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# **SIMULATION OF SYLVATIC PLAGUE EPIDEMICS IN CENTRAL ASIA BY USING A SEASONALLY FORCED BOTTOM-UP MODELING CHAIN**

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# Plague in Kazakhstan

Main host: great gerbil *Rhombomys opimus*

Main vector : flea of species *Xenopsylla gerbilli* Minax

Particularities:

- an intensive eco-epidemiological monitoring
- strong seasonal effects



Source : Kausrud et al., 2007



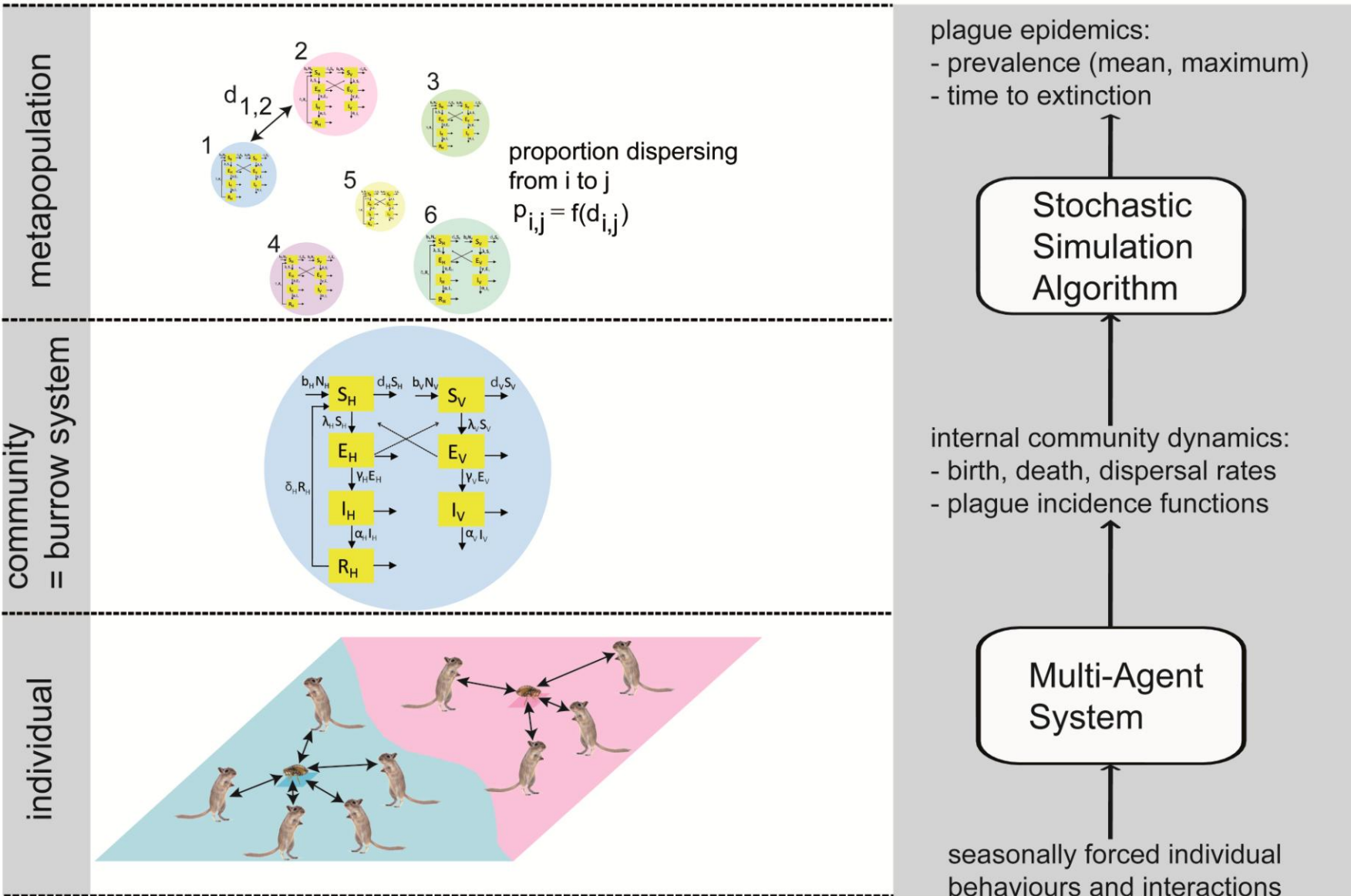
Source : Wikipedia

# A bottom-up modeling chain for a multi-level system

levels

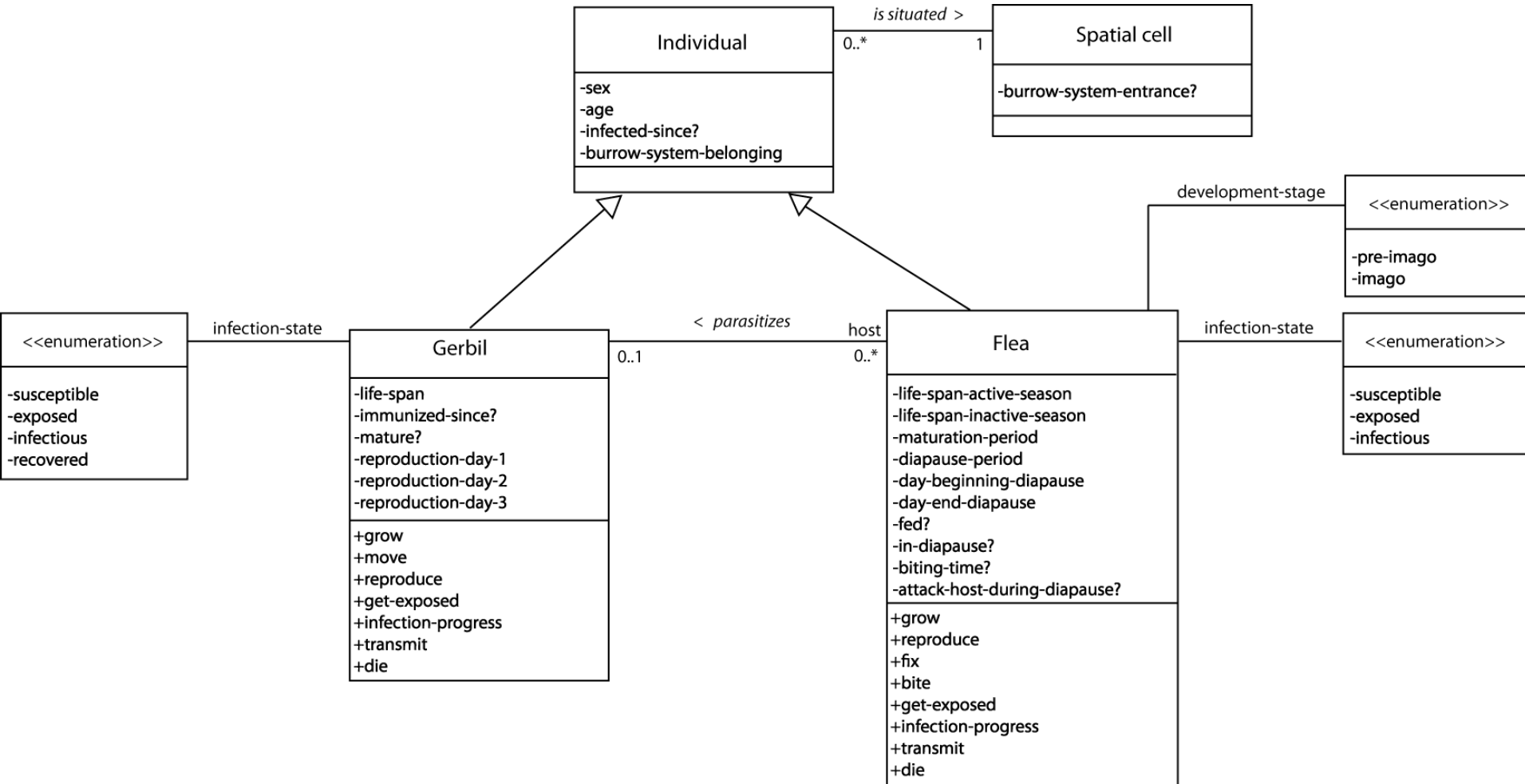
conceptualization

modeling chain



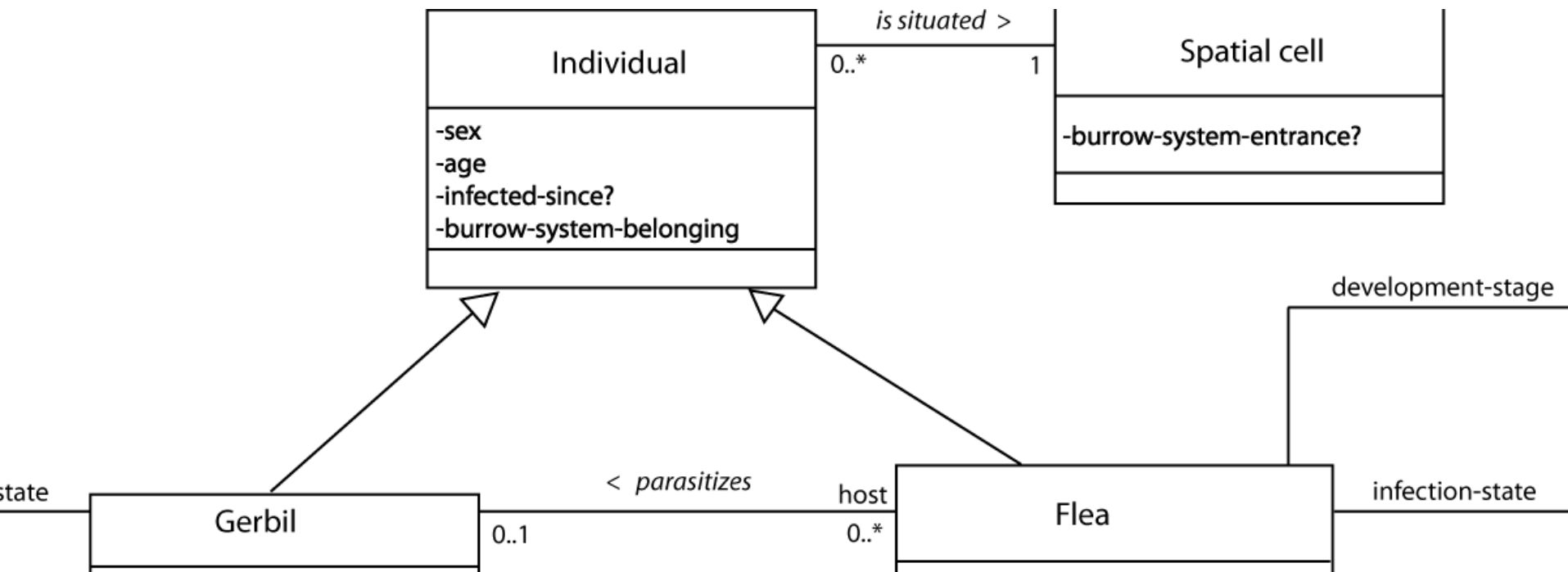
# The Individual Based Model a Multi-Agent System

## Class diagram



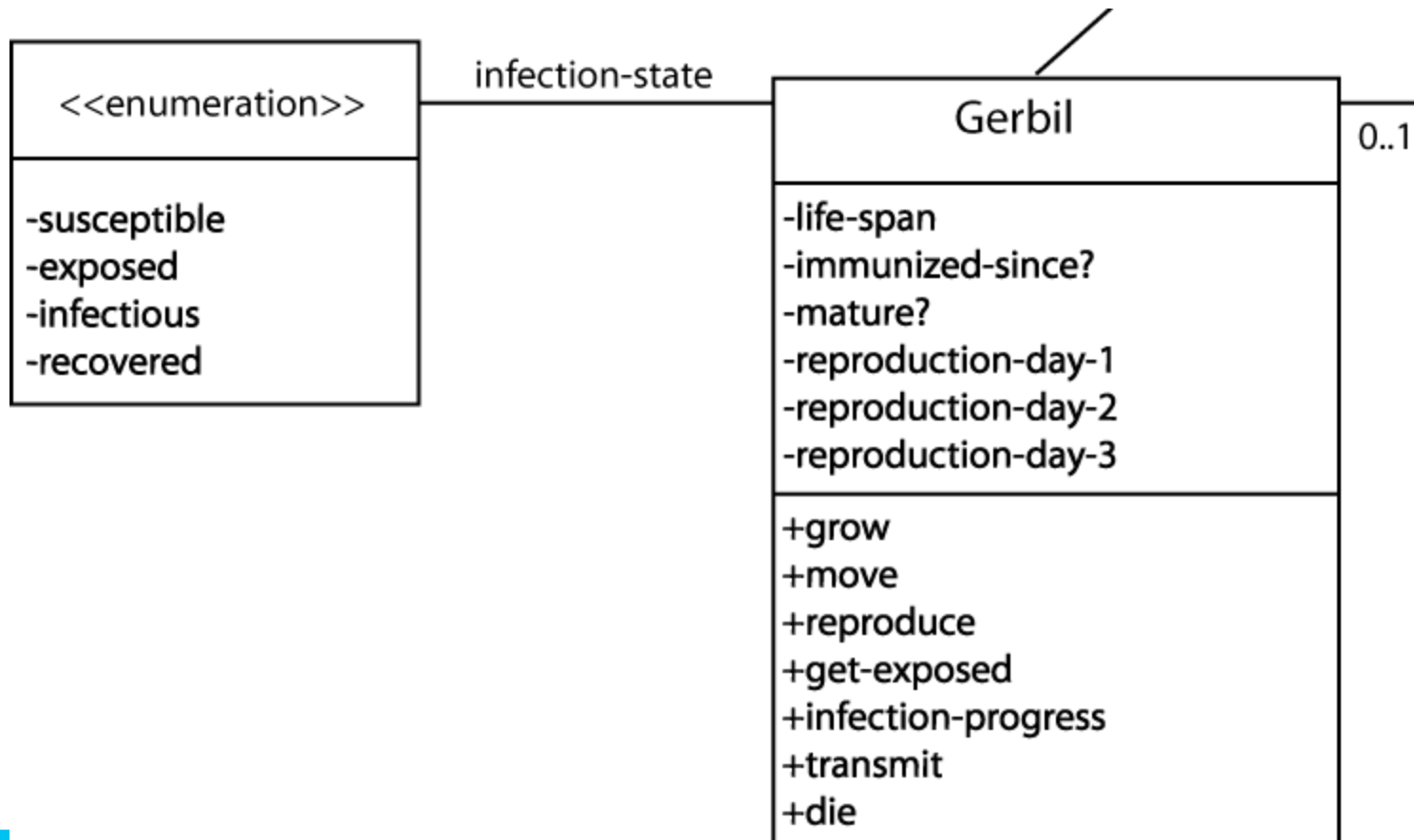
# The Individual Based Model a Multi-Agent System

