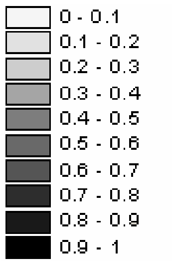
Surveys to monitor the spread (FR & DE)





Interpolated distribution Germany 1996-1999

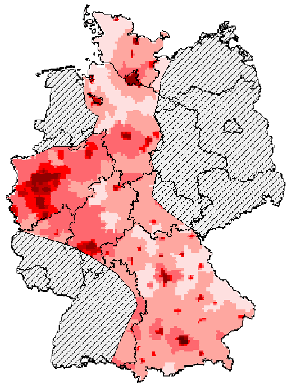




Irregular invasion front line

Accelerating spread rate

Apparent association with human population density



Monte-Carlo simulation model: cellular automata

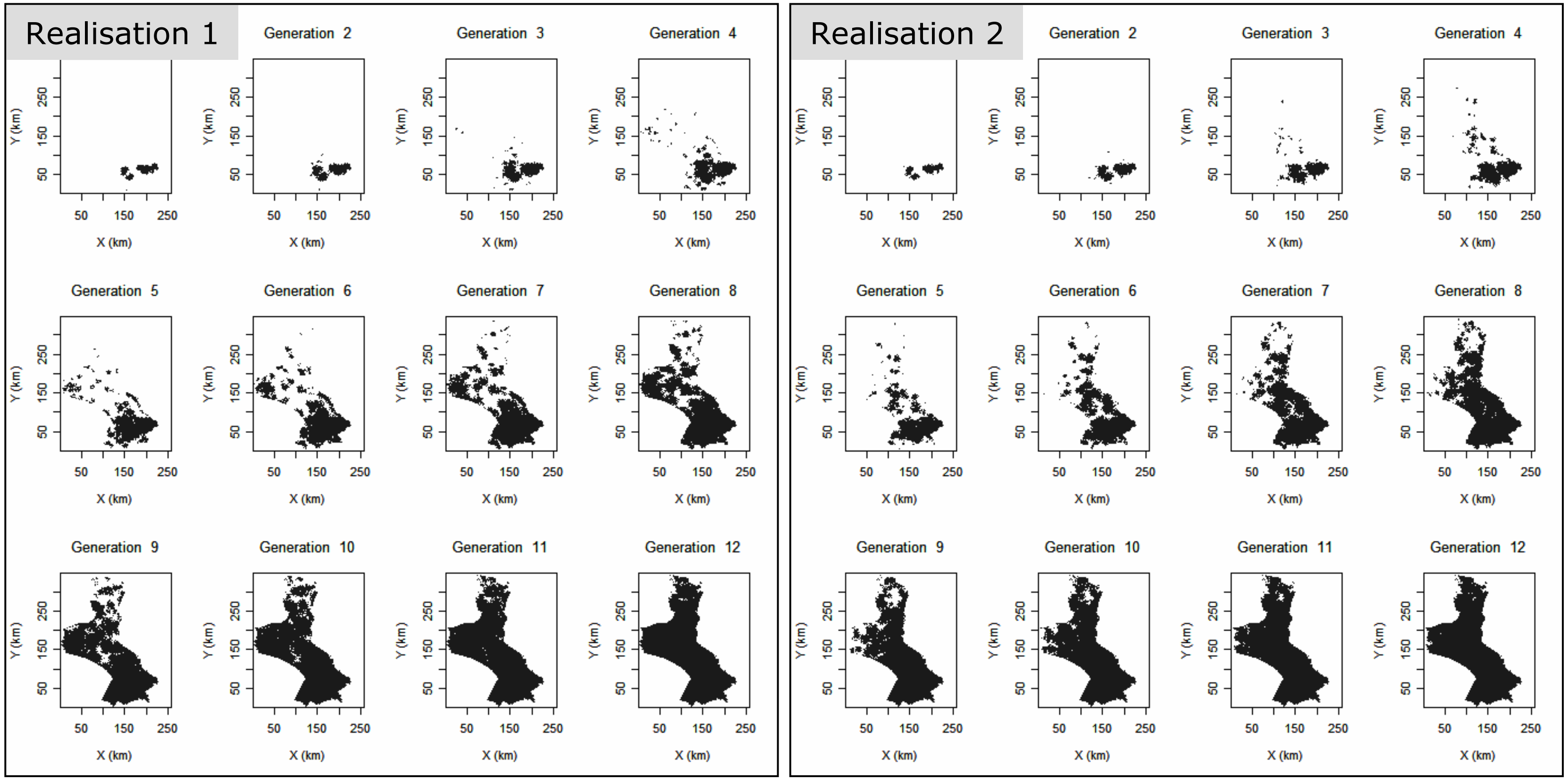
- (a) the spatial domain is divided in cells of equal size, occupied (1) or empty (0). All simulations start from the same t_0 distribution (in this case the distribution of *Cameraria ohridella* in southeastern Germany in 1995)

- (b) For each pixel, the probability of presence is estimate as a function of the distance to the nearest occupied cell in the previous time step, and as a function of an external variable.

