

### QUESTIONS POSÉES :

Effet du nombre de villes  $k$  à population globale constante sur le taux d'extinction ? A phase constante 0,  $\pi/4$ ,  $\pi/2$ ,  $3\pi/4$  et  $\pi$

- a. tau décroît-il avec la synchronie (à  $N$  et  $k$  constant) ? Comment en fonction de  $N$  et  $k$  ?
- b. tau croît-il avec  $k$  ( $N$  constant) ? Comment en fonction de la synchronie ?
- c. tau décroît-il avec  $N$  ( $k$  constant) ? Comment en fonction de  $\Phi$  ? CCS Critical Community Size.
- d. Influence du taux de contact.
- e. Influence du couplage.
- f. Comment augmenter le taux d'extinction (i.e augmente la synchronie) par une vaccination optimale ?

### DISCUSSION :

- Discussion sur Code EpiDynamics.
  - Giang a utilisé le package ode dans le cas déterministe.
  - Sur les aspects stochastiques ; Pb de la comparaison des résultats.
  - On peut utiliser deux méthodes suivantes pour comparer les résultats : **Kullback-Leibler Divergence**  
**Kolmogorov-Smirnov test**
- Analyse des résultats Garder  $N$  constants et  $k$  sous-populations de  $N/k$ , ajouter l'intervalle de confiance.

### A faire :

- Connaitre date de fin de troisième année : Partager le plan de thèse
- Donner le temps nécessaire pour répondre à chaque question.
- Enregistrer le nombre des extinctions locales et le nombre de recolonisation locale.
- ECRIRE : un rapport en latex/knitrR qui contient au moins les 3 sections :

## REMETTRE LES RESULTATS

Here, we use the formula given by YANN. The fore of infection is proposed for city  $i$  :

$$(0.1) \quad \lambda_i = \sum_j \rho_{ij} \kappa_j \log \left[ 1 - \sum_{k=1}^M \left( \frac{|I_{k,t}|}{N_k} \times c_{ik} \times \xi_{jk} \right) \right]$$

where  $c_{i,k}$  ( $0 \leq c_{ij} \leq 1$ ) is the probability that a susceptible individual native from  $i$  being in contact with another infected individual native from  $k$  gets infected.  $\xi_{jk}$  ( $0 \leq \xi_{ij} \leq 1$ ) refers to the probability that an individual  $y$  meeting  $x$  in  $C_j$  comes from  $C_k$ .  $\kappa_j$  is the average number of contacts per unit of time a susceptible will have when visiting city  $j$ .  $\rho_{i,j}$  ( $0 \leq \rho_{ij} \leq 1$ ) is denoted as the probability that an individual from subpopulation  $i$  visits subpopulation  $j$ , of course,  $\sum_{j=1}^M \rho_{ij} = 1$ . We can verify that in the limit case on one single subpopulation in the metapopulation ( $i = j$  and  $n = 1$ ) we have

$$(0.2) \quad \lambda_i = -\kappa_i \log(1 - \frac{I_i}{N_i} \times c_{ii})$$

Consider that the average number of contacts per unit of time  $\kappa_i$  is seasonally forced and seasonality is an annually periodic function of time. As a result, for the subpopulation  $i$  :

$$(0.3) \quad \kappa_i(t) = \kappa_{i0} \left[ 1 + \kappa_{i1} \cos \left( \frac{2\pi t}{T} + \varphi_i \right) \right]$$

In order to run simulations, we use the same values of all parameters for all subpopulations. We have a table of the convenient values for parameters of measles as follows :

TABLE 1. Some Disease Parameter Values for Measles from the Literature

parameter	description	value	unit
$\mu$	birth and death rate per day	$1/(70 * 365)$	1/(people*day)
$\kappa_0$	mean value of the number of contacts $\kappa$ per unit of time	$\{30, 50, 80, 100, 150\}$	people/day
$\kappa_1$	amplitude of the number of contacts $\kappa$ per unit of time	$\{0.01, 0.1\}$	
$\gamma$	recovery rate per day	$1/8$	1/(people*day)
$\sigma$	average exposed duration per day	$1/5$	1/day
$\rho$	coupling rate	$\{0, 0.001, \dots, 0.5, 0.8, 1\}$	
$\varphi_{max}$	synchrony parameter in radian	$\{0, \pi/4, \pi/2, 3 * \pi/4, \pi\}$	radian
$N$	population size of subpopulation	$\{5e5, 7e5, 1e6, 2e6, 5e6\}$	people
$n$	number of subpopulation	$\{2, 3, \dots, 10, 15, 20, 30\}$	subpopulation
$t_{max}$	simulation time	100	day

