

# Physics of Life Data Epidemiology

*Lect 16: epidemics in space 1*

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# Spatial spread of epidemics

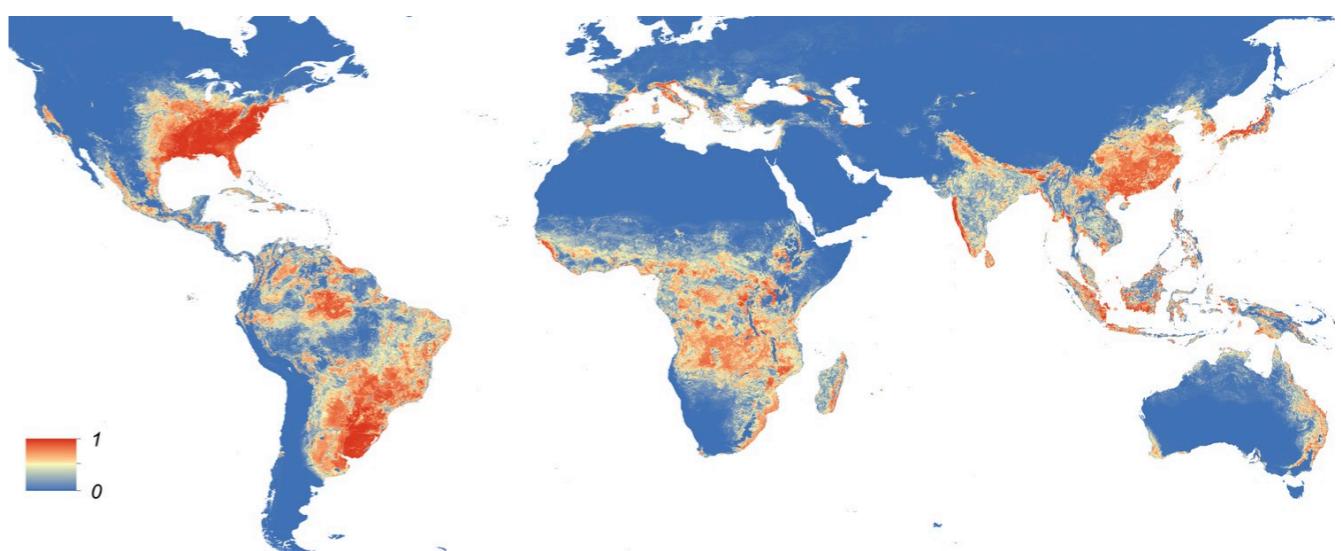
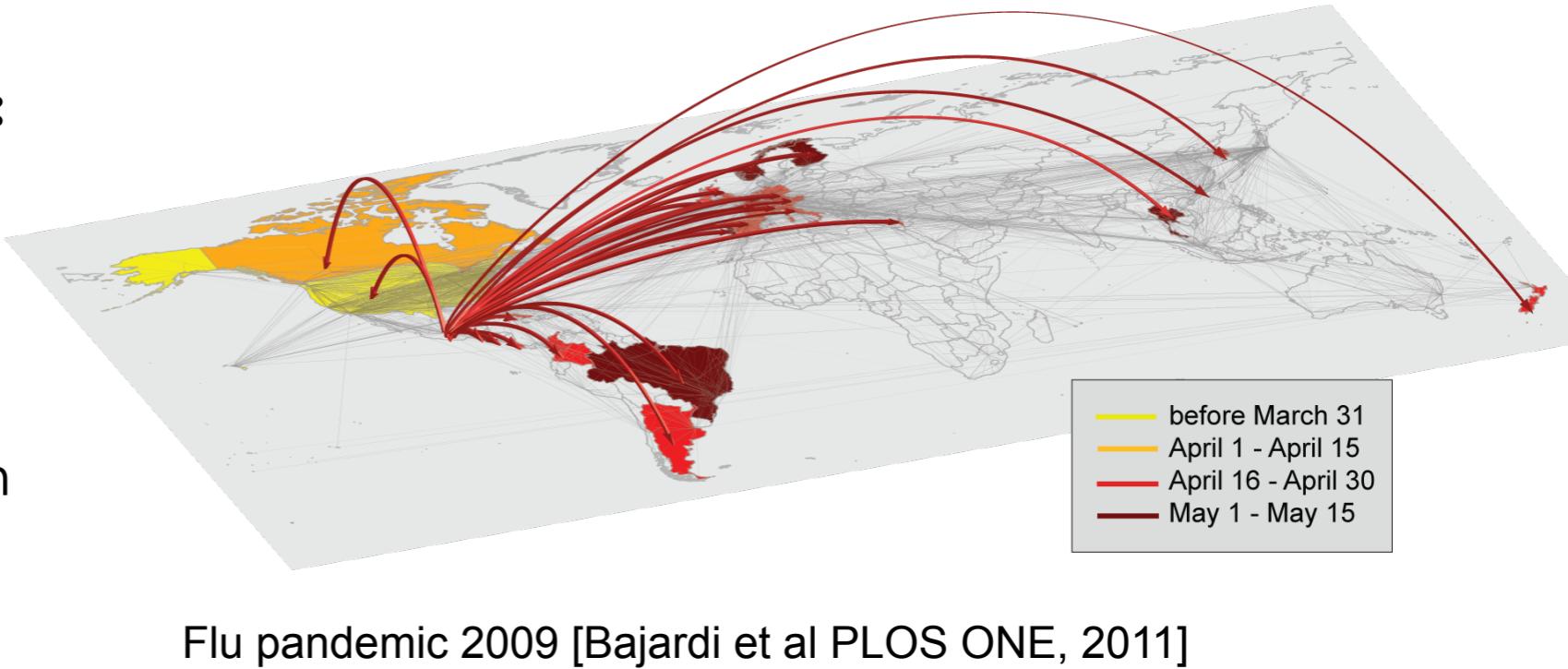
## **understanding the spatial spread of epidemics is important**

- spatial information is an essential ingredient in epidemiology: we need to know where the epidemic is
- estimate the invasion risk for a given territory
- understand the conditions for containment (containing an epidemic spatially helps the epidemic management)
- understand the *spatial coupling*: how the epidemic in a given area influences the epidemic in another