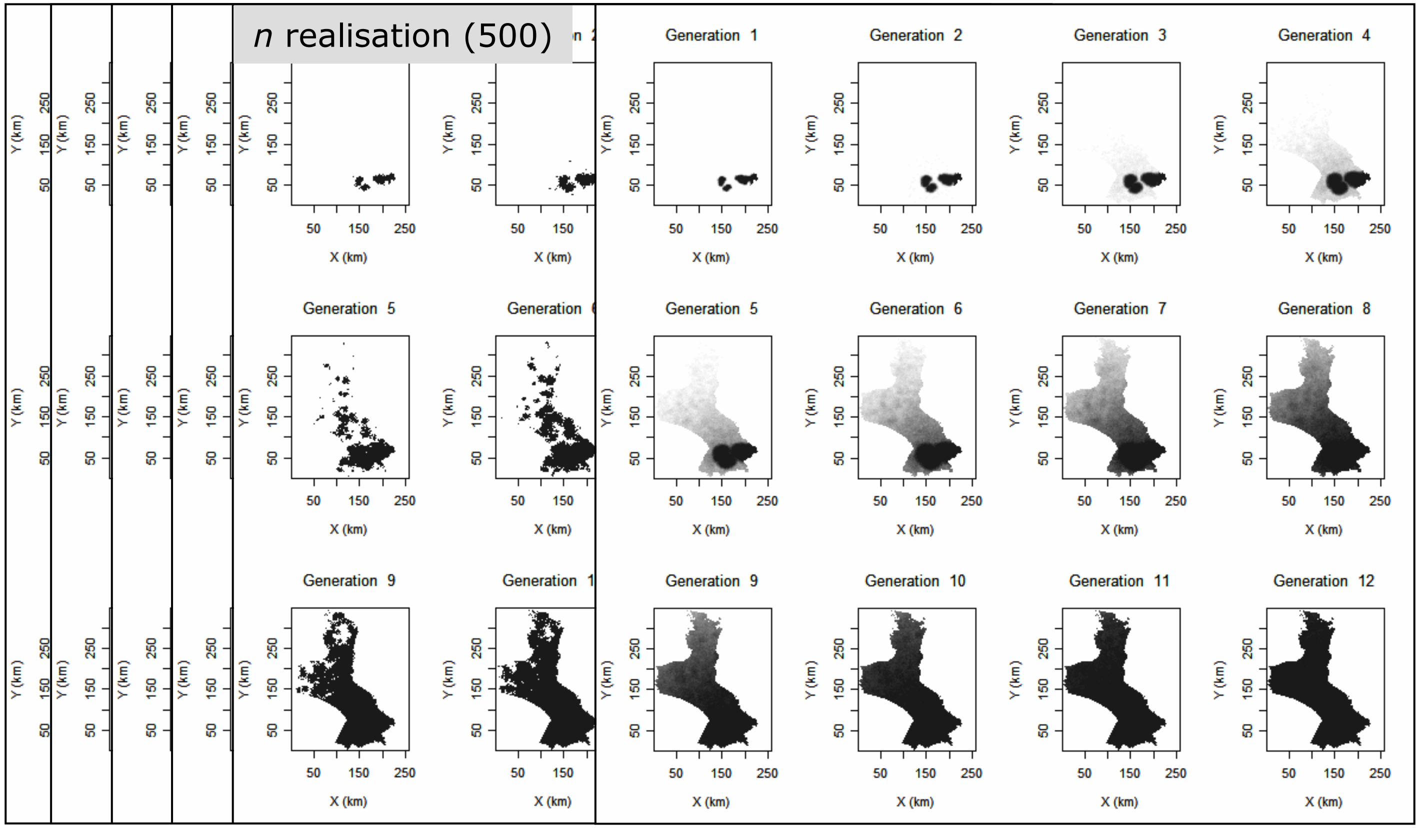
- (c) Based on a random trial the probability of presence in each pixel is set as occupied (1), or empty (0), which provides the presence/absence distribution at time t_{+1}

