



SCHOOL OF INFORMATICS  
AND COMPUTING

INDIANA UNIVERSITY  
Bloomington

*Pervasive Technology Institute*

# ***Predicting the behavior of techno-social systems***

**Alessandro Vespignani**



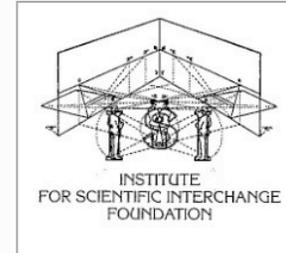
Center for Complex Networks  
and Systems Research

# Collaborators....



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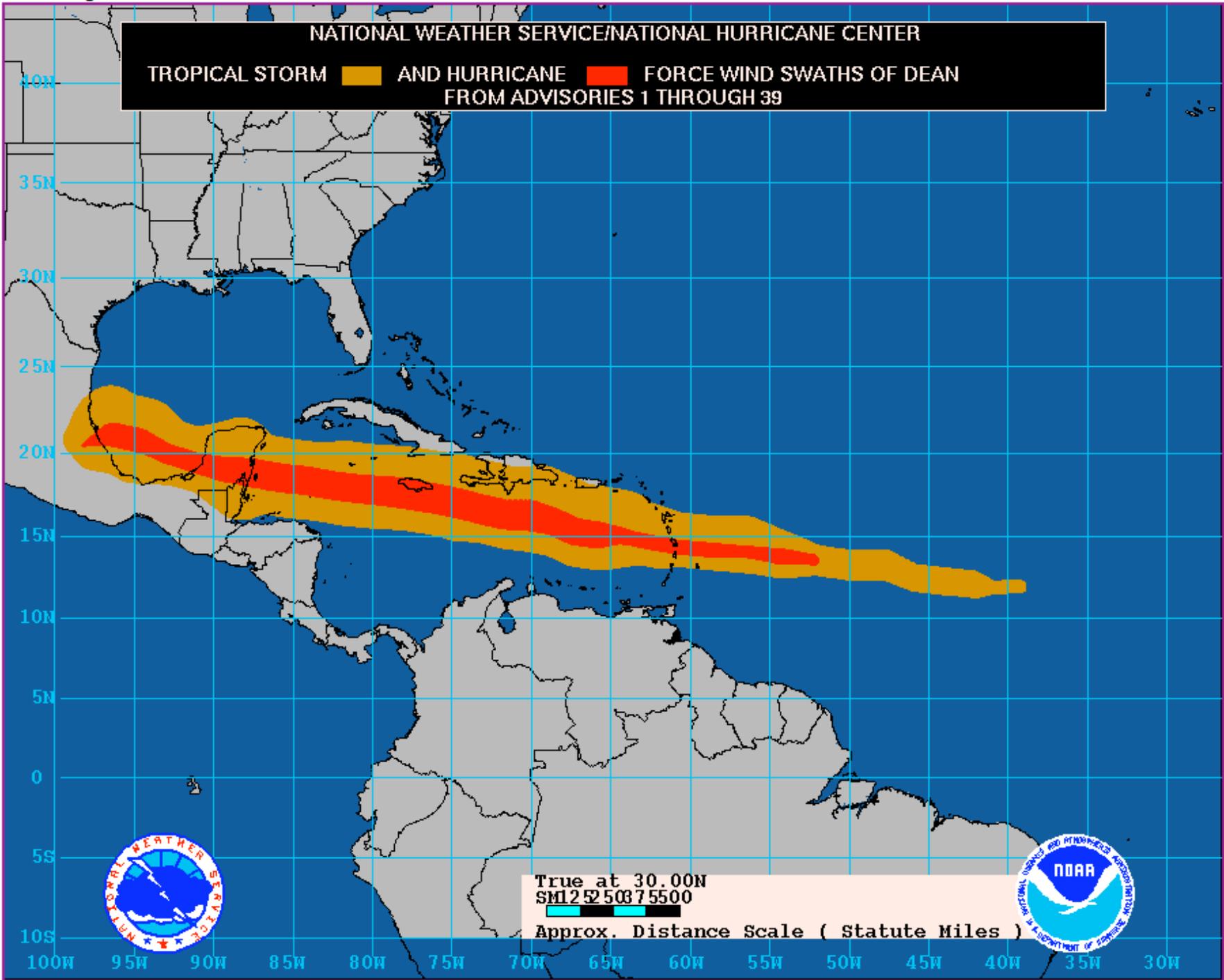


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NIH, DTRA, NAKFI,  
Lilly foundation, Abbott  
FET-program



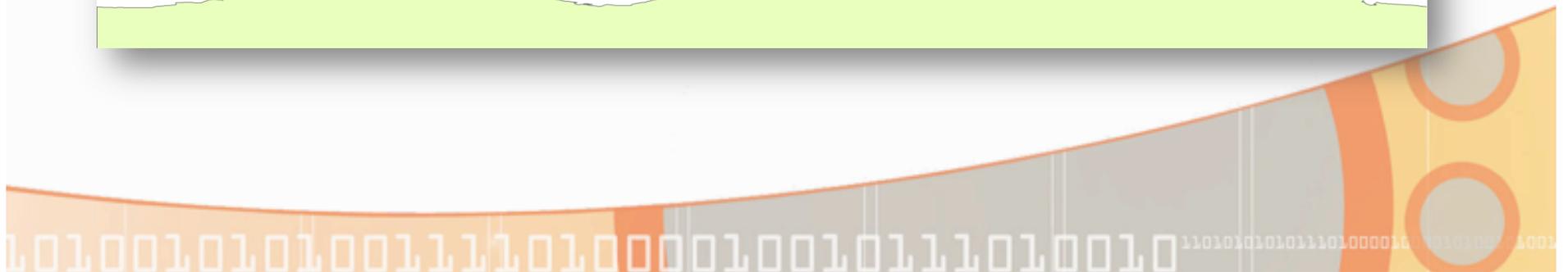
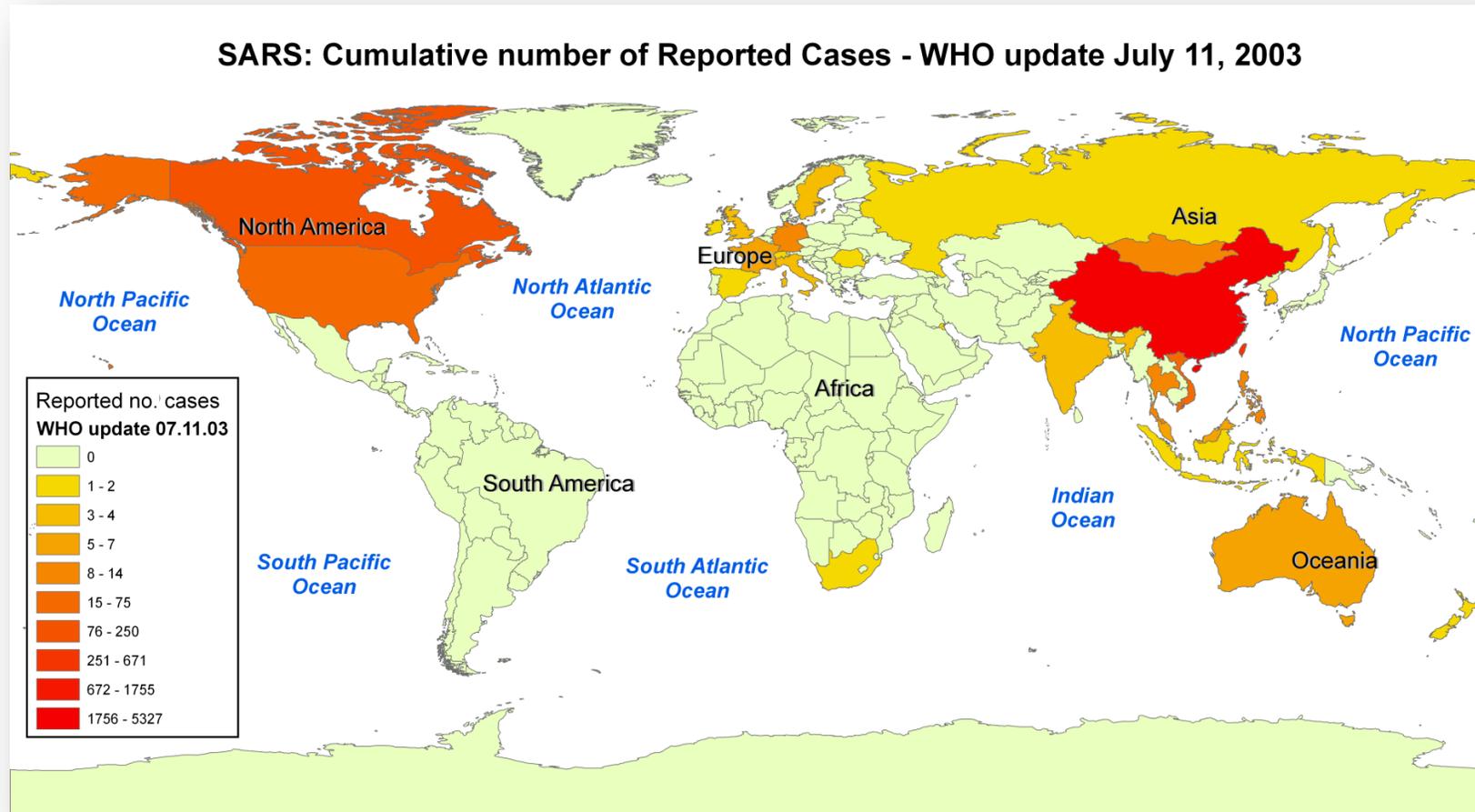
NATIONAL WEATHER SERVICE/NATIONAL HURRICANE CENTER  
TROPICAL STORM AND HURRICANE FORCE WIND SWATHS OF DEAN  
FROM ADVISORIES 1 THROUGH 39



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# Why we do not forecast pandemic evolution



# Collective Bio-Techno-social problems ....

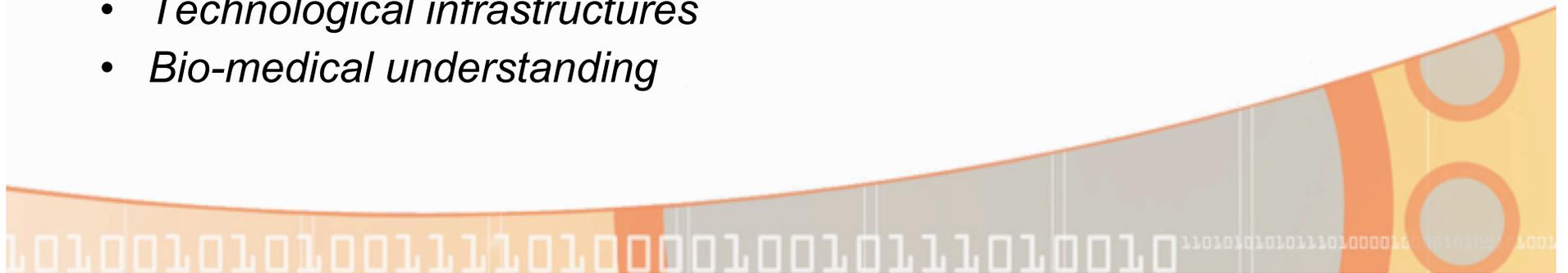
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## *In other words*

*The complete temperature analysis of the sea surface, and satellite images of atmospheric turbulence are easier to get than the large scale knowledge of commuting patterns or the quantitative measure of the propensity of a certain social behavior, or the spreading rate of a given pathogen.*

## *Complexity+complications*

- *large numbers of heterogeneous individuals*
- *over multiple time and size scales*
- *Non-linearity, threshold effects, discreteness, cooperation*
- *huge richness of cognitive/social science problems*
- *Technological infrastructures*
- *Bio-medical understanding*



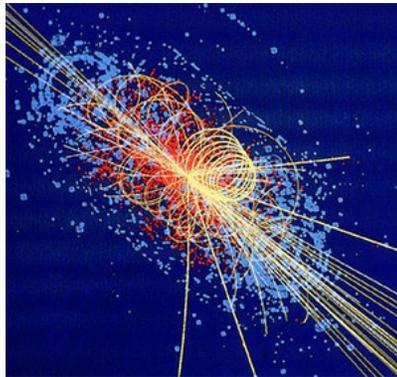
# Limits in the forecast of techno-social systems...

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- Lack of large scale-data on human behavior and social adaptation (>million individuals, worldwide dimension).
- Undersatnding of the feedback loop  
system behavior->prediction -> information+adaptation -> new system behavior...
- Formal models and understanding of social adaptation/ reaction during social disruptive events.
- Large scale characterization of interdependencies between technology, infrastructures and social behavior.

# WHY A MAJOR FUNDING EFFORT: IT AND THE SOCIETY “TOMOGRAPHY”

- × Data integration and assimilation
- × Mobile telephone and devices..
- × Web 2.0, Proxy networks
- × Pervasive and embedded technology/sensors



“Social collider” where the trace of human behavior can be harvested, characterized, rationalized....