# Spatial spread of epidemics

## Drivers of spatial transmission:

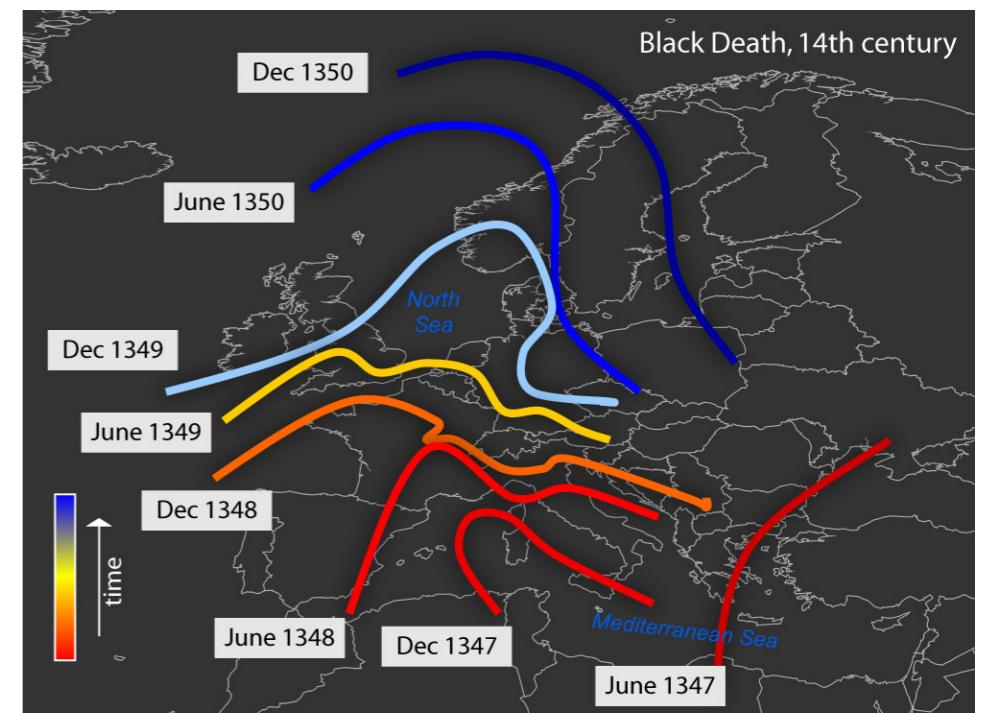
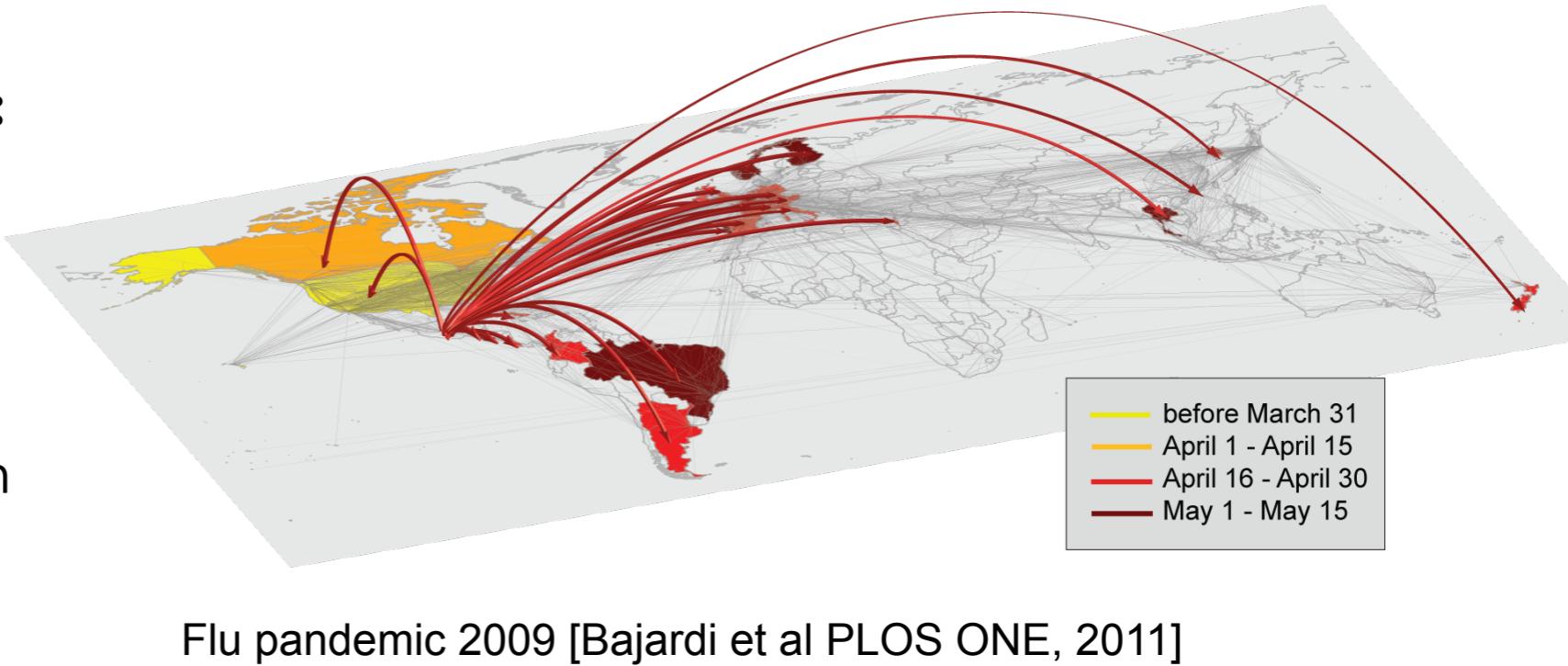
- directly transmitted human diseases: spatial spread of epidemics is determined by human mobility. The pathogen spreads carried by traveling individuals
- vector borne diseases: the spatial propagation requires human mobility but also the local presence of the competent vector. Vector mobility is also possible
- food borne, environmental diseases, zoonotic pathogens, etc.: different drivers



# Spatial spread of epidemics

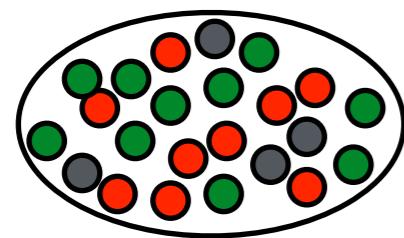
## Drivers of spatial transmission:

- **directly transmitted human diseases:** spatial spread of epidemics is determined by human mobility. The pathogen spreads carried by traveling individuals
- human mobility behaviour determines the spatiotemporal pattern of spread.
- Different kinds of mobility become relevant according to the epidemic of interest and the epidemiological question (spatial scale, time scales, recurrence)

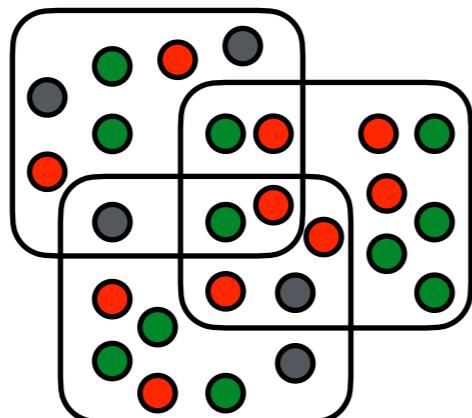


# integrating human mobility in epidemic models

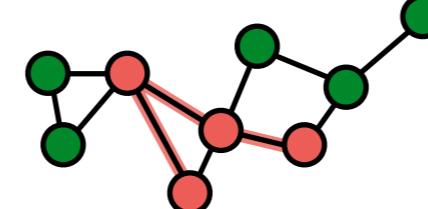
**How to integrate mobility into epidemic modelling?**