- Steps (b) – (c) are repeated over *n* time steps (in this case, the simulations were run over 4 years x 3 generations; 12 time steps)

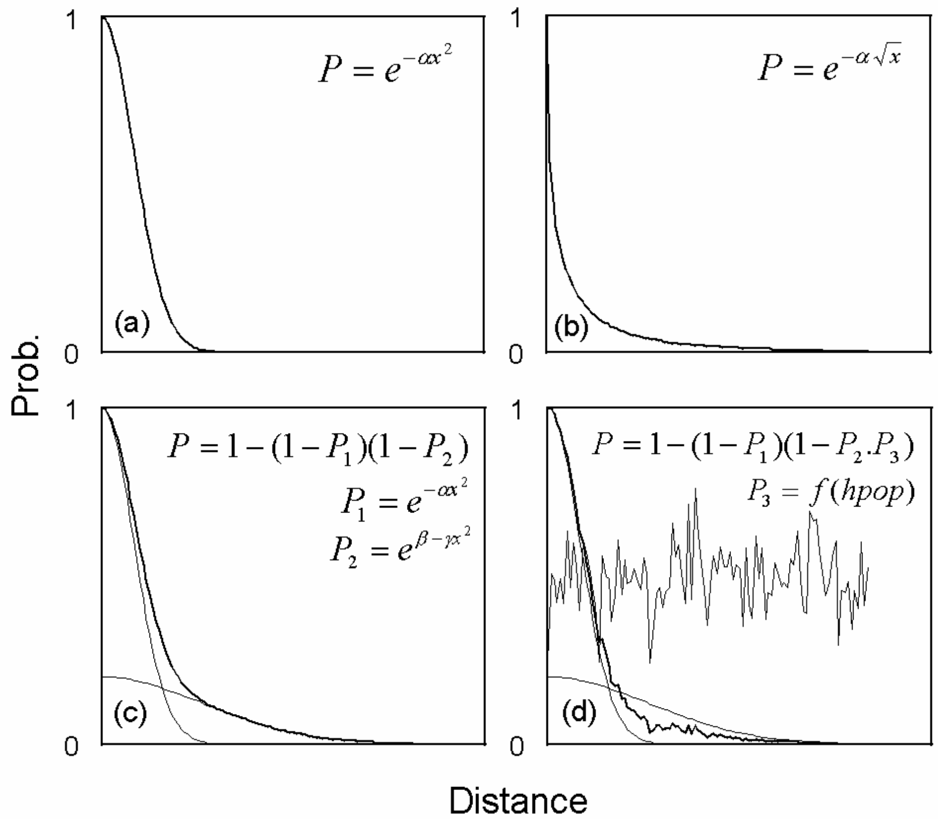
Monte-Carlo simulation model: cellular automata



