



EMORY

ROLLINS
SCHOOL OF
PUBLIC
HEALTH

Summer Institute in
Statistics and Modeling
in Infectious Diseases

17TH ANNUAL SISIMID

JULY 7 - 30, 2025

EMORY UNIVERSITY
ATLANTA, GA

ONLINE - JULY 7-11, 2025

IN-PERSON - JULY 14-30, 2025

Spatial and Metapopulation Modeling

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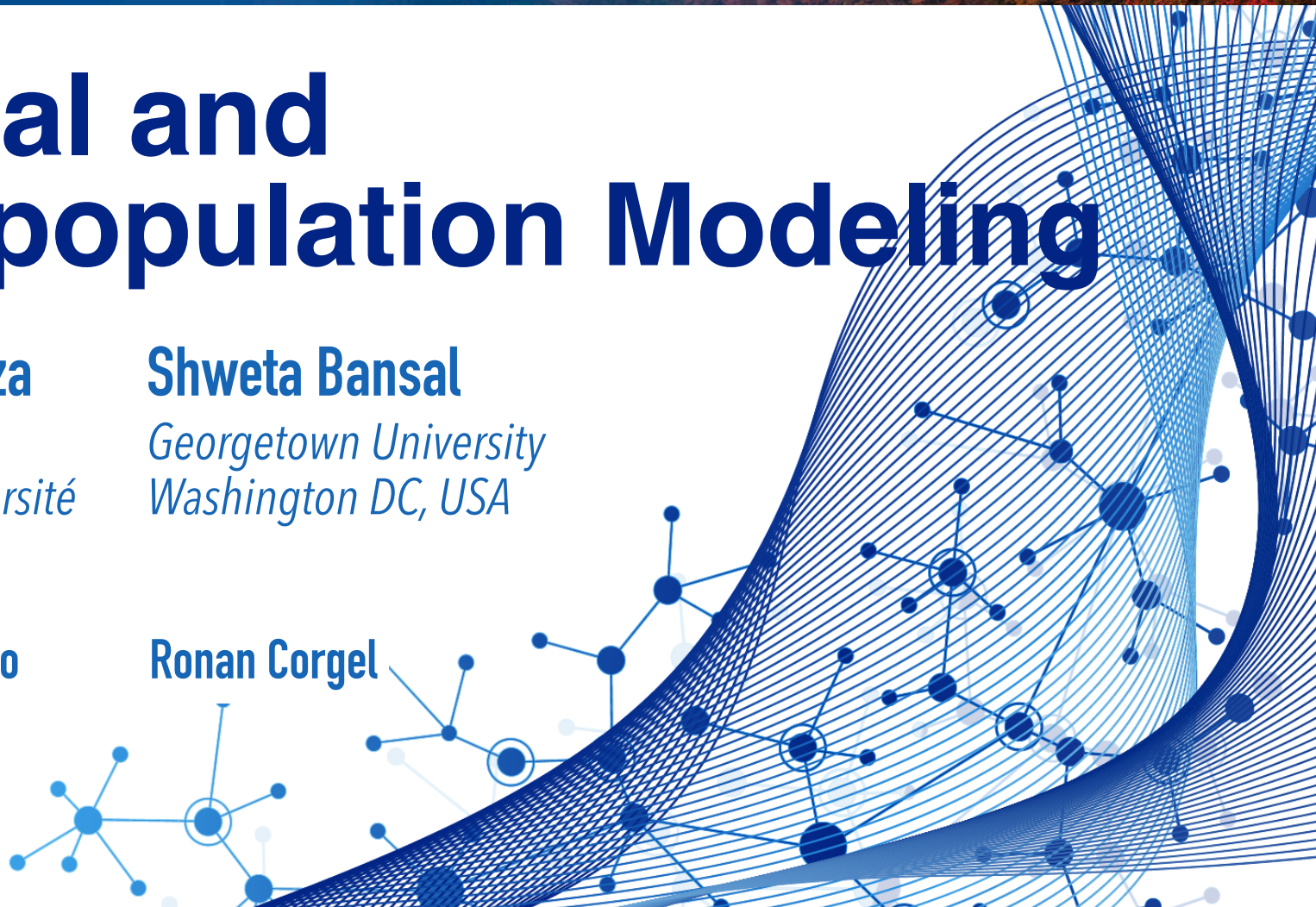
Shweta Bansal

Georgetown University

Washington DC, USA

Francesco Parino

Ronan Corgel



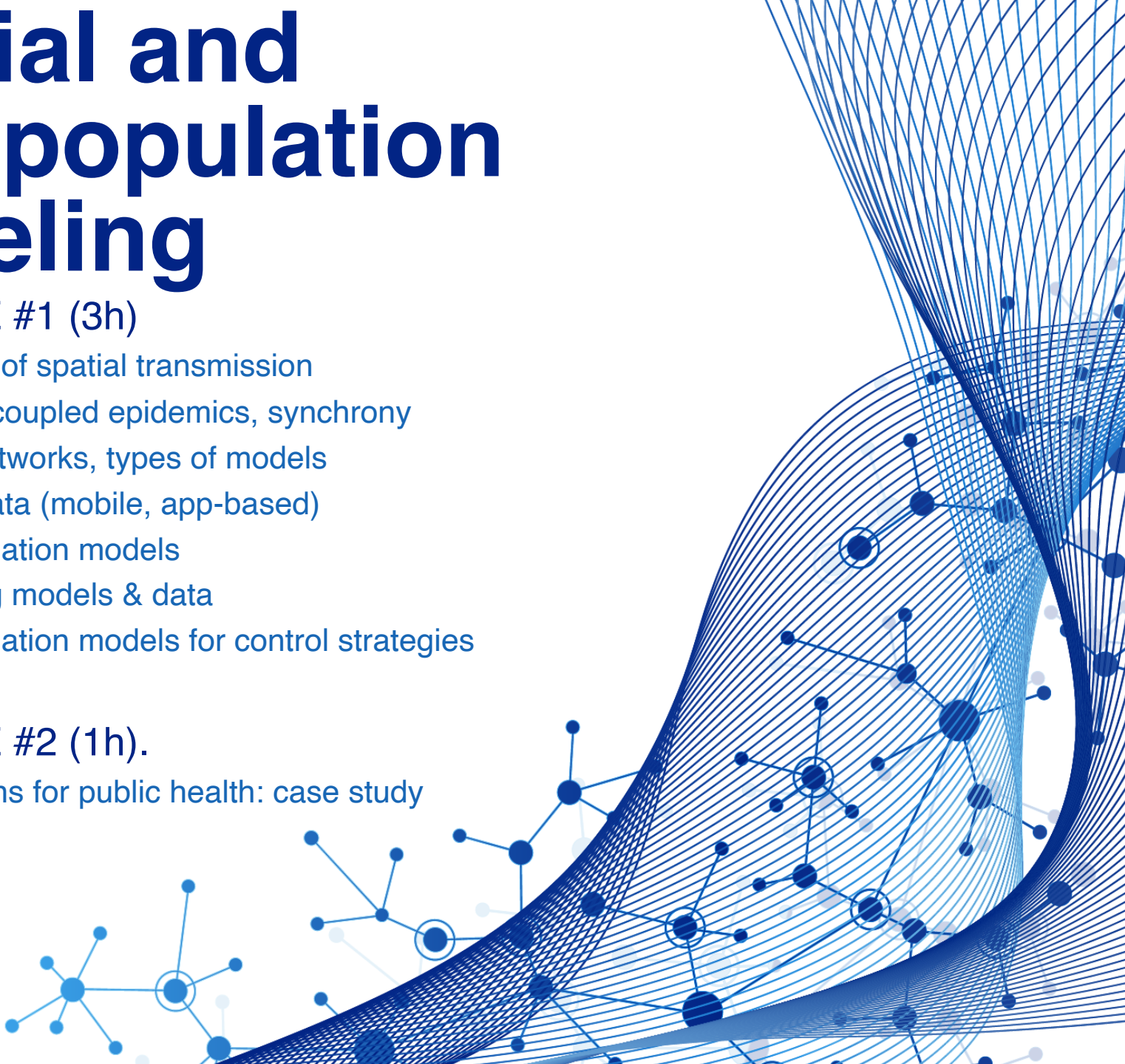
Spatial and Metapopulation Modeling

► LECTURE #1 (3h)

- Examples of spatial transmission
- Invasion, coupled epidemics, synchrony
- Role of networks, types of models
- Mobility data (mobile, app-based)
- Metapopulation models
- Integrating models & data
- Metapopulation models for control strategies

► LECTURE #2 (1h).

- Applications for public health: case study



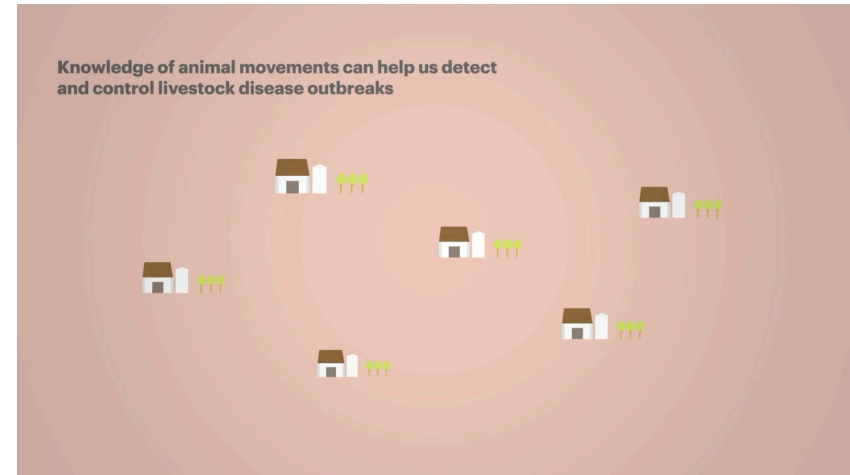
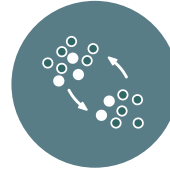
Spatial and Metapopulation Modeling

LECTURE #1.

Mobility networks and spatial
disease transmission



Networks in spatial disease transmission

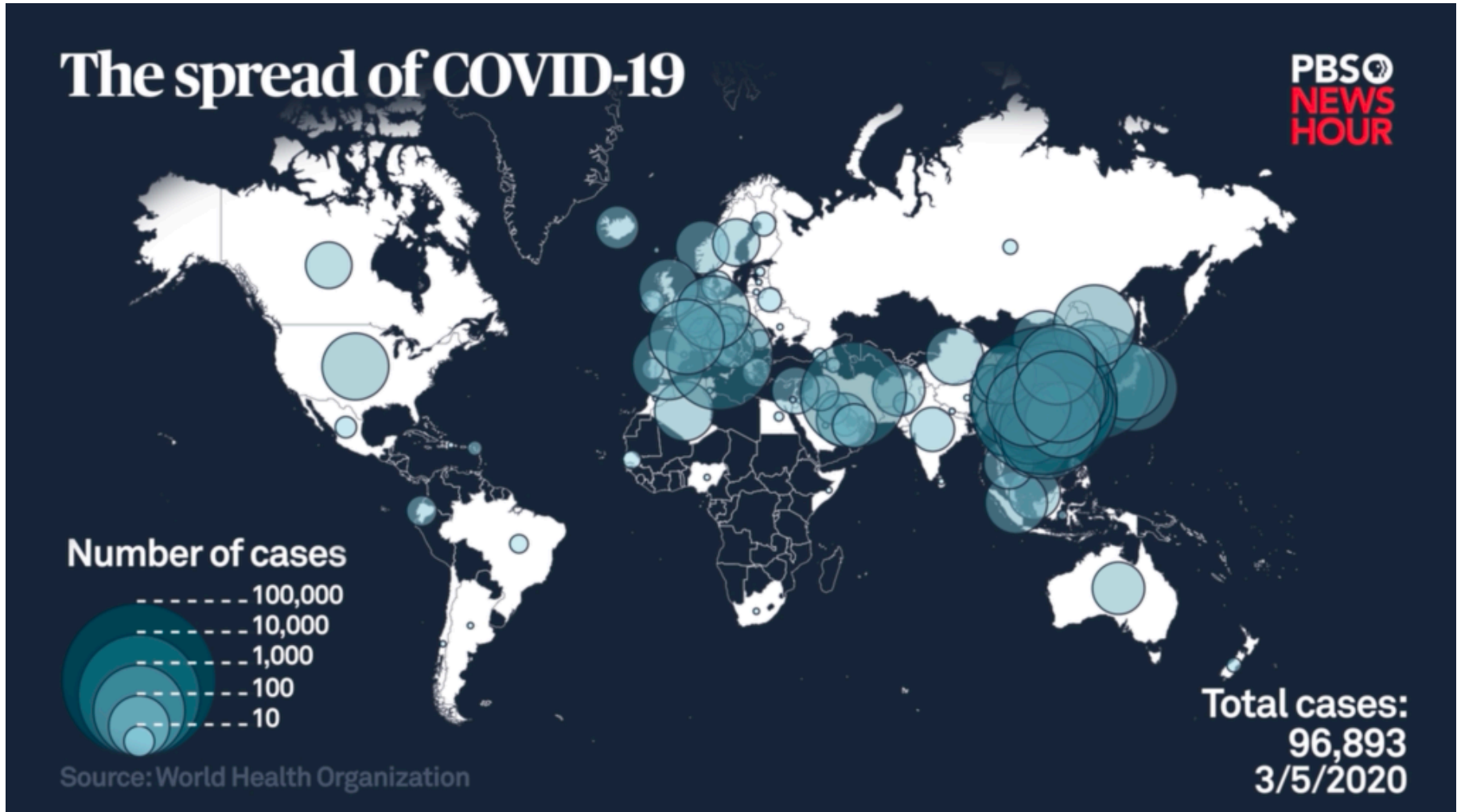


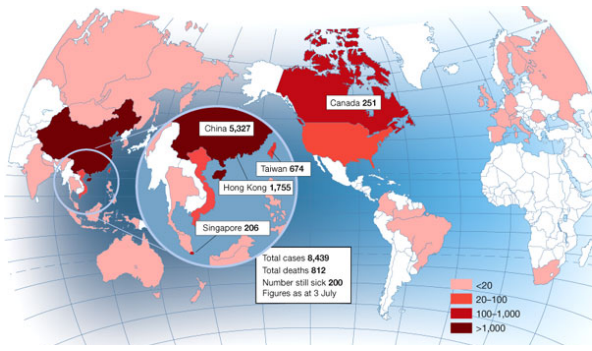
Colizza et al. PLOS Medicine 2007
Balcan et al PNAS 2009
Tizzoni et al BMC Med 2012

Bajardi et al PLOS One 2009
Bajardi et al Proc Roy Soc Interface 2012
Valdano et al PLOS Compute Bill 2015

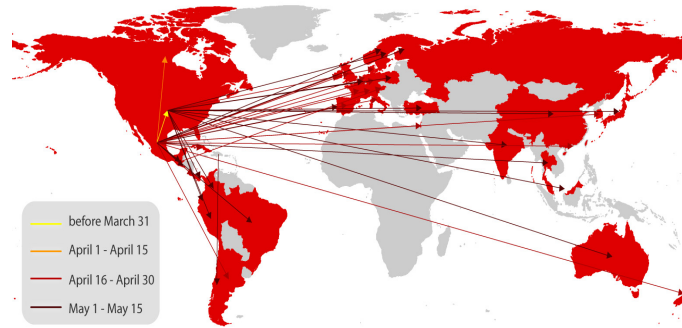
“PROFESSIONAL EPIDEMIOLOGISTS APPEAR OBLIVIOUS TO WHERE THE EPIDEMIC IS, ASKING ONLY WHEN NUMBERS WILL APPEAR ALONG THE TIME HORIZON.” (GEOGRAPHER PETER GOULD, 1991)

Spatial disease transmission

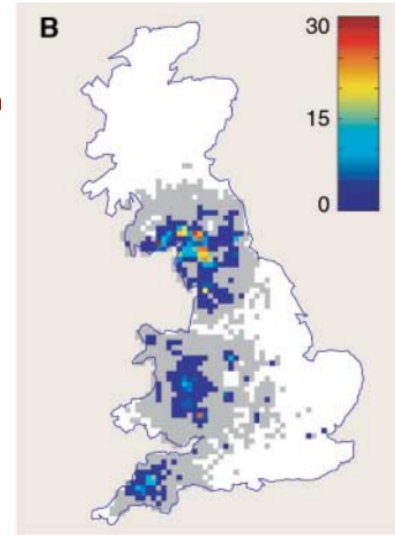




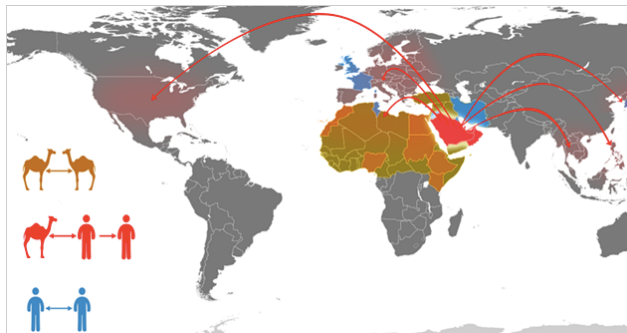
2002-2003: SARS



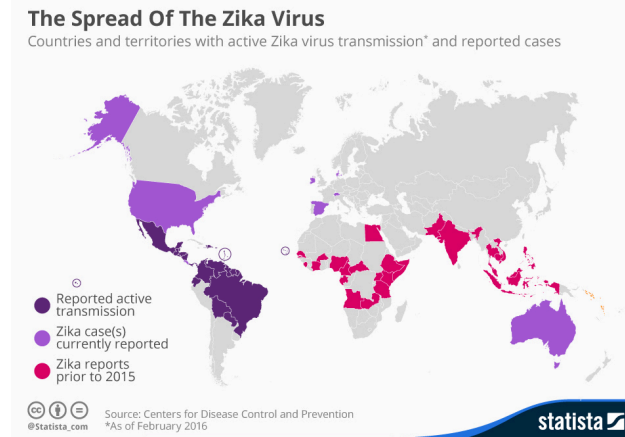
2009: H1N1 pdm



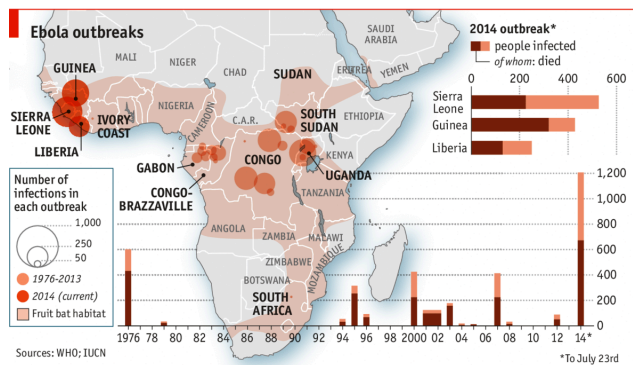
2001: FMD



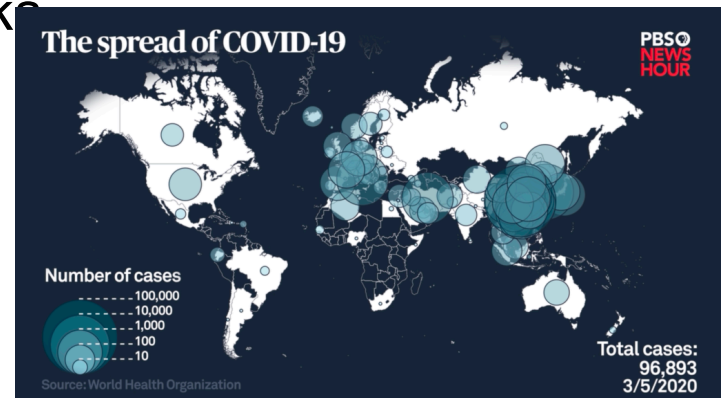
2012—: MERS



2014: Zika

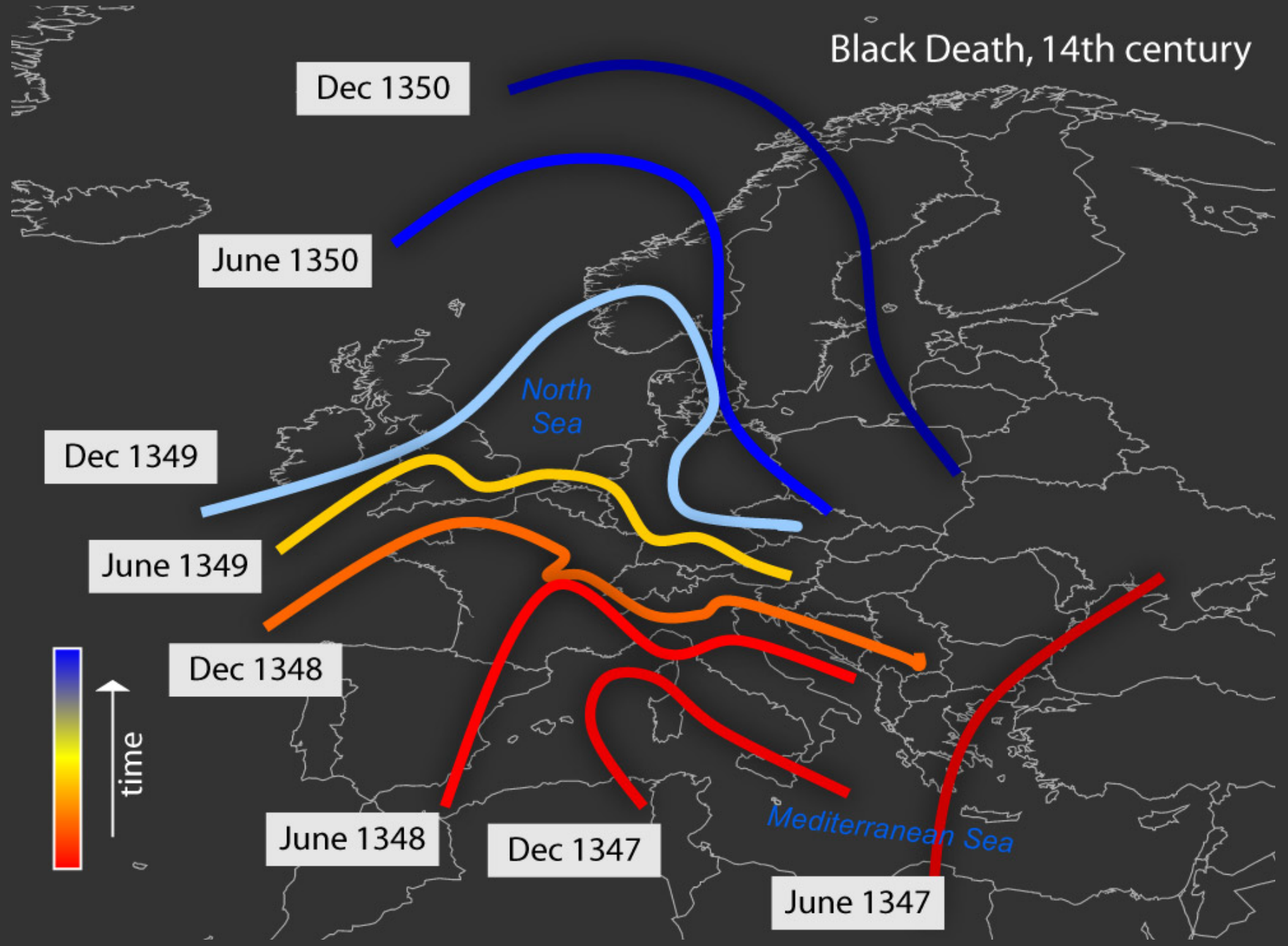


2014: Ebola



2020: SARS-CoV-2

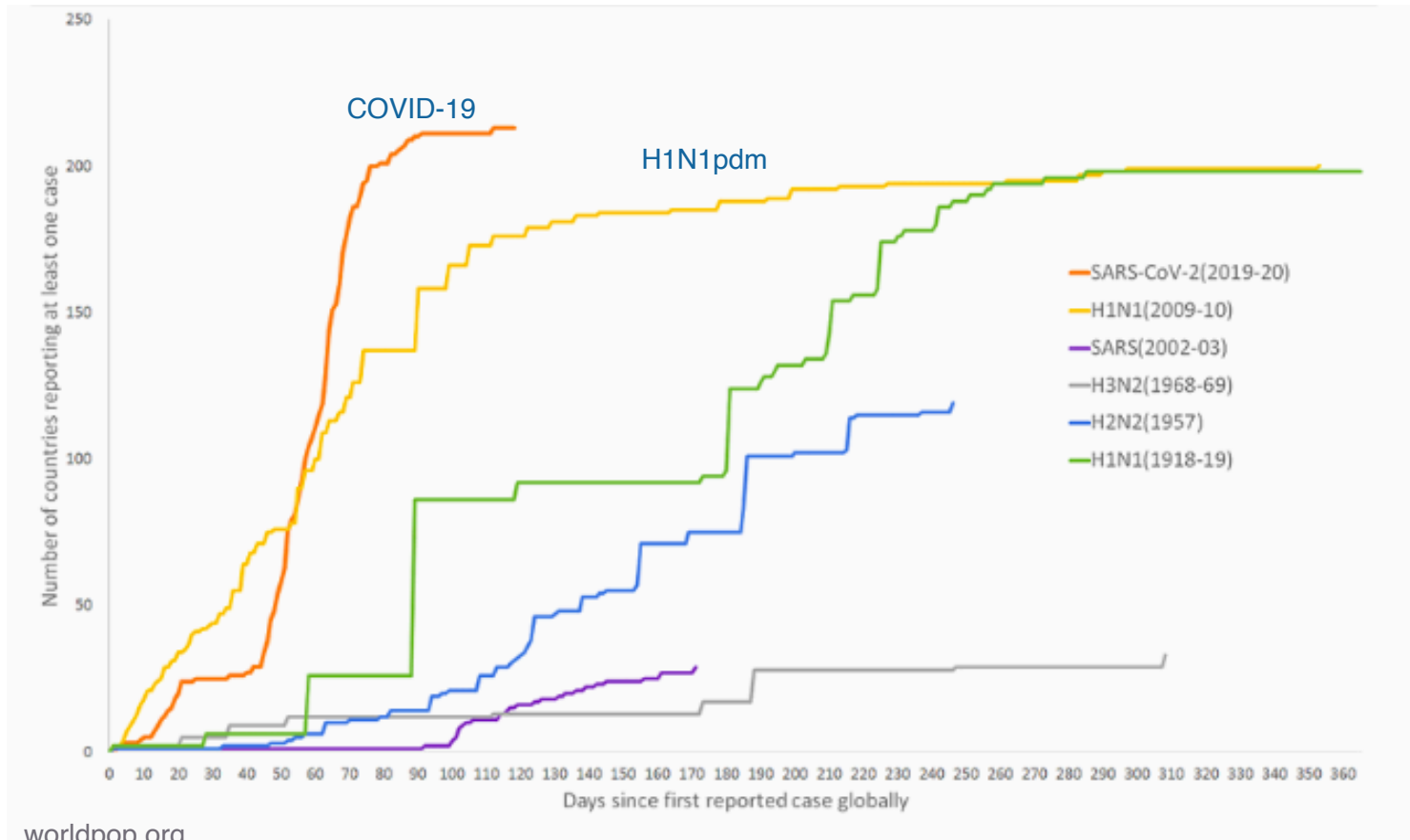
Black Death, 14th century



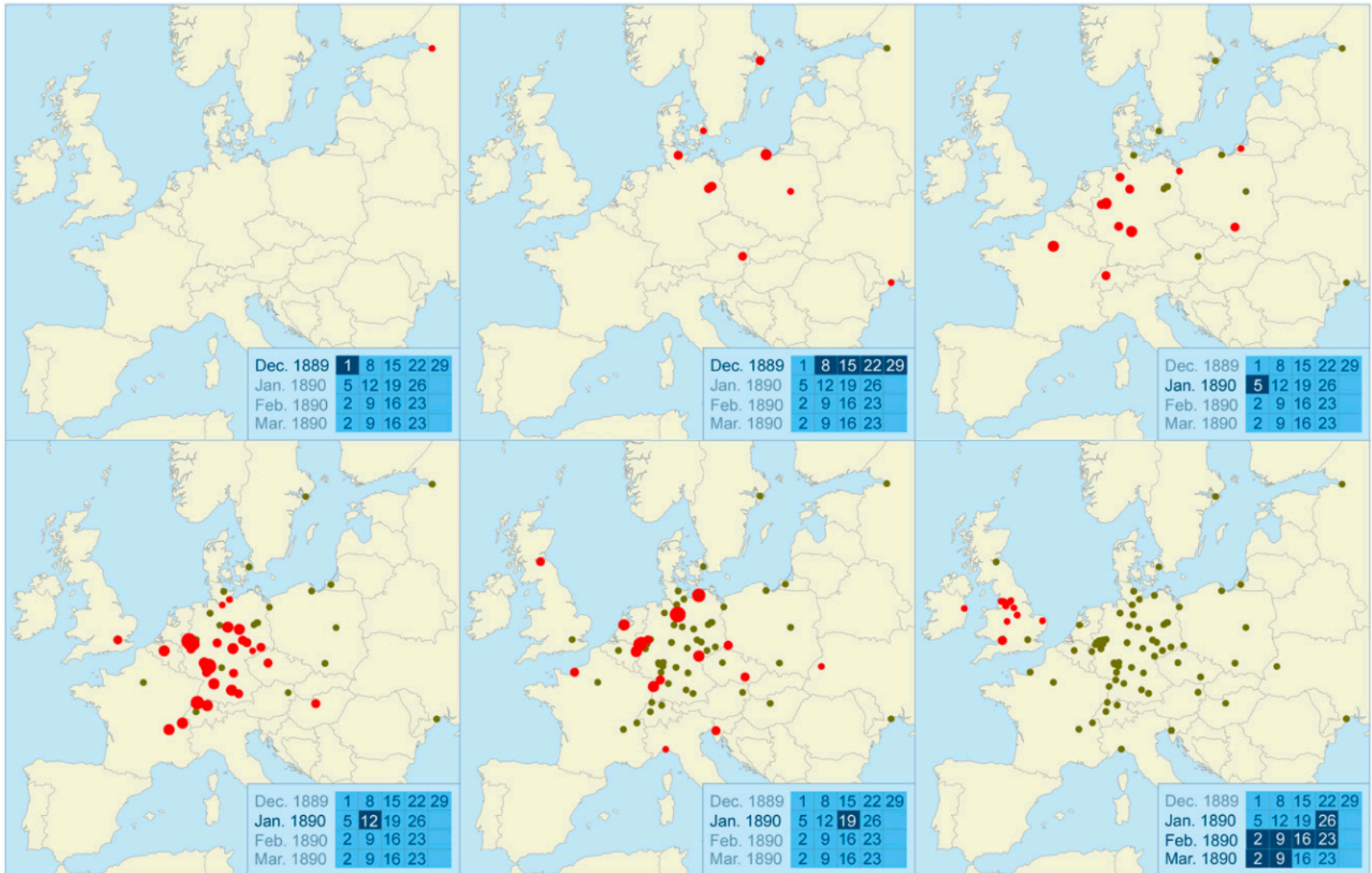
**Black Death pattern vs.
recent epidemics patterns**



Acceleration

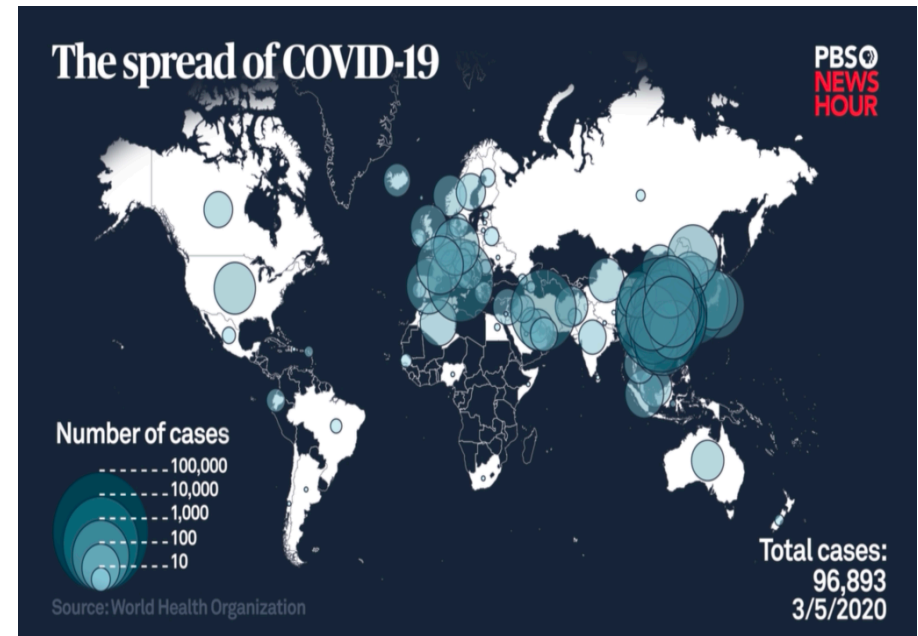
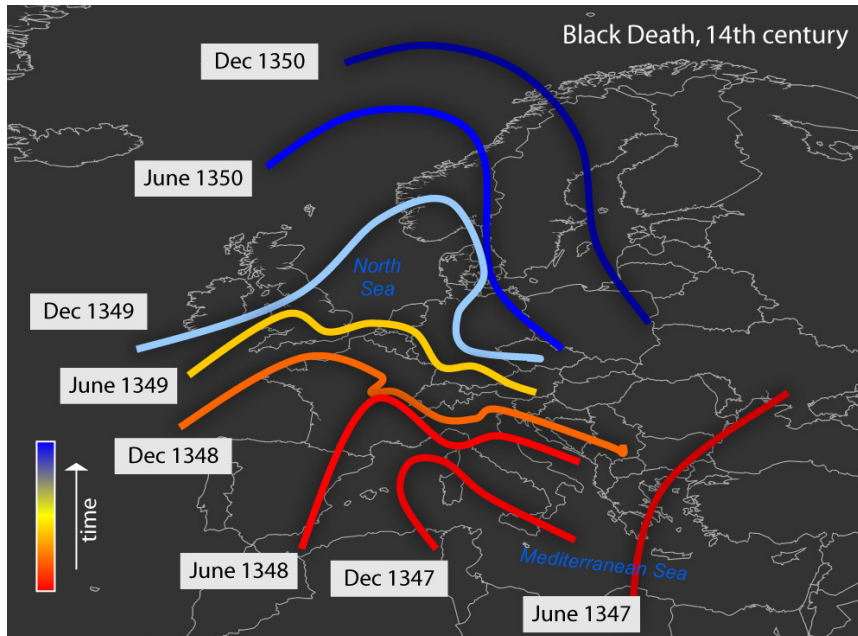


But... 1889 flu pandemic



Peak size ● [0.25-1[● [1-1.75[● [1.75-2.5[● [2.5-3.25[● [3.25-4[

Wave vs. non-local jumps



Accelerated Article Preview

Effect of non-pharmaceutical interventions to contain COVID-19 in China

Received: 12 March 2020

Shengjie Lai, Nick W. Ruktanonchai, Liangcai Zhou, Olivia Prosper, Wei Luo, Jessica R. Floyd, Amy Wesolowski, Mauricio Santillana, Chi Zhang, Xiangjun Du, Hongjie Yu & Andrew J. Tatem

Accepted: 23 April 2020

Article

Population flow drives spatio-temporal distribution of COVID-19 in China

<https://doi.org/10.1038/s41586-020-2284-y>Jayson S. Jia¹, Xin Lu^{2,3}, Yun Yuan⁴, Ge Xu⁵, Jianmin Jia^{6,7,8} & Nicholas A. Christakis⁸

Received: 18 February 2020

Articles

Effects of non-pharmaceutical interventions on COVID-19 cases, deaths, and demand for hospital services in the UK: a modelling study

Nicholas G Davies, Adam J Kucharski*, Rosalind M Eggo*, Amy Gimma, W John Edmunds, on behalf of the Centre for the Mathematical Modelling of Infectious Diseases COVID-19 working group



The impact of non-pharmaceutical interventions on SARS-CoV-2 transmission across 130 countries and territories

Yang Liu^{1,2}, Christian Morgenstern^{2,3}, James Kelly², Rachel Lowe¹, CMMID COVID-19 Working Group, Mark Jit^{1,2}¹Centre for Mathematical Modelling of Infectious Disease, London School of Hygiene & Tropical Medicine, London, United Kingdom²Informed Portfolio Management, United Kingdom

RESEARCH

CORONAVIRUS

The effect of human mobility and control measures on the COVID-19 epidemic in China

Moritz U. G. Kraemer^{1,2,3*}, Chia-Hung Yang⁴, Bernardo Gutierrez^{1,5}, Chieh-Hsi Wu⁶, Brennan Klein⁴, David M. Pirotti⁷, Open COVID-19 Data Working Group†, Louis du Plessis¹, Nuno R. Faria¹, Ruoran Li⁸, Yanyan Li⁸, John S. Brownstein^{2,3}, Maylis Layan^{9,10}, Alessandro Vespignani^{4,11}, Huaiyu Tian¹², Yiye¹, Oliver G. Pybus^{1,13*}, Samuel V. Scarpino^{4*}Di Domenico et al. *BMC Medicine* (2020) 18:240
<https://doi.org/10.1186/s12916-020-01698-4>

