

# LIFE DATA EPIDEMIOLOGY

*lect. 1: Introduction to computational epidemiology*

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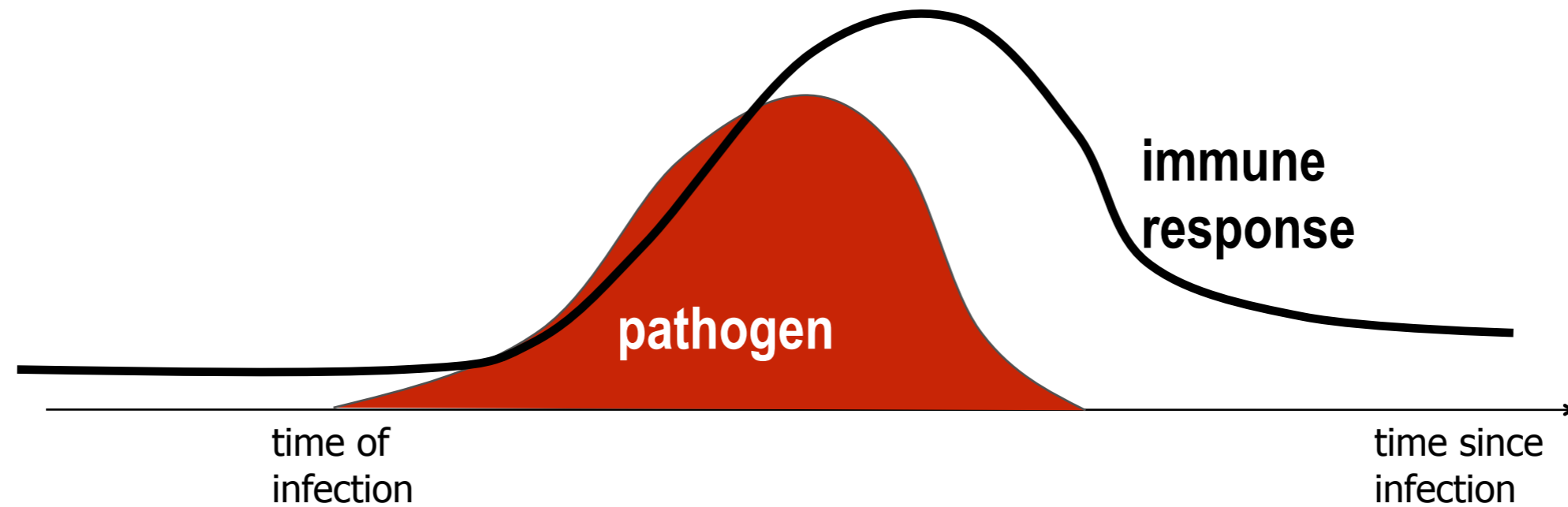
# Life data epidemiology

- What is computational epidemiology?
- modelling epidemics in space - the meta population models
- Introduction to temporal network epidemiology
- Confronting models with data introduction to model fitting

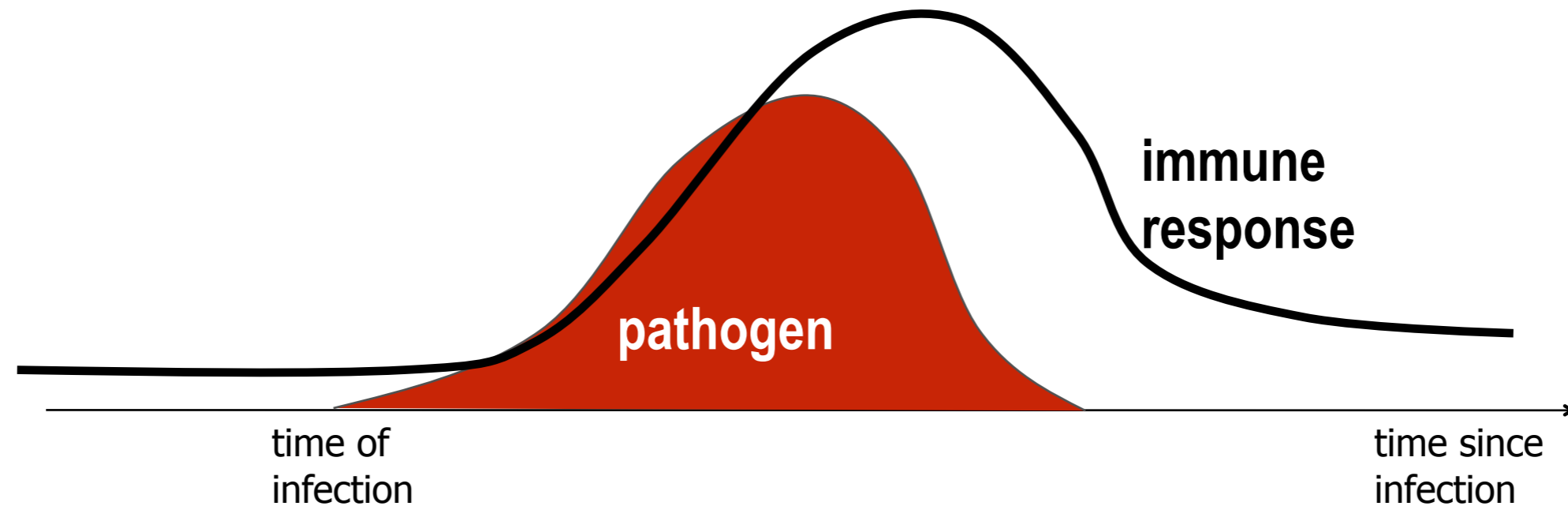
# Epidemiology is interdisciplinary

- **Public health:** because of the emphasis on disease prevention
- **Clinical medicine:** because of the emphasis on disease classification and diagnosis (numerators)
- **Pathophysiology:** because of the need to understand basic biological mechanisms in disease (natural history)
- **Social sciences:** because of the need to understand the social context in which disease occurs and presents (social determinants of health phenomena)
- **Statistics [+ Mathematics + Physics + ...]:** because of the need to quantify disease frequency and its relationships to antecedents

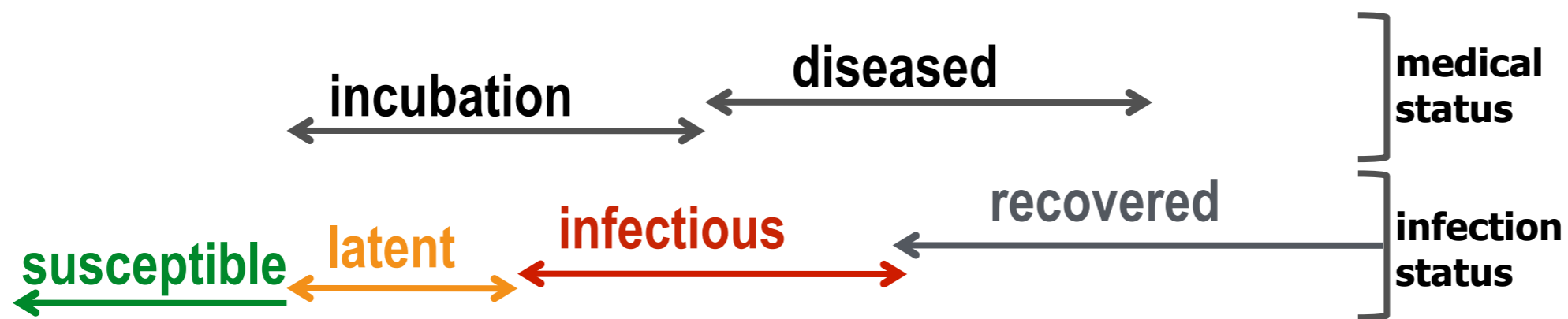
# epidemiological vs. clinician point of view



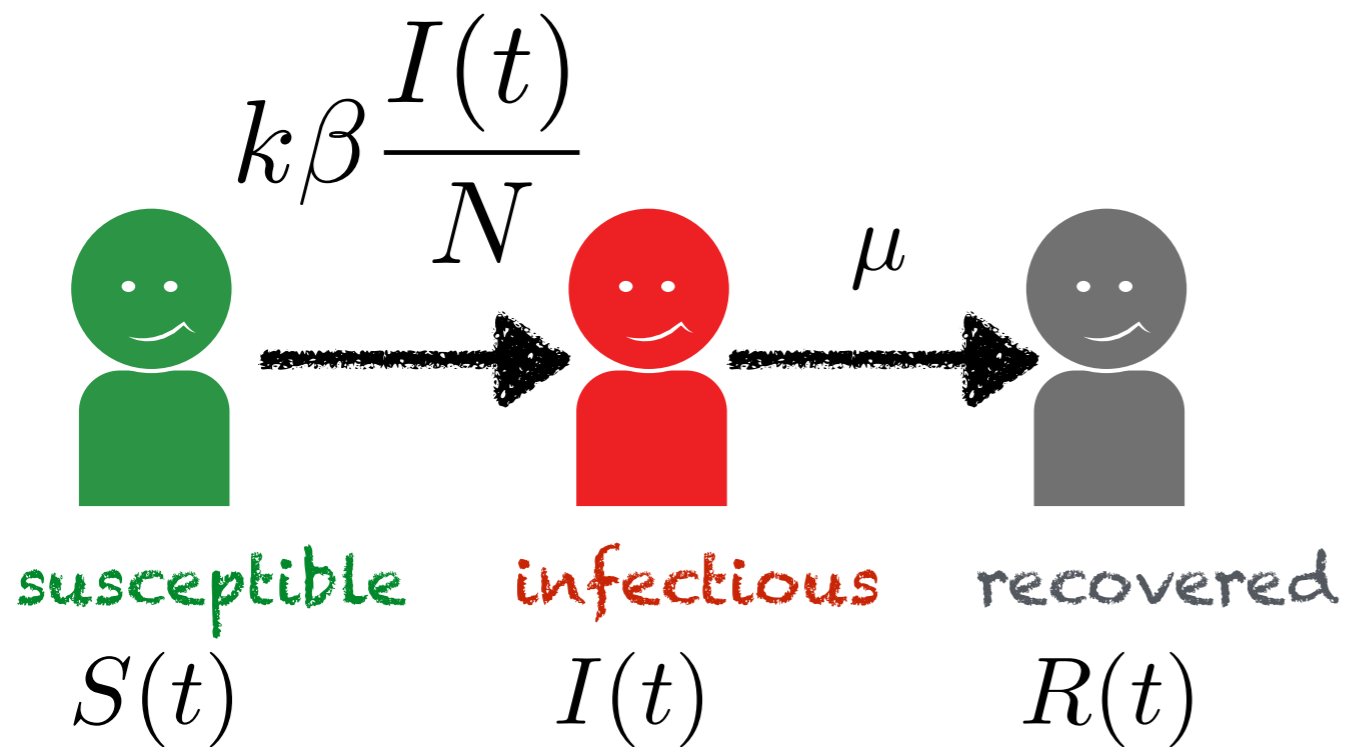
# epidemiological vs. clinician point of view



Coarse graining of the dynamics:



