

Multi-level modeling, simulation for optimizing vaccination policies

Phd: TRAN Thi Cam Giang

Directors : Yann CHEVALEYRE, Marc CHOISY

VU Dinh Thiem, Jean-Daniel ZUCKER

Doctoral School : EDITE 130, Université Pierre et Marie CURIE

Commencement day : 01/10/2012

Cotutelle scholarship : UPMC/NIHE

Funding: PDI MSI, UPMC/IRD

Context et Objective

- Many infectious diseases such as measles, dengue in Asia and most countries of southeast Asia. (REF)
- Vaccination: Mass policy, the oldest and still most widely used in the world, is to vaccinate a maximal number of children before a certain age. It is already getting a significant decrease about the incidence in many countries,
- Problem : is too expensive, ineffective and absolutely impossible to implement in many poor countries, in particular in Africa, Southeast Asia..as at the same time financial and logistical problems. (ex. the projet of the WHO about extinction of measles in Vietnam before 2012 is failed).

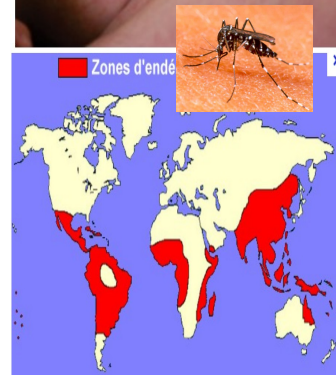
OPTIMIZING vaccination policies that would be more effective, less expensive than the mass policies.



Context et Objective

- Many infectious diseases such as measles, dengue in Asia and most countries of southeast Asia. (REF)
- Vaccination: Mass policy, the oldest and still most widely used in the world, is to vaccinate a maximal number of children before a certain age. It is already getting a significant decrease about the incidence in many countries,
- Problem : is too expensive, ineffective and absolutely impossible to implement in many poor countries, in particular in Africa, Southeast Asia..as at the same time financial and logistical problems. (ex. the projet of the WHO about extinction of measles in Vietnam before 2012 is failed).

OPTIMIZING vaccination policies that would be more effective, less expensive than the mass policies.



Tool?

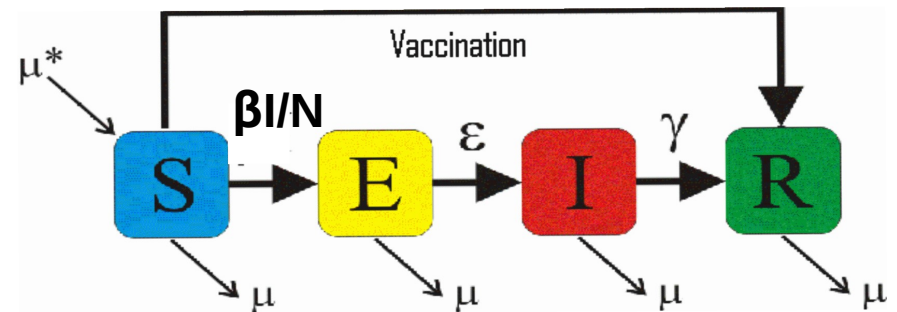


- There exists the R package : very slow !
- Using C++ to do stochastic simulation with $N = 10M \rightarrow$ excellent !
- Developing a package integrating R/C++.

Method

(1) Stochastic Epidemiological model

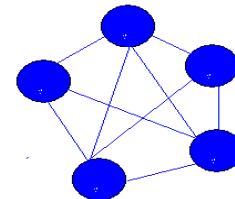
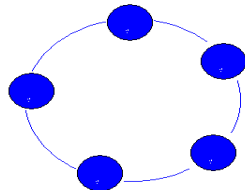
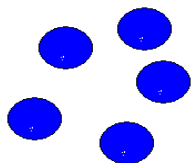
→ SEIR Model of population :



→ Gillespie's Stochastic Algorithm (1977)

- Motivation : no extinction in deterministic model
- Approach: population-based time-to-event model, 2 steps:
 - Searching the time of next event
 - Searching the nature of next event

(2) Spatial Epidemiological Modeling



Method

(3) Optimizing vaccinations policies : reinforcement learning

For a structure à population given, where and when we must vaccinate to vacciner afin de decrease at most the global incidence or crease at most the probability of global eradication.