- 2 classes of individuals
- 1 class of spatial cells



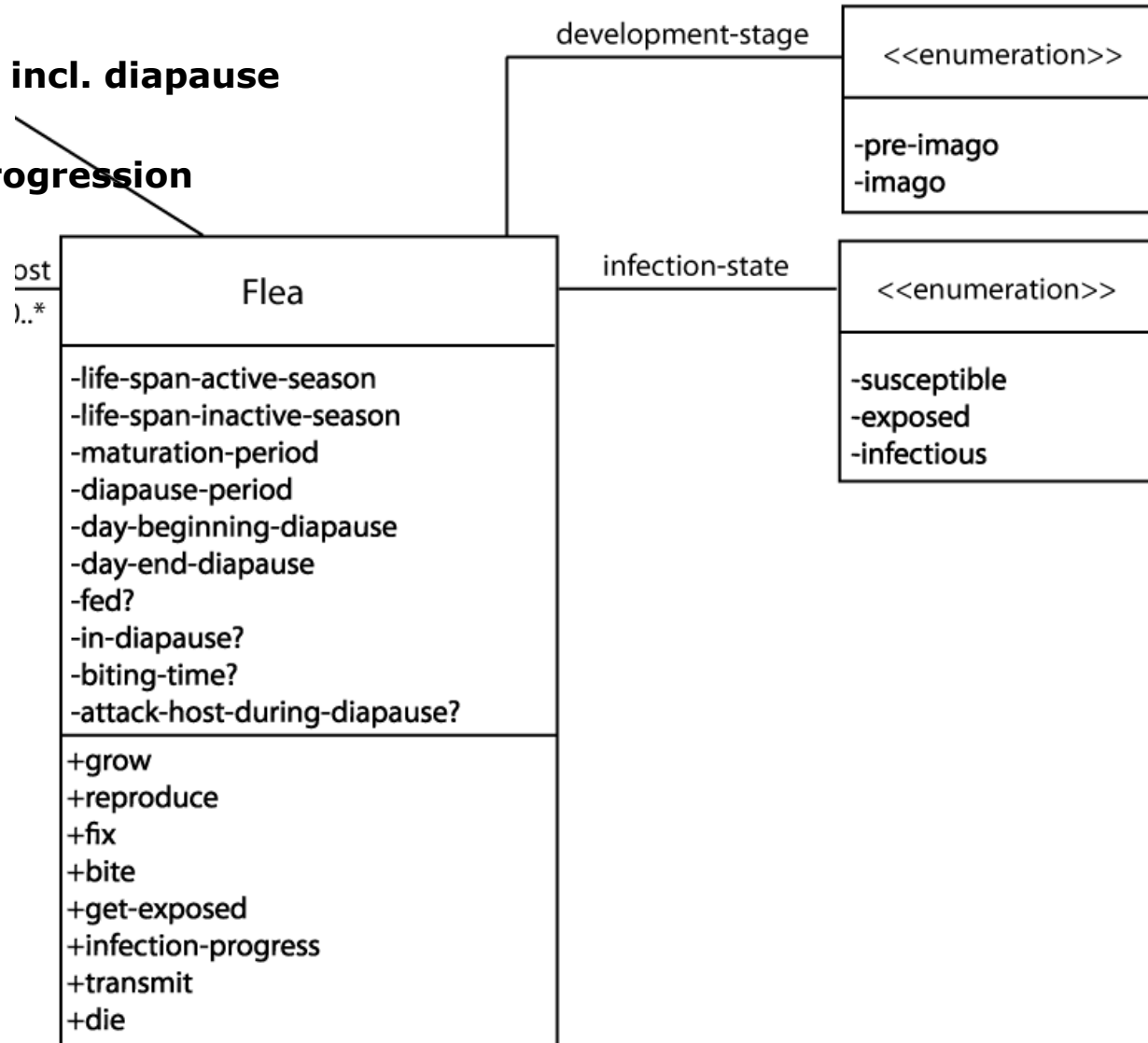
# The Individual Based Model a Multi-Agent System

- growth, reproduction and death
- foraging activity
- pathogen transmission and progression



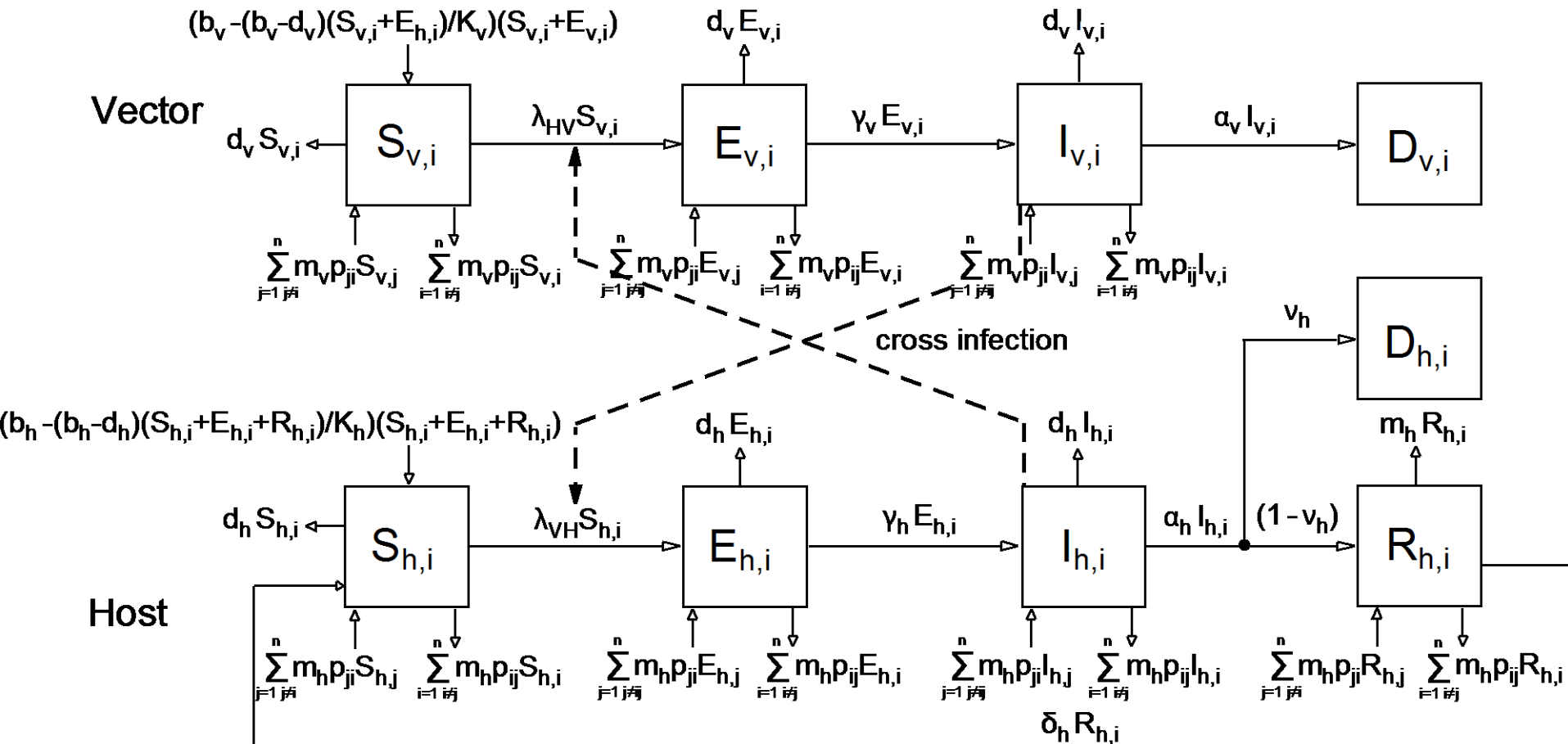
# The Individual Based Model a Multi-Agent System