Computational predictive tools to inform policy making, drawing scenarios, communicate to the public opinion, anticipate impact, produce knowledge

# UNPRECEDENTED AMOUNT OF DATA.....

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- ❑ Transportation infrastructures
- ❑ Behavioral Networks
- ❑ Census data
- ❑ Commuting/traveling patterns
  - ❑ Different scales:
    - ❑ International
    - ❑ Intra-nation (county/city/municipality)
    - ❑ Intra-city (workplace/daily commuters/individuals behavior)

# MAJOR OBSTACLES..

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- ❑ Many data layers (method/language divide)
- ❑ New computational tools (skill divide)
- ❑ Expertise/cultural divide
- ❑ Data sharing-practice divide
- ❑ Data Collection
- ❑ Ethics/security
  - ❑ Different scales:
    - ❑ International
    - ❑ Disciplines
    - ❑ methodology

# ETHICAL AND PRIVACY ISSUES

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- Geo-localization ✓
- Telephone logs ✓✓
- E-mail/social networks ✓✓✓
- Health data ✓✓✓✓

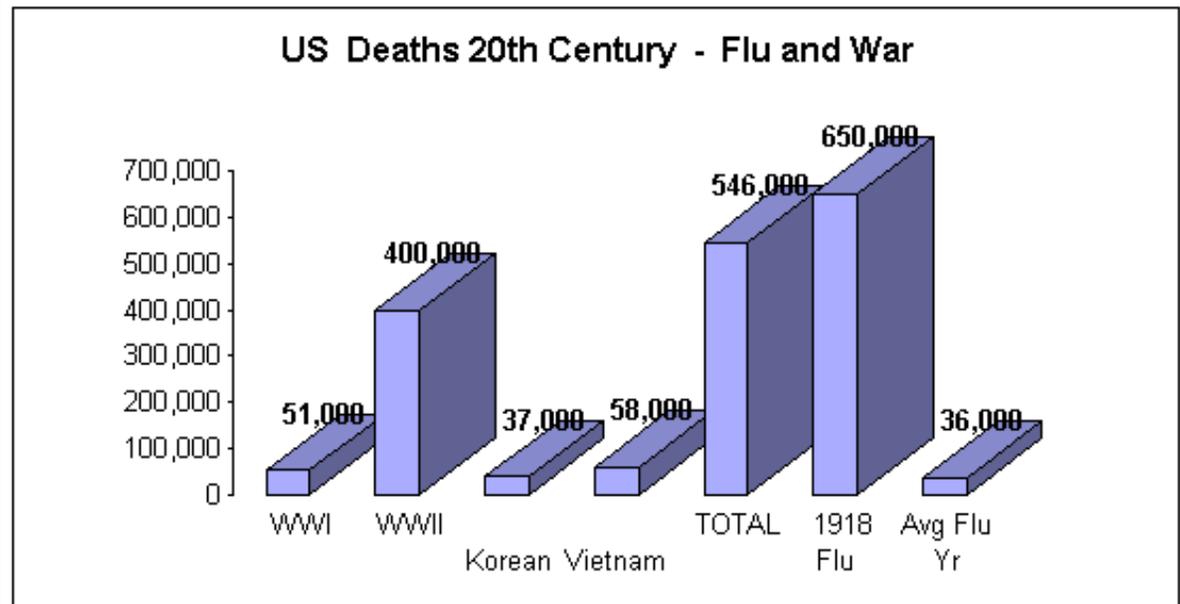
- **Research focus:**

From “social atom” or “social molecules” (i.e. small social groups) to the quantitative analysis of “social aggregate states”.

“social aggregate states”= large-scale social systems consisting of millions of individuals that can be characterized statistically in space (geographic and social) and time.

# 1918 Pandemic

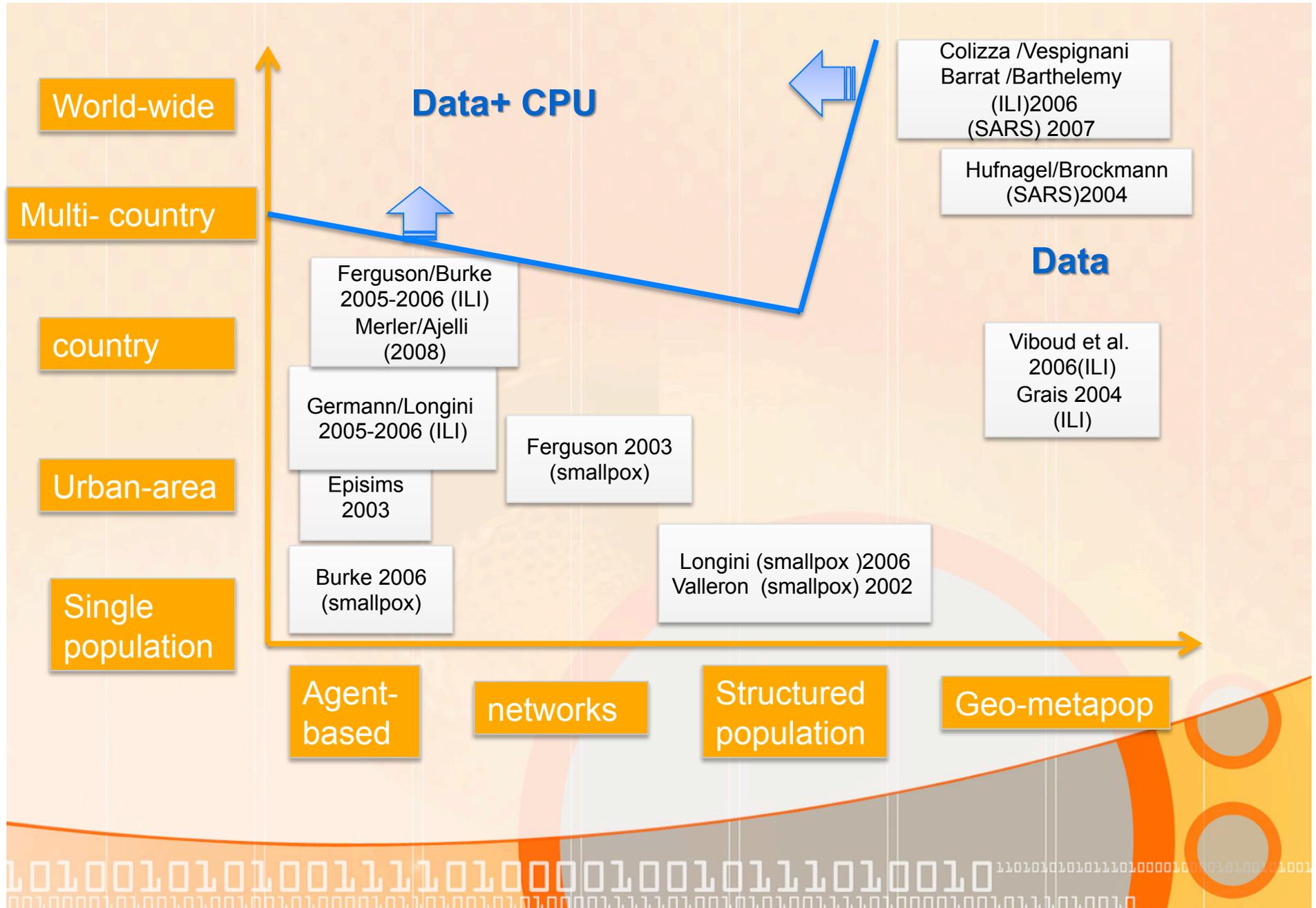
- An estimated 50 million people, about 3% of the world's population (approximately 1.6 billion at the time), died of the disease.
- An estimated 500 million, or 1/3 were infected.[5]
- In the U.S., about 28% of the population suffered, and 500,000 to 675,000 died



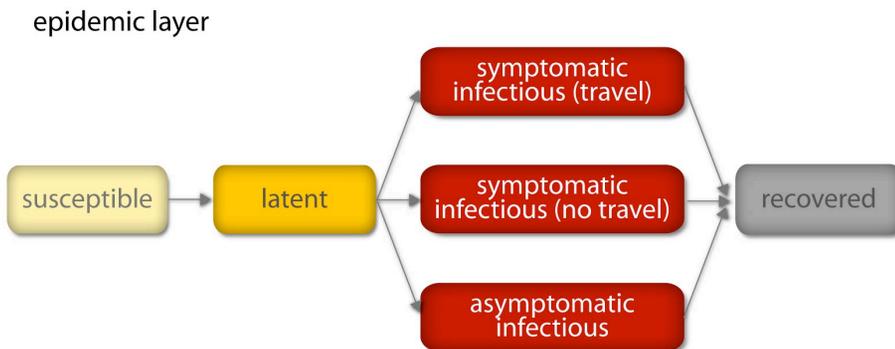
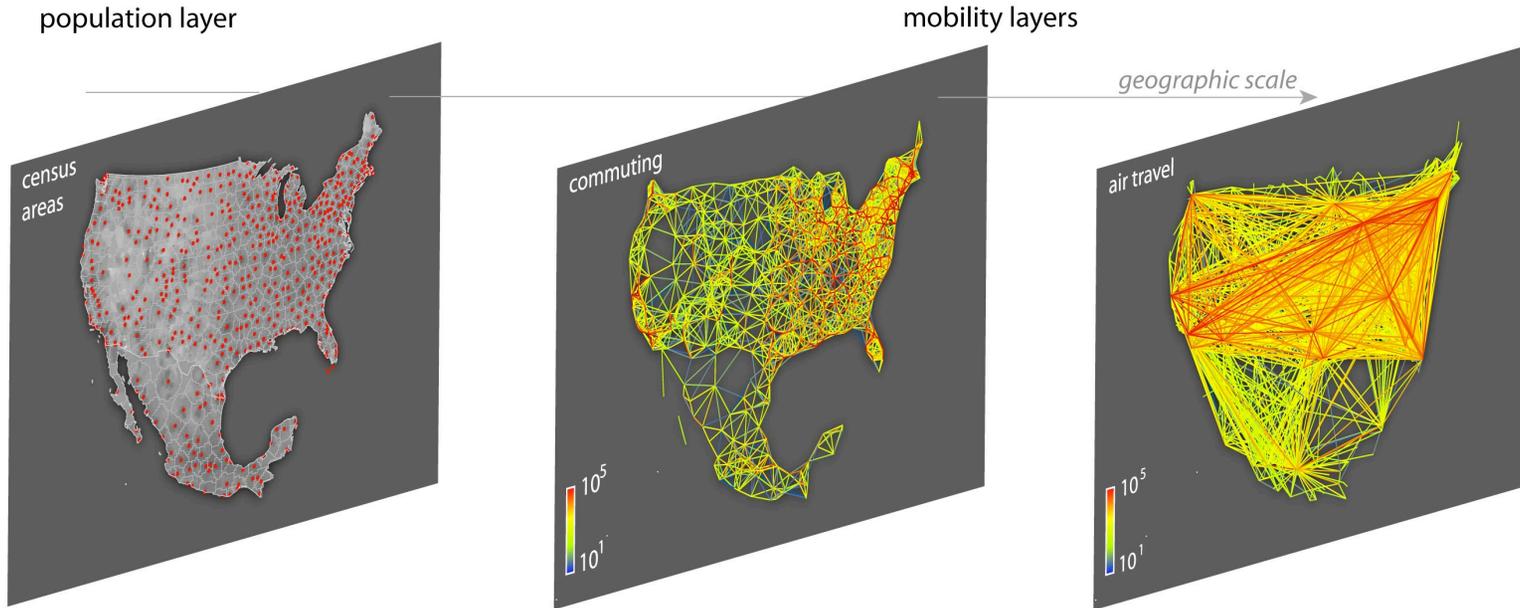
# Pandemics & Travel

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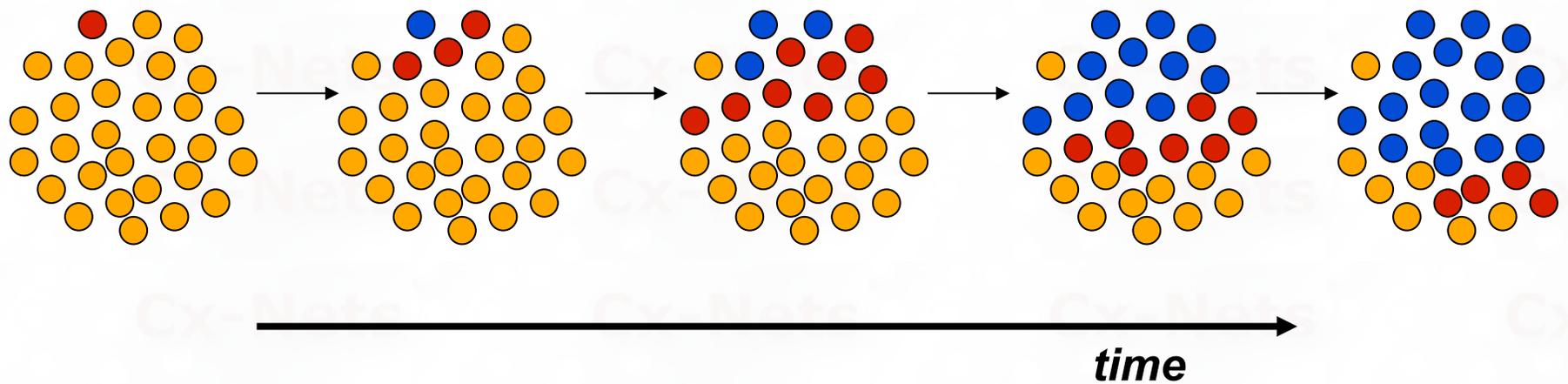
# Large scale computational model...GLEaM