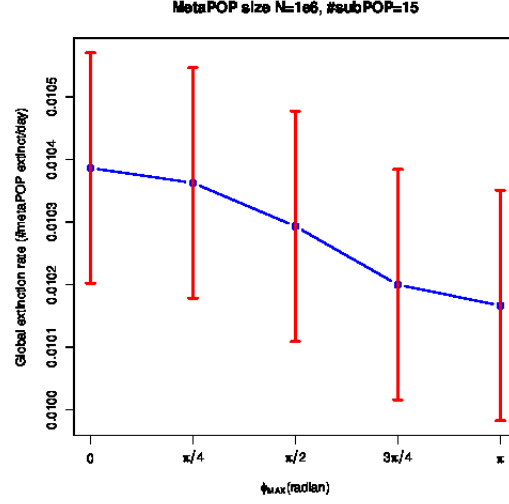


FIGURE 0.1. Estimated global etinction rates in the metapopulation of fifteen subpopulations after 100 different simulations with the metapopulation size  $N = 10^6$ , coupling rate  $\rho = 0.1$ . Here, with 95% confidence interval, the red lines and the blue points are respectively the confidence intervals and the estimated rates for the global extinction rate of each value of  $\varphi_{max}$ .

- Running time : 4.188hours
- Analysis : The figure 0.1 shows to us that the amplitude of the confidence intervals for each value of  $\varphi_{max}$  are quite far to each other. Furthermore, it goes down robustly when  $\varphi_{max}$  runs from 0 to  $\pi$ . The phase difference strongly influences the global disease extinction rate. The figure 0.1 indicates the trend of the extinction rate with decreasing the level of asynchrony. The asynchrony between subpopulations is the main reason why the infectious disease goes extinct in the slow way.

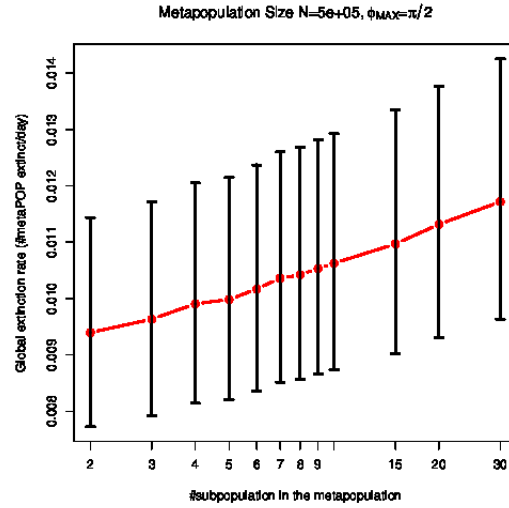


FIGURE 0.2. Estimated global etinction rates in different metapopulations after 100 different simulations with the metapopulation size fixed  $N = 5 \times 10^5$ , coupling rate  $\rho = 0.1$  and  $\varphi_{max} = \pi/2$ . Here, with 95% confidence interval, the black lines and the red points are respectively the confidence intervals and the estimated rates for the global extinction rate of each metapopulaion.