- growth, reproduction & death incl. diapause
- on-host / off-host mobility
- pathogen transmission and progression



# the Metapopulation Level Model:

- within-community population & infection dynamics
- between-community dynamics due to gerbil dispersal

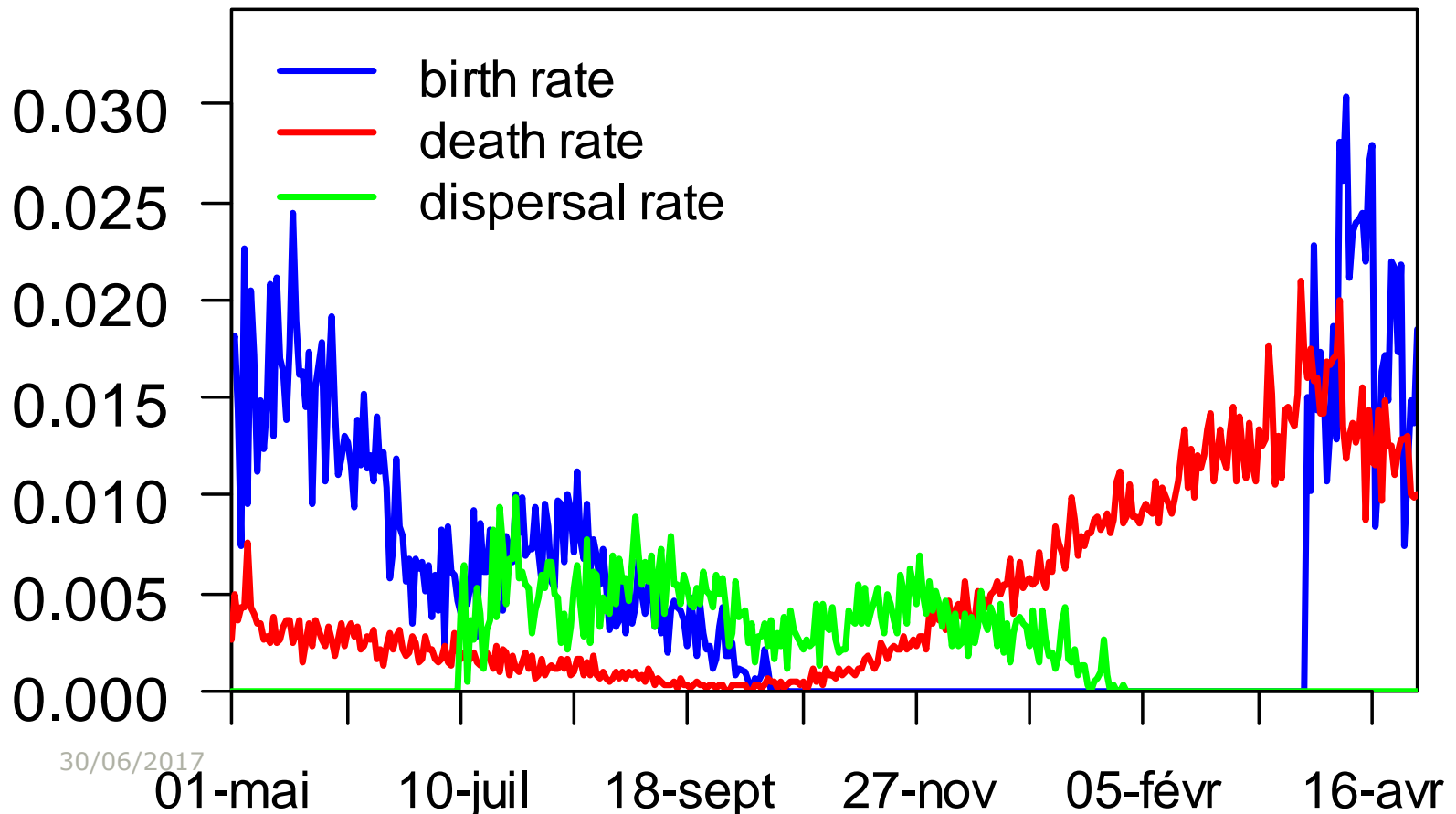