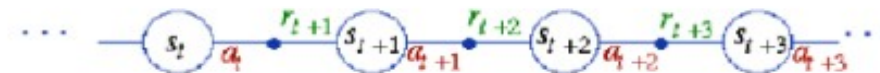
- SARSA : State - Action - Reward – State – Action

- A state at time t : $(\in \mathbb{N}^4)$

$$S = \left((s_1, e_1, i_1, r_1), (s_2, e_2, i_2, r_2), \dots, (s_n, e_n, i_n, r_n) \right)$$

- Set of states : $\mathbb{N}^{4 \times \text{nbVilles}}$

- Action at time t, vaccination ou non vaccination



- Sum of rewards for a policy : $\Pi : S \rightarrow A$

$$\sum_{t=0}^{\infty} \gamma^t r_t = r_0 + \gamma r_1 + \gamma^2 r_2 + \gamma^3 r_3 + \dots$$

Expected Results



- The results of this thesis are: an efficient **algorithm** for optimizing vaccination policies evaluated by **spacial and stochastic simulation**.
- An informatic tool supporting decision of vaccination policies used by health professionals available in the form of an R package (R/C++)

Results 1

- Finding the formula of the force of infection in spatial structure.

$$\lambda_i = \left(1 - \sum_{\substack{k=1 \\ k \neq i}}^n \rho_{ik} \right) \beta_i \frac{I_i}{N_i} + \sum_{\substack{k=1 \\ k \neq i}}^n \rho_{ik} \frac{(1 - \varepsilon_{ik})\beta_i N_k + \varepsilon_{ik}\beta_k N_i}{N_i N_k} I_k$$

- Modeling and simulation of deterministic and stochastic SEIR model in programming languages.

Result 1: package dizzys



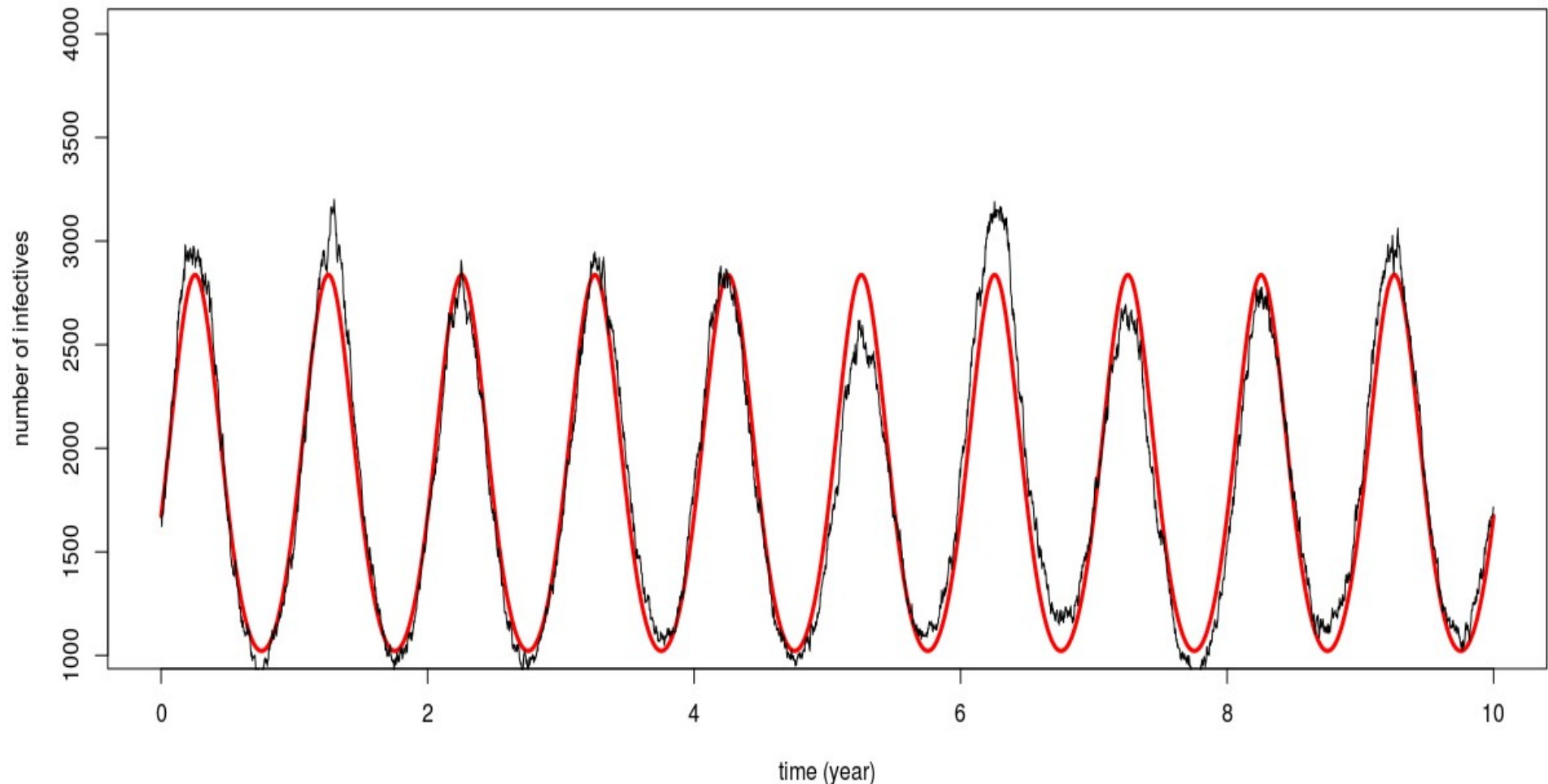
- The package dizzys simulating temporal epidemic models.
 - Allow to integrate C ++ in R.
 - Make deterministic / stochastic simulations for SIR and SEIR epidemic models by using deterministic equations, stochastic algorithms and adaptivetau Gillespie algorithm.
 - Make simulations for n sub-populations in a meta-population.
 - Interface displayed by R in 2D, in 3D.