- Running time : 8.589hours
- Analyse : The result (figure0.2) exhibits to us that the number of subpopulations strongly has an influence for the disease persistence time. The global extinction rate of an infectious disease in a metapopulation increases when the number of subpopulations in this metapopulation increases. With the metapopulation size is fixed, when the number of cities in the metapopulation goes up, it means that the population size of each city is declined. In particular, the population size of each city is very small when the number of cities reaches to 30. The dynamic in a small population goes fastly extinct. Although, the model used is the coupling metapopulations, there are interactions among subpopulations and recolonisations of disease. But because the population size is small, the number of visiteurs going to other city is very little. The time of disease persistence in a population having the small size is short. We fastly find the mass extinction in the metapopulation. In addition to the resultat above, we have the relation between the local extinction number of the metapopulation and its number of cities as follows (figure0.3)

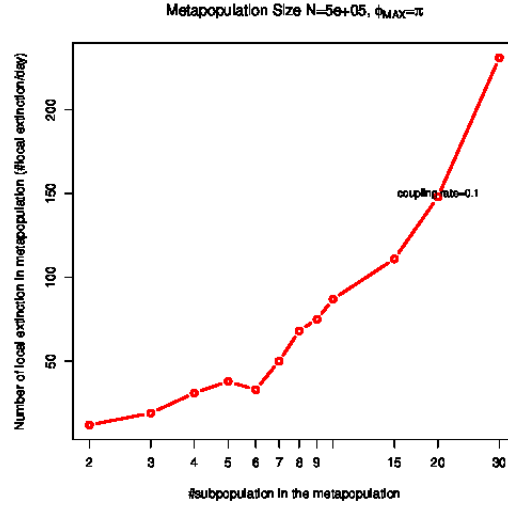


FIGURE 0.3. Number of local extinction in the metapopulation with the size  $N=5e+05$ ,  $\phi_{max} = \pi/2$

As showed in the figure 0.3, the number of the local extinction in the metapopulation has an increase when the number of subpopulation in the metapopulation rises from 2 to 30. This is obvious that in the coupling metapopulation, there are the interactions between cities. One city gets the local extinction but it is fastly reinfected because of the migration of infected individuals of the other cities.

# SECTION{ANALYSIS OF THE VARIATION OF TAU IN FUNCTION OF N}

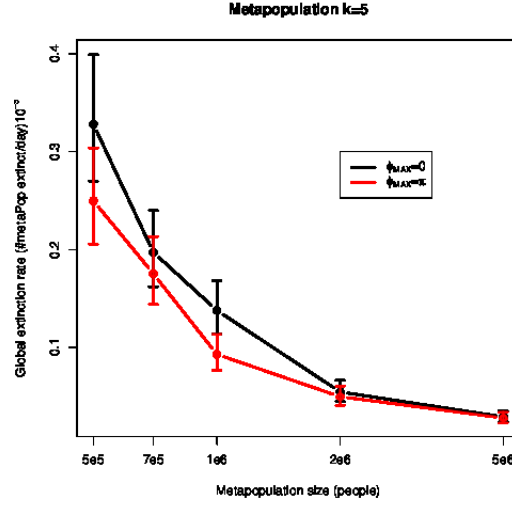


FIGURE 0.4. The relation between the metapopulation size and the global extinction rate for the metapopulation of five cities.

- Running time : 3 hours (3.231257hours)
- Analysis : From the figure 0.4, we find that the mass extinction rate goes down when the metapopulation size augments, at the same time, these rates decreases when the asynchrony  $\phi_{max}$  goes up. It is obvious that the metapopulation size is big, then the time of disease persistence augments, then the mass extinction rates is declined.

# SECTION{INFLUENCE DU TAUX DE CONTACT}

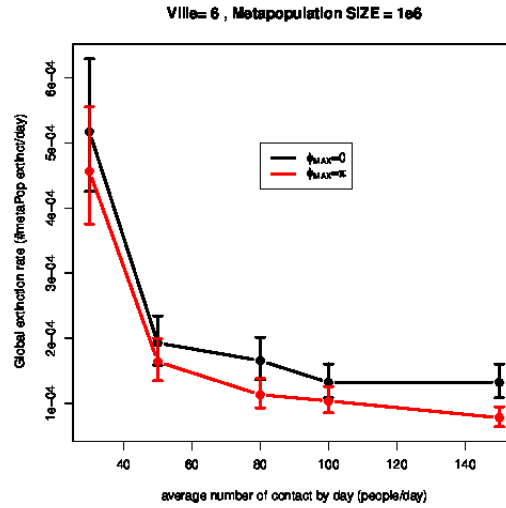


FIGURE 0.5. Influence of the average number of contact per day

- Running time : 3.369hours
- Analyse : Here we find that the average number of contact per day of a susceptible influences also the mass extinction rates. When we change the average number of a contact person per day. We have (1) The global extinction rate also is declined when the asynchrony parameter  $\phi_{max}$  increases, and (2) the mass extinction rate decreases when the average number of contacts per day increases. It is found that the curves highly