# IBM derived seasonally forced parameters

for a typical year

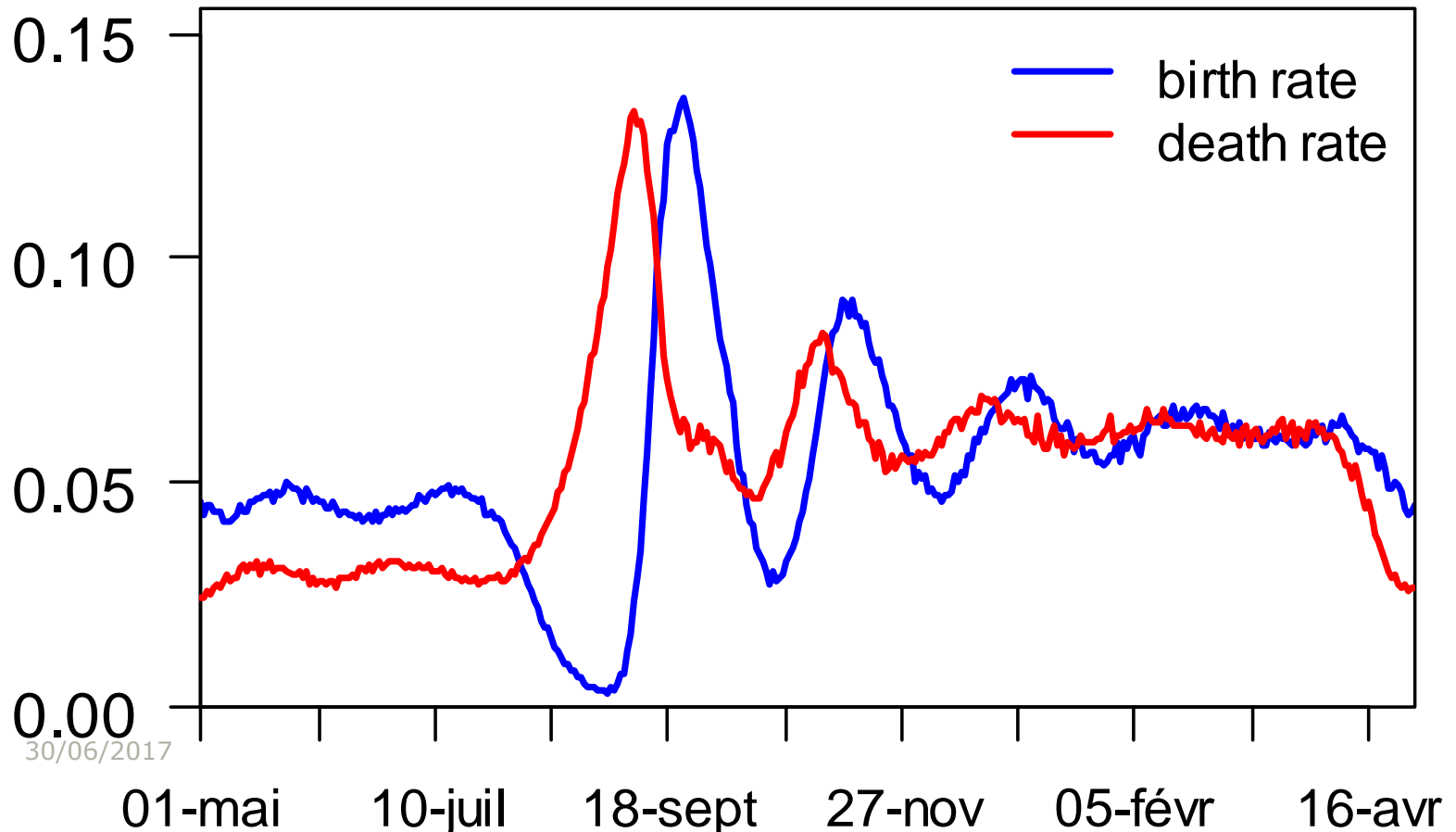
host



# IBM derived seasonally forced parameters

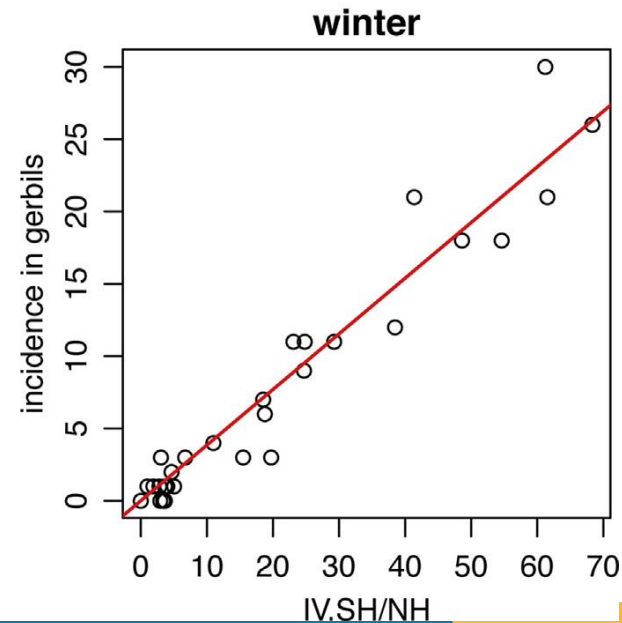
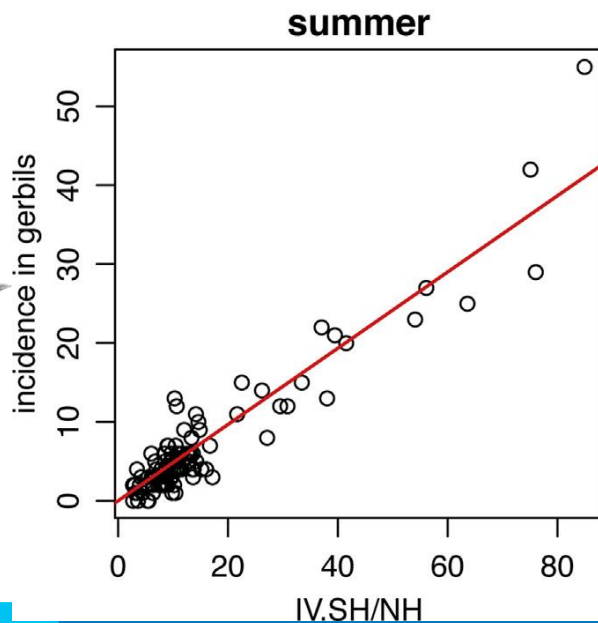
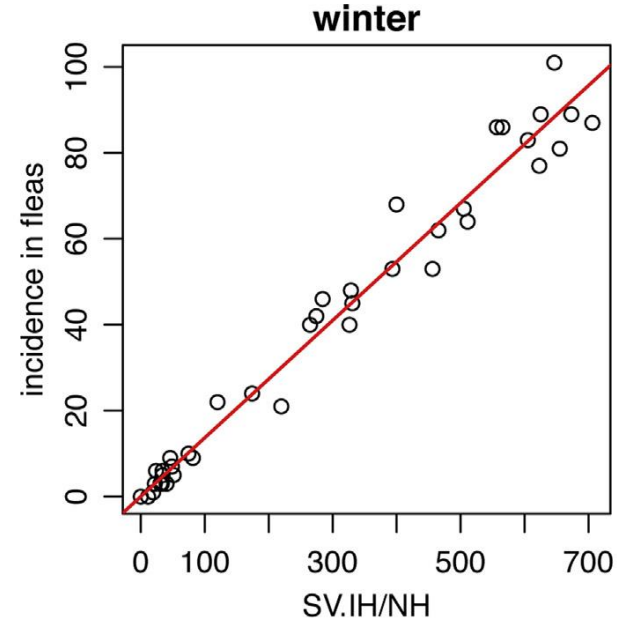
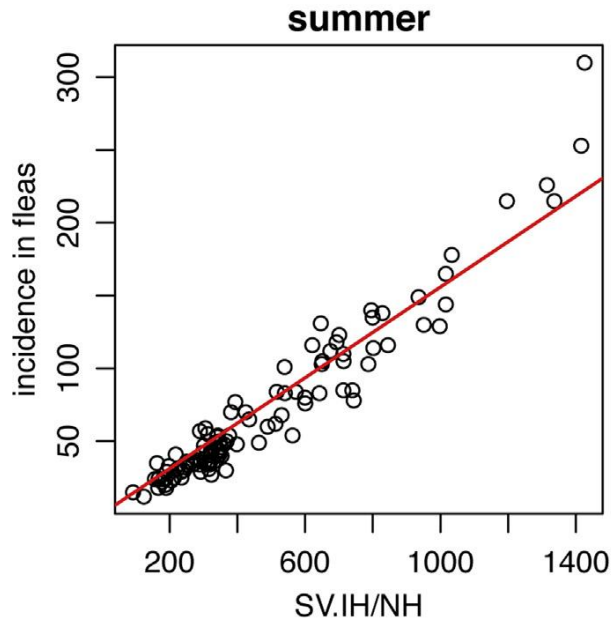
for a typical year

