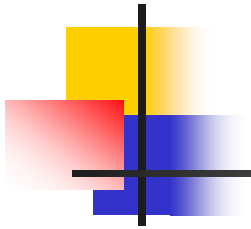

Bridging "Would Be" Agent-based Worlds with the Emergent Real-World Epidemic Dynamics

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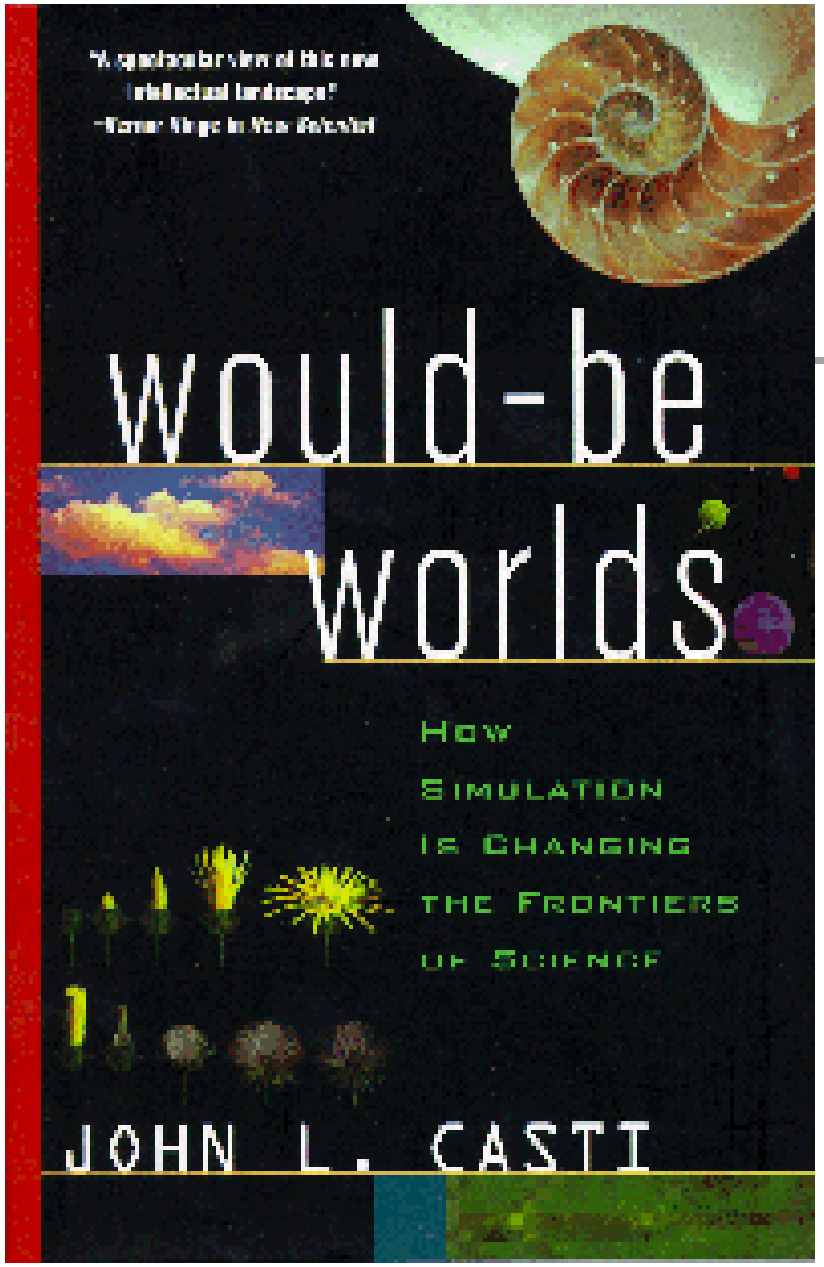
National Technical University of Athens, Greece

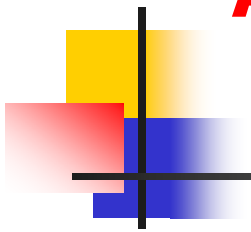
8th Workshop Dynamical Systems Applied to Biology and Natural Sciences |
DSABNS, 31 Jan-3 Feb. 2017, Universidade de Évora, Portugal



....the ability to create surrogate versions of real complex systems inside our computing machines changes the way we do science. In particular, emphasis will be laid upon the idea that these so-called, "artificial worlds" play the role of laboratories for complex systems, laboratories that are completely analogous to the more familiar laboratories that have been used by physicists, biologists, and chemists for centuries to understand the workings of matter.

Because the ability to do controlled, repeatable experiments is a necessary precondition to the creation of a scientific theory of anything, the argument will be made that, for perhaps the first time in history, we are now in a position to think realistically about the creation of a theory of complex systems.

Agent-based Models and Complexity



Agent-Based models that simulate the simultaneous operations and interactions of multiple objects (atoms, molecules, agents) in an attempt to re-create and predict the appearance of complex phenomena.

The process is one of emergence from the lower (micro) level of systems to a higher (macro) level.

As such, a key notion is that simple behavioral rules generate complex behavior.

Complex vs. Complicated

Collective patterns emerging from many interacting components,

The emergent dynamics is more than the sum of the properties of the individual units

…decomposing the system and analyzing subunits does not necessarily give us an idea of the behavior as a whole

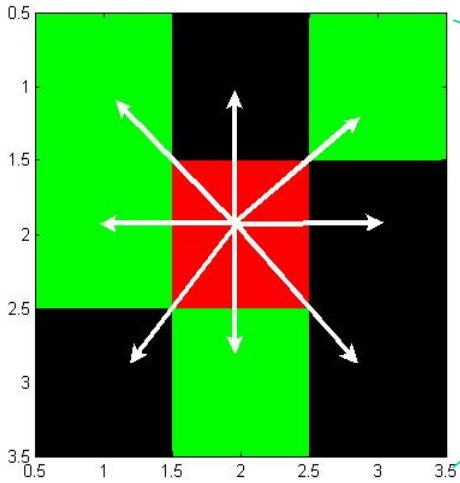
…the behavior of complex systems is therefore unpredictable

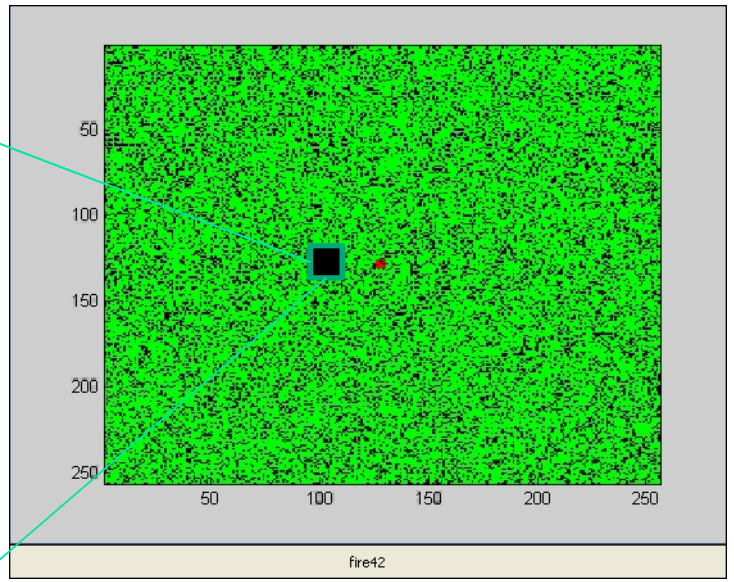
…subunits are designed and connected so that they accomplish a pre-determined (predictable) function

The notion of Complexity: a simplistic! model of Tumor Growth

A cell can take each time one of the three states:

- 1:Black, tumor cell
- 2:Green, healthy cell.
- 3:Red: micro vessel cell





The evolution rules are the following:

- Micro vessel on a site will invade to nearest neighbors healthy cells at the next time step with probability **p**.

Cells with Micro vessel

at time t → **With probability** → **at time t+1**

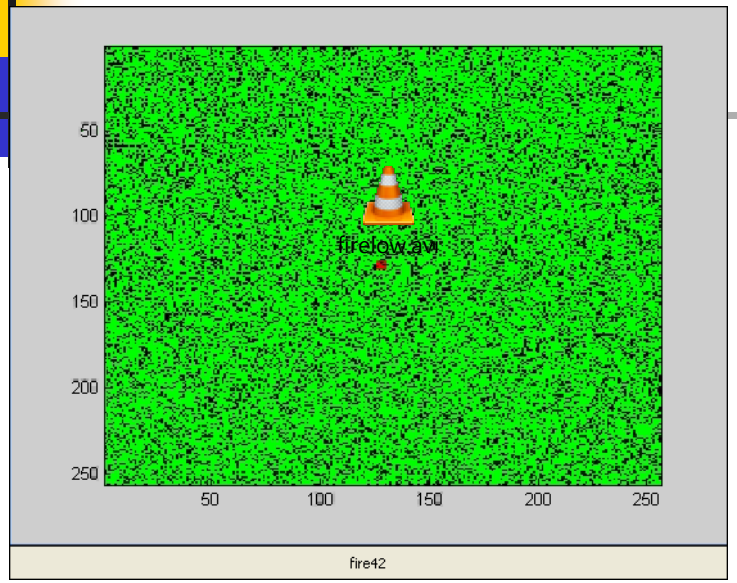
at cell (i, j) **p** **At neighbor cells**

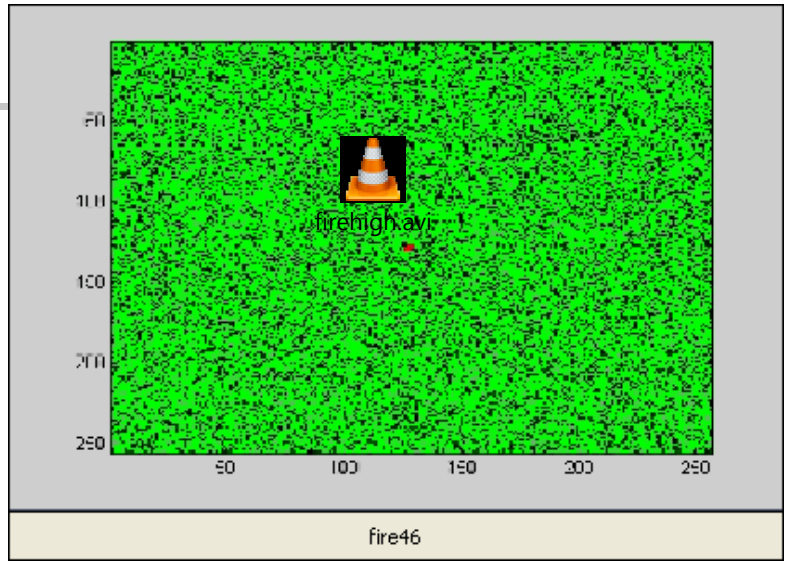
- All cells with micro vessel will turn to tumor at the next time step.

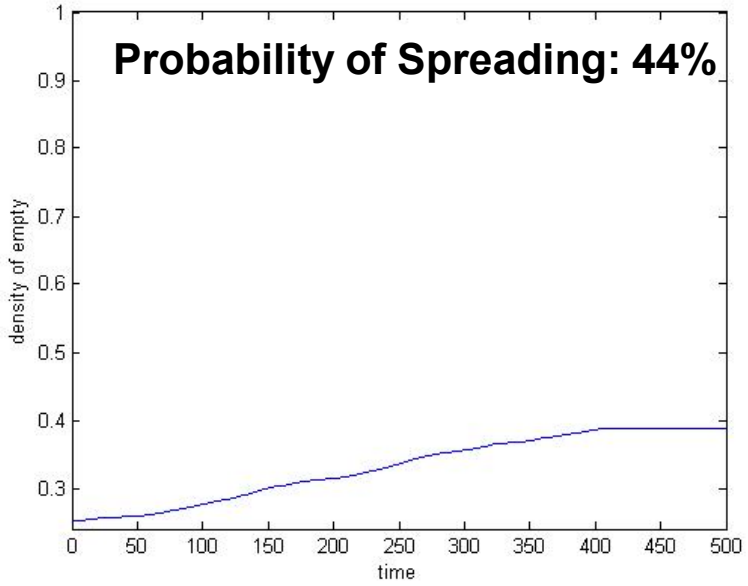
Cell with micro vessel → **Tumor Cell**

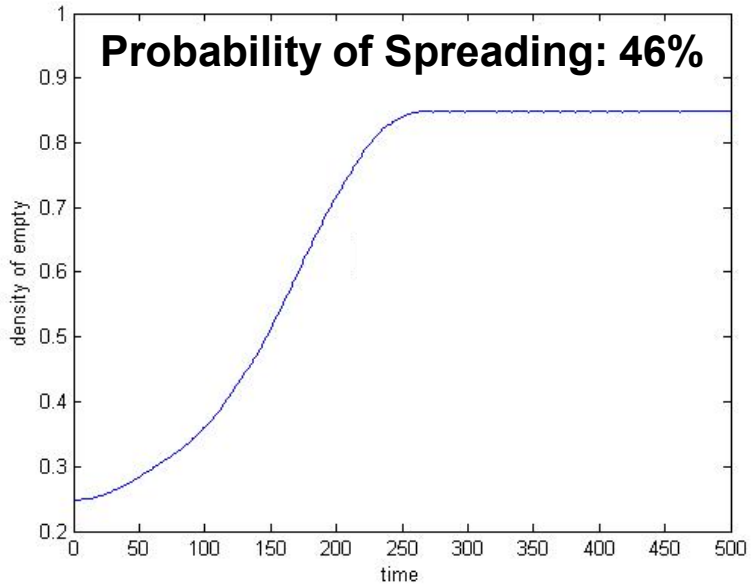
At time t **At time t+1**

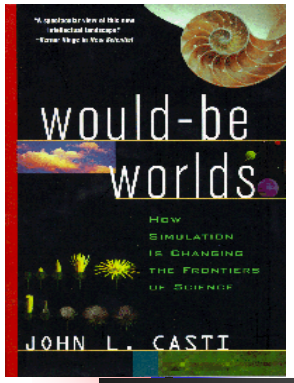
The notion of Complexity: small changes can cause unpredictable behaviour









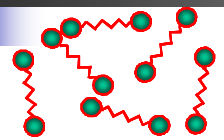


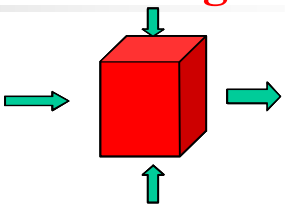
20 years after....