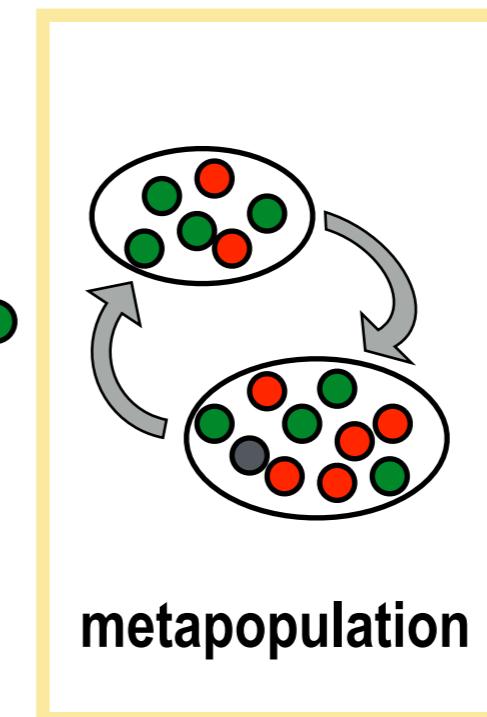
homogeneous  
mixing



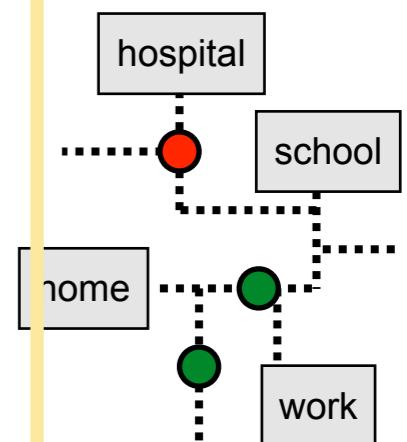
population  
structure



network



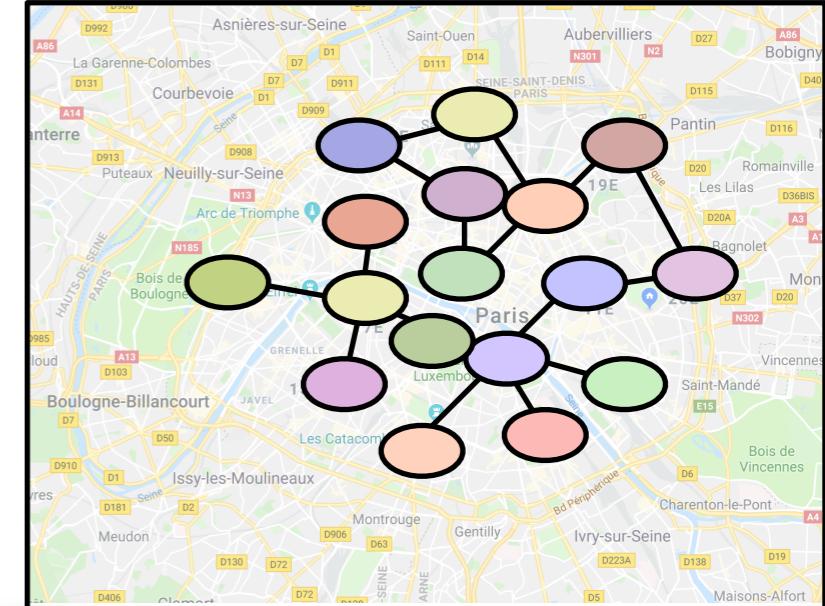
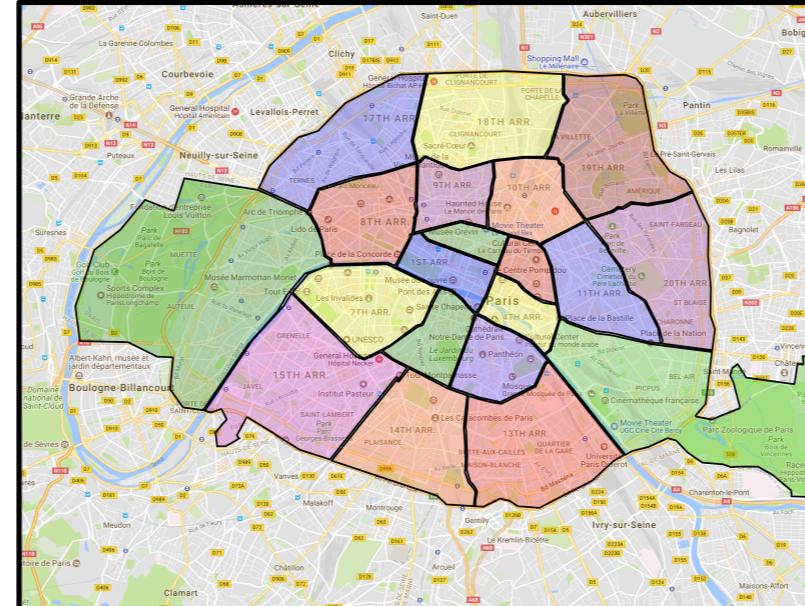
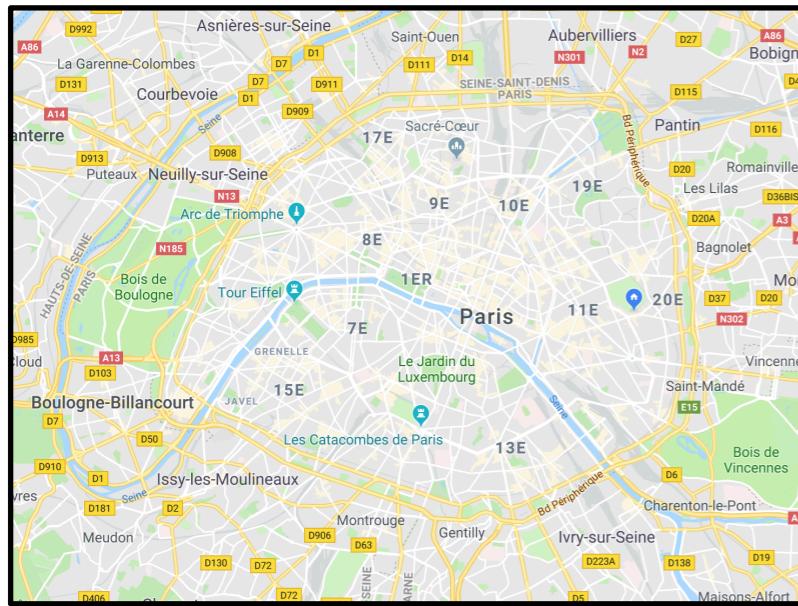
metapopulation