vector



30/06/2017

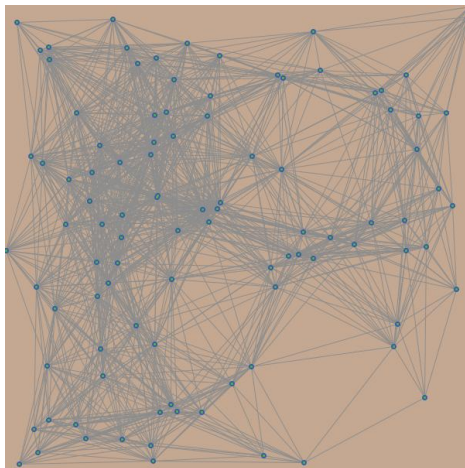
# IBM derived transmission coefficients



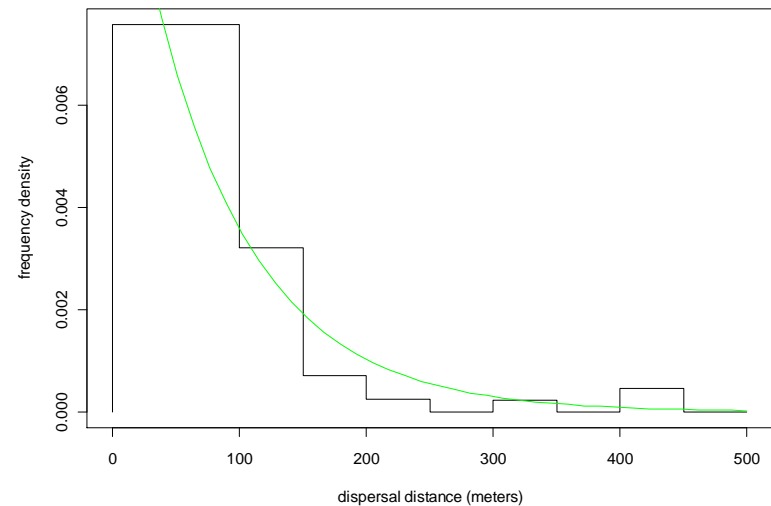
# The Metapopulation Level Model:

## Host dispersal

Exponential density function fitted to dispersal distribution (Davis et al., 2008)



+



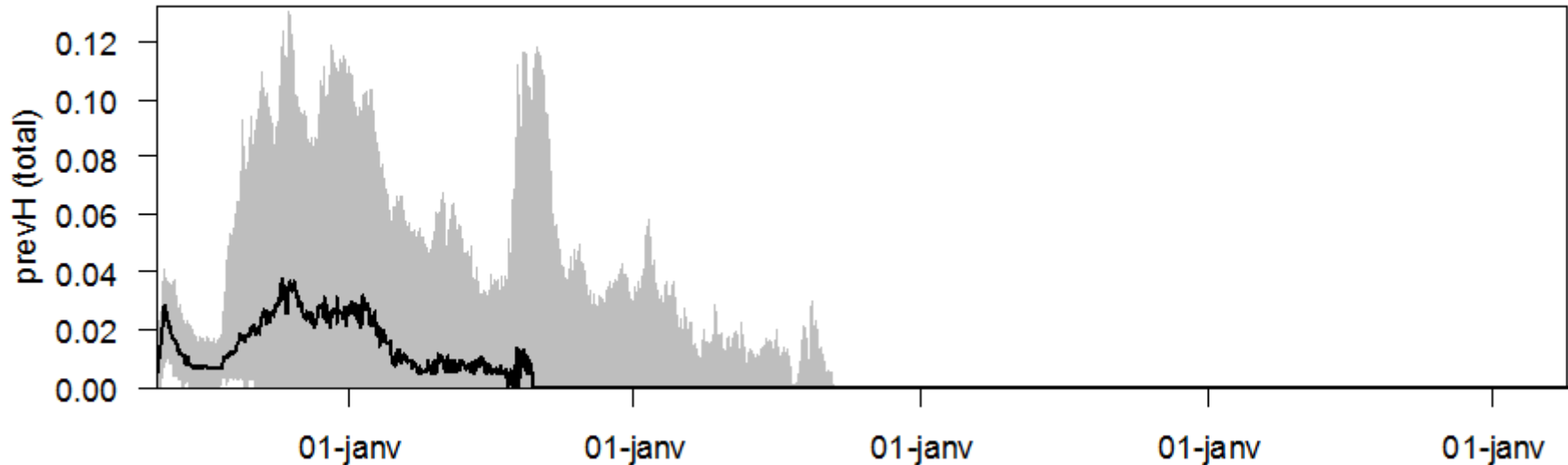
Flux distribution  $p_{i,j}$

Proportion moving from  $i$  to  $j$

$$p_{i,j} = f(d_{i,j})$$

	1	2	3	4	5	sum	
1		0	0.08999955	0.42916617	0.4259499	0.05488437	1
2	0.1860359		0	0.06231696	0.1080404	0.64360671	1
3	0.8040972	0.05648497		0	0.1211829	0.01823489	1
4	0.6568	0.08059435	0.09973163		0	0.16287399	1
5	0.1139613	0.64650657	0.02020826	0.2193239		0	1