Result 1: Prototype developed under C++ : Example

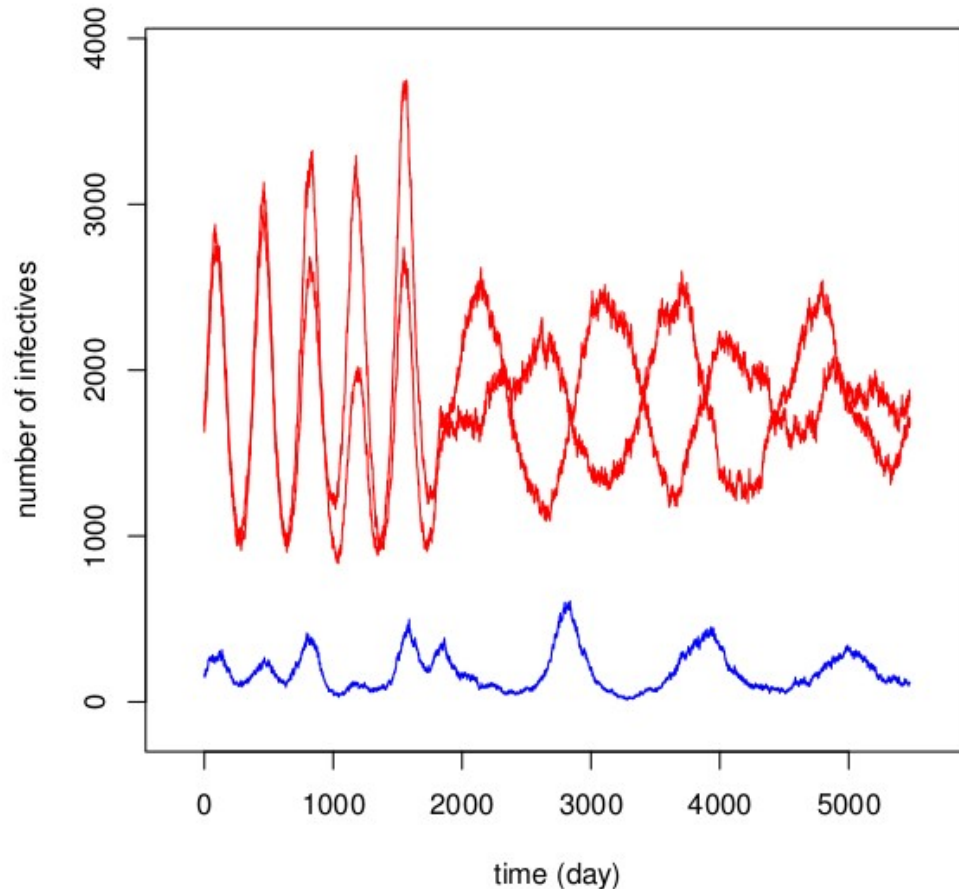
Number of infected for 1 city of 10M individuals



SIMULATION: -nbVilles 1 -tmax 3650 -sigma 0.125 -gamma 0.2
-mu 3.91389432485323e-05 -epsilon 0 -topology 0 -rho 0 -unitTemps 1 -graine 1355734407.61301
-S0 741559.447874164 -E0 2794.62443191756 -I0 1673.21742231949 -R0 9253972.7102716 -N0 1e+07 -beta0 2.73972602739726 -beta1 0.1
-phiMIN 0 -phiMAX 0 -nbSimu 1 -typeFonc 0