A Big! number of available microscopic/ agent-based models simulating the time evolution of Complex Systems (Biological Systems, Material Science, Complex Fluids, Epidemics, Neurons)

Micro-Scale

Macro Emergent) Scale





Large-Scale Microscopic Models

Mean-field (moments)

Agent-Based

Brownian D

Monte Carlo

Molecular Dynamics

Different time and space scales
Macro scales much much bigger than the bigger Microscopic scale

ODE's-PDE's

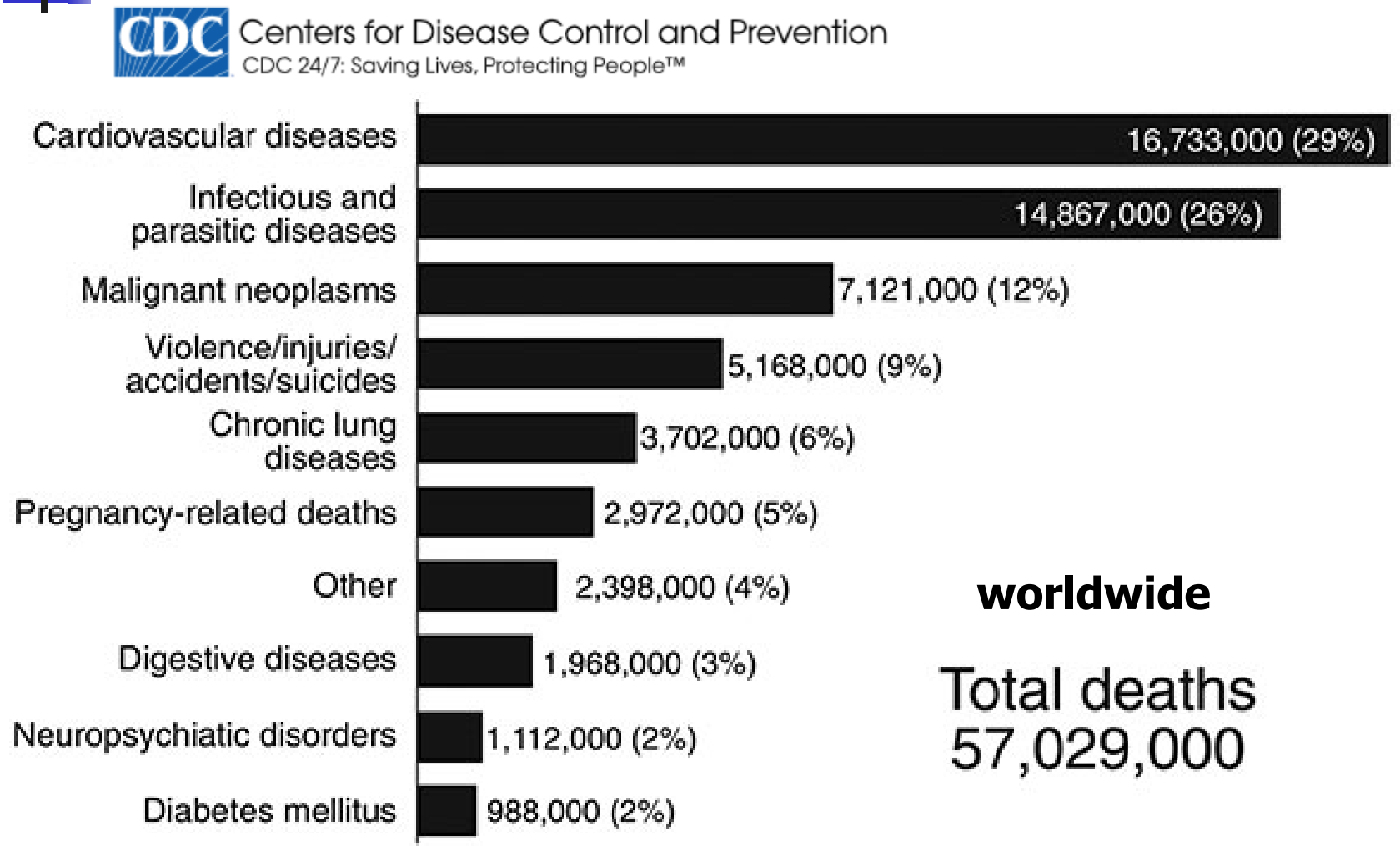
The analysis is usually sought at this level (system-level analysis

- **Material Science**
- **Epidemiology**
- **Bio**
- **Neurons**
- **Markets**

… but such good models not always exist in closed form

Epidemics: One of the major challenges nowdays

The surveillance, analysis and ultimately the efficient long-term prediction and control of epidemic dynamics appear to be (the) major challenges nowdays



Epidemics: One of the major challenges nowdays

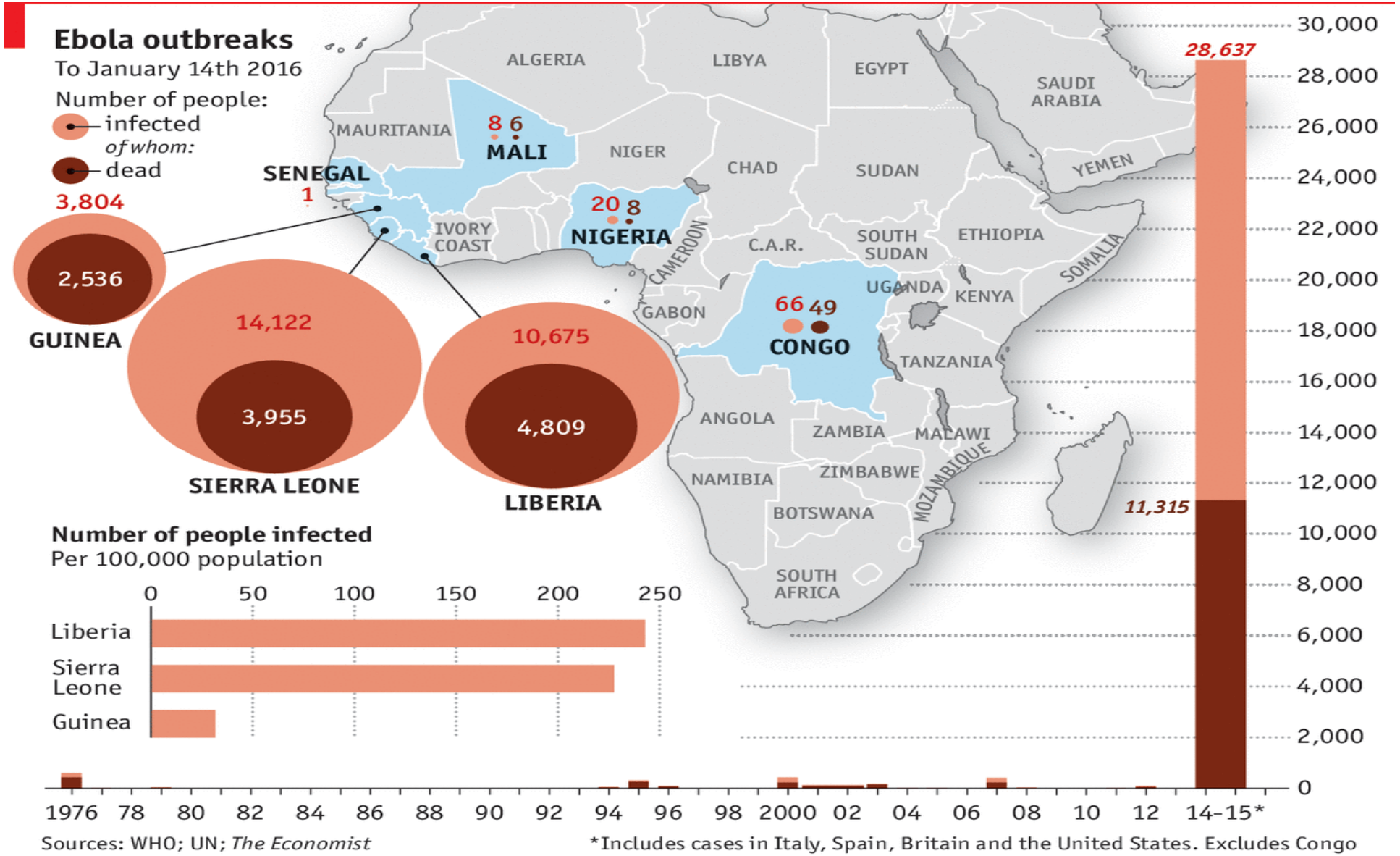
The surveillance, analysis and ultimately the efficient long-term prediction and control of epidemic dynamics appear to be (the) major challenges nowdays

Influenza Pandemics
20th Century

Credit: US National Museum of Health and Medicine

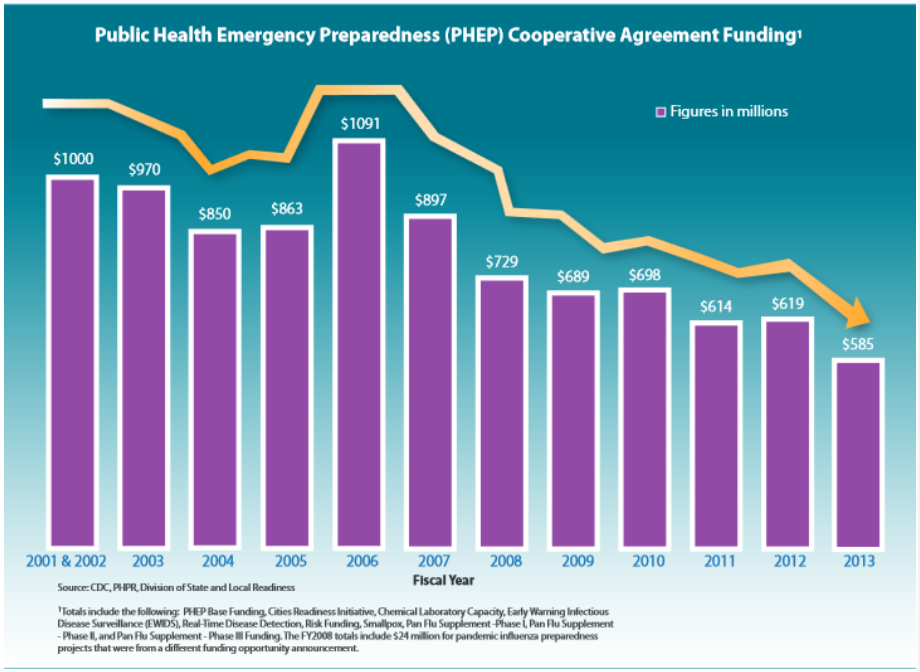
1918: "Spanish Flu" A(H1N1)	**1957: "Asian Flu"** A(H2N2)	**1968: "Hong Kong Flu"** A(H3N2)
20-40 m deaths	1-4 m deaths	1-4 m deaths
675,000 US deaths	70,000 US deaths	34,000 US deaths

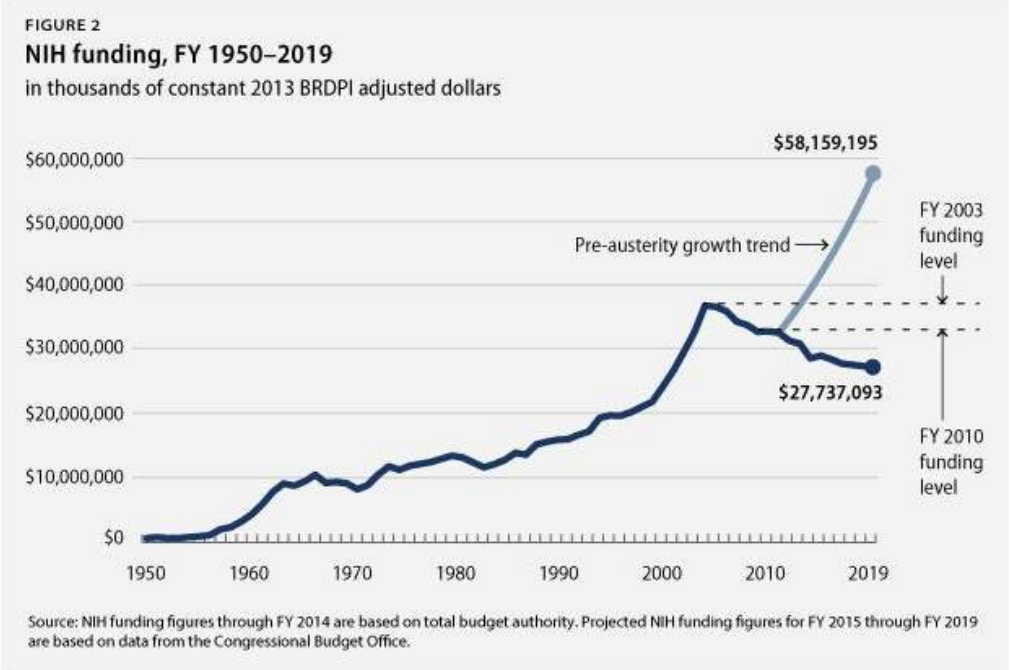
Epidemics: One of the major challenges nowdays



Epidemics arise: funding… declines…

CDC continues to work with reduced financial resources, which similarly affects state, local, and insular area public health departments





Modelling Epidemics : the diffuculties

Modelling difficulties stem mainly from three reasons:

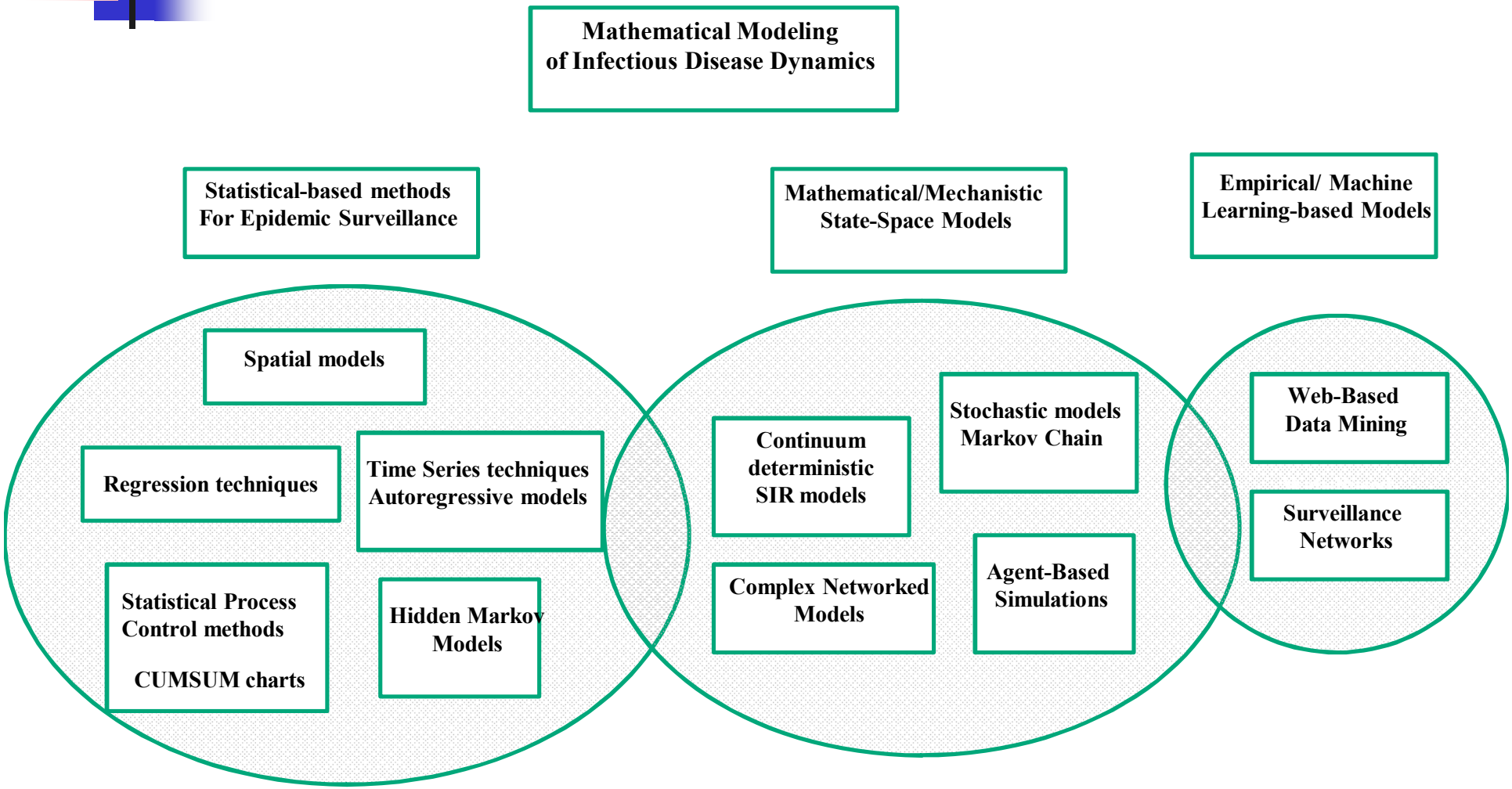
(a) the continuous and ever-lasting mutations of pathogens, particularly of viruses