Monte-Carlo simulation model: cellular automata



Different invasion models

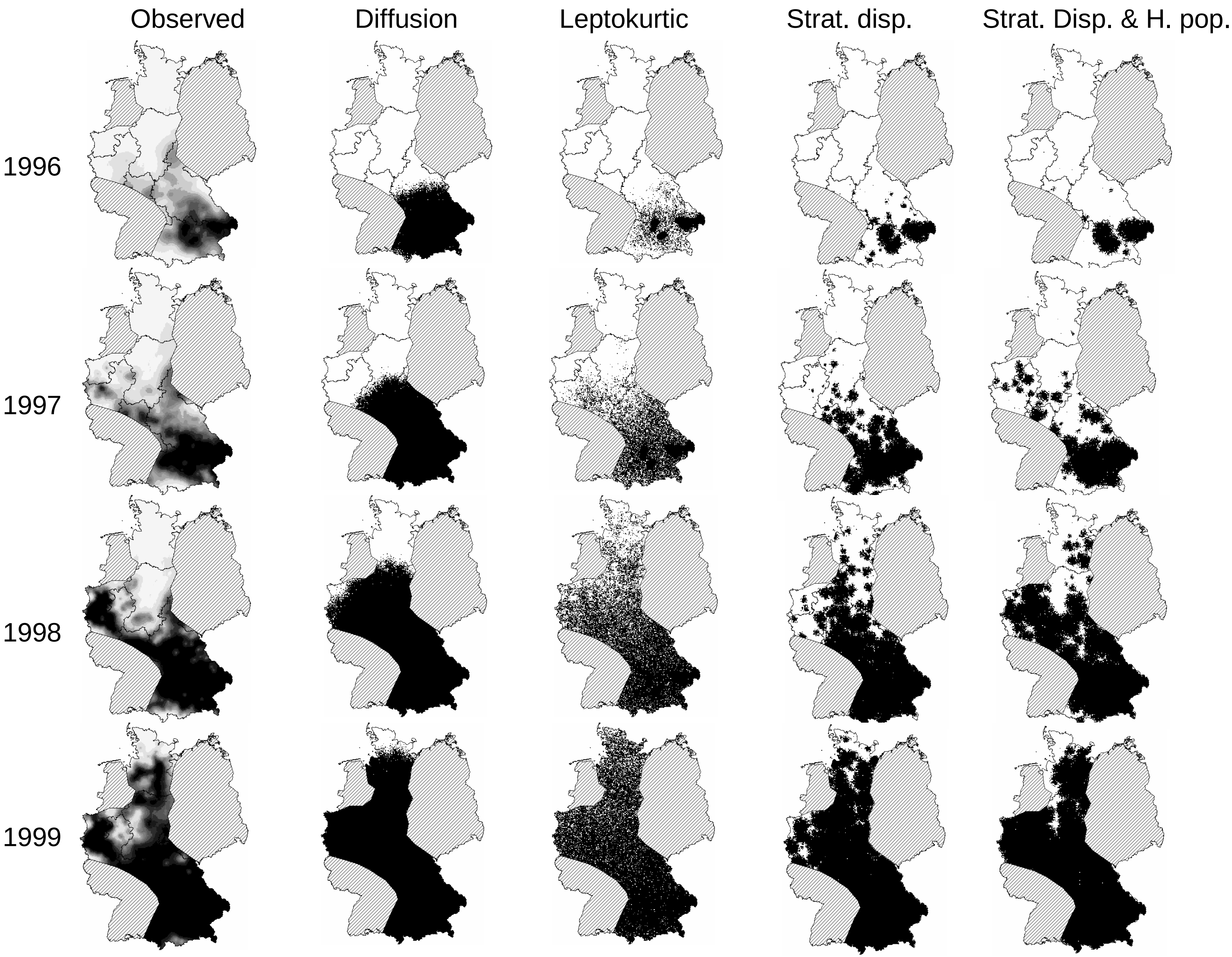


(a) Diffusion (Gaussian kernel)

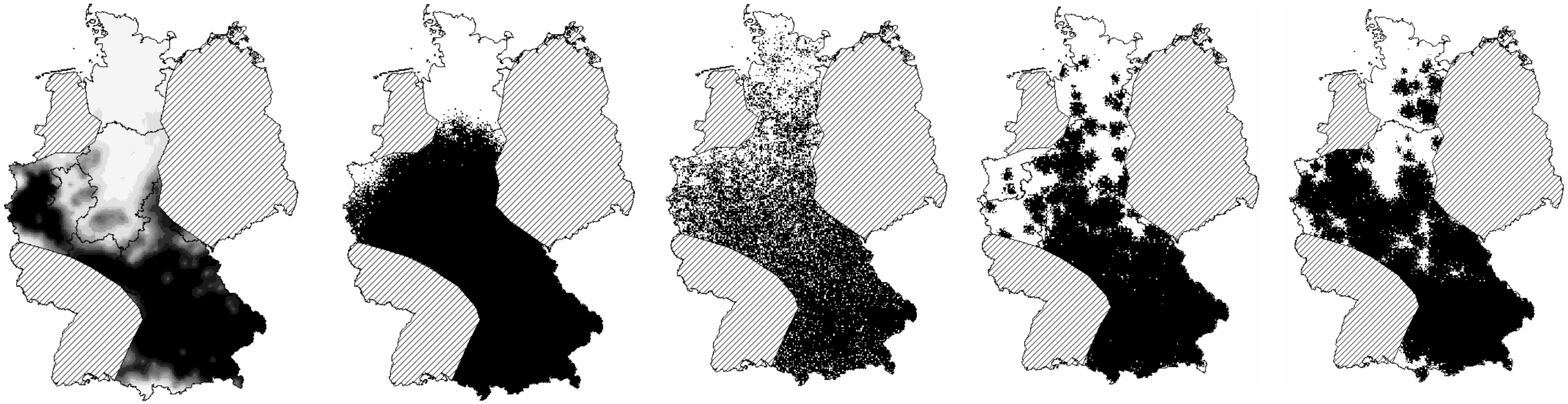
(b) Leptokurtic kernel

(c) Stratified dispersal

(d) Stratified dispersal with effect of human population density


Observed
Diffusion
Leptokurtic
Strat. disp.
Strat. Disp. & H. pop.
1996
1997
1998
1999