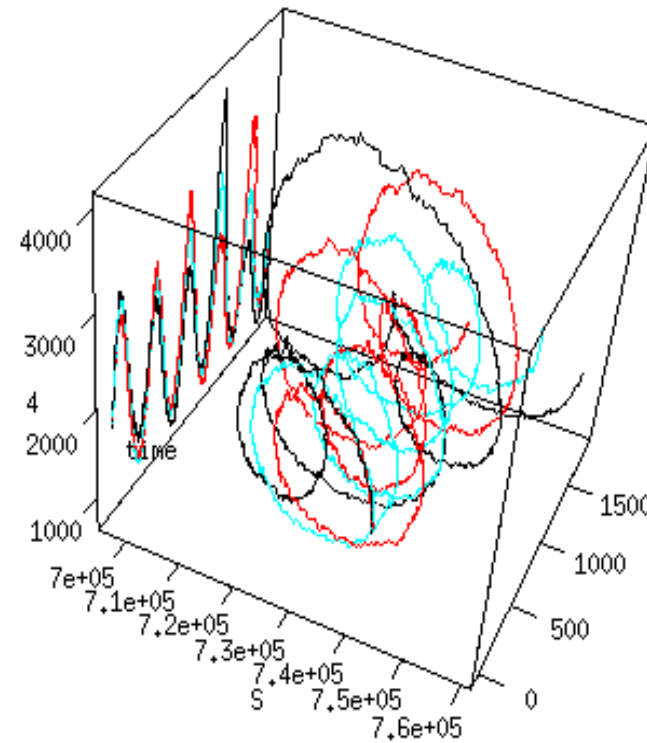


Result 1: : package **dizzys** simulation in 2D and 3D

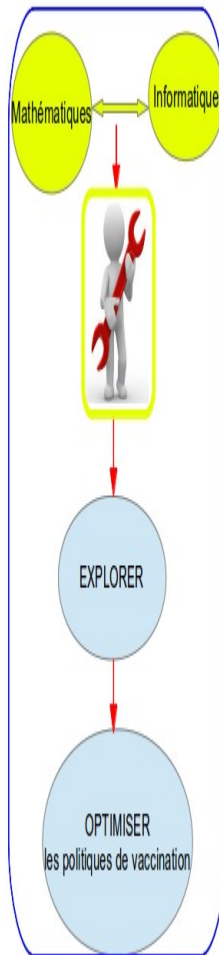


Metapopulation of three cities,
 $N = \{10^6, 10^6, 10^5\}$, $\varphi_{\text{Max}} = \{0, \pi\}$

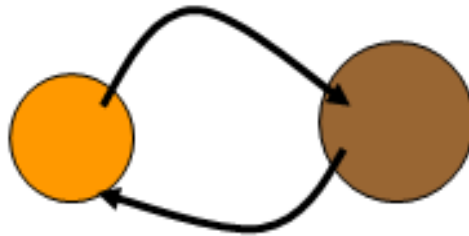
$\mu = 1/(70 \times 365)$ par jour, $\beta_0 = 1250/365$ jour, $\beta_1 = 0.1$ jour, $1/\sigma = 8$ jours, $1/\gamma = 5$ jours, $\varphi = 0$, temps de simulation = 10 ans.



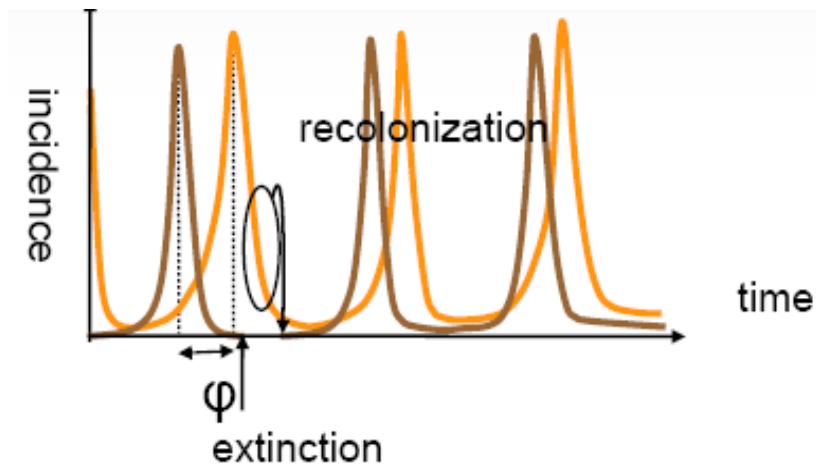
Metapopulation of three cities,
 $N = \{10^6, 10^6, 10^6\}$, $\varphi_{\text{Max}} = \{0\}$