BMC Medicine

RESEARCH ARTICLE

Open Access

Impact of lockdown on COVID-19 epidemic in Île-de-France and possible exit strategies

Laura Di Domenico¹, Giulia Pullano^{1,2}, Chiara E. Sabbatini¹, Pierre-Yves Boëlle¹ and Vittoria Colizza^{1*}

Article

Estimating the effects of non-pharmaceutical interventions on COVID-19 in Europe

138/s41586-020-2405-7

2020

020

June 2020

98

Seth Flaxman^{1,2}, Swapnil Mishra^{2,7}, Axel Gandy^{1,7}, H. Juliette T. Unwin², Thomas A. Mellan², Helen Coupland², Charles Whittaker², Harrison Zhu¹, Tresnia Berah¹, Jeffrey W. Eaton², Mélodie Monod¹, Imperial College COVID-19 Response Team¹, Azra C. Ghani¹, Christl A. Donnelly^{2,3}, Steven Riley², Michaela A. C. Vollmer², Neil M. Ferguson², Lucy C. Okell¹ & Samir Bhatt^{2,7,8}Following the detection of the new coronavirus¹ severe acute respiratory syndrome

Importation vs. persistence

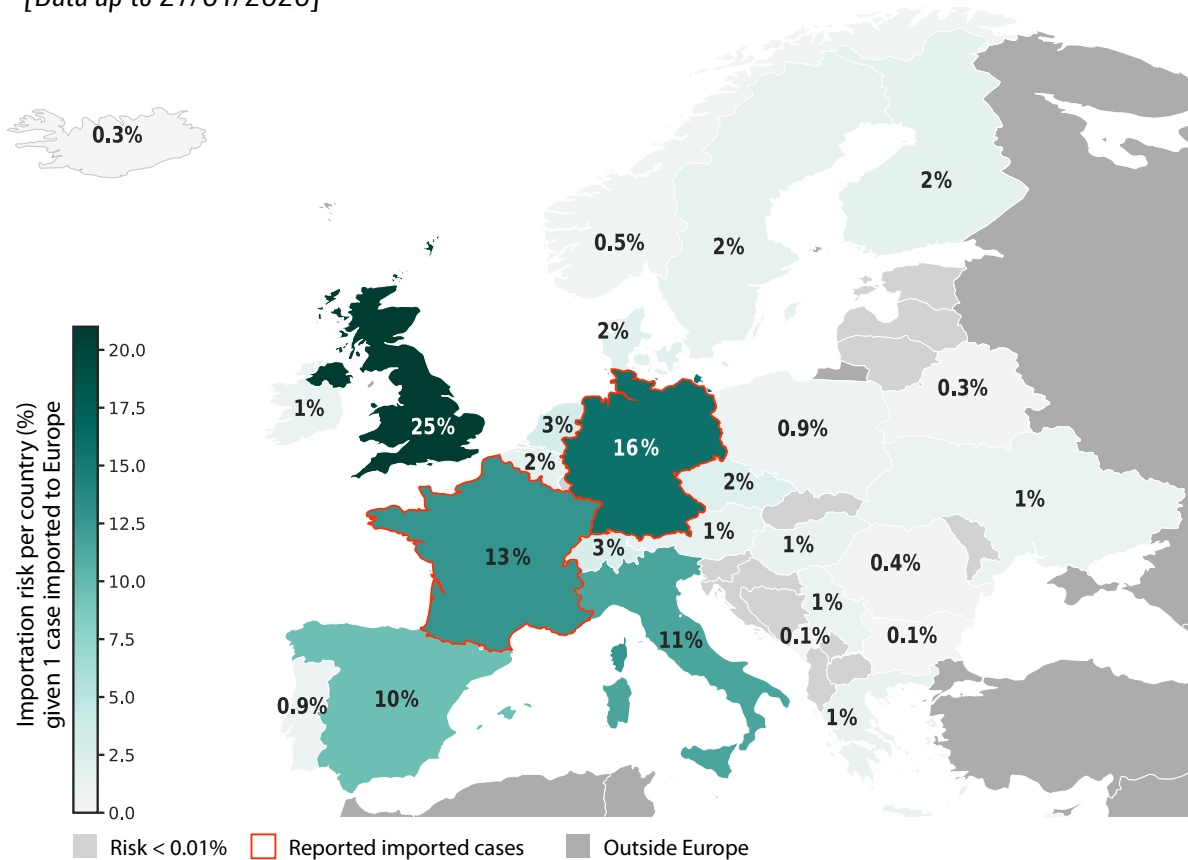
- ▶ invasion
- ▶ Coupled epidemics
- ▶ Recolonization and synchrony

► invasion

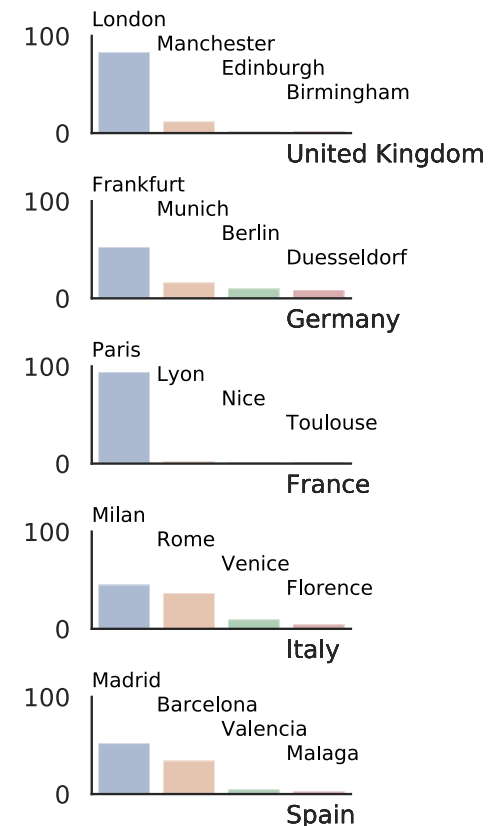
COVID-19 importation risk

Risk of importation per country, given 1 case imported to Europe

[Data up to 27/01/2020]

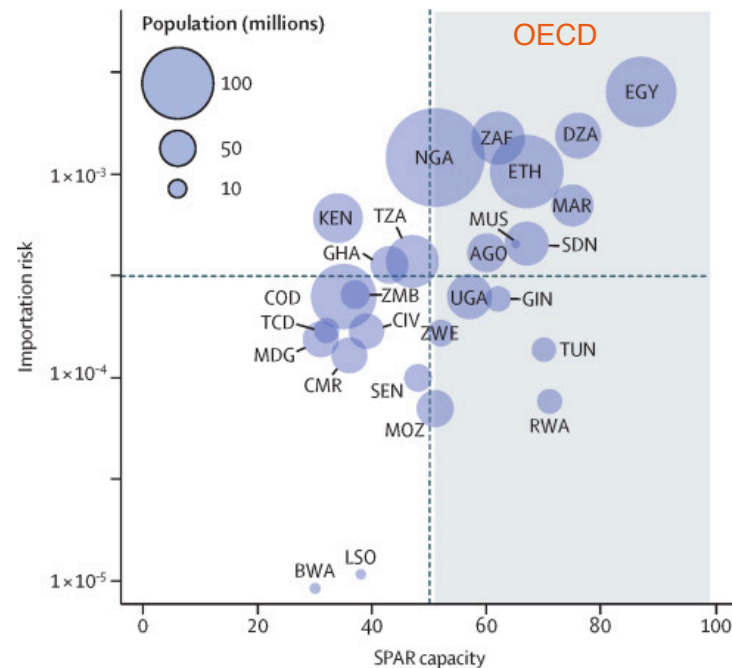
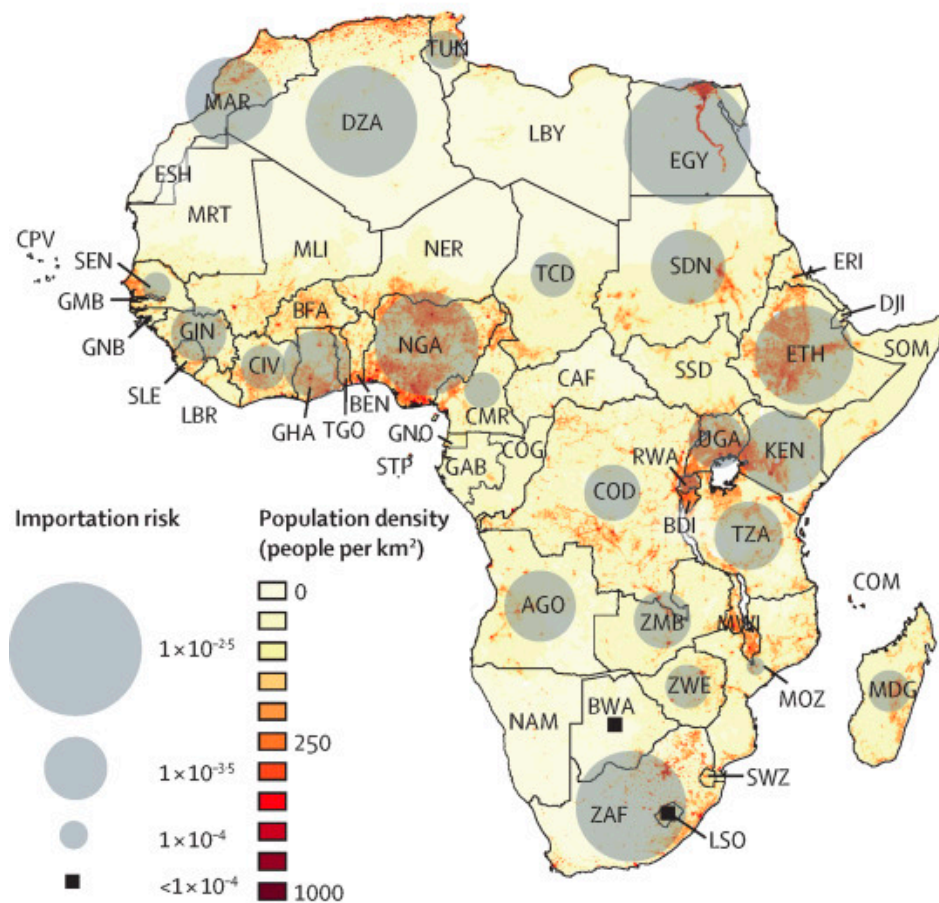


Relative risk by airport*

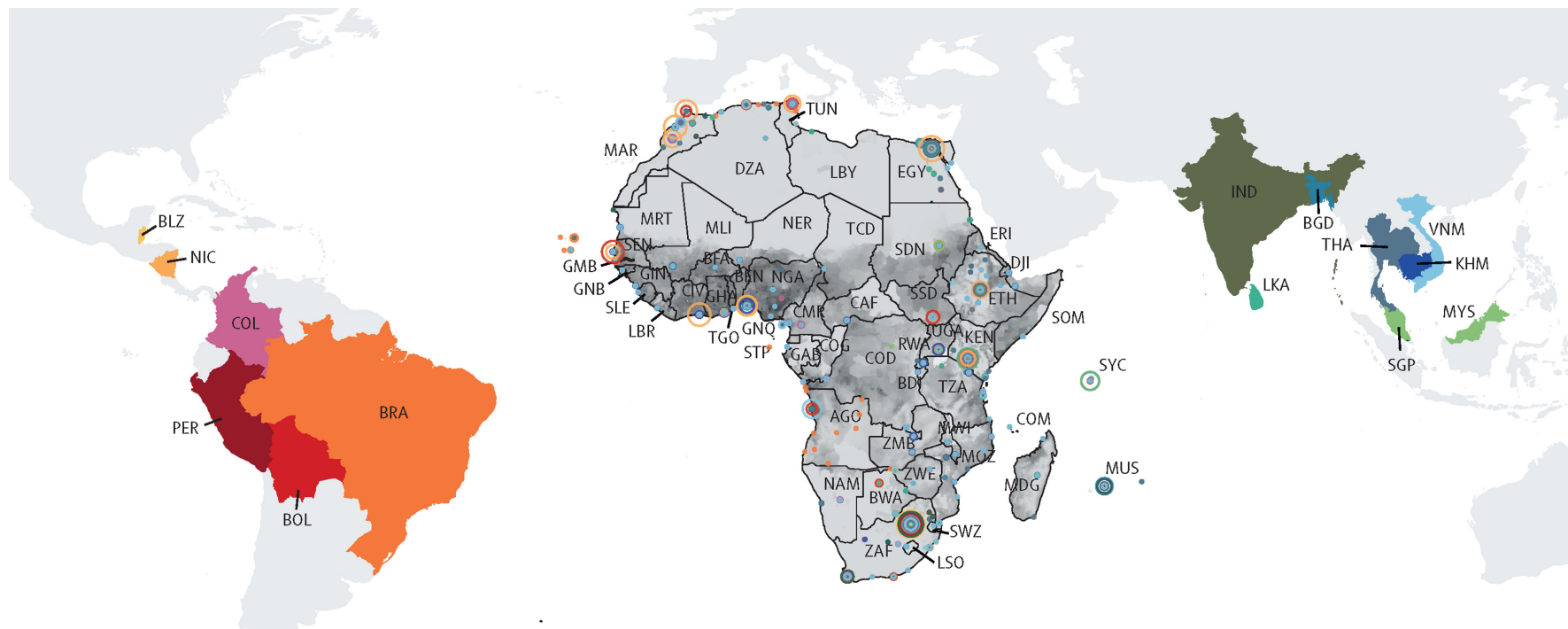


*Only the top 4 airports with largest contributions are shown

COVID-19 importation risk & preparedness



Dengue importation risk



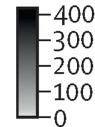
Origin country

- | | | | | |
|---------|-----------|------------|-----------|----------|
| Belize | Colombia | Bangladesh | Singapore | Viet Nam |
| Bolivia | Nicaragua | India | Sri Lanka | Cambodia |
| Brazil | Peru | Malaysia | Thailand | |

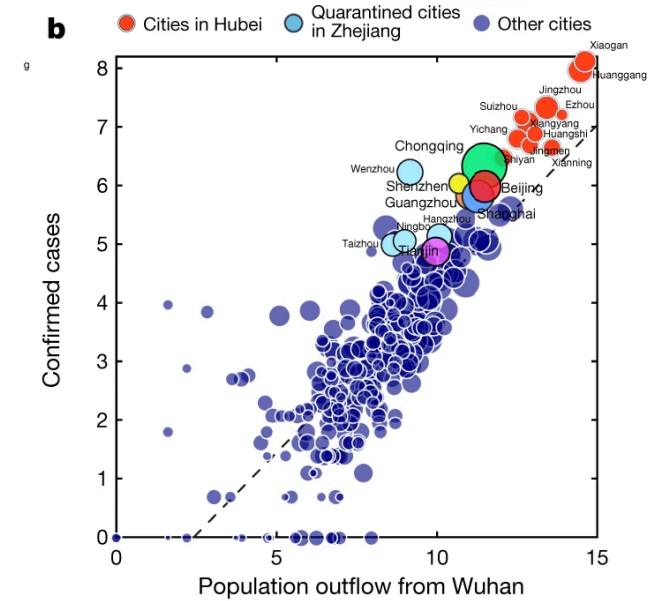
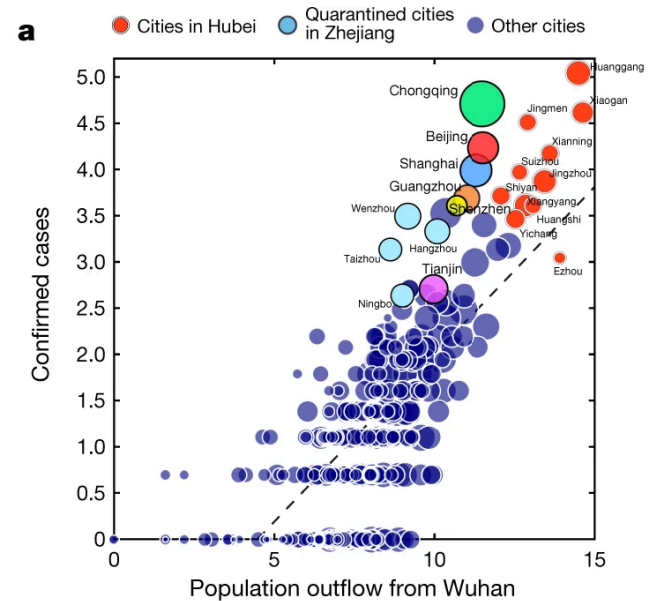
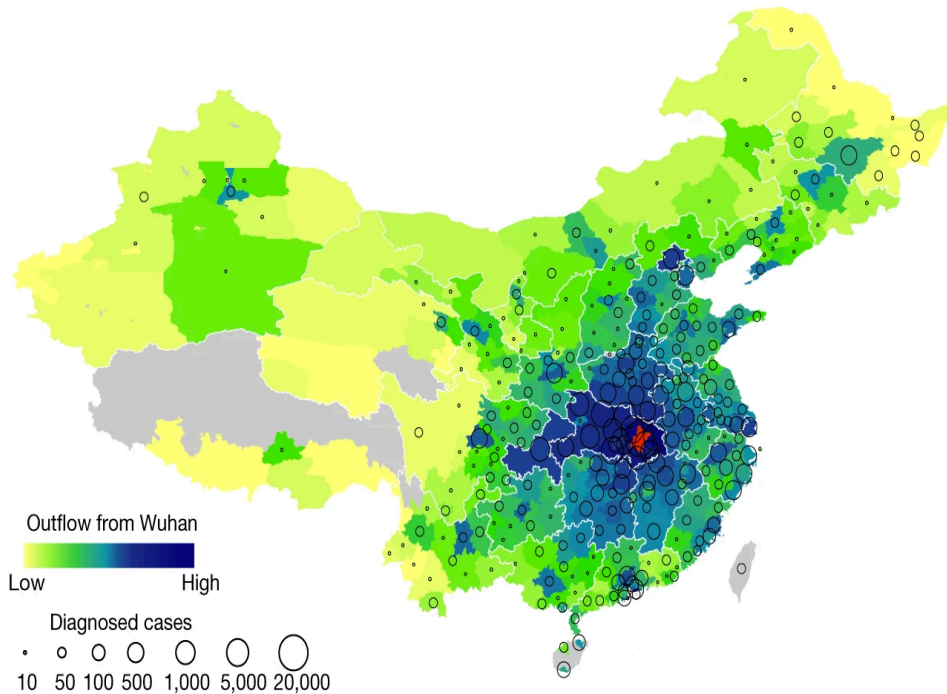
Mean annual risk of importation

- | | |
|------|------|
| 0.01 | 0.04 |
| 0.02 | 0.05 |
| 0.03 | |

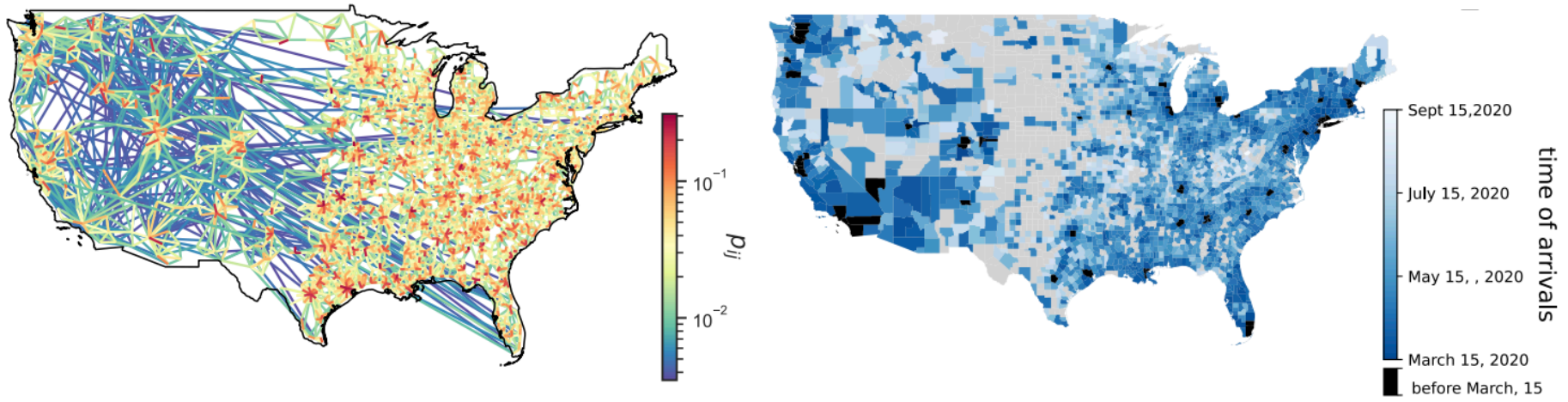
Transmission suitability × population density



COVID-19 observed invasion

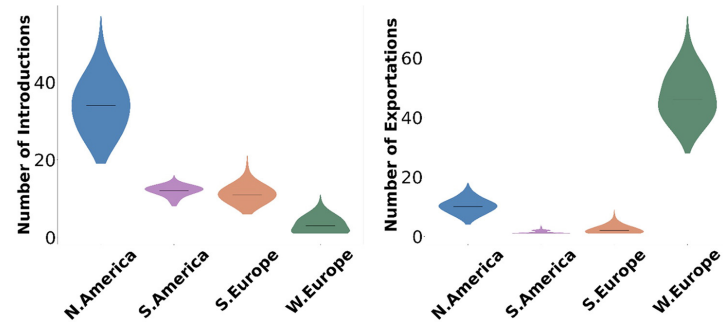
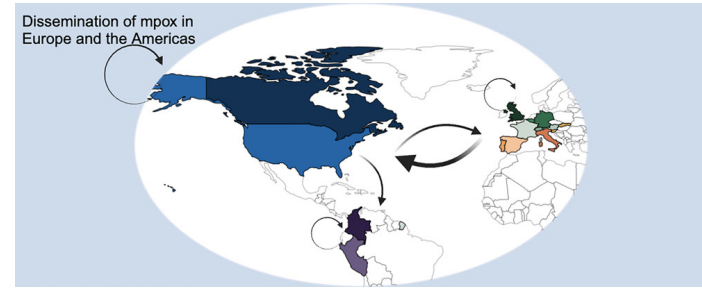


COVID-19 observed invasion



From sequence data

MPOX



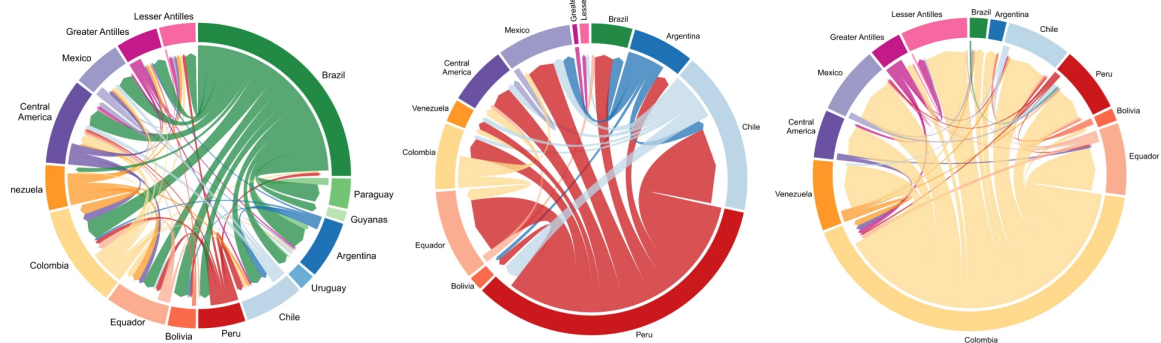
Paredes et al Cell 2024

SARS-CoV-2 variants

Gamma

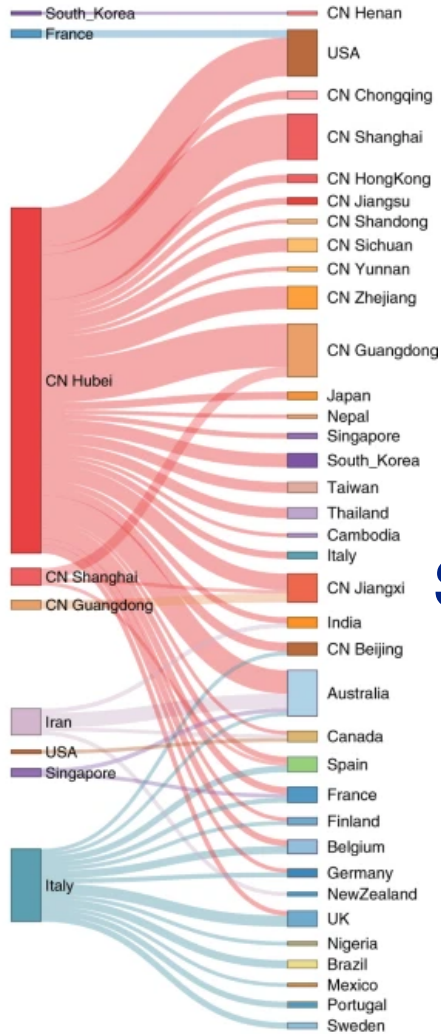
Lambda

Mu



Graf et al Nature Communications 2024

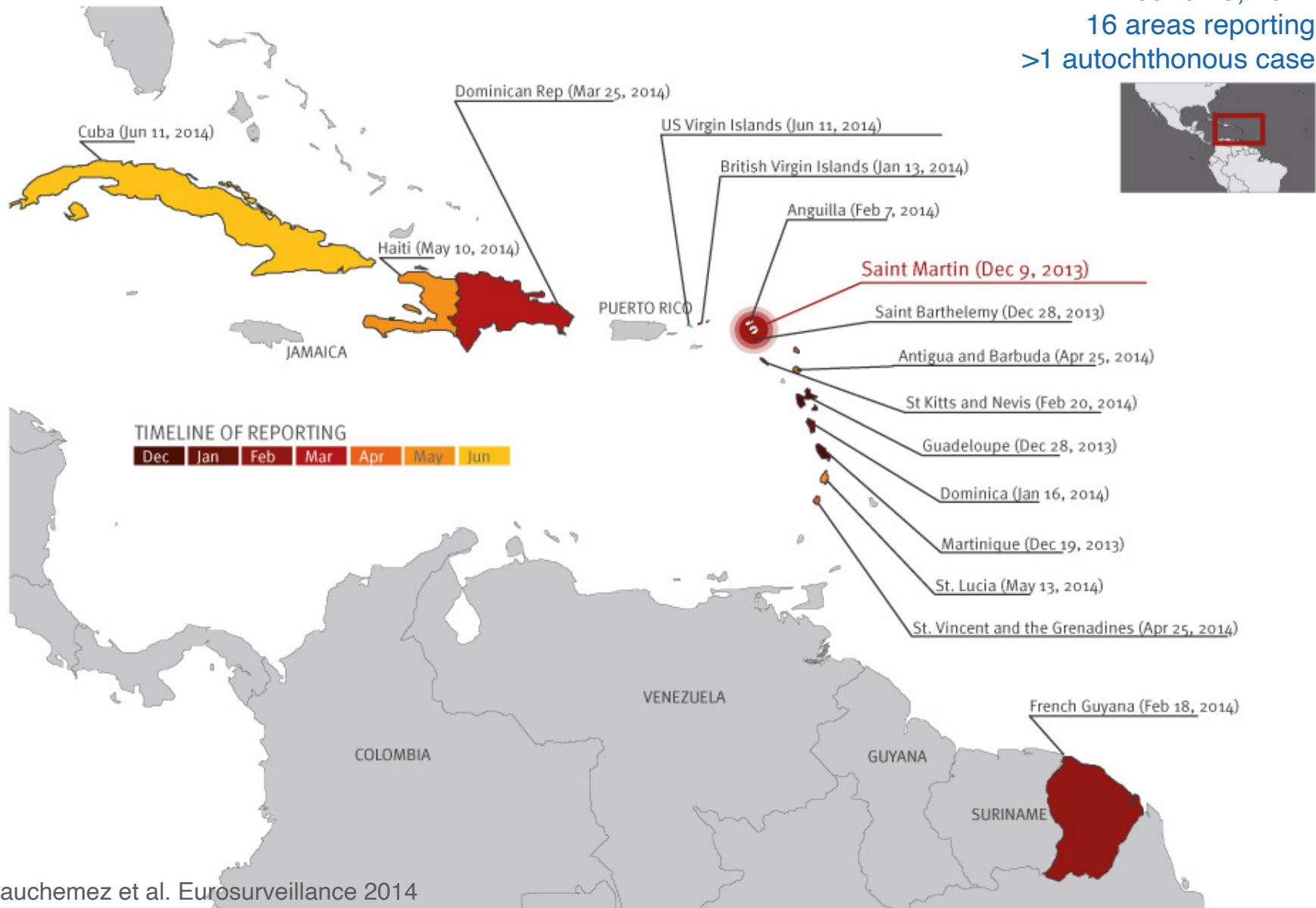
COVID-19



Lemey et al Nature Communications 2020

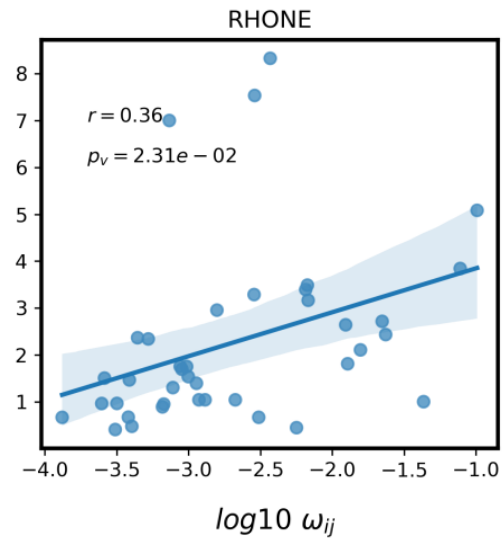
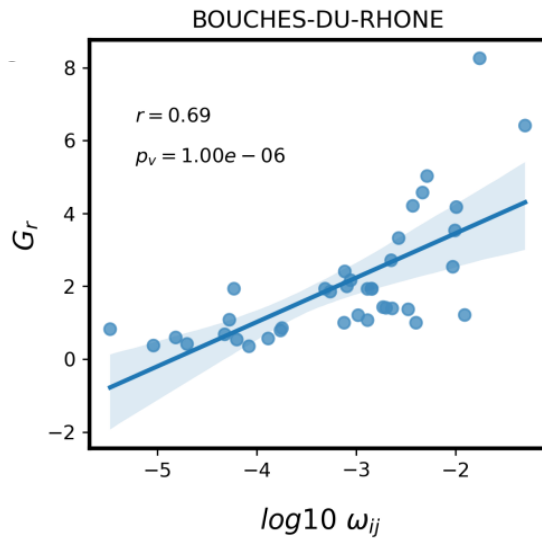
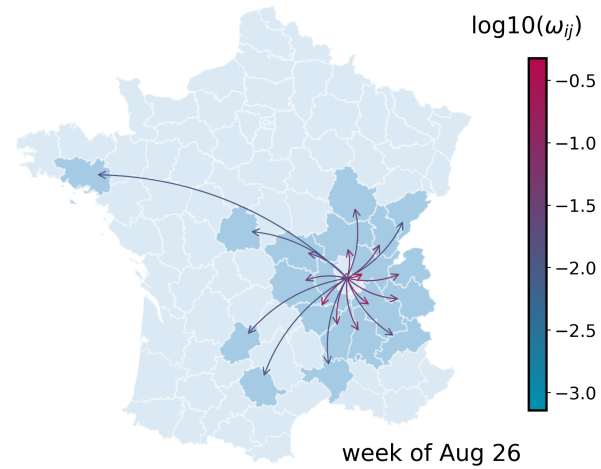
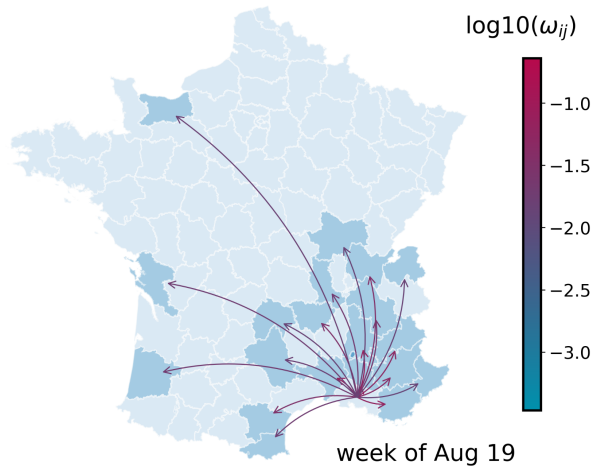
Chikungunya observed invasion

June 15, 2014
16 areas reporting
>1 autochthonous case

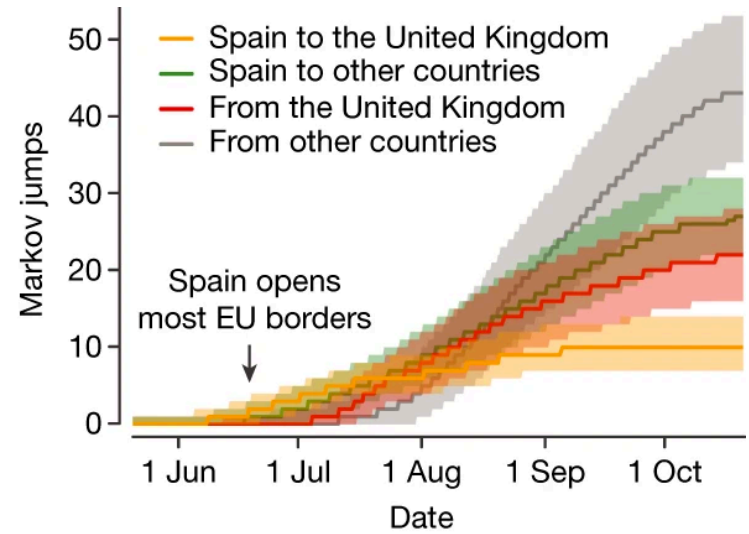
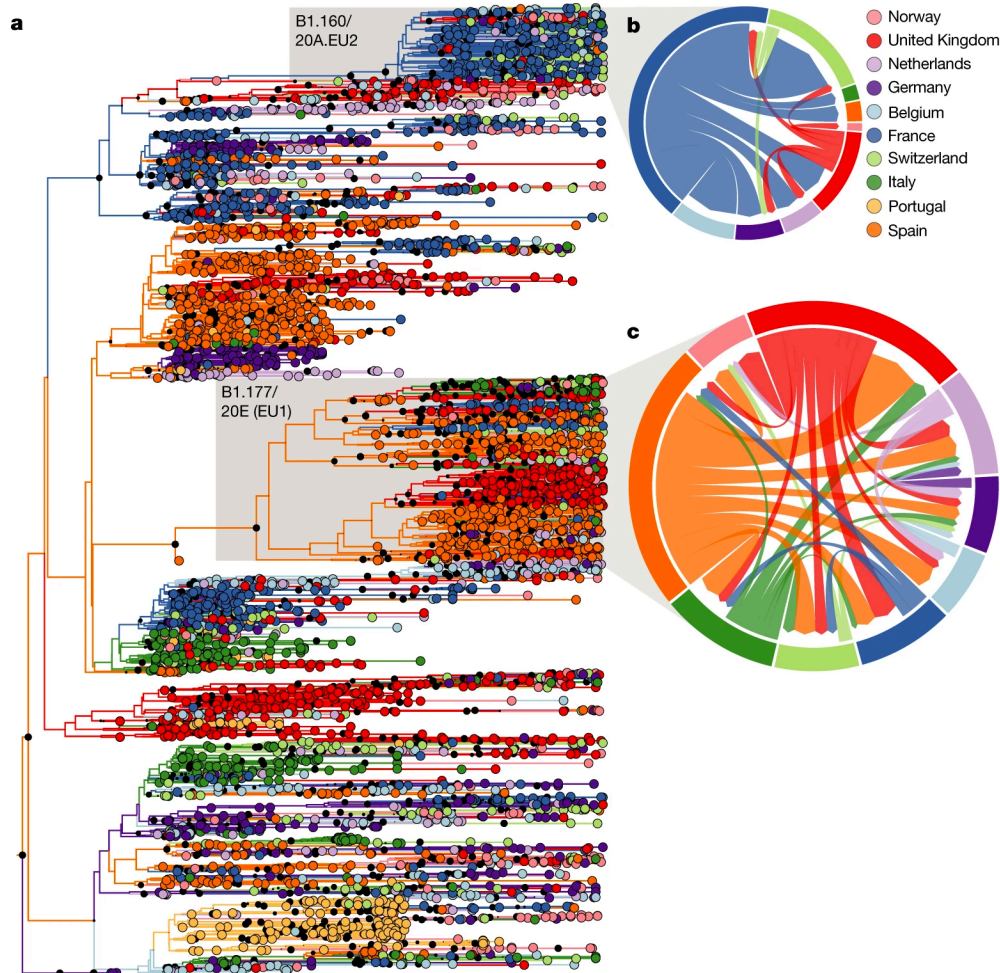