agent based

**COMPLEXITY**

# metapopulation models: a compromise

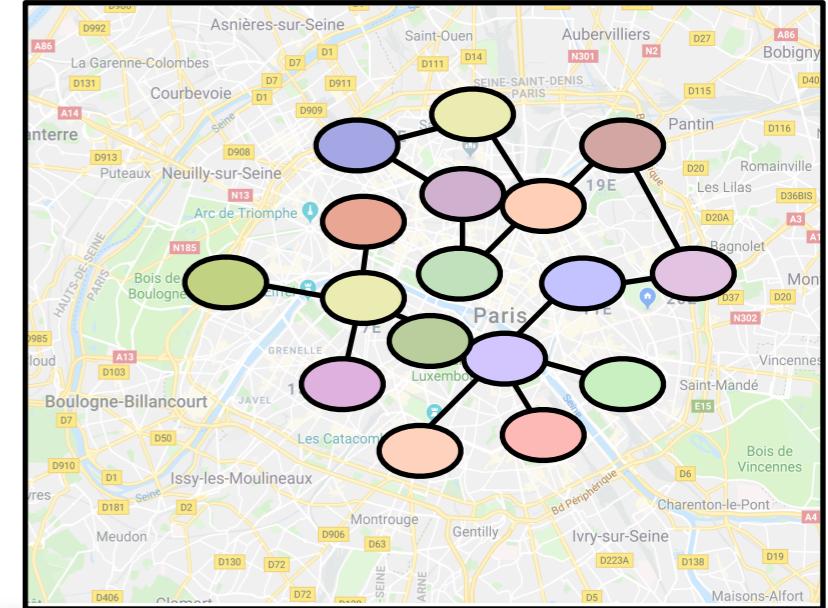
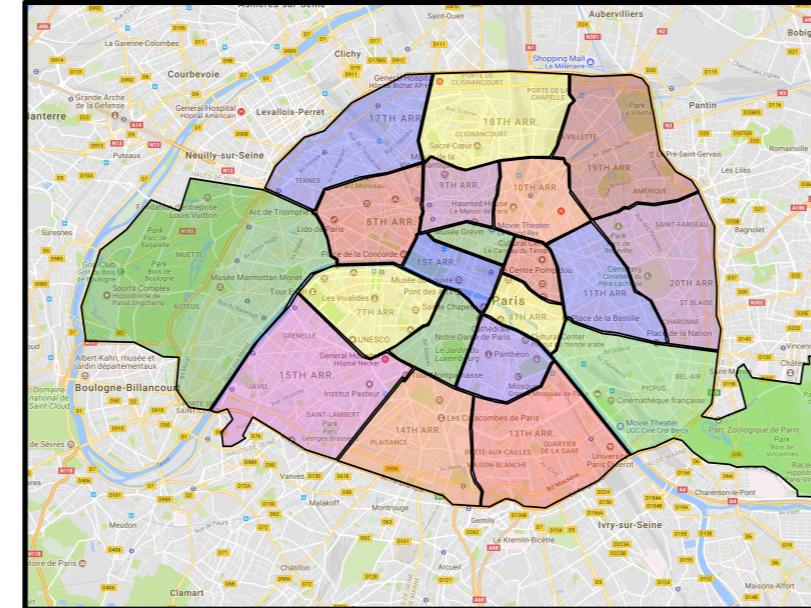
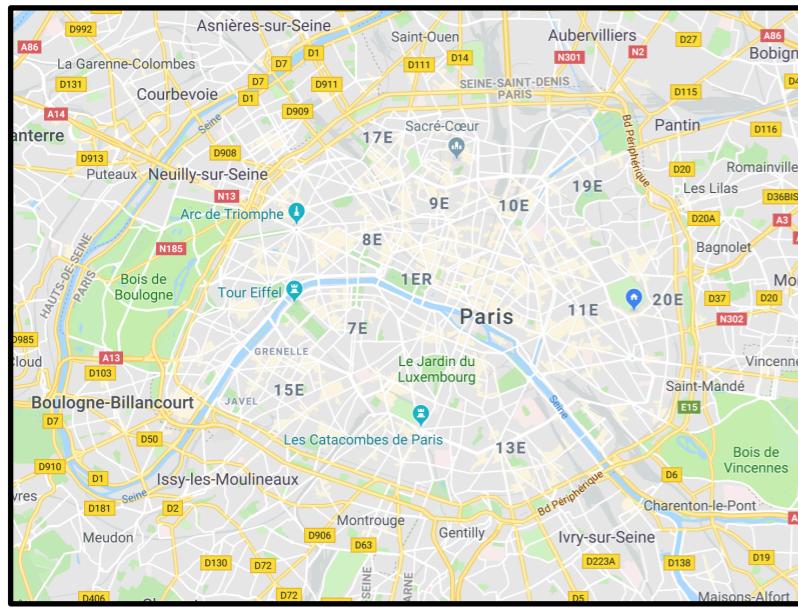


Introduced in ecology to study the interplay between stochasticity and spatial heterogeneities

[Levins Bull. Entomol. Soc. Am., 15 (3) (1969)]

- population divided in discrete entities, *patches or subpopulations*
- two level of mixing: *local* (within a patch), *global* (among patches)
- coarse grained description: patches can be seen as elementary units