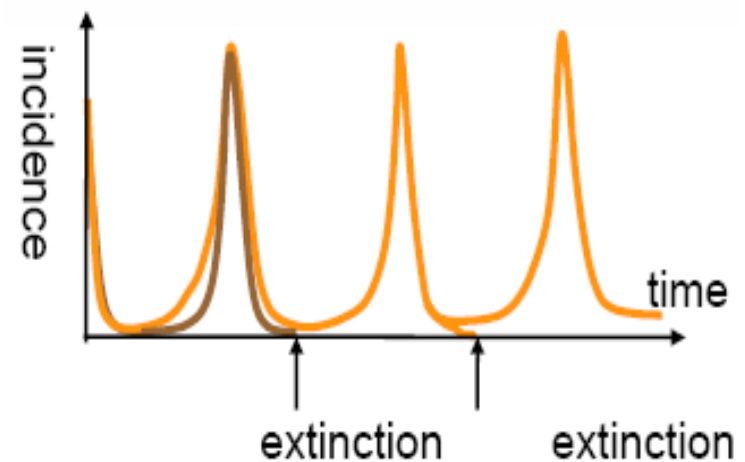
Question 1: persistence in the simulated model



Spatial Asynchrony
no extinction at larger scale



Spatial synchrony
Extinction at larger scale



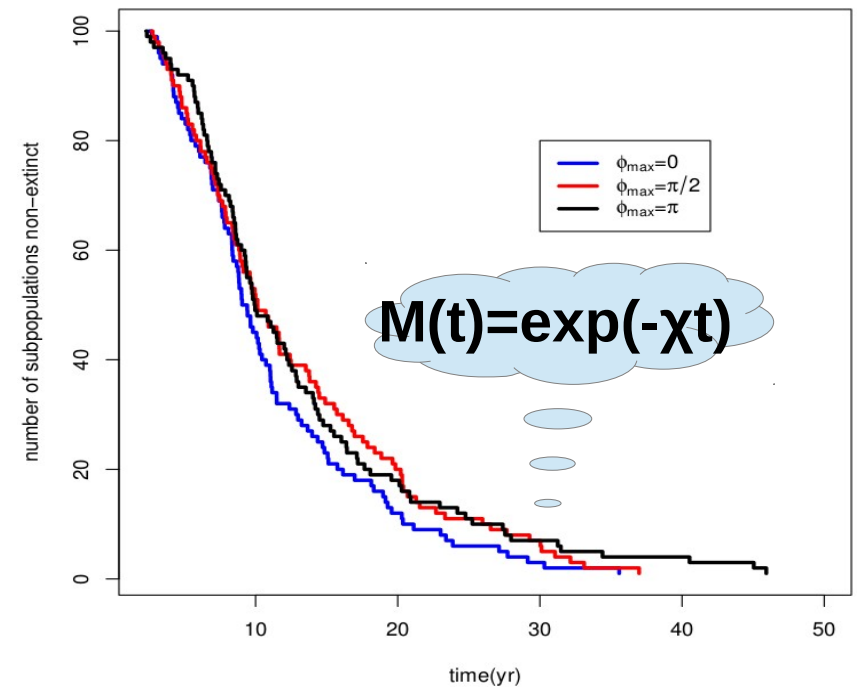
Solution of Q1 : EXPLOITING **dizzys**

- EXPLOITING the tool dizzys for the persistence in the model simulated.
- FINDING the characteristics of the global persistence. This is the survival curve which is shaped

$$M(t) = \exp(-\chi t)$$

where $M(t)$ is the number of meta-populations that are not extinct at time t .