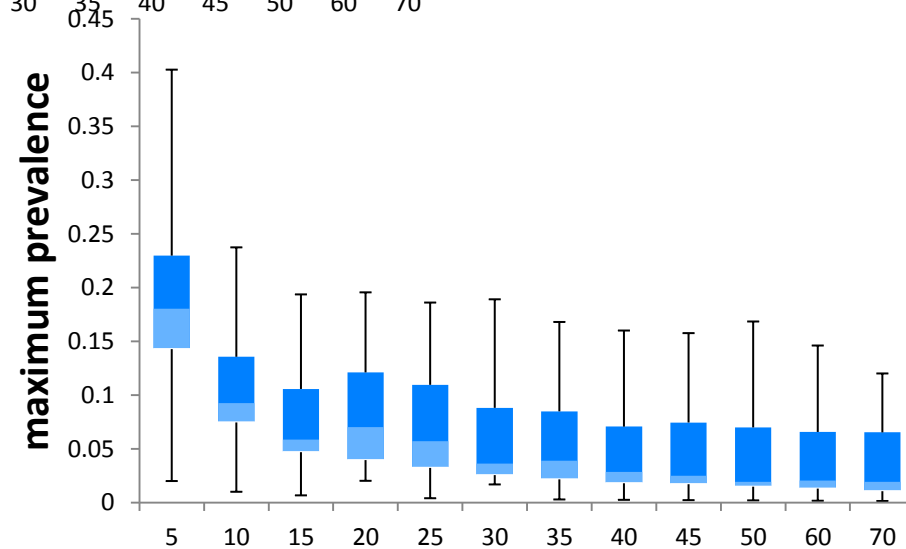
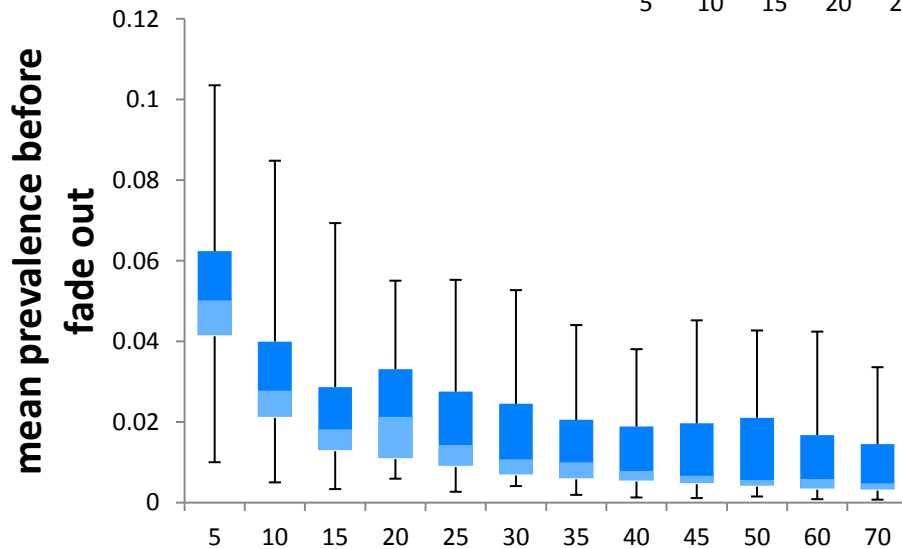
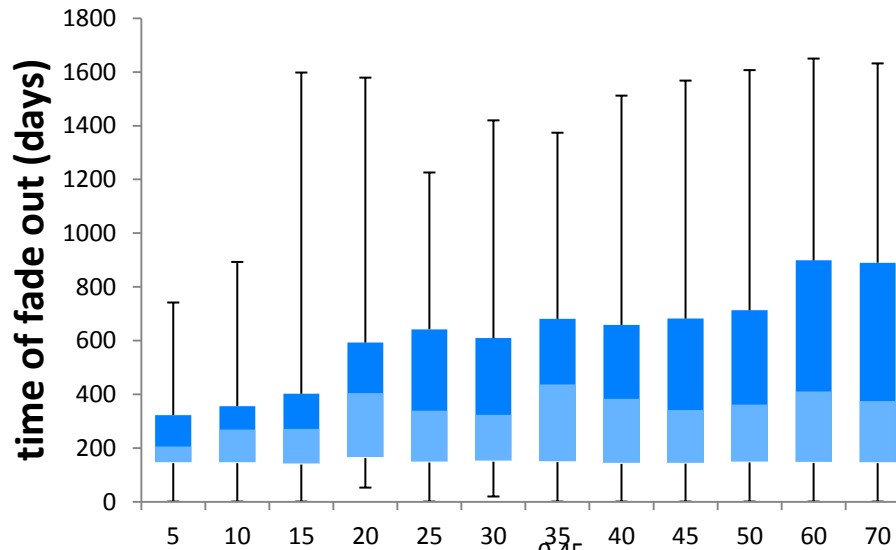
100 replications with 20 communities and 1 infected individual introduced (median, 5th-95th percentiles):



SIMULATION Scenario 2	Host prevalence	FROM OBS. TIME-SERIES	Host prevalence	source
Mean before fade out	0.023	Mean	1. 0.008-0.012 in spring ; 0.011-0.012 in fall (GTMM) 2. 0.01-0.06 (autoregressive modelling)	1. Stenseth et al., 2006 2. Kausrud et al., 2007
Mean 1800 days	0.0077			
Max recorded	0.1955 (0.2 on raw data)			
		Max	1. 0.19 2. 0.065 3. 0.3-0.8 (autoregressive modelling)	1. Stenseth et al., 2006 2. Davis et al., 2004 3. Kausrud et al., 2007

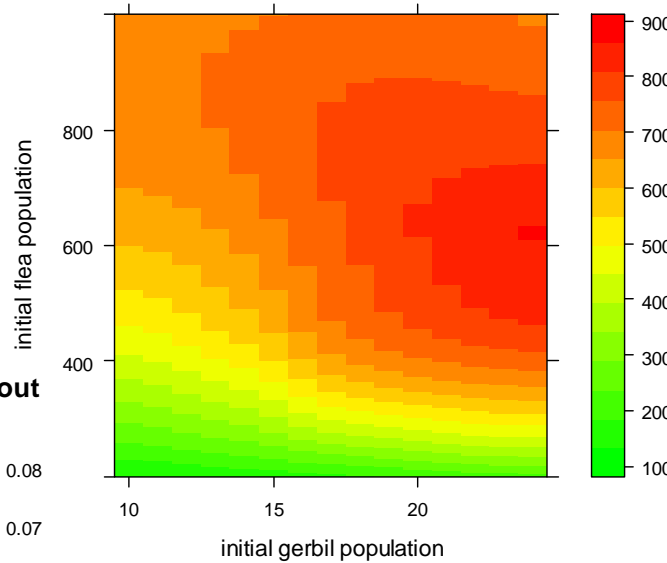
Kazakh Scientific Centre for Quarantine and  
Zoonotic Diseases:  
**Serious concern at host prevalence 0.008**