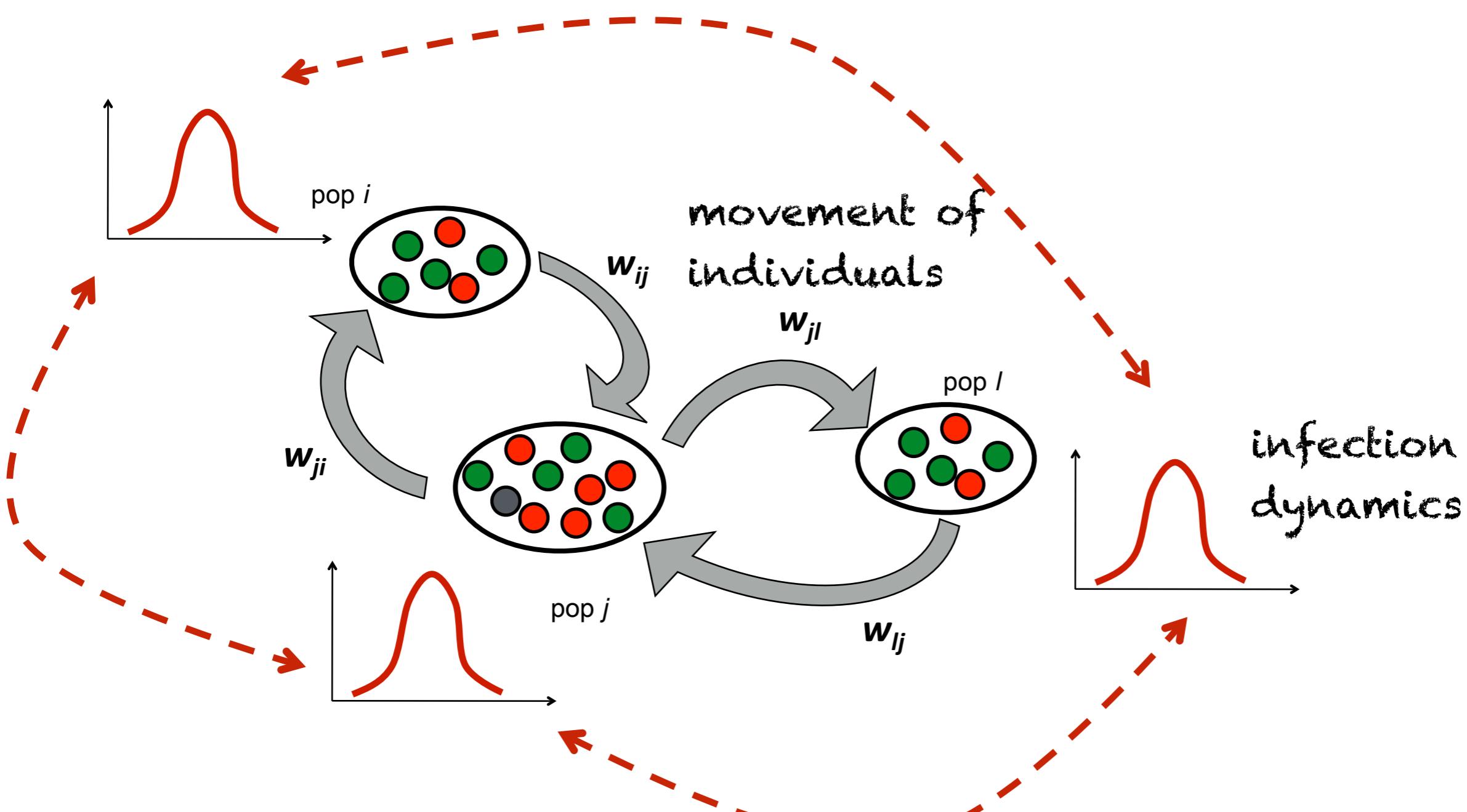
# metapopulation models: a compromise



- dynamics driven by stochastic effects: extinction, recolonisation
- discrete nature of individuals essential ingredients to describe the dynamics - If I let half an individual travel I obtain an unrealistic mixing
- early works: mixing among patches homogeneous
- more recently: mixing among patches mediated by the human mobility network: coupling the metapopulation perspective with network theory

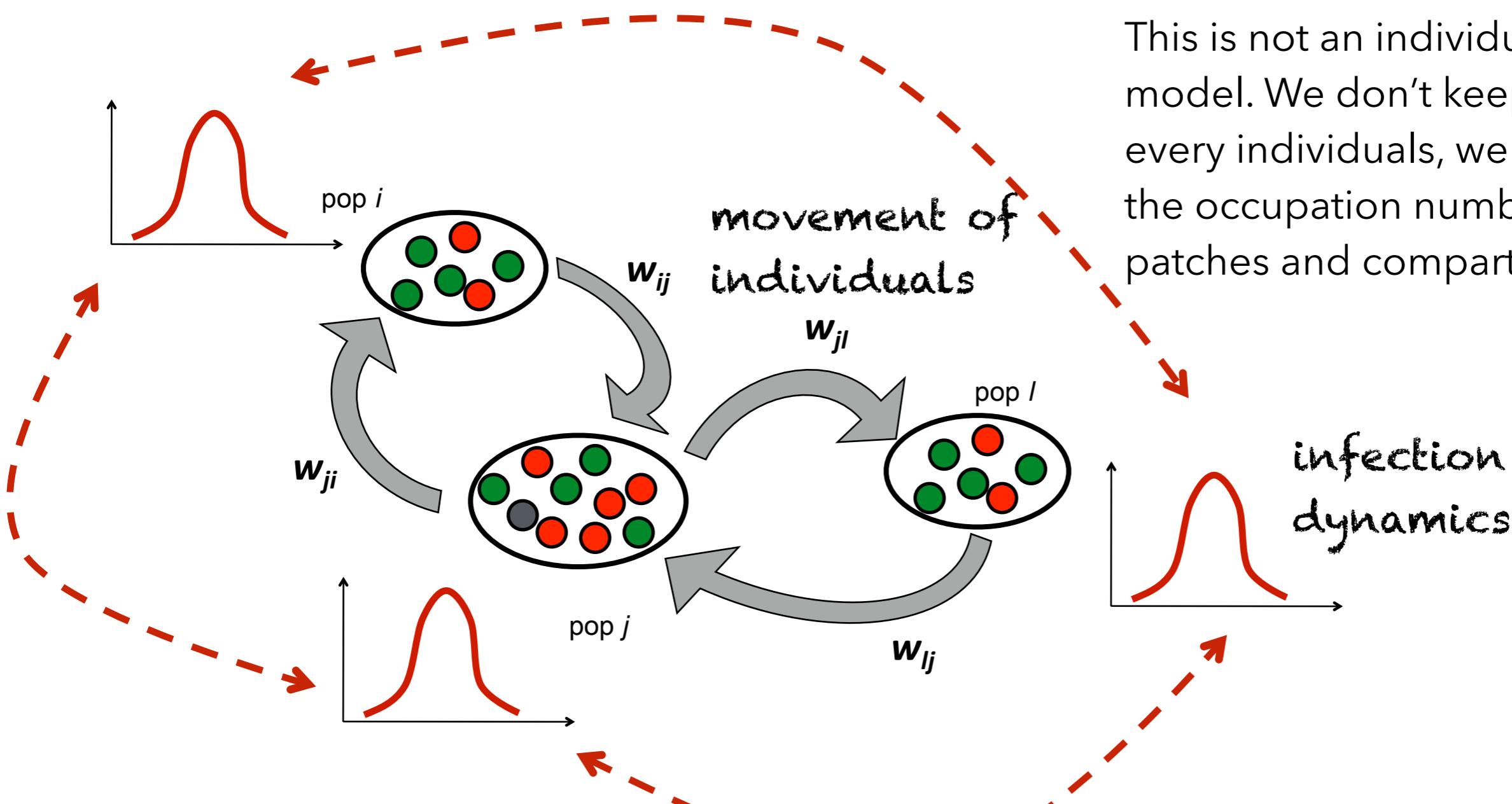
# SIR metapopulation model

modelling of mobility AND transmission dynamics



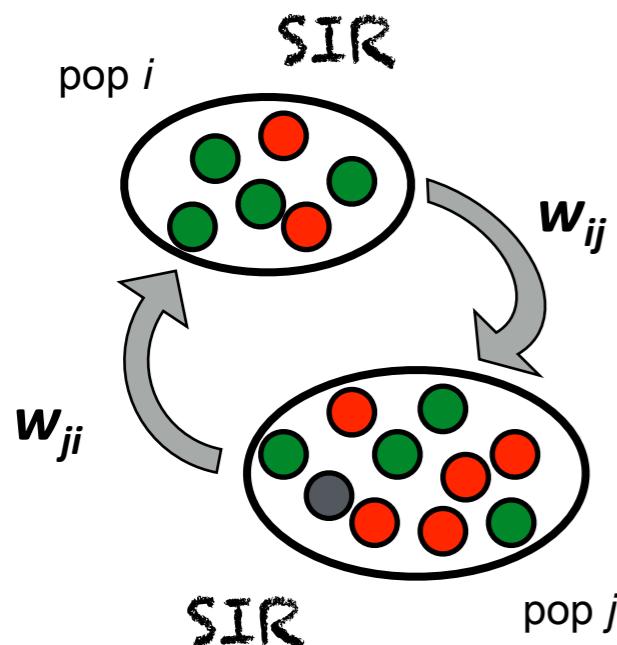
# SIR metapopulation model

modelling of mobility AND transmission dynamics



This is not an individual-based model. We don't keep track of every individuals, we monitor the occupation number of patches and compartments

# SIR metapopulation model



$V$ : # populations

$S(t)$        $S_i(t)$

$I(t)$        $I_i(t)$

$R(t)$        $R_i(t)$

$N(t)$        $N_i(t) = S_i(t) + I_i(t) + R_i(t)$

global variables

$$S(t) = S_1(t) + S_2(t) + S_3(t) + \dots + S_V(t) = \sum_i S_i(t)$$
$$I(t) = I_1(t) + I_2(t) + I_3(t) + \dots + I_V(t) = \sum_i I_i(t)$$
$$R(t) = R_1(t) + R_2(t) + R_3(t) + \dots + R_V(t) = \sum_i R_i(t)$$
$$N(t) = N_1(t) + N_2(t) + N_3(t) + \dots + N_V(t) = \sum_i N_i(t)$$