▶ Coupled epidemics

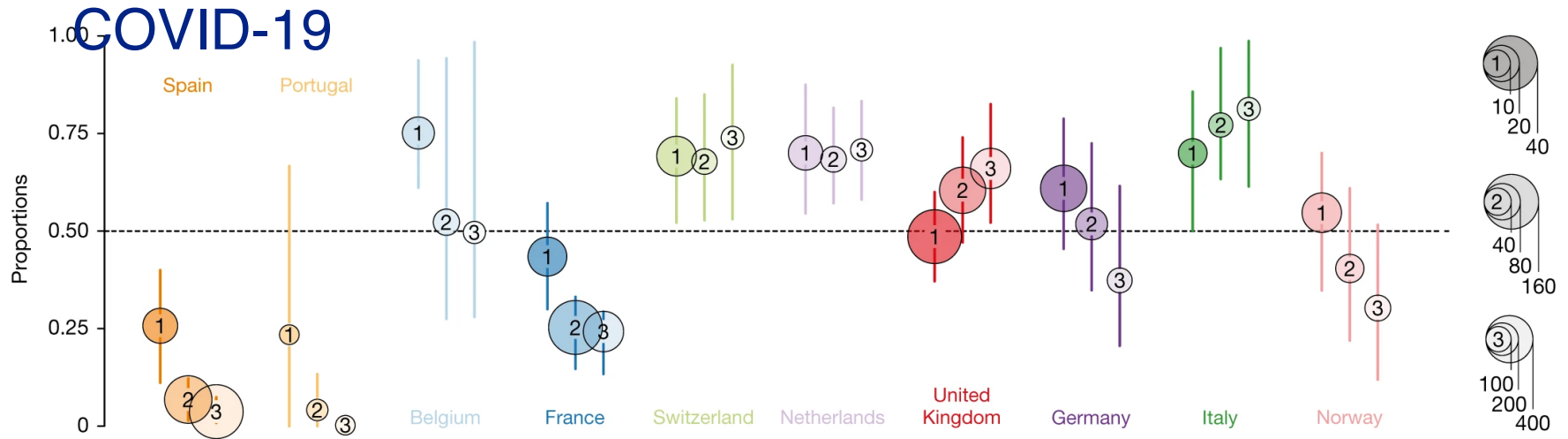
COVID-19 re-seeding



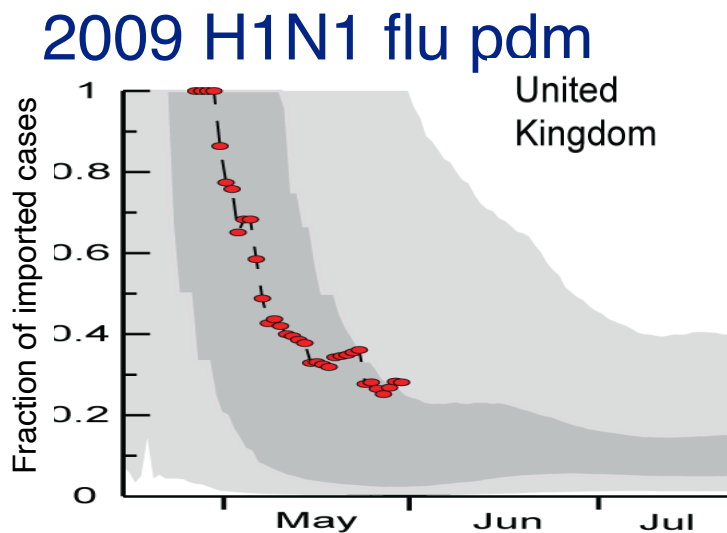
COVID-19 re-seeding



Introductions vs. persistence



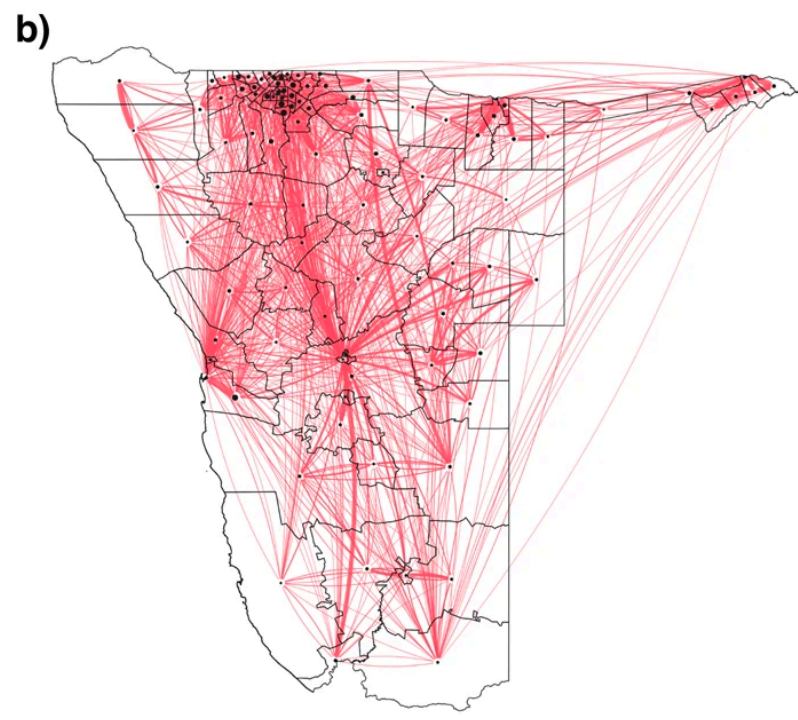
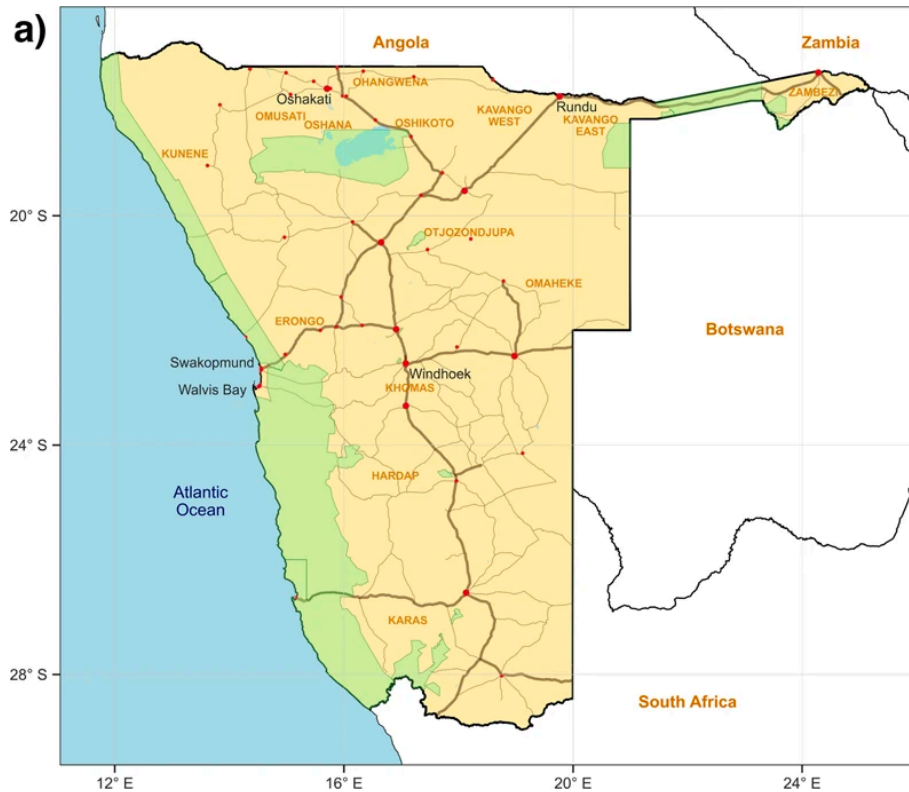
Lemey et al Nature 2021



- surveillance data
- 50% ref. range
- 95% ref. range

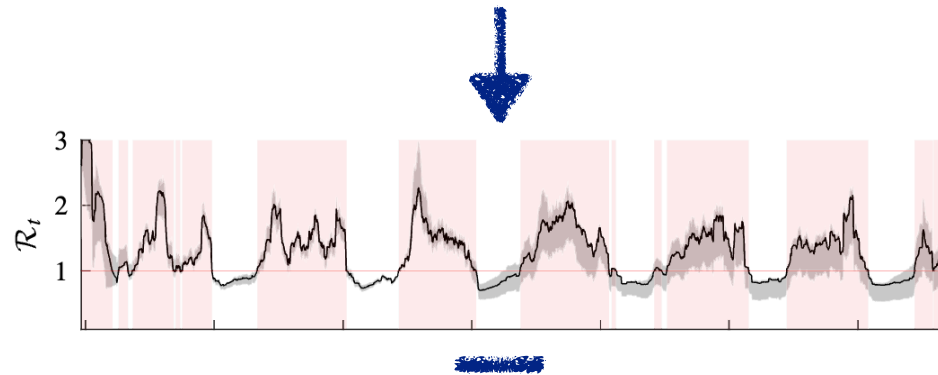
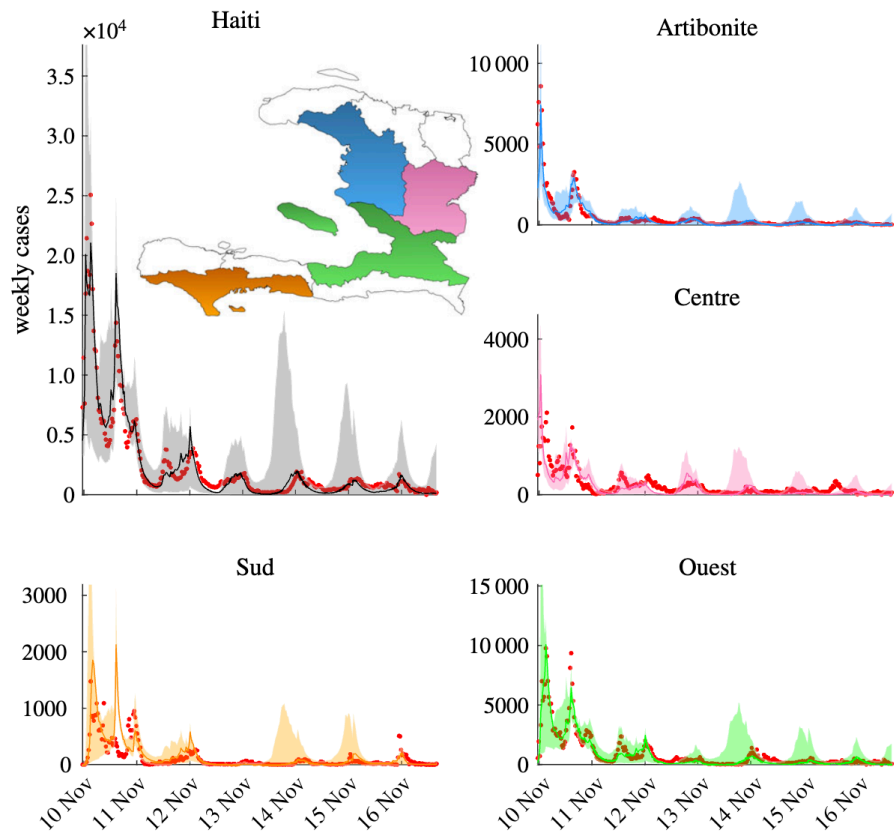
Bajardi et al PLOS One 2011

HIV risk flow networks



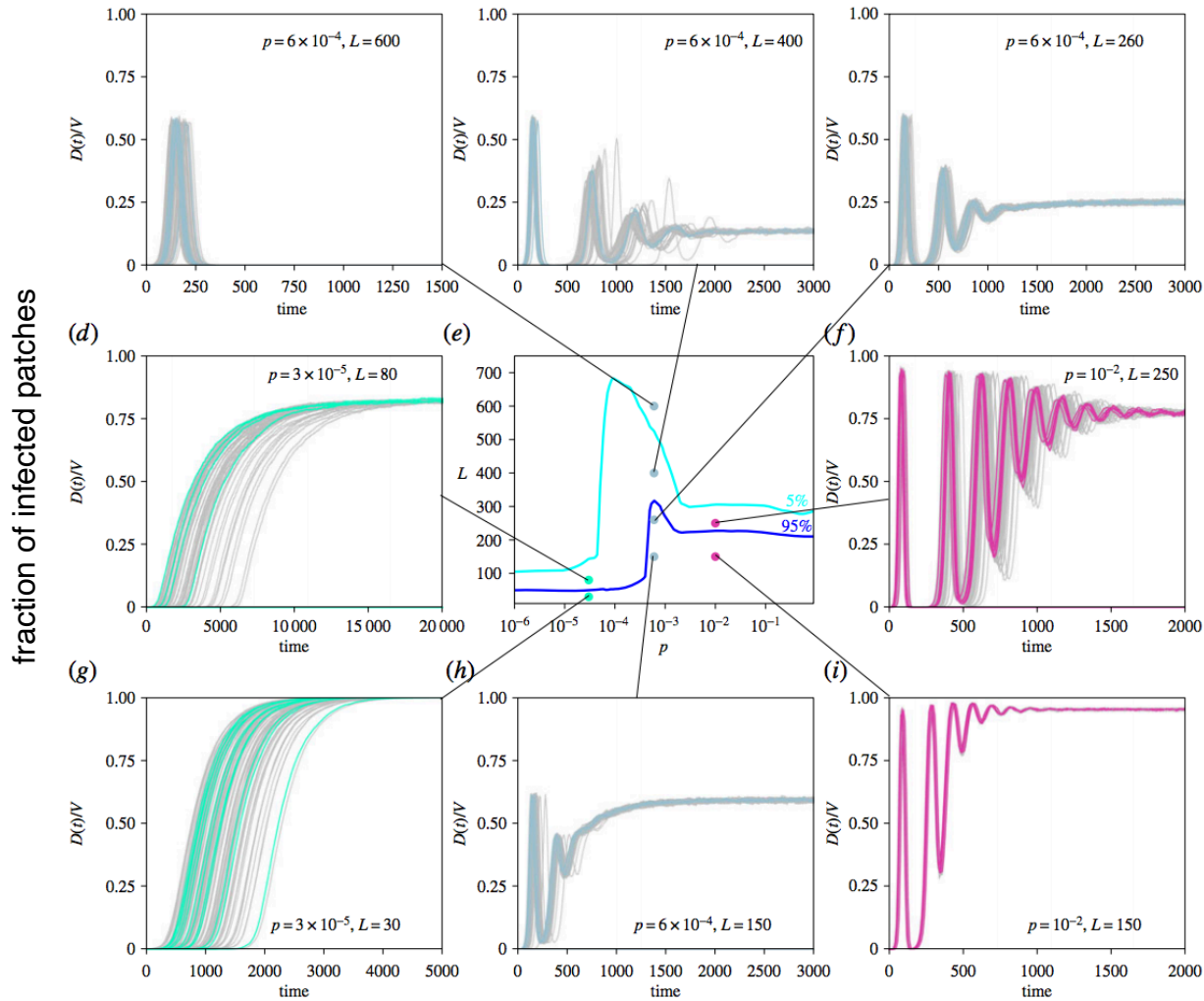
Valdano et al. Nature Comms 2021
Valdano et al. The Lancet HIV 2022

Cholera

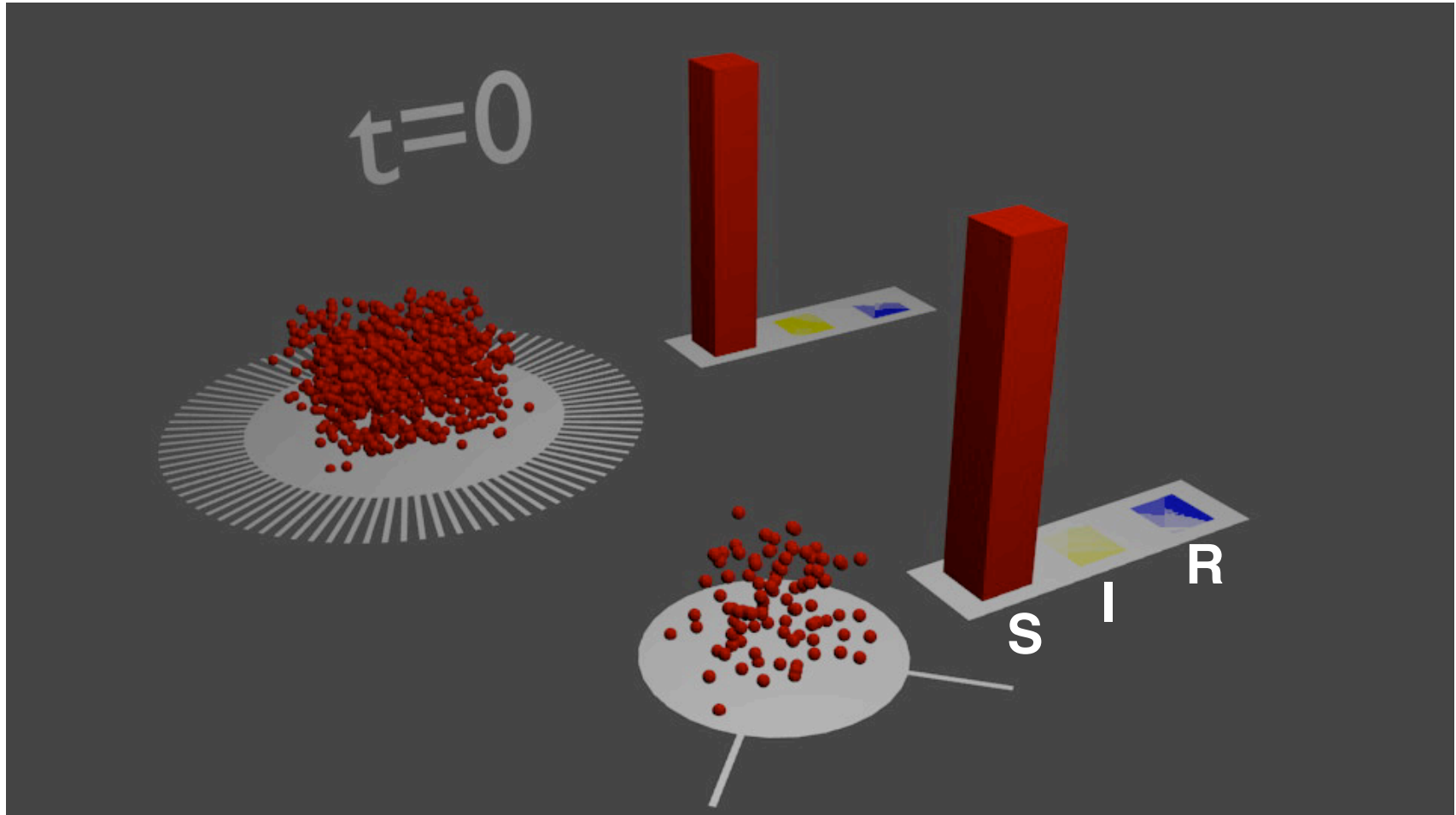


► Recolonization and synchron

Recolonization and synchrony

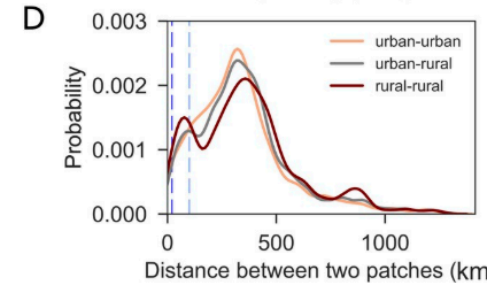
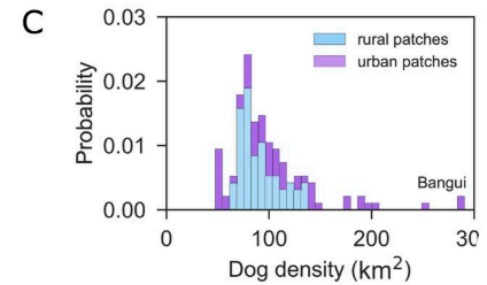
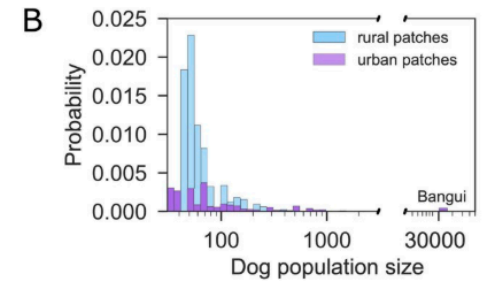
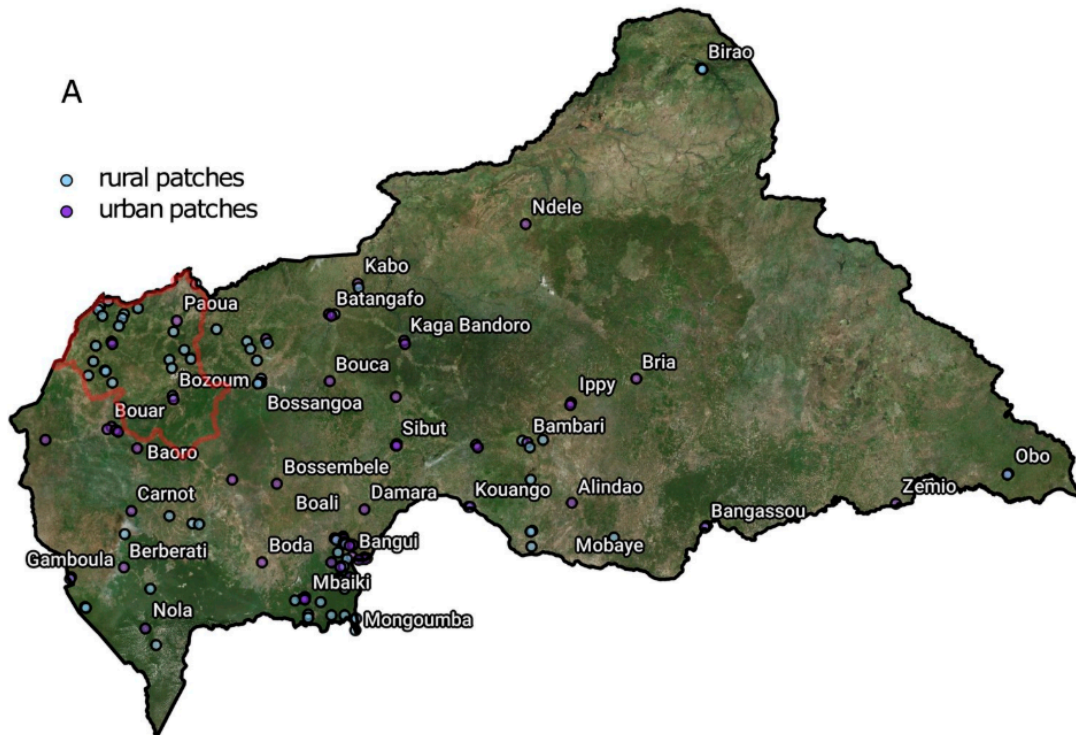