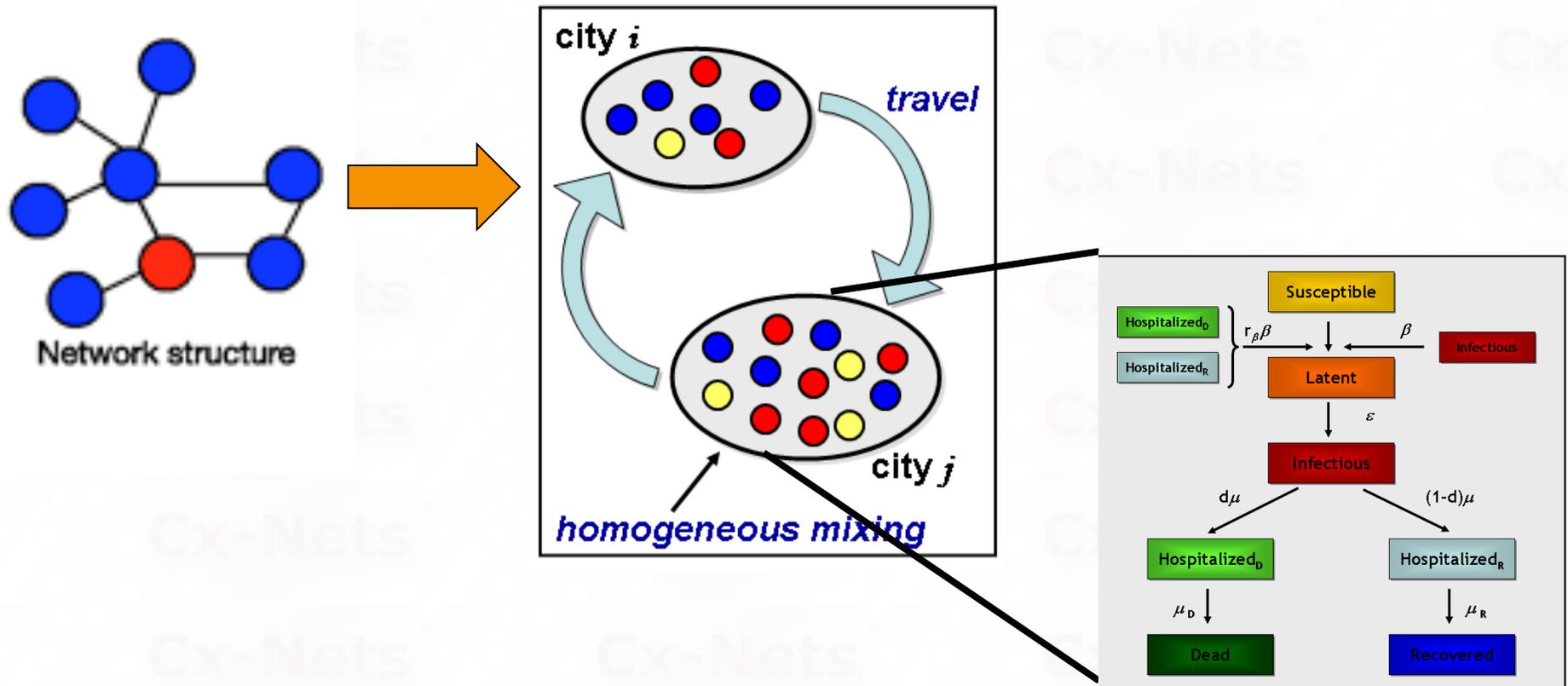
Parameter	Value	Description
$\beta$	from $R_0$	transmission probability
$\varepsilon^{-1}$	1.9 [1.1-2.5] d	average latency period
$\mu^{-1}$	3 [3-5] d	average infectious period
$p_t$	50%	probability of traveling for infectious individuals
$p_a$	33%	probability of being asymptomatic
$r_\beta$	50%	relative infectiousness of asymptomatic infectious individuals



# INTRA-POPULATION: THE **SIR** MODEL

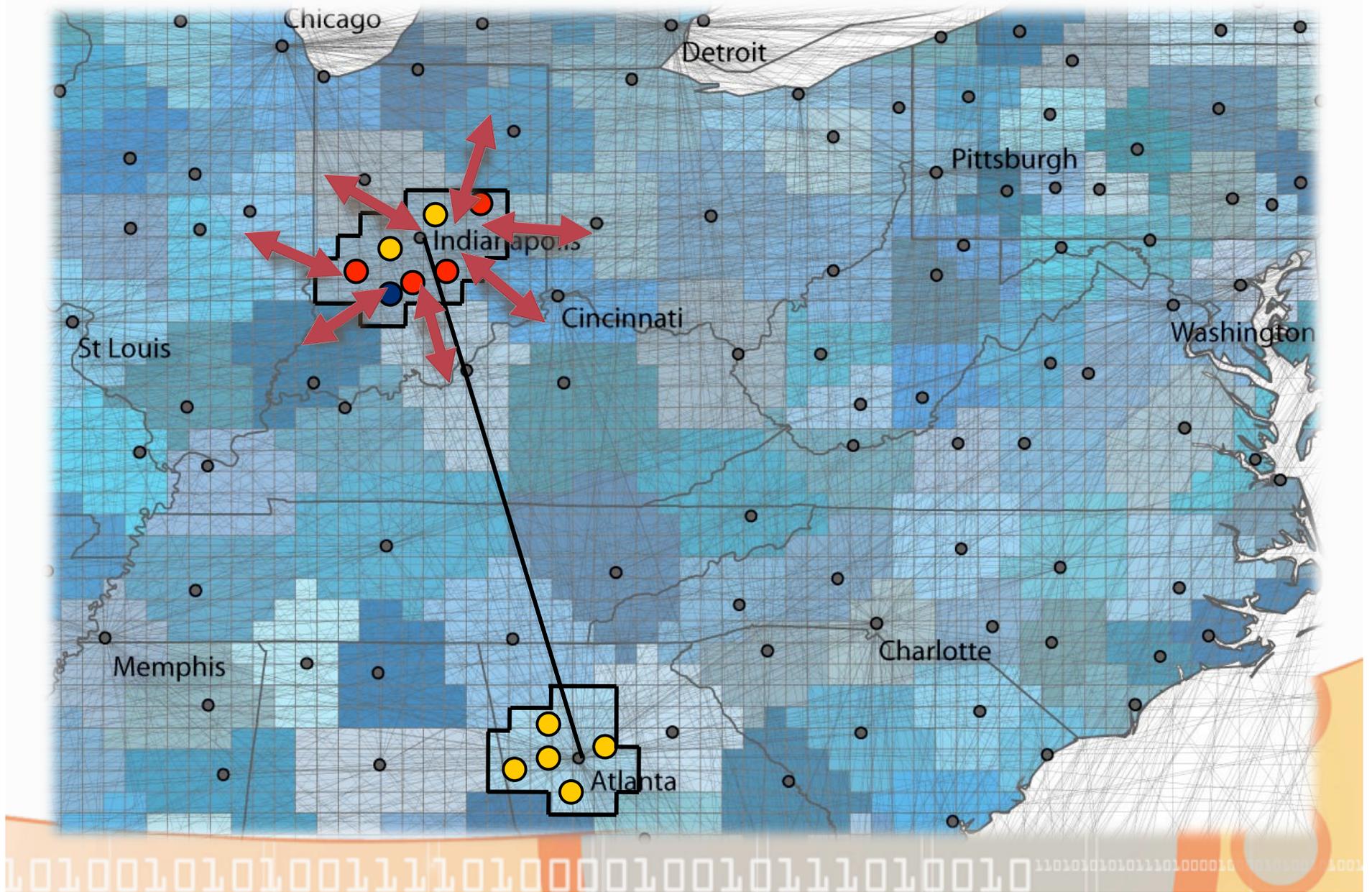


# Mechanistic metapopulation models...



Intra-population infection dynamics

# Long and Short range mobility (I)



# COMPLEX MOBILITY AND TRAFFIC NETS....

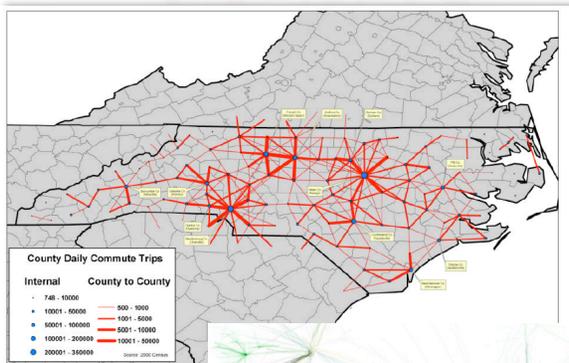
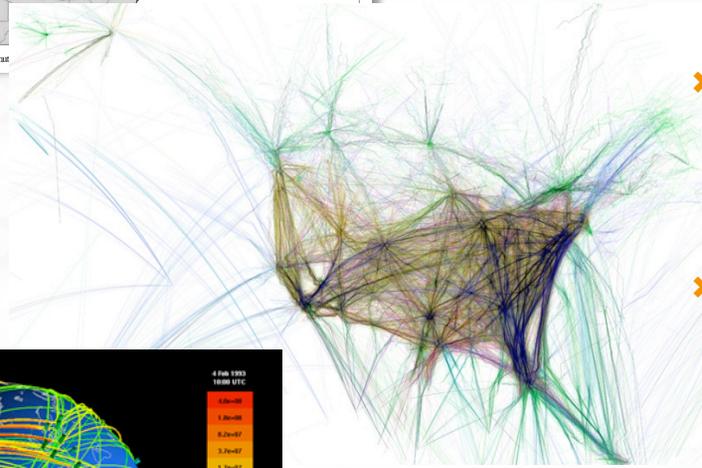
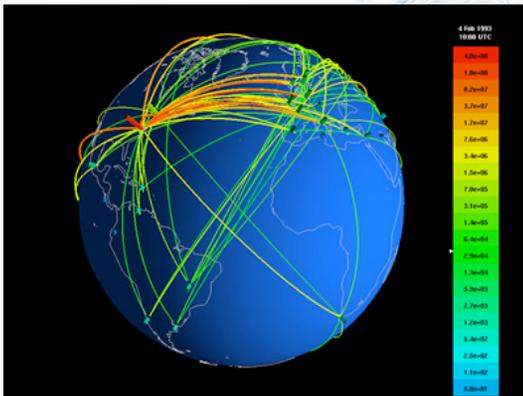


EXHIBIT A - North Carolina County-to-County Commute



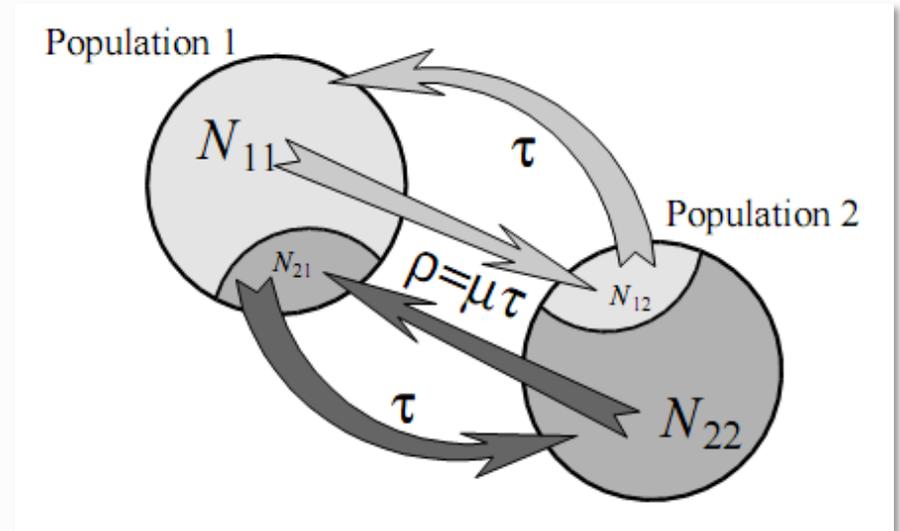
- ✗ spatially structured models depend on the notion of identifiable populations in a meta-population.
- ✗ For instance, cities, town and villages (on a smaller scale schools, workplaces) and homes, cell tower, WiFi base station area range, etc.
- ✗ intuitive segmentations is often fuzzy, ill defined, arbitrary and lacks a systematic backbone.
- ✗ How much geography, cultural diversity, spatial and technological variability is encoded in the topology and mobility/diffusion of multi-scale networks
- ✗ Which are the topology and traffic/flows statistical properties of real world networks.