(b) the complexity in the disease host-pathogen and host-host transmission mechanisms,

(c) the complexity in the structure of underlying social network,

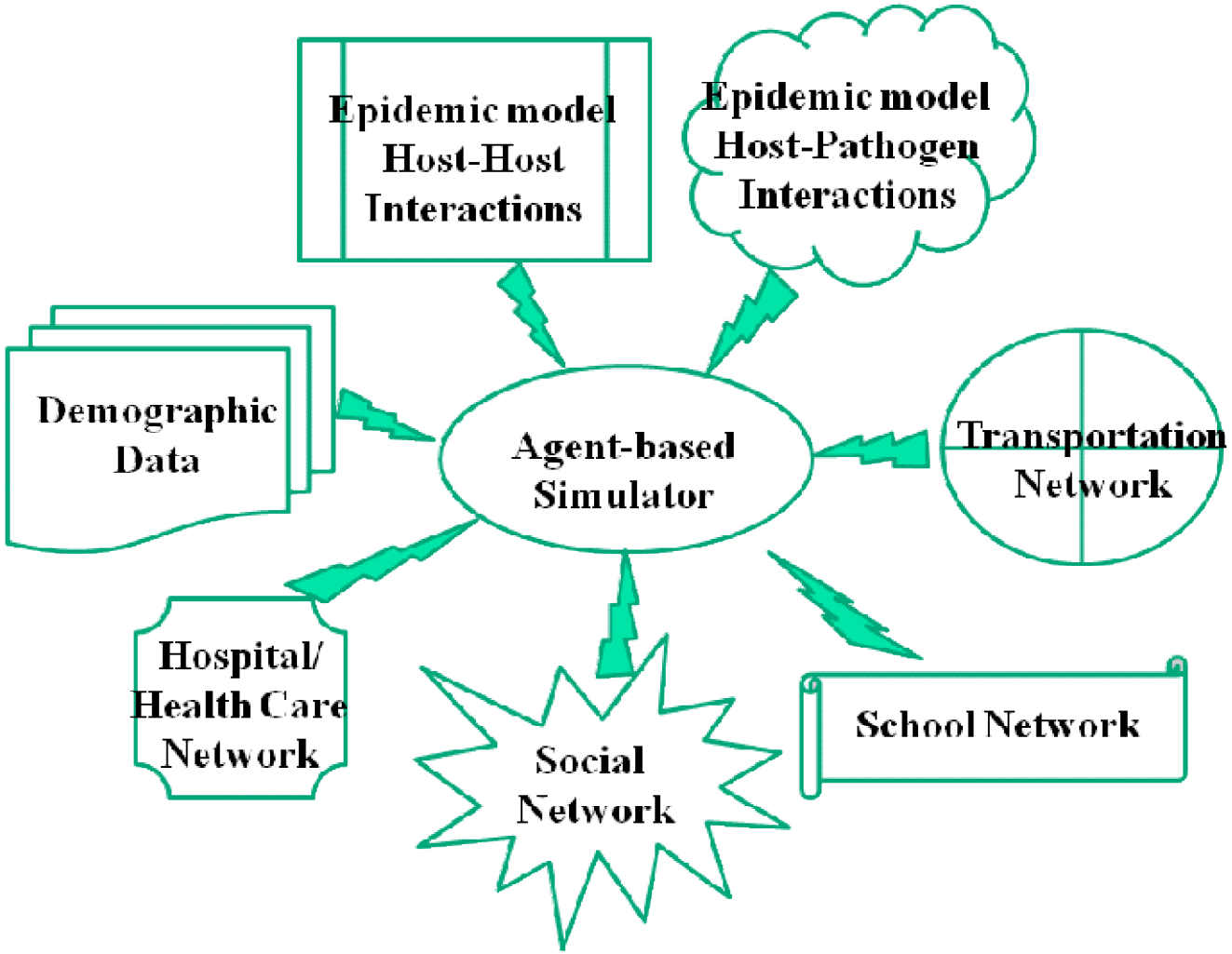
Epidemic modelling: an overview

Siettos, C. I., Russo, L., 2013, Mathematical Modeling of Infectious Disease Dynamics: A Review, Virulence, 4 (4), 295-306.



An Agent-Based Simulator

the Models of Infectious Disease Agent Study **(MIDAS),** a network launched on May, 1, 2004 and funded by the U.S. National Institutes of Health has as its pilot effort the detailed modeling of the dynamics of a hypothetical flu pandemic



What is done until now with Agent-Based Simulators

(A) Run in time:

running many scenarios with different initial conditions and for long times to get the relative macroscopic information.

(B) Try to find Macroscopic equations in a closed form
→ Statistical Mechanics

What is done until now: an example for obtaining closures with the pencil

Example: The SIRS model for Epidemics.
Use of stochastic dynamics on a lattice
(or more general graphs)

Description

A site x of a d-dimensional graph can be:

S **(healthy and susceptible)**

I **(infected)**

R **(recovered, i.e., healthy and immune).**

The rules:

$S \longrightarrow I$ with rate $\lambda\,\eta(x)$,
$\eta(x)$ number of Infected Neighbors

$I \longrightarrow R$ with rate δ

$R \longrightarrow S$ with rate γ

What is done until now: an example for obtaining closures with the pencil

Mathematical individual description of SIRS

$$\frac{dP_t(S_x)}{dt} = -\lambda \sum_{y \in N(x)} P_t(S_x, I_y) + \gamma P_t(R_x)$$

$$\frac{dP_t(I_x)}{dt} = +\lambda \sum_{y \in N(x)} P_t(S_x, I_y) - \delta P_t(I_x)$$

$$\frac{dP_t(R_x)}{dt} = \delta P_t(I_x) - \gamma P_t(R_x) \quad (\delta = 1)$$

N(x) **: Is the neighborhood (nearest-neighbor sites) of a site x**

$P_t(a_x)$ **: is the probability of having a state a at site x at, a=*S,I,R***

$P_t(a_x, b_y)$ **: is the joint probability to have state a at site x and state b at site y.**

Problem : Equations are, as is usual for moment equations, not in a closed system.

What is done until now: an example for obtaining closures with the pencil

Problem : This leads to an infinite hierarchy.

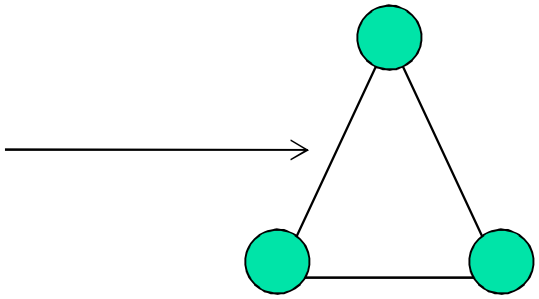
To solve such a hierarchy, one usually resorts to some approximation-reduction scheme, which expresses the higher-order moments in terms of the lower-order ones and truncates the equations at some point.

To close the system and derive a set of autonomous equations we approximate the triad joint probability

$$P\left(a_x, b_y, x_w\right) = \frac{P\left(a_x, b_y\right) P\left(b_y, x_w\right)}{P\left(b_y\right)}$$

Assumption

Three adjacent sites can not form a triangular



Reppas, A., De Decker Y., Siettos, C.I., 2012, On the Efficiency of the Equation-Free Closure of Statistical Moments: Dynamical properties of a Stochastic Epidemic Model on Erdos-Renyi networks, ***Journal of Statistical Mechanics: Theory and Experiment***, **8**, P08020.

Objective

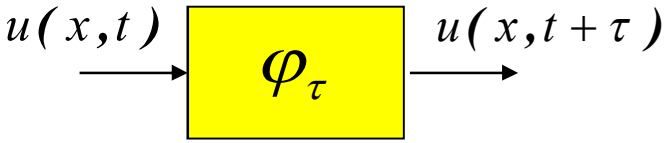
Bridge the gap between micro (where the information is available) and macro scales (where the analysis is sought)

Enable microscopic simulators through a computational superstructure to perform tasks beyond simple simulation

- **Obtain coarse stable and unstable!!! steady state solutions from microscopic simulator**
- **Accelerate convergence of microscopic simulator to the corresponding coarse steady state**
- **Calculate "coarse" slow eigenvalues and eigenvectors**
- **Design linear and nonlinear controllers : Nonlinear feedback linearization**
- **Deal with Rare Events**

without having the equations!

I don't know the coarse equations, but I have a black box agent-based simulator



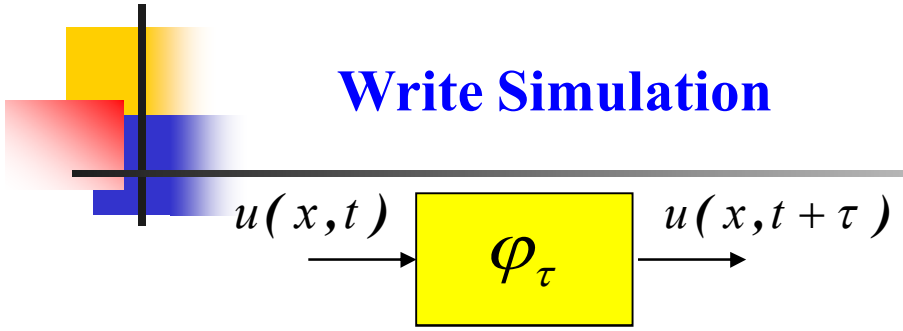
Use the agent-based simulator as an experiment!

Identify coarse information on demand

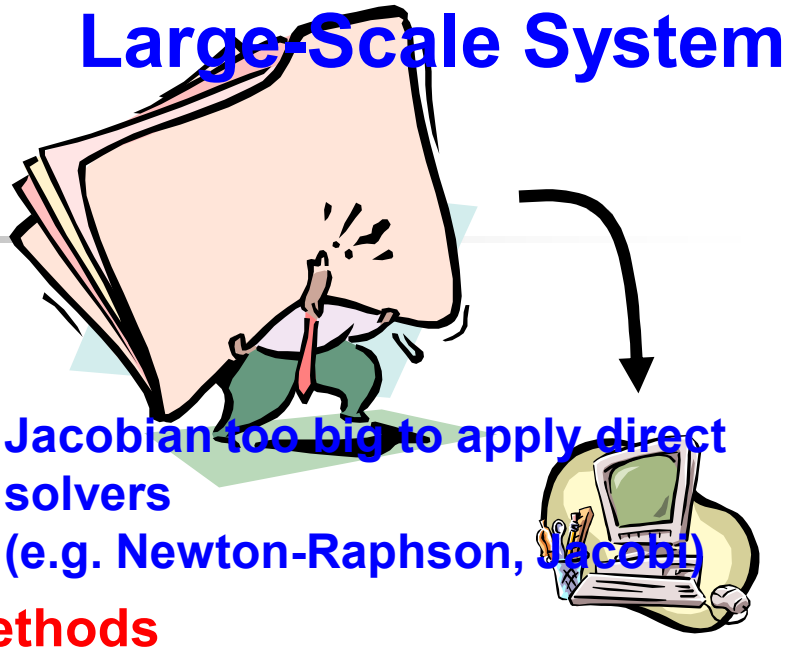
THE CONCEPT: What else can I do with an integration code ?

Have Equations (PDE's)

Write Simulation



Large-Scale Systems

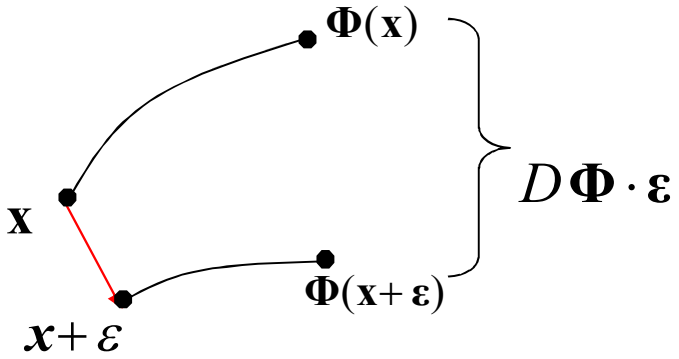


Jacobian too big to apply direct solvers
(e.g. Newton-Raphson, Jacobi)

-Instead, use iterative linear algebra methods

(matrix-free methods)

Also



Estimate

matrix-vector product

⇓

Matrix free iterative linear algebra

⇓

The World

⟺

CG, GMRES
Arnoldi
Newton-Krylov

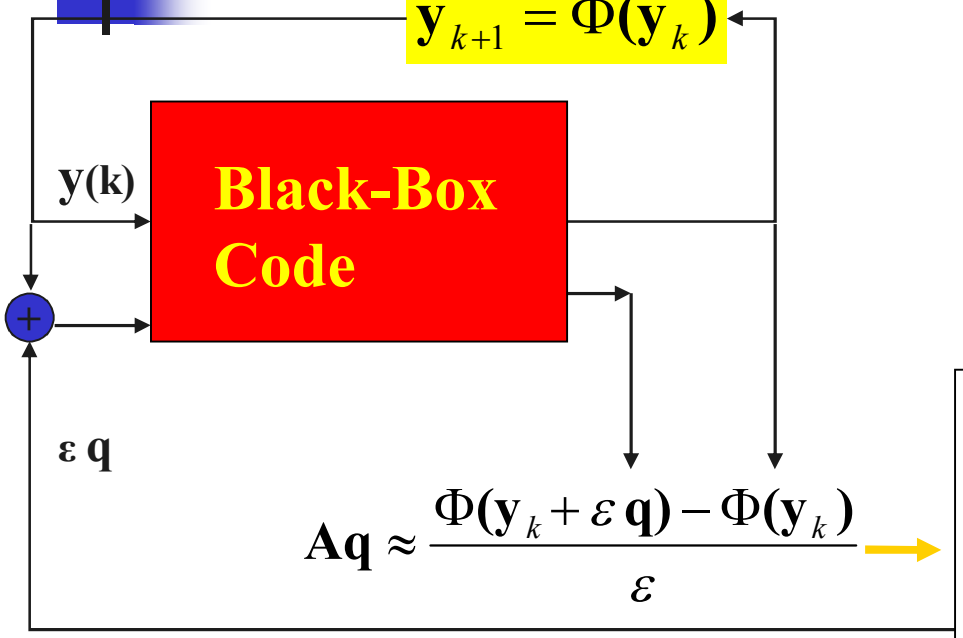
Matrix-free methods: Arnoldi Eigensolver & GMRES

No need of "transparent" equations, just a black box code that will integrate it over a step size that it has been chosen.