Recolonization and synchrony



Recolonization

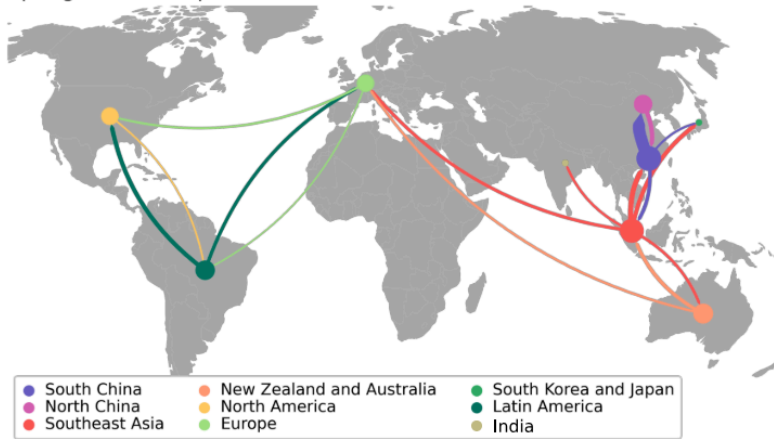
Dog rabies



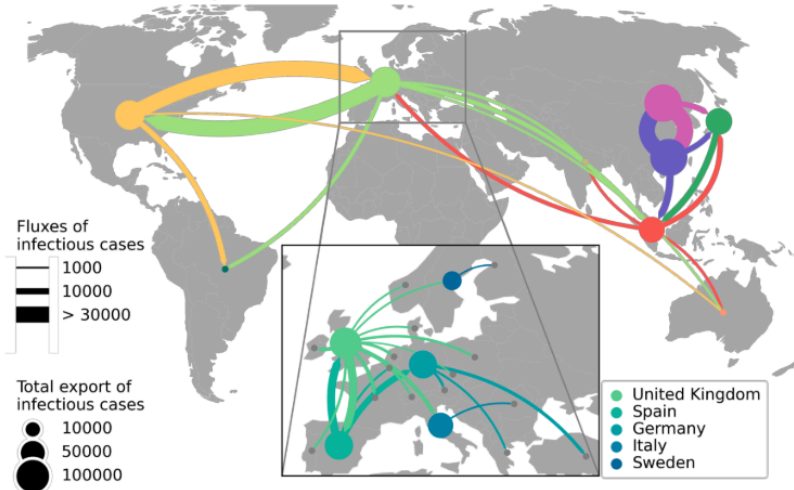
Global spread

Seasonal flu

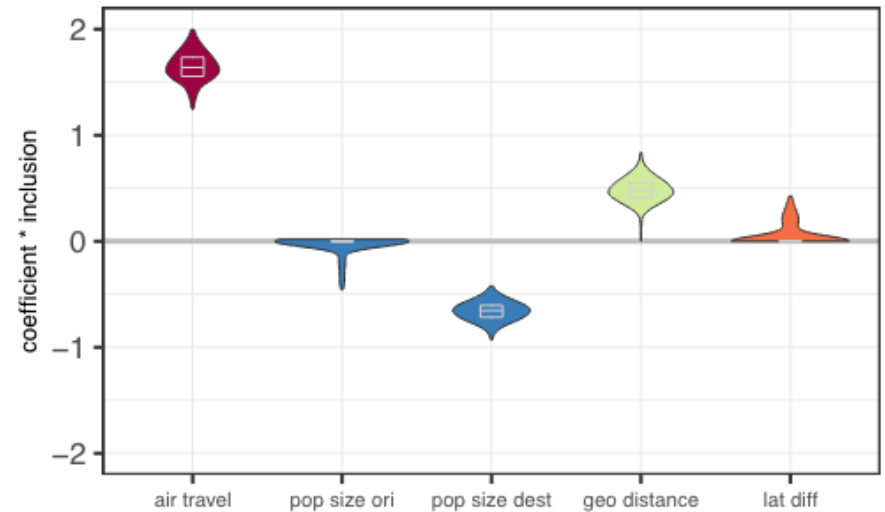
Spring & summer period



Autumn & winter period



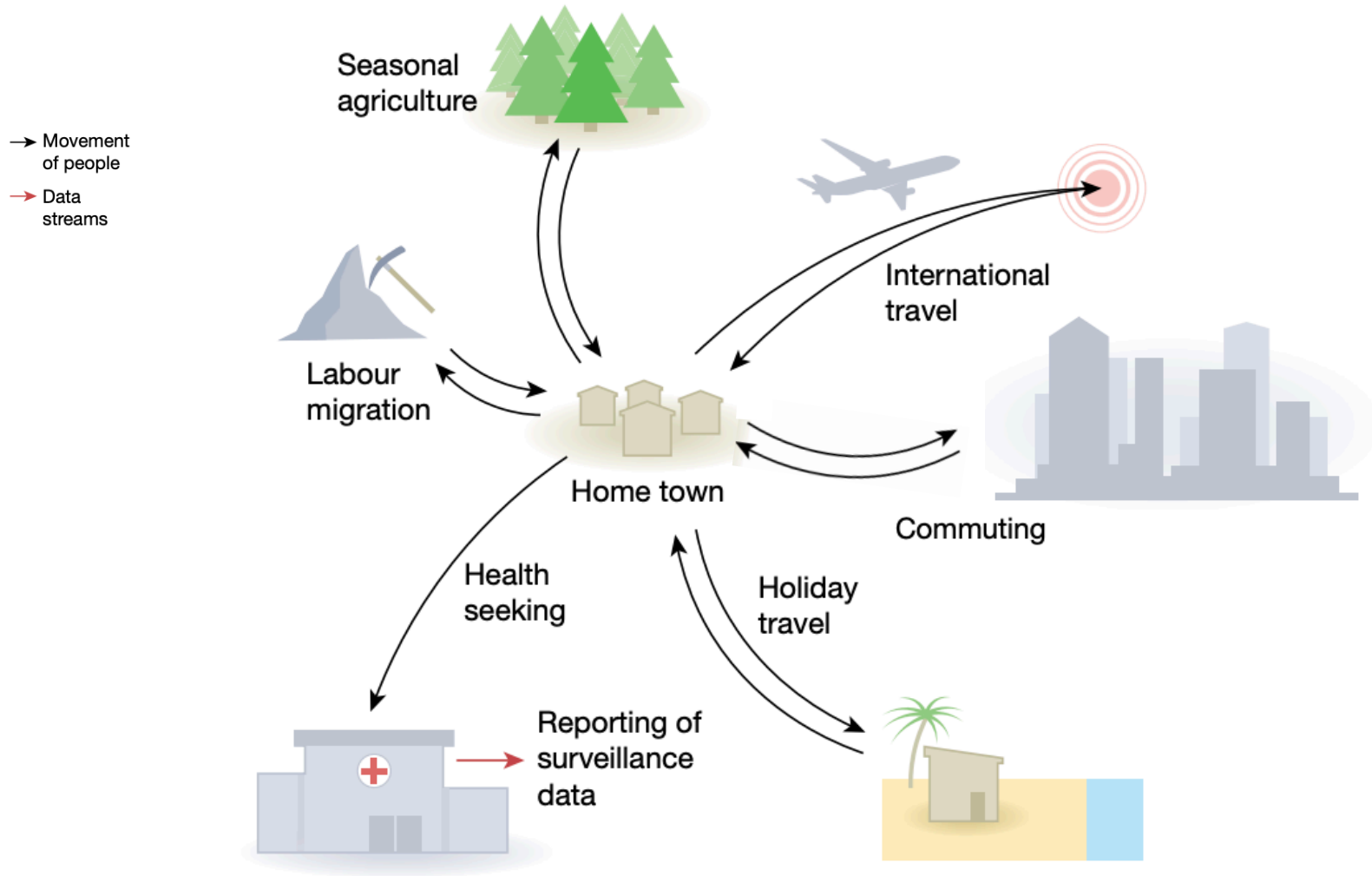
RSV



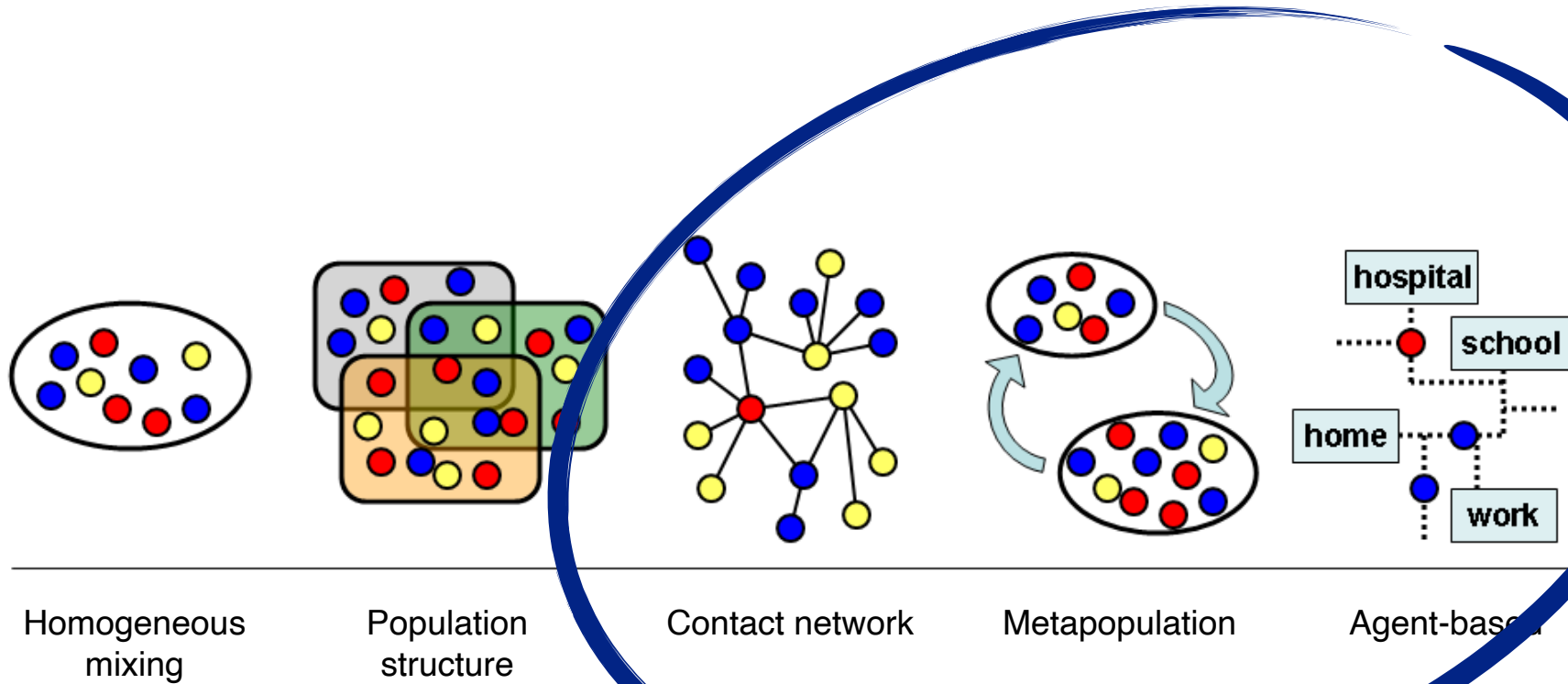
Langedijk et al Nature Comms 2024

MODELS  **DATA**

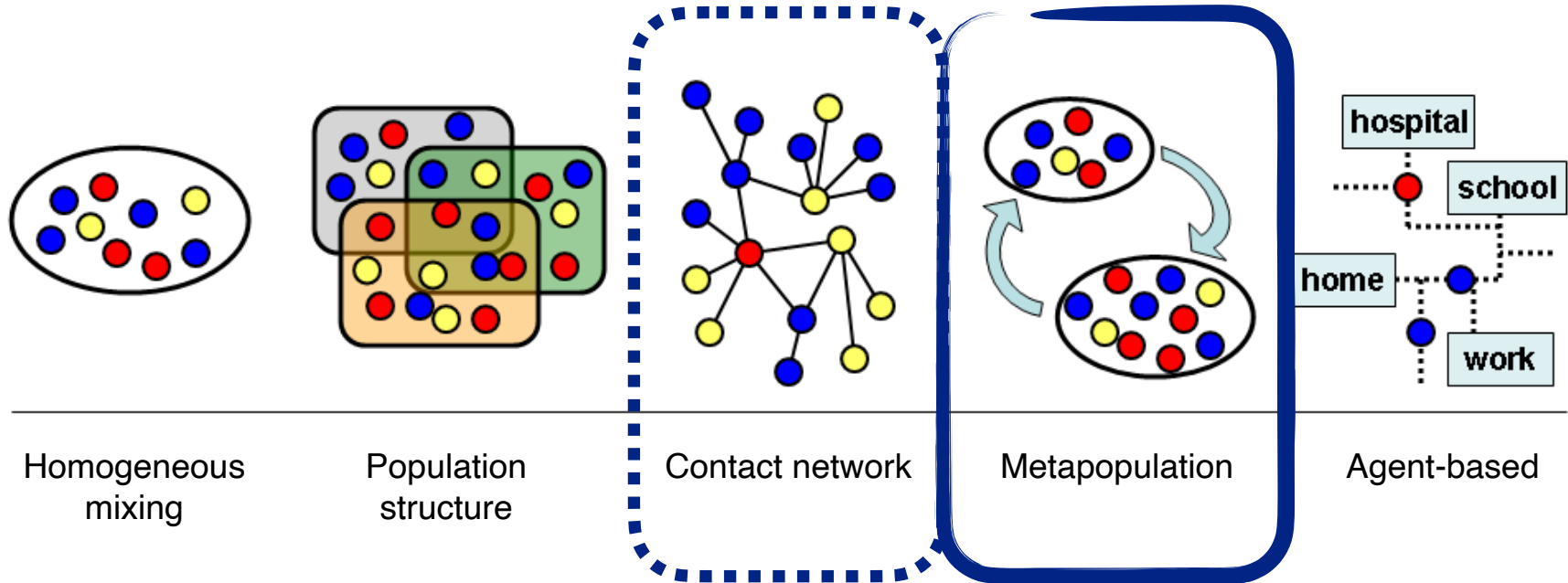
Mobility to inform spatial transmission



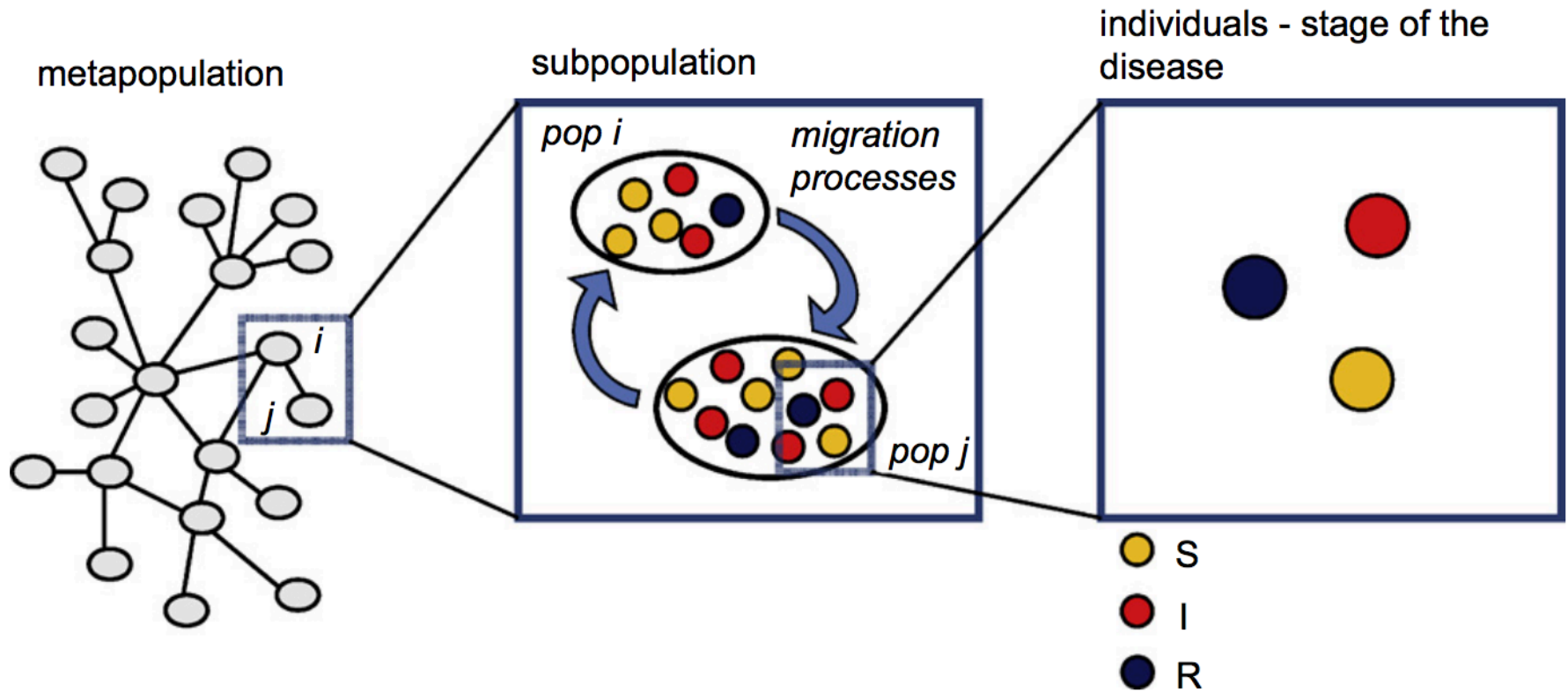
Models



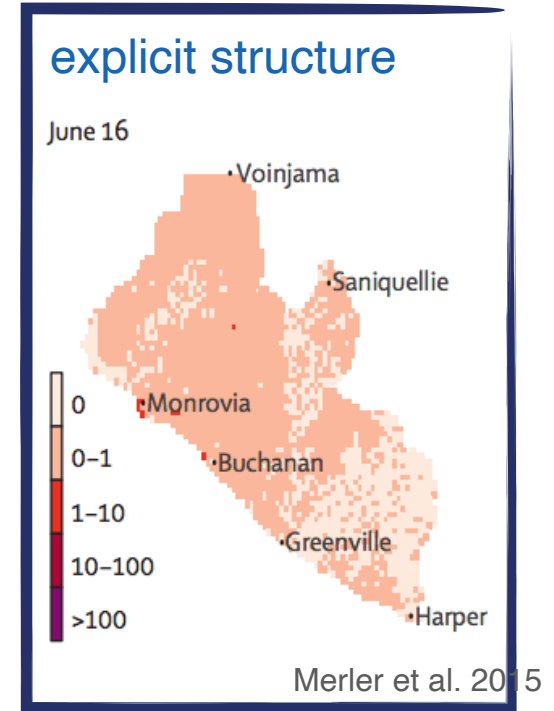
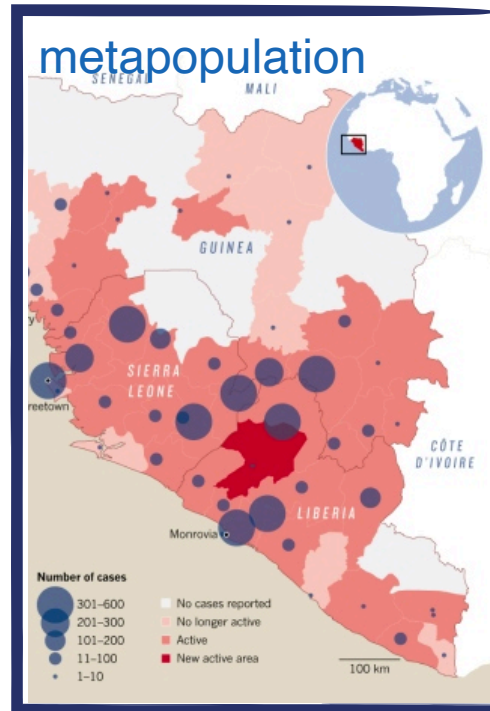
Models



Metapopulation models



Metapopulation models: a compromise



- discrete entities in space: *patches, subpopulations*
- interaction between populations : *coupling, flows*

Coupling across scales

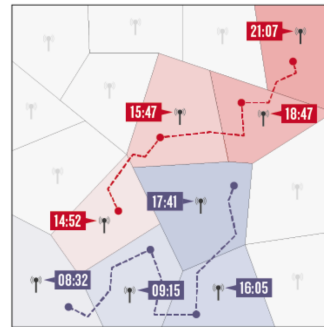
Colizza et al PNAS 2006



Balcan et al PNAS 2007



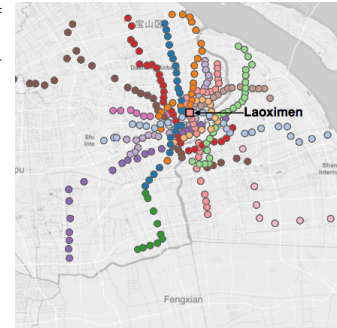
Tizzoni et al PCB



Maximen Nature

Eubank et al Nature 2004
Diet et al arxiv 2018

Person ID	Location ID	Arrival time	Departure time	Activity type
115	4225	0.0000	7.00	Home
115	49 296	8.00	11.00	Work
115	21 677	11.2	13.00	Work
115	49 296	13.2	17.00	Work
115	4225	18.00	19.00	Home
115	4225	0.0000	7.00	Home
115	49 296	8.00	11.00	Work
115	21 677	11.2	13.00	Work
115	49 296	13.2	17.00	Work
115	4225	18.00	19.00	Home
115	4225	0.0000	7.00	Home
115	49 296	8.00	11.00	Work
115	21 677	11.2	13.00	Work



International scale



Air travel

- metropolitan areas
- airport 'basins of attraction'
- air travel flows (market/segment)

Rvachec, Longini 1985, Longini 1988

Grais et al 2003, Flahault et al 1991, Hufnagel et al 2004

Colizza et al PNAS 2006, PLOS Med 2007

Balcan et al PNAS 2009

Country scale



Balcan et al. PNAS 2009

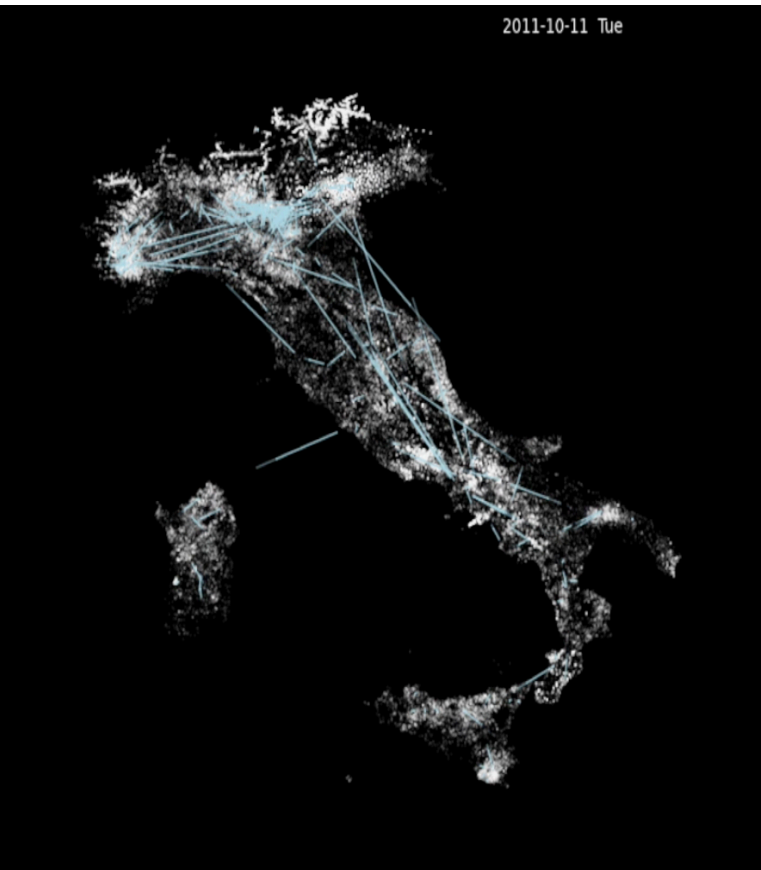
- Air travel
- Ground transportation (trains, buses, ...)
- Commuting
- All movements: mobile phone data

- Administrative subdivisions

Crepey et al Am J Epic 2007
Balcan et al PNAS 2009
Tizzoni et al. PLOS Comput Biol 2014
Wesolowski et al Science 2012
Deville et al PNAS 2014
Lai et al JTM 2019

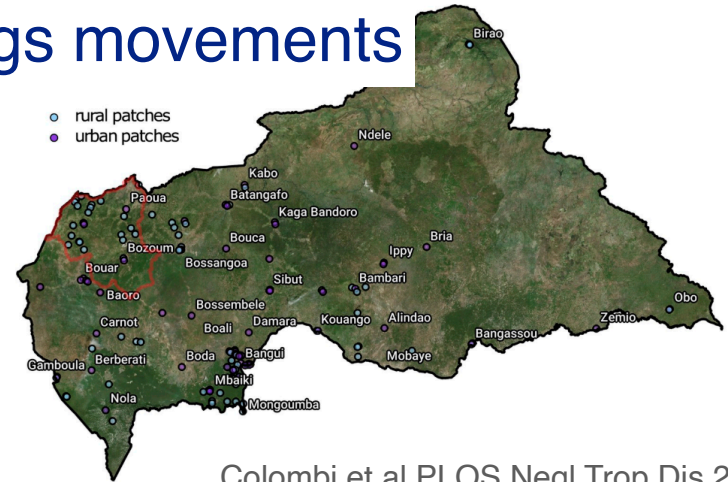
Country scale

livestock movements



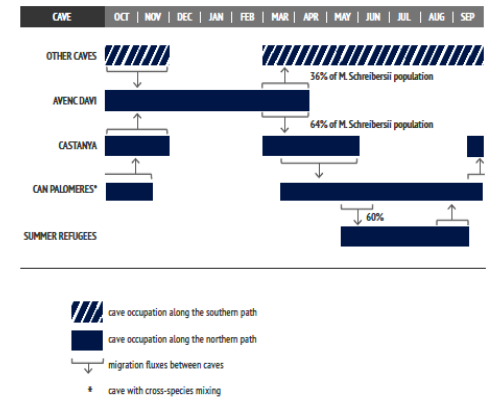
2011-10-11 Tue

Dogs movements



Colombi et al PLOS Negl Trop Dis 2020

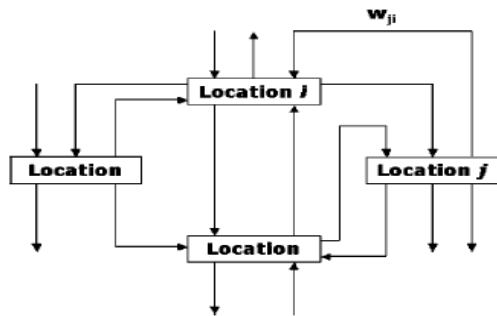
Bats migration



Colombi et al Sci Rep 2019

Woolhouse et al. 2005, Christley et al 2005, Bigras-Poulin et al 2006, Ortiz-Pelaez et al 2006, Kao et al 2007, Natale et al 2009, Vernon et al 2009, Bajardi et al 2009, Rautureau et al 2010, Volkova et al 2010

City scale

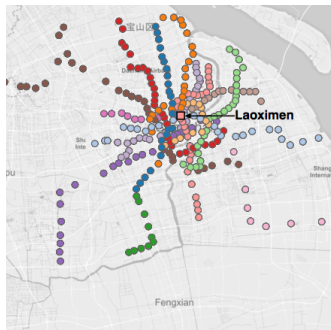


Person ID	Location ID	Arrival time	Departure time	Activity type
115	4225	0.0000	7.00	Home
115	49 296	8.00	11.00	Work
115	21 677	11.2	13.00	Work
115	49 296	13.2	17.00	Work
115	4225	18.00	19.00	Home

Survey data

- locations...?

Eubank et al. Nature 2004

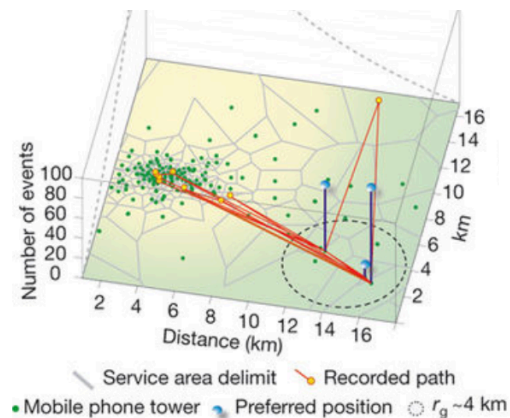
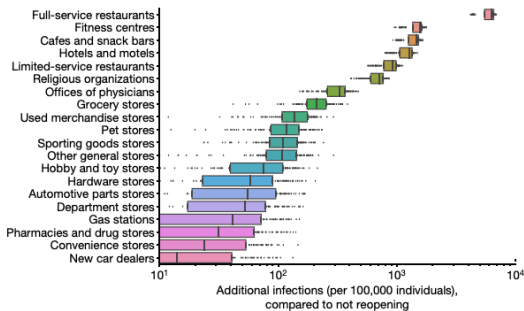


Public transportation data

- stations...?

Batty. Dialogues in Hum. Geo. 2013

Du et al arxiv 2018



Mobile phone data

- cell towers, POIs
- administrative divisions

Gonzalez et al. Nature 2008

Blondel et al. EPJB Data Sci 2015

Chang et al Nature 2020

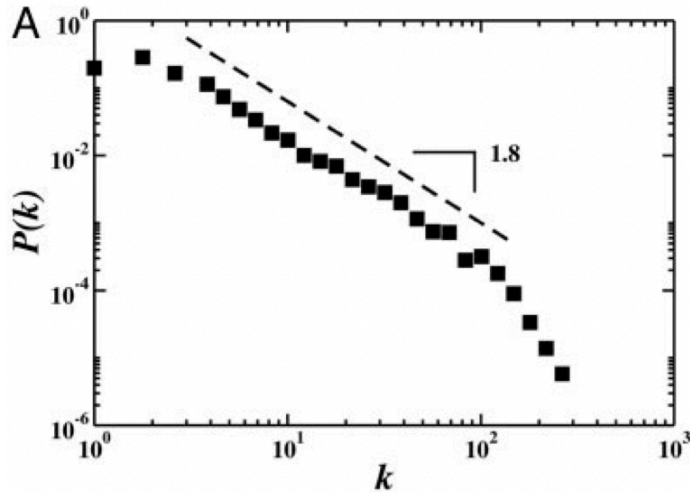
Human vs. animal hosts



- ▶ Resident vs. non-resident

Mobility NETWORK FEATURES

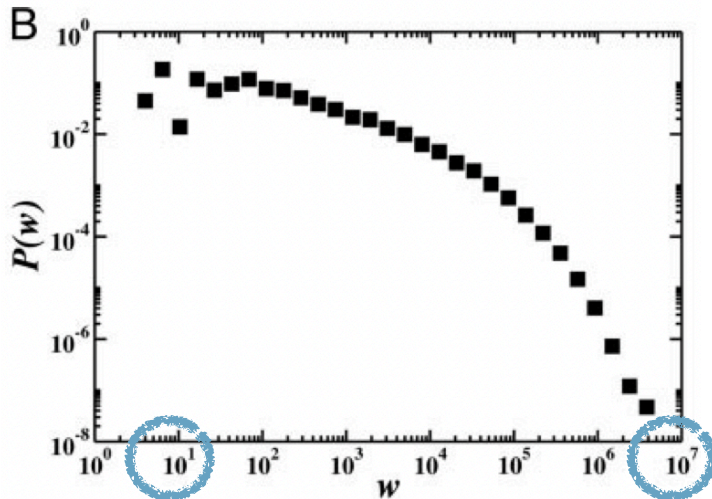
Air transportation network



AIRPORT connections

$$P(k) \sim k^{-1.8}$$

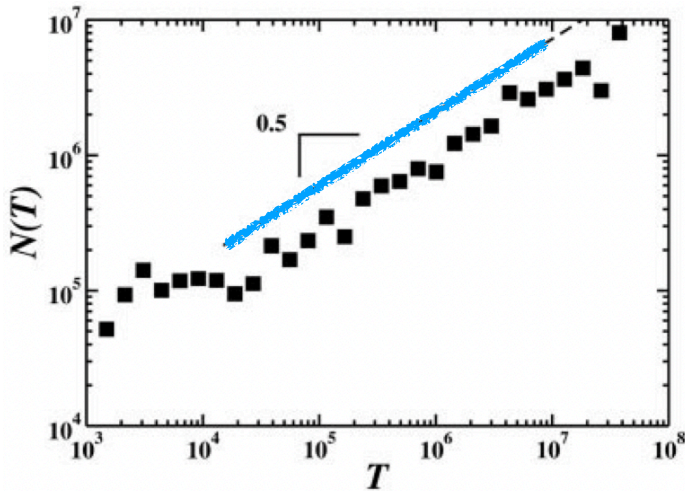
- ▶ long tail distributions



Passenger Fluxes

- ▶ long tail distributions
- ▶ >6 orders of magnitude

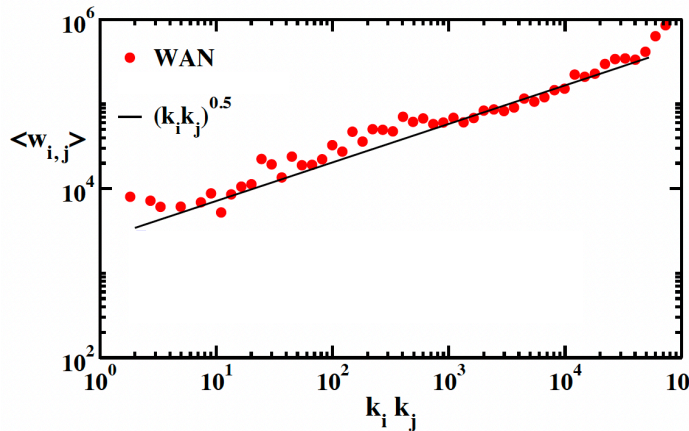
Air transportation network



City population vs. Airport traffic

$$N(T) \sim T^{0.5}$$

- larger population \leftrightarrow larger traffic

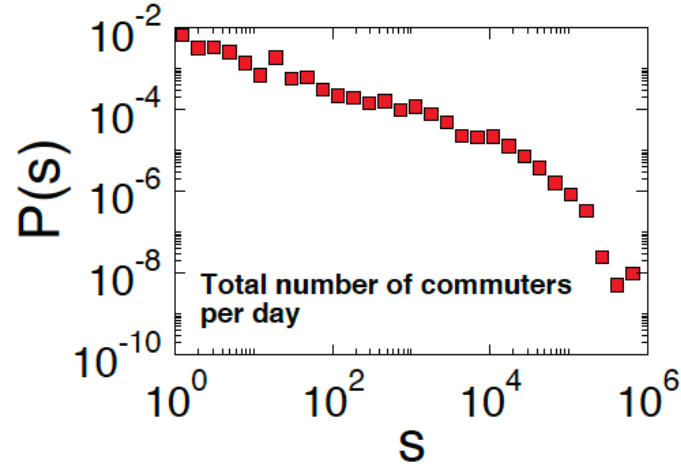


Passenger Flux vs. airport connectivity

$$w_{ij} \sim (k_i k_j)^{0.5}$$

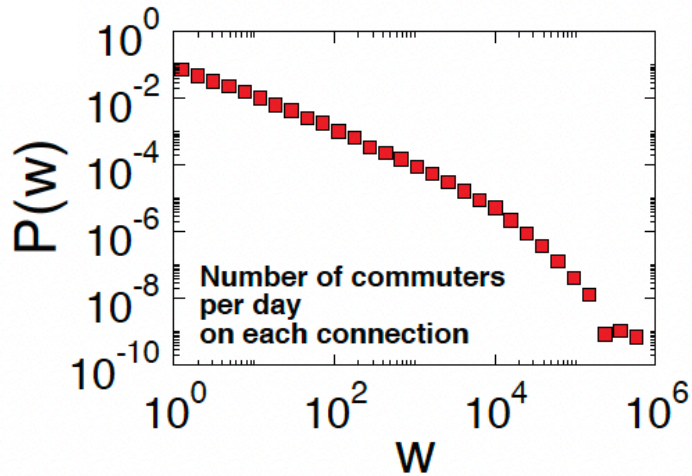
- hubs \leftrightarrow larger traffic

Commuting



COMMUTERS of a city

- ▶ long tail distributions



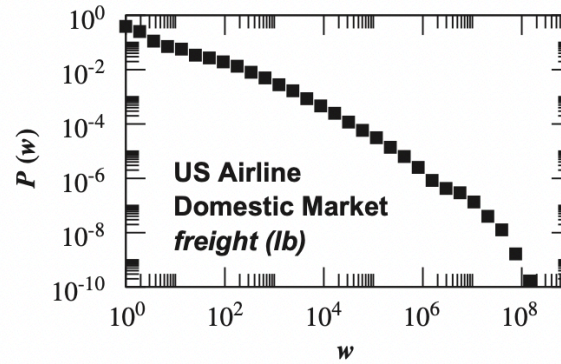
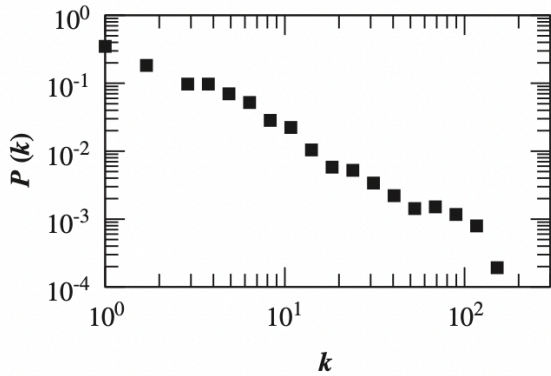
Commuters between cities

- ▶ long tail distributions
- ▶ >5 orders of magnitude

Mobility from mobile phone data

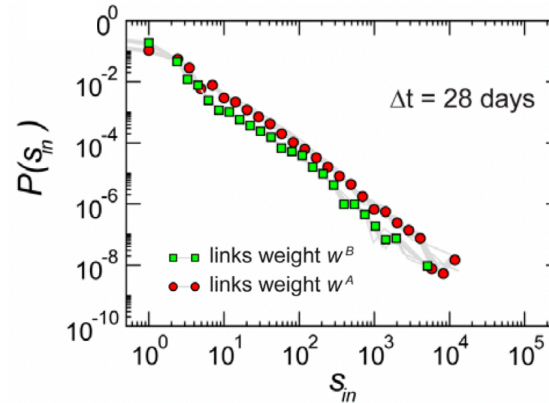
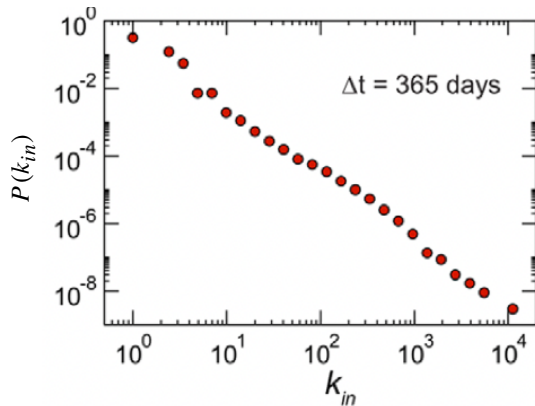


Transportation of goods and animals



Freight transportation

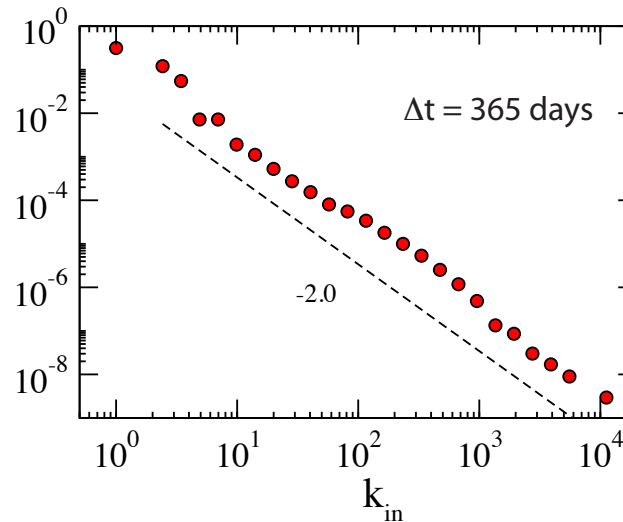
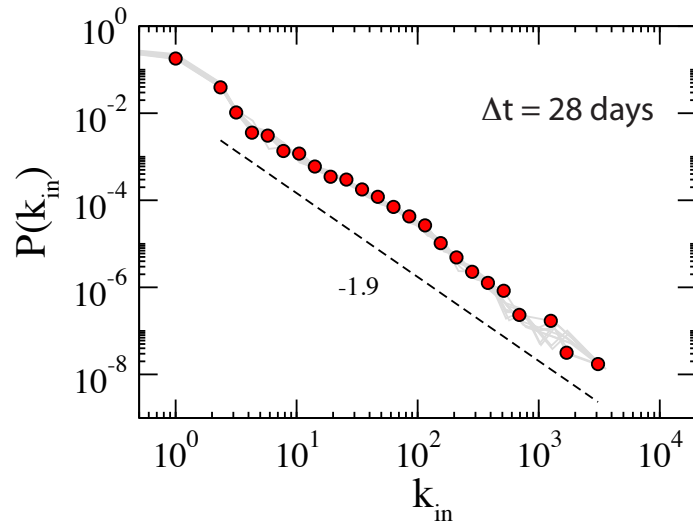
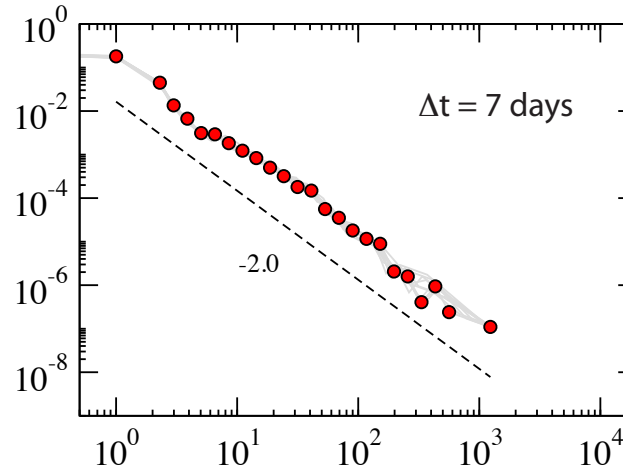
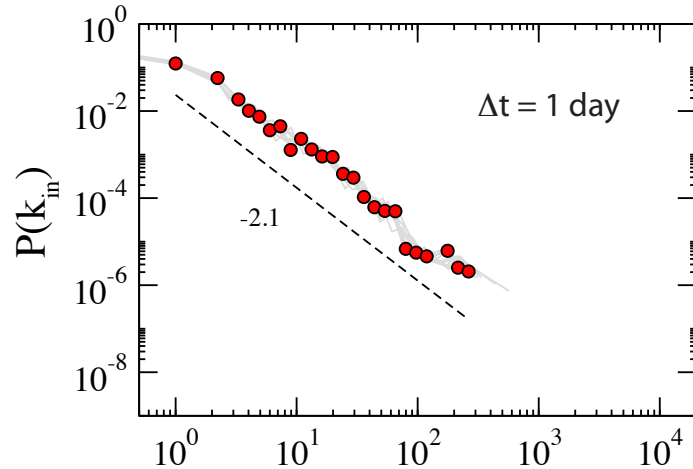
- long tail distributions



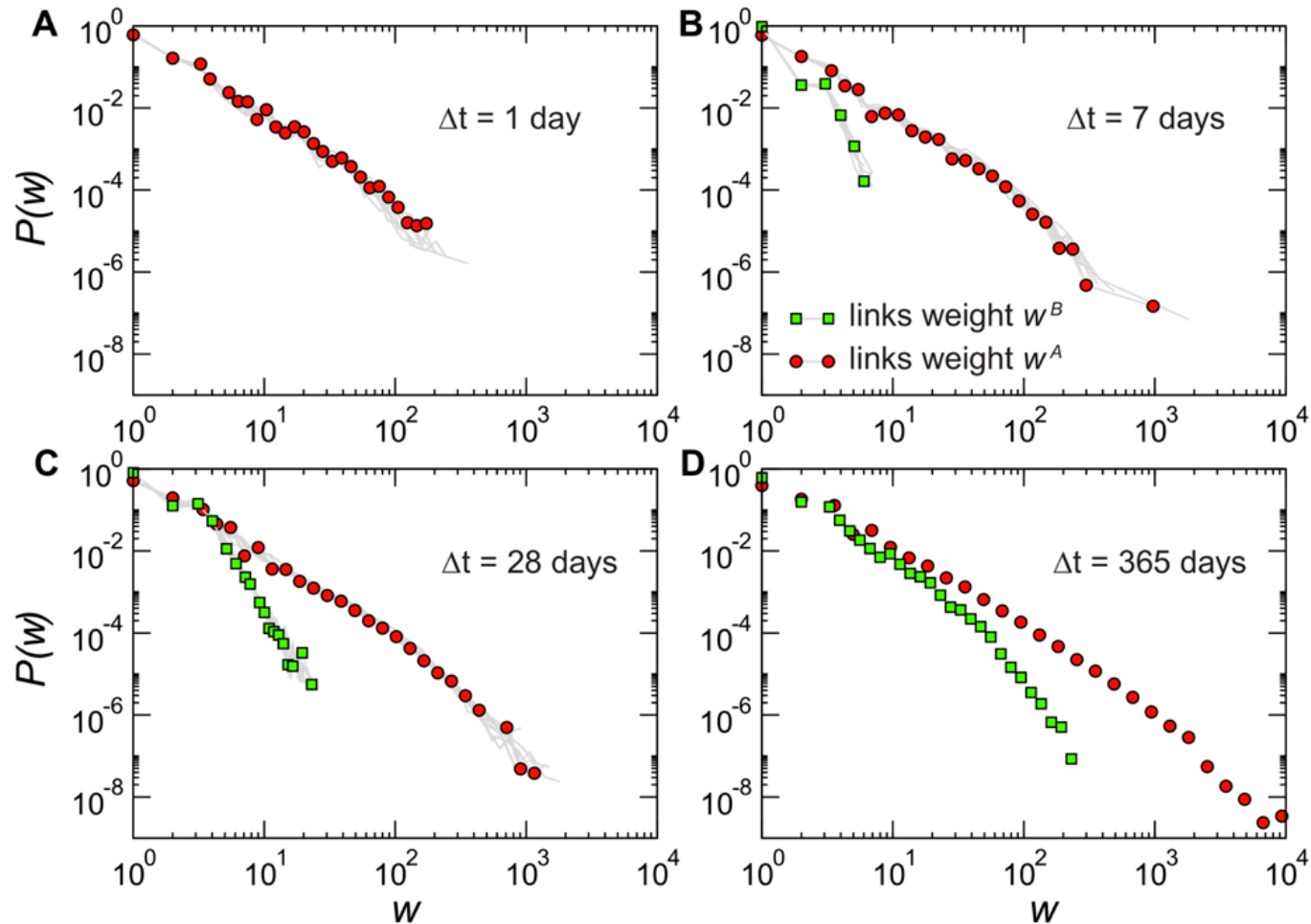
Livestock movements

- long tail distributions

Across timescales



Across timescales



Mobility models

Mobility models

- **What they do:** capture and reproduce the spatiotemporal structures of human trajectories based on various factors such as population distribution, geographical distance, socio-economic factors, ...
- **WHY:**
 - Understanding the mechanisms
 - Handling incomplete data
 - Generate synthetic mobility where data are not available

Gravity model

$$T_{ij} = C \frac{N_i^\alpha N_j^\gamma}{f(d_{ij})}$$

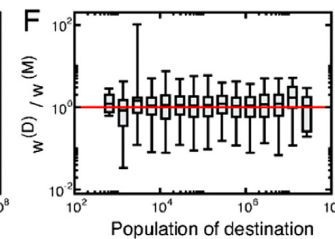
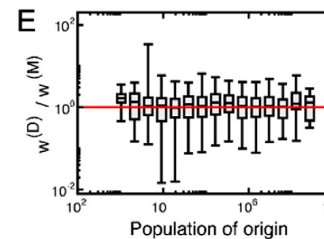
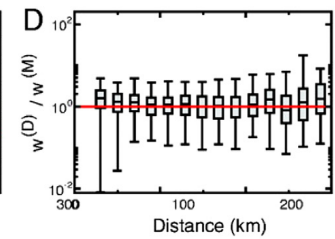
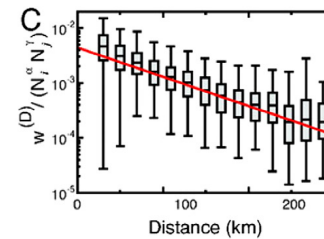
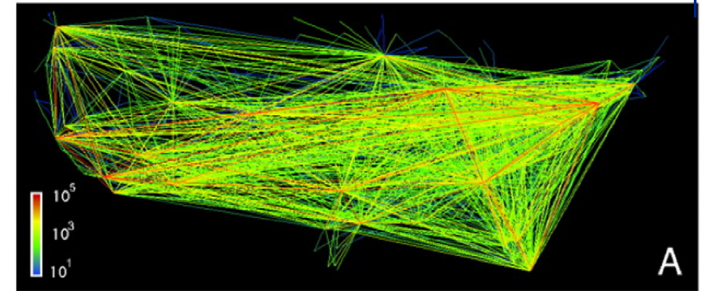
- ▶ T_{ij} : flow $i \rightarrow j$
- ▶ Analogous to Newton's law of gravitation where the populations represent masses
- ▶ The distance function $f(d_{ij})$ is commonly modeled with a power-law or an exponential form
- ▶ Other socio-economic factors can be used as masses or distances