# Kermack & McKendrick model



$$d_t S(t) = -k\beta \frac{I(t)}{N} S(t)$$

$$d_t I(t) = k\beta \frac{I(t)}{N} S(t) - \mu I(t)$$

$$d_t R(t) = \mu I(t)$$

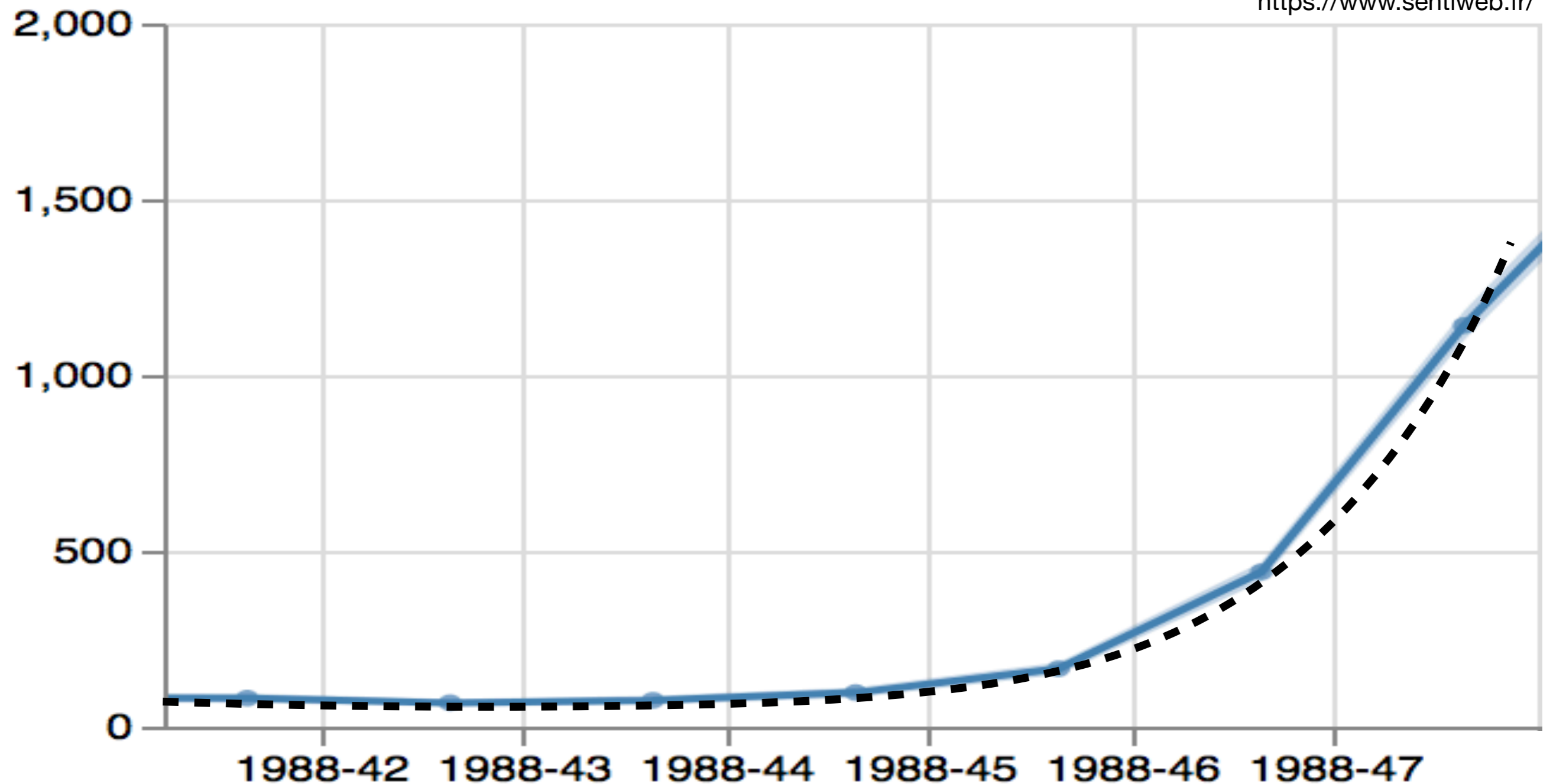
$$S(t) + I(t) + R(t) = N$$

# Kermack & McKendrick model

**epidemiology = making sense of data**

**Sentinelles**  
Réseau Sentinelles

<https://www.sentiweb.fr/>



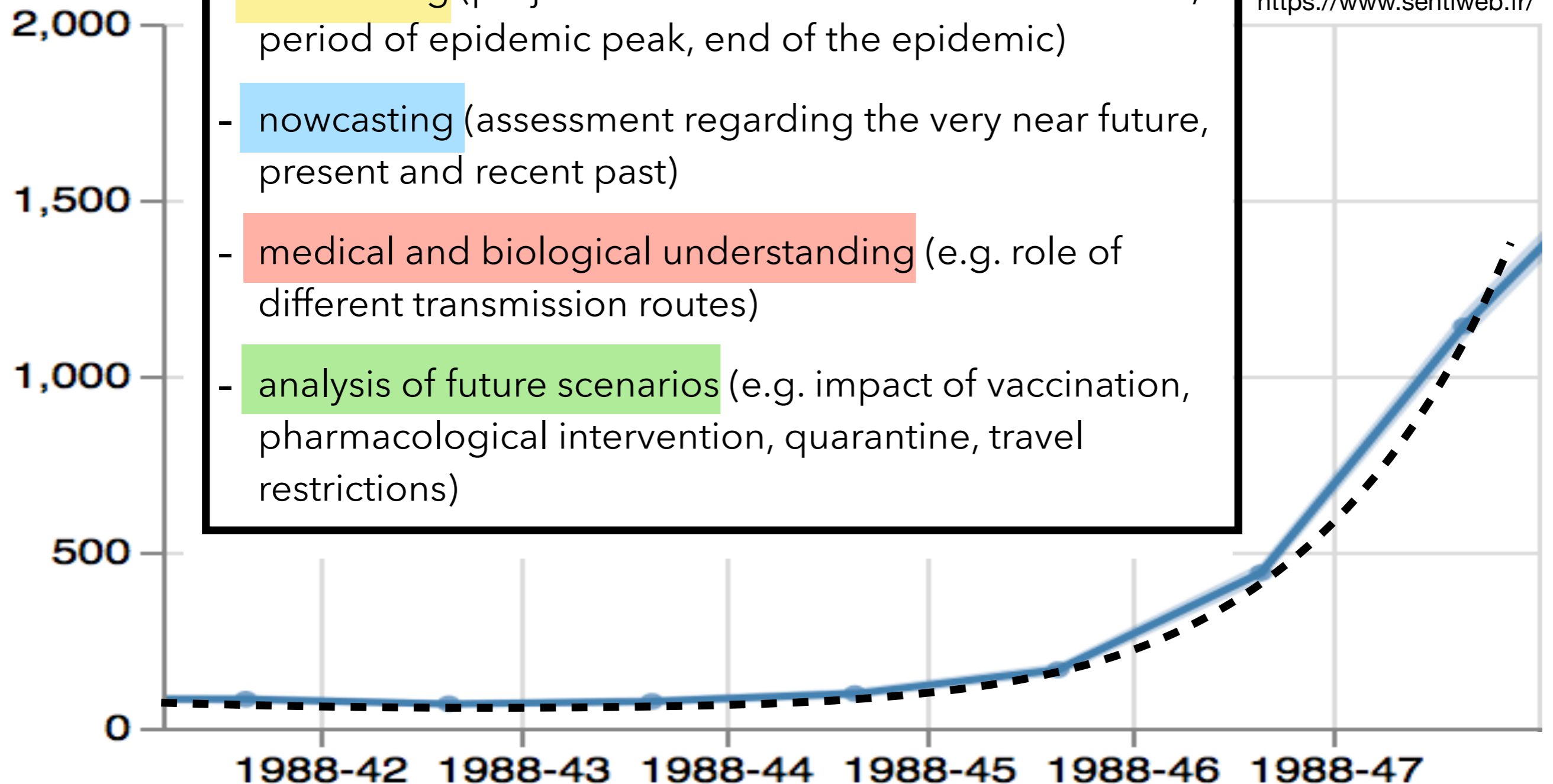
# Kermack & McKendrick model

## epidemiology = making sense of data

Sentinelles  
Réseau Sentinelles

<https://www.sentiweb.fr/>

- forecasting (projections on the future number of cases, period of epidemic peak, end of the epidemic)
- nowcasting (assessment regarding the very near future, present and recent past)
- medical and biological understanding (e.g. role of different transmission routes)
- analysis of future scenarios (e.g. impact of vaccination, pharmacological intervention, quarantine, travel restrictions)





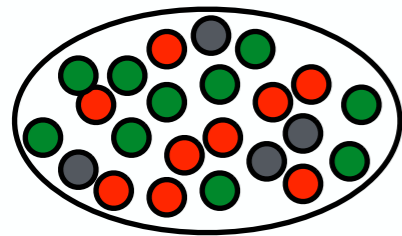
pathogen polymorphism,  
evolution, interaction with  
other pathogens

Host immunological &  
genetical profile,  
microbiome

COMPLEXITY

COMPLEXITY

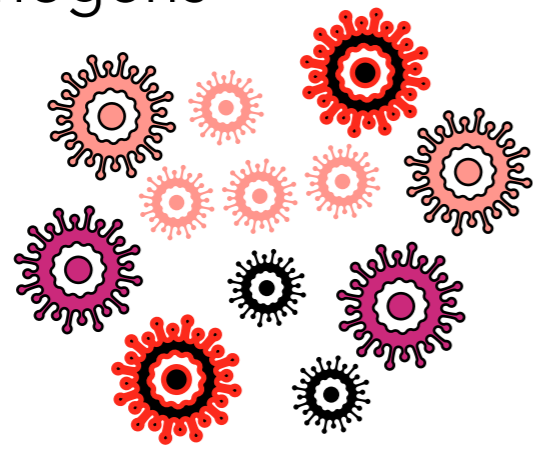
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homogeneous mixing  
compartmental models

Host demography - behaviour -  
contacts - spatial structure

pathogen polymorphism,  
evolution, interaction with  
other pathogens

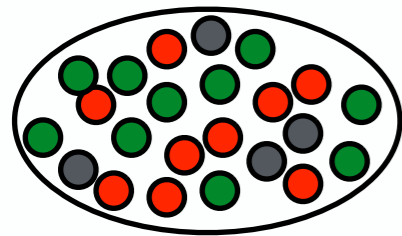


multi strain, evolution

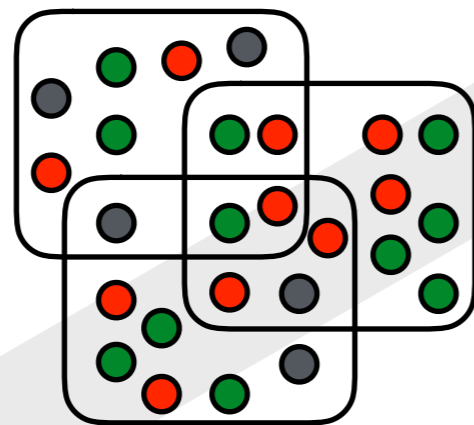
Host immunological &  
genetical profile,  
microbiome

COMPLEXITY

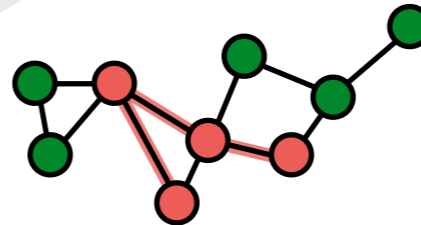
COMPLEXITY



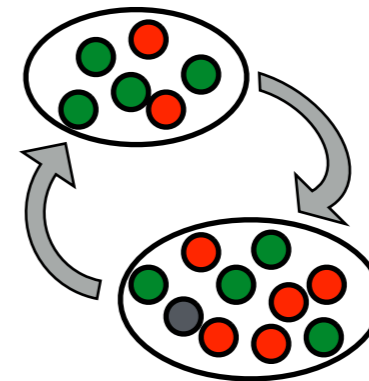
homogeneous mixing  
compartmental models



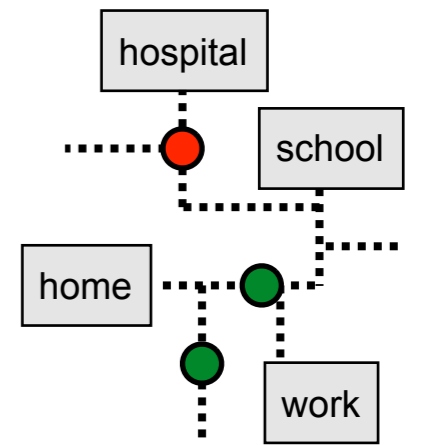
population  
structure



network



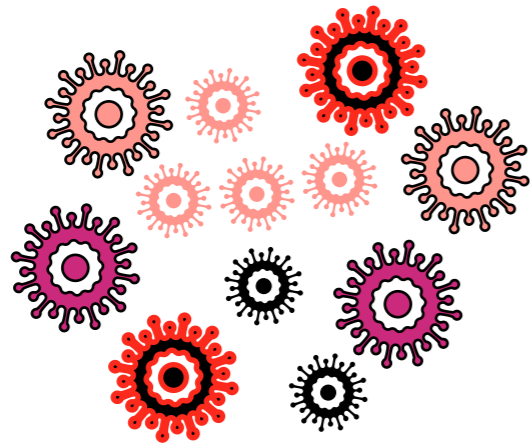
metapopulation



agent based

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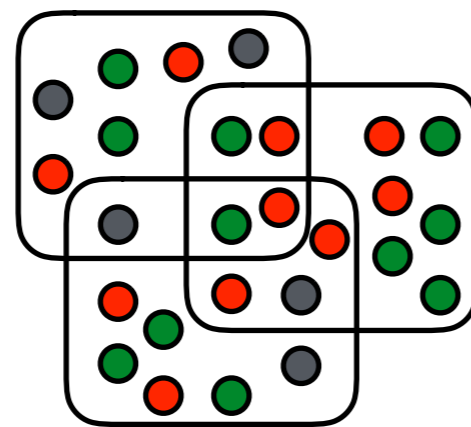
Host demography - behaviour -  
contacts - spatial structure