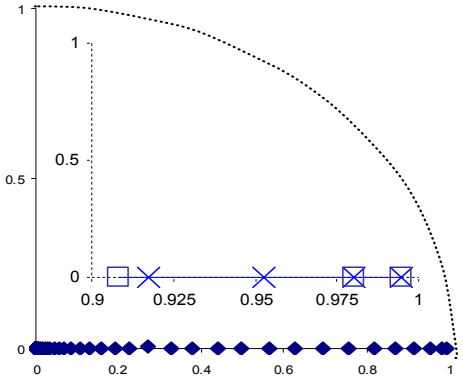
GMRES → **SOLVE AX=B**

SYSTEM AROUND THE STEADY STATE

$$\mathbf{y}_{k+1} = \Phi(\mathbf{y}_k)$$



Critical Eigenvalues



ARNOLDI

Set q_1 **with** $\|q_1\| = 1$

For j =1,m

(1) **Calculation** Aq_j

(2) **Calculation** $h_{t,j} = \langle Aq_j, q_t \rangle, t = 1,2,\ldots,j$

(3) $r_j = Aq_j - \sum_{t=1}^{j} h_{t,j} q_t$

(4) $h_{j+1,j} = \langle r_j, r_j \rangle^{1/2}$

(5) $q_{j+1} = r_j / h_{j+1,j}$

End For

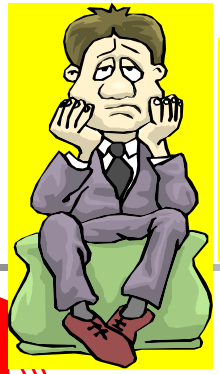
In step m the algorithm creates an orthogonal basis in Krylov subspace K_m

$\boldsymbol{Q}_m = \{q_1, Aq_1, \ldots, A^{m-1}q_{m-1}\}$

The projection of A in K_m results to an upper Hessenberg $H_m = Q_m^T A Q_m$ with elements h_{ij}

Computational Methods for System-Level Analysis

What if physics are known in a more detailed (microscopic) level?



…but there is no description (in moments of distribution) of the macroscopic behavior;

SIMPLE SIMULATION: LIKE EXPERIMENTAL EXPERIMENTS

i.e. run atomistic-based models for many agents and for different parameters and for long time to get macroscopic (system-level) information

MICRO-scopic

MACRO-scopic

FINITE ELEMENTS

KRYLOV SUBSPACE ARNOLDI-GMRES

NEWTON/ (QUASI-NEWTON)

CONTROL

OPTIMIZATION

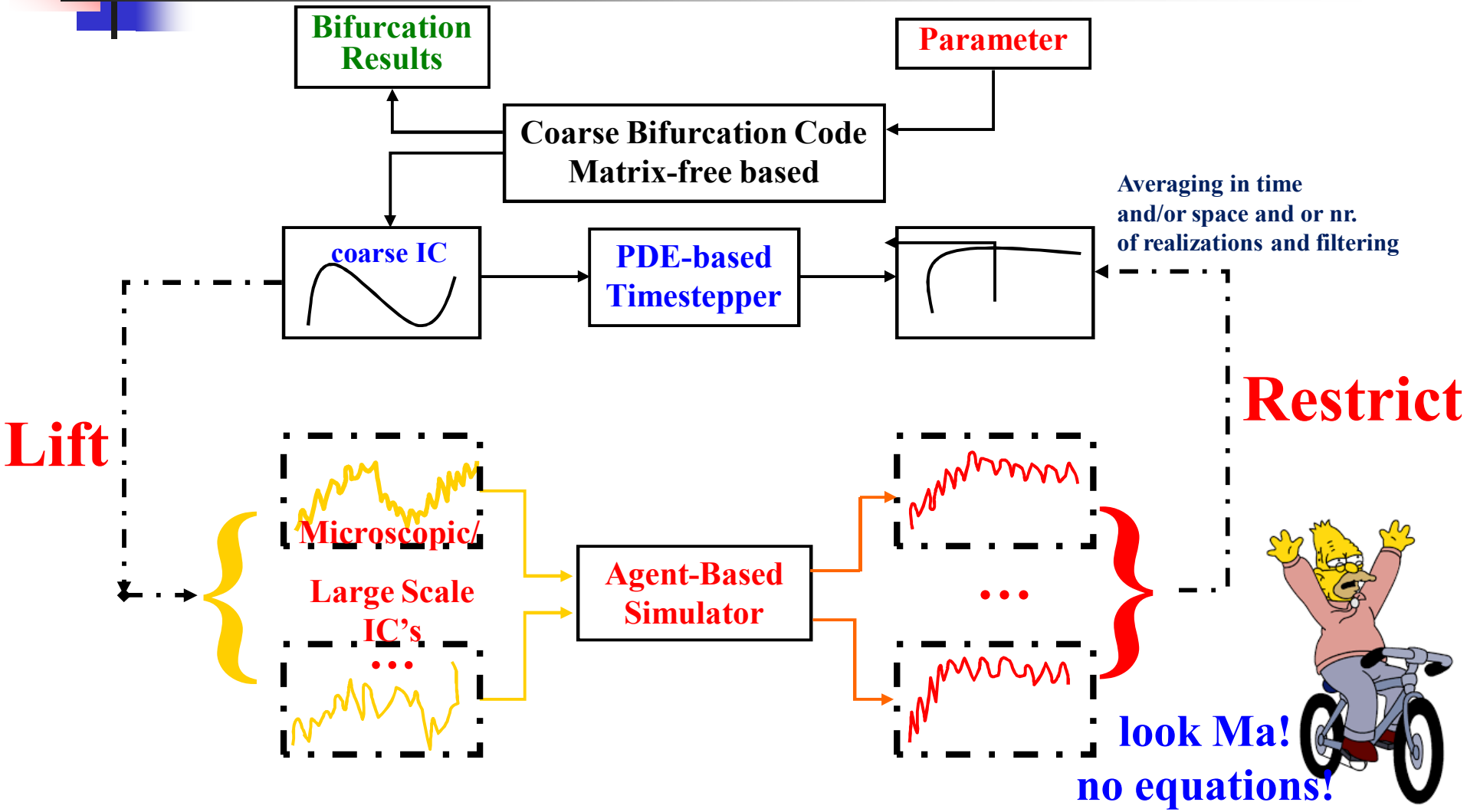
AIM: Systematically bridge the gap between Micro-scopic and Macro-scopic (system-level) World

But good macroscopic models do not always exist in closed form ….

An Equation-Free Approach for Agent-based Models

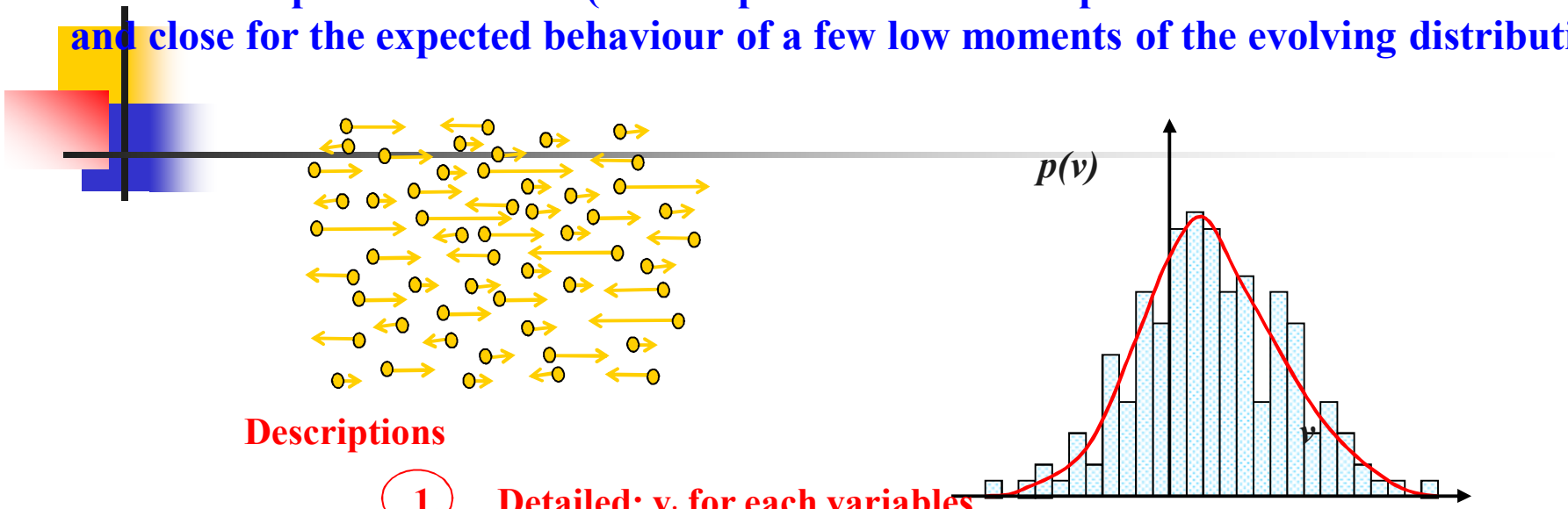
…. or else How to perform systems-level analysis without the equations

[Kevrekidis et al., *Comm. Math. Sciences*, 1, 715-762, 2003;
Siettos, Gear and Kevrekidis, EPL, *EPL*, 99, 48007, 2012]



The Assumption: Time Scale Separation of Distributions and Moments

Macroscopic models exist (but the problem is too complex & we cant'derive them) and close for the expected behaviour of a few low moments of the evolving distributions



Descriptions

1. **Detailed: v_i for each variables**
2. **Moments**

m_0 **Zeroth moment: density ρ** $\int p(v)dv$

m_1 **First moment: momentum ρv** $\int p(v)vdv$

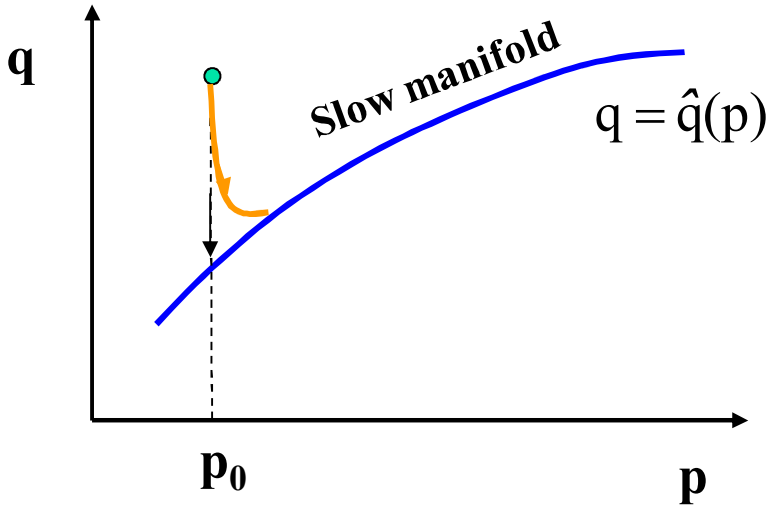
Time scale separation

m_2 **Second moment**

m **Third Moment**

^{3} ……

SLOW & FAST DYNAMICS



$$\frac{dp}{dt} = f(p,q)$$

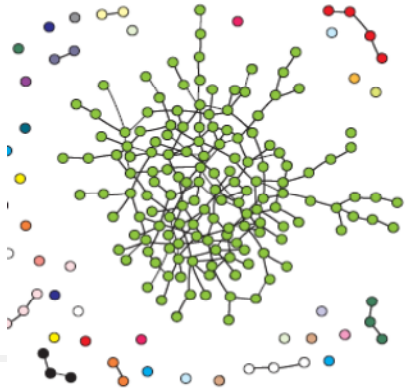
$$\frac{dq}{dt} = \frac{1}{\varepsilon} g(p,q)$$

ε small➔ $g(p,q) \approx 0$, $q \approx \hat{q}(p)$ } very fast

So soon $\dot{p} = f(p,q) \approx f(p,\hat{q}(p)) \equiv \tilde{f}(p)$ **Singular perturbed systems**

Motivation/Scope:

The topology of the Transmission Network Matters!



✓ Introduce methods for analysing the EMERGENT DYNAMICS of detailed Agent-based evolving on complex networks (BIFURCATION ANALYSIS, STABILITY…)

✓Introduce methods for tuning topological characteristics of contact transmission networks to get closer to the structure of real-world observations.

✓Explore the effects of the network topology on the Emergent Dynamics of Agent-Based Epidemic Models.

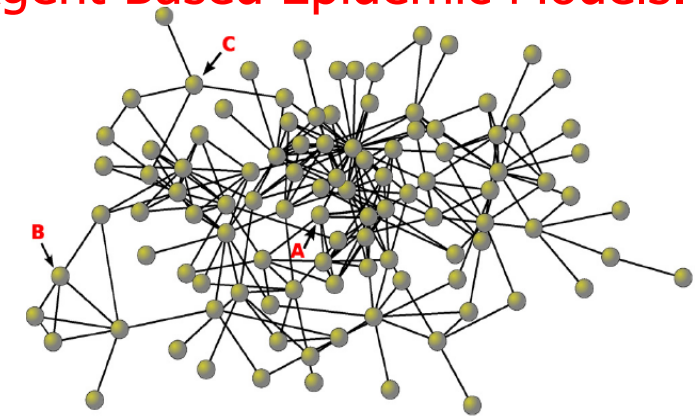
✓Examine how graph-base intervention policies can be introduced along with the use of the network topological characteristics (CONTROL DESIGN)

USING THE AGENT-BASED SIMULATOR AS EXPERIMENT, THUS BYPASSING THE NEED FOR DERIVING ANY MACROSCOPIC MODEL IN A CLOSED FORM

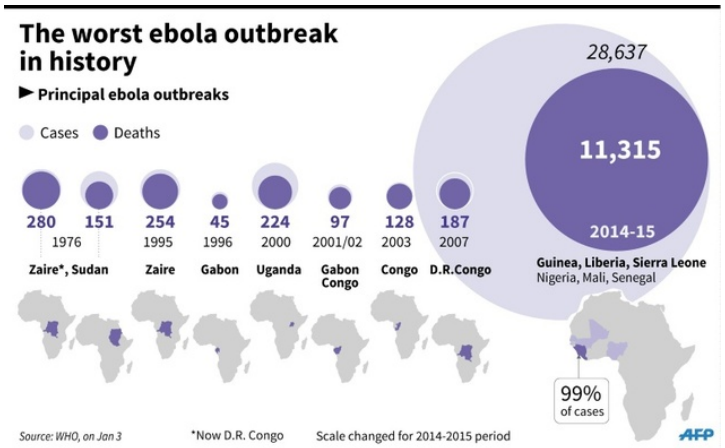
The Problems

1. Comparison between closed Models and Equation-Free Computations

2. Exploring the effects of the Network Topology on the Emergent Dynamics of Agent-Based Epidemic Models.



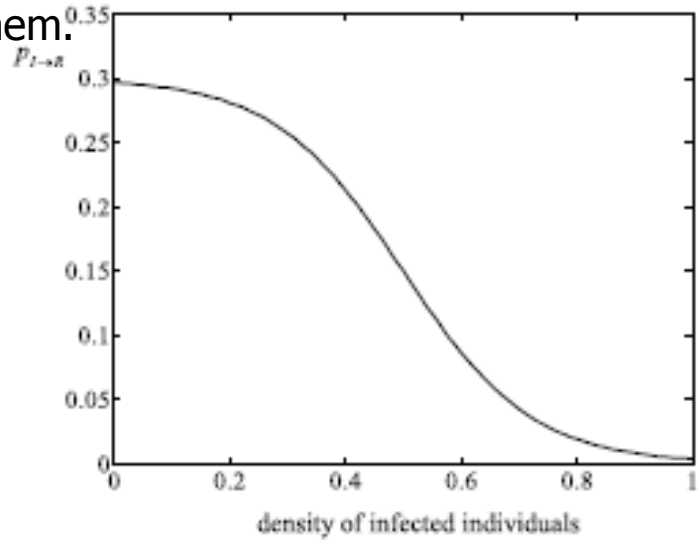
3. Forecasting 2014 Ebola Epidemics



1. The Epidemic model: The Efficiency of Closures

Reppas, A., De Decker Y., Siettos, C.I., 2012, On the Efficiency of the Equation-Free Closure of Statistical Moments: Dynamical properties of a Stochastic Epidemic Model on Erdos-Renyi networks, *Journal of Statistical Mechanics: Theory and Experiment*, 8, P08020.

