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, 3pi/4 et pi

a. tau décroit-il avec la synchronie (à N et k constant) ? Comment en fonction de N et k ?

b. tau croit-il avec k (N constant) ? Comment en fonction de la synchronie ?

c. tau décroit-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 le taux d'extinction local.
  - Utiliser la fonction "fitdistr" du package MASS
- Discussion sur le taux de durée de recolonation.
  - Utiliser la fonction "fitdistr" du package MASS ".

A faire :

- Envoyer un email à Christophe Cambier sur quelle language écrite pour le mémoire.
- Essayer de lancer des simulations sur une grille avec le nombre de simulations différentes. (100,500,1000) : Sang, il a fait ça, mais il n'est pas réussit. Maintenant, je continue à utiliser la fonction "mclapply" de R pour lancer des simulations parallèles.
- Calculer le taux d''extinction locale et le taux de durée de recolonisation :
  - Etape 1 :
    - On a : n souspopulations, M simulations différentes. Alors, on a n*M souspopulations simulée.
    - Pour chaque souspopulation simulée : on calcule la table comme suite :

temps	EtatExtLocl	nbExtLoclCul	DurReclT
100	1	1	7
120	1	2	10
125	1	3	3
300	1	4	8
...	1	...	...

  - Etape 2 : On a n*M tables comme ci-dessus.
    - Intégrer les tables en une seule grande table.
    - Arranger la grande table en augmentation selon le temps t.

temps	EtatExtLocl	nbExtLoclCul	DurReclT
100	1	1	7
120	1	2	10
125	1	3	3
300	1	4	8
500	1	5	3
557	1	6	20
600	1	7	36
...	...	....	....
...	....	...	....

  - Etape 3 :
    - Le processus de recolonisation est un processus de Poisson de taux lambda alors les durées d'extinction suivent une distribution exponentielle de taux lambda. Donc, pour estimer ton taux de recolonisation, on peux tout simplement fitter une distribution exponentielle à la distribution de tes durées d'extinction. Tu peux faire ça avec la fonction fitdistr du package MASS.
    - Utiliser la fonction "fitdistr" du package MASS pour trouver le taux lambda et son interval de confience "confint".

1. \section{#localExtinction/#souspop en fonction de #souspop selon-Variation de Phi (asynchronie)}

1.1. Taux d'extinction locale et #souspopulation - Variation de Phi.

- Figure

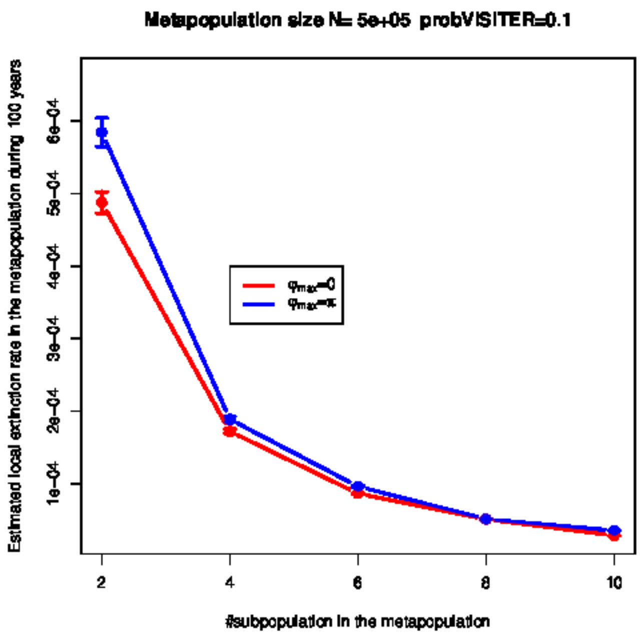

Figure 1.1. Relation between #subpopulation in the metapopulation and the rate of the number of local extinction when φ_{max} is changed

- Running time : 5.3 hours
- Analyse :
  - The rate of the number of local extinction goes down when the number of subpopulation in the metapopulation rises : the rate of local extinction decreases, so the curve of density of the number of local extinctions correspondent to each the number of subpopulation augments. It means that the number of local extinctions scales proportionately that of subpopulations in the metapopulation.
  - The rate of the number of local extinctions goes down when the number of subpopulations is small (2,4 or 6). In this case, the rate of local extinctions with $\varphi_{max} = 0$ is smaller than that with $\varphi_{max} = \pi$. Because there are the phase differences among subpopulations, thus there are recolonisations among them too. We are difficult to find the local extinction in a metapopulation of many subpopulations. And this becomes more difficult than when the number of subpopulation increases.