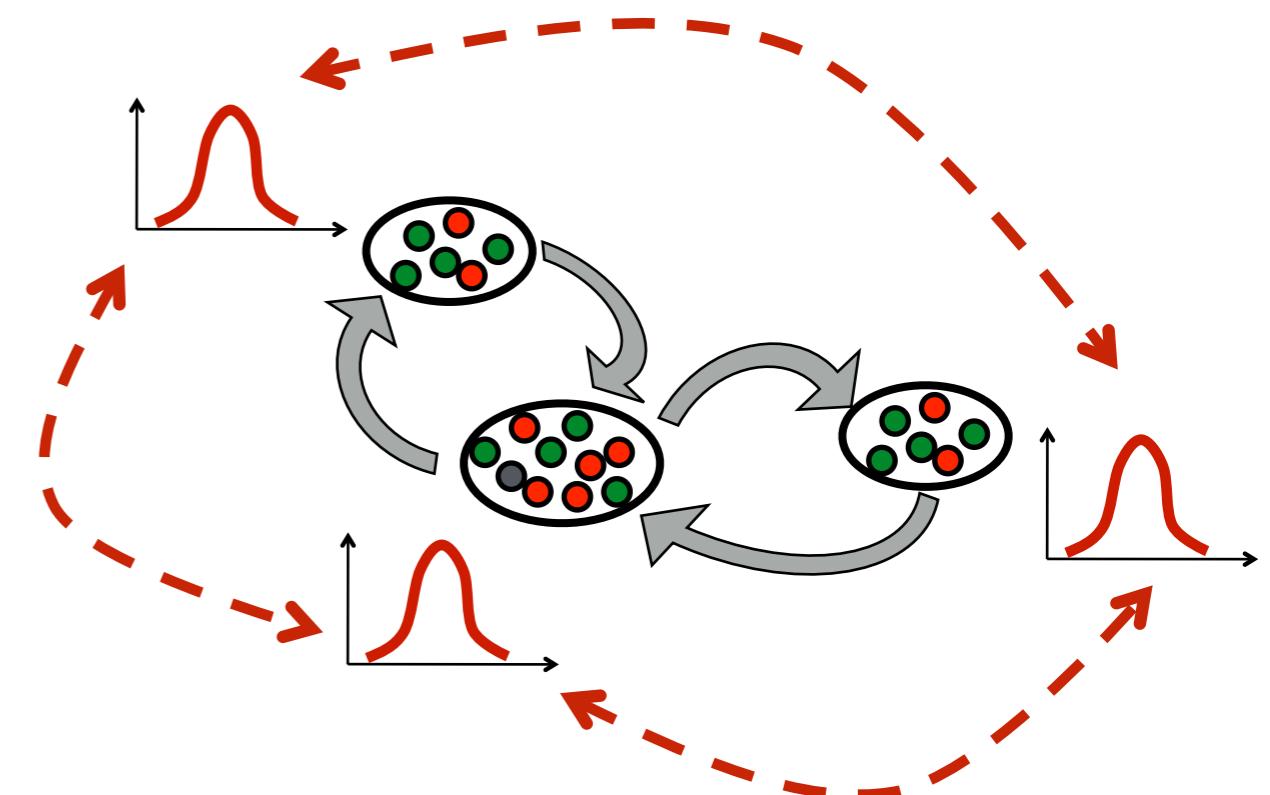
# SIR metapopulation model

$$\frac{dS_i}{dt} = -\beta \frac{I_i(t)S_i(t)}{N_i} + \Omega_i^S$$

$$\frac{dI_i}{dt} = \beta \frac{I_i(t)S_i(t)}{N_i} - \mu I_i(t) + \Omega_i^I$$

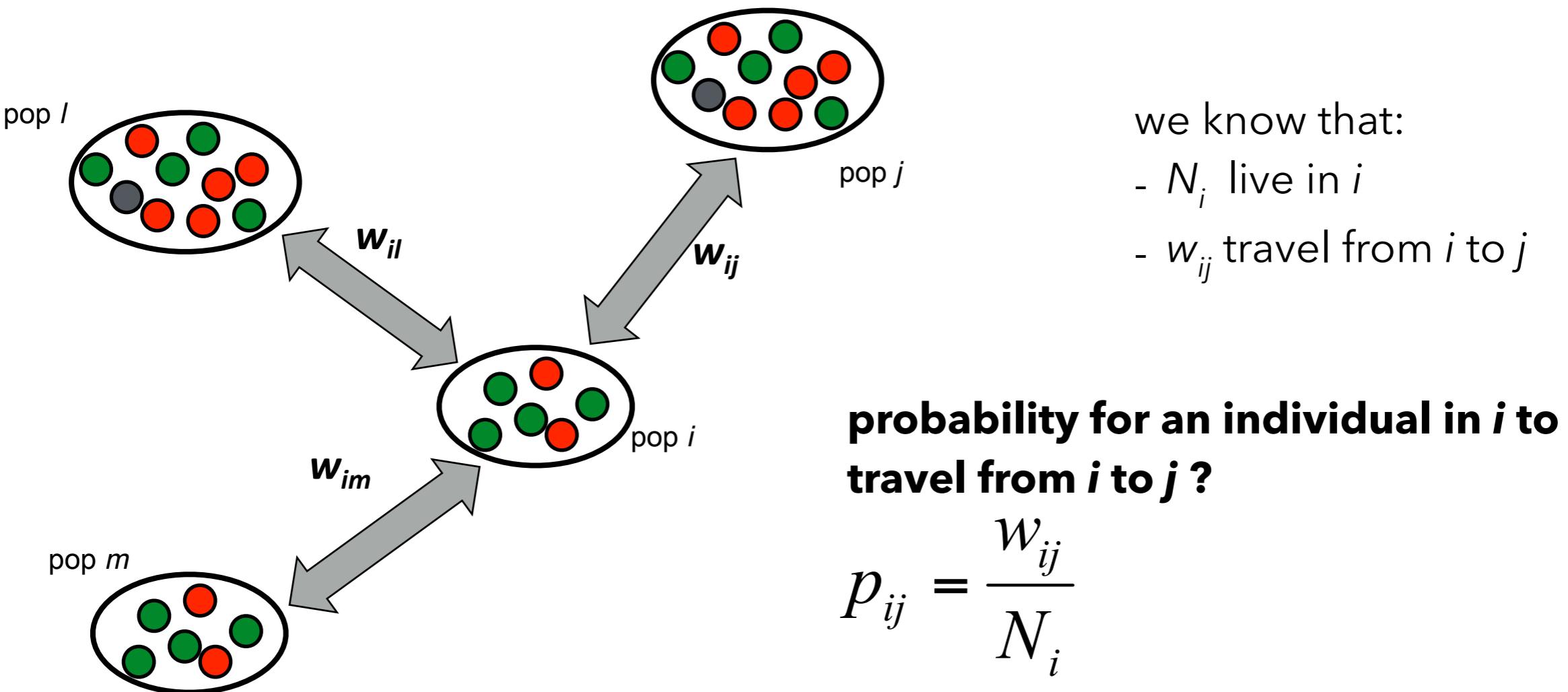
$$\frac{dR_i}{dt} = \mu I_i(t) + \Omega_i^R$$