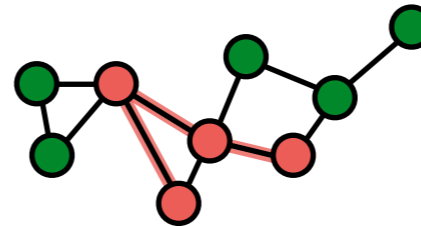
**multi strain, evolution**

pathogen sequences

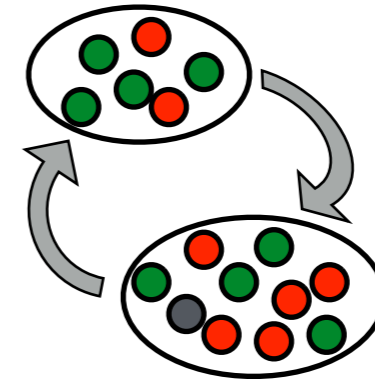
phenotypic information



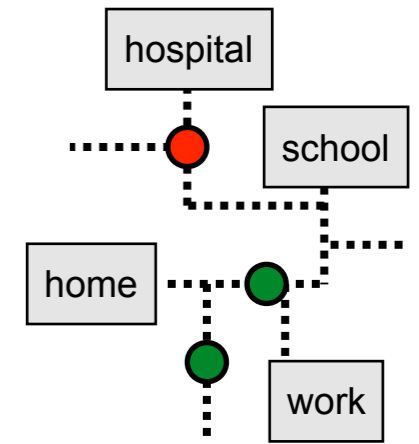
**population structure**



**network**



**metapopulation**



**agent based**

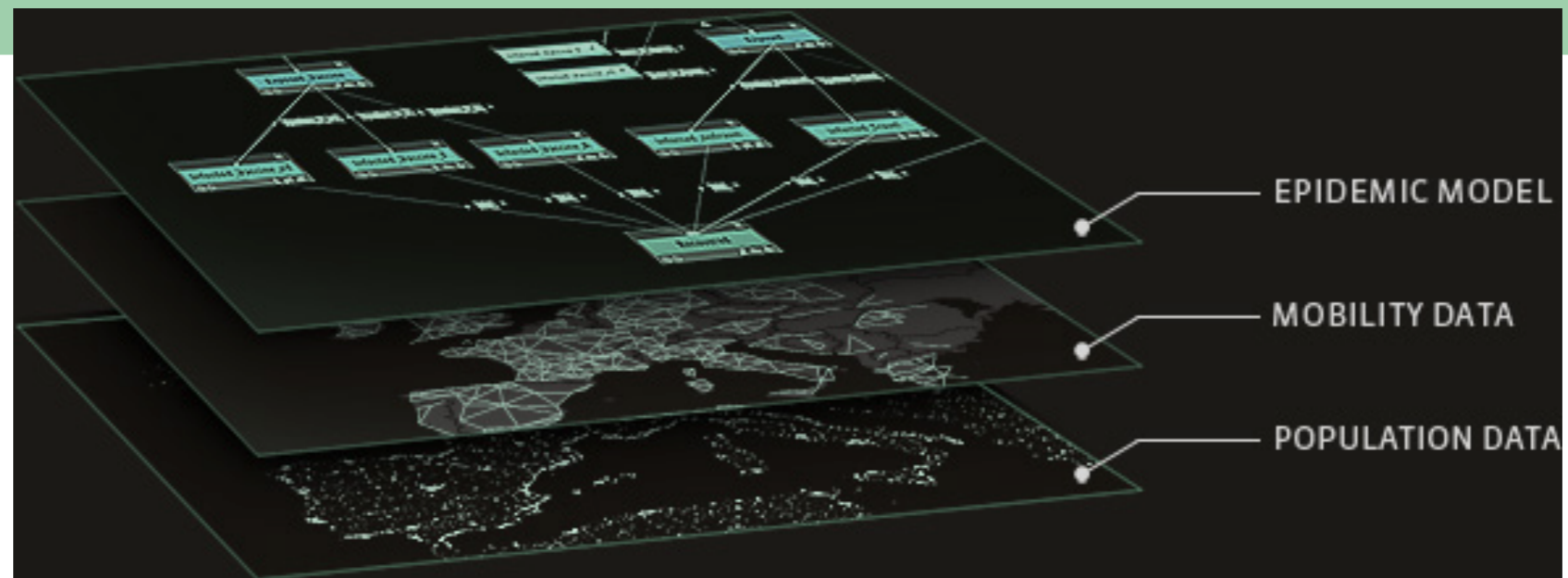
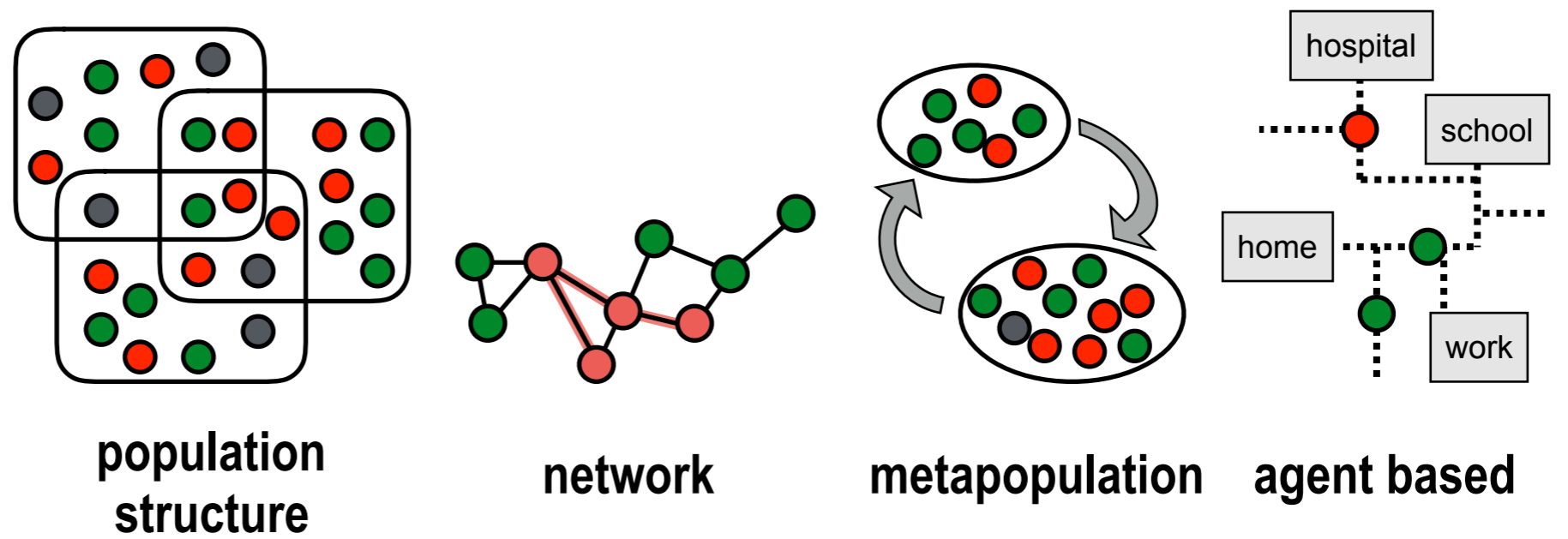


age profile,  
contact statistics  
risk classes

individual level  
contact dynamics

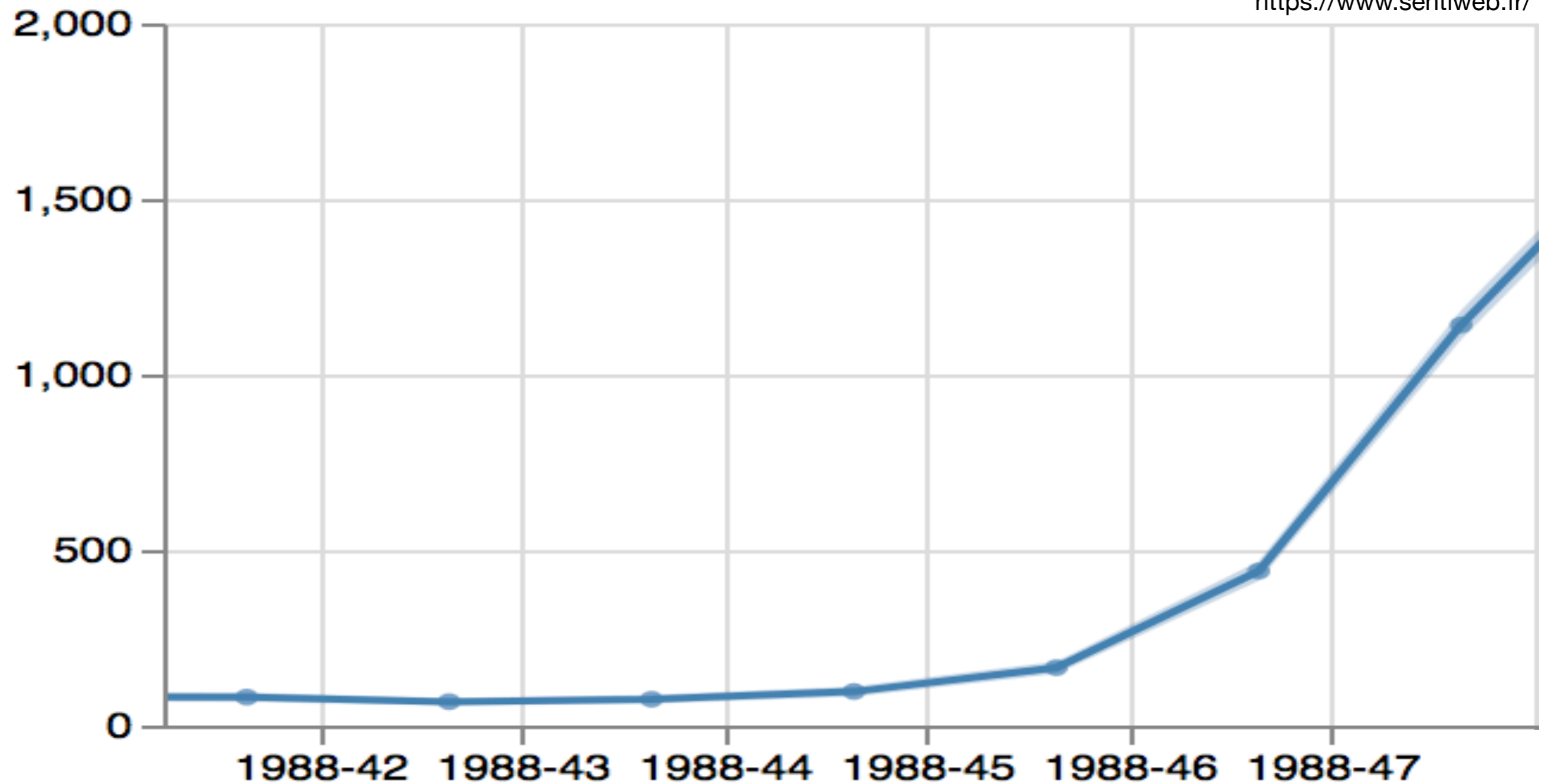
spatial  
distribution,  
mobility

detail  
statistics of  
the  
population  
(households,  
workplaces,  
schools)