Application to the US

- A gravity model for commuting in the US
- Airport basins of attraction (change of scale)

$$T_{ij} = C \frac{N_i^\alpha N_j^\gamma}{e^{\beta d_{ij}}}$$

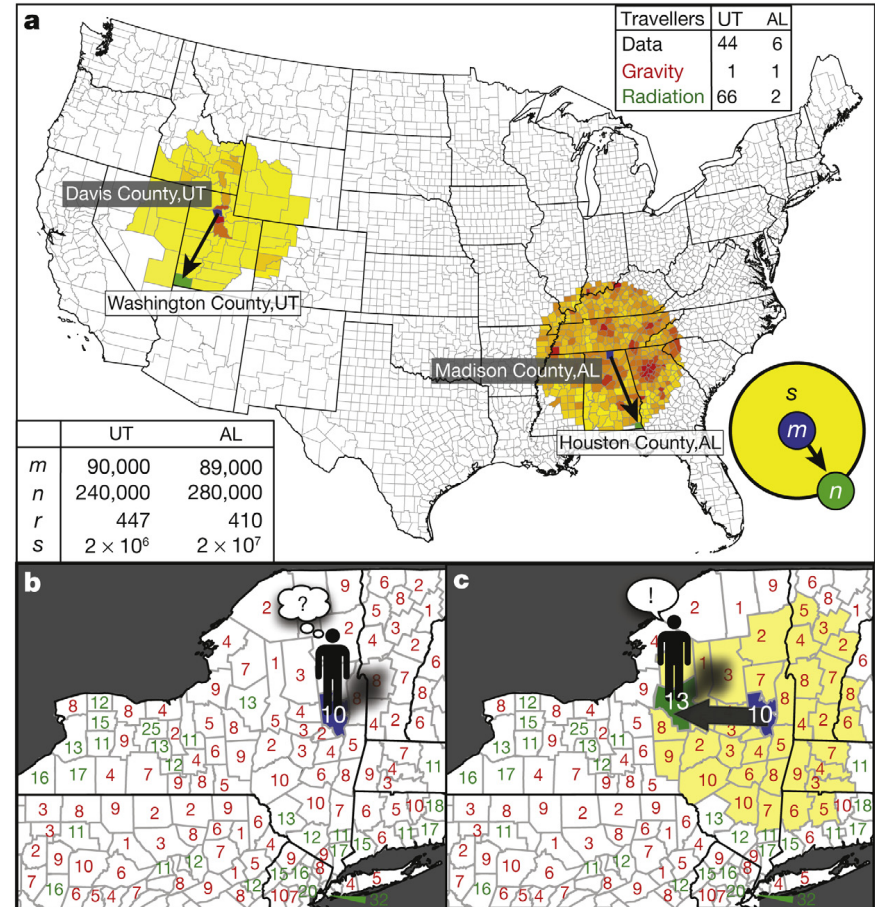
d (km)	Parameter	Estimate	Standard Error	p-value	R ²
≤ 300	α	0.46	0.01	< 2E - 16	0.7972
	γ	0.64	0.01	< 2E - 16	
	β	0.0122	0.0002	< 2E - 16	
> 300	α	0.35	0.06	6.91E - 09	0.5369
	γ	0.37	0.06	2.12E - 09	



Radiation model

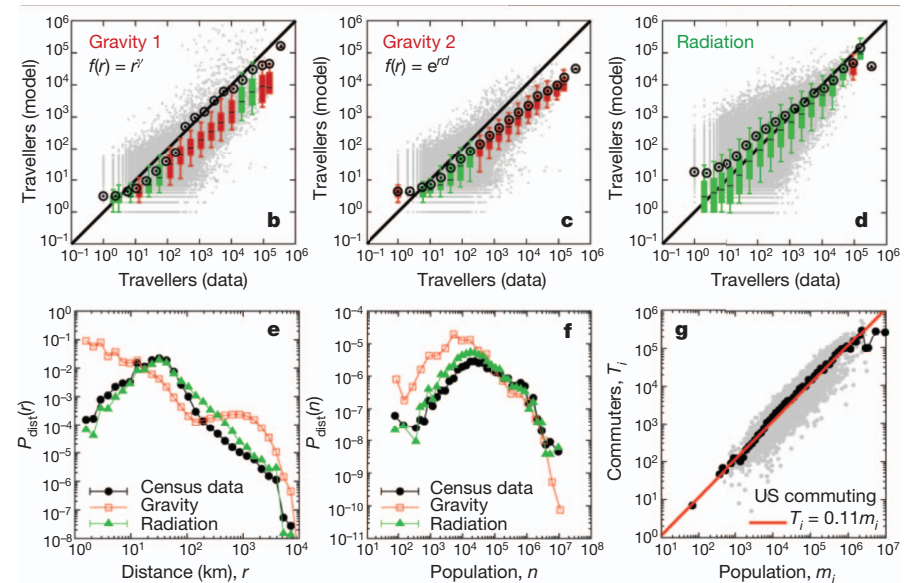
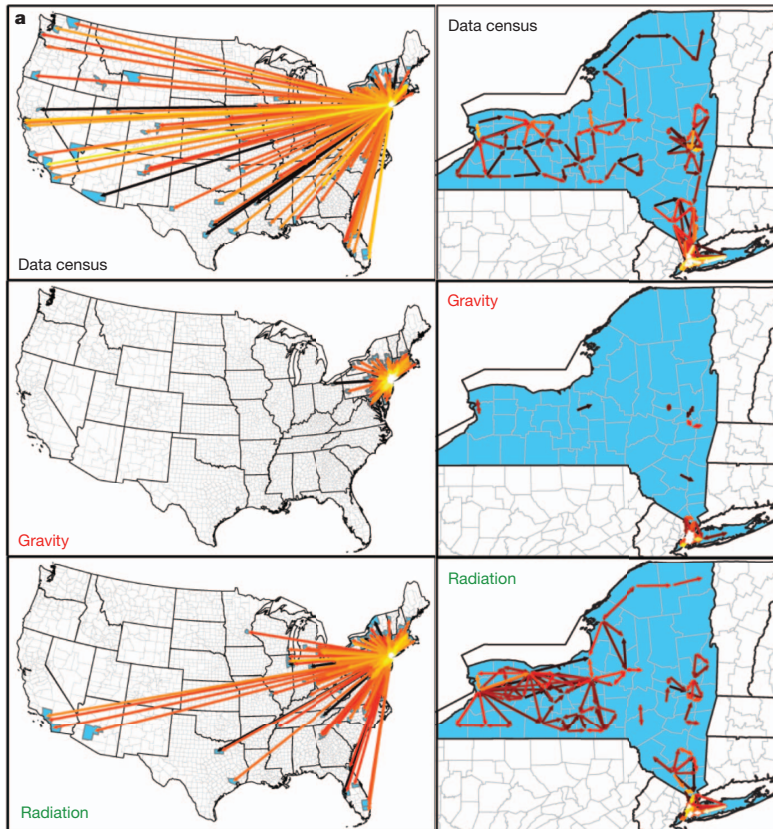
$$T_{ij} = O_i \underbrace{\frac{1}{1 - \frac{m_i}{M}}}_{\text{Normalization term}} \frac{m_i m_j}{(m_i + s_{ij})(m_i + m_j + s_{ij})}$$

- The flow T_{ij} depends on the opportunities (m_i, m_j) available at the origin and at the destination compared to those in the surrounding area of the origin (s_{ij})
- Opportunities can be approximated by the population size



Gravity vs. radiation model

National mobility fluxes from New York County



► Small fluxes...

Gravity vs. radiation model

Gravity model

- Based on population (or socio economic factors) and distances of source and destination
- Adjustable parameters and multiple option for the distance function
- Widely used and accepted framework
- **Requires detailed mobility data for calibration**
- Inconsistent predictive power (e.g., overestimation in sparsely populated areas)
- Needs for different calibration at different scale

Radiation Model

- Based on population (or opportunities) and distances of source and destination
- Requires only population data
- Intervening opportunities between source and destination
- **Parameter-free (no need for calibration)**
- Accurate in diverse scenarios and large-scale predictions
- Less precise for short-distance trips
- Assumes uniform distribution of opportunities

CORONAVIRUS

Mobile phone data for informing public health actions across the COVID-19 pandemic life cycle

Nuria Oliver^{1,2}, Bruno Lepri^{2,3}, Harald Sterly⁴, Renaud Lambiotte^{5,6}, Sébastien Deletaille⁷, Marco De Nadai³, Emmanuel Letouzé^{2,8}, Albert Ali Salah^{2,9}, Richard Benjamins^{10,11}, Ciro Cattuto^{12,13}, Vittoria Colizza¹⁴, Nicolas de Cordes¹⁵, Samuel P. Fraiberger^{2,16,20}, Till Koebe^{2,17}, Sune Lehmann¹⁸, Juan Murillo¹⁹, Alex Pentland²⁰, Phuong N Pham^{2,21}, Frédéric Pivetta²², Jari Saramäki²³, Samuel V. Scarpino²⁴, Michele Tizzoni¹³, Stefaan Verhulst²⁵, Patrick Vinck^{2,21*}

Telco metadata grab is for modelling COVID-19 spread, not tracking citizens, says EC

Natasha Lomas @ripart / 5:05 PM GMT+1 • March 27, 2020

 Comment



Mobile phone data

Aggregated mobility data could help fight COVID-19

As the coronavirus disease 2019 (COVID-19) epidemic worsens, understanding the effectiveness of public messaging and large-scale social distancing interventions is critical.

Caroline O. Buckee^{1*}, Satchit Balsari², Jennifer Chan^{3,4}, Mercè Crosas⁵, Francesca Dominici⁶, Urs Gasser⁷, Yonatan H. Grad¹, Bryan Grenfell⁸, M. Elizabeth Halloran^{9,10}, Moritz U. G. Kraemer^{11,12}, Marc Lipsitch¹, C. Jessica E. Metcalf⁵, Lauren Ancel Meyers¹³, T. Alex Perkins¹⁴, Mauricio Santillana^{15,12}, Samuel V. Scarpino¹⁵, Cecile Viboud¹⁷, Amy Wesolowski¹⁸, Andrew Schroeder¹⁹

PERSPECTIVE

<https://doi.org/10.1038/s41467-020-18190-5>

OPEN

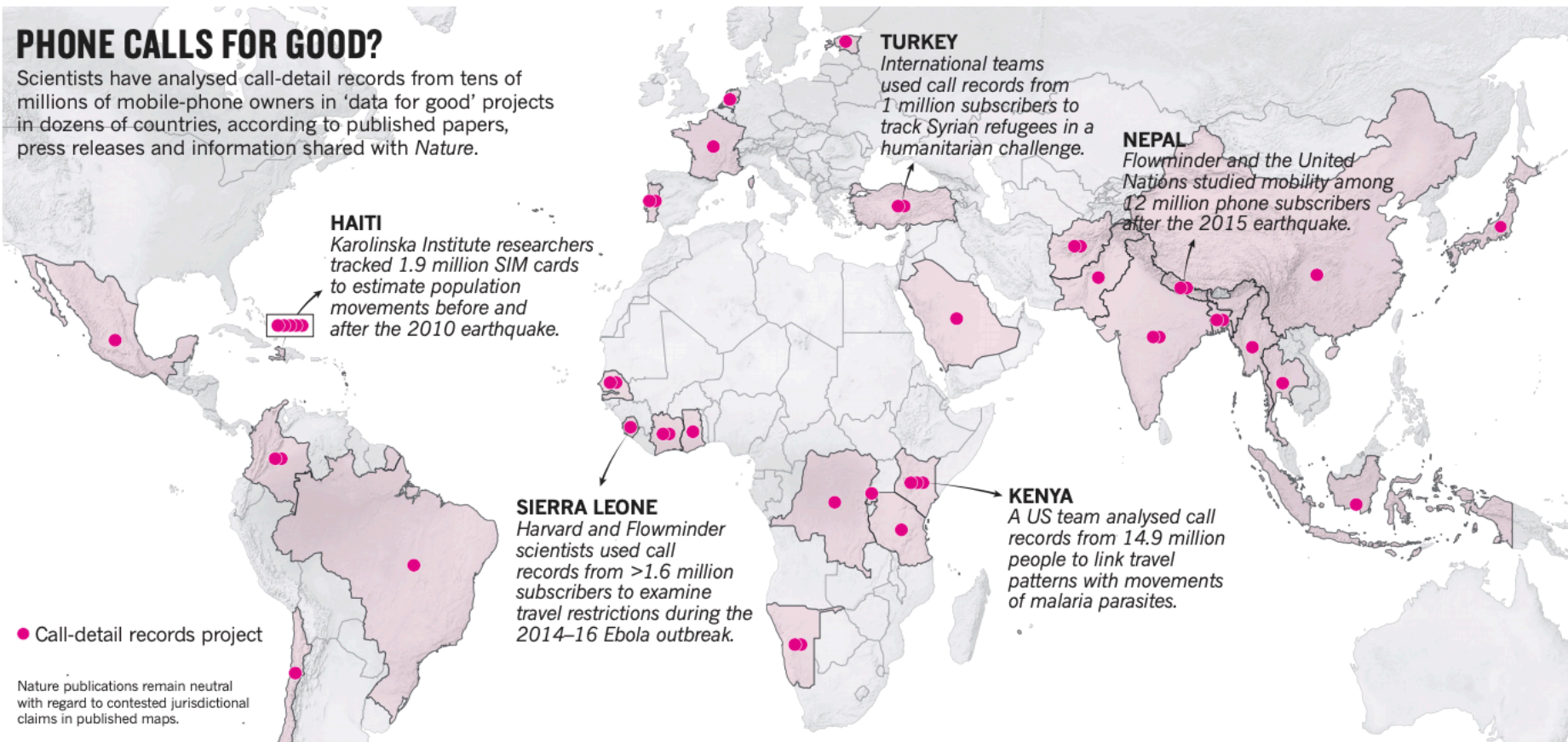
The use of mobile phone data to inform analysis of COVID-19 pandemic epidemiology

Kyra H. Grantz¹, Hannah R. Meredith¹, Derek A. T. Cummings², C. Jessica E. Metcalf³, Bryan T. Grenfell³, John R. Giles¹, Shruti Mehta¹, Sunil Solomon¹, Alain Labrique⁴, Nishant Kishore⁵, Caroline O. Buckee⁵ & Amy Wesolowski¹✉

FEATURE NEWS

PHONE CALLS FOR GOOD?

Scientists have analysed call-detail records from tens of millions of mobile-phone owners in 'data for good' projects in dozens of countries, according to published papers, press releases and information shared with *Nature*.



Nature publications remain neutral with regard to contested jurisdictional claims in published maps.

Quantifying the Impact of Human Mobility on Malaria

Amy Wesolowski,^{1,2} Nathan Eagle,^{3,4} Andrew J. Tatem,^{5,6,7} David L. Smith,^{6,8} Abdisalan M. Noor,^{9,10} Robert W. Snow,^{9,10} Caroline O. Buckee^{4,11*}

Human movements contribute to the transmission of malaria on spatial scales that exceed the limits of mosquito dispersal. Identifying the sources and sinks of imported infections due to human travel and locating high-risk sites of parasite importation could greatly improve malaria control programs. Here, we use spatially explicit mobile phone data and malaria prevalence information from Kenya to identify the dynamics of human carriers that drive parasite importation between regions. Our analysis identifies importation routes that contribute to malaria epidemiology on regional spatial scales.



Mobile phone data highlights the role of mass gatherings in the spreading of cholera outbreaks

Flavio Finger^a, Tina Genolet^a, Lorenzo Mari^b, Guillaume Constantin de Magny^c, Noël Magloire Manga^d, Andrea Rinaldo^{a,e,1}, and Enrico Bertuzzo^{a,1}

^aLaboratory of Ecohydrology, École Polytechnique Fédérale Lausanne, 1015 Lausanne, Switzerland; ^bDipartimento di Elettronica, Informazione e Bioingegneria, Politecnico di Milano, 20133 Milano, Italy; ^cMaladies Infectieuses et Vecteurs: Ecologie, Génétique, Evolution et Contrôle, Institute of Research for Development, 64501 Montpellier, France; ^dService des Maladies Infectieuses et Tropicales de l'Hôpital de la Paix, Unité de Formation et de Recherche en Sciences de la Santé, Université Assane Seck de Ziguinchor, 27000 Ziguinchor, Senegal; and ^eDipartimento dell'Ingegneria Civile, Edile ed Ambientale, Università di Padova, 35131 Padova, Italy



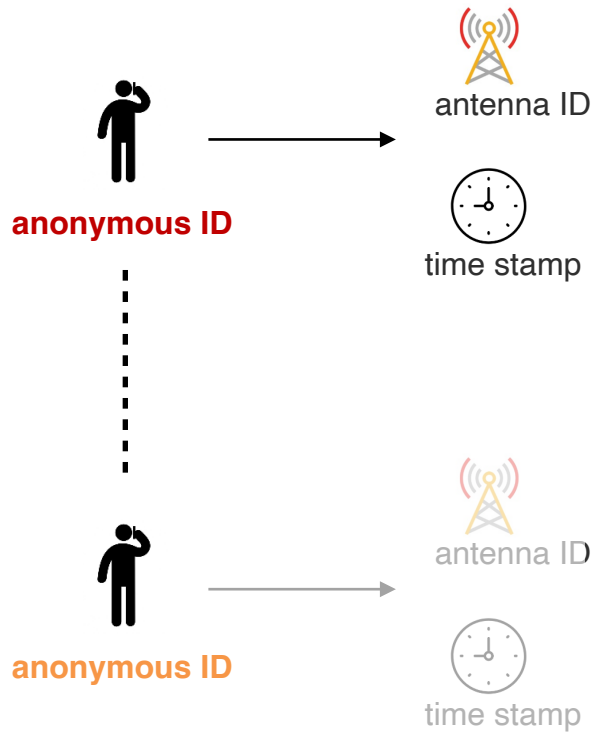
Predictability of population displacement after the 2010 Haiti earthquake

Xin Lu^{a,b,1,2}, Linus Bengtsson^{a,1,2}, and Petter Holme^{a,b,c,d}

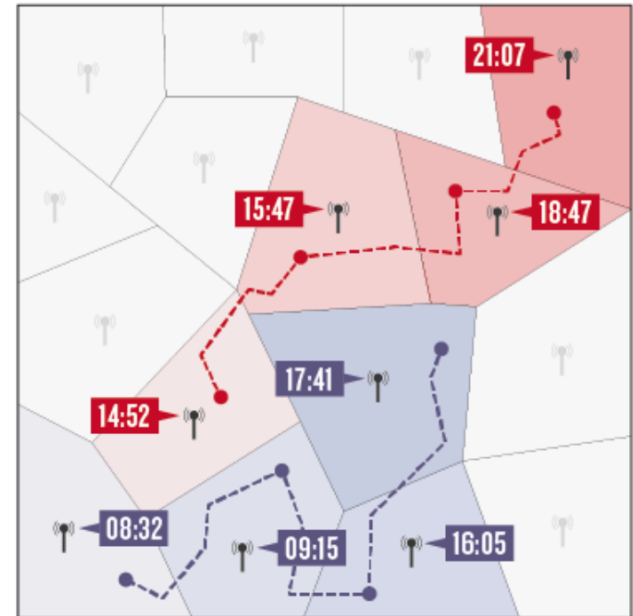
^aDepartment of Public Health Sciences, Karolinska Institutet, 17177 Stockholm, Sweden; ^bDepartment of Sociology, Stockholm University, 10691 Stockholm, Sweden; ^cDepartment of Physics, Umeå University, 90187 Umeå, Sweden; and ^dDepartment of Energy Science, Sungkyunkwan University, Suwon 440-746, Korea

Edited by* H. Eugene Stanley, Boston University, Boston, MA, and approved May 16, 2012 (received for review March 6, 2012)

Mobility phone data: CDR



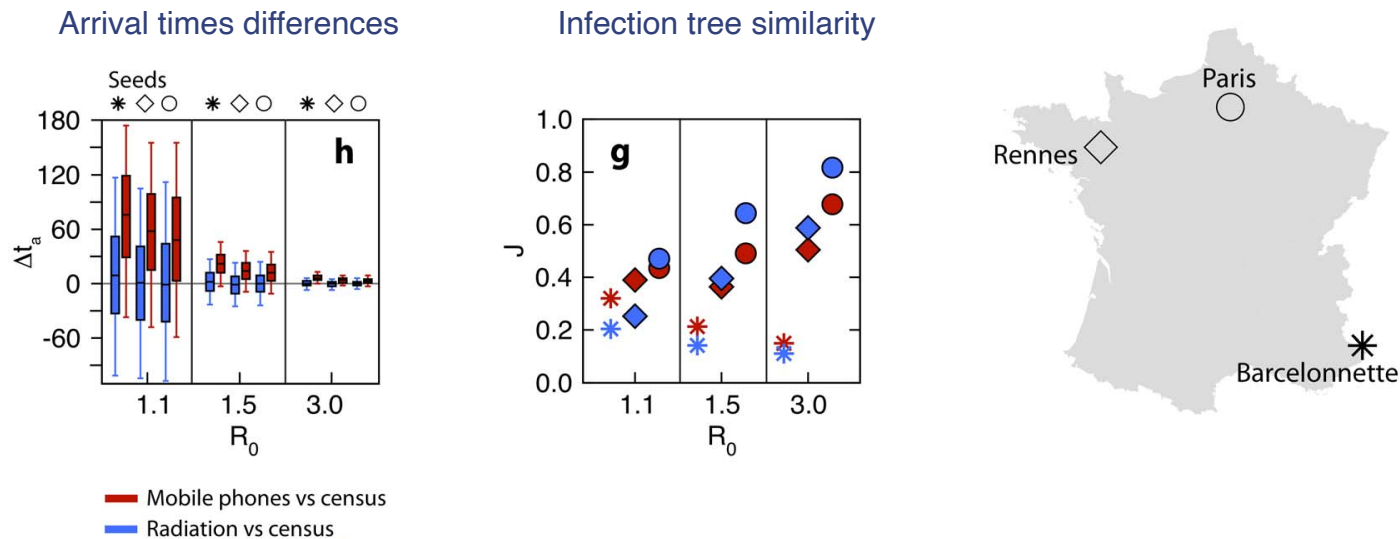
Mobile Phones Data Call Detail Records (CDRs)



Maximen 2019

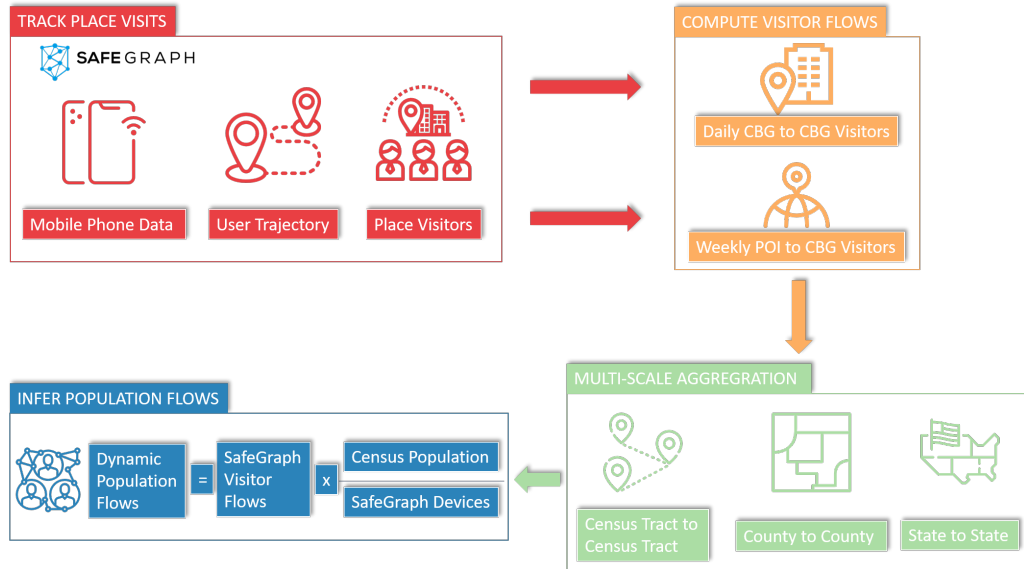
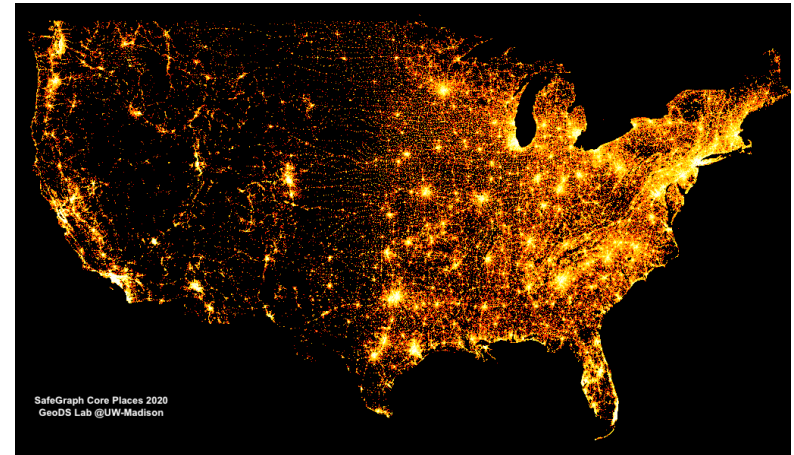
Mobility phone data for routine displacements

- ▶ CDR captures 87% of the empirical flow, is highly correlated, but systematically overestimate → faster epidemic with order preserved
- ▶ Adjustment needed (on census data, on epidemic data)
- ▶ Proxy/models perform differently at different resolution scales. Radiation model showing higher accuracy for central seed (the opposite for peripheral locations)



Mobility phone data: GPS

- From GPS ping
- Cluster of GPS pings are used to identify individuals' home location and POIs
- Spatial aggregation at Census Tract, County and State level



SPATIAL AND METAPOPULATION MODELING

LAB #1.
Mobility data introduction

Beyond telcos



Google COVID-19 Community Mobility Reports



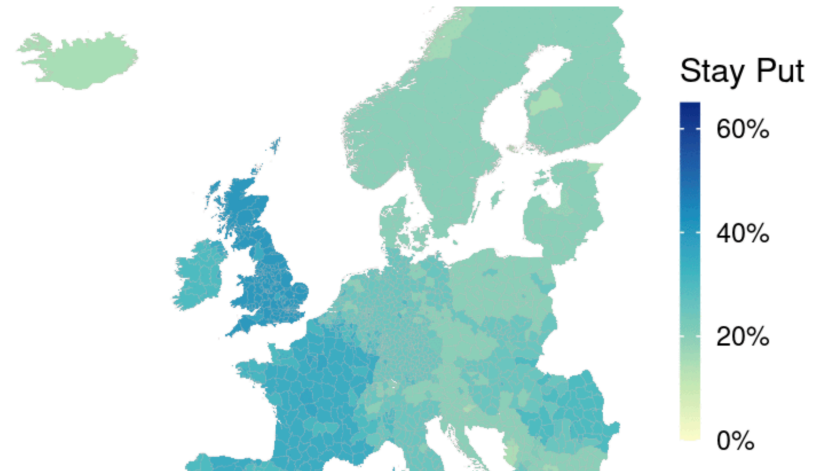
See how your community is moving around differently due to COVID-19

FACEBOOK Data for Good



Movement Range Maps

Movement Range Maps inform researchers and public health experts about how populations are responding to physical distancing measures. These datasets have two different metrics: Change in Movement and Stay Put. The Change in Movement metric looks at how much people are moving around and compares it to a baseline period that predates most social distancing measures. The Stay Put





SAFE GRAPH

Why SafeGraph ▾

Data ▾

Resources ▾

Docs [↗](#)

Geospatial Data: A Comprehensive Guide

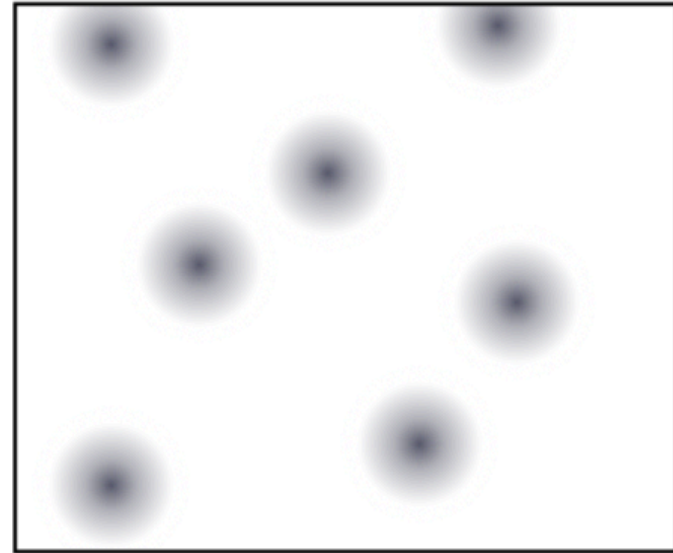
<https://www.safegraph.com/guides/geospatial-data>

Resolution

Definition of patches, borders



e.g. commuting



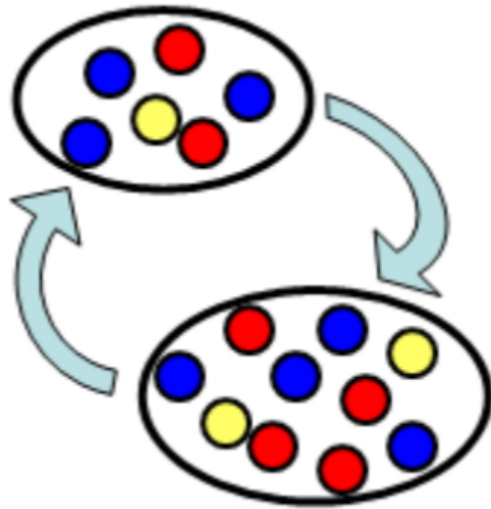
e.g. air travel

but also

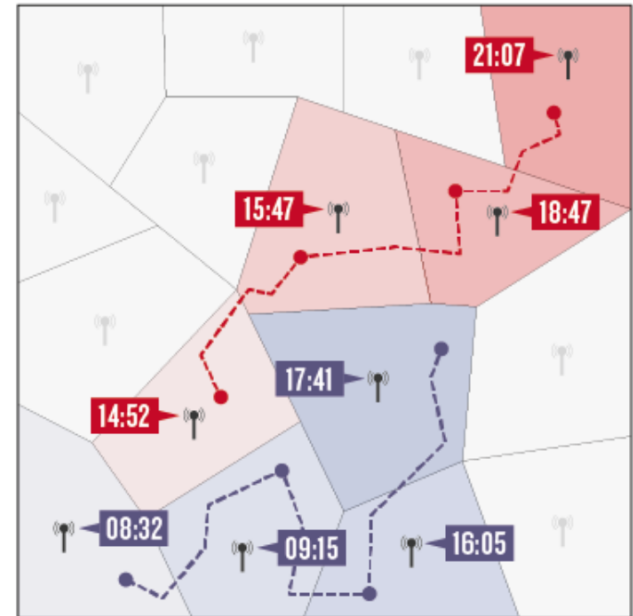
livestock farms →

- network approaches
- metapopulation

From individual movements to fluxes

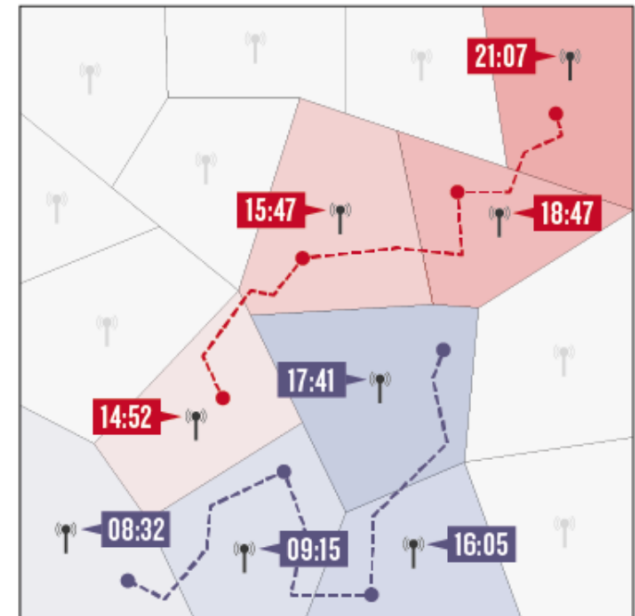
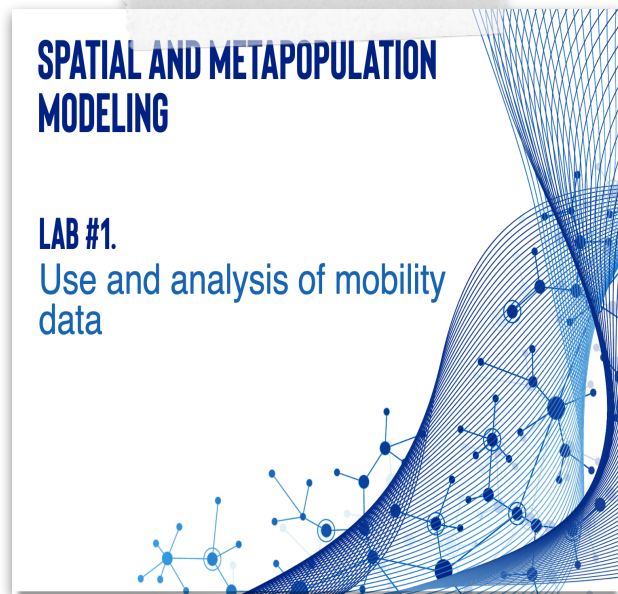


?



Maximen 2019

Home location, ...