# Sensitivity to the number of communities

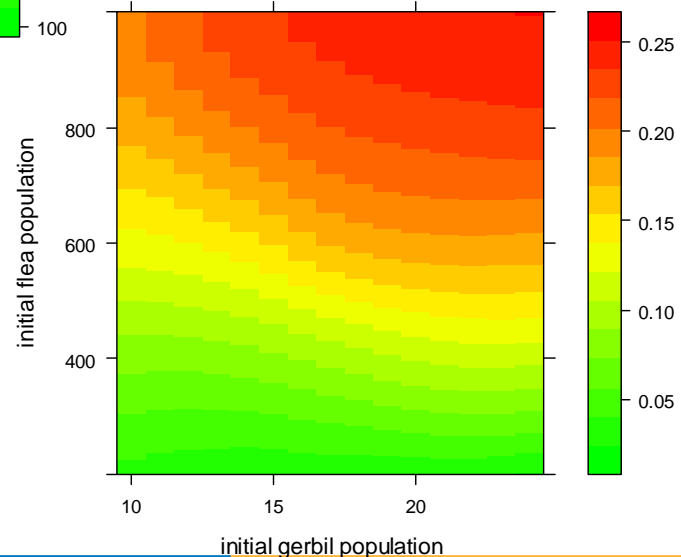


# Sensitivity to host & vector initial community sizes

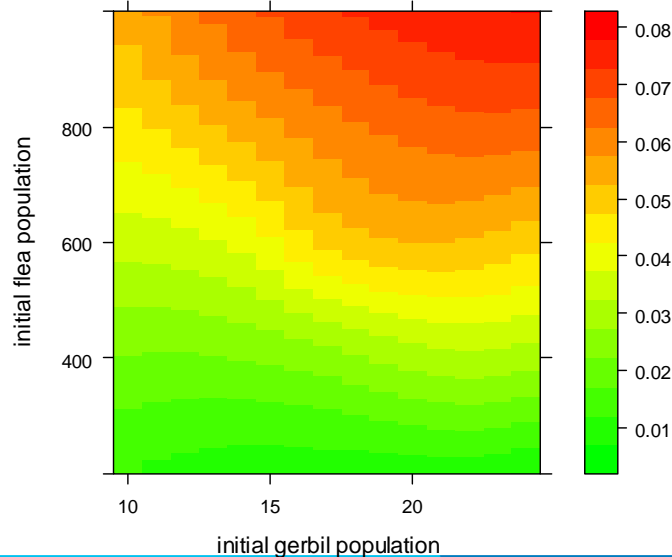
median time of fade out



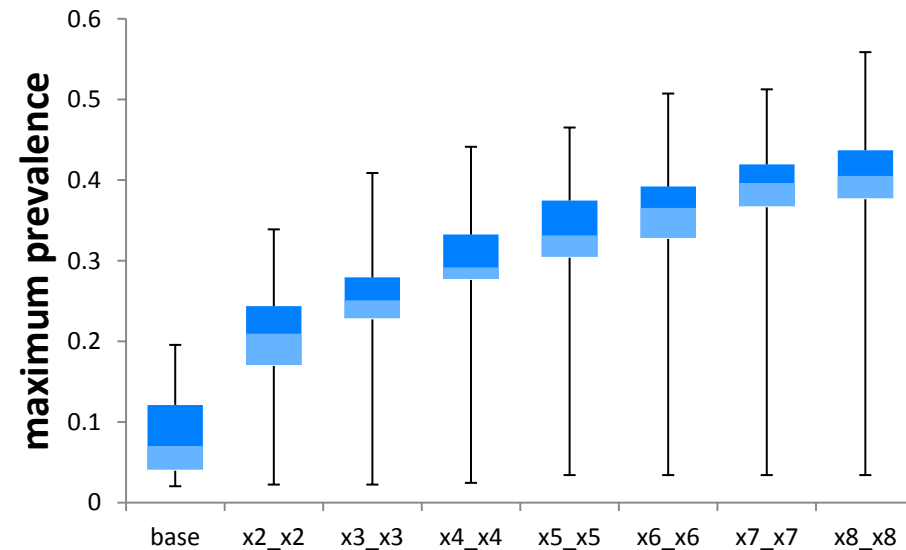
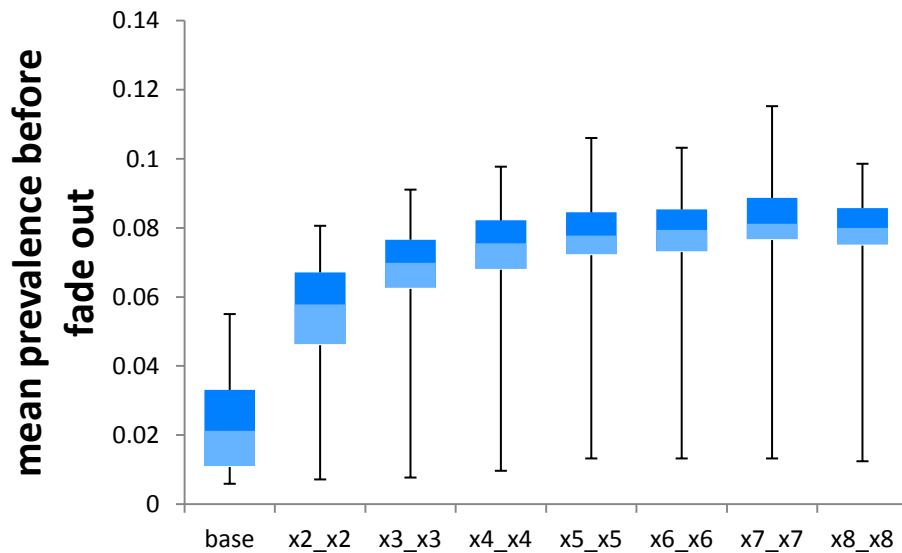
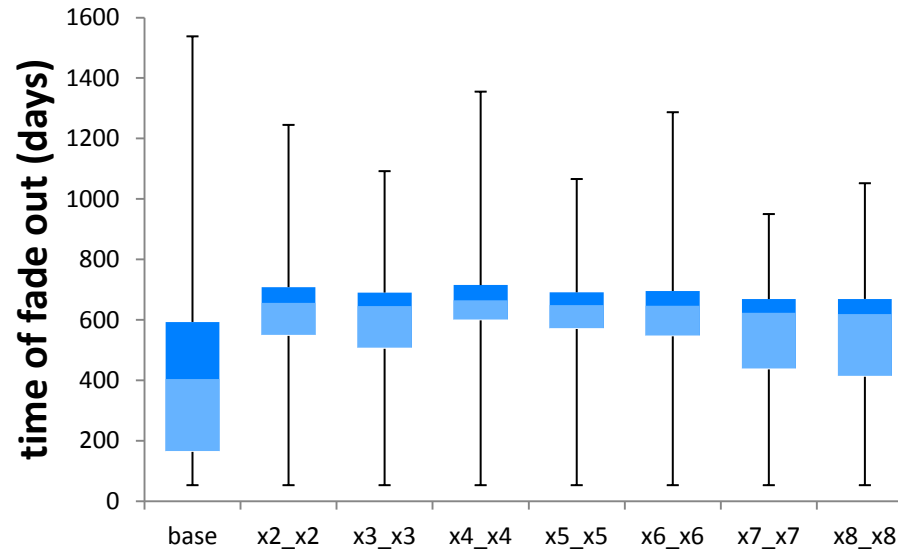
median prevalence at the epidemic peak



median time averaged prevalence before fade out



# Sensitivity to the intensity of mobility of host & vector





# Discussion:

## From the individual to the metapopulation:

- ⊙ Metapopulations are finite and made of heterogeneous spatially distributed individuals arranged in communities
- ⊙ The PLM is always an approximation to the underlying IBM

## About the plague system in Kazakhstan:

- ⊙ Strong ability for the infection to persist very locally for multiple years
- ⊙ Metapopulation sizes considered in the model too low to act as autonomous hotspots

# For further reading:

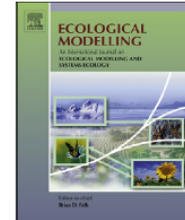
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journal homepage: [www.elsevier.com/locate/ecolmodel](http://www.elsevier.com/locate/ecolmodel)



### Cross-scale modeling of a vector-borne disease, from the individual to the metapopulation: The seasonal dynamics of sylvatic plague in Kazakhstan



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#### ABSTRACT

Individual-based or population-level simulation approaches are often employed alternatively in eco-epidemiological modeling. In this paper, we introduce an original coupling approach applied to bubonic plague zoonotic infection in the Pre-Balkhash focus (central Asia), with main host *Rhombomys opimus* (Rodentia: Gerbillidae) and vector its associated ectoparasite flea *Xenopsylla gerbilli minax*. An Individual-Based Model (IBM) is first developed as a Multi-Agent System (MAS), addressing the seasonally forced internal dynamics of a typical burrow system based upon individual processes and interaction rules of the host-vector parasitoid system. Key population parameters and incidence functions are derived from