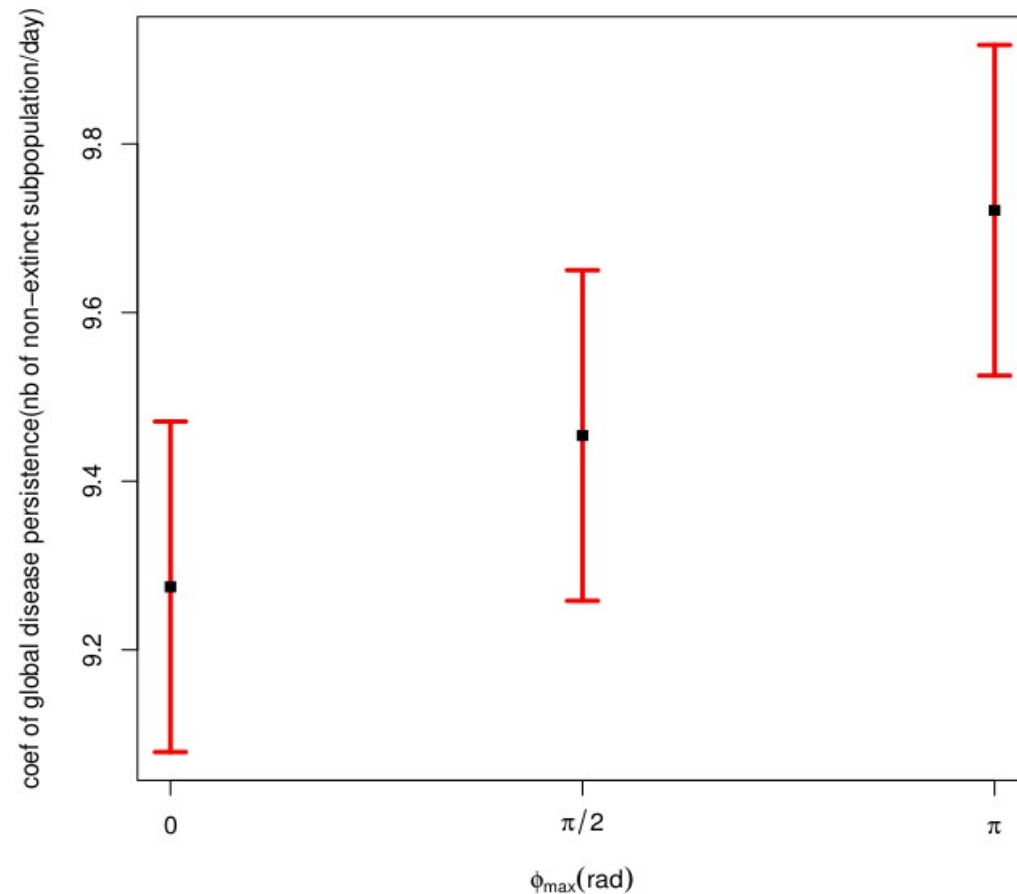
Survival curve Kaplan-Meier



NbVilles=02, $N=3 \cdot 10^5$ tmax=50 ans, $p=0.001$

Result 2 : Persistence 1

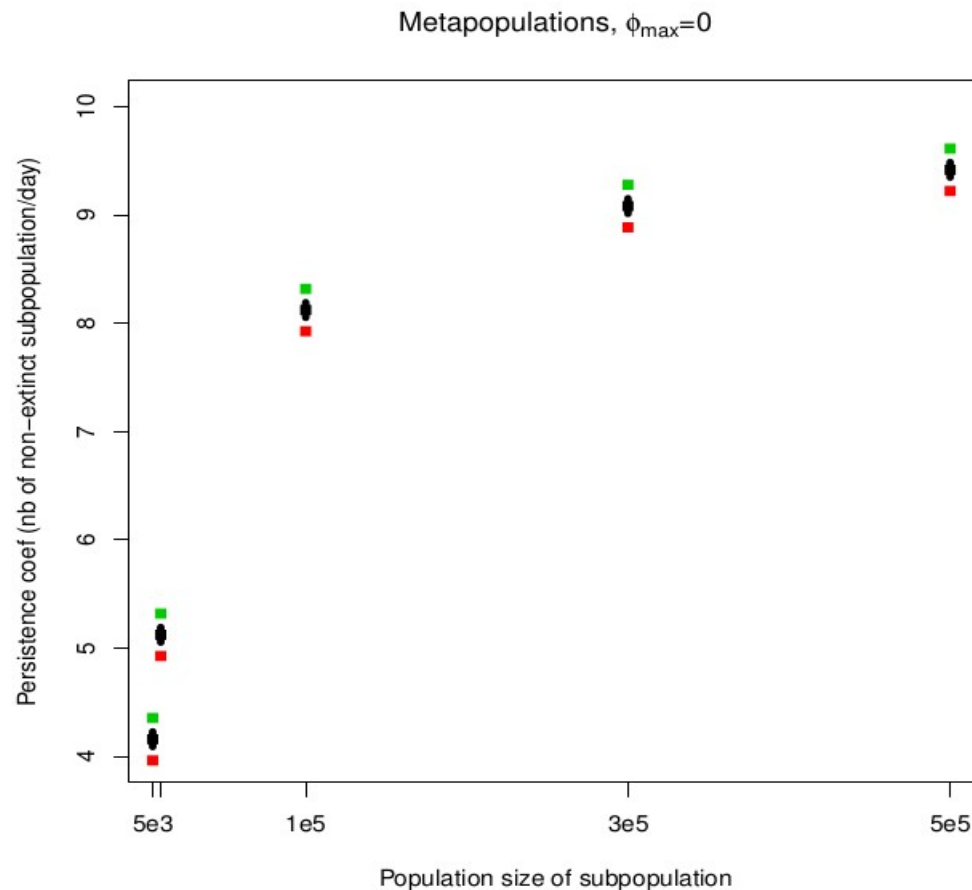
ESTIMATING the global persistence of an infectious disease and φ_{Max}



Estimated rate of global disease persistence in the metapopulation of 08 subpopulations₁₄ after 100 different simulations $N=3e5$, coupling rate $\rho=0.1$.