**big data!**

# epidemiological data - surveillance

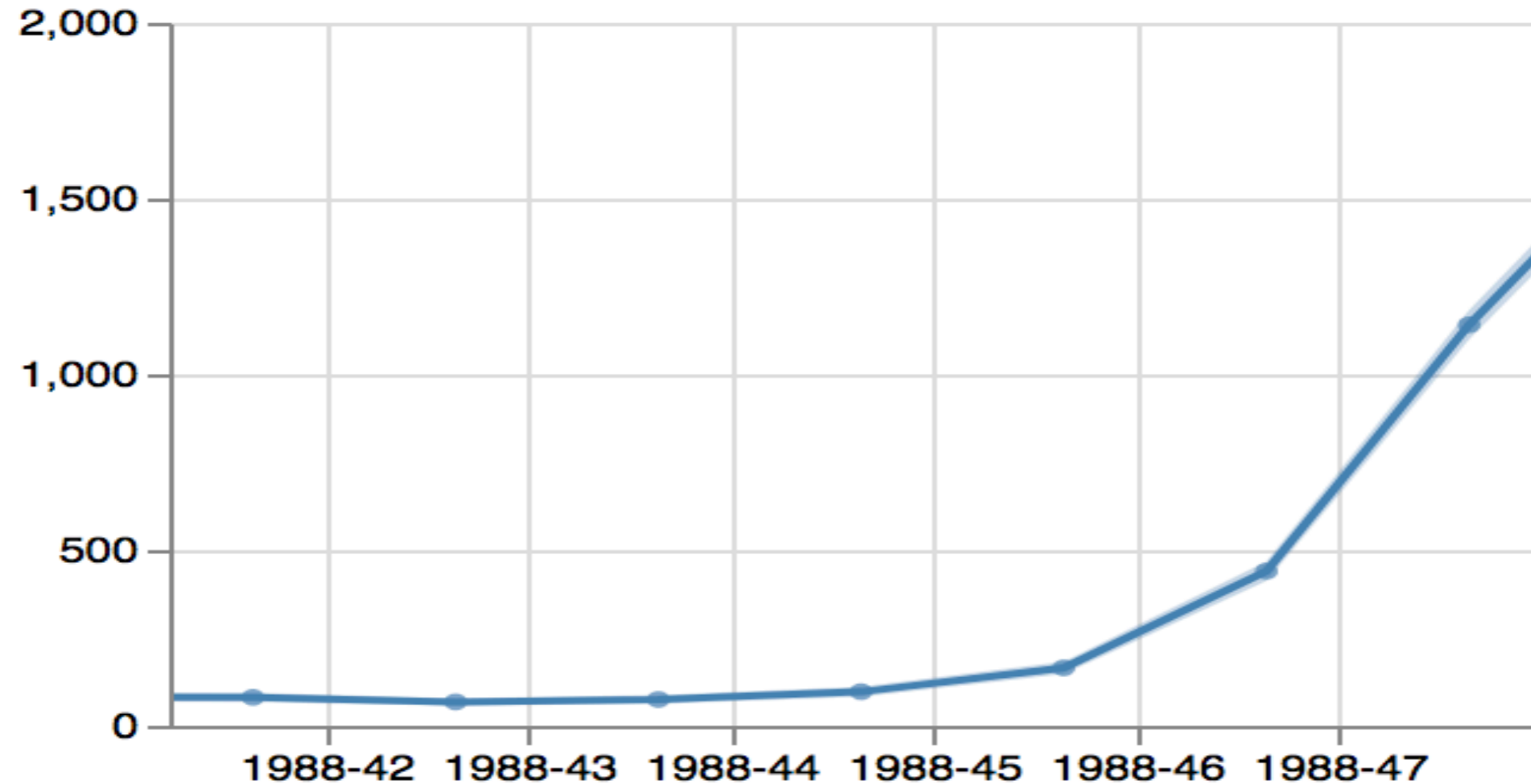


# incidence: flu

1988-1989 Influenza season in France



<https://www.sentiweb.fr/>



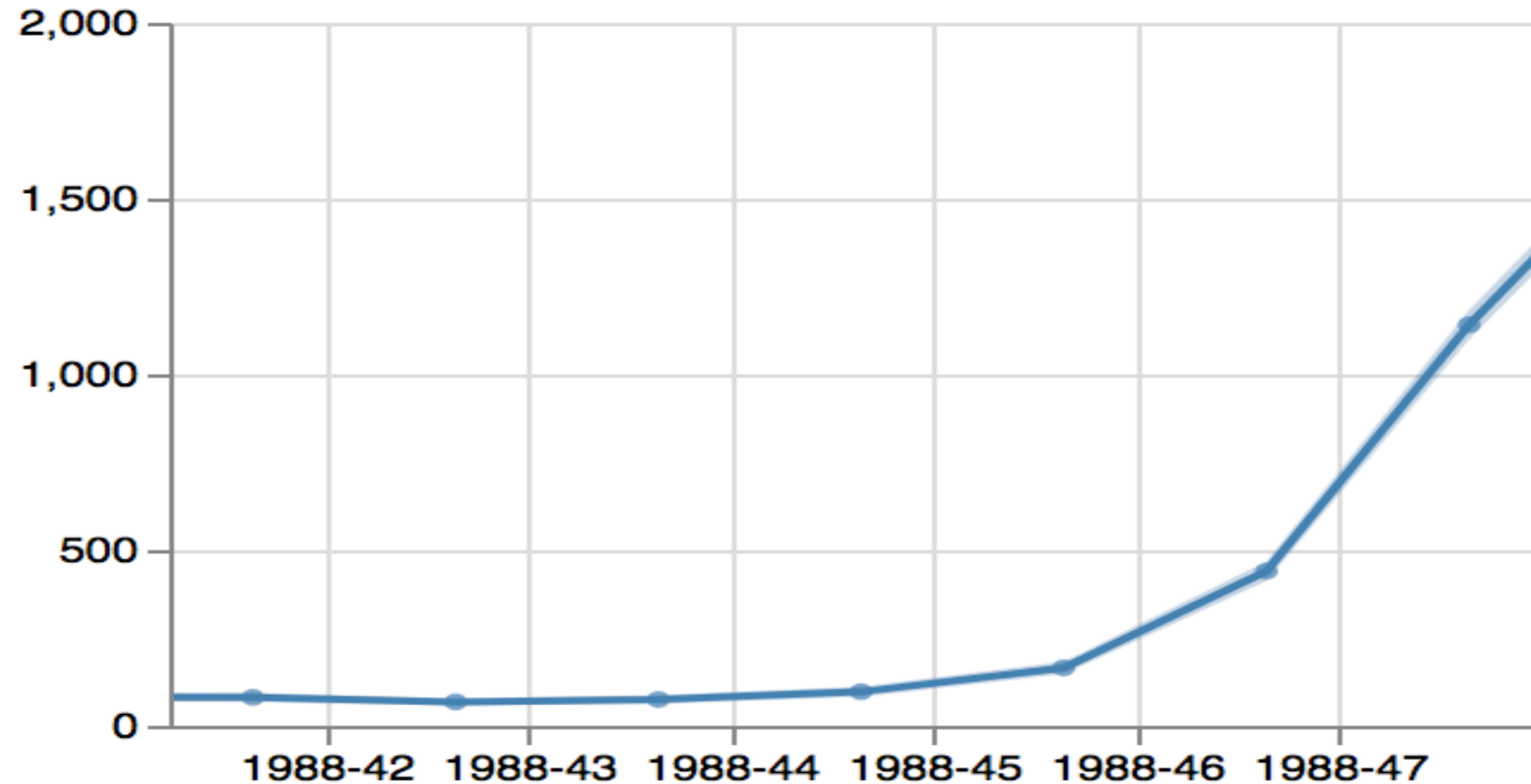
**Incidence in a given area  $a$  at time  $t$**  = fraction of the population catching flu in  $a$  at  $t$

# incidence: flu

1988-1989 Influenza season in France



<https://www.sentiweb.fr/>



**Incidence in a given area  $a = \text{numerator}_a / \text{denominator}_a$**

**numerator** = the number of people hit by flu

**denominator** = the population at risk



numerator: case definition

**case definition = set of criteria used in making a decision as to whether an individual has a disease or health event of interest**

possible criteria: clinical, laboratory

characteristics, information regarding the person

cases can be classified: confirmed, probable,

possible

# case definition: sensitivity and specificity

A **sensitive** case definition will detect many cases but may also count as cases individuals who do not have the disease.

A **specific** case definition is more likely to include only persons who truly have the disease under investigation but also more likely to miss some cases

	Disease is truly present	Disease is truly absent	Total
complies to case definition	a	b	all cases
does not comply to case definition	c	d	all non-cases
	all 'diseased'	all 'non-diseased'	all people in the study sample

Sensitivity = [ a / (a+c) ]

Specificity = [ d / (b+d) ]

# numerator: flu

**numerator for a area a** = cases seen by General Practitioners defined based on *clinical criteria*. These are in fact possible cases. Laboratory confirmation available only for a small proportion of cases.

## symptoms of flu

- no symptoms (~30%)
- upper respiratory symptoms, e.g. nasal stuffiness, runny nose, sore throat, sneezing, hoarseness, ear pressure, or earache (~60%)
- lower respiratory symptoms, e.g. cough, breathing difficulty, and chest discomfort (~2%)
- fever (~35%)

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- fever (~35%)
- from early to peak symptoms ~1 day

## clinical case definition

- fever  $> 39\text{ }^{\circ}\text{C}$  AND myalgia
- sudden onset
- respiratory symptoms

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## clinical case definition

- fever OR malaise OR headache OR myalgia
- sudden onset
- cough OR sore throat OR shortness of breath

# numerator: flu

**numerator for a area a** = cases seen by General Practitioners defined based on *clinical criteria*. These are in fact possible cases. Laboratory confirmation available only for a small proportion of cases.

## clinical case definition



- fever > 39 °C AND myalgia
- sudden onset
- respiratory symptoms

**higher specificity**



- fever OR malaise OR headache OR myalgia
- sudden onset
- cough OR sore throat OR shortness of breath

**higher sensitivity**

# numerator: flu

**numerator for a area a** = cases seen by General Practitioners defined based on *clinical criteria*. These are in fact possible cases. Laboratory confirmation available only for a small proportion of cases.

