

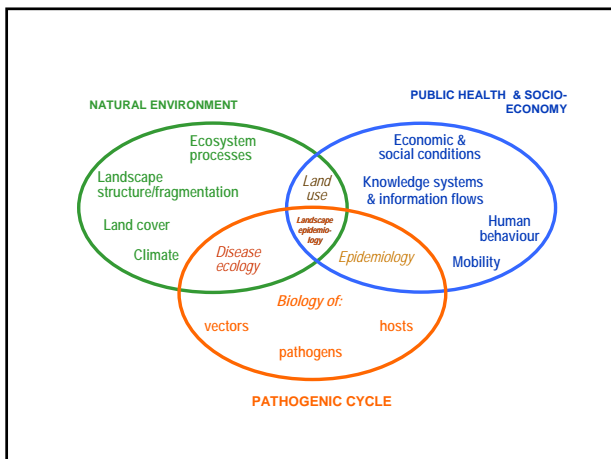
Land change and infectious diseases: The emerging discipline of spatial epidemiology

Eric Lambin
with Sophie Vanwambeke, Catherine Linard

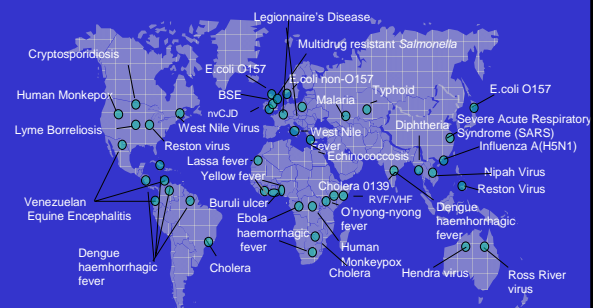
Département de Géographie
UCL

Spatial epidemiology

- The study of spatial variation in disease risk or incidence (Ostfeld et al. 2005)
- Disease risk mapping based on ecological factors affecting the distribution of vectors, reservoir hosts or human cases
- Pavlovsky (1930s): « *Landscape epidemiology* »
Integration of landscape ecology with epidemiology

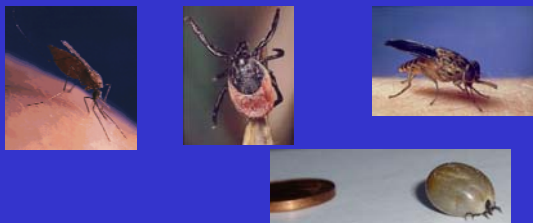


Emerging and re-emerging infectious diseases, 1996–2004



WHO, 2004

Zoonotic & vector-borne diseases

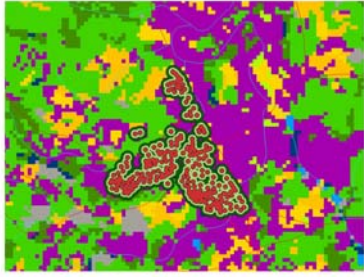


Close association between life history variables of a vector or intermediate host species, and environmental features

Estimating the risk of emergence

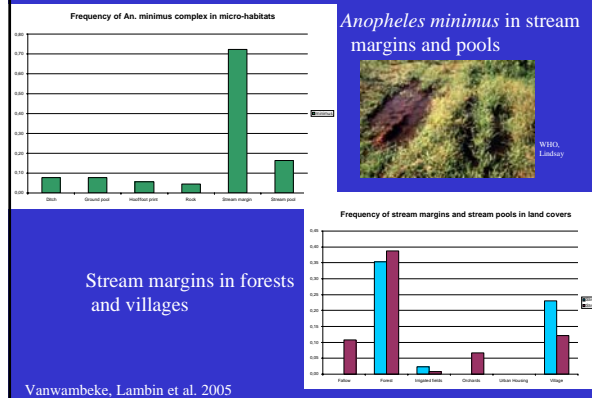
- Statistical models based on remote sensing
- Biological model (R_0)
- Integrated model at landscape scale
- Multi-agent simulation

Habitat mapping & spatial analyses

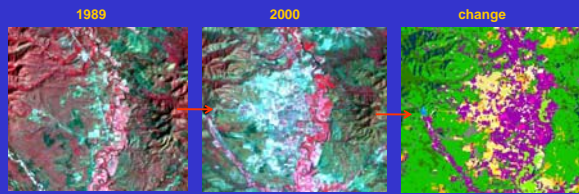


- Distance to...
- Land cover within a distance x (buffers)
- Habitat fragmentation
- Corridors ...