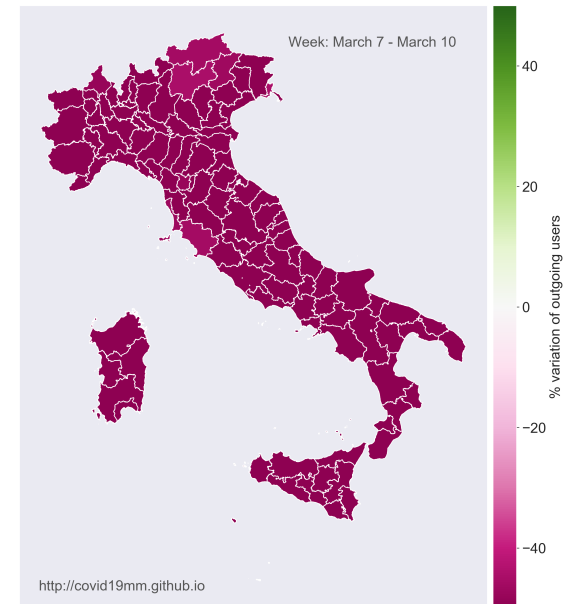
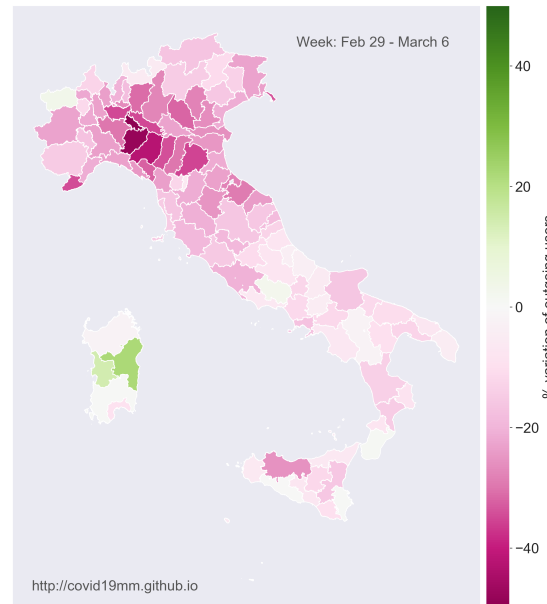
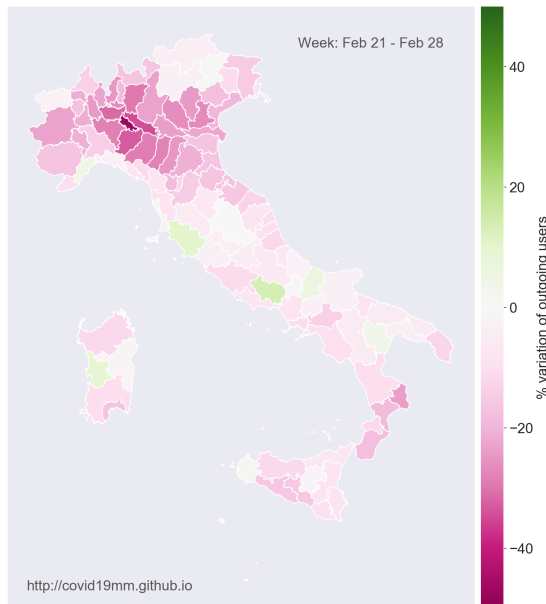
Maximen 2019

Time-varying mobility

- ▶ Changes in mobility over time
- ▶ Can we anticipate them
- ▶ What are the drivers
- ▶ Applications for social distancing

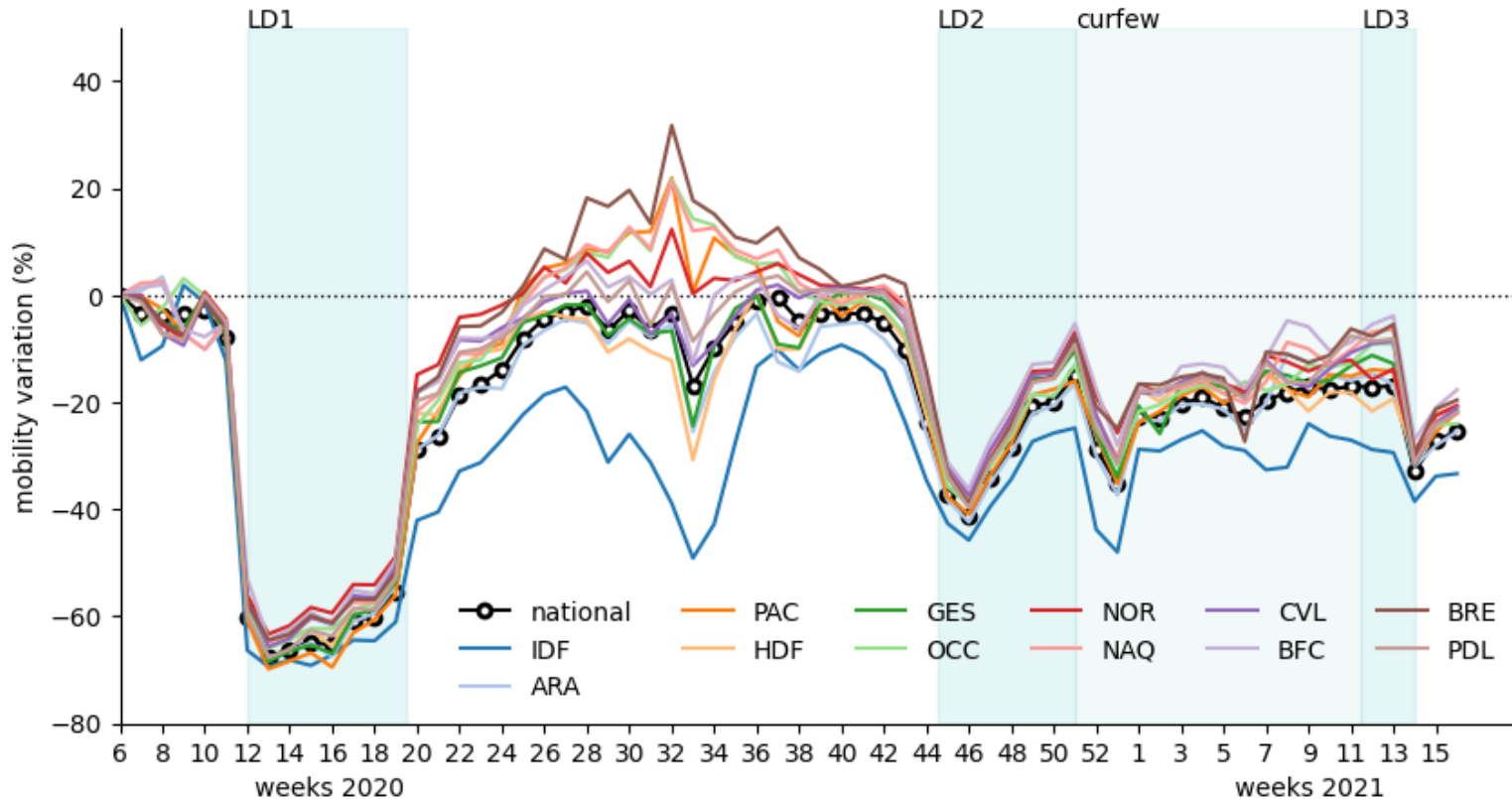
Mobility changes during COVID-19 pdm

Italy



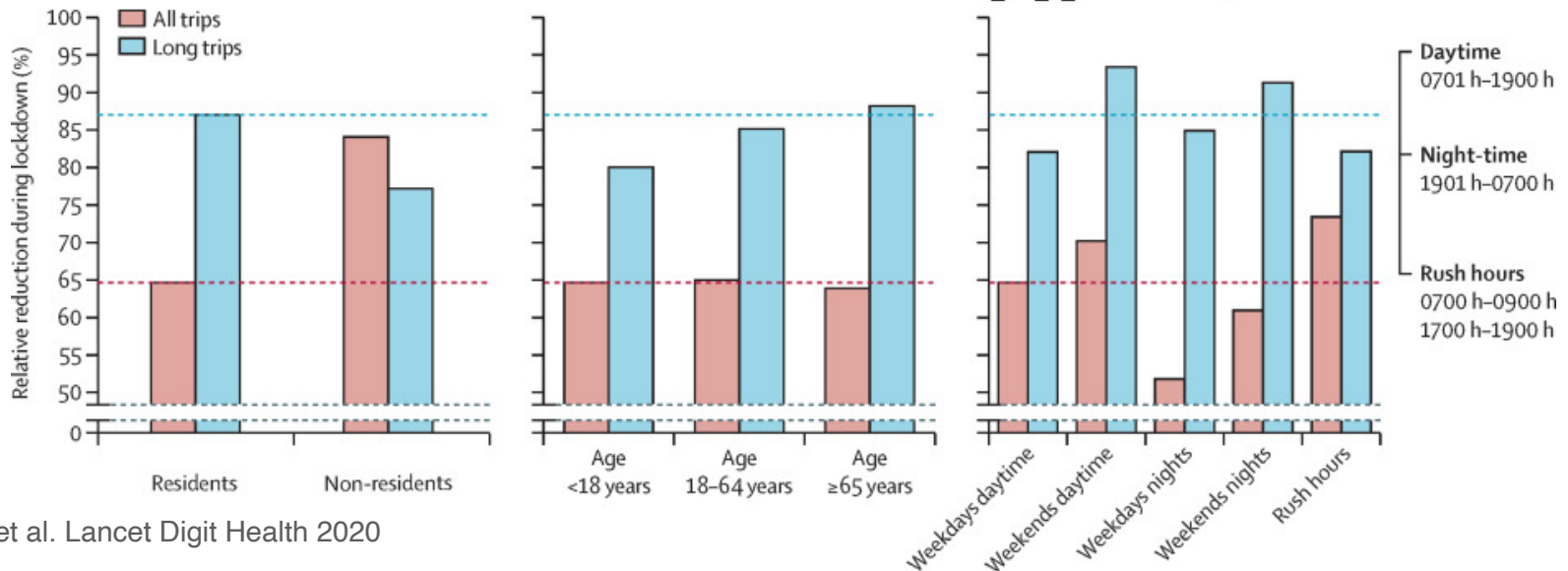
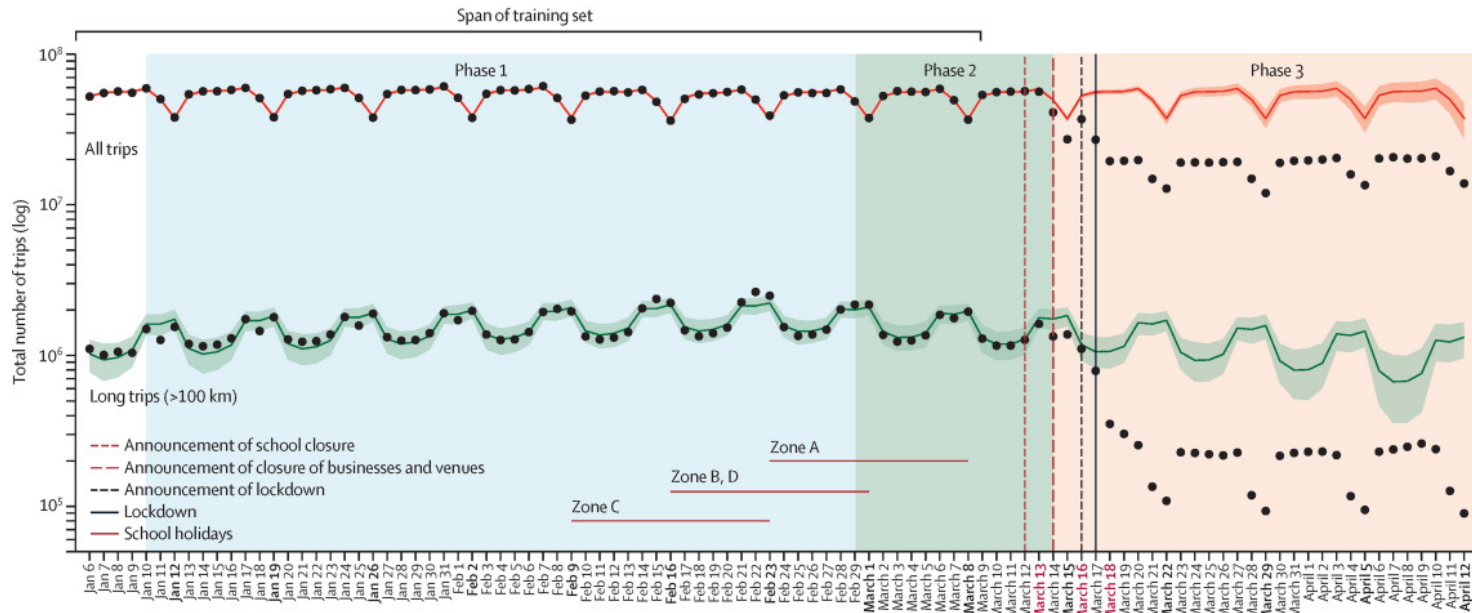
Mobility changes during COVID-19 pdm

France



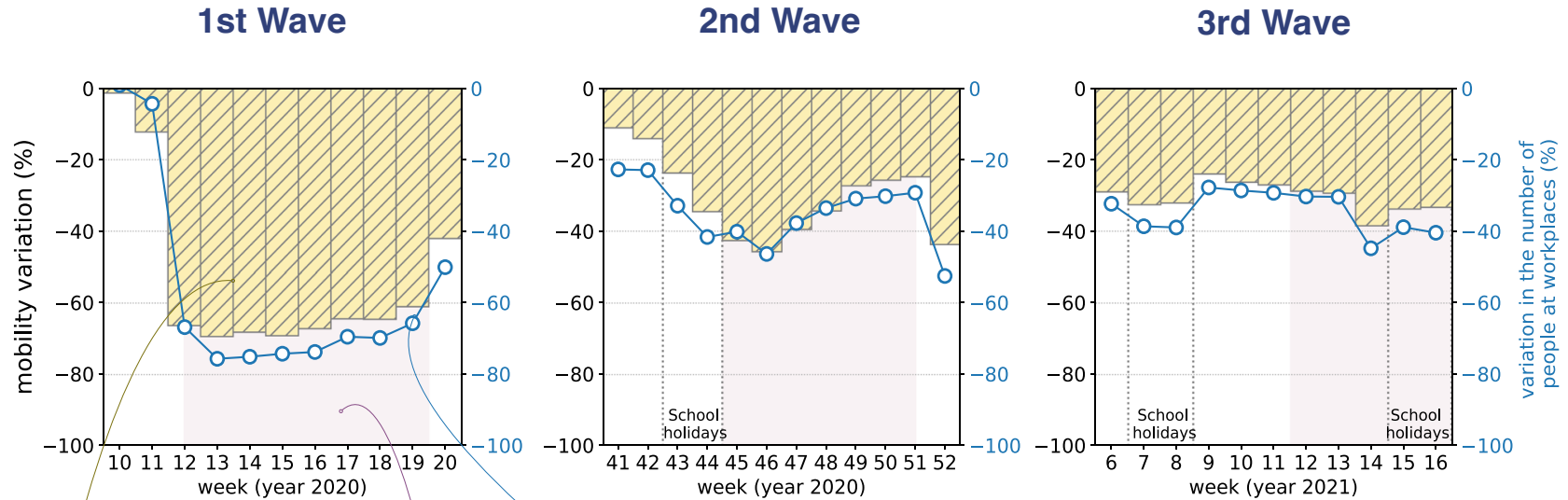
Mobility changes during COVID-19 pdm: strata

France



Mobility changes during COVID-19: lockdowns

France





Reduction in **number of trips** from mobile phone data

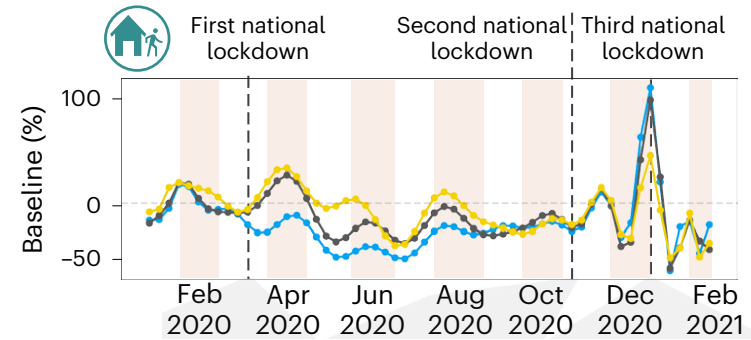
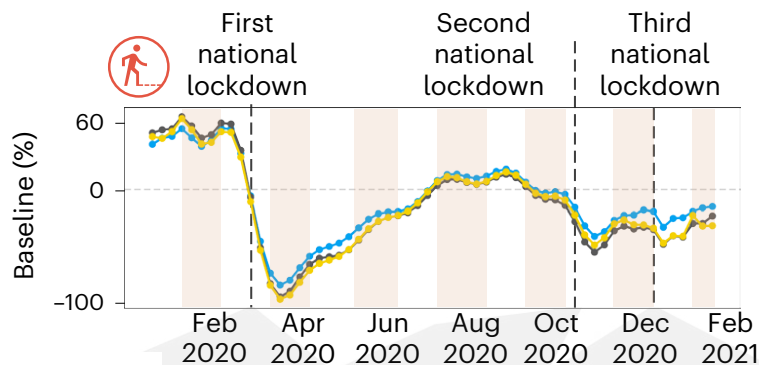
social distancing measures

Estimated change in presence at **workplace locations** based on Google location-history data

Mobility changes during COVID-19: space/time

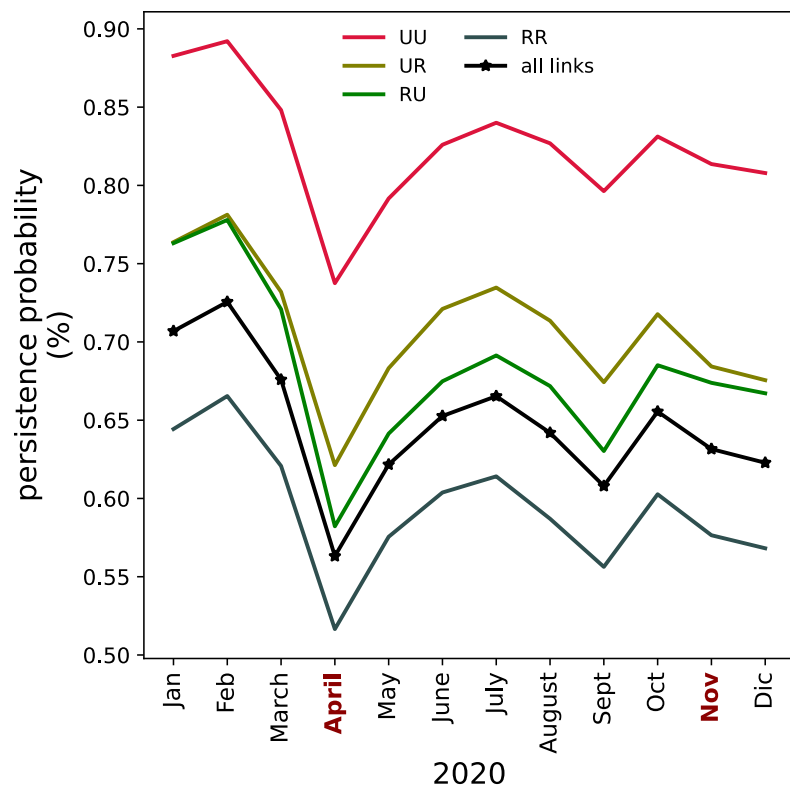
 **radius of gyration:** how far user's visited locations are spread

 **mobility synchronization:** temporal regularities related to when people leave their residences (quantify travel rhythms of the populations)



 Mixed  Urban  Rural

Mobility changes during COVID-19: persistence

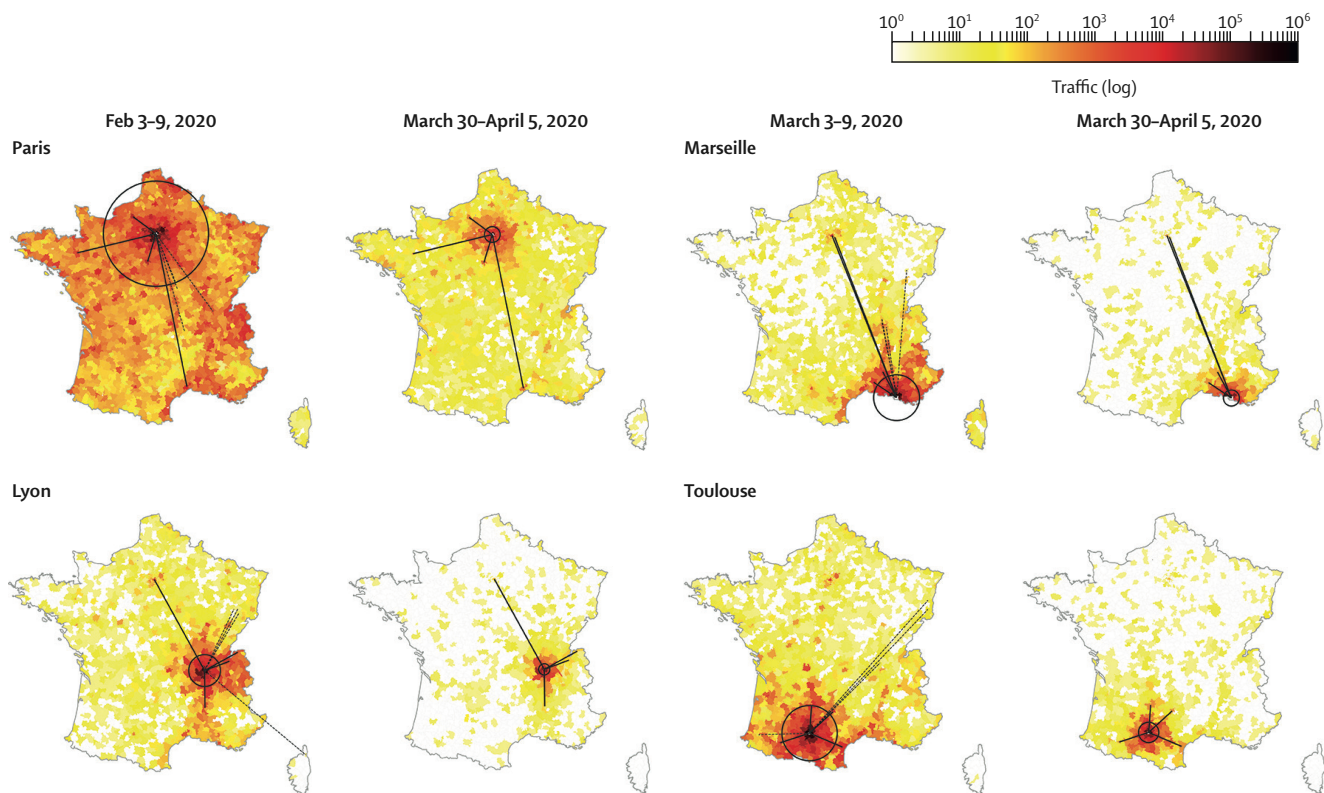


Likelihood that existing connections remain present

UU urban-urban / UR urban-rural
RU rural-urban / RR: rural-rural

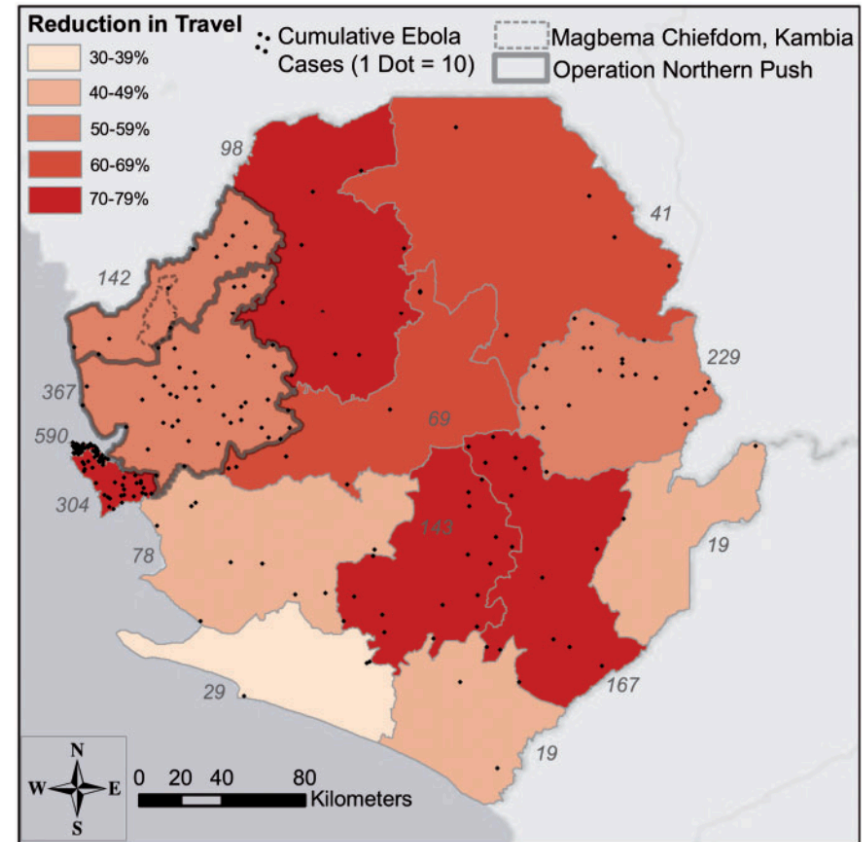
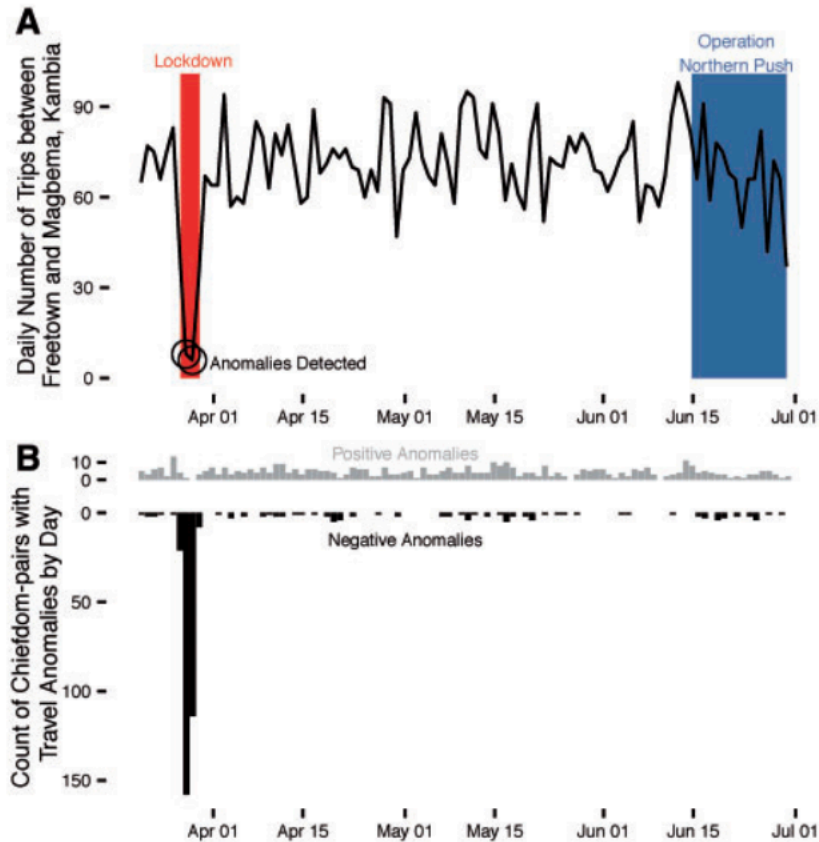
Mobility changes during COVID-19: persistence

France



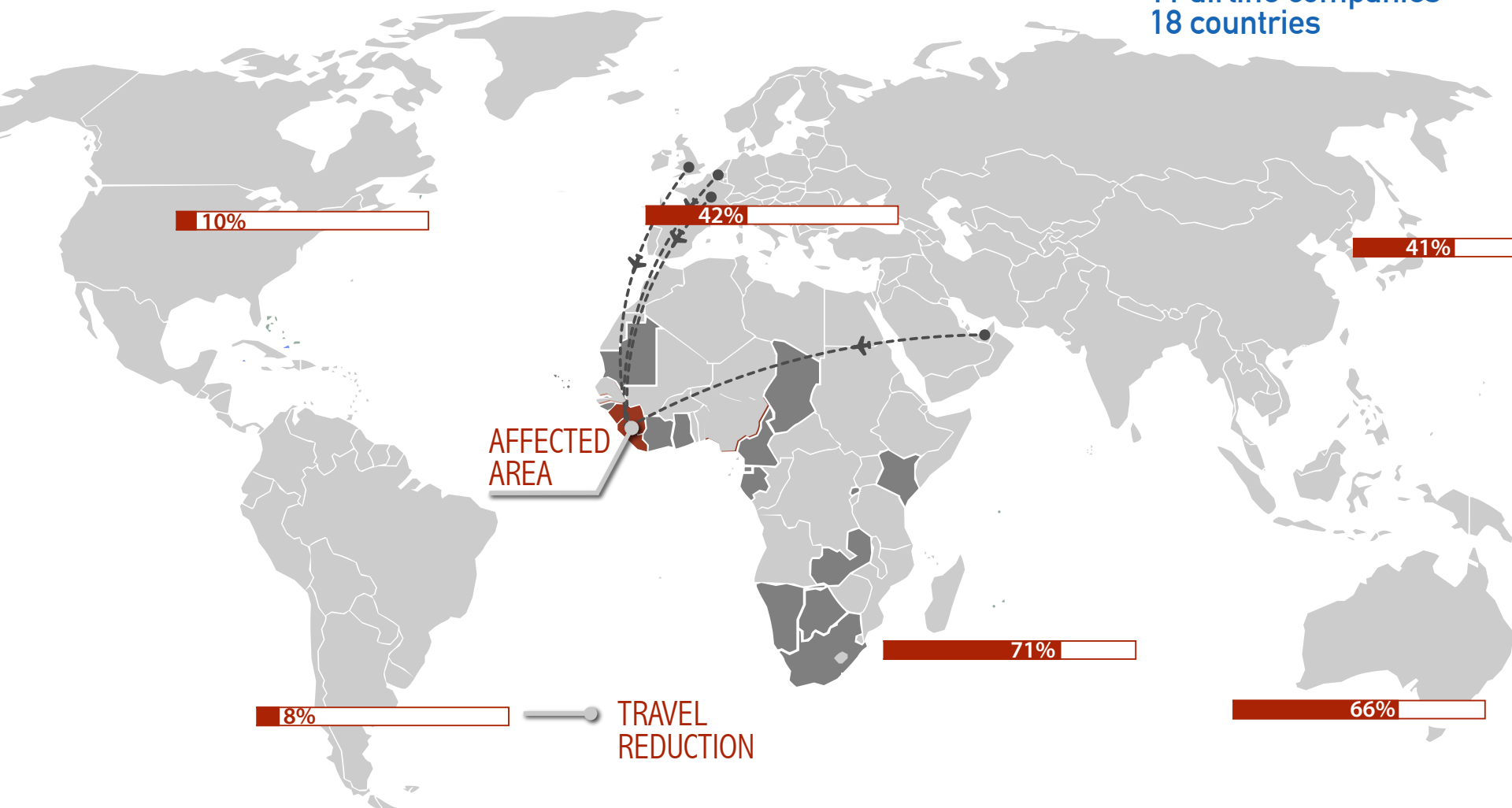
Mobility changes during 2014 Ebola outbreak

Sierra Leone



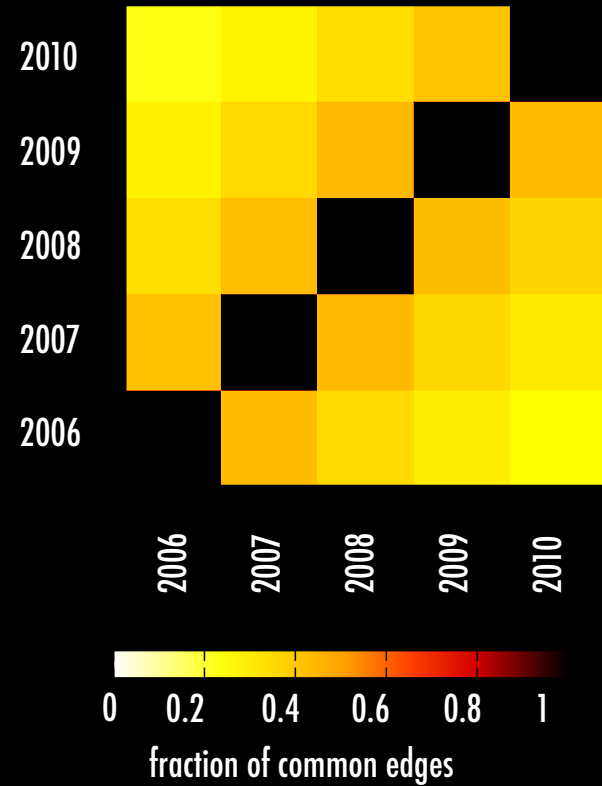
Mobility changes during 2014 Ebola outbreak

11 airline companies
18 countries



Time-varying livestock movements

2011-10-10 Mon

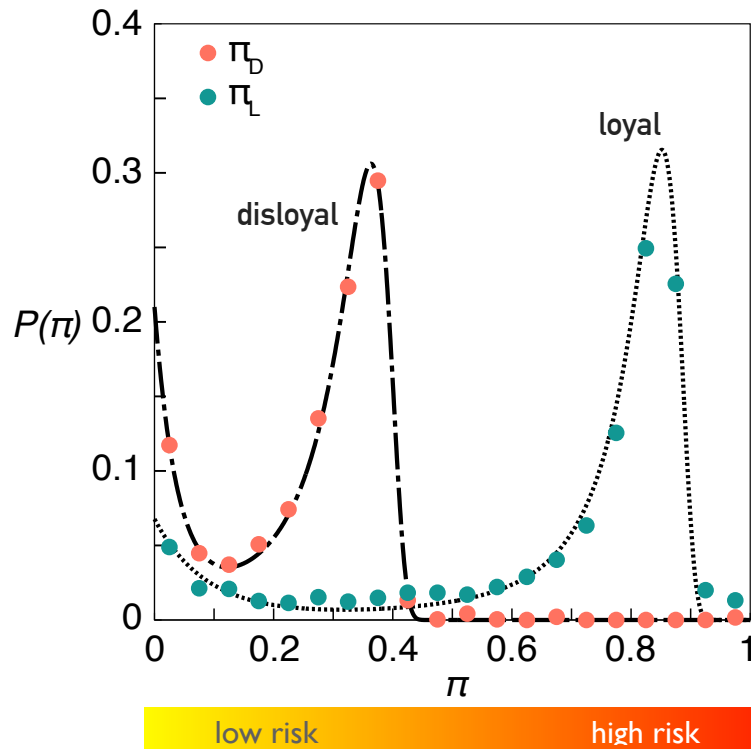


Bajardi et al. PLOS One (2011)
Bajardi et al. J Roy Soc Interface (2012)
Valdano et al. PLOS Comput Biol (2015)

Anticipating change (seasonality)

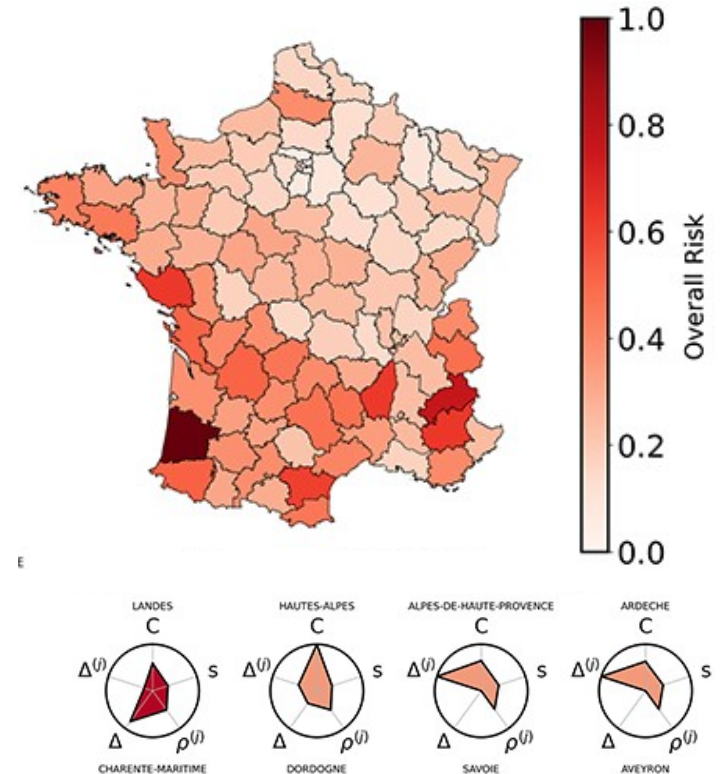
Livestock infections

Risk measure for 2008 based on 2007 movement data + loyalty assessment

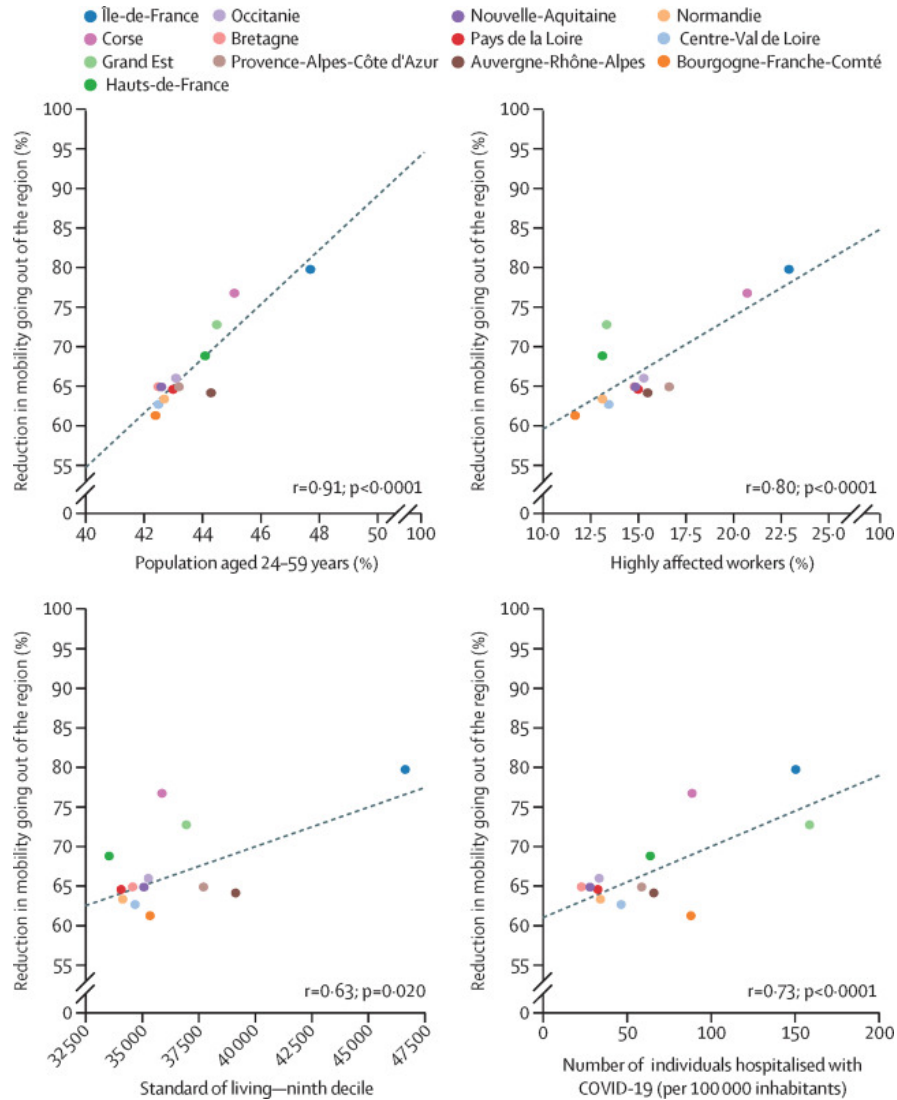


COVID-19

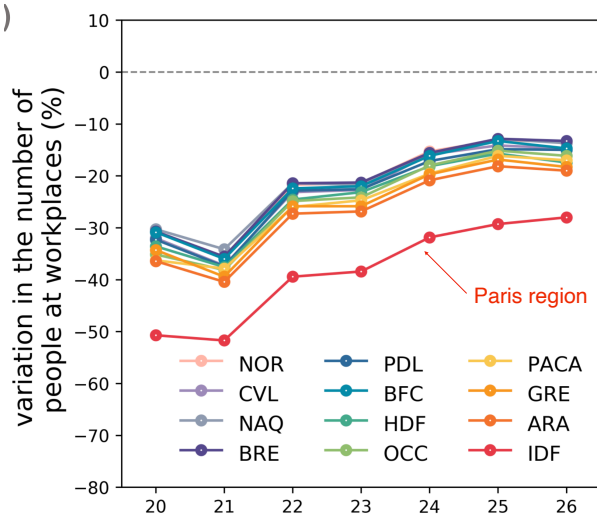
Composite risk measure for summer 2021 based on 2020 summer mobility data