## clinical case definition



- fever > 39 °C AND myalgia
- sudden onset
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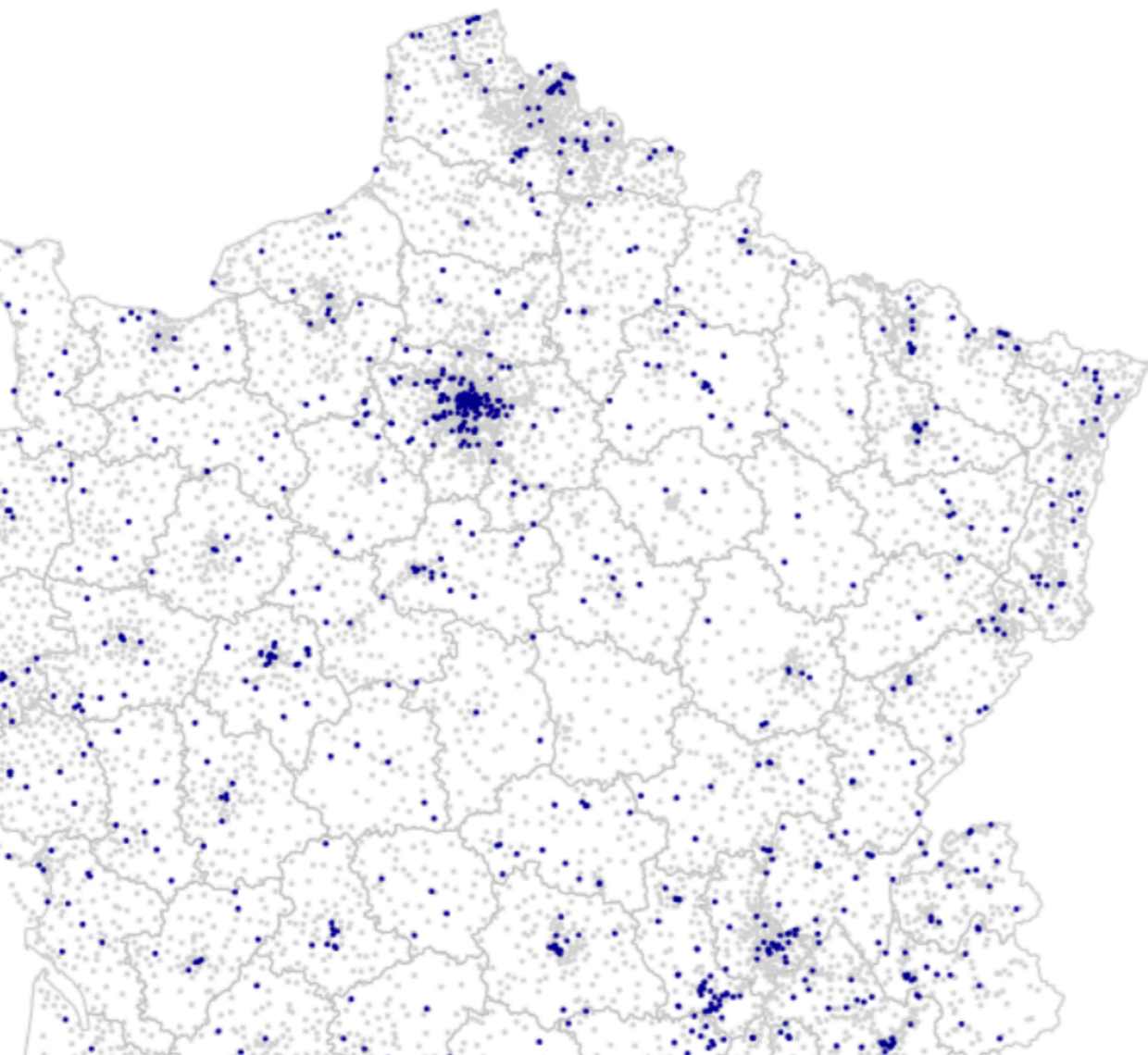
**higher specificity**

**higher sensitivity**

many cases are missed (no symptoms for ~30%)

# denominator: flu

**denominator for the area  $a$**  = catchment population, i.e. all the people living in the catchment area of the General Partitioner reporting the cases, who would usually seek healthcare at the site when they get sick



The Surveillance Networks (SN) is based on a *fraction of General Partitioner* (~1%), who are volunteers

denominator  $a$  =  $\text{Population}_a \cdot \text{GP}_{\text{SN},a} / \text{GP}_a$

(Horvitz DG, Thompson DJ. A JASA. 1952;47:663–85)



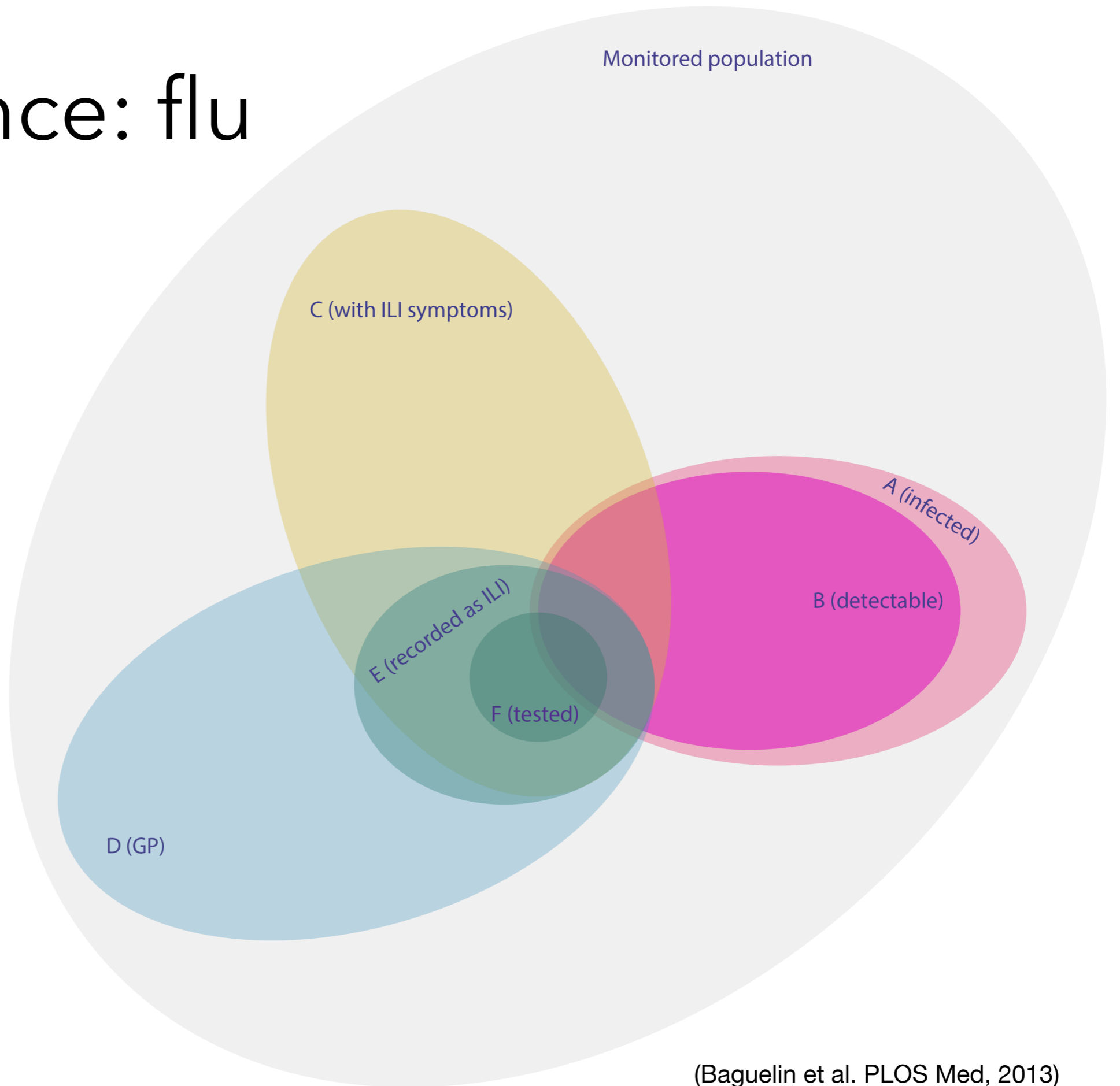
# incidence: flu

**Incidence in a given area  $a = \text{numerator}_a / \text{denominator}_a$**

**but ... consultancy rate**

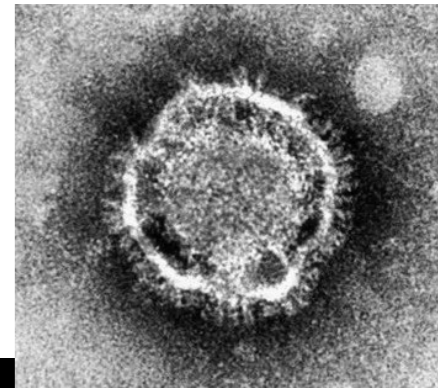
- highly variable by age
- variable geographically (e.g. dependent on the GP density)
- variable according to the period of the year
- highly dependent on the health-care system (how expensive is going to the GP? Do you need a permit for staying at home from work?)