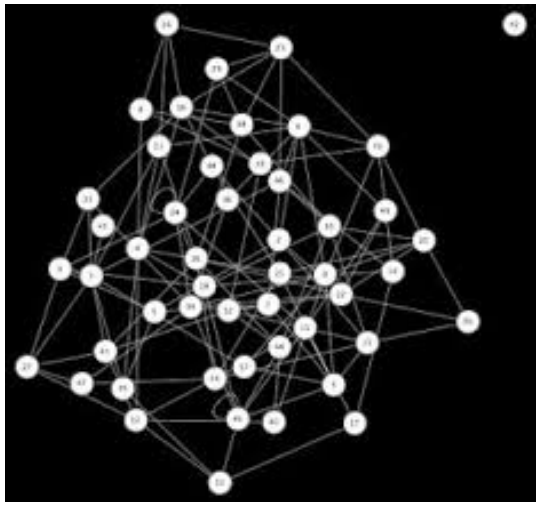
Rule #1: An infected individual *[I]* infects a susceptible (*S*) neighbor with a probability $p_{S\to I} = \lambda$ if an active link exists between them.



Rule #2: An infected (*I*) individual recovers with a probability $p_{I\to R} = \delta$

Rule #3: A recovered individual becomes susceptible with a probability $p_{R\to S} = \gamma$

Contact transmission Network: Erdős–Rényi



1. The Epidemic model: the Efficiency of Closures

Reppas, A., De Decker Y., Siettos, C.I., 2012, On the Efficiency of the Equation-Free Closure of Statistical Moments: Dynamical properties of a Stochastic Epidemic Model on Erdos-Renyi networks, *Journal of Statistical Mechanics: Theory and Experiment*, 8, P08020.

Mean Field

$$P_t(a_x, b_y) = P_t(a_x)P_t(b_y)$$
$$P_t(a_x, b_y, c_w) = P_t(a_x)P_t(b_y)P_t(c_w).$$

$$\frac{\mathrm{d}[S]}{\mathrm{d}t} = -\lambda z[S][I] - \gamma(1 - [S] - [I])$$
$$\frac{\mathrm{d}[I]}{\mathrm{d}t} = \lambda z[S][I] - \delta[I]$$

Kirkwood (pairwise)

$$P_t(a_x, b_y, c_w) = \frac{P_t(a_x, b_y)P_t(b_y, c_w)}{P_t(b_y)}.$$

$$\frac{\mathrm{d}[I]}{\mathrm{d}t} = \lambda z[SI] - \delta[I]$$
$$\frac{\mathrm{d}[R]}{\mathrm{d}t} = \delta[I] - \gamma[R]$$
$$\frac{\mathrm{d}[SR]}{\mathrm{d}t} = \delta[SI] + \gamma([R] - [RI] - 2[SR]) - \frac{(z-1)\lambda[SI][SR]}{1 - [R] - [I]}$$
$$\frac{\mathrm{d}[RI]}{\mathrm{d}t} = -(2\delta + \gamma)[RI] + \delta([I] - [SI]) + \frac{(z-1)\lambda[SI][SR]}{1 - [R] - [I]}$$
$$\frac{\mathrm{d}[SI]}{\mathrm{d}t} = \gamma[RI] - (\lambda + \delta)[SI] + \frac{(z-1)\lambda[SI]}{1 - [R] - [I]}(1 - [R] - [I] - [SR] - 2[SI])$$

1. The Epidemic model: the Efficiency of Closures

Reppas, A., De Decker Y., Siettos, C.I., 2012, On the Efficiency of the Equation-Free Closure of Statistical Moments: Dynamical properties of a Stochastic Epidemic Model on Erdos-Renyi networks, *Journal of Statistical Mechanics: Theory and Experiment*, 8, P08020.

Ursell Expansion (pairwise)

$$P_t(S_x, S_y, I_w) = P_t(S_x)P_t(S_y, I_w) + P_t(I_w)P_t(S_x, S_y) - P_t(S_x)P_t(S_y)P_t(I_w)$$
$$P_t(I_w, S_x, I_y) = 2P_t(I_w)P_t(S_x, I_y) - P_t(I_w)P_t(S_x)P_t(I_y)$$
$$P_t(I_w, S_x, R_y) = P_t(R_x, S_y, I_w) = P_t(I_w)P_t(S_x, R_y) + P_t(R_y)P_t(I_w, S_x)$$
$$- \,]$$

$$\frac{\mathrm{d}[I]}{\mathrm{d}t} = \lambda z[SI] - \delta[I]$$
$$\frac{\mathrm{d}[R]}{\mathrm{d}t} = \delta[I] - \gamma[R]$$
$$\frac{\mathrm{d}[SR]}{\mathrm{d}t} = \delta[SI] + \gamma([R] - [RI] - 2[SR]) - (z-1) \times \lambda([I][SR] + [R][SI] - [I][R](1 - [I] - [R]))$$
$$\frac{\mathrm{d}[RI]}{\mathrm{d}t} = -(2\delta + \gamma)[RI] + \delta([I] - [SI]) + (z-1)\lambda([I][SR] + [R][SI] - [I][R](1 - [I] - [R]))$$
$$\frac{\mathrm{d}[SI]}{\mathrm{d}t} = \gamma[RI] - (\lambda + \delta)[SI] + (z-1)\lambda([SI](1 - [I] - [R]) + [I] \times (1 - [I] - [R] - [SR] - [SI]) - [I](1 - [I] - [R])^2) - (z-1)\lambda(2[I][SI] - [I]^2(1 - [I] - [R])).$$

1. The Epidemic model: the Efficiency of Closures

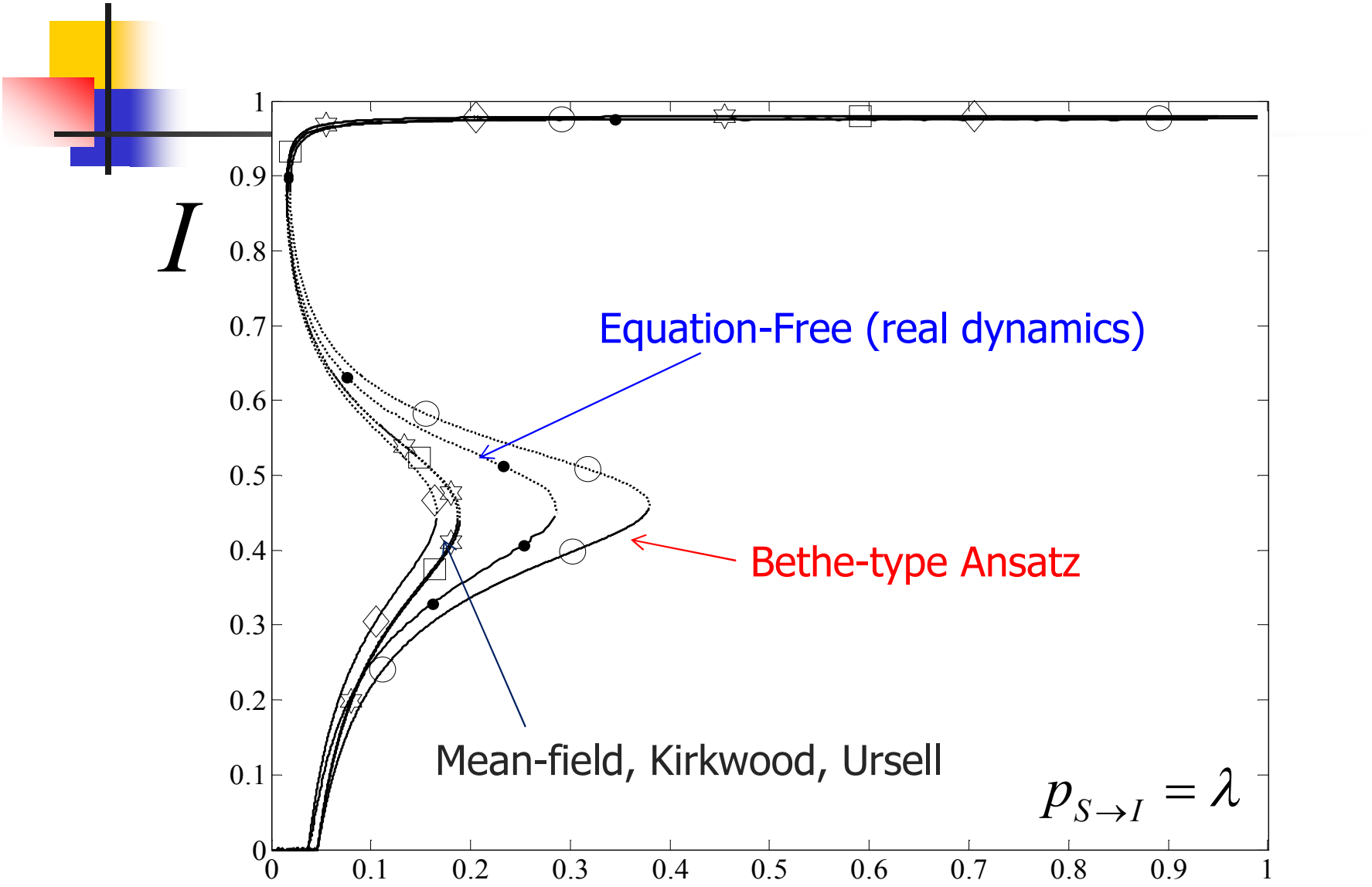
Reppas, A., De Decker Y., Siettos, C.I., 2012, On the Efficiency of the Equation-Free Closure of Statistical Moments: Dynamical properties of a Stochastic Epidemic Model on Erdos-Renyi networks, *Journal of Statistical Mechanics: Theory and Experiment*, 8, P08020.

Bethe-type Ansatz (pairwise)

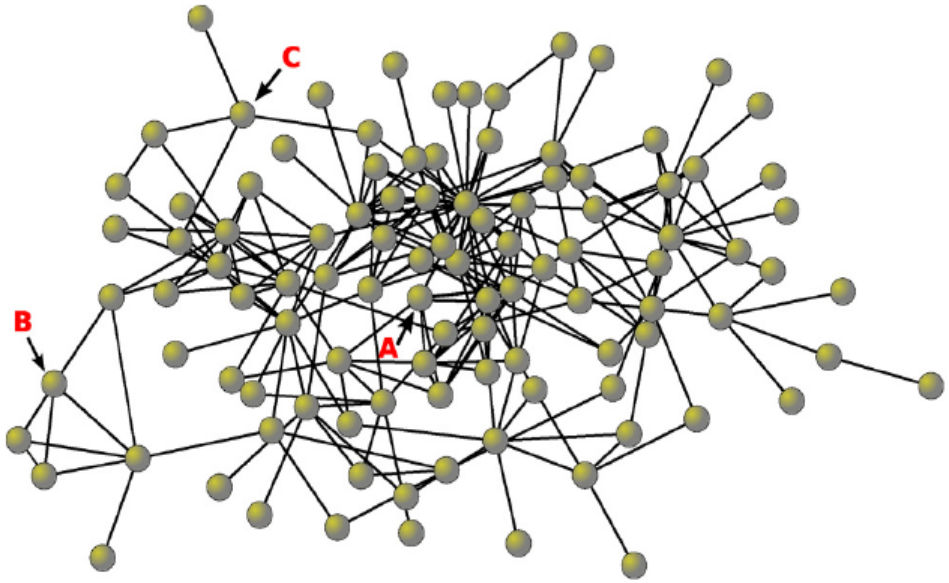
$$
\begin{aligned}
P_t(S_x, S_y, I_w) &= P_t(S_x)P_t(S_y, I_w) \\
P_t(I_w, S_x, I_y) &= P_t(I_y)P_t(I_w, S_x) \\
P_t(I_w, S_x, R_y) &= P_t(R_y)P_t(I_w, S_x) \\
P_t(R_x, S_y, I_w) &= P_t(R_x)P_t(S_y, I_w).
\end{aligned}
$$

$$
\begin{aligned}
\frac{\mathrm{d}[I]}{\mathrm{d}t} &= \lambda z[SI] - \delta[I] \\
\frac{\mathrm{d}[R]}{\mathrm{d}t} &= \delta[I] - \gamma[R] \\
\frac{\mathrm{d}[SR]}{\mathrm{d}t} &= \delta[SI] + \gamma([R] - [RI] - 2[SR]) - (z-1)\lambda([R][SI]) \\
\frac{\mathrm{d}[RI]}{\mathrm{d}t} &= -(2\delta + \gamma)[RI] + \delta([I] - [SI]) + (z-1)\lambda([R][SI]) \\
\frac{\mathrm{d}[SI]}{\mathrm{d}t} &= \gamma[RI] - (\lambda + \delta)[SI] + (z-1)\lambda[SI](1 - [R] - 2[I]).
\end{aligned}
$$

1. Closures vs Equation-Free/Bifurcation Diagram



2. Epidemics: The Topology of the Transmission Network Matters!



Christakis N., Fowler J., Social Network Sensors for Early Detection of Contagious Outbreaks, PLoSONE 5(9) 2010.

A real network of students in the University of Harvard which is used to examine the progress of a disease (Christakis & Fowler, 2010).

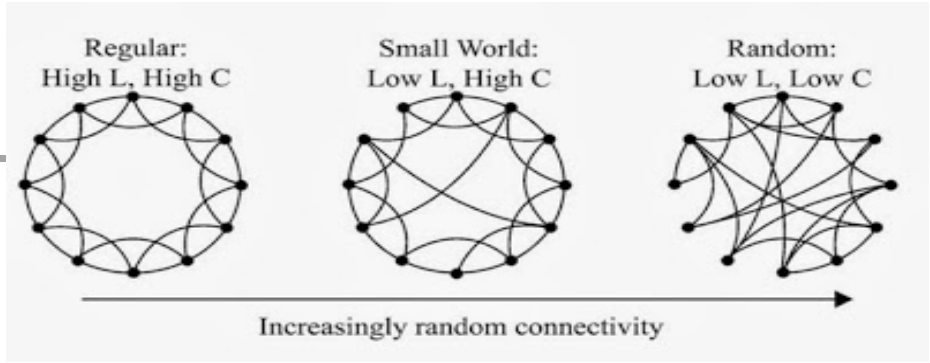
Node A is a central node with 6 friends around him was more likely to get infected sooner because of its shortest path length from other individuals in the network (e.g. B & C)

Nodes B and C: although they have the same number of connections, they have different clustering coefficients

with node C being more likely to get infected earlier in the epidemic.