goes down when the average number of contact increases from 30 to 80 per day. However, they are in the form of a gentle slope when the number of contacts is bigger from 100 to 150. It means that there is a threshold of the number of contact here, if the number of contacts is greater than 150, I think that the global extinction rates are smaller than the rates of nbCONTACT = 150 but not too small. Thus, the probability of infection of a person has a limit. A susceptible will be contaminated when he meets a threshold of the number of personnes daily.

\SECTION{INFLUENCE DU COUPLAGE}

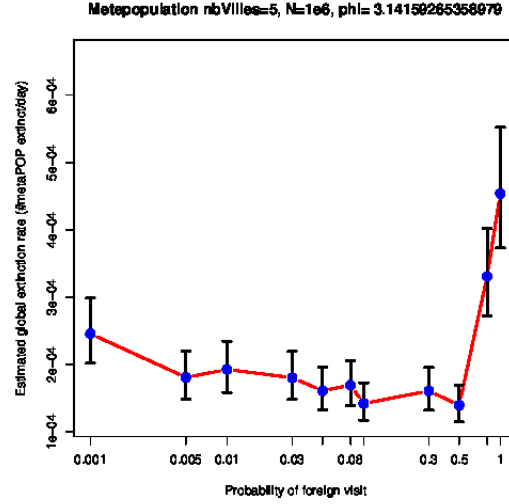


FIGURE 0.6. Correlation between the coupling rate and the mass extinction rate in the metapopulation of five subpopulations. Here, the coupling rate  $\rho$  runs from 0 to 1. The level of asynchrony  $\varphi_{max}$  is  $\pi$  and the metapopulation size  $N=1e6$ .

- Running time : 8.884 hours
- Analyse : One more factor that was pointed is coupling strength between subpopulations. Here, the coupling rate or the dispersal rate  $\rho$  can be considered as migration strength. The disease transmission speed grows fast when coupling rate goes up in metapopulations, but the global extinction rate is inverse. In this part, we permit coupling rate change from weak to strong in a metapopulation of five subpopulations with the metapopulation size  $N = 10^6$ . The dispersal rate  $\rho$  is divided into three intervals. These are low, intermediate and high coupling rate intervals. In each interval, we chose some coupling rates that highlight the coupling strength among subpopulations in a metapopulation. When the coupling rate is small from 0.0 to 0.005, the mass extinction rate decreases very slowly. Because, in this case, the subpopulations seem to be independent. They fluctuate independently. They are easy to go extinct. We are also easy to find the mass extinction in the metapopulation. However, this extinction rate is declined in a sudden way when the coupling rate changes from 0.01 to 0.3. Lastly, the extinction rate increases when the coupling rate is so robust from 0.5 to 1.0. Based on this figure, the mass extinction rate in a metapopulation is one inverse bell for the coupling rate. The medium coupling rate (from 0.01 to 0.1) minimizes the mass extinction rate in metapopulation. As in the case of the small and average coupling rates, the coupling rate and the speed of migration among subpopulations are directly proportional. The dispersal speed increases, thereby the local recolonization speed rises, the duration of persistence grows. However, this trend of global extinction rate with decreasing coupling rate, is not right any more when the dispersal rate is strong. The duration of persistence falls, because the metapopulation has tendency to become one big population. In this case, the phase difference or the recolonization among subpopulations are no longer significant.