# Time scale separation technique

(Sattenspiel & Dietz 1995)  
(Keeling & Rohani, 2002)

- *Theoretical description of reaction diffusion processes with memory and “return rates”.*
- *define  $\mu = \rho / \tau$  (leaving rate / returning rate),*
- *$N_{ij}$ : population in  $i$  who is visiting region  $j$*
- *$N_{ii}$ : population in  $i$  who is actually present in the home region*

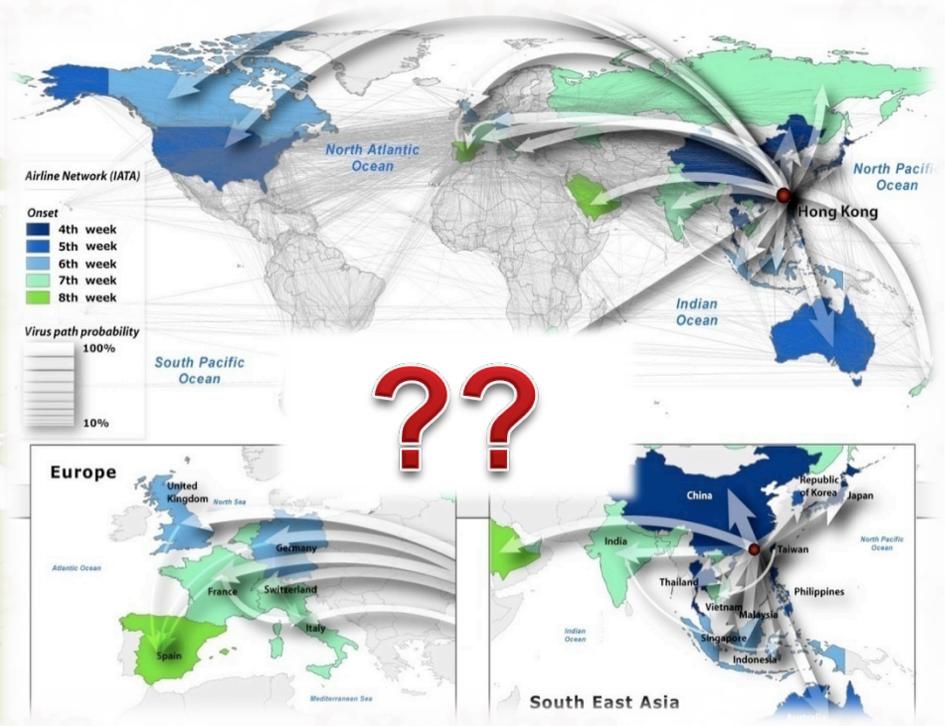
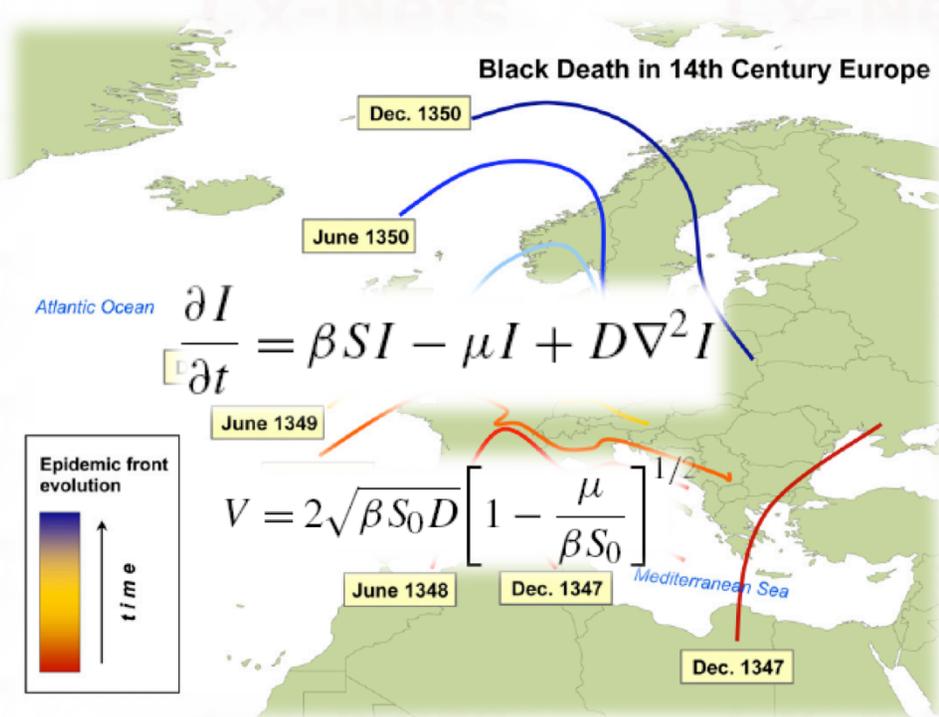


Time scale separation  $\mu \ll 1$  ; heterogeneous population sizes

$$\begin{aligned}
 p_\ell^D(S \rightarrow L) &= \frac{\beta_\ell}{(1 + \tilde{\mu}_\ell)N_\ell^*} \left[ \frac{r_\beta I_\ell^a + I_\ell^t}{1 + \tilde{\mu}_\ell} + I_\ell^{nt} + \sum_k \frac{\tilde{\mu}_k \tilde{\nu}_{k\ell}}{1 + \tilde{\mu}_k} (r_\beta I_k^a + I_k^t) \right] \Delta t \\
 &+ \sum_k \frac{\beta_k \tilde{\mu}_\ell \tilde{\nu}_{\ell k}}{(1 + \tilde{\mu}_\ell)N_k^*} \left[ \frac{r_\beta I_k^a + I_k^t}{1 + \tilde{\mu}_k} + I_k^{nt} \right] \Delta t
 \end{aligned}$$

# BLACK DEATH IN 1347: A CONTINUOUS DIFFUSION PROCESS

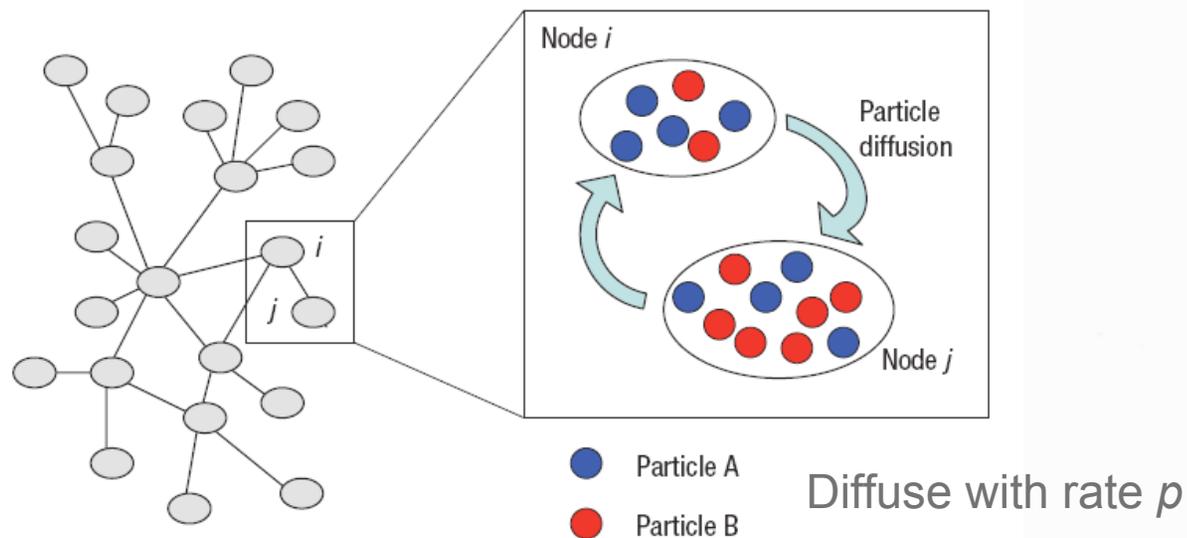
# SARS EPIDEMICS: A DISCRETE NETWORK DRIVEN PROCESS



# NETWORKS AND NETWORK THINKING

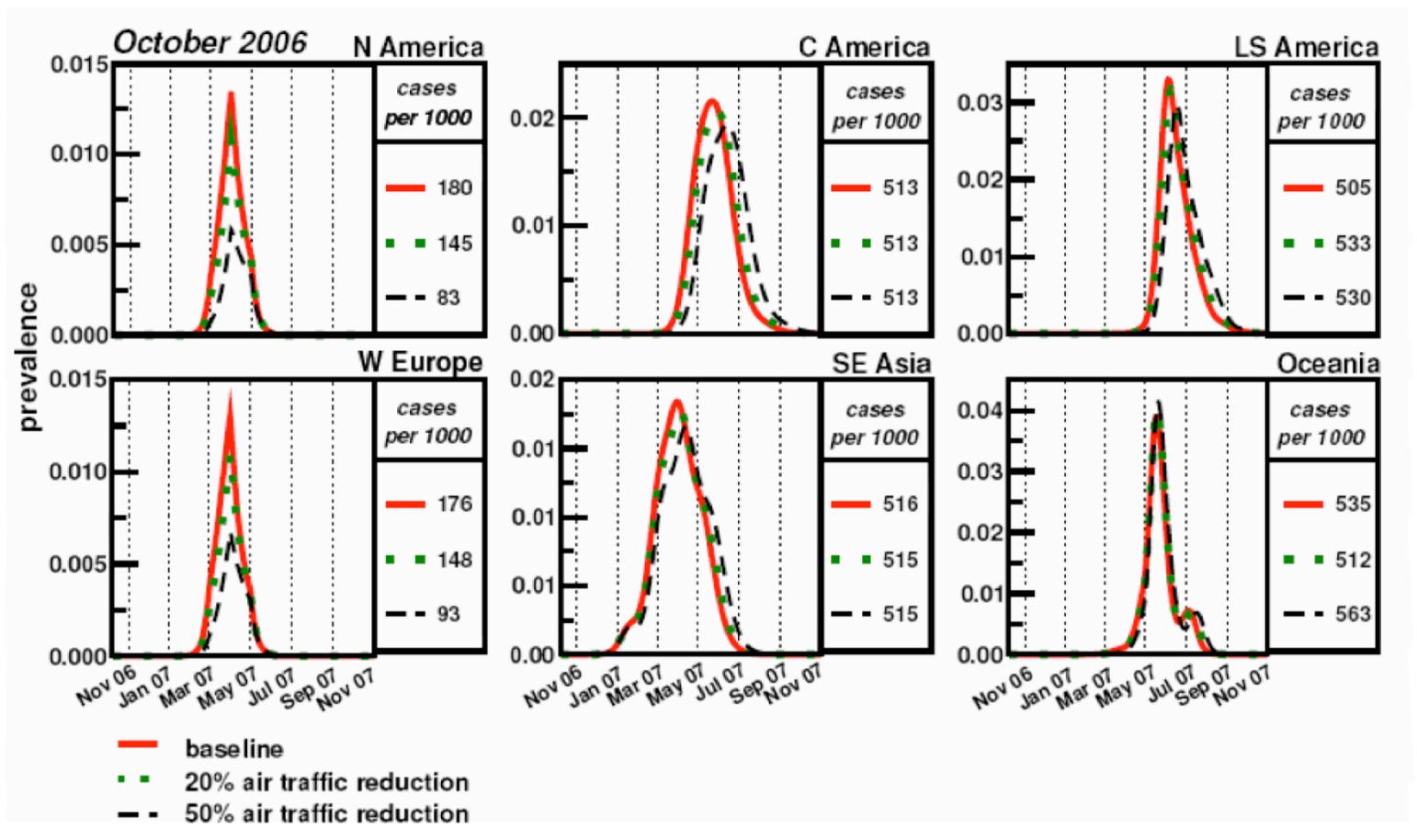
# Complex networks approach

- Understanding of non-linear/tipping points due to the complexity of the network system
  - Global Threshold and Mobility reduction,
  - Epidemic pathways,
  - mitigation-vs-containment



# PROTOTYPICAL RESULT

## ✘ Travel restriction inefficacy



# THEORETICAL FINDING....VS REAL WORLD DATA

$$p_c \bar{N} \geq \frac{\langle k \rangle^2}{\langle k^2 \rangle} \frac{\mu R_0^2}{2(R_0 - 1)^2}$$



	Airport network
Average population $N$	$\approx 10^5$
$\langle k \rangle^2 / \langle k^2 \rangle$	$\approx 10^{-1} - 10^{-2}$
$\mu$	1/3
$R_0$	1.1
$p_c$	$\approx 10^{-5} - 10^{-6}$
$p_{real}$	$\approx 10^{-3} - 10^{-4}$

Tenfold traffic reduction is needed to achieve containment effects

## What's in GLEaM...

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- Refined census data (up to 2.5 arc/min resolution)
- IATA/OAG airline database
- Commuting data for about ~35 countries in 5 continents (definition of a world-wide commuting networks)
- Disease structure and population heterogeneity.
- Multiscale force of infection
- Intervention scenarios (vaccination, contact tracing, secondary infections, quarantine..)



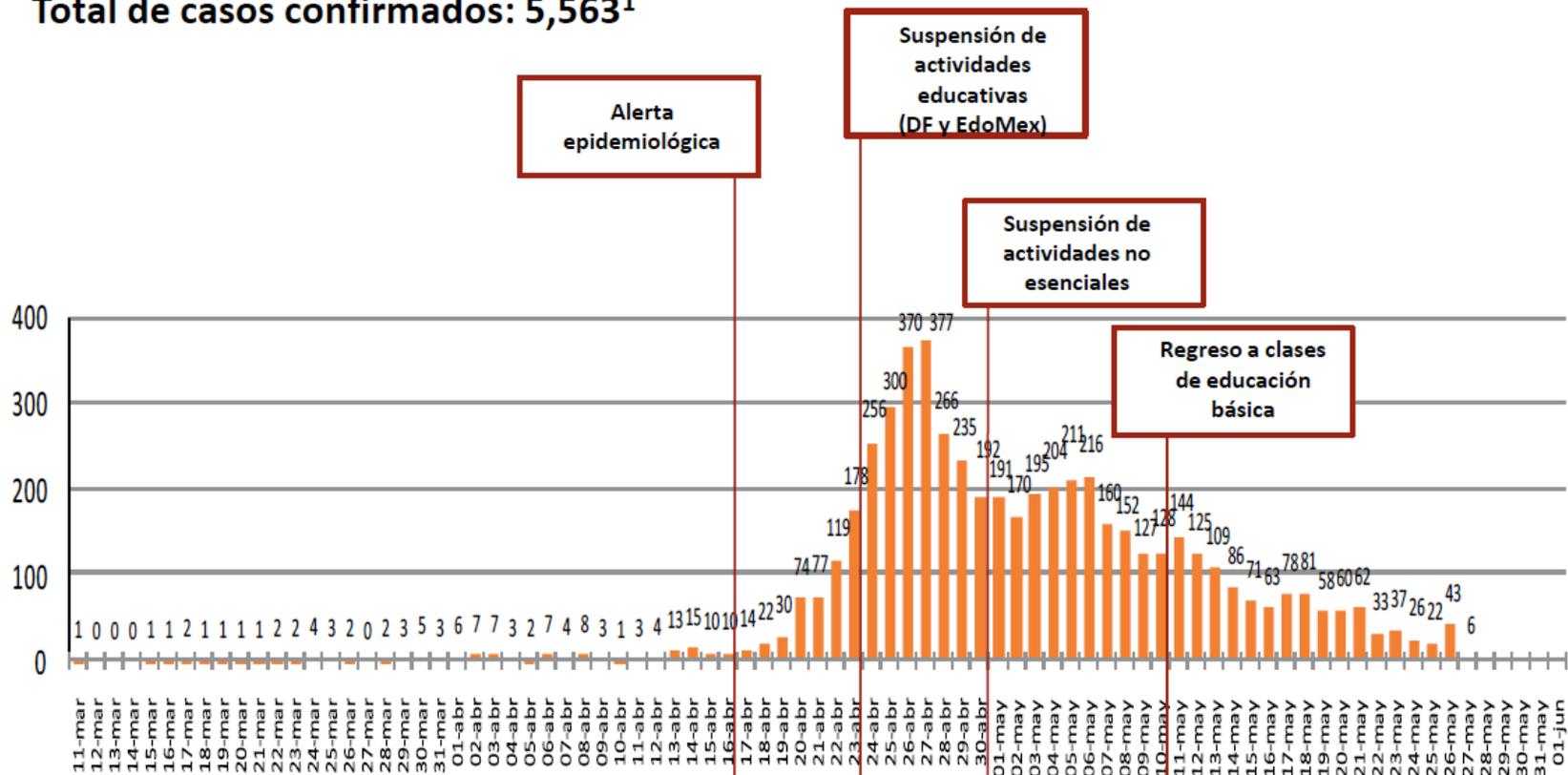
# H1N1 epidemic (Feb. 2009, Mexico):

Can we do projections in real time ?