Mosquito ecology: micro-habitats



Land cover change mapped based on Landsat



Vanwambeke and Lambin, 2007

Basic reproductive rate of a disease

Average number of new cases of the disease that will arise from the introduction of an infective host in a susceptible population

$$R_0 = \frac{a^2 m c b e^{-uT}}{\mu r}$$

a : vector biting rate

m : ratio of vectors to hosts

c : transmission coefficient from vertebrate to vector

b : transmission coefficient from vector to vertebrate

μ : vector mortality rate

T : incubation period of the infection within the vector

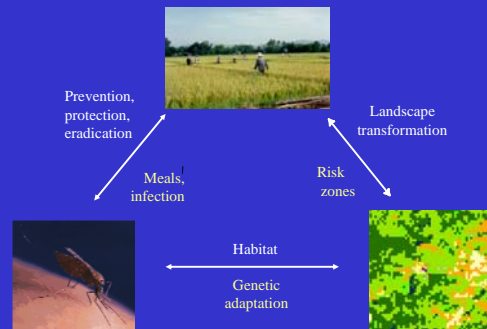
r : rate of recovery of the vertebrate from infection (host)

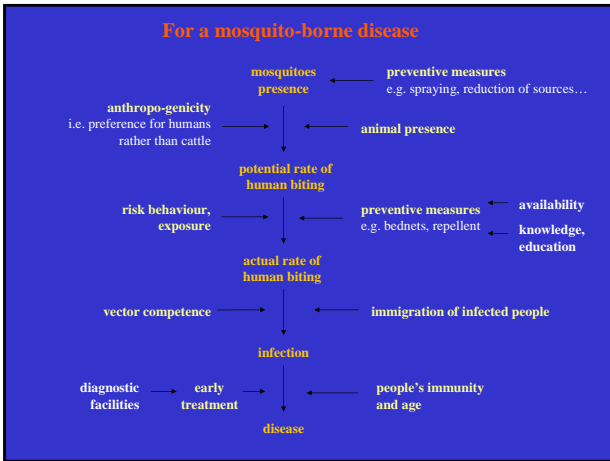
Limitations of R_0

- Assumes a homogenous geographical space
- Assumes stable environmental attributes through time
- Vector/host ratio: requires data on distribution of susceptible hosts

Integrated approach:

humans - landscape - vectors - pathogens





Integrated model

$$D_{cdvy} = PBR_{cdvy} * AIBP_{dv} * INFP_c * DISP_{dv}$$

DISP: probability for an infection to lead to a *disease*
 PBR: *potential biting rate*
 AIBP: *actual biting probability* (daytime, evenings, night-time)
 INFP: probability of a potential biting to be *infectious*

c: mosquito complex
 d: disease
 v: village
 y: year

Vanwambeke, Lambin et al. (2007) *Ecohealth*

Multi-level analysis

Mosquito ecology:

- *Vectors:* mosquitoes
- *Breeding sites:* micro-habitats
- *Land cover:* landscape patches

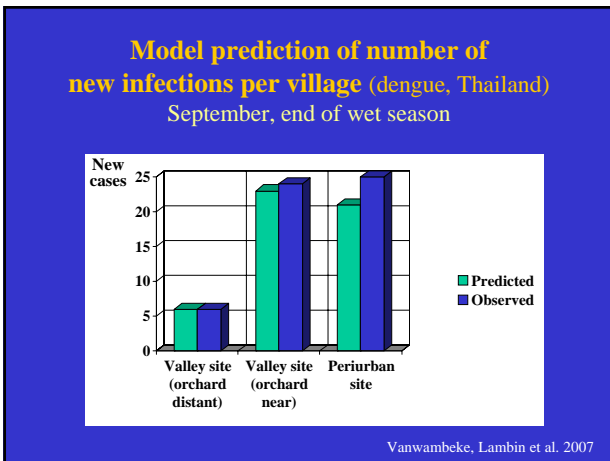
Disease and land use:

- *Epidemiology:* individuals
- *Land use:* households
- *Public health/disease prevention:* villages

Data collection Thailand project

- 7 villages
- Time series of Landsat data
- Socio-economic survey: 223 households
- Field sampling of larvae: 790 habitats surveyed
- Human-baited captures of adult mosquitoes: 4-7 sites per village, 6:00 pm-10:00 pm, 6 times per year, 3 years
- Mosquito identification by molecular methods (PCR and generation of DNA sequence data): 1,867 adults, 1,272 larvae
- Blood collection (antibody testing) & questionnaire: 1,208 (malaria) + 1,928 (dengue) persons followed-up over 3 years

Picture: Biyong van Benthem

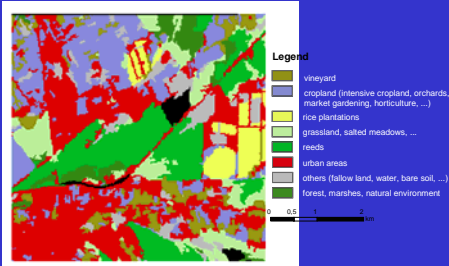


Multi-agent simulations

- Cellular-spatial model
- Agents:
 - represent animals, people, landscape units
 - are goal-oriented, purposeful
 - are interdependent, interact
 - move and adapt
- Patterns of interactions produce emergent properties that are not easy to predict by analysing the separate system components (Holland, 1995)