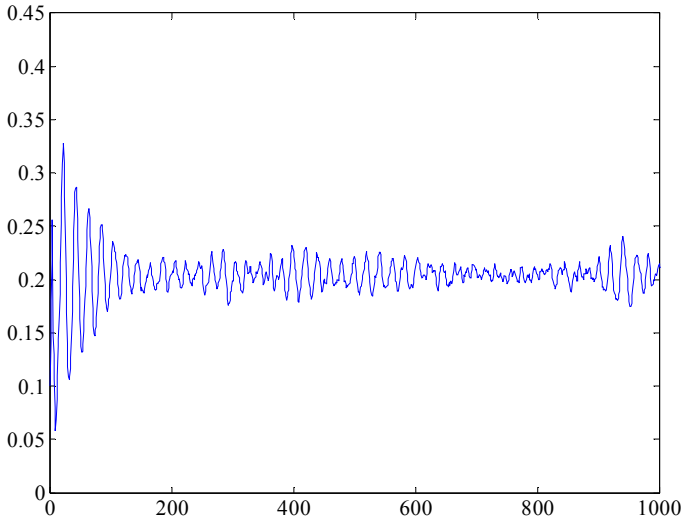
2. The importance of Network Topology

Contact transmission Network:
Watts and Strogatz Small World



Small-world network
constructed with ***p=0.1***

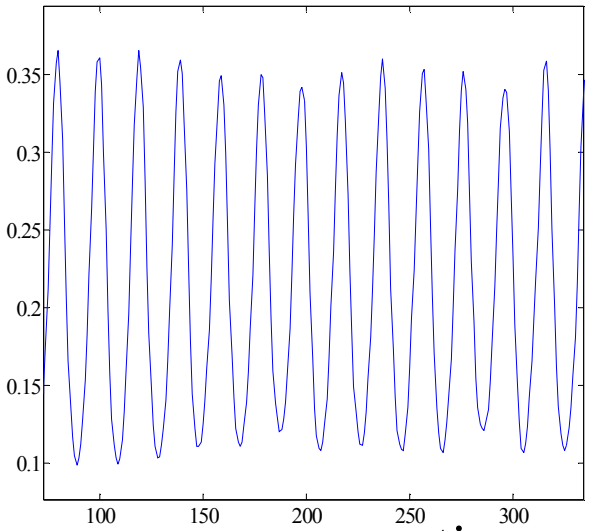
density of susceptible



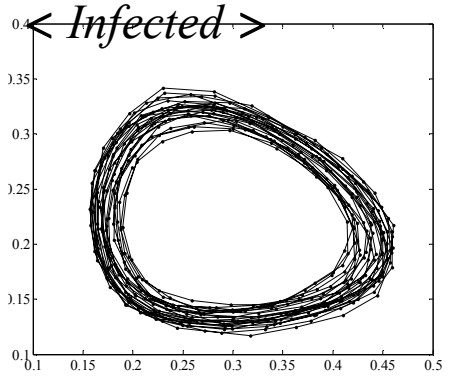
time

small-world network
constructed with ***p=0.3***

density of susceptible



time



< Susceptible >

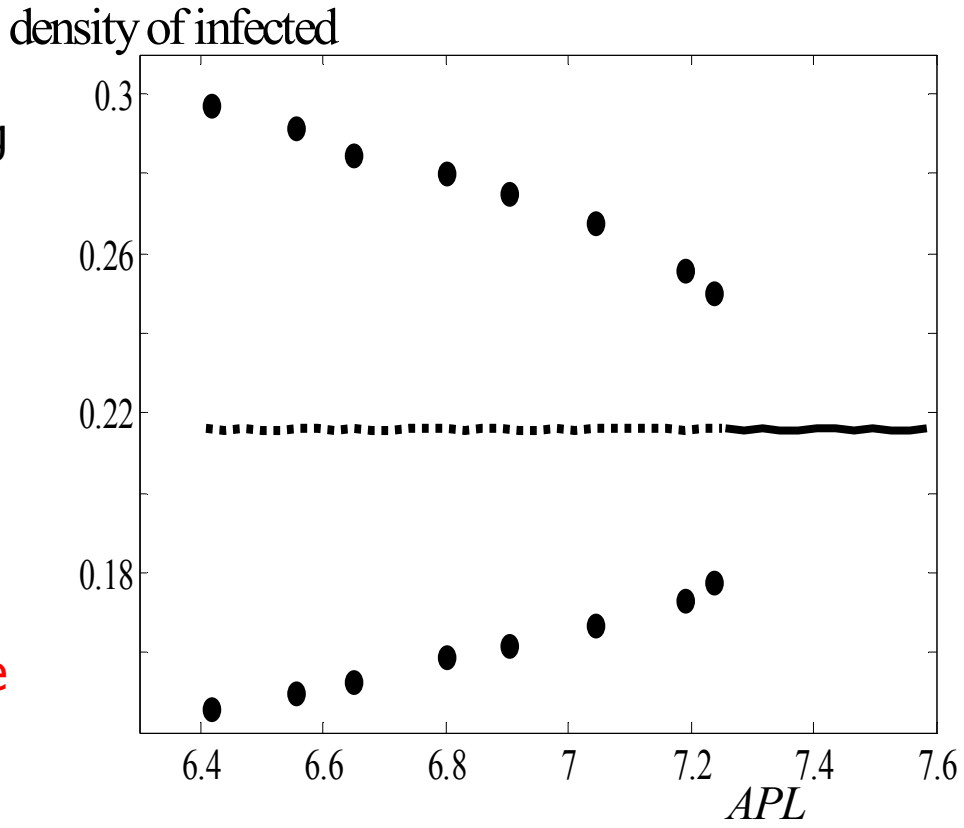
Coarse-grained Bifurcation diagram w.r.t theAPL

Reppas, A.I., Spiliotis, K.G., Siettos, C.I., 2015, Tuning the Average Path Length of Complex Networks and its Influence to the Emergent Dynamics of the Majority-Rule Model, *Mathematics and Computers in Simulation*, 109, 186-196.

- We started with small-world networks constructed with a rewiring probability=*0.25*

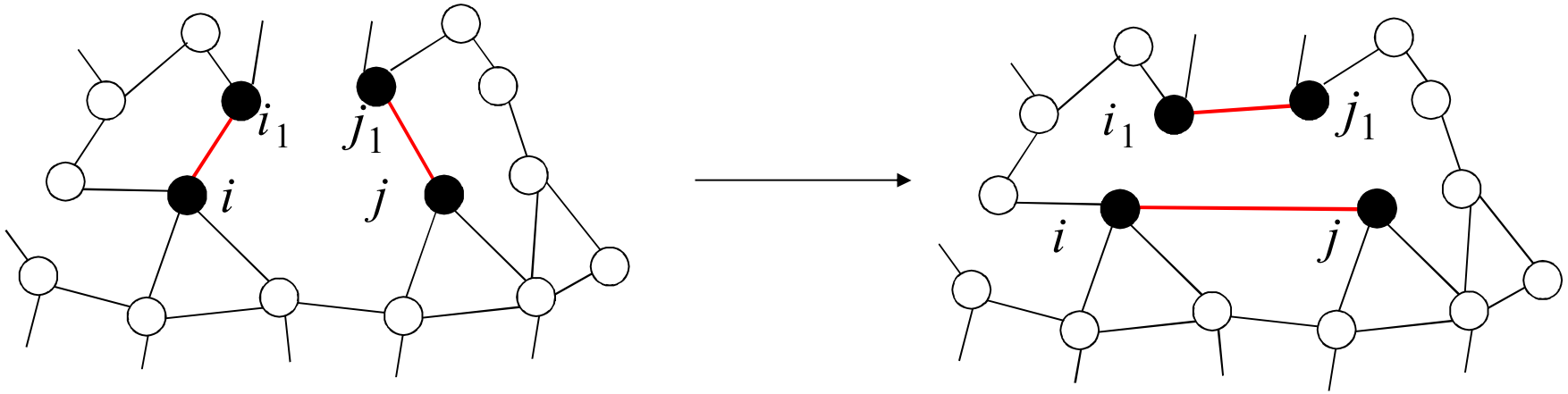
•Adjust the Average Path Length (APL); Degree and Clustering distributions are kept constant

•Equation-Free approach to trace the unstable branch



A Schematic for Adjusting the Average Path Length (APL)

Mutual rewiring of edges; Degree and Clustering distributions are kept constant



Select randomly two nodes i , j

(a) which do not have any common neighbours and

(b) each one of them has at least one neighbour (say i_1 ***and*** j_1 ***) that does not form any triangle with any other neighbour of*** i ***and*** j ***nor any common neighbours exist between*** i_1 ***and*** j_1 **.**

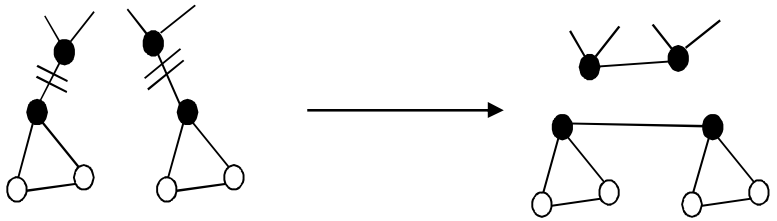
Reppas, A.I., Spiliotis, K.G., Siettos, C.I., 2014, **Tuning the Path Length in Complex Networks: a Metropolis Monte Carlo-based Approach**, *Mathematics and Computers in Simulation*, *doi: 10.1016/j.matcom.2014.09.005*

The proposed algorithm for adjusting the mean path length

The implementation of the algorithm to converge to the target value L^* of the Characteristic Path Length is based on a **Simulated Annealing process:**

Do until Convergence {

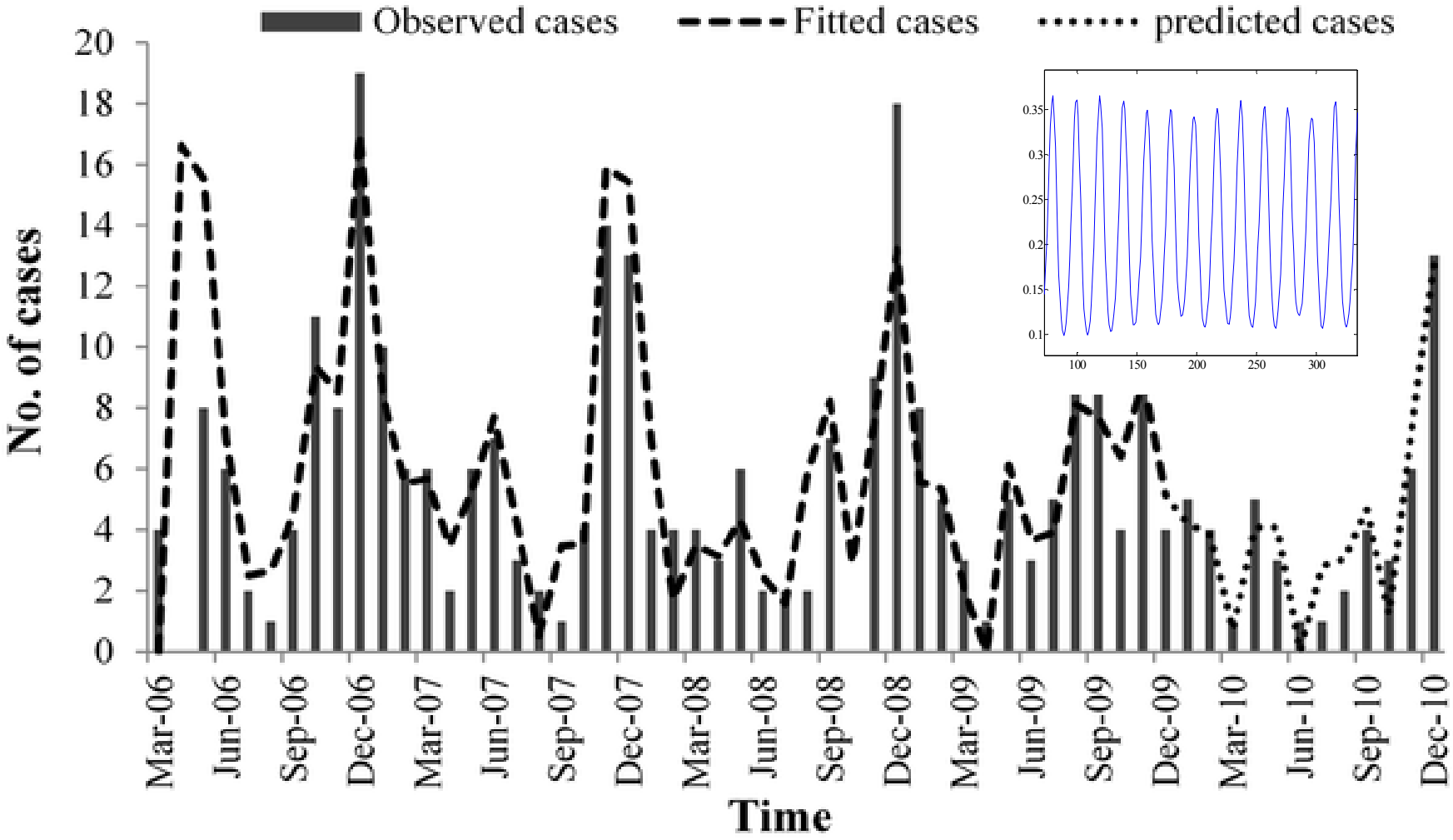
1) *Evaluate the initial characteristic path length of the network, L.*
2) *Make the appropriate rewiring of edges according to the proposed algorithm.*



3) *Evaluate the new characteristic path length, L′.*
4) *Accept or reject the new configuration using the Metropolis procedure.*

}

Hemorrhagic Fever with Renal Syndrome in Chenzhou, China



Xiao H, Tian H-Y, Gao L-D, Liu H-N, et al. (2014) Animal Reservoir, Natural and Socioeconomic Variations and the Transmission of Hemorrhagic Fever with Renal Syndrome in Chenzhou, China, 2006–2010. PLoS Negl Trop Dis 8(1): e2615. doi:10.1371/journal.pntd.0002615

http://www.plosntd.org/article/info:doi/10.1371/journal.pntd.0002615

3. Forecasting the EBOLA 2014-2015 Epidemics in West -Africa

The worst Ebola Virus Disease (EVD) epidemic in history ravaged West Africa.