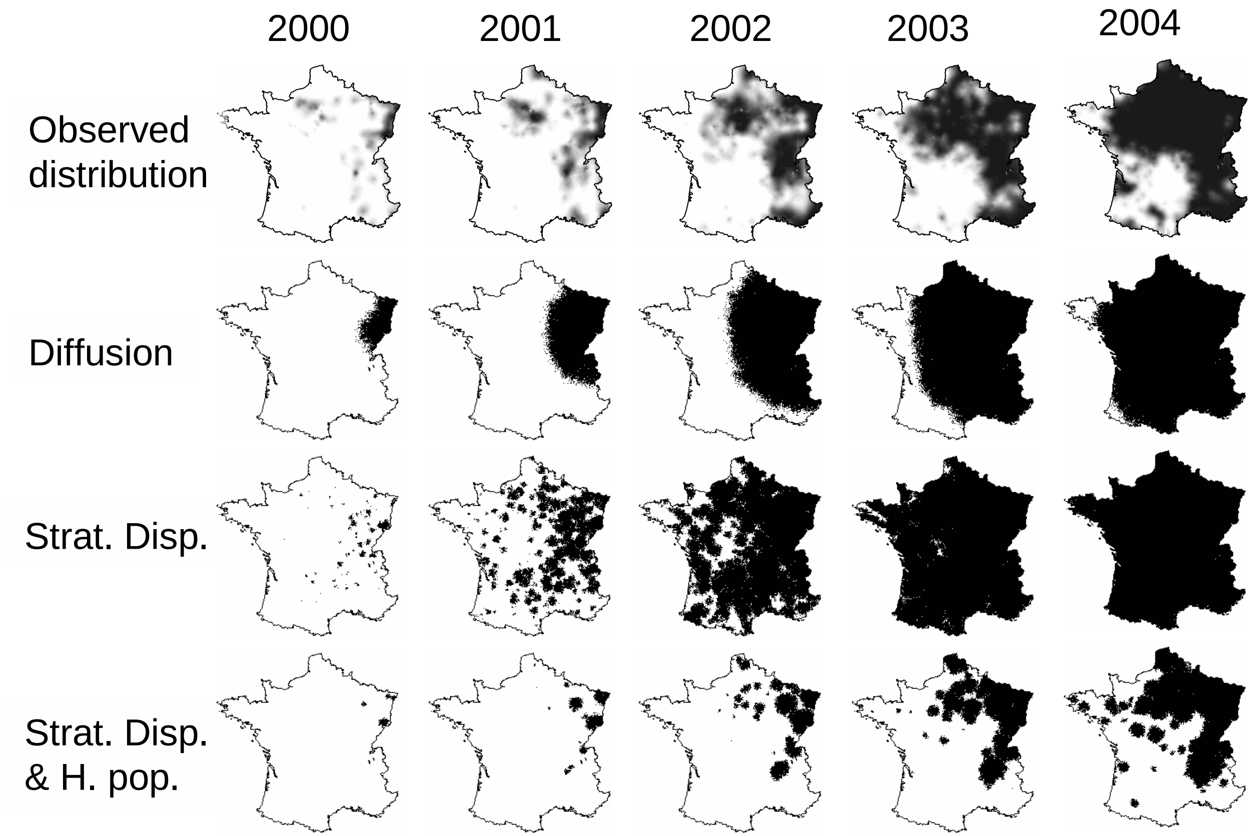
Qualitative and quantitative assessment



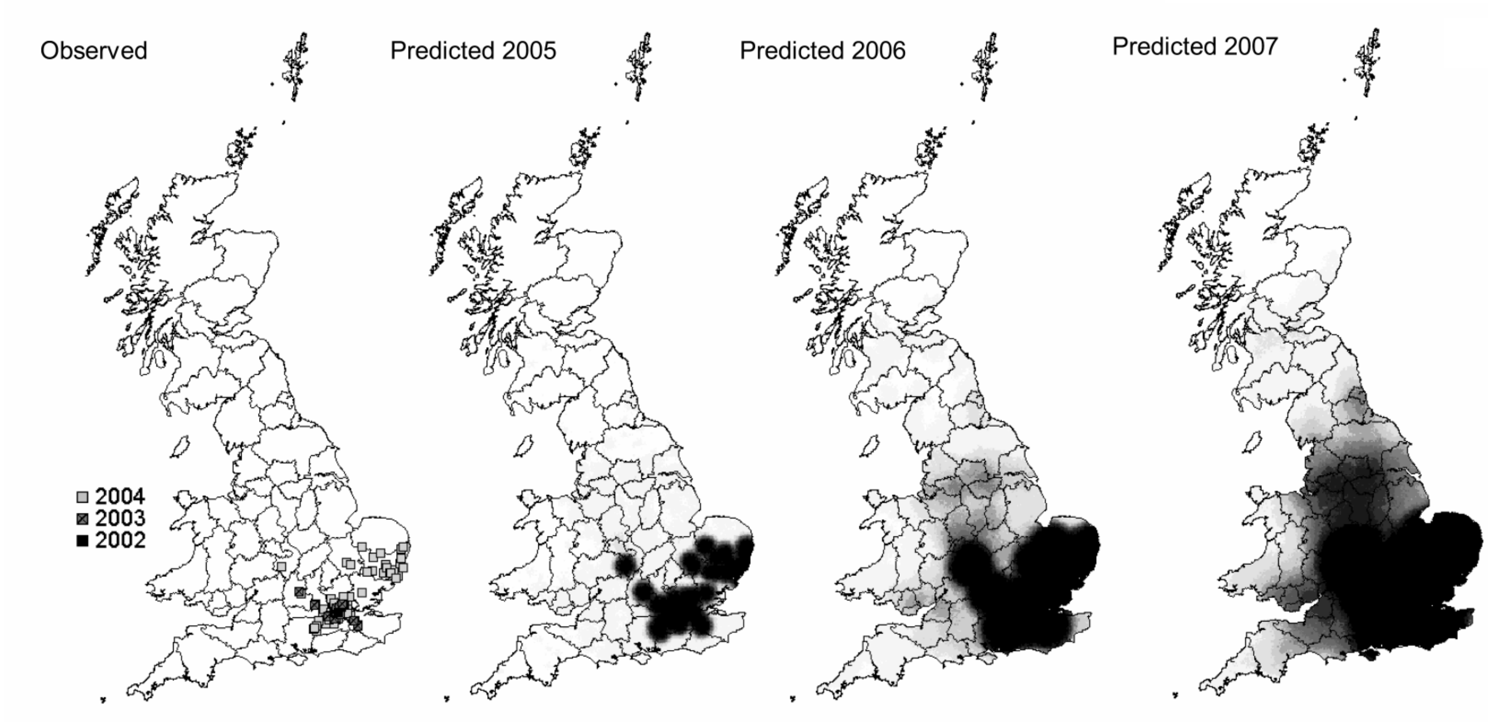
FD 1.806 ± 0.0075

Model	Parameters	SSE	R^2	Fractal dimension
Diffusion	$\alpha = 1.58\ 10^{-9}$	956.6	0.218	1.540 ± 0.0243
Leptokurtic dispersal	$\alpha = 0.0229$	761.2	0.378	1.953 ± 0.0074
Stratified dispersal	$\alpha = 2.5\ 10^{-8}$, $\beta = -7.0$, $\gamma = 4.0\ 10^{-11}$	760.1	0.379	1.806 ± 0.0122
Stratified dispersal & H. pop.	$\alpha = 2.5\ 10^{-8}$, $\beta = -6.7$, $\gamma = 4.2\ 10^{-11}$, $\phi = 2.1$	663.5	0.458	1.771 ± 0.0118