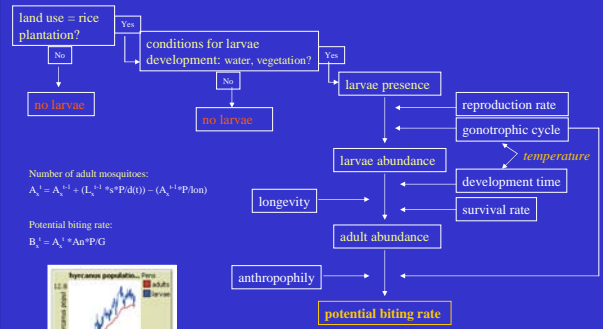
Risk of re-emergence of malaria in Camargue

- potential malaria vector: *Anopheles hyrcanus*
- model human-vector contacts with environmental changes
- test impact of land-use change scenarios by 2025



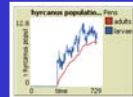
Linard, Ponçon et al.

Decision rules for mosquitoes



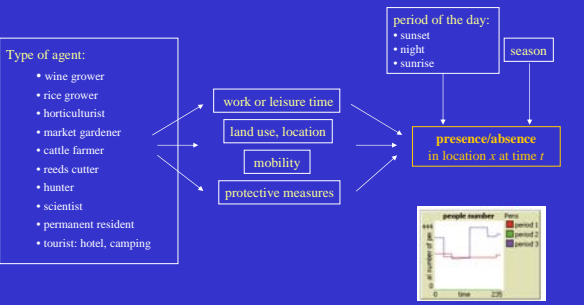
Number of adult mosquitoes:
 $A_t = A_{t-1} + (L_{t-1} * \mu * P/d(t)) - (A_{t-1} * P/d(t))$

Potential biting rate:
 $B_t = A_t * An * P * G$



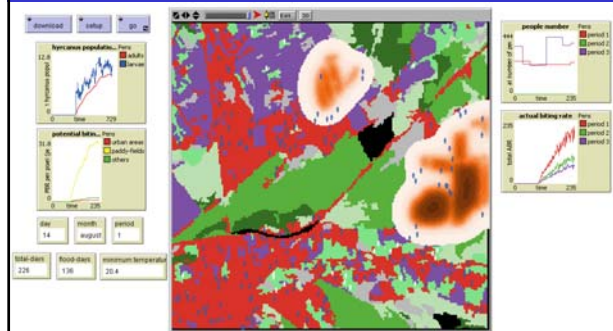
Linard, Ponçon et al., 2007

Decision rules for humans



Linard et al., 2007

Model output: spatially-explicit and dynamic vector-host ratio



Linard et al., 2007

Disease transmission is influenced by fine-grained land-use/cover patterns through:

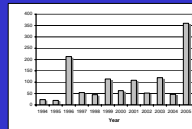
Habitat suitability for vectors and intermediate hosts

Probability of contact between infected vector or animal host, and human host

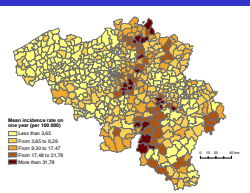
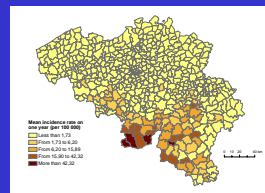
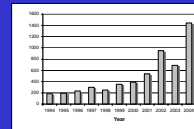
direct transmission: vector/host ecology
 indirect transmission: pathogen ecology

Hantavirus and Lyme borreliosis infections in Belgium

Puumala hantavirus incidence (1994-2004)



Lyme borreliosis incidence (1998-2004)



Data from: Institute of Public Health Belgium

Binomial negative regressions of disease incidence

Hantavirus

Parameter	estimate
Proportion of forest	0.11***
Mean income	-0.0001***
Urbanisation level	-0.67***
Hunters	0.008**
Dispersion	1.50

Deviance/DF = 0.74; Pearson Chi-Sq/DF = 0.98

Higher infection risk in
remote forest areas;
Low incomes

Lyme borreliosis

Parameter	estimate
Proportion of forest	0.023***
Mean income	0.0001***
Separated houses	0.009***
Deer density	0.10**
Dispersion	0.98

Deviance/DF = 1.14; Pearson Chi-Sq/DF = 1.13

Higher infection risk in wealthy
and forested periurban zones

* p < 0.1
** p < 0.01
*** p < 0.001

Linard, Lamarque and Lambin, 2007

Fusion of different scientific cultures

Different emphasis:

- Public health policies, human behaviour, biology, physical environment (climate, vegetation, landscape structure)
- Value of integration *versus* hyper-specialization

Study design:

- Exhaustive survey, statistical sampling or case identification
- Modelling *versus* lab experiments
- Statistical *versus* biological modelling
- Spatially-explicit *versus* non-spatial analyses

Research process:

- Joint fieldwork to promote interdisciplinary interactions
- Jointly construct an *integrated* conceptual model and then a simulation model to engage all project participants on a common goal