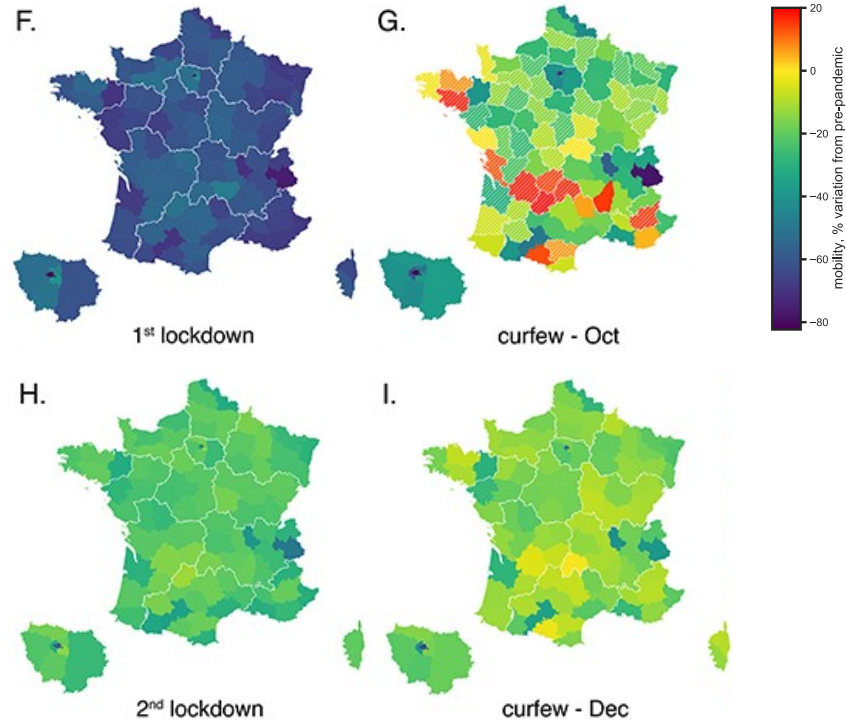
Identifying drivers for change



Identifying drivers for change



Pullano et al. Nature 2021



- job sector
- house crowding

Pullano et al. The Lancet Digital Health 2020

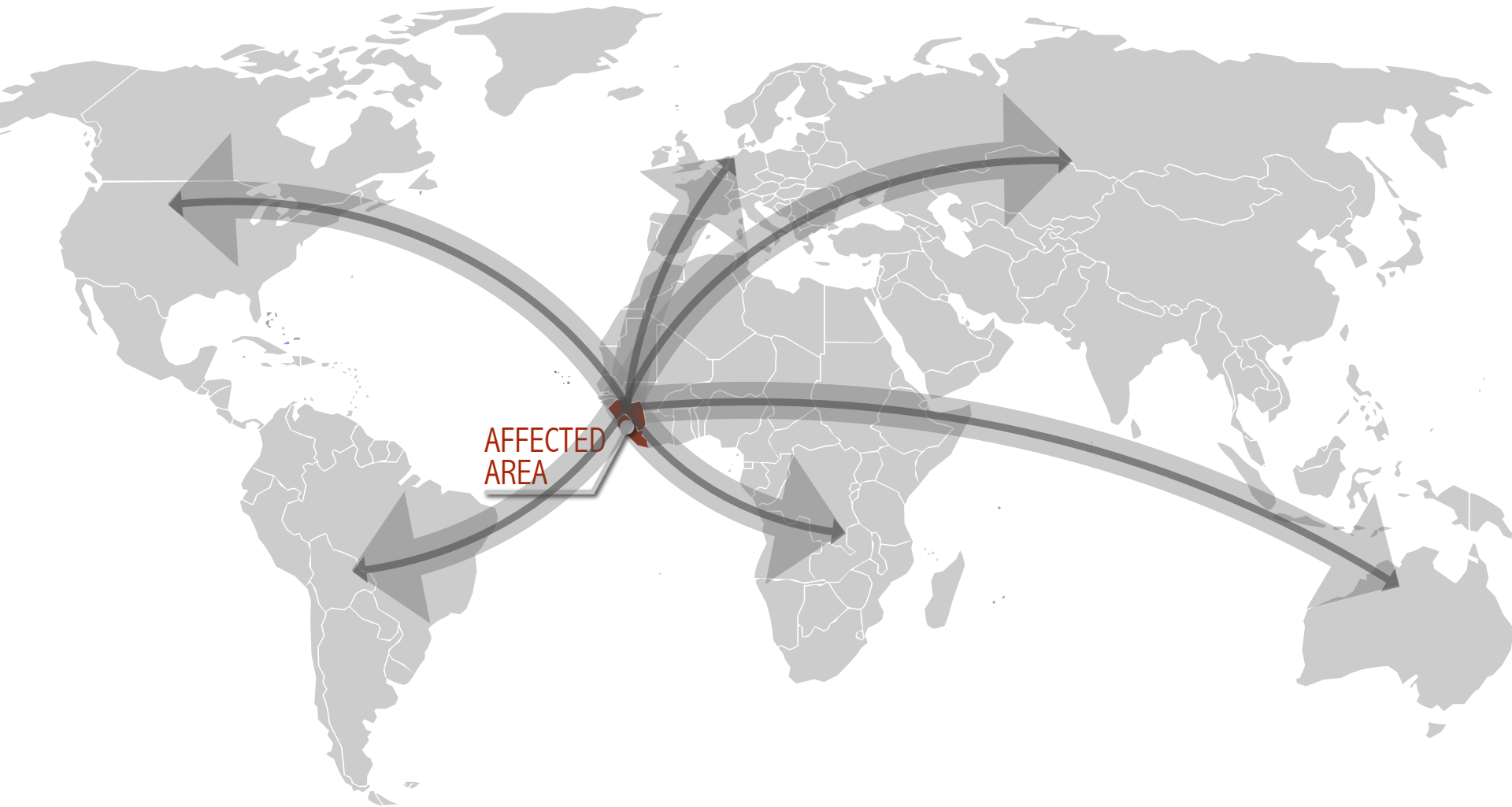
Valdano et al. J Travel Medicine 2021

Tizzoni et al Nature Communications 2022

Risk assessment

- ▶ Importation risk
- ▶ Source size estimate
- ▶ Time of arrival
- ▶ Identification of means of spatial transmission

Importation risk: single source

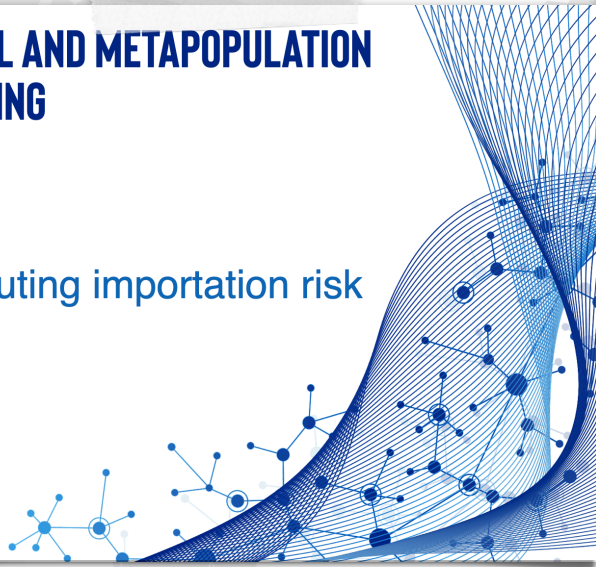


Importation risk: single source

SPATIAL AND METAPOPOPULATION MODELING

LAB #2.

Computing importation risk

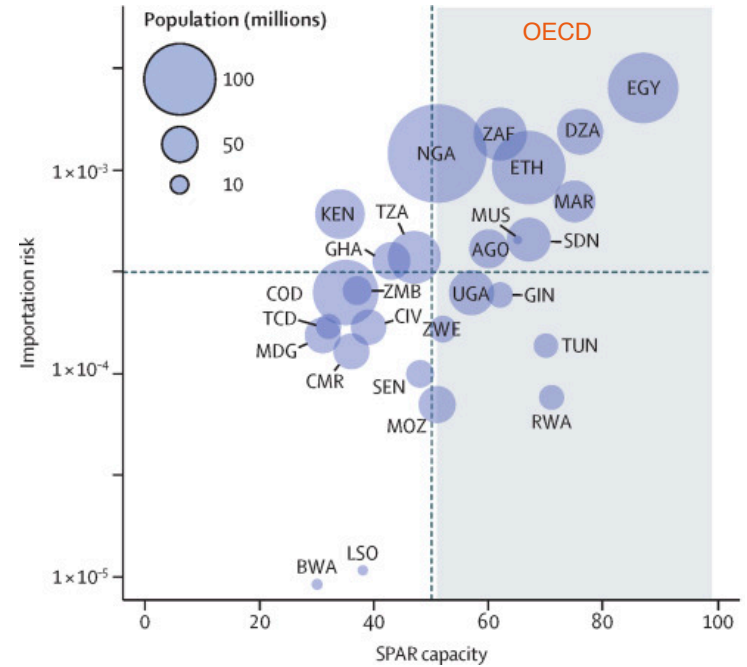
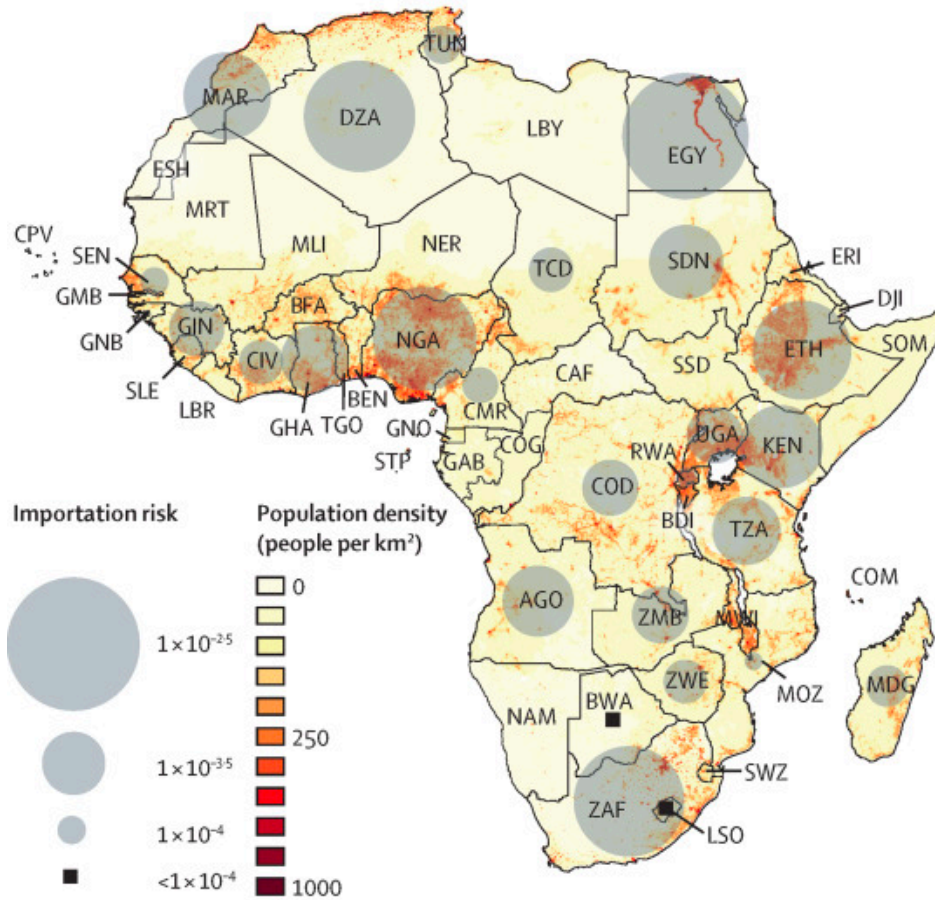


- Importation risk of country α from city i :

$$r_{i\alpha} = A_{i\alpha}$$

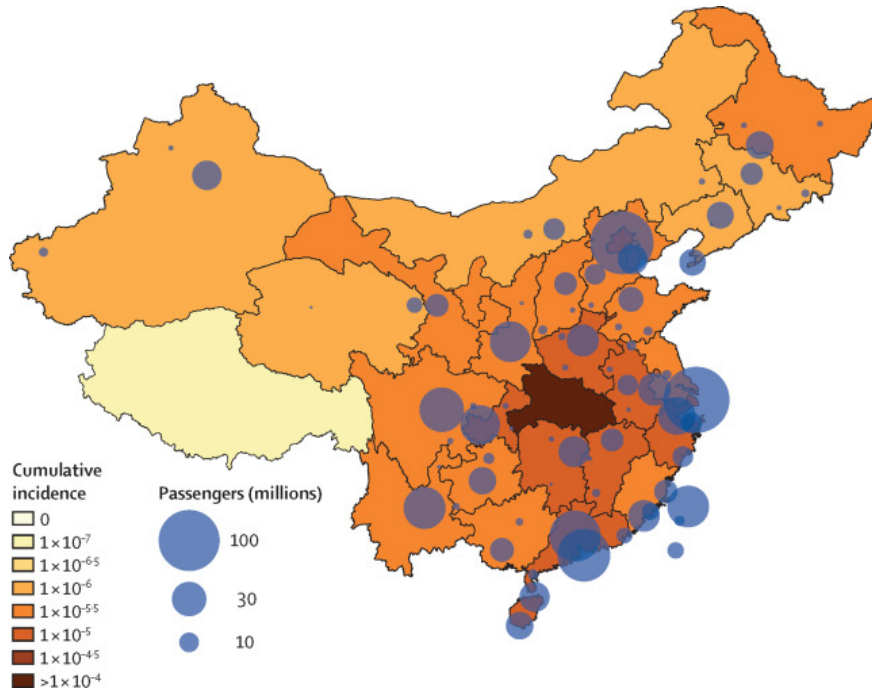
$A_{i\alpha}$: probability to travel from i to α if travel
(== proportion of travelers $i \rightarrow \alpha$ from travel data)

Importation risk: multiple source



Importation risk: multiple source

COVID-19 incidence in China as of Feb 11, 2020, and annual volume of outflow passenger per airport



- Importation risk of country α from city i :

$$r_{i\alpha} = \frac{e_i n_i A_{i\alpha}}{\sum_j e_j n_j}$$

- Importation risk of country α :

$$R_\alpha = \sum_i r_{i\alpha}$$

n_i : number of individuals leaving i

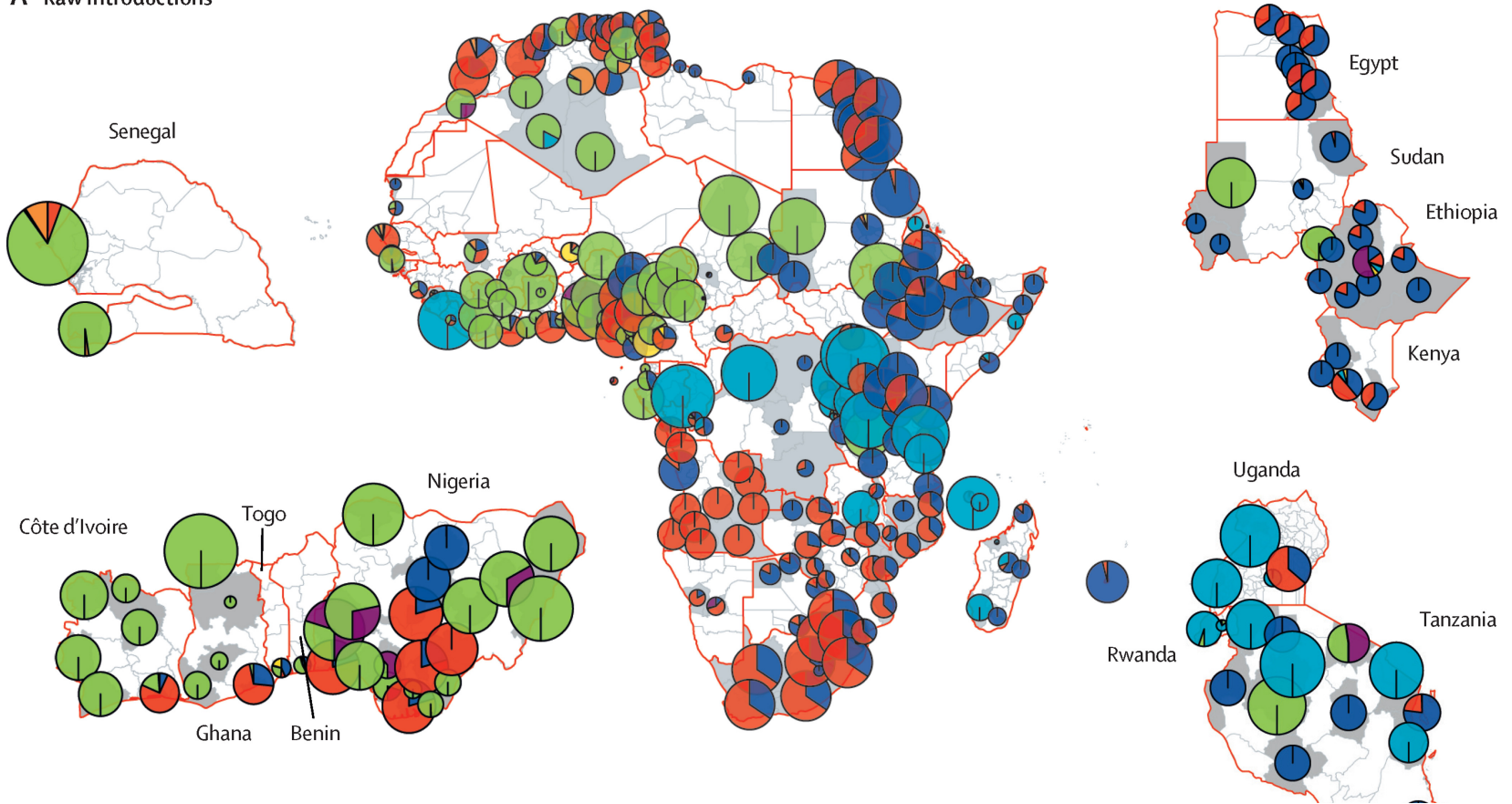
e_i : cumulate incidence in city i

$A_{i\alpha}$: probability to travel from i to α if travel

Dengue importation risk

■ Asia ■ South America ■ East Africa ■ Central Africa ■ West Africa ■ Northern Africa ■ Southern Africa

A Raw introductions



Source size estimate

COVID-19

17 January 2020

Imperial College London COVID-19 Response Team

Report 1: Estimating the potential total number of novel Coronavirus cases in Wuhan City, China

Natsuko Imai, Ilaria Dorigatti, Anne Cori, Steven Riley, Neil M. Ferguson

WHO Collaborating Centre for Infectious Disease Modelling

MRC Centre for Global Infectious Disease Analysis

Abdul Latif Jameel Institute for Disease and Emergency Analytics (J-IDEA)

Imperial College London

	Baseline	Scenario 1	Scenario 2	Scenario 3	Scenario 4
Exported number of confirmed cases*	3	3	3	2	4
Daily international passengers travelling out of Wuhan International airport ¹	3,301	3,301	3,301	3,301	3,301
Effective catchment population of Wuhan airport	19 million	11 million	19 million	19 million	19 million
Detection window (days)	10 days	10 days	8 days	10 days	10 days
Estimated Total number of cases (95% CI)	1,723 (427 – 4,471)	996 (246 – 2,586)	2,155 (535 – 5,590)	1,149 (190 – 3,549)	2,298 (712 – 5,341)

$$I_{source} = \frac{I_{dest}^{det}}{p_{dest}^{det}}$$

$$p_{dest}^{det} = \frac{W_{source \rightarrow dest}}{N_{source}} \cdot \Delta t$$

I_{dest}^{det} : detected cases at destination

p_{dest}^{det} : probability that a case is detected at destination

$W_{source \rightarrow dest}$: travel flow from source to destination

N_{source} : source population

Δt : mean time to detection

January 16, 2020:

- 41 cases in Wuhan
- 2 in Thailand
- 1 in Japan



1,723
(427-4,471)

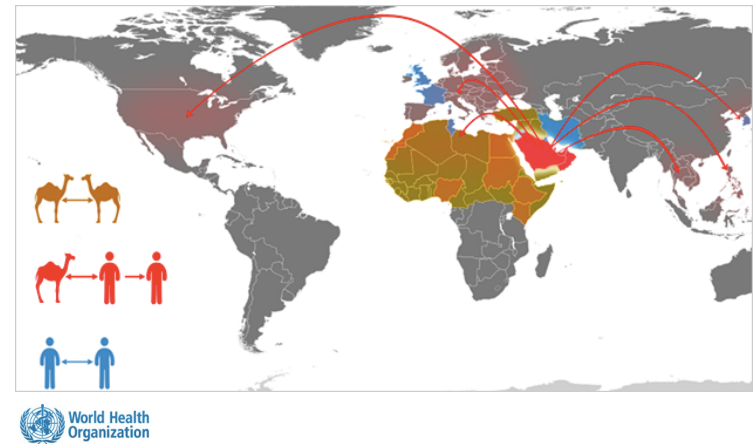
Source size estimate

2009 H1N1 pandemic



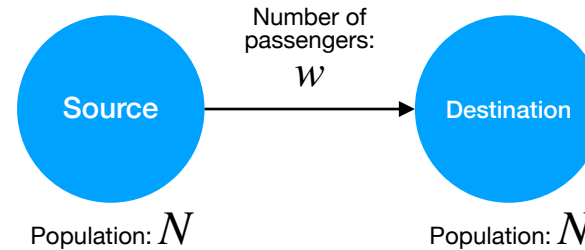
Fraser et al. Science 2009
Balcan et al PNAS 2009

MERS epidemic



Poletto et al Eurosurveillance 2014

Arrival time: two cities

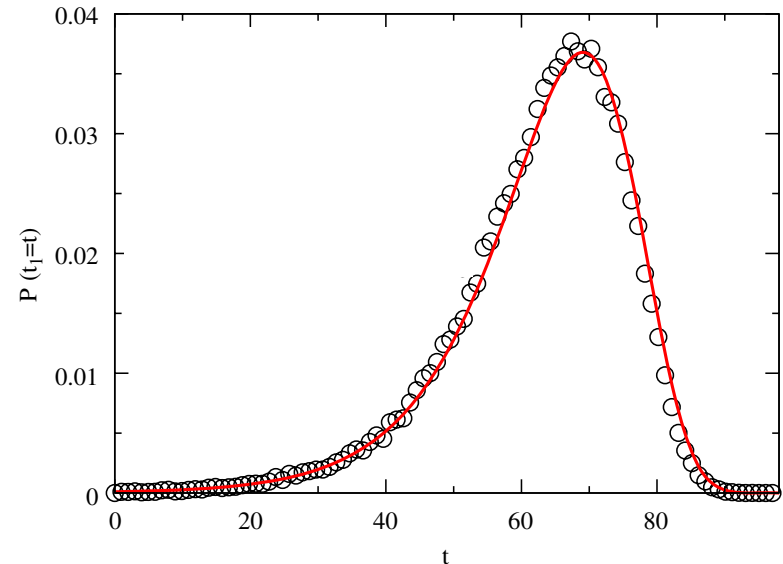


Travel probability: $p = \frac{w}{N} \Delta t$

Probability arrival at time t : $P(t_1 = n\Delta t) = \underbrace{\left(1 - (1 - p)^{I_0(n\Delta t)}\right)}_{\text{Probability to travel at time } t_1} \times \underbrace{\prod_{i=1}^{n-1} (1 - p)^{I_0(i\Delta t)}}_{\text{Probability never traveled before}}$

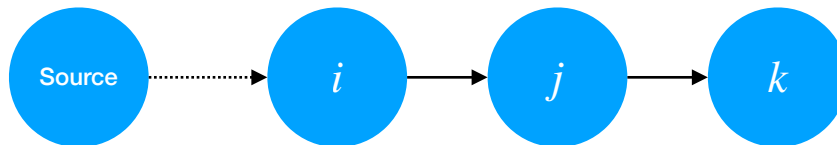
Suppose at the source: $I(t) = I_0 e^{\lambda t}$

$$\langle t \rangle = \frac{1}{\lambda} \left(\ln \left(\frac{N\lambda}{w} \right) - \gamma \right)$$

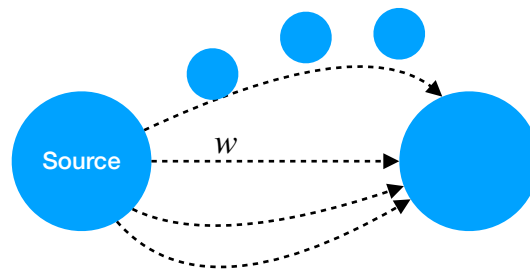


Extensions

Line of cities

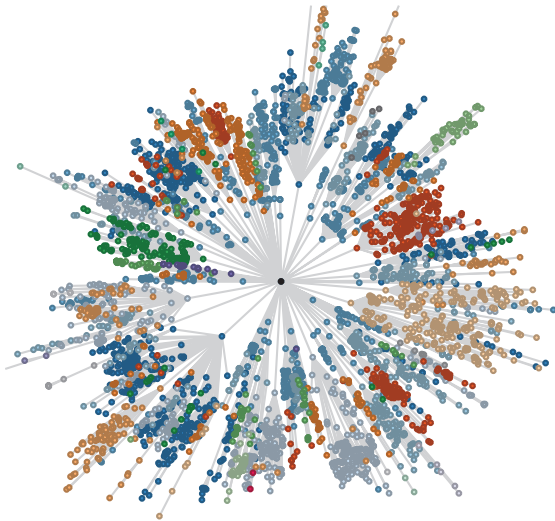


Network of cities



Logarithm of traffic

Arrival time



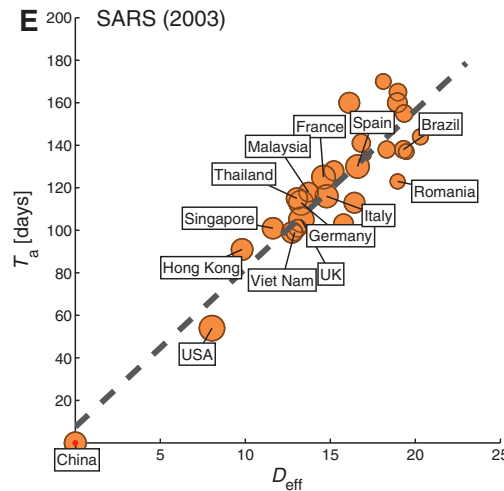
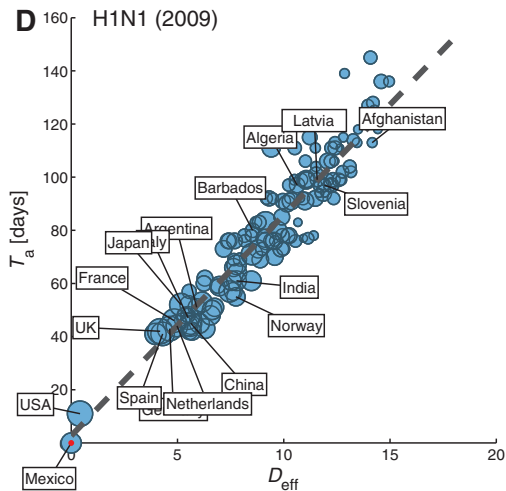
Alternative view: **Effective distance**

- d_{mn} : distance between connected patches
- D_{mn} : distance taking the path that minimize the sum effective distances

Probability of travel

$$d_{mn} = (1 - \log P_{mn}) \geq 1$$

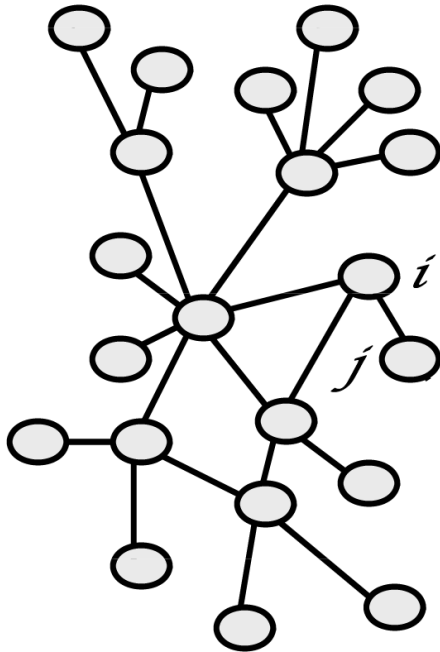
$$D_{mn} = \min_{\Gamma} \lambda(\Gamma)$$



MEtapopulation models

- ▶ Levins-type (no pop structure)
- ▶ Kernel transmission
- ▶ Explicit coupling
- ▶ Effective coupling

#1: Levins type



$$\frac{dp_i}{dt} = C_i(\vec{p})(1 - p_i) - p_i E_i(\vec{p})$$

Rate of change in p_i ,
the probability that
infection is present in
population i

Viana et al. TREE 2014

Invasion rate C_i of
population i from other
populations \vec{p} when
infection absent

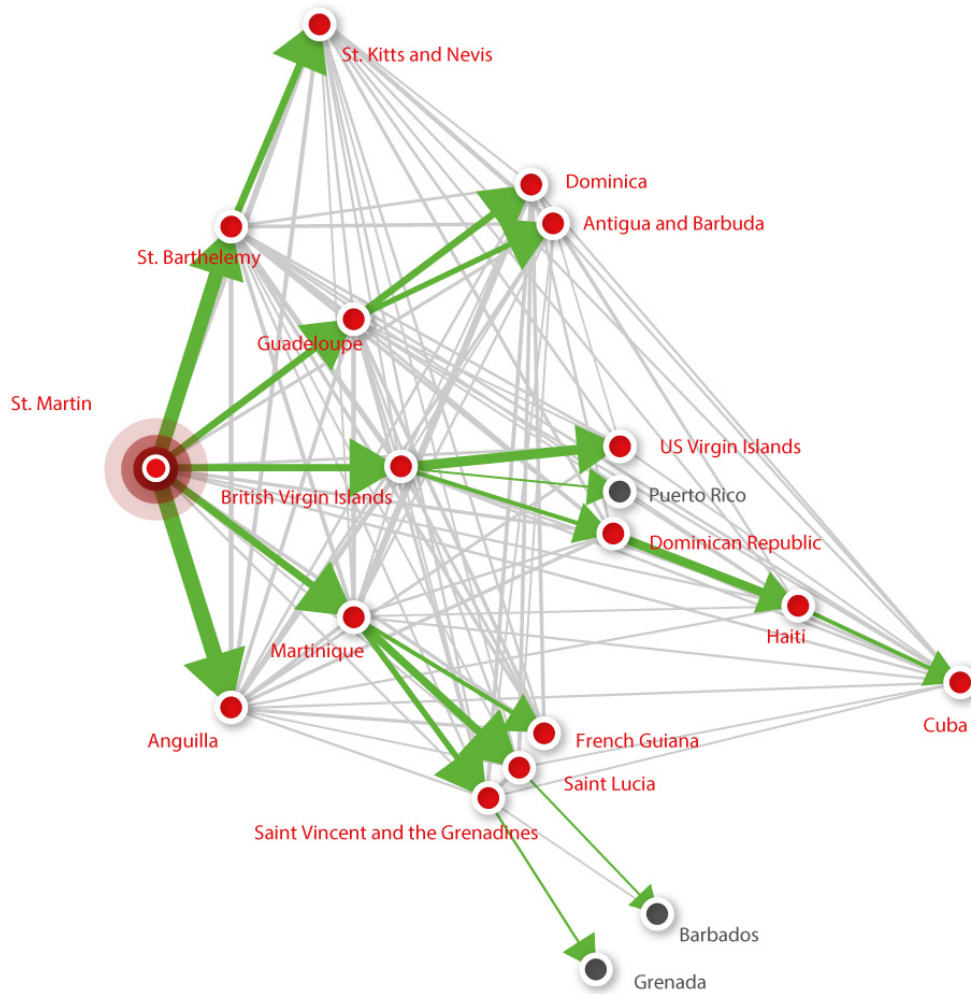
Fadeout rate E_i of
pathogen in population i
when infection present

Ecology \longleftrightarrow Epidemiology

Grenfell et al. TREE 1997

Levins Bull Entomol Soc Am 1969

Chikungunya spread



$\lambda_{i \rightarrow j}$: risk of transmission from venue i to venue j

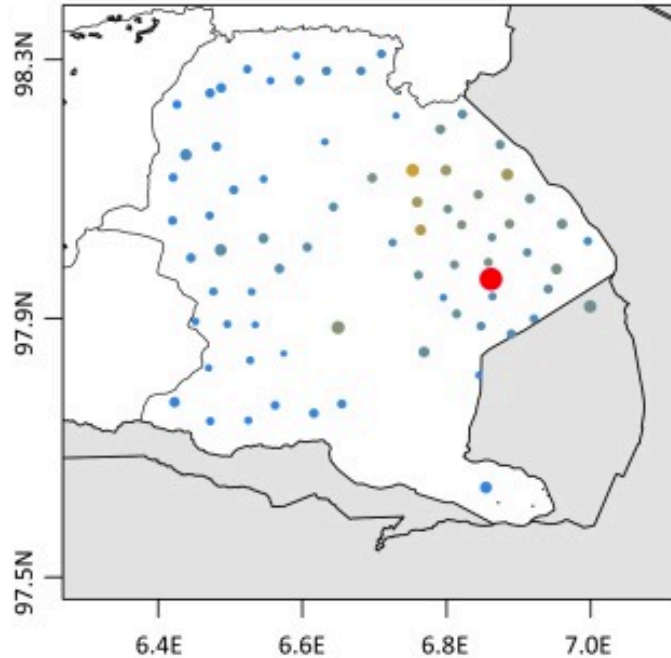
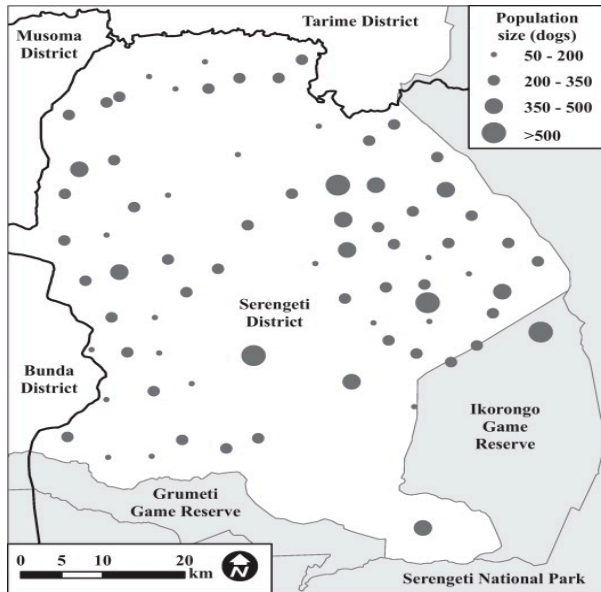
I_i $\left\{ \begin{array}{l} =0 \text{ if } i \text{ not invaded yet} \\ =1 \text{ if } i \text{ invaded} \end{array} \right.$

Force of invasion on location j

$$\Lambda_j(t) = \sum_{i | t_i < t} \lambda_{i \rightarrow j}$$

Assumed coupling model or selected through fitting

Rabies metapopulation dynamics



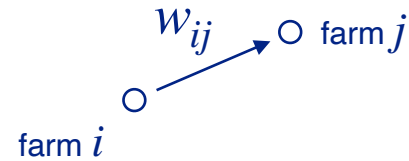
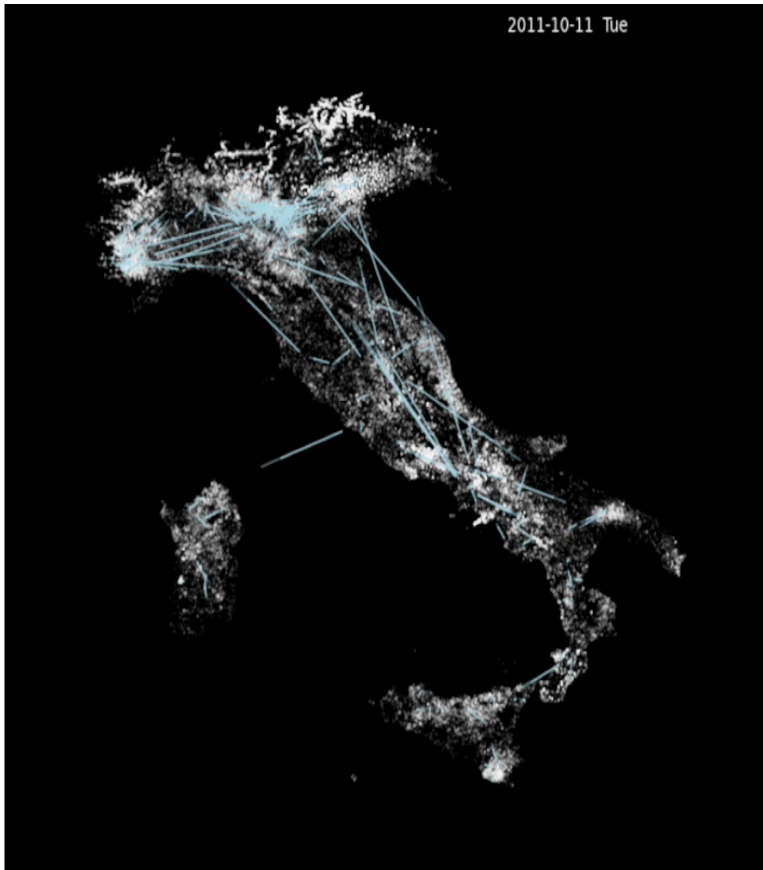
Infectious state of village i at time t

$$\mathbf{I}_{i,t} \sim \text{Bern}[1 - e^{-c_{i,t}}]$$

Hazard rate

$$c_{i,t} = \beta(1 - e^{-\delta S_{i,t-1}}) \sum_j^V [\mathbf{I}_{j,t-1} e^{-\kappa d_{i,j}} (1 - e^{-\psi S_{j,t-1}})]$$