Validating the model in France



Predicting the spread in the United Kingdom

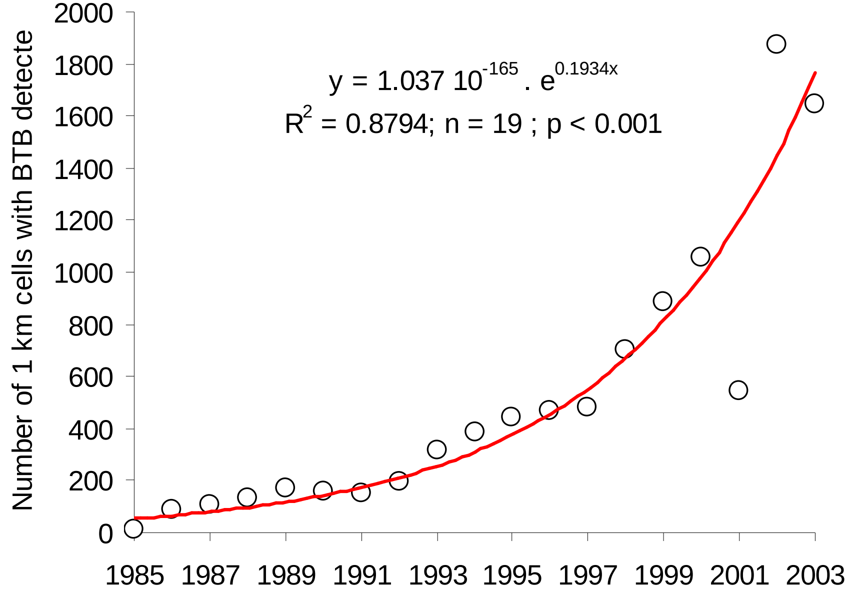


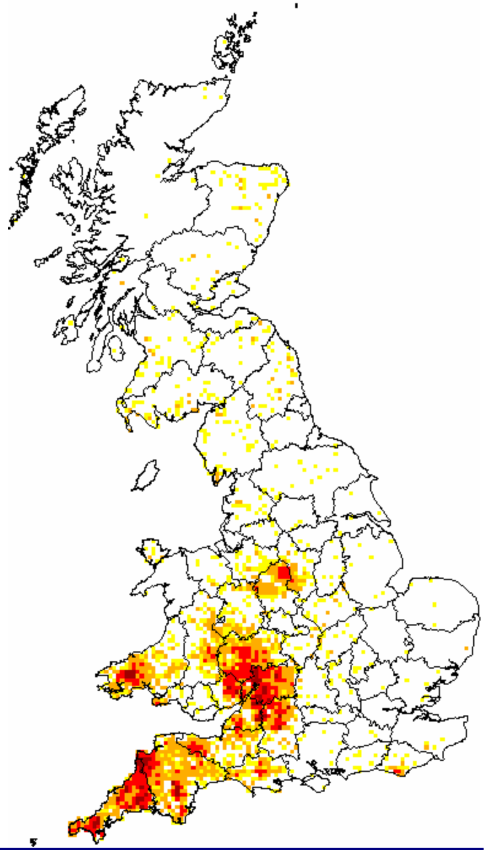
Accounting for long-distance dispersal and landscape heterogeneity

- Long distance dispersal is accounted for by the long-distance component of the stratified dispersal kernel.
- Landscape heterogeneity is viewed through one single variable, i.e. human population density.
- Can we accommodate multiple variables ?
- How can we circumvent the problem of finding the best-fit parameters ?

J. Appl. Ecol. (2005) 42:805-813.
J. Anim. Ecol (2004) 73:459-468.

Bovine tuberculosis in Great-Britain





Nature (2005) 435: 491-496.
J. Anim. Sci. (2005) 80:265-273.

Invasion model

In a previous analysis the distribution was found associated to

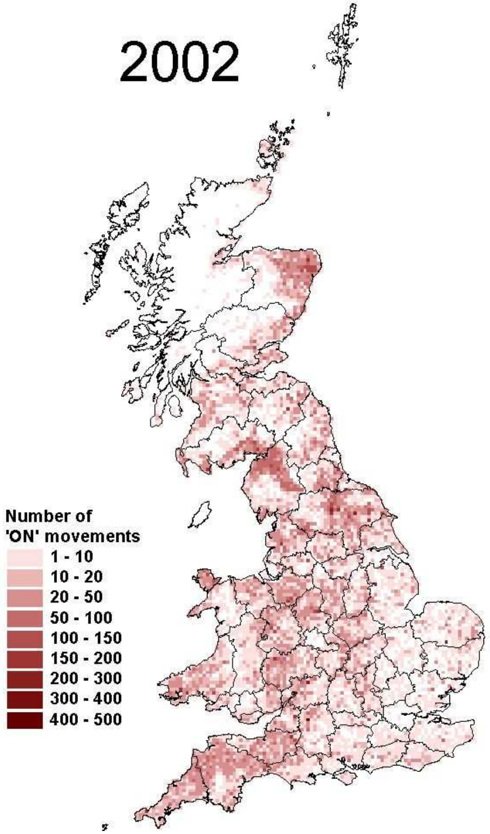
- Distance to the nearest previous TB case
- Cattle density
- Landuse and climatic variables

Attempt to develop a stratified dispersal model including:

- Short-distance spread (adjacent cells only)
- Long-distance spread: movement of animals as recorded in the Cattle Tracing System (CTS, VLA)
- External factors: variable already identified.