# incidence: flu

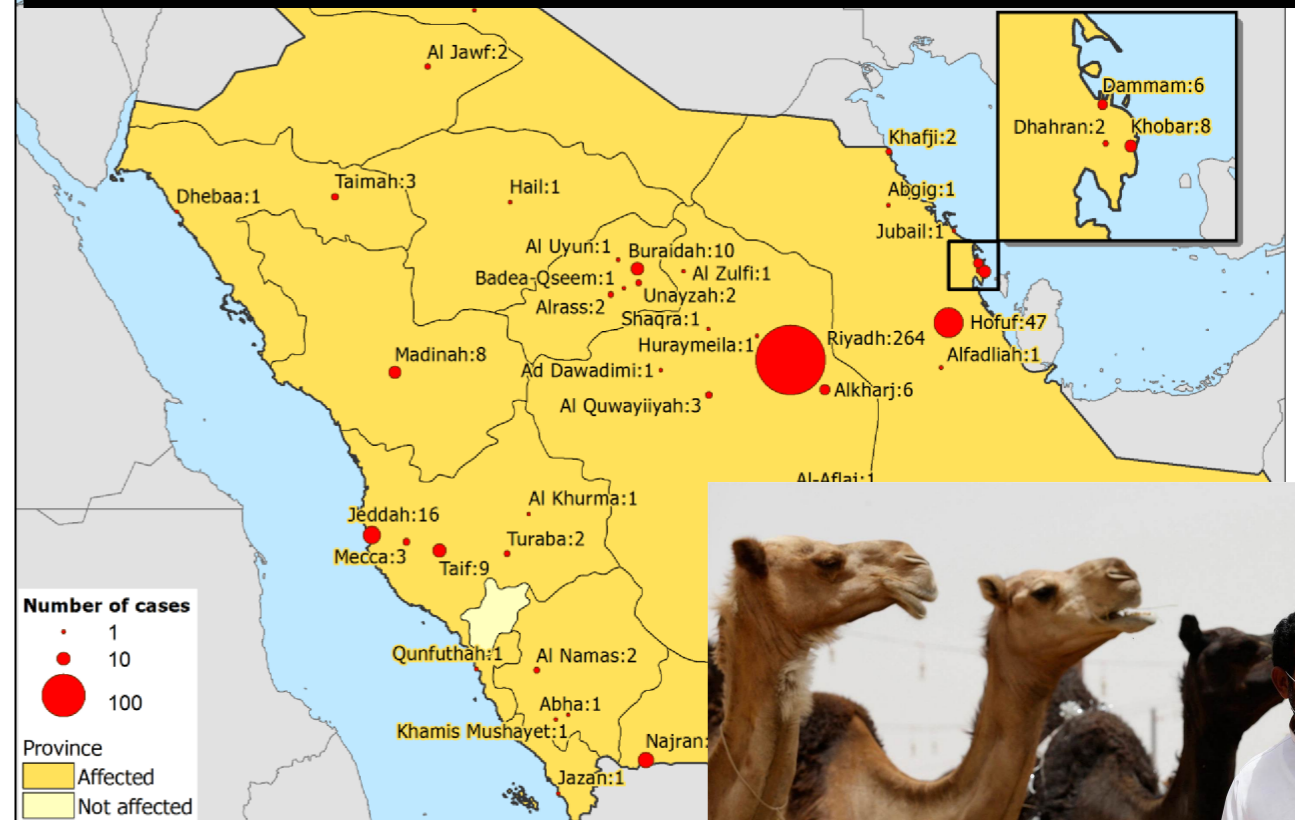


# incidence: MERS

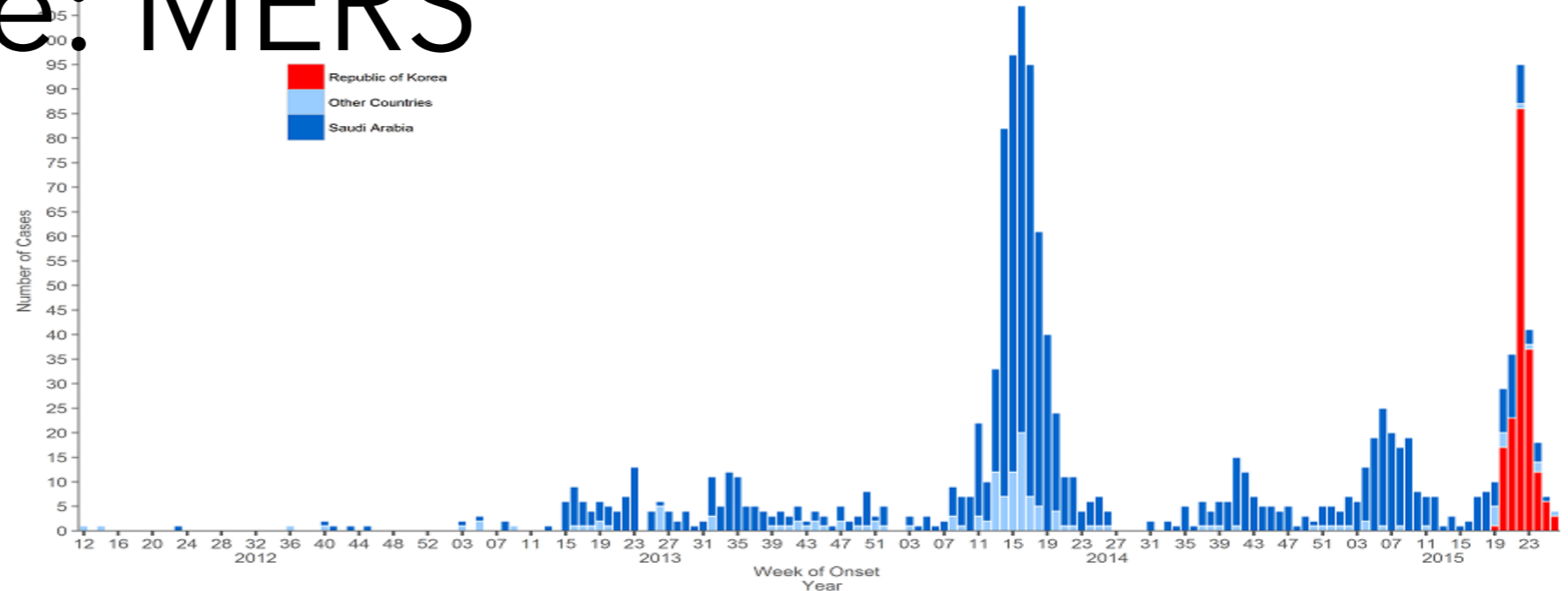
- emerging disease (first detected in 2012)
- severe respiratory infection (mortality rate ~35%)
- zoonotic origin (dromedary camels)
- limited human-to-human transmission
- zoonotic transmission (from camel to human)



## Middle East Respiratory Syndrome (MERS) Coronavirus



# incidence: MERS

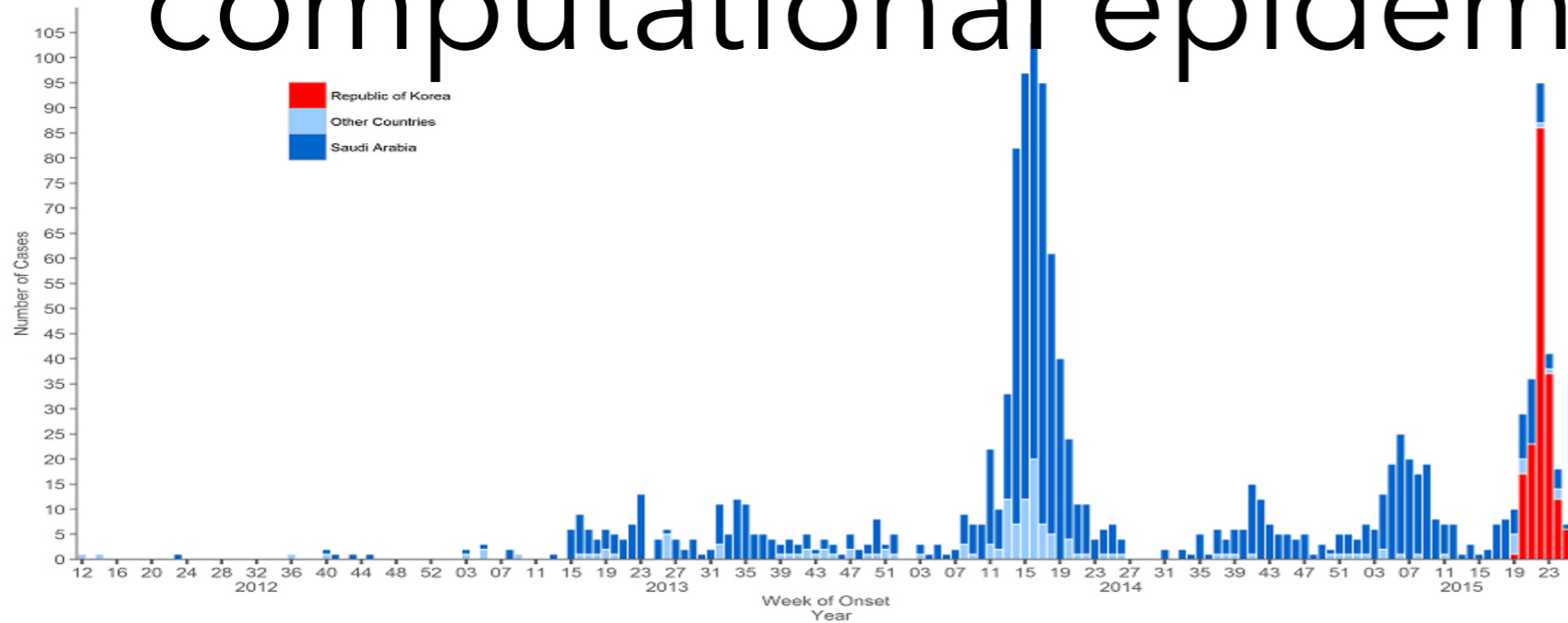


- case definition varying in time: range of symptoms unknown
- not wide spread: unclear the region where it is spreading, thus denominator hard to estimate
- quality and coverage of the health care systems unknown
- reporting rate highly variable in time: from passive to active surveillance, to saturation of the surveillance system
- there can be a retrospective correction for the number of cases: further source of biases in case of a real time analysis

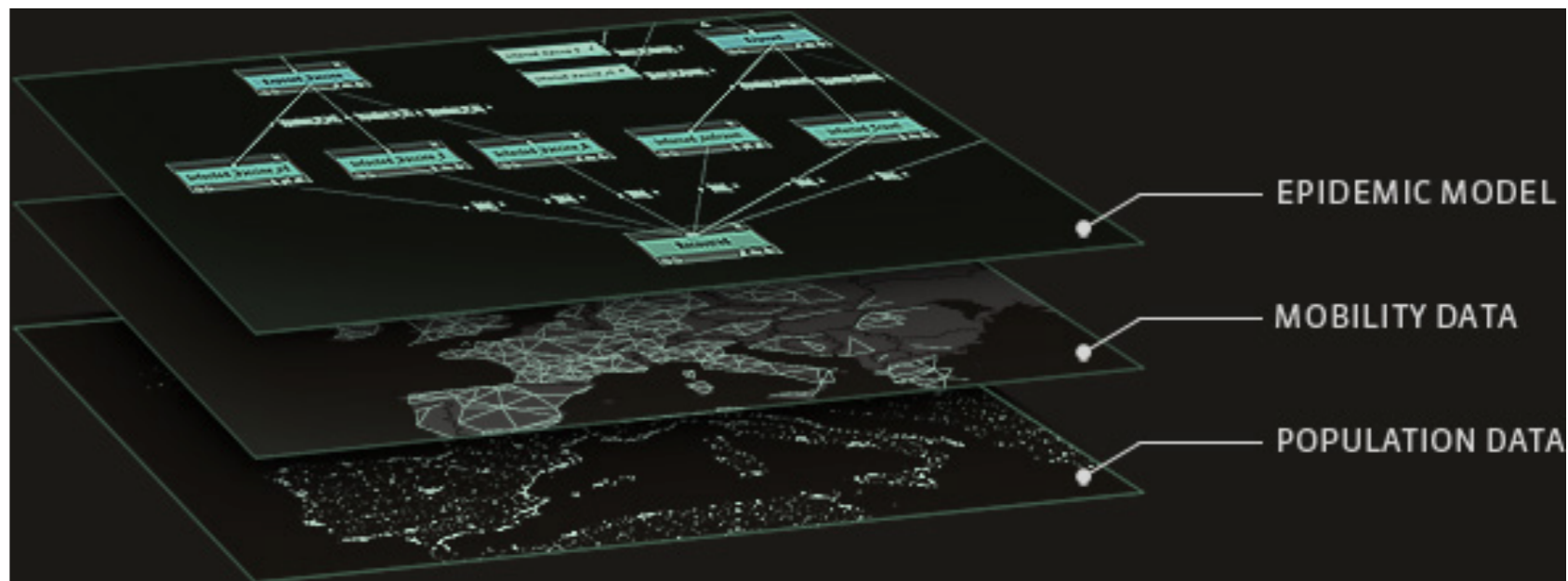
# computational epidemiology

**epidemiology = making sense of data**

# computational epidemiology



**computational** epidemiology = making sense of **scarse**  
**data** using big data

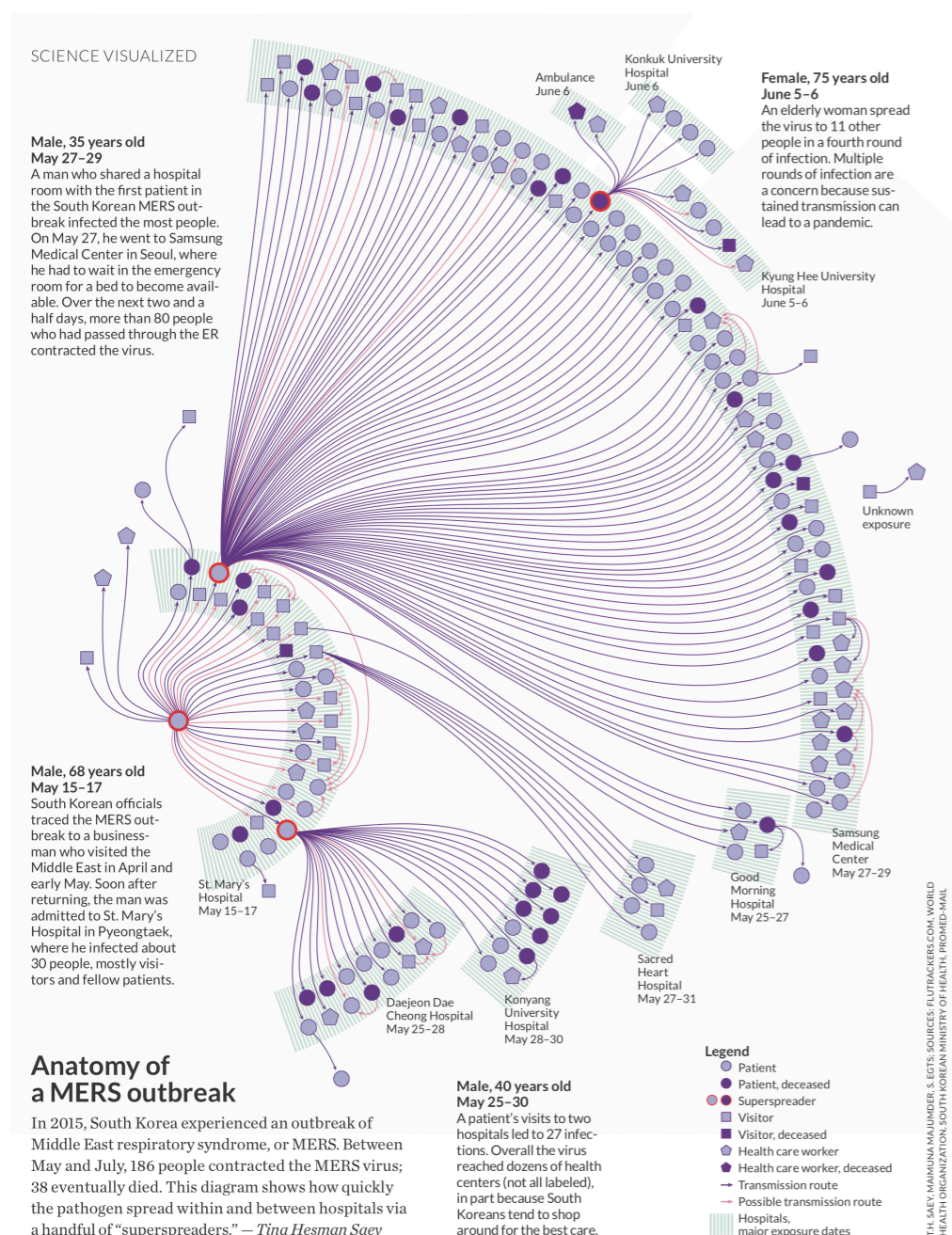


# projects

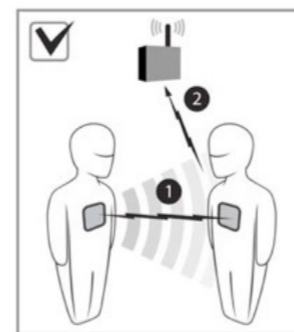
- MERS outbreak in South Korea and role of super-spreading events
- 2014 Ebola outbreak
- Competition between strains of influenza virus
- Spread of sexual-transmitted-diseases (STDs) on a prostitution network
- Measles spread and vaccine hesitancy
- Critical community size and effect of spatial structure

# project 1: MERS

## Hospital outbreak of MERS in South Korea, 2015: 186 cases and 36 deaths



Heterogeneities in contacts can lead to super-spreading events



data on face-to-face contacts in a hospital from [sociopattern.org](http://sociopattern.org)

- Characterise the properties of the network from the data
- Simulate a MERS epidemic starting from the different nodes comparing different level of transmissibility. Is this different according to the node initially infected?
- What are the properties of the node that mostly affect the outbreak size? What are the category of people sensible to cause bigger outbreak?