What we need to do projections?

Are projections reliable?

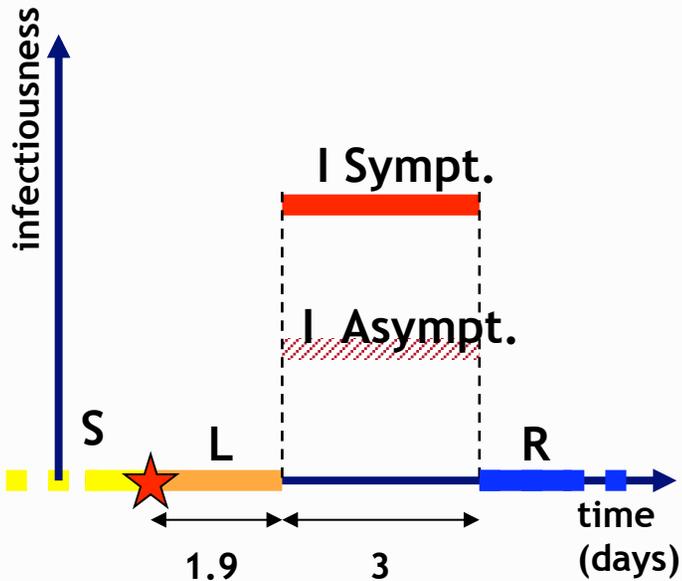
Total de casos confirmados: 5,563<sup>1</sup>



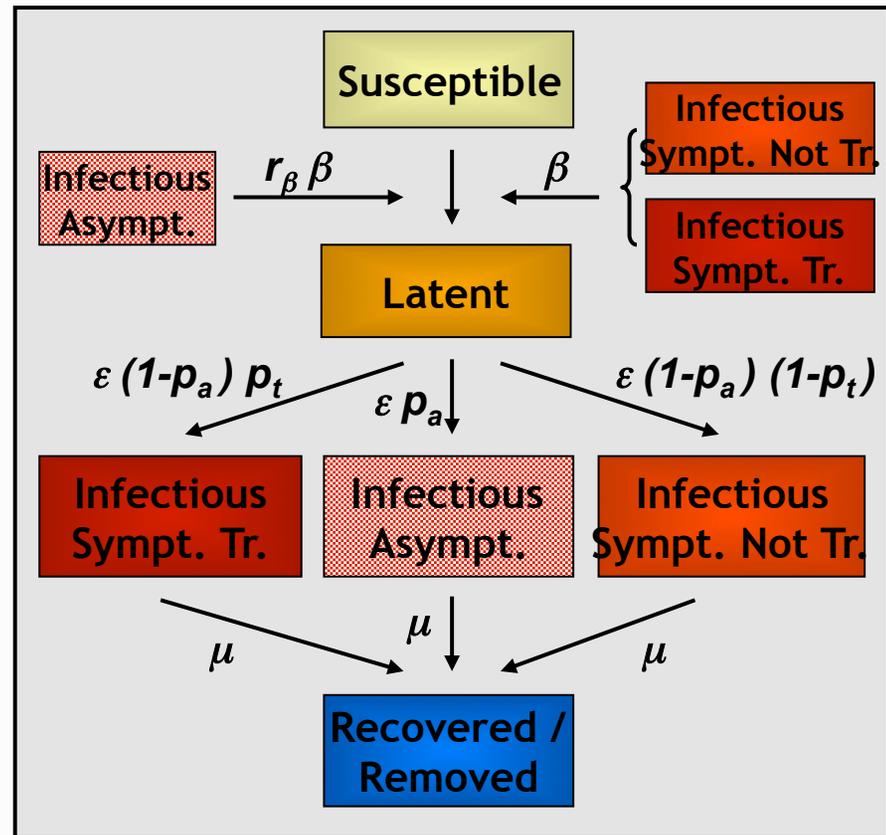
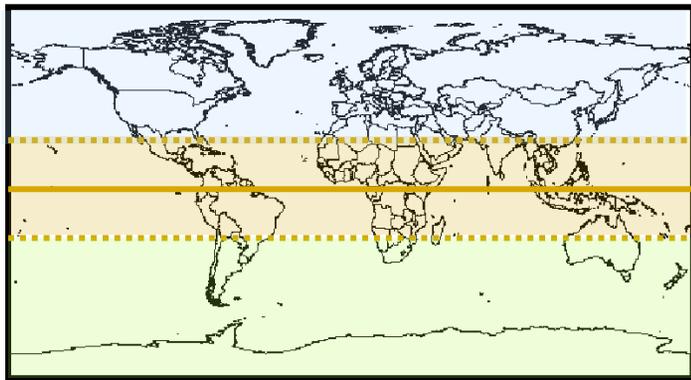
# Influenza Transmission



# Scenarios and policy making



Seasonality



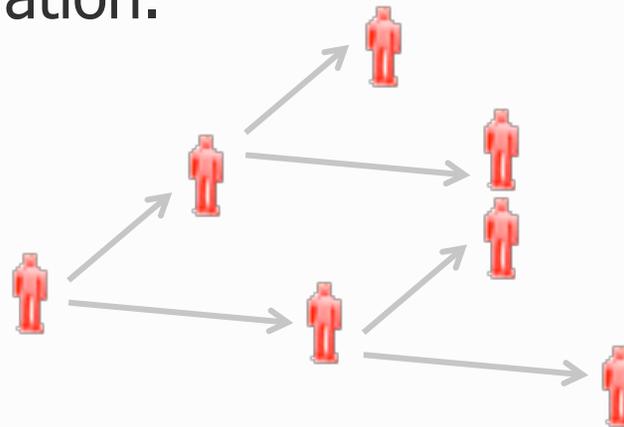
Longini et al. Am. J. Epid. (2004)



# Epidemic evolution

**reproductive number  $R_0$**  : average # of infectious individuals generated by one infected in a fully susceptible population.

e.g.  $R_0=2$



**pandemic influenza:  $R_0$  unknown**

Choose transmission scenario

2

mild

$R_0=1.5$

medium

$R_0=1.9$

high

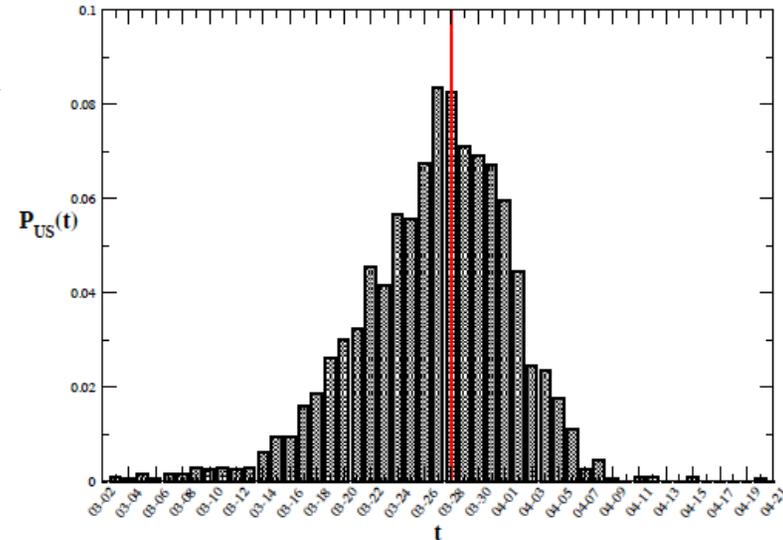
$R_0=2.3$

very high

$R_0=2.7$

# Monte Carlo Likelihood analysis (BMC Medicine 7,45 (2009))

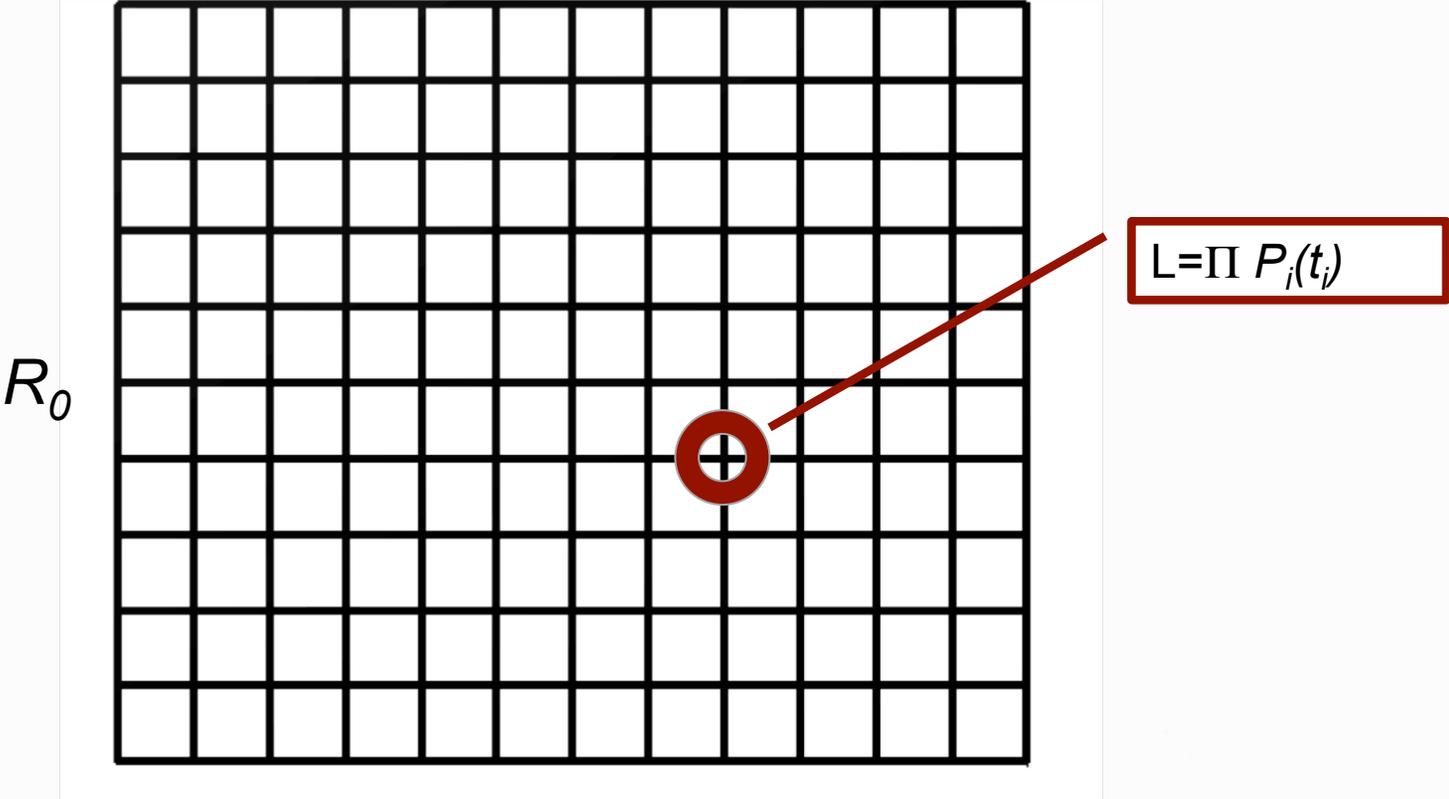
- Probability of arrival in each country depend depend on the disease parameter  $R_0$
- For each set of parameter we can use a Monte Carlo estimate of the arrival time distribution.
- We can therefore construct the likelihood function and then maximize it to find the best estimate of  $R_0$
- Just one problem:  
We need to simulate  $10^6$  epidemics for a total of 50 Terabyte of data and 2Million minutes of state-of-the-art CPU time.