$\Omega_i^X$  Measure of *in-flow* and *out-flow* of people in compartment  $X$

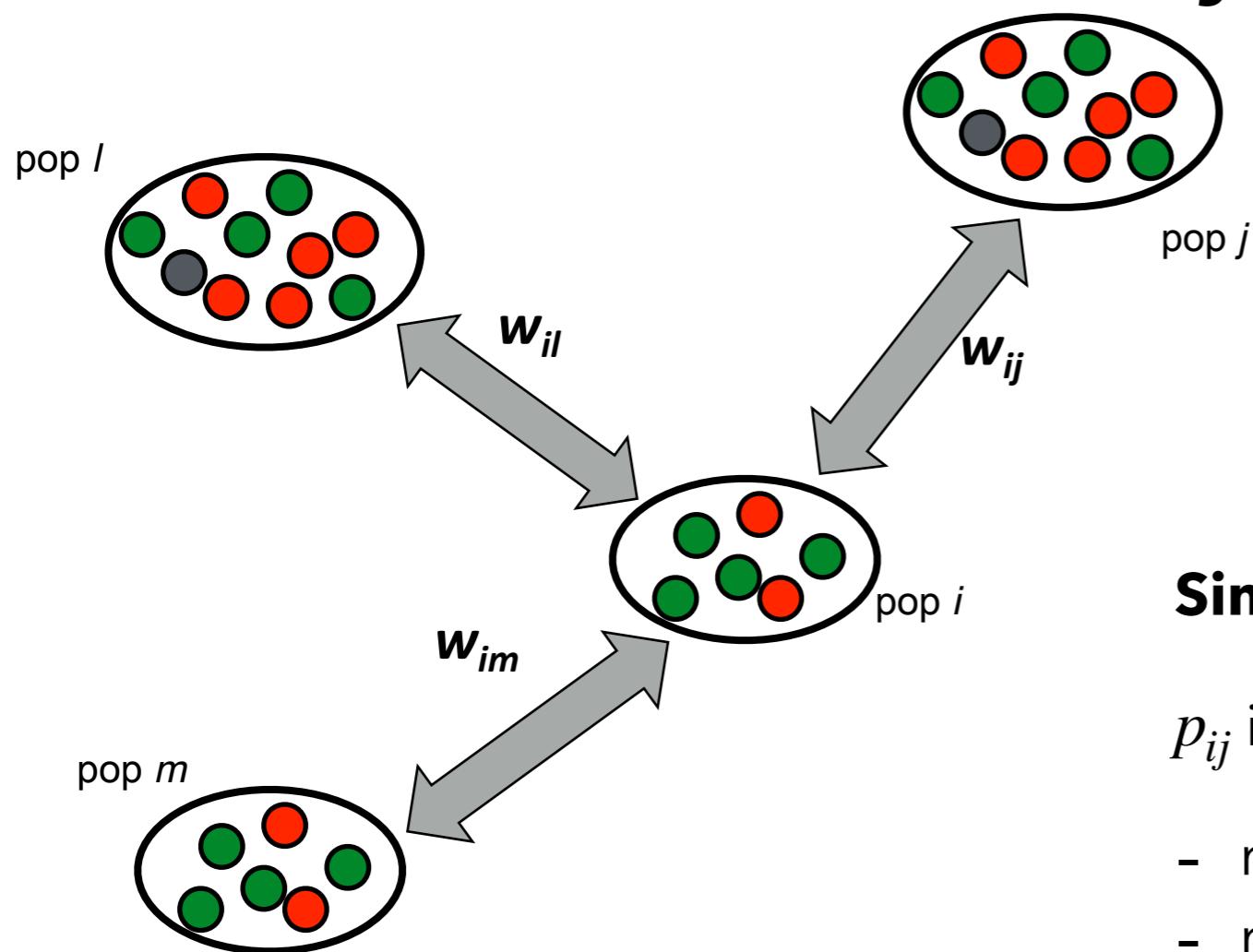


# SIR metapopulation model: markovian mobility

To  $\Omega_I^X$  compute we need to model human mobility



# SIR metapopulation model: markovian mobility



**probability for an individual in *i* to travel from *i* to *j* at each time?**

$$p_{ij} = \frac{w_{ij}}{N_i}$$

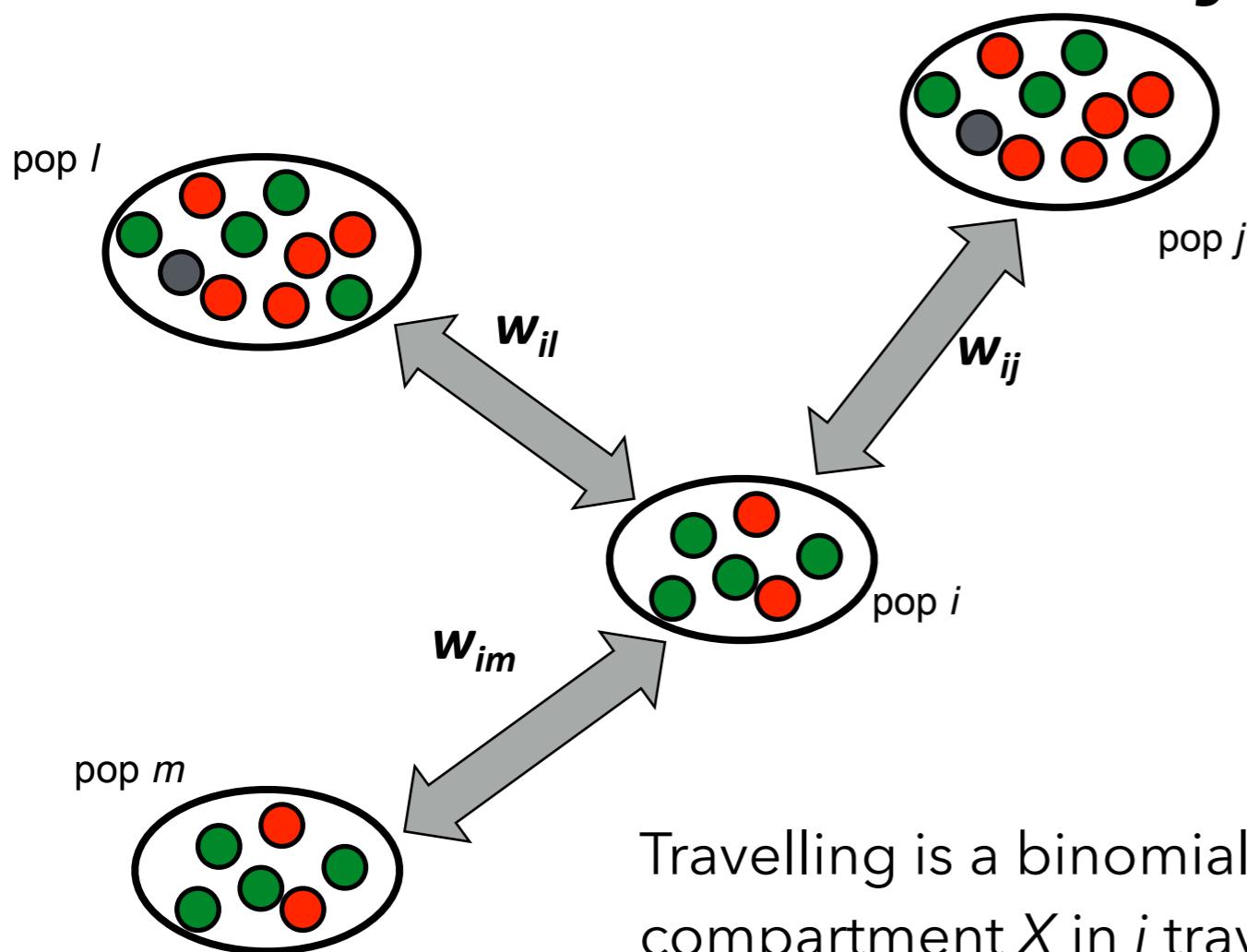
**Simplest possible model:**

$p_{ij}$  is the same for all individuals:

- regardless their infectious status (S,I,R)
- regardless their travel history (time since last travel, previous patch of origin)

as soon as an individuals enter in a new population, it mixes completely with the other individuals of that population

# SIR metapopulation model: markovian mobility



**probability for an individual in *i* to travel from *i* to *j* ?**

$$p_{ij} = \frac{w_{ij}}{N_i}$$

Travelling is a binomial process. Average number of individuals in compartment  $X$  in *i* traveling from *i* to *j* at each  $t$ :

$$\langle T_{ij}^X \rangle = p_{ij} X_i(t) = \frac{w_{ij}}{N_i} X_i(t)$$

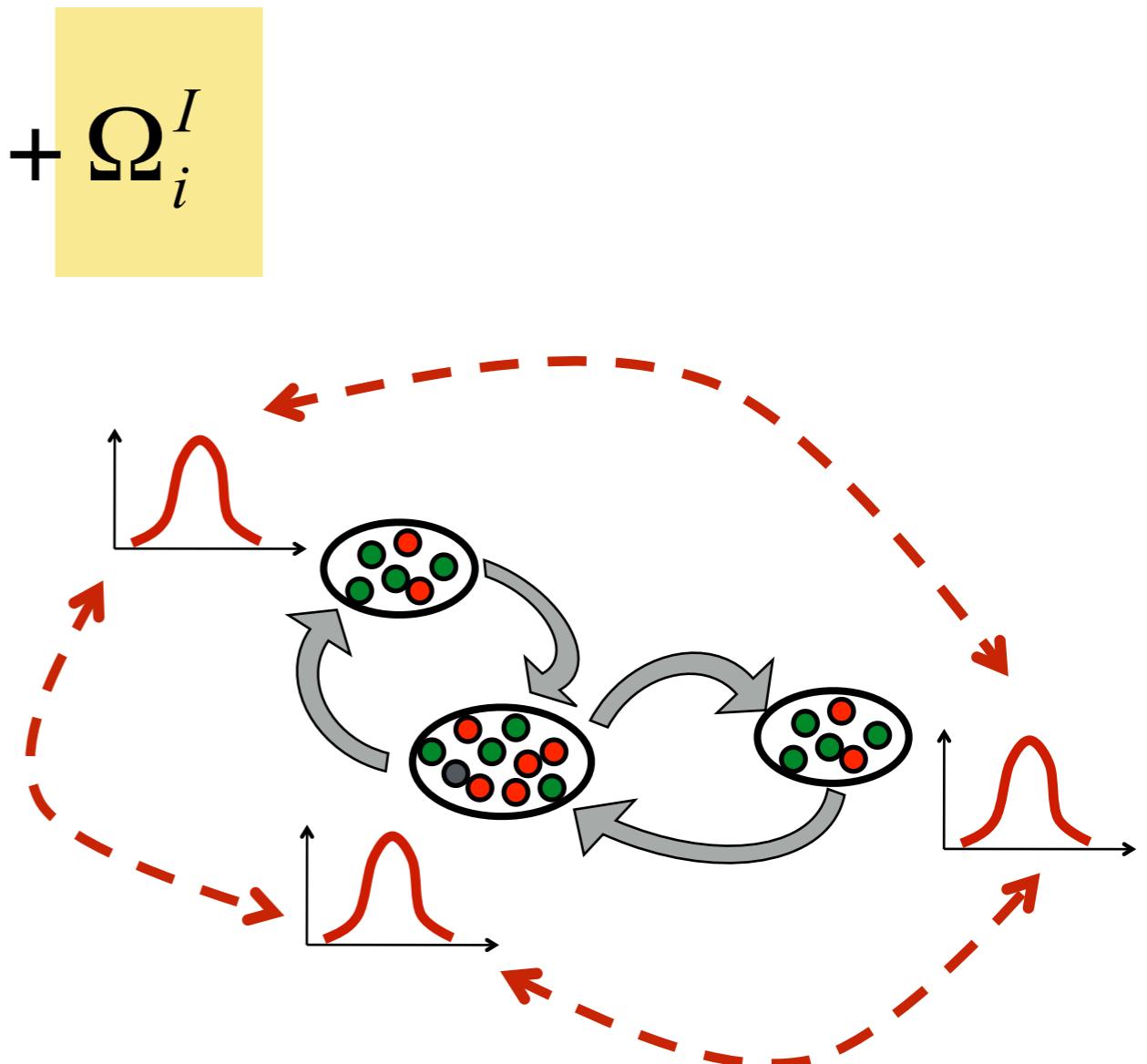
# SIR metapopulation model: markovian mobility

$$\frac{dS_i}{dt} = -\beta \frac{I_i(t)S_i(t)}{N_i} + \Omega_i^S$$