1.2. Taux de durée de recolonization et #souspopulation - Variation de Phi.

- Figure :

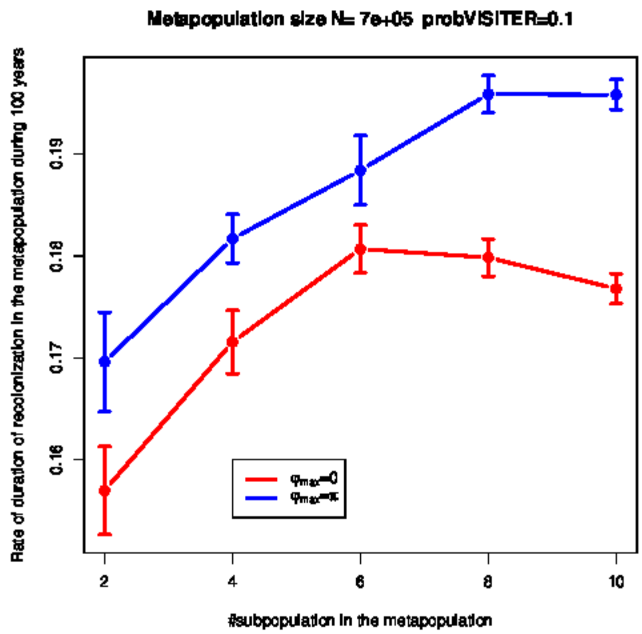

FIGURE 1.2. Relation between #subpopulation in the metapopulation and the rate of the duration of recolonisation among subpopulations when φ_{max} is changed

- Running time : 5.1 hours
- Analyse:
  - The rate of the duration of recolonisation goes up when the number of subpopulation climbes. It means that the duration of recolonisation among subpopulation decreased when the number of subpopulation augments. Because, the number of subpopulation augments, the emigration speed among subpopulation have a significant increase. The recolonisation of disease is very easy in subpopulation where the disease is temporally extint.
  - The rates of the duration of recolonisation with $\varphi_{max} = 0$ are smaller than that with $\varphi_{max} = \pi$. It mean that the duration of recolonisation among subpopulations with $\varphi_{max} = \pi$ is smaller than that with $\varphi_{max} = 0$. It is right, because due to the recolonisation among subpopulations, thus the duration of local extinction of a subpopulation is shorter.

2. \section{#localExtinction/#souspop en fonction de #souspop selon - Variant de N (pop globale)}

2.1. Taux d'extinction locale et #souspopulation - Variation de N (Metapopulation size).

- Figure

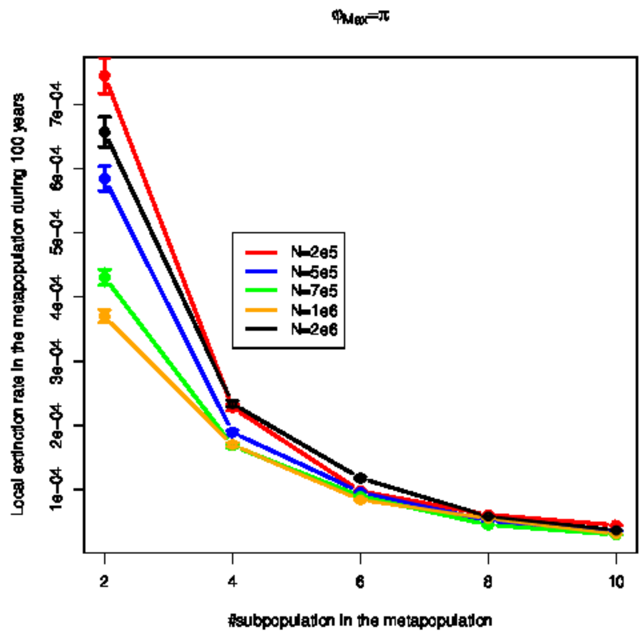

FIGURE 2.1. Relation between #subpopulation in the metapopulation and the rate of the number of local extinction when the metapopulation size N is changed

- Running time:
- Analyse:
  - The rate of the number of local extinction goes down when the number of subpopulation in the metapopulation rises : the rate of local extinction decreases, so the curve of density of the number of local extinctions correspondent to each the number of subpopulation augments. It means that the number of local extinctions scales proportionately that of subpopulations in the metapopulation.
  - The rates of the number of local extinctions are bigger than when the metapopulation size is very big or very small ($N = 2e5$ or $N = 2e6$). In the case N very small, it is easy to find local extinctions in subpopulations, however, the global persistence time of the metapopulation is short. In the case N very big, it is more difficul to find local extinction in subpopulations, however, the global persistence of the metapopulation is very long. Therefore, in both cases, the total of local extinctions in the metapopulation is bigger than when the metapopulation size is medium.