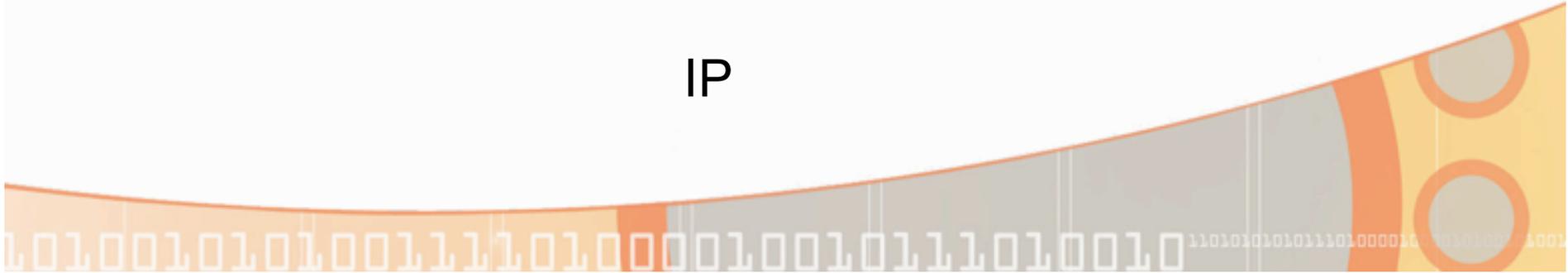
Country	Onset of symptoms	Flight arrival	Confirmed on
United States	March 28 [20]	–	April 21 [20]
Canada	April 11 [21]	April 8 [22]	April 23 [23]
El Salvador	–	April 19 [24]	May 3 [25]
United Kingdom	April 24 [26]	April 21 [27]	April 27 [23]
Spain	April 25 [28]	April 22 [29]	April 27 [23]
Cuba	–	April 25 [30]	May 13 [23]
Costa Rica	April 25 [31]	April 25 [31]	May 2 [23]
Netherlands	–	April 27 [32]	April 30 [32]
Germany	April 28 [33]	–	April 29 [23]
France	–	–	May 1 [34]
Guatemala	May 1 [35]	–	May 5 [36]
Colombia	–	–	May 3 [37]



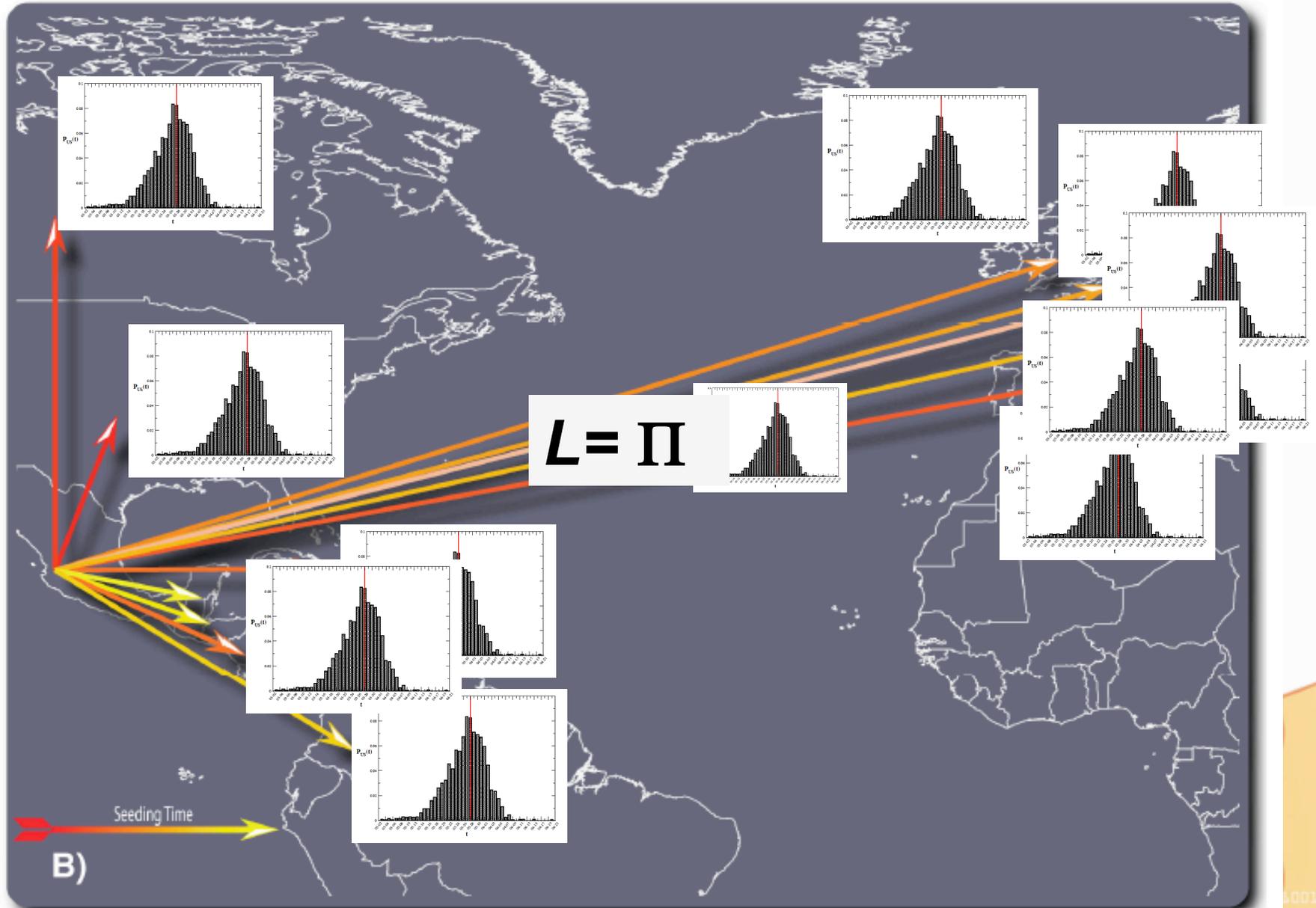
# Monte Carlo likelihood sampling



IP

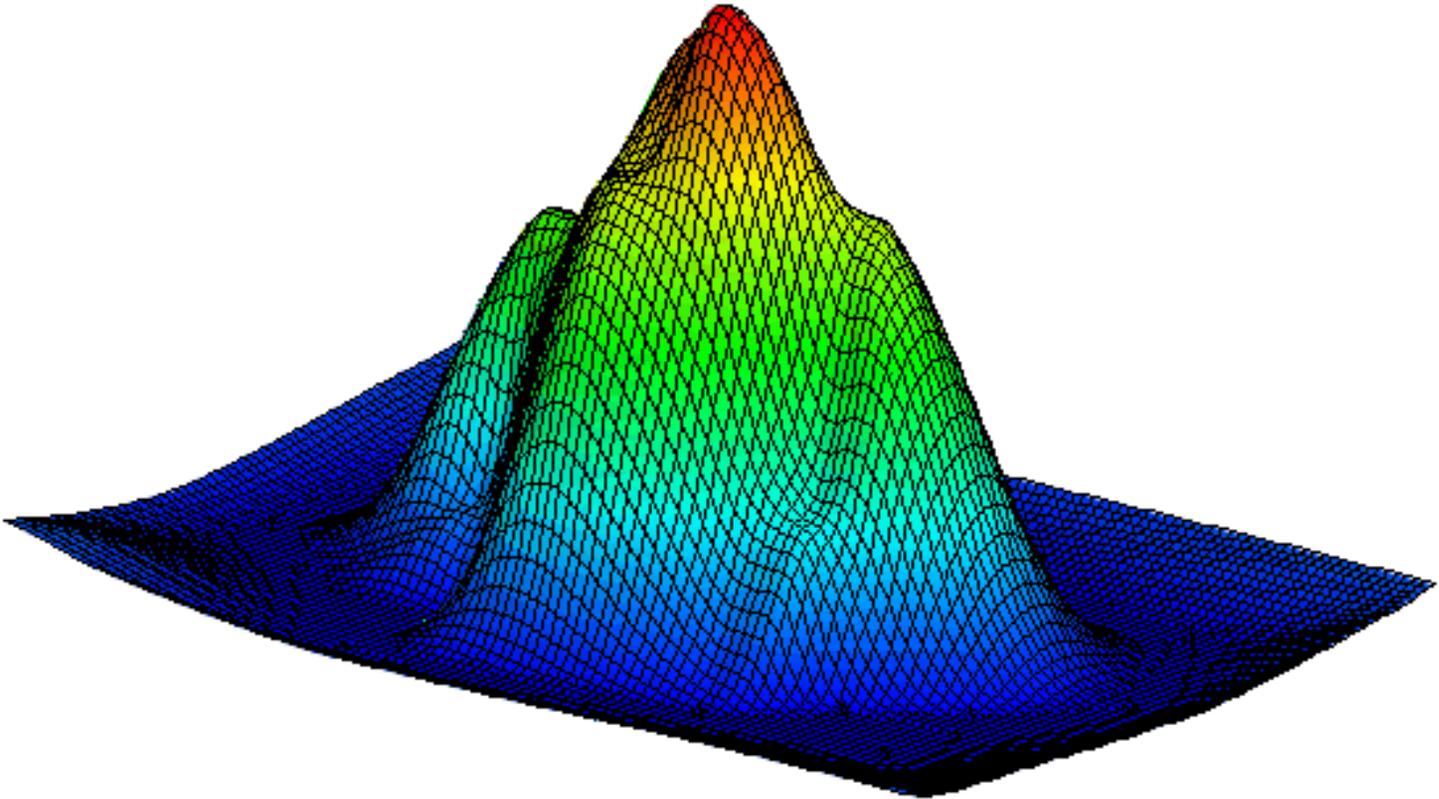


# Parameter set likelihood



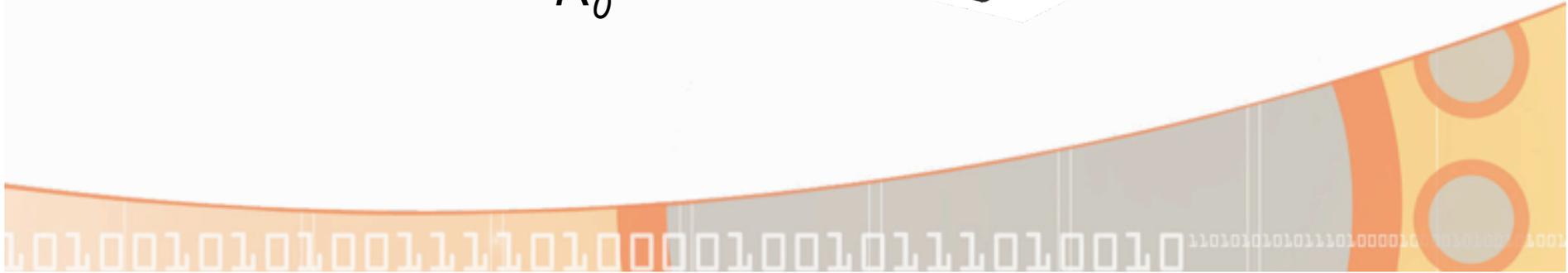
B)

# Monte Carlo likelihood sampling



$R_0$

IP

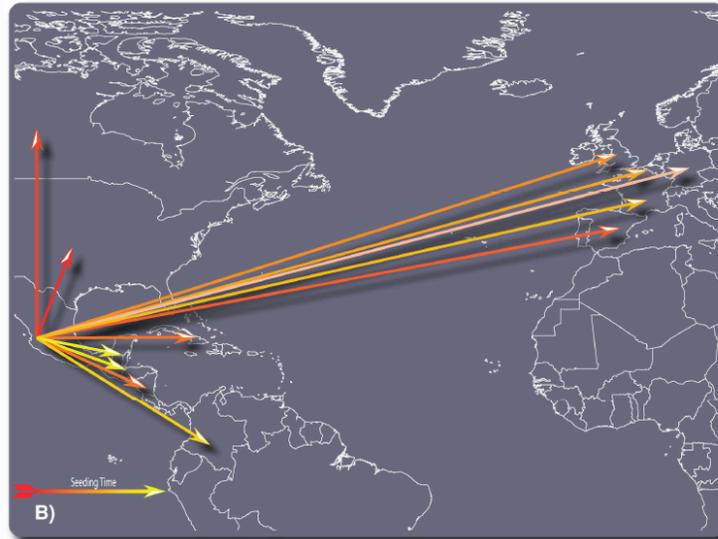


# Parameter estimates

Parameter	Best Estimate	Confidence Interval	Description
$R_0$			number
$G_t$	<b>Month</b>	<b><math>R(t)</math> in Northern hemisphere</b>	ne (days)
$\mu^1$			riod (days)
$\alpha_{min}$	May	[1.19-1.49]	asonality
	June	[1.07-1.33]	
	July	[1.05-1.24]	
	August	[1.07 - 1.33]	on
$\varepsilon^1$	September	[1.19 - 1.49]	od (days)
$\alpha_{max}$			seasonality rescaling



# Anticipate the spreading pattern



- Repeated stochastic realizations  $\sim 10^5$
- For each subpopulation pair we define  $p_{ij}$  as the probability of infection transmission from  $i$  to  $j$ .
- Define a distance
- The minimum spanning tree is then calculated using Chu-Liu-Edmunds Algorithm.