\SECTION{EXTINCTION/ #SOUSPOP EN FONCTION DE #SOUSPOP SELON-VARIATION DE PHI (ASYNCHRONIE)}

- Running time : 2.5 hours
- Analyse : As the result shown in the figure , the rate of asynchrony  $\phi_{MAX}$  robustly affects the relation between the average local extinction number and the number of subpopulation in a metapopulation. We

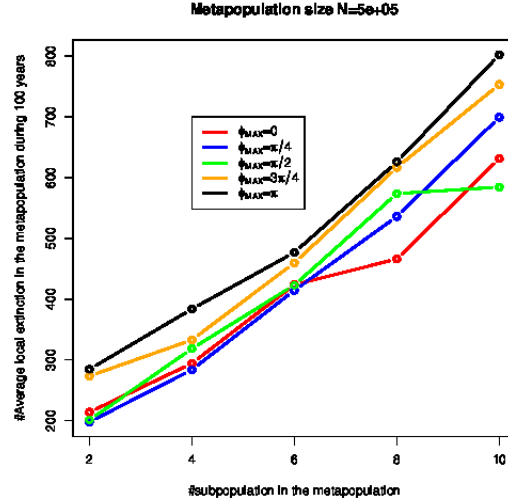


FIGURE 0.7. Influence of the variation of asynchrony  $\phi_{MAX}$  on the relation between the average local extinction number and the number of subpopulation in a metapopulation.

can find two main results here. First, the average local extinction number in any metapopulation has an clear increase when the rate of asynchrony  $\phi_{MAX}$  augments. At the rate  $\phi_{MAX} = 0.0$ , it means to set the entire metapopulation in the synchrony state, the dynamics of all subpopulations are synchronous and the local extinction positions of the subpopulation may be also synchronous. Therefore, this average number in the metapopulation is minimum. Inversely, when the rate of asynchrony  $\phi_{MAX}$  starts tending to increase, the fluctuations are also changed and fallen into the difference phase. It is the reason why when a subpopulation goes locally extinct and after it is dominated back by disease due to the recolonisation among subpopulations. At the rate  $\phi_{MAX} = \pi$ , the difference phase is maximum. The average number of local extinction in a metapopulation is maximum. Second, in a metapopulation, if the subpopulation number increases, then the local extinction number augments also. Because when the subpopulation number is directly scaled with the metapopulation size and the time of disease persistence. In addition, the interaction among subpopulation increases with the subpopulation number. One subpopulation is easy to be dominated by the other subpopulations due to the recolonisation.

\SECTION{EXTINCTION/#SOUSPOP EN FONCTION DE #SOUSPOP SELON - VARIANT DE N (POP GLOBALE)}

- Running time : 35,5 hours
- Analyse : The figure 0.8 shows the relation between the average local extinction number and the number of subpopulation in a metapopulation. We find that the local extinction number is minimum when the metapopulation size is maximum. Because with a big metapopulation, the size of a subpopulation is great. It is the reason why this subpopulation is very difficile to find the local extinction. Inversely, when the metapopulation size is small, then the persistence time is short. Thus, this metapopulation goes to the global extinction in the easy way. On the other hand, we can find that the metapopulation size in the interval from  $5e+05$  to  $1e+06$ , the local extinction number is high. It means that the size of a subpopulation is approximately from  $1e+05$  to  $5e+05$ . This is the interval that permit a disease to spread and permit the time of disease persistence to be enough long to study. Finally, we get also the same result, the local extinction number are in increase with the number of subpopulation in a metapopulation.

\SECTION{EXTINCTION/#SOUSPOP EN FONCTION DE #SOUSPOP SELON -VARIATION DU COUPLAGE}

- Running time: 4 hours
- Analyse : The results are found in the figure , the local extinction number is minimum when the coupling rate is equal 0.0. It is obvious that in a metapopulation where the subpopulations are isolated, there is no recolonisation among subpopulation. After the local extinction number strongly increases when the coupling rate augments. However, this number is biggest when the coupling rate  $\rho = 0.01$ . Because at this rate where the subpopulations are in the mediate interaction. Moreover the coupling rate and the speed of migration among subpopulations are directly proportional. The dispersal speed increases, thereby the local