2.2. **Taux de durée de recolonization et #souspopulation - Variation de N (Metapopulation size).**

- Figure

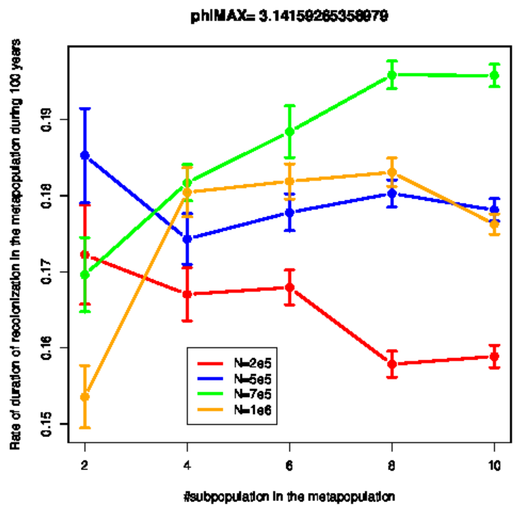

FIGURE 2.2. Relation between #subpopulation in the metapopulation and the rate of the duration of recolonisation among subpopulations when the metapopulation size N is changed

- Running time :3.45 hours
- Analyse :
  - The CCS (Critical community size) is the minimum size of a closed population within which a human-to-human.
  - In the case N small (N=2e5 and N=5e5), the curves have a trend towards going down. We find that, when the bigger the number of subpopulation is, the smaller the subpopulation size is. In this case, the subpopulation size falls below the CCS level. (1) the metapopulation is easy to get global extinct and (2) the number of people emigrating to other subpopulation is very small. The duration of recolonisation is longer when the number of subpopulation is larger.
  - In the case N big (N=7e5 and N=1e6), the curves have a trend towards going up. Because, here the subpopulation size starts being large. It is in the CCS level. The emigration rate is larger and thus the duration of recolonisation is shorter.

3. \section{#localExtinction/#souspop en fonction de #souspop selon -Variation du couplage}

3.1. Taux d'extinction locale et #souspopulation - Variation du taux de couplage.

- Figure

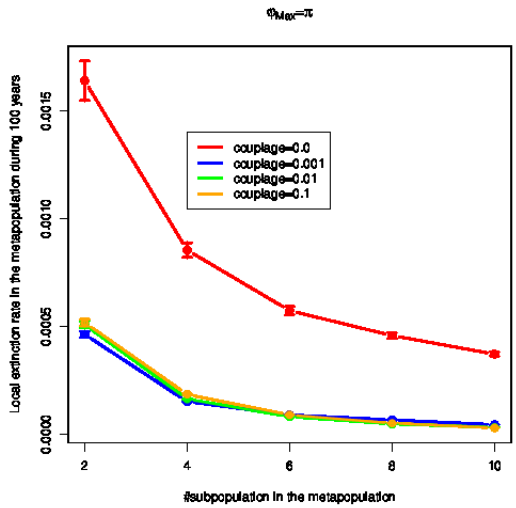

FIGURE 3.1. Relation between #subpopulation in the metapopulation and the rate of the number of local extinction when the coupling rate is changed

- Running time :
- Analyse:
  - In the case $coupling = 0.0$, subpopulations are independent in a metapopulation. The number of local extinctions is the smaller. Hence, the rate of the local extinction in the metapopulation is maximum.
  - In the case $coupling = 0.001/0.01/0.1$, the subpopulation are interactive. The power of interaction between two subpopulation is presented by the coupling rate. The time of disease persistence is longer than in the case $coupling = 0.0$. Thus, the number of local extinction is larger. The rate of local extinction is smaller.