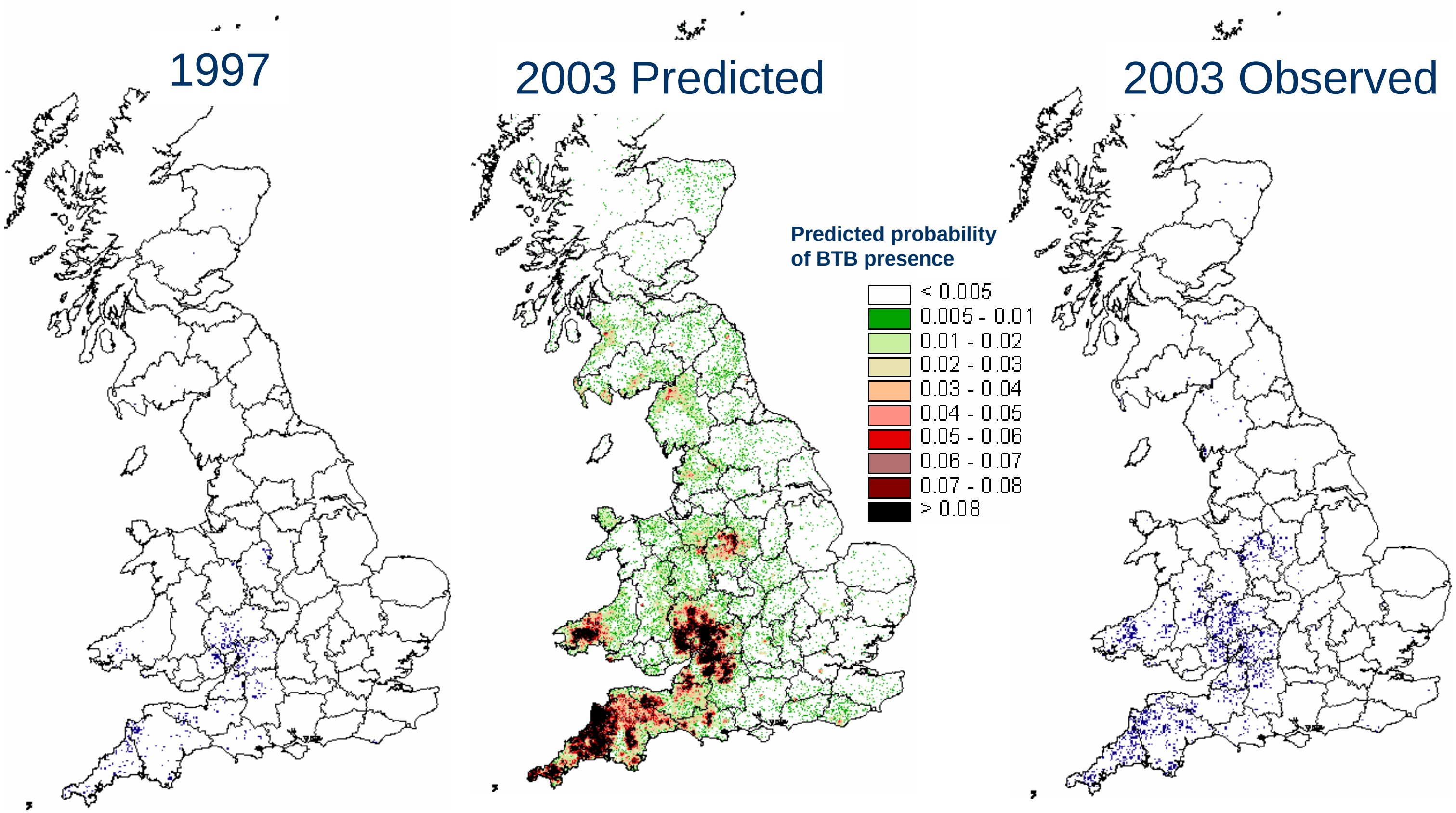
Use of logistic regressions to identify best-fit parameters for the model.

Cattle movements



CTS DATA 2002
MONTHLY MOVEMENTS
PER SQUARE KILOMETRE
INTO CELLS

Predictive model



Conclusions

- Long-distance dispersal events are accounted for by a two-scale dispersal kernel
- Landscape heterogeneity is accounted for by differential probabilities of as a function of local conditions
- Allows short-term predictions provided that the invasion is under a stationary regime, and in similar environmental/landscape conditions

- Does not allow quantitative population estimates
- Difficult to relate to life-history parameters (e.g. growth rate, Diffusion etc.)
- Heavy processing