# project 2: Ebola

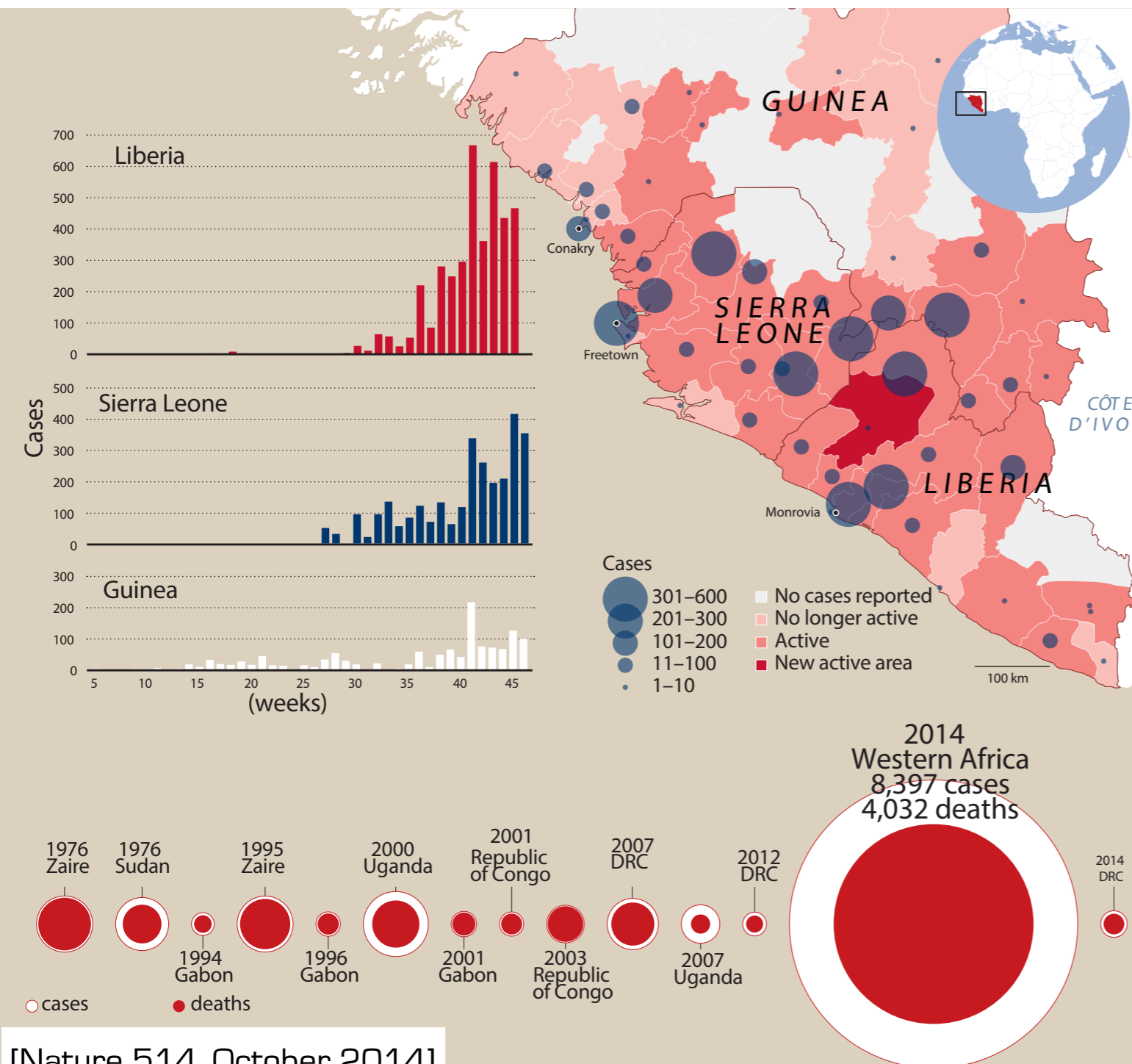
**Largest Ebola outbreak in the history: 28,000 cases; 10,000 deaths; 10 countries affected**

Ebola data and Statistics

[<http://apps.who.int/gho/data/node.ebola-sitrep>]

Althaus CL. PLOS Currents Outbreaks. 2014. doi: 10.1371/currents.outbreaks.91afb5e0f279e7f29e7056095255b288.

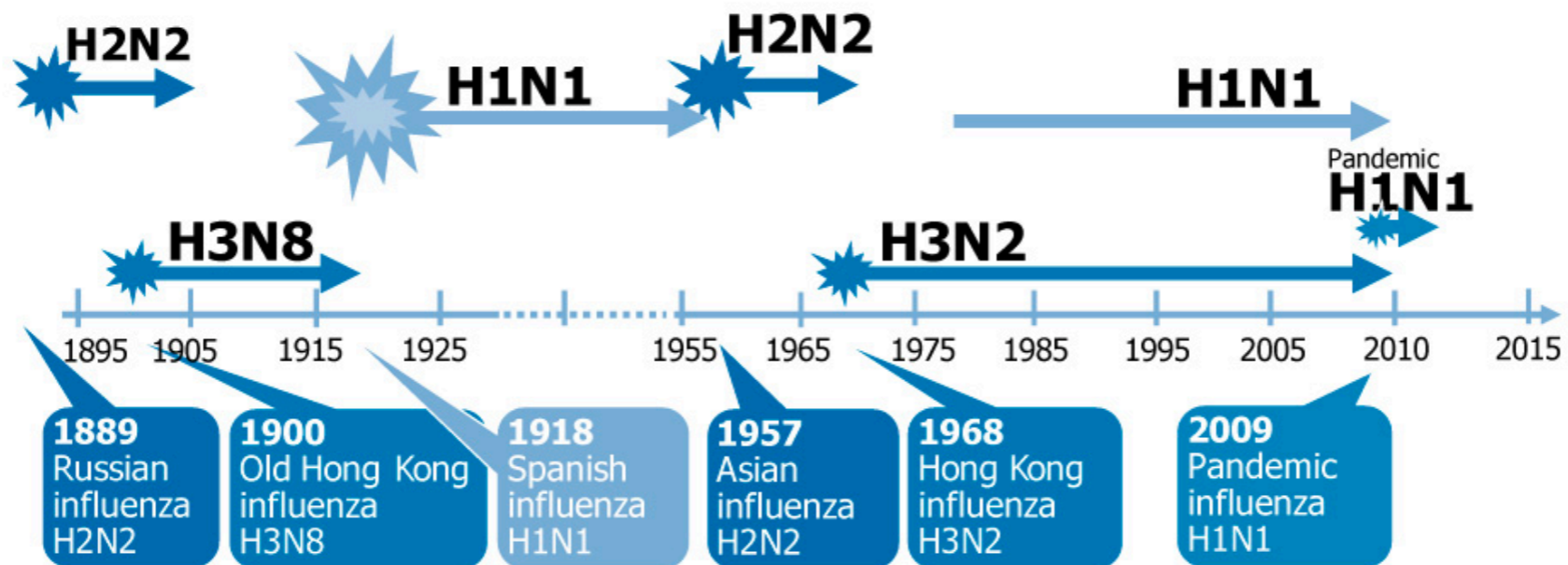
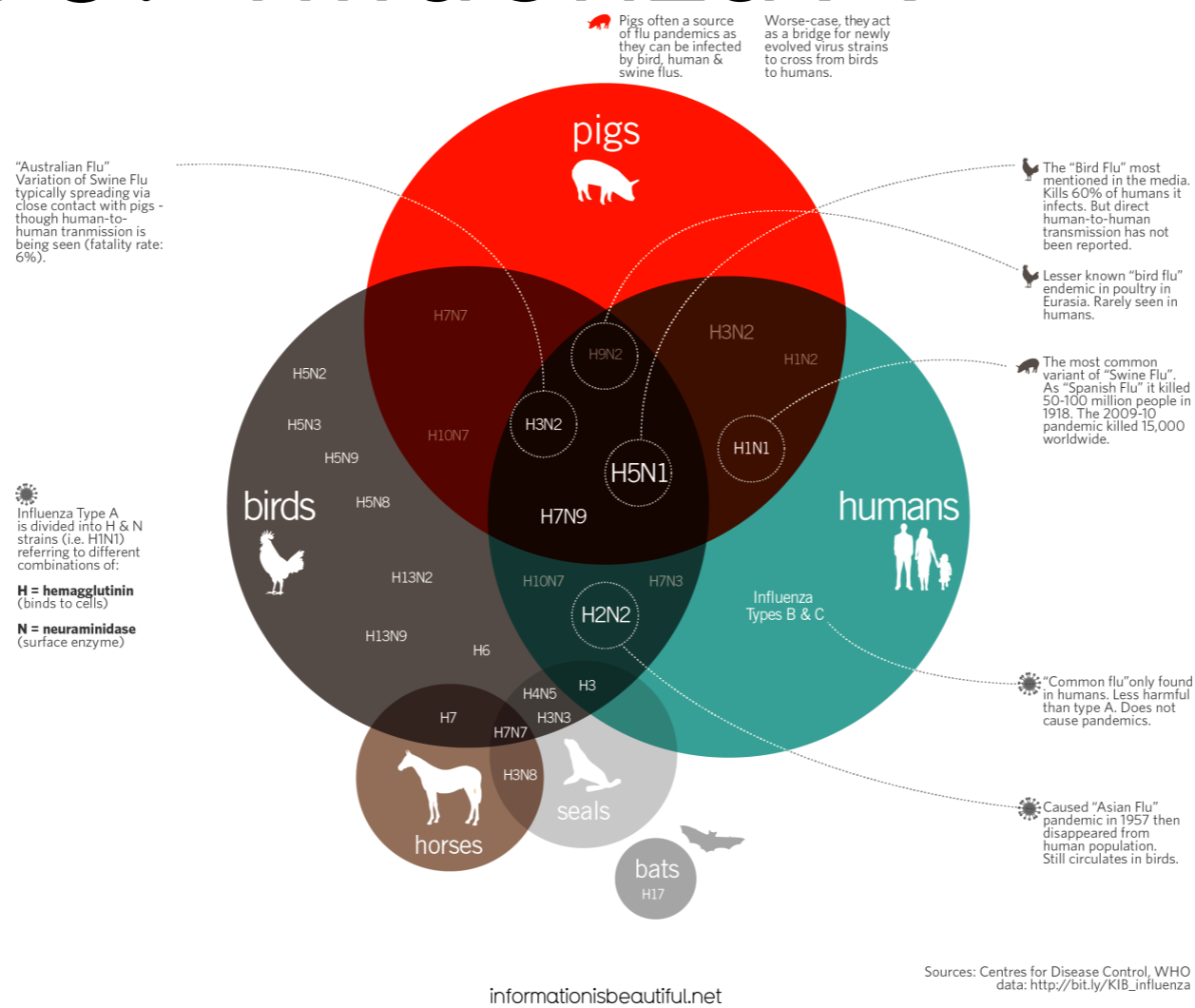
Legrand J, Grais RF, Boelle PY, Valleron AJ, Flahault A. Epidemiol Infect. 2007;135(4):610-21.