- **The epidemic began with the report of 49 cases and 29 deaths in Guinea on March 22, 2014.**

- **Liberia reported its first laboratory-confirmed cases on March 30, 2014,**

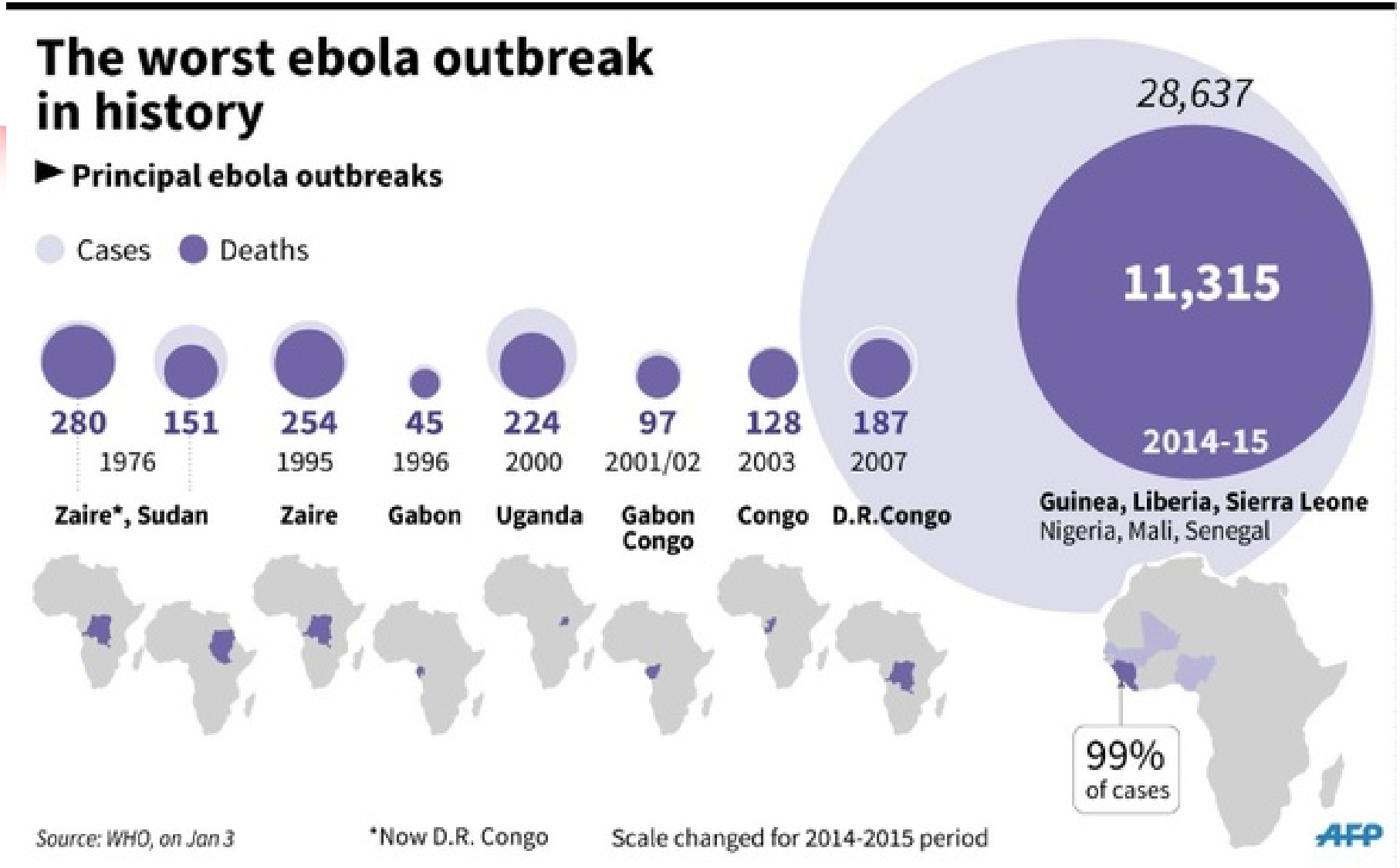
- **the first cases in Sierra Leone were reported on May 28, 2014.**

- **the virus crossed the local porous international borders, establishing chains of transmission not just in small villages, where it would have been easier to contain it, but also in large urban centers.**

- **Insufficient public health infrastructure, poor sanitation conditions, and unsafe traditional burial practices were the main reasons to the spread of the epidemic in the region.**

According to the WHO only the total death toll exceeded 17000 people.

The map of the Epidemic



Mathematical Models: the Ebola Epidemic

- Both deterministic and stochastic SEIR dynamic models have been used to study the 1995 and 2000 Ebola outbreaks in DR Congo and Uganda, which were caused by the Zaire and Sudan virus strains, correspondingly (e.g. Chowell et al., 2004; Lecone and Finkenstädt, 2006).

- Legrand et al. (2007), analyzed data from these two epidemics with a sixth-order stochastic compartmental model that incorporated explicitly the settings of transmission in the community, in the hospital and during traditional burial ceremonies.

- For the current Ebola outbreak in West Africa, Rivers et al. (2014) utilized the model proposed by Legrand (2007) to approximate and forecast the evolution of the spread in Liberia and Sierra Leone. Their model forecasted a continuously increasing epidemic until December 31, 2014, with medians of 117,877 and 30,611 cases for Liberia and Sierra Leone, respectively.

3. Forecasting the EBOLA 2014-2015 Epidemics in West -Africa

Factors such as:

- **Incubation period, recovery period, time to death,**

- **Per- Contact transmission probability (the most difficult to predict just from clinical studies)**

- **Reproductive number – number of secondary infected from an infectious!!!**

- **Age-Specific distributions (age-structured parameters)**

- Topological characteristics of the underlying transmission network is of outmost importance,

Mathematical Models: the Ebola Epidemic

- **Althaus (2014) used a deterministic SEIR dynamic model to estimate two vital epidemiological parameters for any infection, describing the spread of EBOV in West African countries, in this case: the basic and the effective reproduction numbers, R_0 and R_e**

- **A compartmental stochastic, individual-based model employed by Gomes et al. (2014) to approximate the dynamics of the Ebola outbreak worldwide at an early period of the outbreak, estimated a rapid increase of the cases in African countries, and a potential international threat on a longer time-scale.**

- **Kiskowski (2014) combined a stochastic SEIR model with a three-scale community network model representing contacts between households and local communities, to demonstrate that the different regional trends of the early growth dynamics of the 2014 EBOV epidemic in Guinea, Sierra Leone and Liberia might be explained by disparate local community mixing rates.**

Mathematical Models: Our contribution

Computer model predicted when the Ebola outbreak in Liberia would fade out

Last updated: Monday 16 March 2015 at 2am PST

Ebola | Adapted media release

Infectious Diseases / Bacteria / Viruses

A novel mathematical approach applied to model the ongoing Ebola outbreak, predicted the current fade out of the epidemic in Liberia almost to the exact date (early March). Using World Health Organization (WHO) data through December 21, 2014, the study that was published online in *PLoS Currents Outbreaks*, was the first to provide an accurate prediction for the epidemic containment.

What's new

Siettos, C., Anastassopoulou, C., Russo, L., Grigoras, C., Mylonakis, E., 2015, Modeling the 2014 Ebola Virus Epidemic – Agent-Based Simulations, Temporal Analysis and Future Predictions for Liberia and Sierra Leone. *PLOS Currents*, 2015 Mar 9.

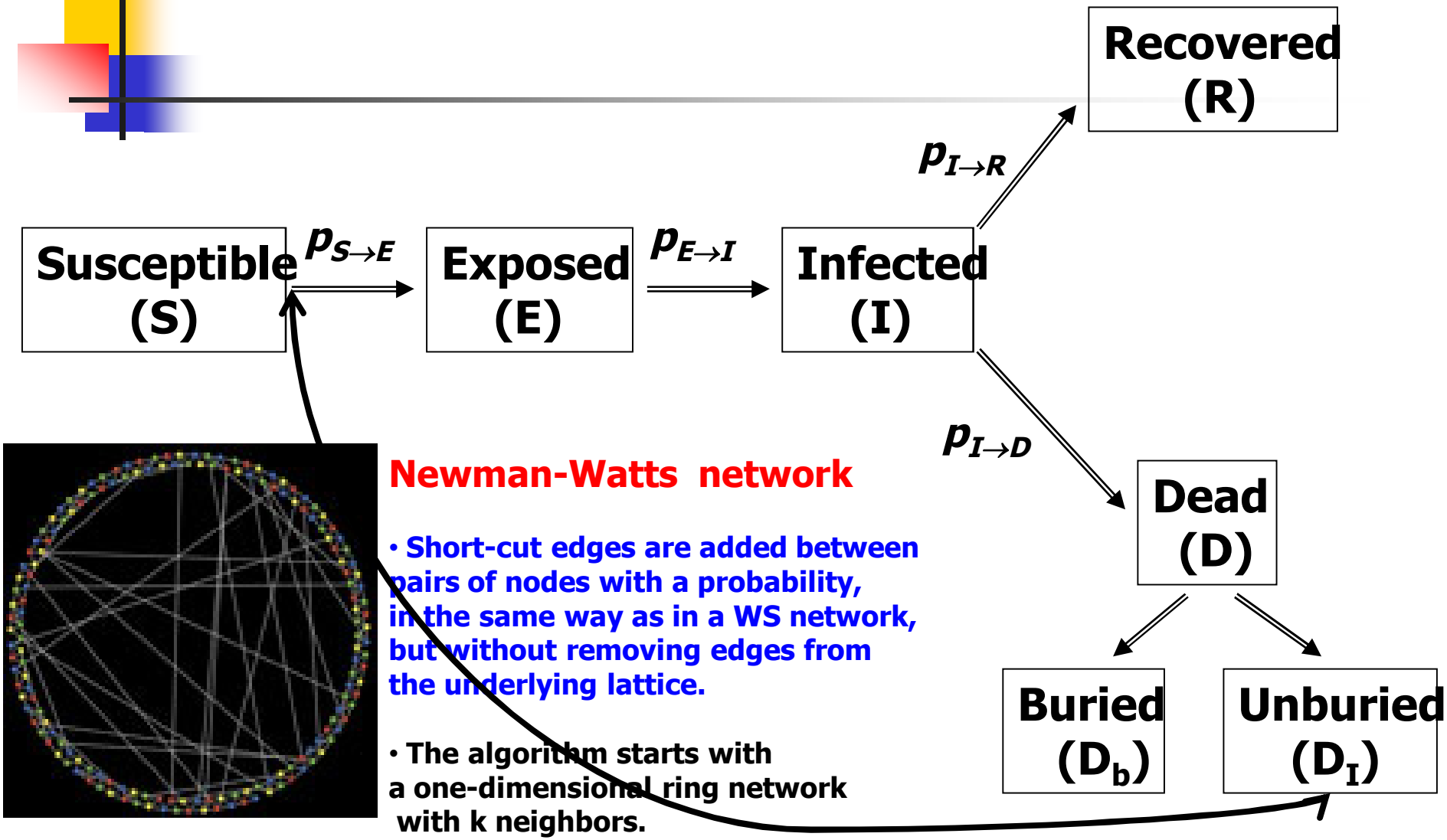
and also

Siettos, C., Anastassopoulou, C., Russo, L., Grigoras, C., Mylonakis, E., 2016, Modeling, Forecasting and Control Policy Assessment for the Ebola Virus Disease (EVD) Epidemic in Sierra Leone Using Small-World Networked Model Simulations, BMJ Open, 6, e008649

Integrating Agent-Based modeling on complex networks and the so-called Equation-Free approach (multiscale bridging)
which allowed us to assess various important epidemiologic parameters including the evolution of the underlying transmission network

Model and Methodology in a Nutshell

Number of Agents = Population ~O(4-6 millions)



Newman-Watts network

- **Short-cut edges are added between pairs of nodes with a probability, in the same way as in a WS network, but without removing edges from the underlying lattice.**

- **The algorithm starts with a one-dimensional ring network with k neighbors.**

Forecasting the Evolution of EBOLA Epidemics: the case of Liberia and Sierra Leone

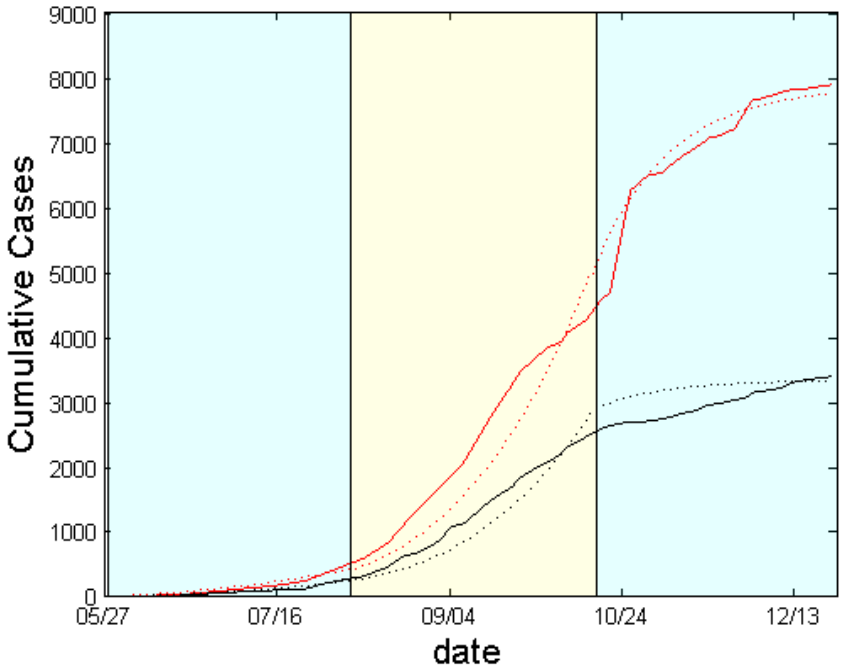
- **Time series of the official case counts from the World Health Organization were used for model fitting (CDC, 2014).**

- **Case data, which included cumulative incidence and cumulative deaths by date of report for Liberia and Sierra Leone retrieved on 5th of January, were found on Wikipedia (2015) and compiled from WHO case reports**

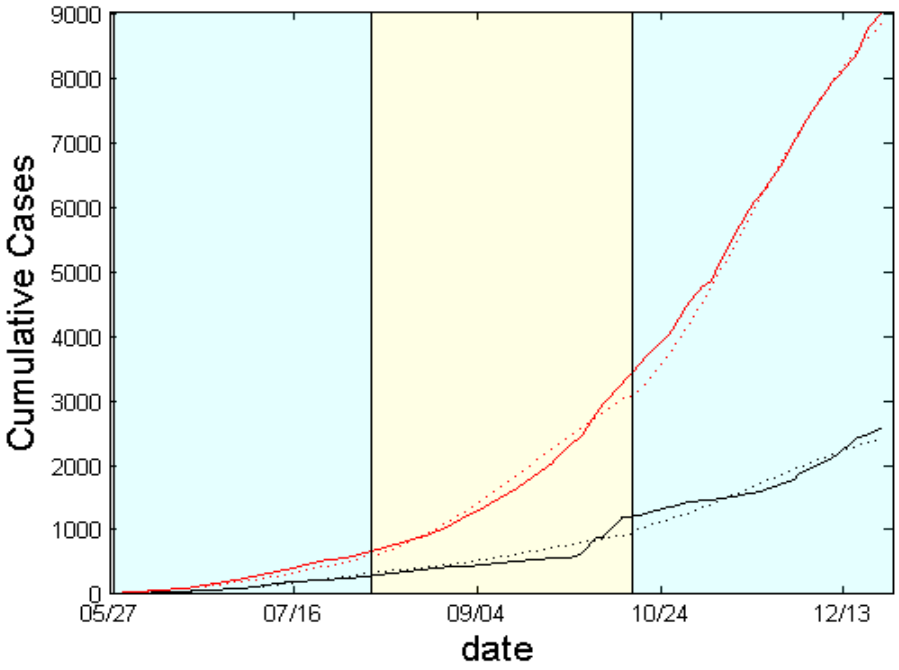
- **Simulations were performed using May 27, 2014 as an initial date and a time horizon of 70 days (10 weeks) with an equal sliding window time interval; the last date was December 21, 2014.**