$$\frac{dI_i}{dt} = \beta \frac{I_i(t)S_i(t)}{N_i} - \mu I_i(t) + \Omega_i^I$$

$$\frac{dR_i}{dt} = \mu I_i(t) + \Omega_i^R$$

$$\Omega_i^X = \sum_j \frac{w_{ji}}{N_j} X_j - \frac{w_{ij}}{N_i} X_i$$



# SIR metapopulation model: markovian mobility

## Assumption so far:

we have modelled mobility as a Markovian process : travellers mix with the population at destination and forget about travel origin.

- The travel trajectory is random: patch  $i \rightarrow$  patch  $j \rightarrow$  patch  $l \rightarrow \dots$
- We do not account for the location of residence
- we do not account for the traveling length of stay.
- We are in fact modelling a migration process

# SIR metapopulation model: markovian mobility

The assumption works well as long as

- travels are not frequent, i.e. traveling rate negligible with respect to the epidemic time scales  $p_{ij} \ll \mu$
- we want to model the short-term dynamics of an epidemic

Situations for which this holds in first approximation:

- air travel and acute infections. E.g. for flu & COVID-19: traveling rate=  $10^{-3}$  days $^{-1}$  vs. recovery rate $> 0.1$  days $^{-1}$ )
- early spread of COVID-19 or flu pandemic. It does not work well if I want to model the long-term continuous circulation