# A test and ....what happened in Mexico

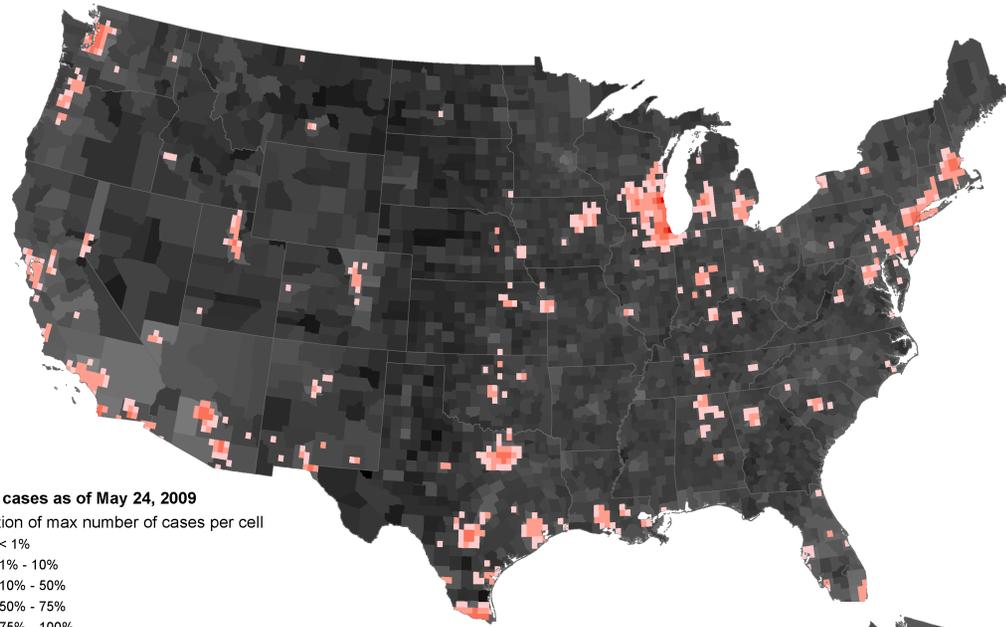
Number imported cases (May 8th)	USA	UK	France	Germany	Brazil
Simulation Results	0 - 534	0 - 44	0 - 62	0 - 55	0 - 45
Surveillance data	85 (170)	17	11	9	3

**Table 1. - Cumulative number of imported cases from Mexico shown as the 99% reference range over 2,000 realizations on May 8 for a few countries.** The simulations are obtained with the best estimate

	Number of symptomatic cases in Mexico (Apr. the 30th)
Simulation Results	[121,000 - 1,394,000]
Lower bound range of Ref. [6]	113,000-375,000
Estimate of Ref. [5]*	2,000 – 280,000
Mexican official report [7] (confirmed cases)	3,350

**Table 2. Predictions of GLEaM for the size of the epidemic in Mexico on April 30 in thousands of cases and comparison with other approaches and with empirical data.** The simulations are obtained with

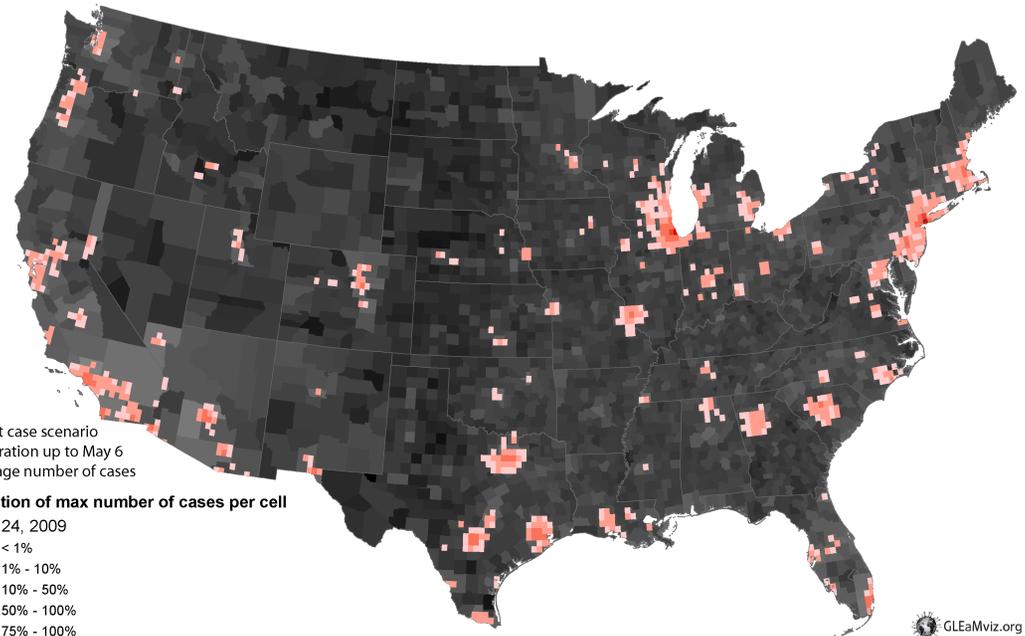
# Anticipate where and when



Real cases as of May 24, 2009

Fraction of max number of cases per cell

- < 1%
- 1% - 10%
- 10% - 50%
- 50% - 75%
- 75% - 100%



Worst case scenario  
Calibration up to May 6  
Average number of cases

Fraction of max number of cases per cell

May 24, 2009

- < 1%
- 1% - 10%
- 10% - 50%
- 50% - 100%
- 75% - 100%

# Where and when continued.....

Estimation of the seasonality rescaling against the arrival time in 96 countries.

Region	Estimated activity peak time
North America	[Sept 25 - Nov 09]
Western Europe	[Oct 14 - Nov 21]
Lower South America	[Jul 30 - Sep 06]
South Pacific	[Jul 28 - Sep 17]

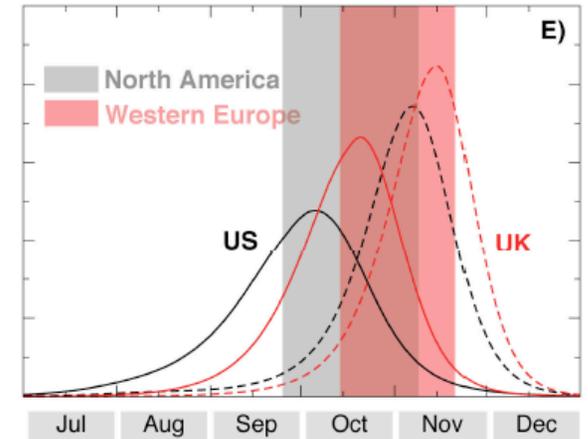
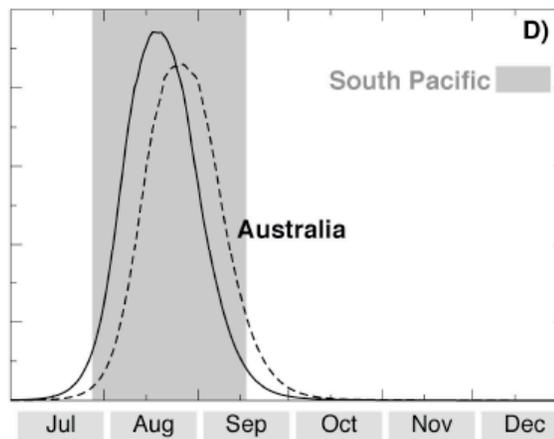
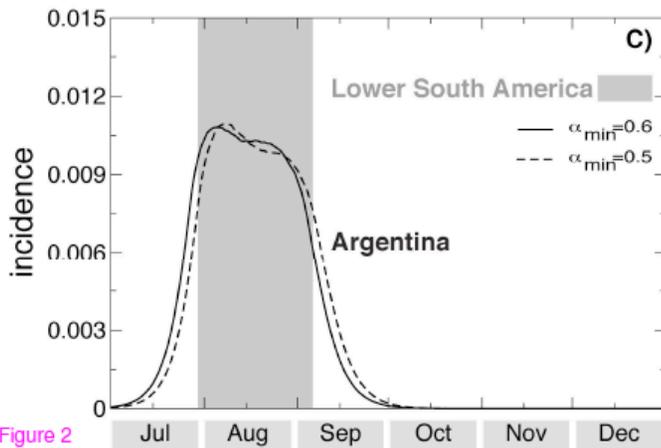
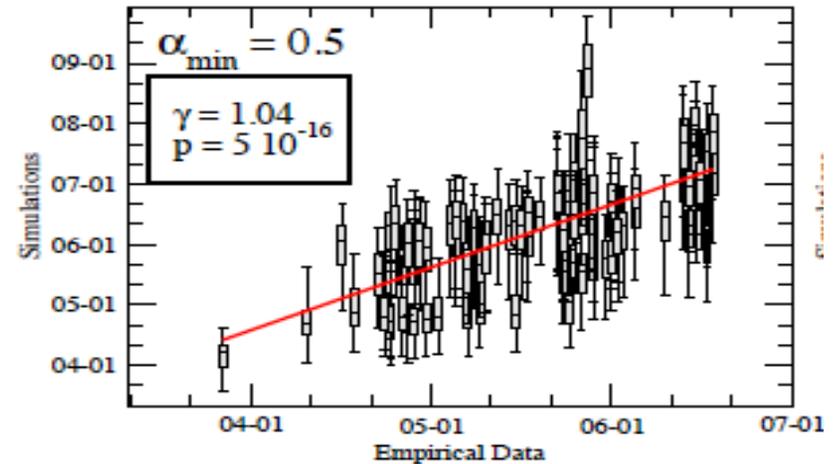
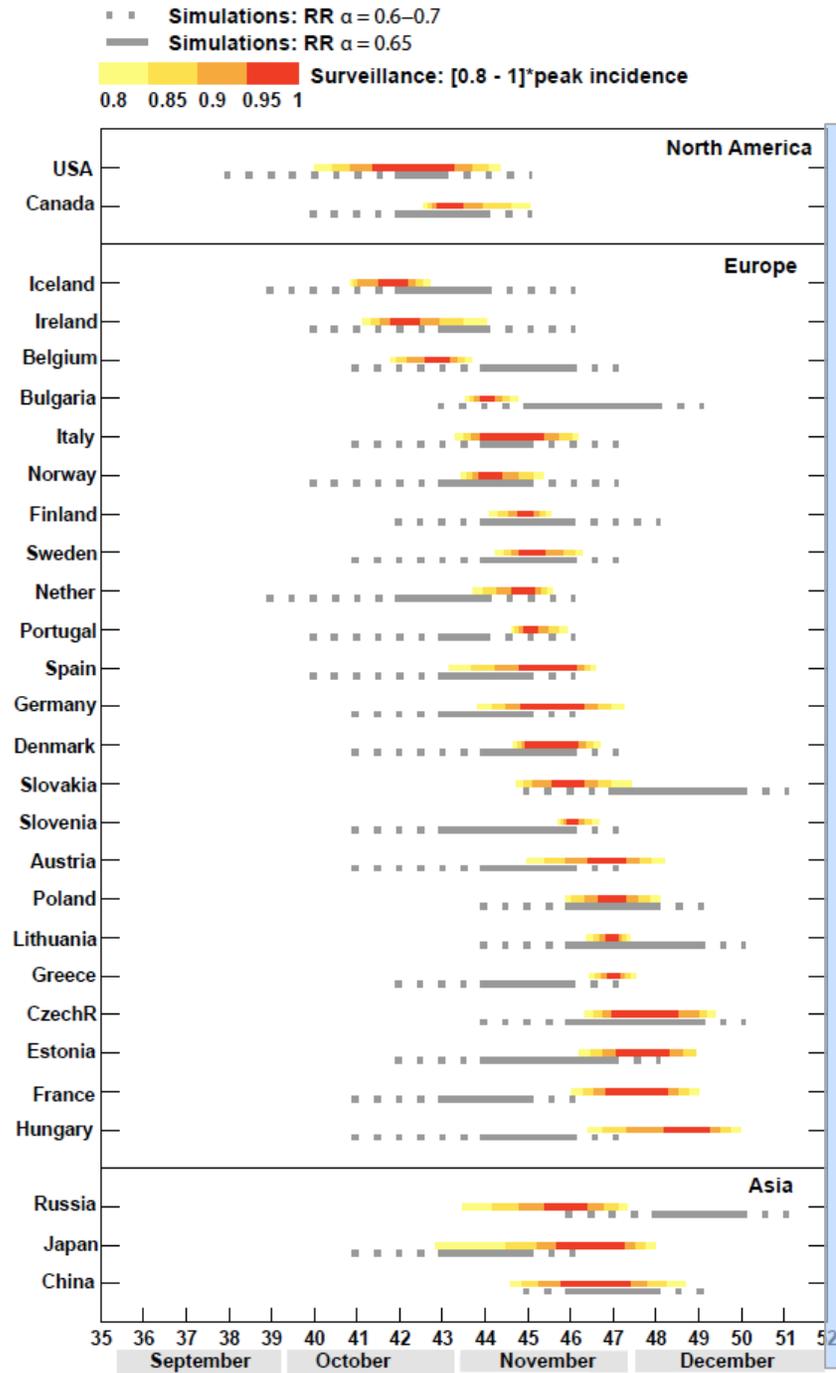