Result 2 : Persistence 2

Influence of the population size on the global persistence of disease

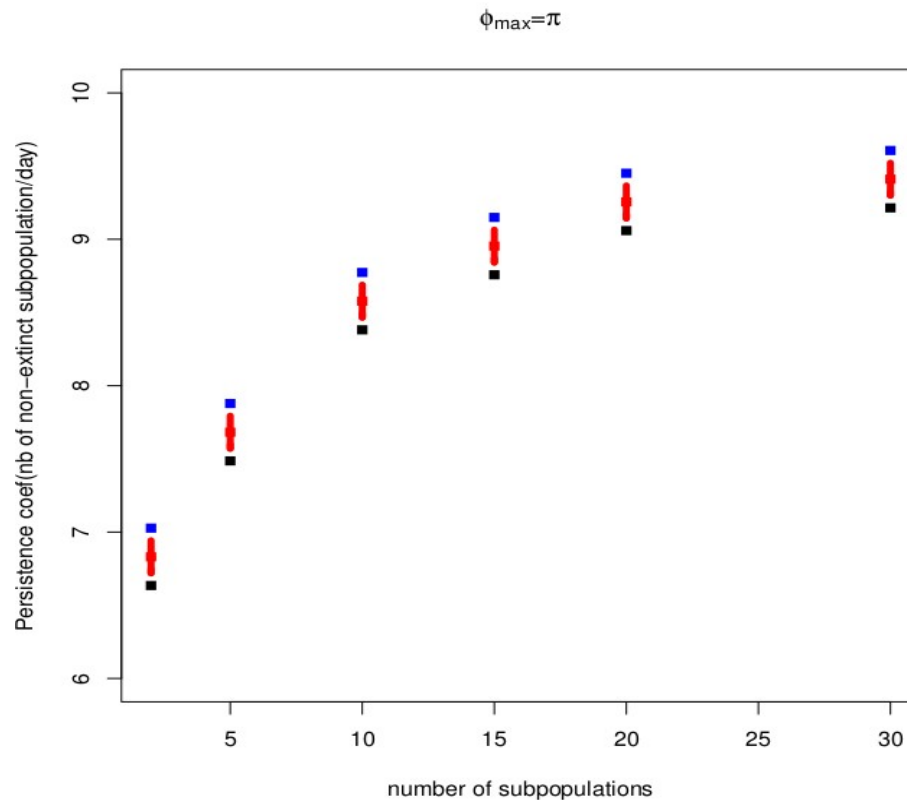


Estimated persistence rate in the metapopulation of 06 subpopulations after 100 different simulations.

The population size of subpopulation is in the set $\{5000, 10000, 1e5, 3e5, 5e5\}$