3.2. **Taux de durée de recolonization et #souspopulation - Variation du taux de couplage.**

- Figure

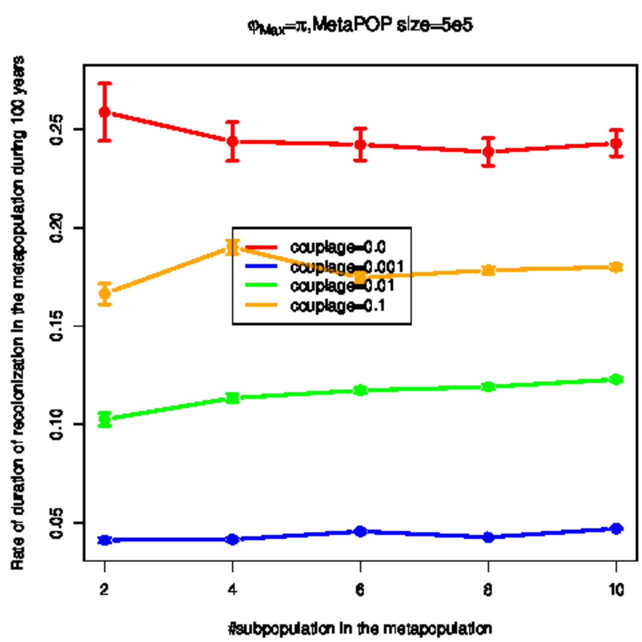

FIGURE 3.2. Relation between #subpopulation in the metapopulation and the rate of the duration of recolonisation among subpopulations when when the coupling rate is changed

- Running time : 4.8 hours
- Analyse:
  - In the case *coupling* = 0.0, the rate of the duration of recolonisation is maximum. It means that the duration of recolonisation at each local extinction moment is minimum. Because here the subpopulation are independent. The time of the infectious disease persistence in a subpopulation only depends on the number of susceptibles and the infection force in this subpopulation. The duration of recolonisation at each local extinction is quickly broken by the represence of the infected persons in the own subpopulation.

3.3. **Taux de durée de recolonization et #souspopulation - Variation du taux de couplage.**

- Figure:

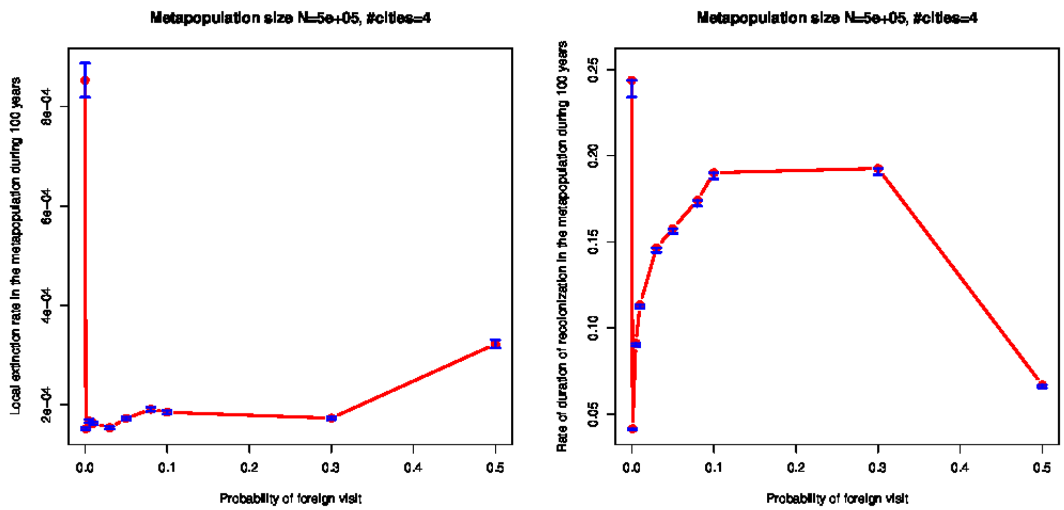

FIGURE 3.3. Relation between the coupling rate in the metapopulation and the rate of the number of local exticntion, and the duration of recolonisation among subpopulations

- Running time: 1.5 hours
- Analyse :
  - When the coupling rate is small, the subpopulations in the metapopulation are independent. The rate of local extinction increases.
  - When the coupling rate is larger, among the subpopulations there are the big interactions, the metapopulation becomes one big population. It is difficul to find local extinction in this population. The rate of local extinction increases.
  - When the coupling rate is medium, the dynamic of the subpopulations depends on the interactions among the subpopulations. In this interval, the rate of local extinction is minimum.