-Analyse the epidemic curves by fitting a compartmental model appropriate for Ebola and estimate  $R_0$ .

-compare the three different countries, different time windows, different compartmental models

# project 3: Influenza A



# project 3: Influenza A

## **2 types (A and B); 2 subtypes of type A (H3N2 and H1N1)**

### known facts about influenza A:

- Subtypes (strains) may have (slightly) different transmissibilities.
- Children and Adults have a different susceptibility to each strain: adults more immune than children; individuals more immune to strains that encountered early in life (antigenic seniority or antigenic sin)
- Social contacts structured by age: individuals enter in contact more with individuals of similar age; children have more contacts than adults.
- Subtypes interact with cross-immunity: after getting infected with a strain I become fully immune to that strain and partially immune to the other (cross-immunity lasts few months)
- Strain specific immunity wanes after some time (estimated to be between 1 to 7 years).

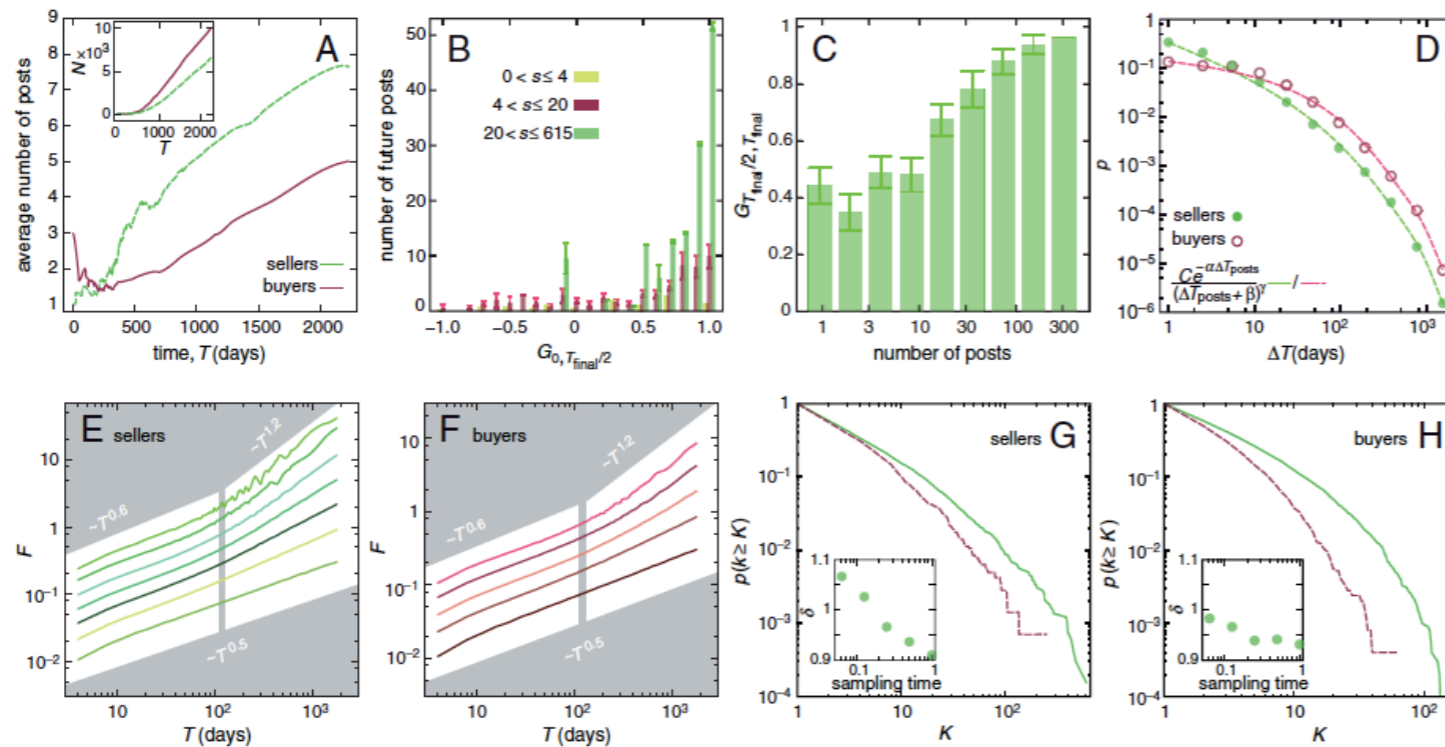
Study the competition between the two strains, considering two age-classes: children ( $\leq 15$  years old), and adults ( $> 15$  years old)

Identify the dominant strain as a function of the strain specific transmissibility and fraction of immune among the two age classes (also strain-specific)

Consider a single influenza season: account for full cross-immunity, and in a second moment partial cross immunity. Bonus: Account also for the waning of immunity

# project 4: STDs

Internet mediated prostitution: sexual contacts between 6,624 escorts and 10,106 sex buyers extracted from an online community



**Fig. 1.** Statistics of the dynamics of the community. (A) Time evolution of the average number of posts by sex buyers and about sex buyers. The *Inset* shows the growth in the number of sex sellers and sex buyers in the data. (B) The number of new posts according to the previous average grade at  $T_{\text{final}}/2 = 1,116$  days for three different activity levels, or total number of posts,  $s$ . The  $R^2$ -values of these data are 0.19 ( $0 < s \leq 4$ ), 0.29 ( $4 < s \leq 20$ ), and 0.33 ( $20 < s$ ). (C) The average future grade of sellers as a function of their number of contacts at half of the total sampling time (the data is logarithmically binned along the abscissa). (D) Shows the distribution of the time elapsed between two posts  $T_{\text{posts}}$  for buyers and sellers. Many posts were written during the same day, respectively,  $p(T_{\text{posts}} = 0) = 0.495$  and  $p(T_{\text{posts}} = 0) = 0.246$ . The distributions are well fitted by  $p(T_{\text{posts}}) = C \exp(-\alpha T_{\text{posts}}) = (T_{\text{posts}} + \beta)^\gamma$ , with:  $C = 2.9 \pm 0.5 \text{ days}^\gamma$ ,  $\alpha = 0.0023 \pm 0.0001 \text{ days}^{-1}$ ,  $\beta = 3.1 \pm 0.4 \text{ days}$ , and  $\gamma = 1.49 \pm 0.04$  (for sellers); and  $C = 12 \pm 8 \text{ days}^\gamma$ ,  $\alpha = 0.0021 \pm 0.0002 \text{ days}^{-1}$ ,  $\beta = 18 \pm 4 \text{ days}$ , and  $\gamma = 1.5 \pm 0.1$  (for buyers). (E) and (F) shows statistics the DFA fluctuation function as a function of the time-scale  $\Delta T$  for sellers and buyers, resp. The different curves correspond to different activity levels—from bottom to top they represent less than 3, 3–7, 8–20, 21–54, 55–148, 149–403, and more than 403 posts (about sellers or from buyers) resp. *Black Lines* are inserted for reference.  $T^{1/2}$  corresponds to uncorrelated interaction. (G) and (H) show degree distributions for sex sellers (G) and buyers (H) cumulative degree distributions for the full sampling time (*Solid Line*) and a yearlong window (starting one year after the full dataset; *Dashed Line*) for sex sellers and -buyers, resp. The *Insets* show the exponent of preferential attachment (Eq. 1).

Dataset made available  
[LEC. Rocha, et al, PNAS 2009]

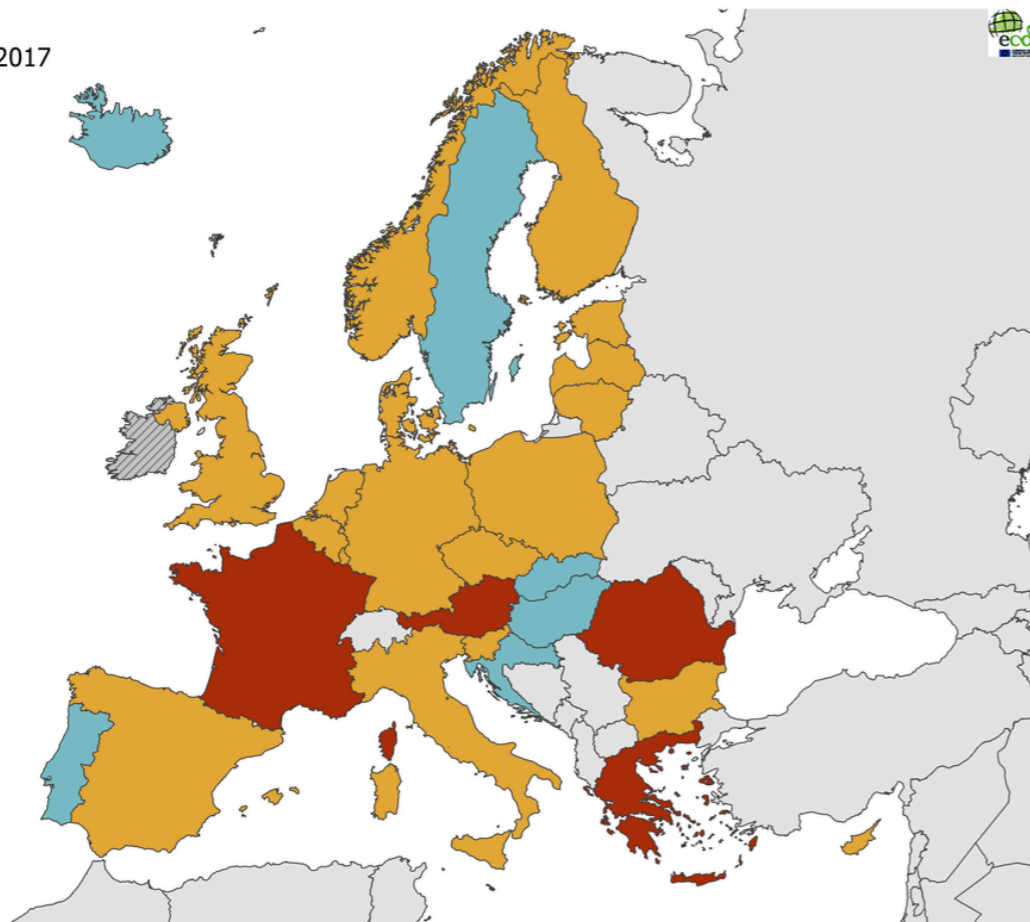
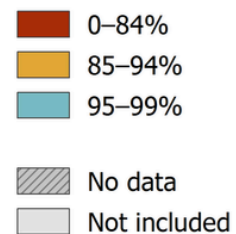
Study the impact of the structure of the network on the dynamics of an infection by comparing simulations on this network with simulations on randomized reference models

# project 5: measles

Vaccine hesitancy listed among the 10 top threats to global health by WHO. Key facts about measles:

- $R_0 = [15-20]$  - vaccination rate to attain eradication 95%
- mortality rate 0.1-0.3%
- 1998: AJ Wakefield publishes on Lancet a paper that links MMR vaccine to autism. The study was later found to be a deliberate fraud, the paper was retracted, Wakefield was struck off the UK medical register
- “pockets” of unvaccinated individuals

Coverage of second dose of measles-containing vaccine, 2017



Study the simultaneous spread of measles and a fake news regarding the measles vaccine. Design a suitable model and simulate its dynamics.

# project 6: measles & critical community size

In 1960, Bartlett defined the critical community size for measles as :

'the size for which measles is as likely as not to fade out after a major epidemic until reintroduced from outside, corresponding to a mean time to fade-out of about two years or about 30 in terms of average weekly notifications'.

[Bartlett MS Journal of the Royal Statistical Society Series A (General). 1960;123(1):37-44. ]

Things are much more complex if we account for realistic ingredients, e.g. spatial structure

Consider the simple case of two cities, with a certain number of individuals traveling from one city to another. Model measles and analyse what are the conditions of persistence / extinction of the disease. Explore in depth the role of mobility and population size.