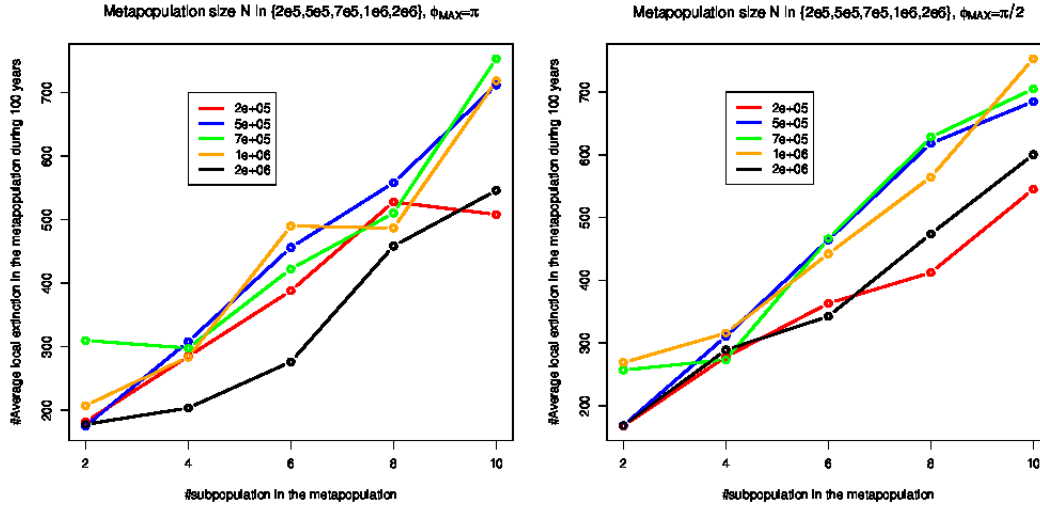


FIGURE 0.8. Influence of the variation of metapopulation size  $N$  on the relation between the average local extinction number and the number of subpopulation in a metapopulation.

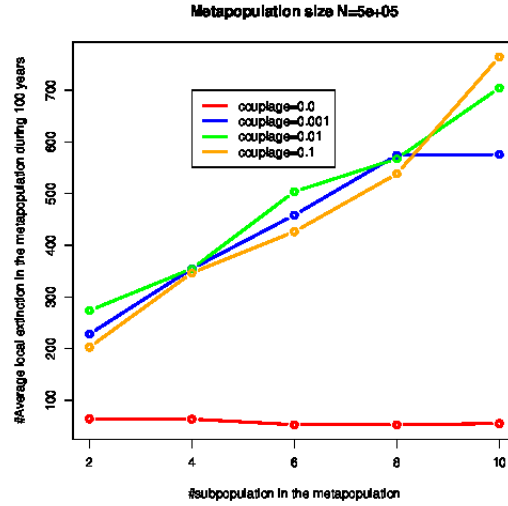


FIGURE 0.9. Influence of the variation of coupling rate on the relation between the average local extinction number and the number of subpopulation in a metapopulation.

recolonization speed rises, the duration of persistence grows. However, when the dispersal rate is more big, this trend of local extinction number decreases. Because the metapopulation has tendency to become one big population, so the phase difference or the recolonization among subpopulations are no longer significant. The following figure is an other resultat for the influence of the coupling rate on the local extinction number in the metapopulation.

- Running time: 1 hours



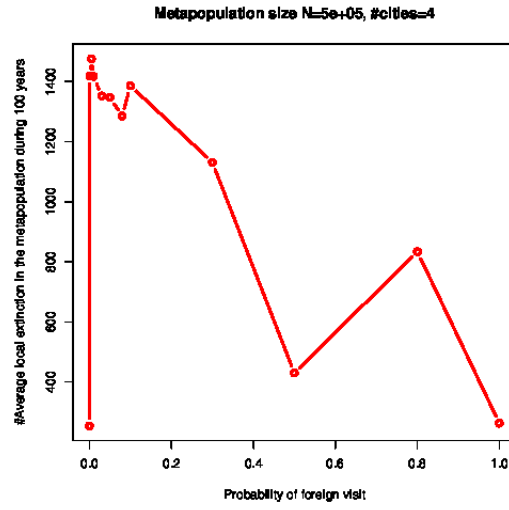


FIGURE 0.10. Relation between the average local extinction number and the coupling rate in the metapopulation of four subpopulations with the metapopulation size  $N=5e5$  and  $\phi_{MAX} = \pi$ .