RESULTS

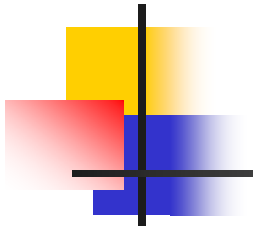
LIBERIA



SIERRA LEONE



Conclusions



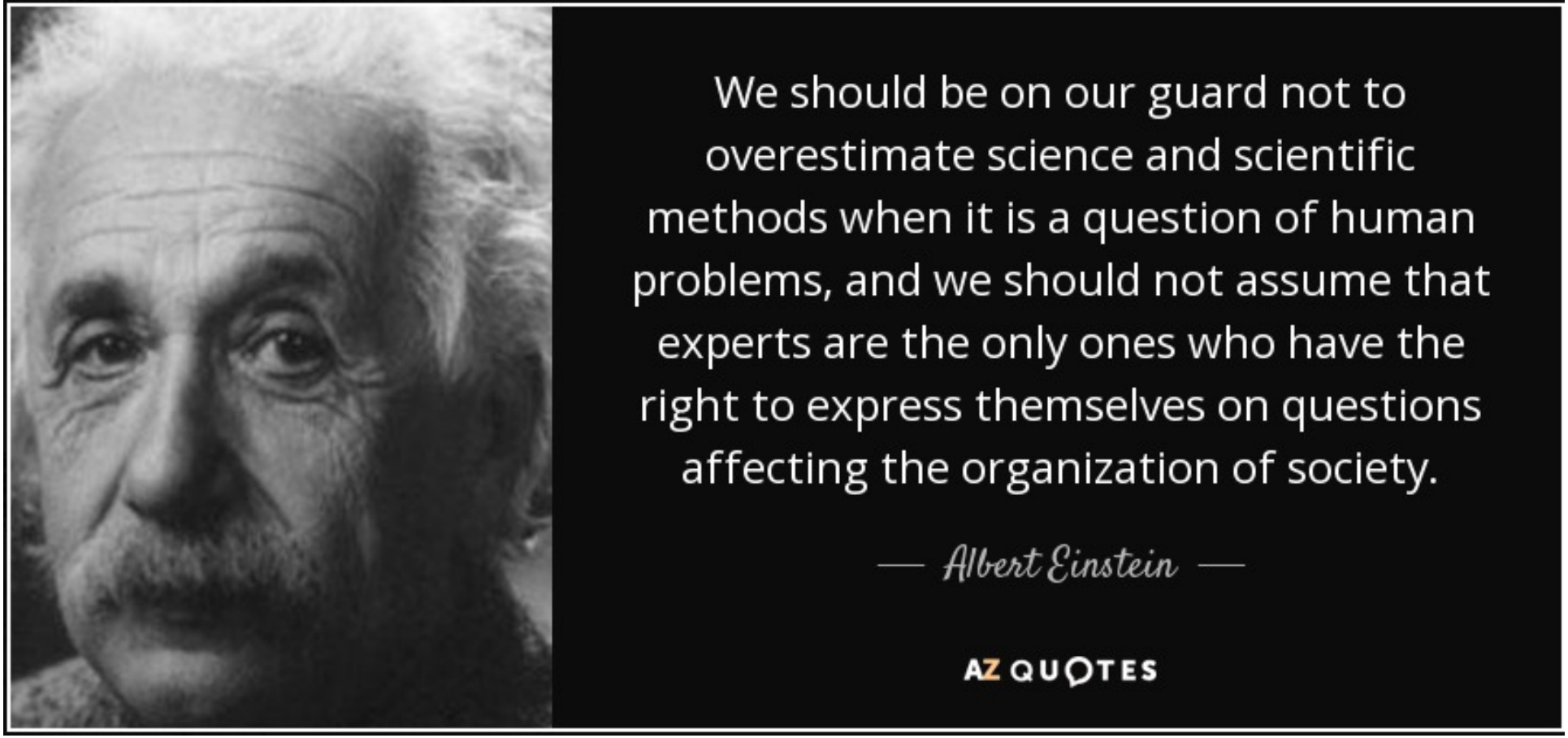
We propose an approach bridging state-of-the-art Agent-Based Models and Numerical Analysis/ Control Techniques for the risk assessment and forecasting of Emerging Infectious Dynamics

-We have successfully forecasted the evolution of the Epidemic in Liberia and Sierra Leone, ahead of time (a time horizon of 3 months)

- Usefulness of Would-Be Worlds/ Mathematical models should not be overestimated.

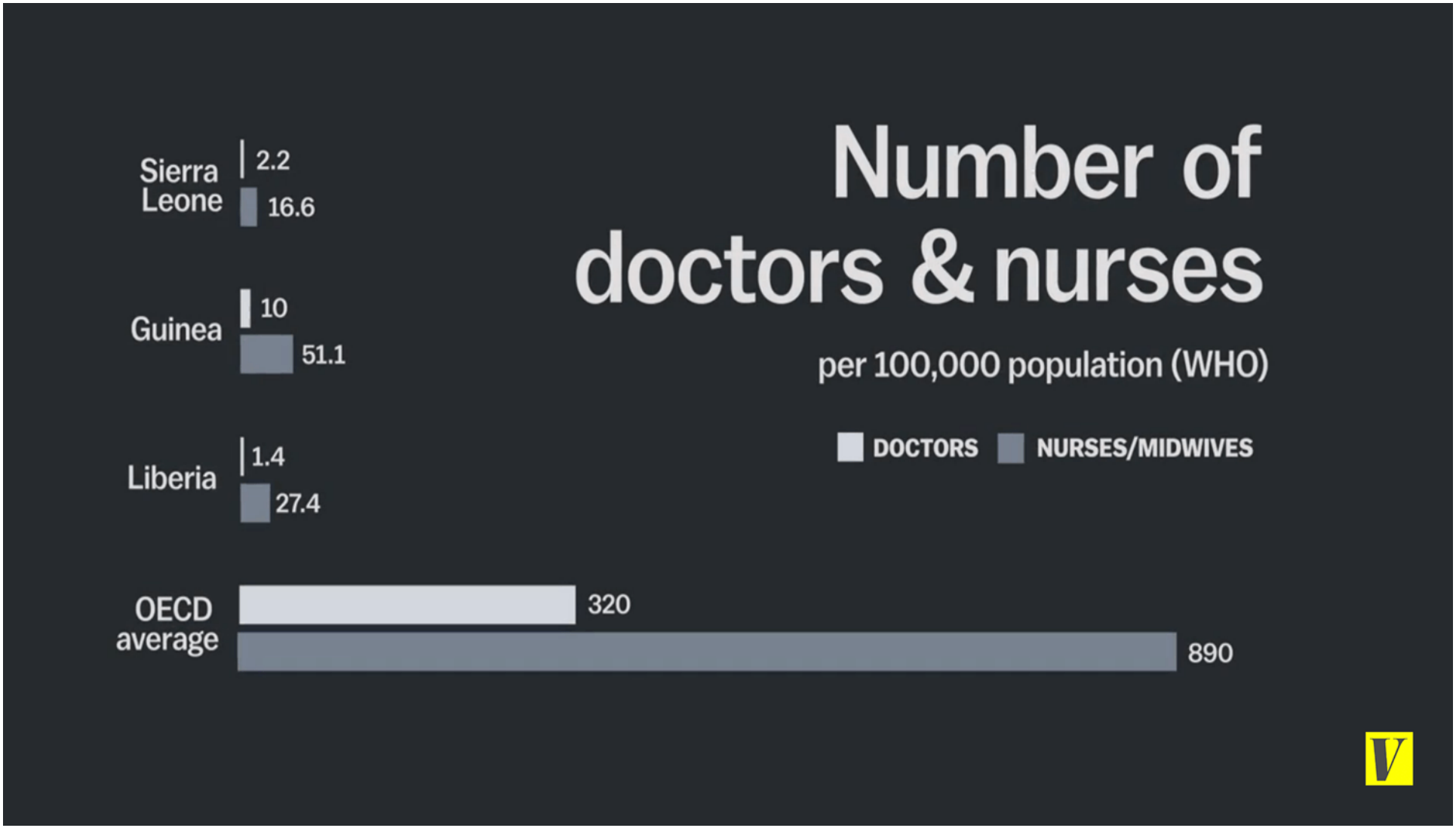
-Despite the significant technological progress and concentrated wealth, breakdowns and cuts in public health infrastructures worldwide are (the) major reasons for boosting epidemics.

Conclusions



On one hand….

On one hand….


Number of doctors & nurses
per 100,000 population (WHO)
DOCTORS
NURSES/MIDWIVES
Sierra Leone
2.2
16.6
Guinea
10
51.1
Liberia
1.4
27.4
OECD average
320
890

On the other hand….

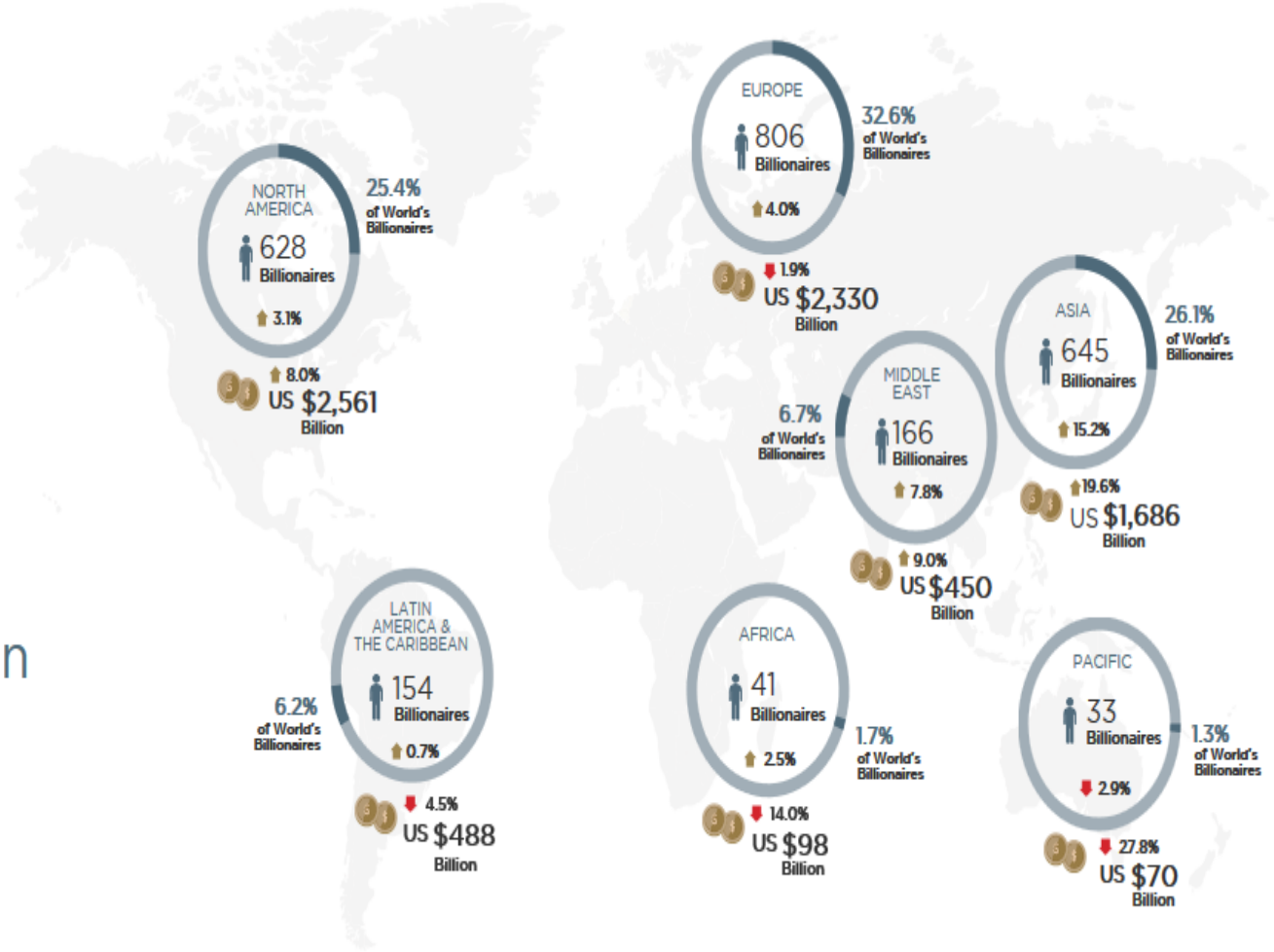
WEALTH-X

Wealth-X Billionaire Census 2015-16

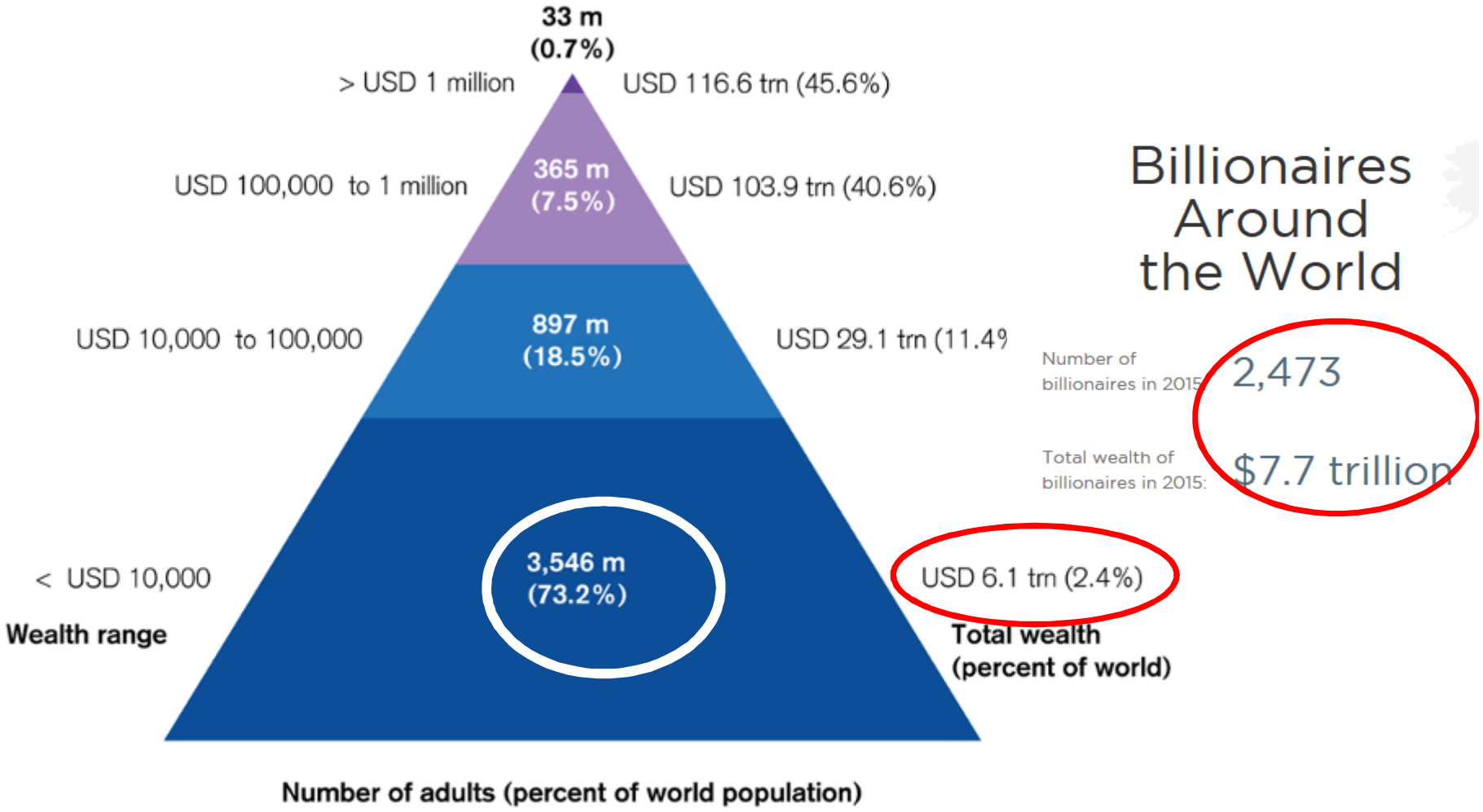
Billionaires Around the World

Number of billionaires in 2015: 2,473

Total wealth of billionaires in 2015: $7.7 trillion



The Global Wealth Pyramid



Billionaires Around the World

Number of billionaires in 2015: 2,473

Total wealth of billionaires in 2015: $7.7 trillion

The Global Wealth Pyramid

Source: James Davies, Rodrigo Lluberas and Anthony Shorrocks, Credit Suisse Global Wealth Databook 2016

Thank you!


HMMM... WE HAVE MORE IN COMMON THAN I THOUGHT...
U.S. WORKERS
ILLEGALS
UNEMPLOYMENT
CARTOONSTOCK .com
Search ID: pfen87
© 2010