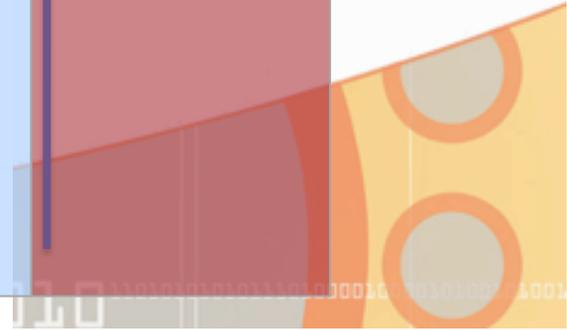
Figure 2

# When...



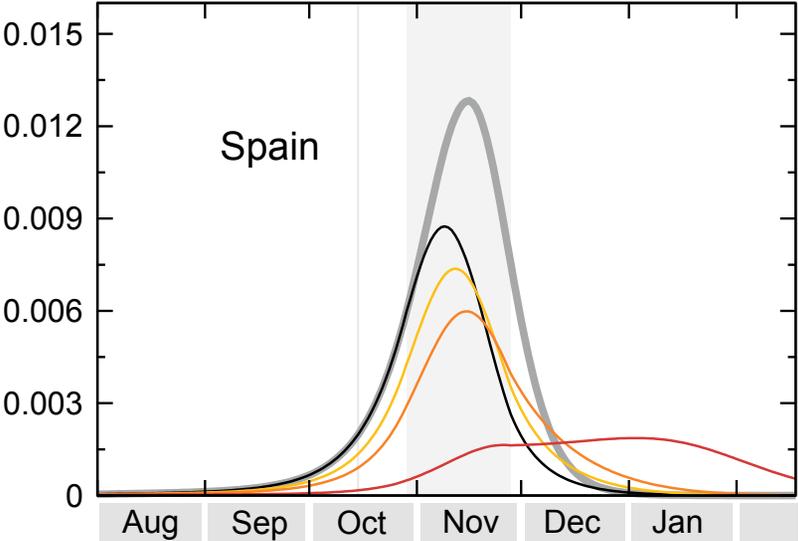
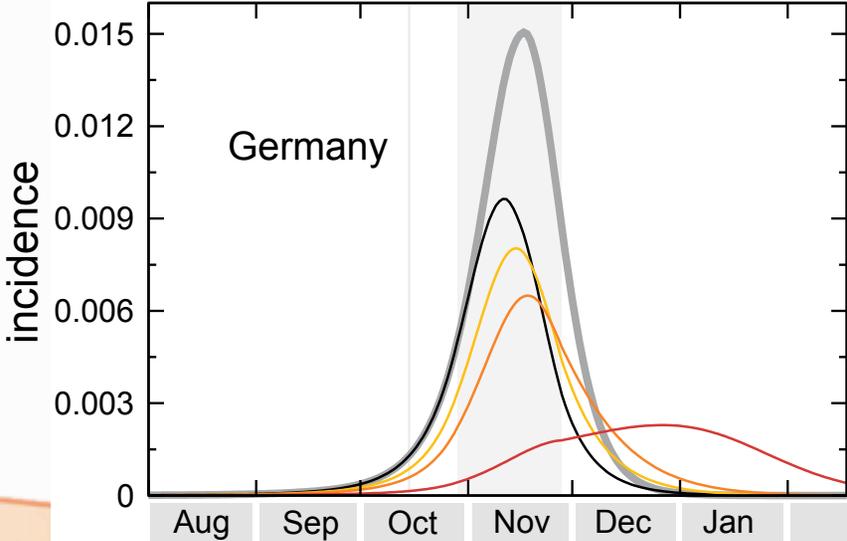
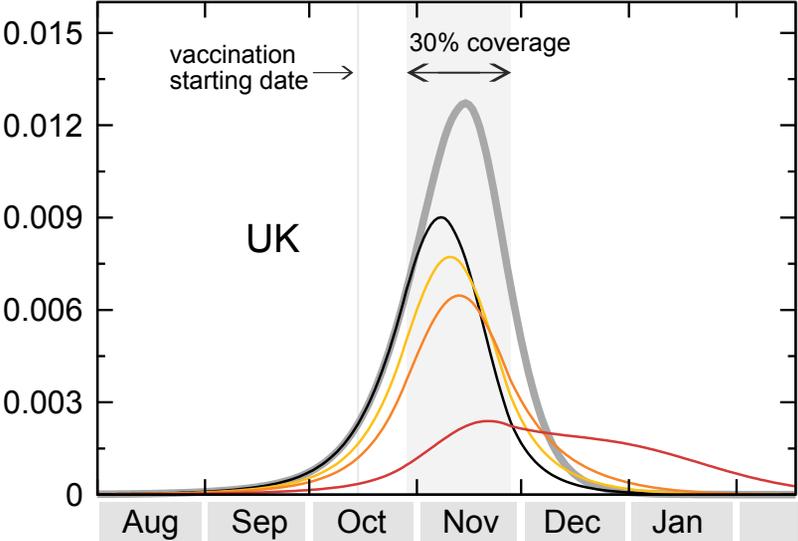
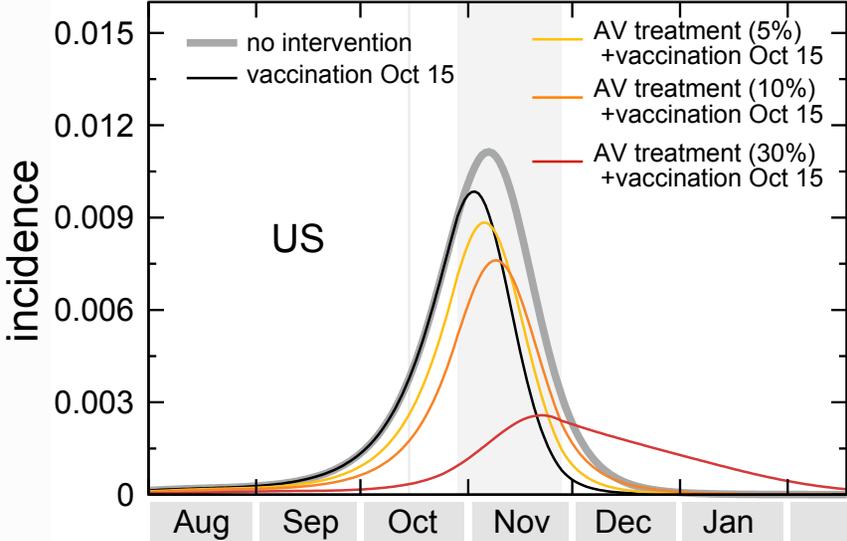
Expected peak time for seasonal

Today



# Vaccination campaigns.....

$\alpha_{\min} = 0.6$



# Where and when continued.....

Delay with the use of systematic AV treatments (30%)

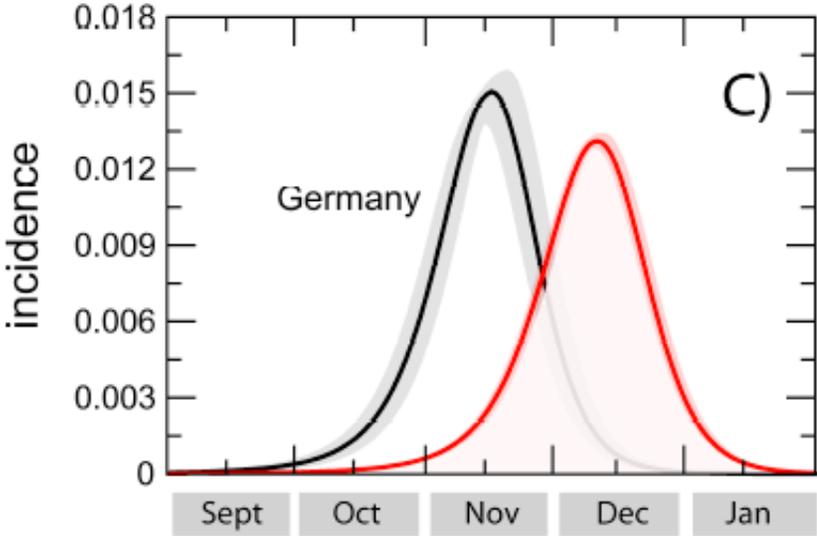
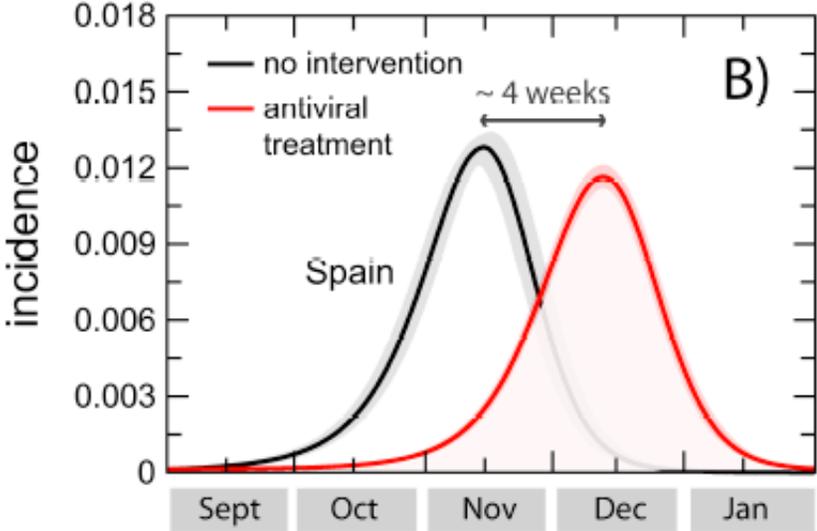
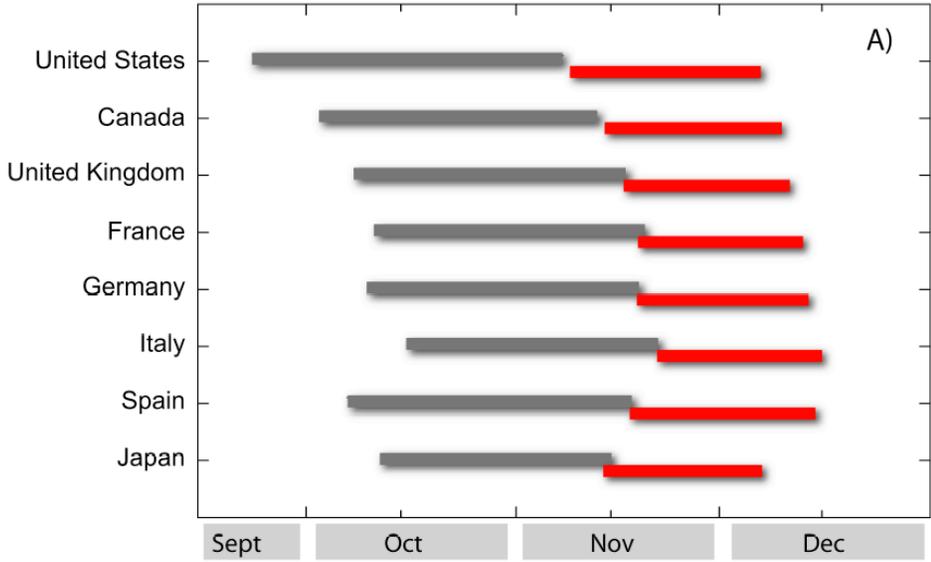


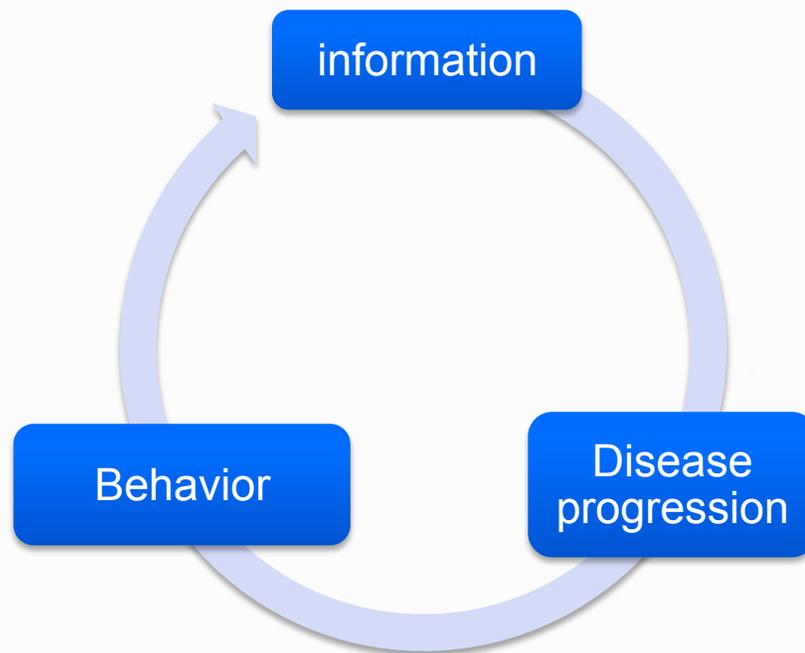
Figure 3



# What's next for...

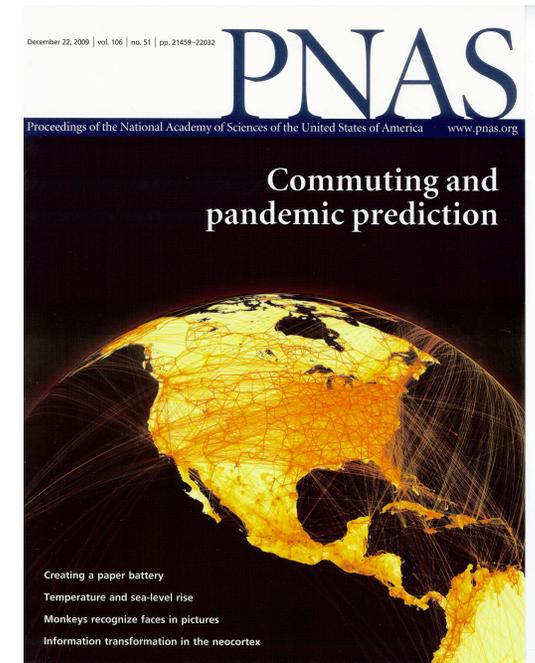
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- Understanding of the feedback loop system behavior -> prediction -> information + adaptation -> new system behavior...
- Formal models and understanding of social adaptation/reaction during social disruptive events.



# Recent papers

- **PNAS**, 106, 21484 (2009)
- **BMC-Medicine** 7, e45 (2009)
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