Result 2 : Persistence 3

**Influence of the number of subpopulation in one metapopulation
On the global persistence of disease.**

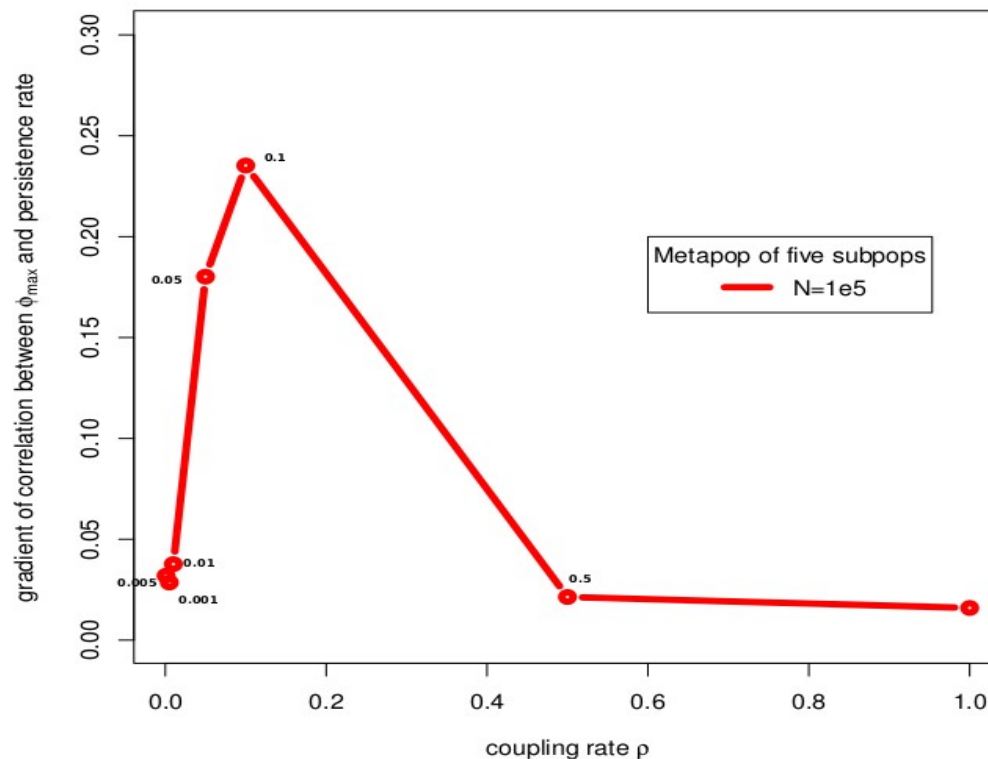


Estimated persistence rate in the metapopulation of multi-subpopulations after 100 different simulations.

The number of subpopulations alters in the set $\{2, 5, 10, 15, 20, 25, 30\}$

Result 2 : Persistence 4

Influence of the coupling rate among subpopulations in a metapopulation on the slope of the coef. of global persistence to φ_{Max}



Coupling rate $\rho = \{0.001, 0.005, 0.01, 0.05, 0.1, 0.5, 1\}$,
 $\varphi_{\text{MAX}} = \{0, \pi/2, \pi\}$ and the population size $N=1e5$.
 $\text{NbVilles} = 05$

Conclusion



- In summary, the degree of asynchrony increases the global persistence time of an infectious disease.
- NOW :
 - GIVING an efficient **algorithm** for optimizing vaccination policies evaluated by **spacial and stochastic simulation**.
 - **Evaluating this algorithm.**

Manuscript in preparation:

T.C.G. Tran, J.D. Zucker, M.Choisy,
Quantifying the effect of synchrony on the
persistence of infectious diseases in a
metapopulation.

Reference

REFERENCES

- 1- Earn, D. J.; Rohani, P. & Grenfell, B. T. Persistence, chaos and synchrony in ecology and epidemiology. *Proceedings of the Royal Society of London B*, **1998**, 265, 7-10
- 2- Grenfell, B. T.; Bjørnstad, O. N. & Kappey, J. Travelling waves and spatial hierarchies in measles epidemics. *Nature*, **2001**, 414, 716-723
- 3- Nokes, D. J. & Swinton, J. Vaccination in pulses: a strategy for global eradication of measles and polio?
S. Altizer, A. Dobson, P. Hosseini, P. Hudson, M. Pascual, and P. Rohani. Seasonality and the dynamics of infectious diseases. *Ecol Lett*, 9(4):467484, Apr 2006.
- 4- R. M. Anderson and R. M. May. *Infectious Diseases of Humans: Dynamics and Control*. Oxford University Press, 1992.
- 5- B. Bolker and B. Grenfell. Space, persistence and dynamics of measles epidemics. *The Royal Society*, 348:309320, 1995.
- 6- D. T. Gillespie. Exact stochastic simulation of coupled chemical reactions. *The journal of physical chemistry*, 81(25):23402361, 1977.
- 7- B.T. Grenfell, B. M. Bolker, and A. Klegzkowski. Seasonality and extinction in chaotic metapopulation. *The royal society*, 259:97103, 1995.
- 8- M. J. Keeling and B. T. Grenfell. Understanding the persistence of measles: reconciling theory, simulation and observation. *Proc Biol Sci*, 269(1489):335343, Feb 2002.
- 10- M. J. Keeling and P. Rohani. *Modeling Infectious Diseases in humans and animals*. Princeton University Press, 2008.
- 11- A. L. Lloyd. Realistic distributions of infectious periods in epidemic models: changing patterns of persistence and dynamics. *Theor Popul Biol*, 60(1):5971, Aug 2001.
- 12- E. Renshaw. *Modelling biological populations in space and time*, volume 11. Cambridge University Press, 1993.
- 13- T. M. Therneau. *A Package for Survival Analysis in S*, 2014. R package version 2.37-7.
- 14- WHO. Reported measles cases with onset date from oct 2013 to mar 2014, 2014.
- 15- <http://microbiology.mtsinai.on.ca/faq/transmission.shtml>
- 16- http://en.wikipedia.org/wiki/Epidemic_model
- 17- Nokes, D. J. & Swinton, J. Vaccination in pulses: a strategy for global eradication of measles and polio? *Trends Microbiol*, 1997, 5, 14-19

.....