Livestock disease spread

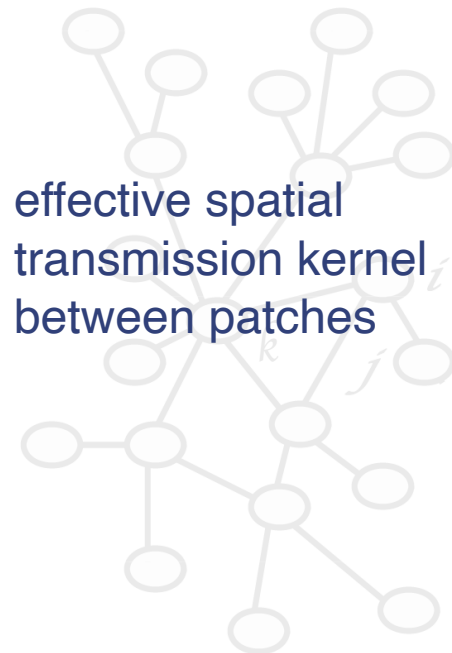


Force of transmission $i \rightarrow j$

$$\Lambda_{ij}(t) = 1 - (1 - \lambda)^{w_{ij}}$$

- λ : transmission rate per bovine

#2: Kernel transmission



Force of infection for **S** in *i*

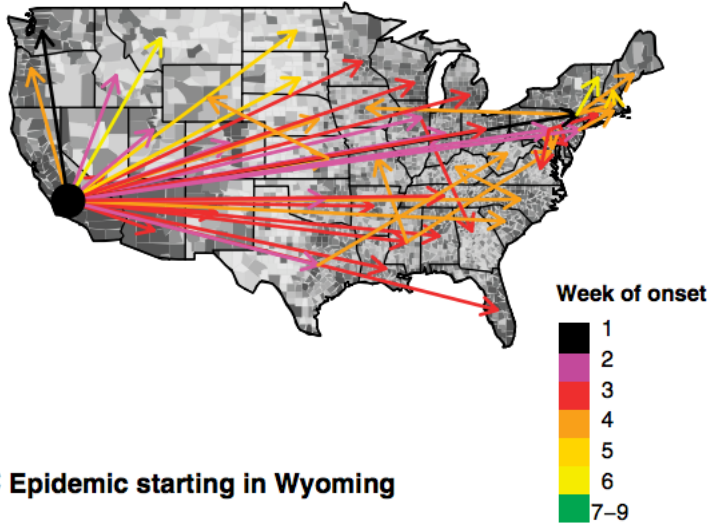
$$\lambda_i = \beta \sum_j f(\mathbf{M}) I_j$$

potential interaction of
S from *i* with **I** from *j*

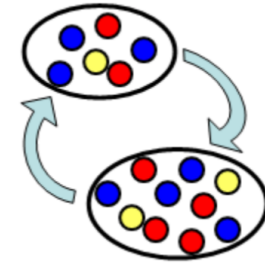
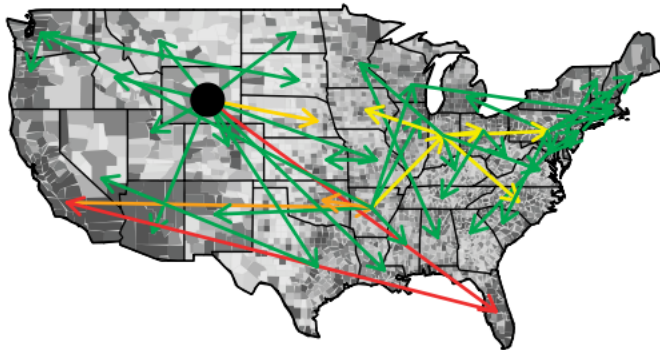
Grenfell et al. Nature 2001 → measles
Hall et al. Epidemiol Infect 2007 → smallpox
Viboud et al. Science 2006 → flu
Keeling et al. PNAS 2010

Synchrony and waves of flu spread

B Epidemic starting in California



C Epidemic starting in Wyoming



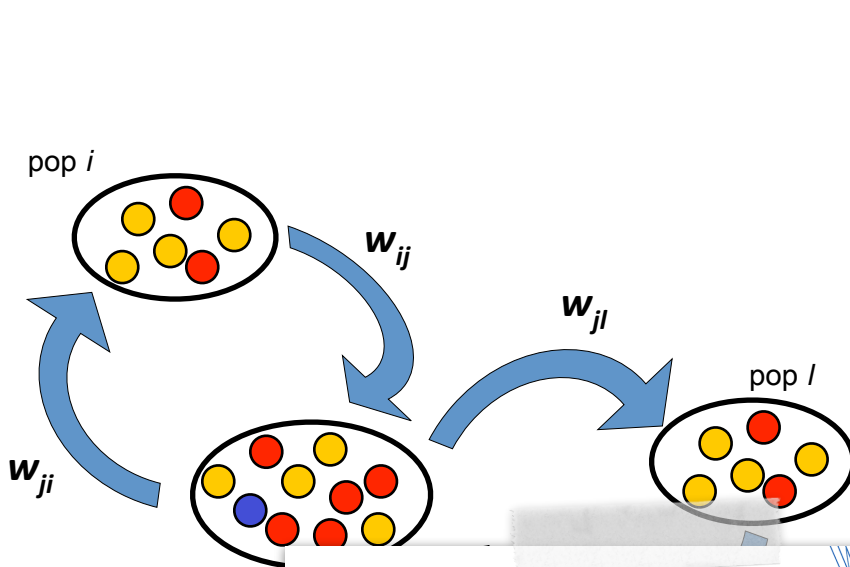
Gravity law

$$C_{ij} = \theta \frac{P_i^{\tau_1} P_j^{\tau_2}}{d_{ij}^{\rho}}$$

Force of infection for **S** in *i*

$$\lambda_i = \beta \left(I_i + \sum_j \gamma C_{ji} I_j \right)$$

#3: Explicit coupling



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

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

SPATIAL AND METAPOPULATION MODELING

LAB #3.
Modeling spatial transmission

Flow balance for compartment X

$$\dot{X}_i = \sum_j (d_{ji} X_j - d_{ij} X_i)$$

mobility rate on a link $j-i$

Data-driven coupling

w_{ij} #passengers from data

$d_{ij} = \frac{w_{ij}}{N_i}$ mobility rate on a link $i-j$

$p_i = \frac{\sum_j w_{ij}}{N_i}$ mobility rate out of i

Markovian diffusion

empirically

$$w_{ij} = w_{ji}$$

Barrat et al. PNAS 2004

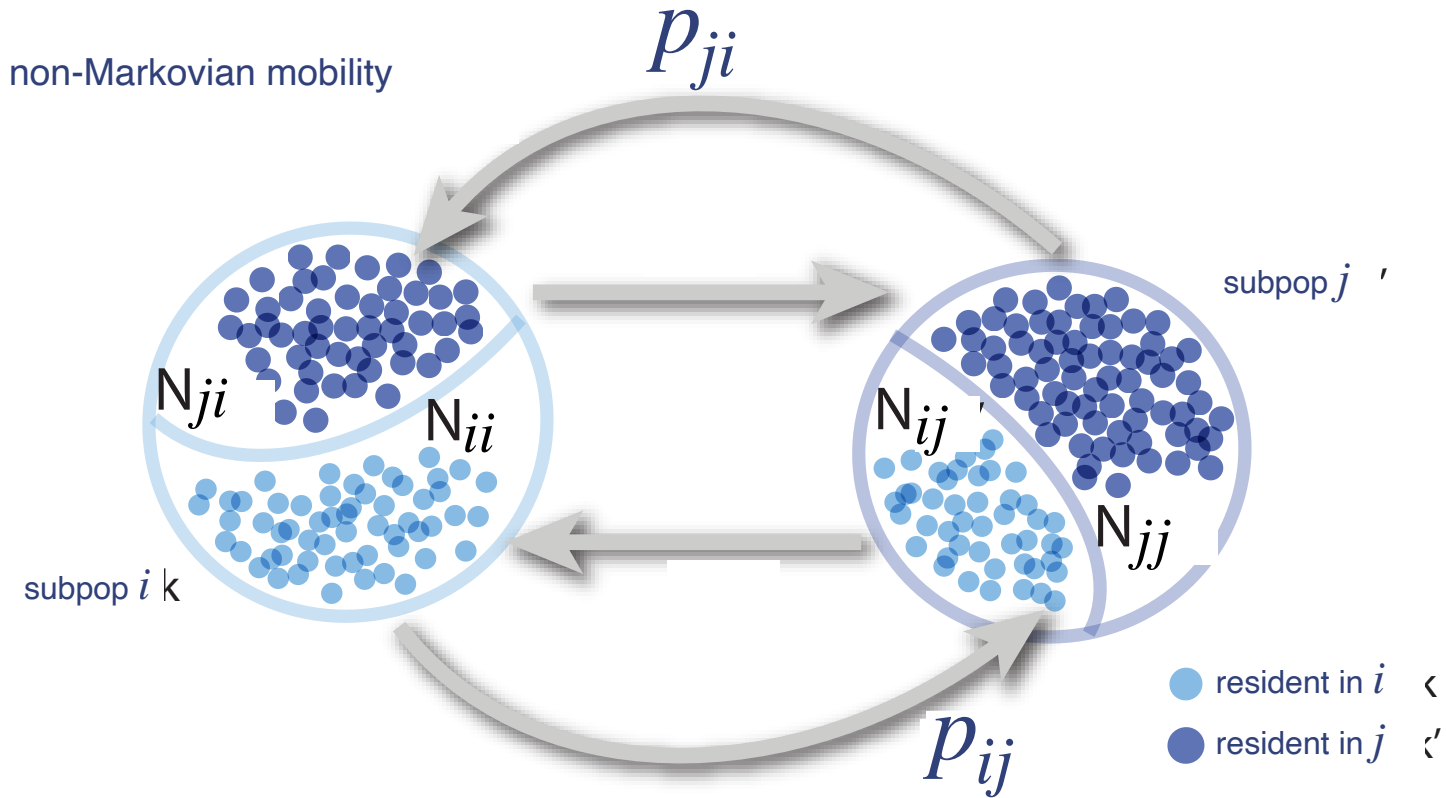
at equilibrium

$$N_i = \text{const}$$

non-Markovian diffusion

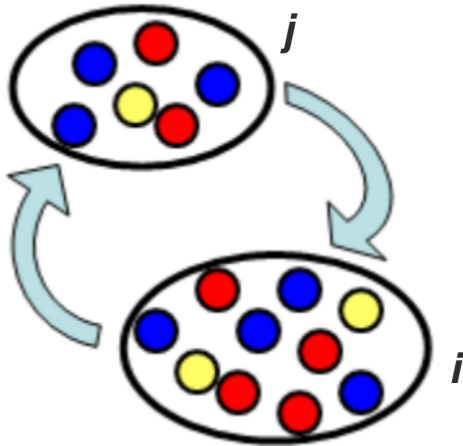
$$N_i = \text{const}$$

#4: Effective coupling



Effective force of infection

non-Markovian mobility



Force of infection for susceptibles in i

$$\lambda_i = \lambda_{ii} + \sum_j \lambda_{ji}^v + \sum_j \lambda_{ij}^r$$

LOCAL
INFECTION
(ρ_{ii})

INFECTION
BROUGHT BY
VISITORS
(ρ_{ji})

INFECTION
BROUGHT BY
RETURNING
RESIDENTS
(ρ_{ij})

Effective force of infection

$$\lambda_i = \lambda_{ii} + \sum_{j \neq i} \lambda_{ji}^v + \sum_{j \neq i} \lambda_{ij}^r$$

LOCAL
INFECTION
(p_{ii})

$$\lambda_{ii} = \beta p_{ii}^2 \frac{I_i}{\hat{N}_i}$$

INFECTION
BROUGHT BY
VISITORS
(p_{ji})

$$\lambda_{ji}^v = \beta p_{ii} p_{ji} \frac{I_j}{\hat{N}_i}$$

$$\hat{N}_i = p_{ii} N_i + \sum_j p_{ji} N_j$$

INFECTION
BROUGHT BY
RETURNING
RESIDENTS
(p_{ij})

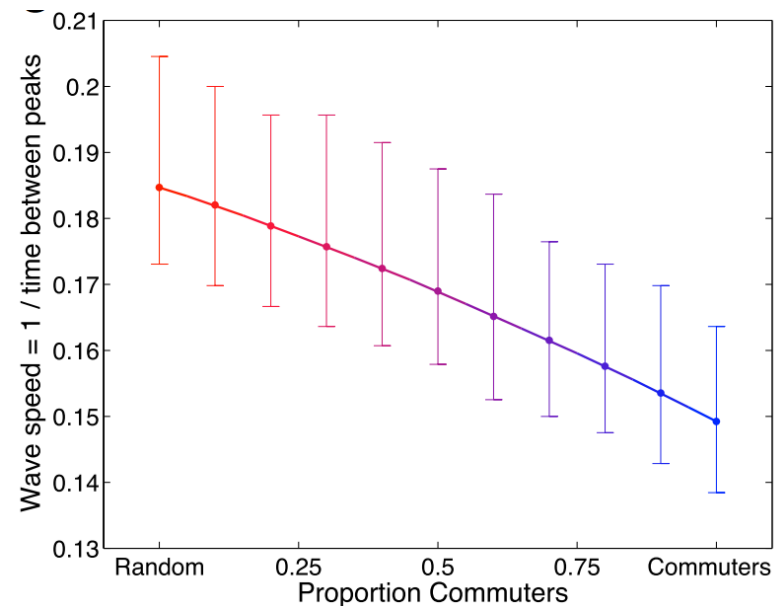
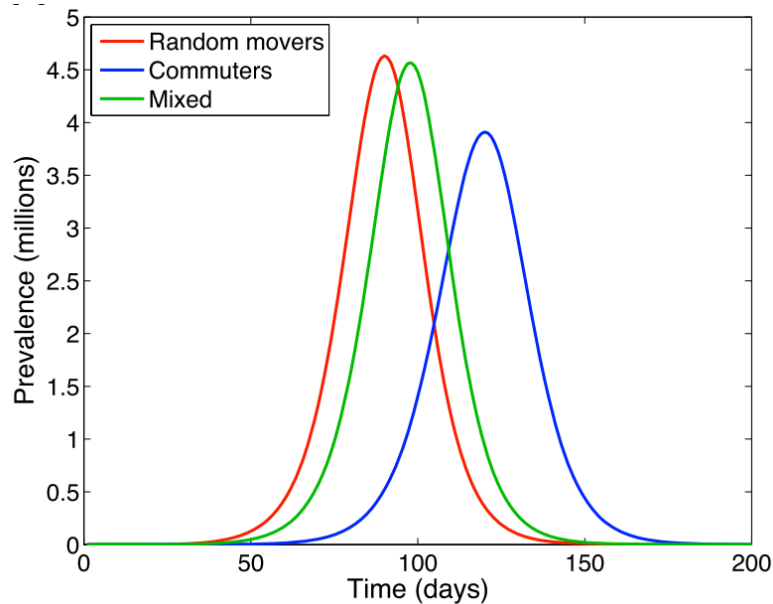
$$\lambda_{ij}^r = \beta p_{ij} \frac{\hat{I}_j}{\hat{N}_j}$$

Markovian vs. individual mobility

Identity of each host and associated movements

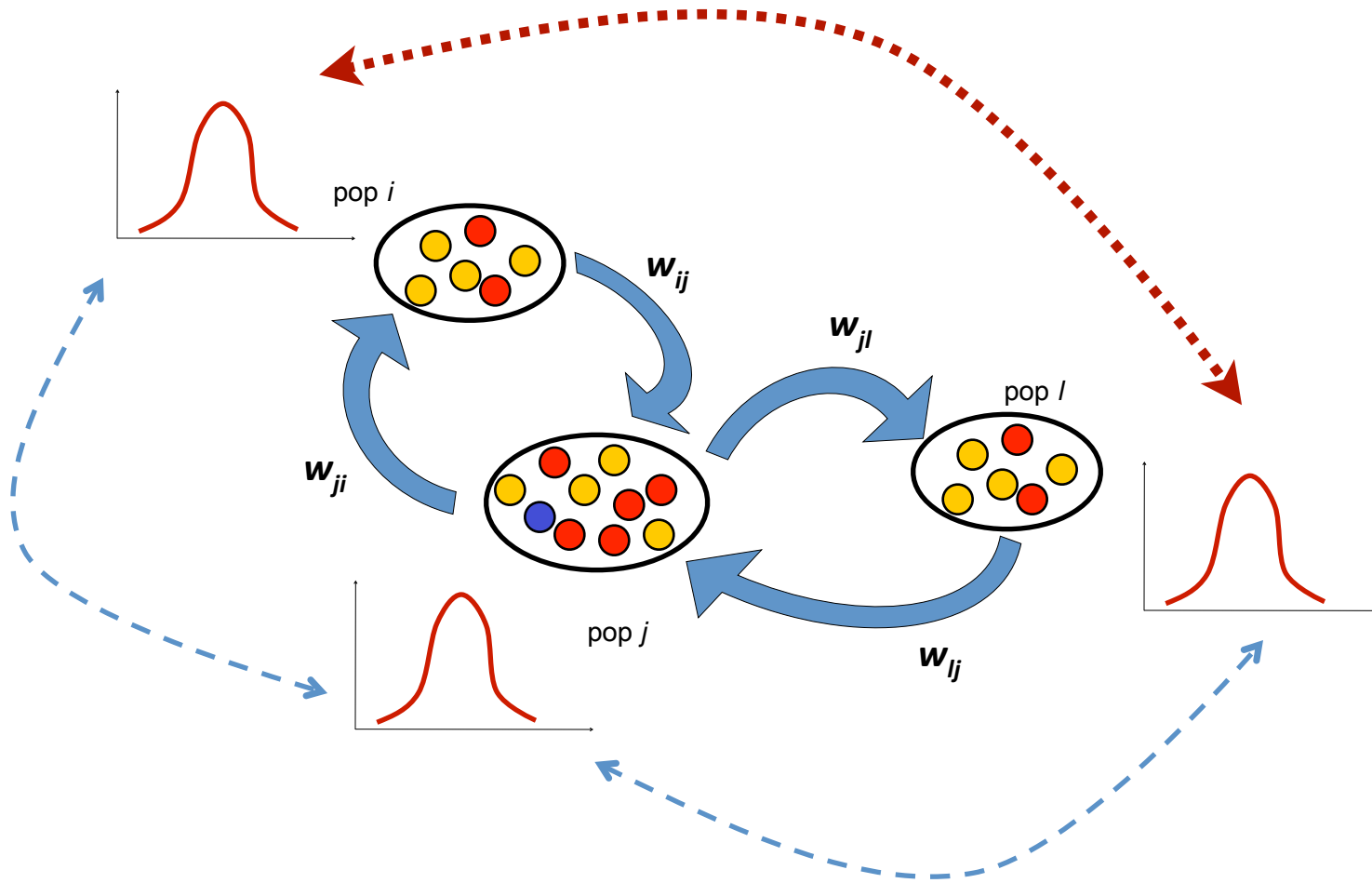
- » commuters in the UK
- » cattle trade movement in the UK

- 'random' = Markovian
- 'commuters' = non-Markovian, individual level

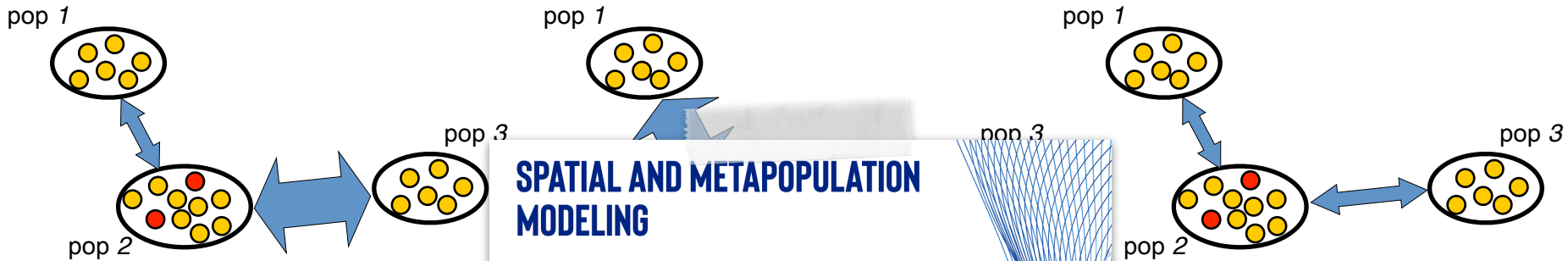


Coupled epidemics

Coupled epidemics

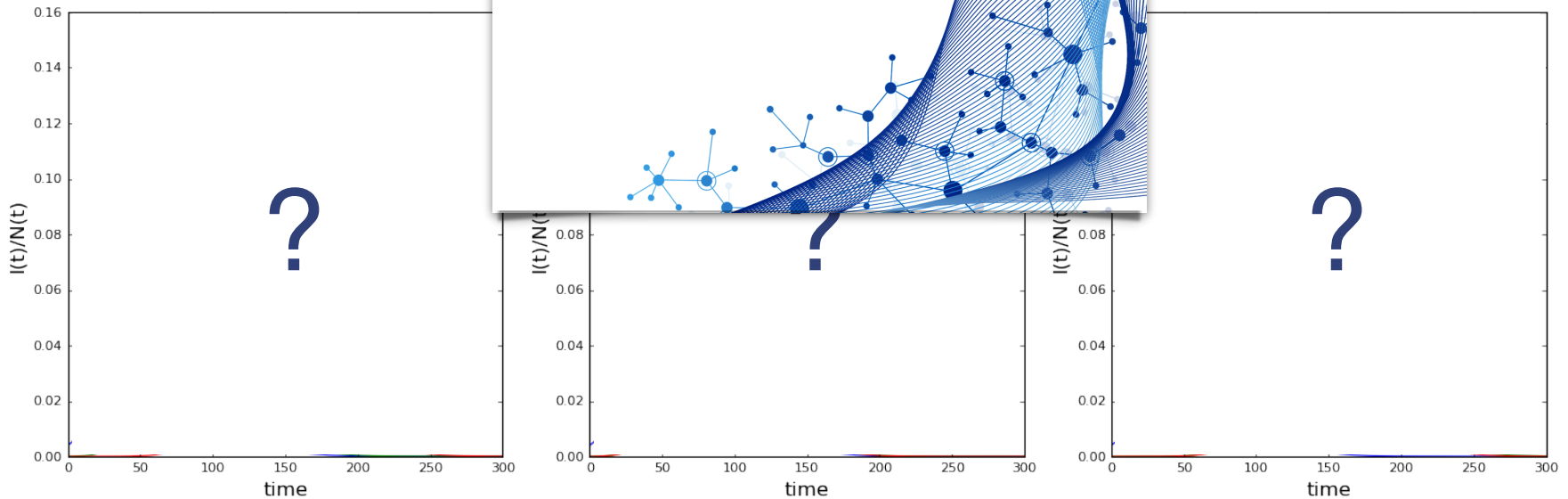


Coupled epidemics



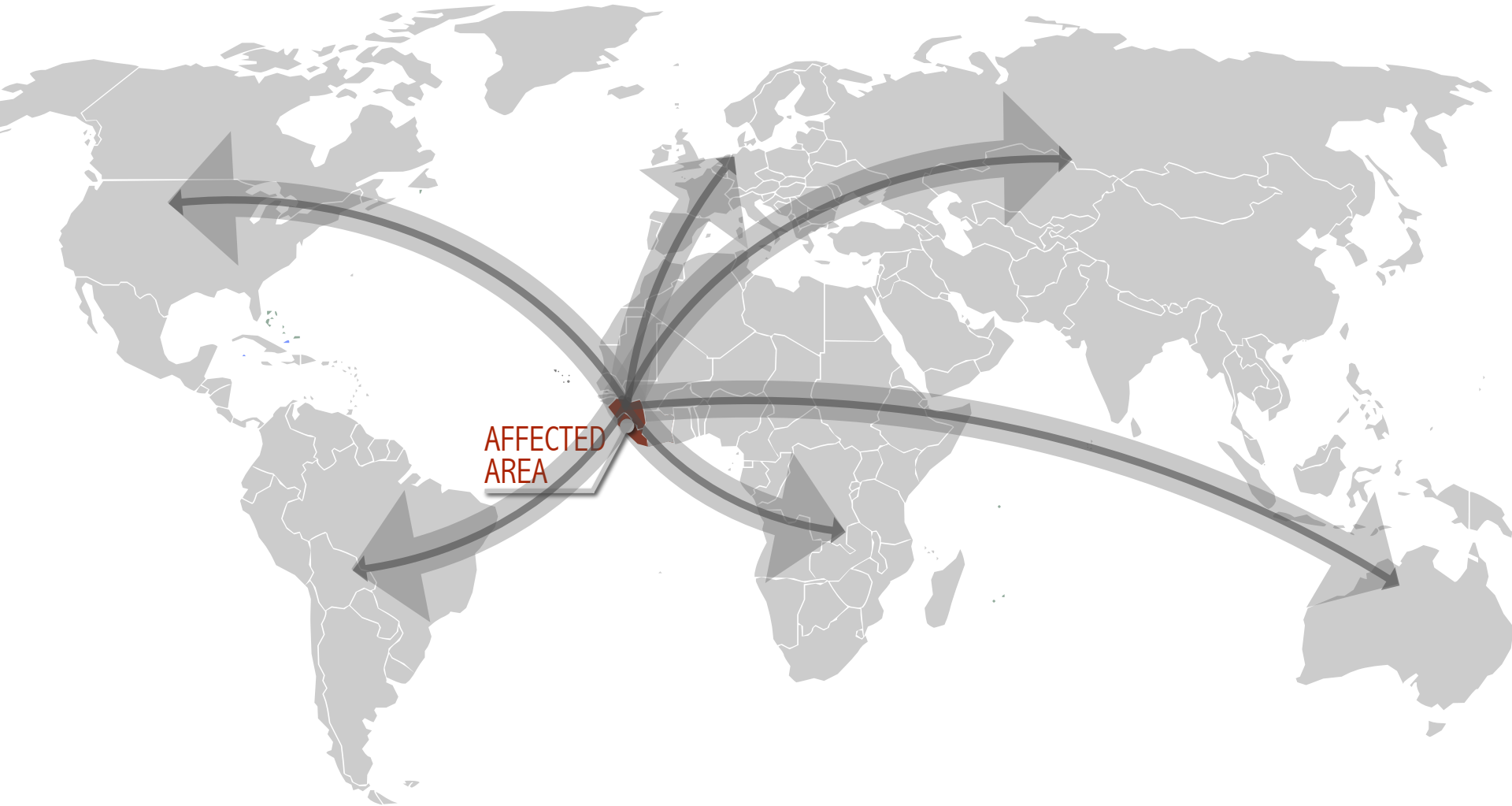
SPATIAL AND METAPOPULATION MODELING

LAB #4.
Impact of connectivity on disease outcomes

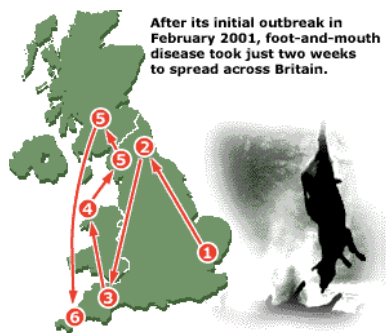


Travel restrictions for containment

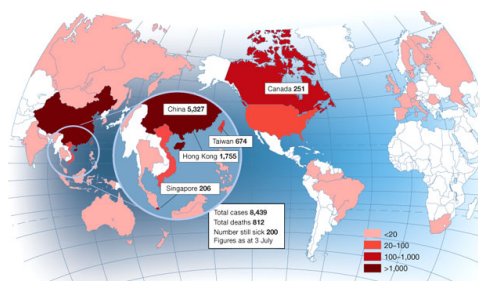
Travel restrictions for containment



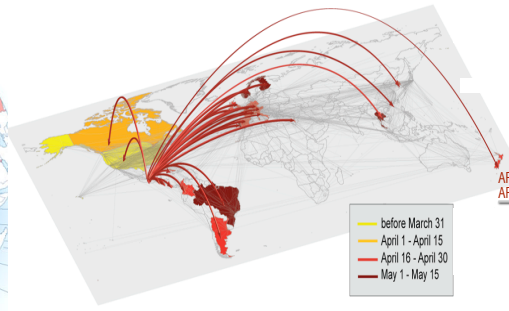
Pre-COVID observed travel reductions



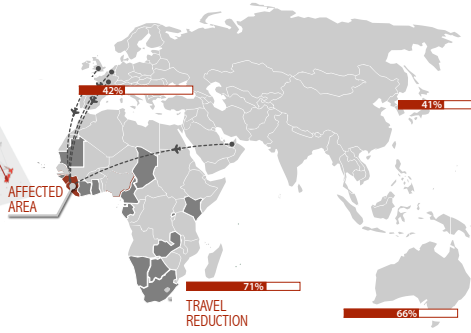
2001: FMD



2002-2003: SARS



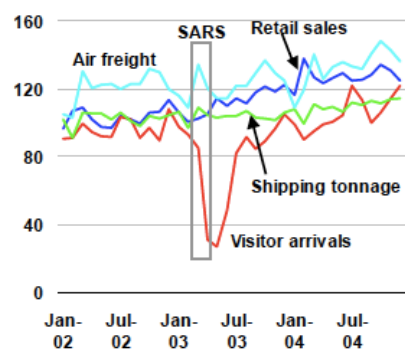
2009: H1N1 pdm



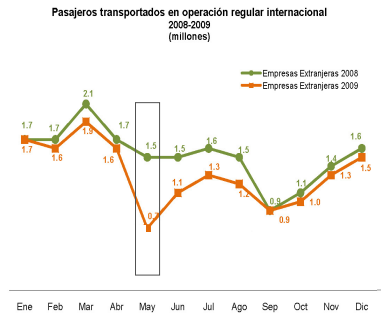
2014: WA Ebola

Losses to tourism:
est. \$44billion

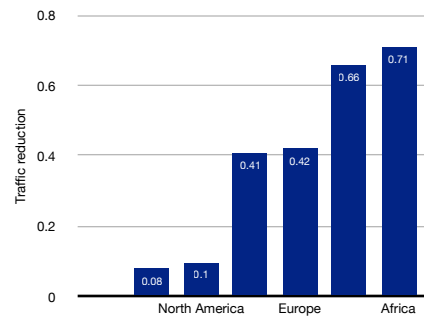
UK



Singapore

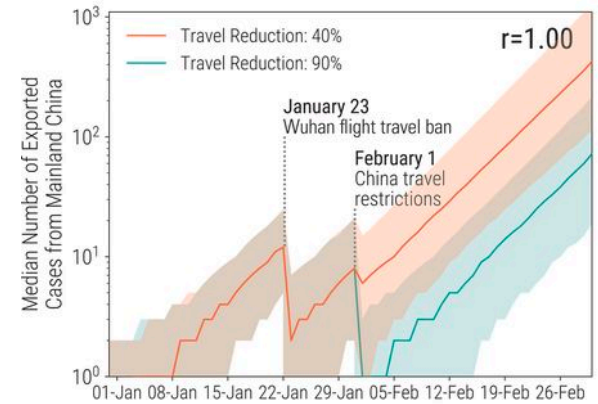
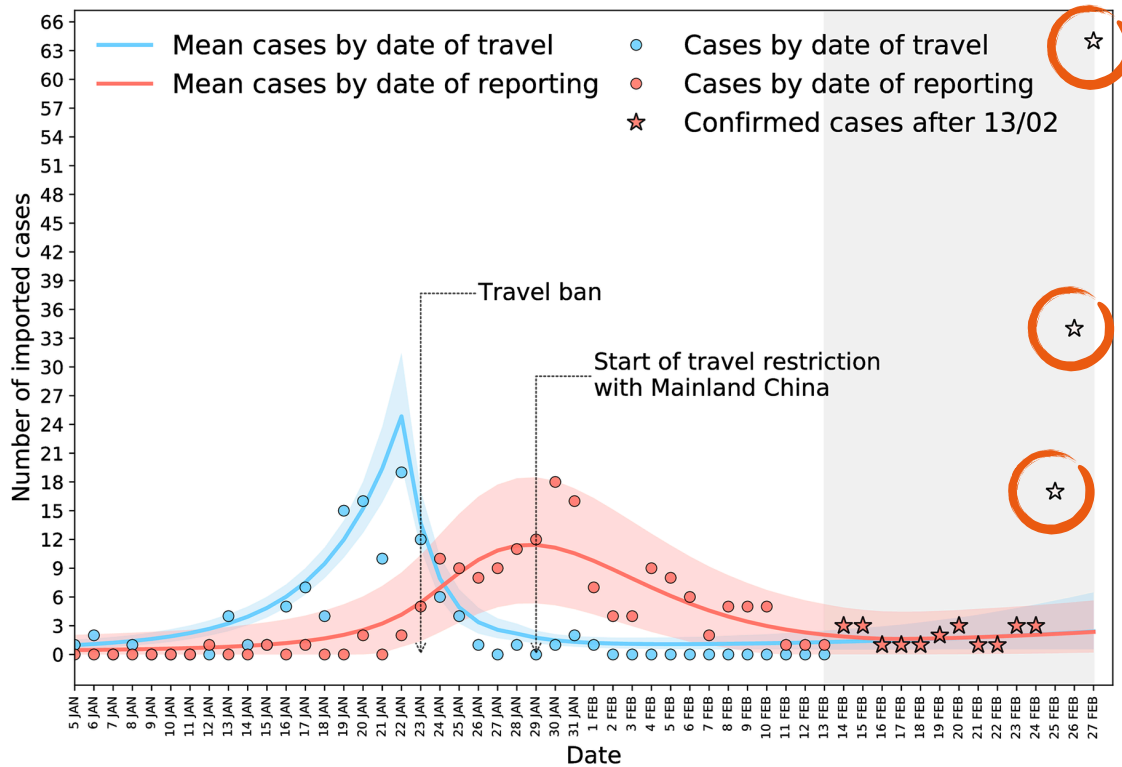


Mexico

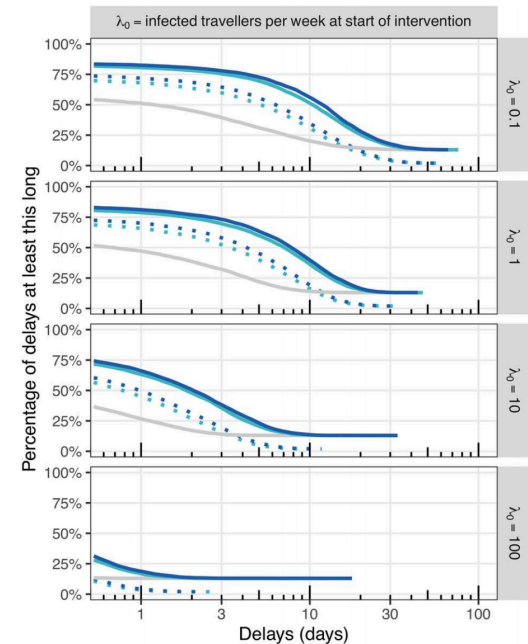


World

COVID-19 travel restrictions

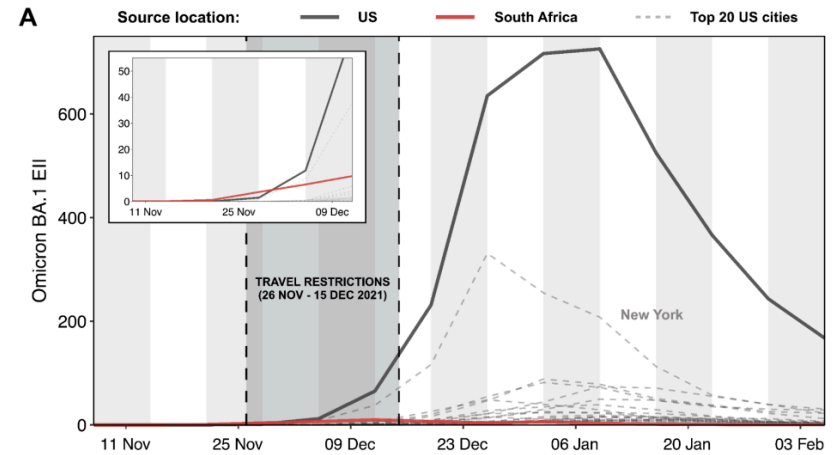
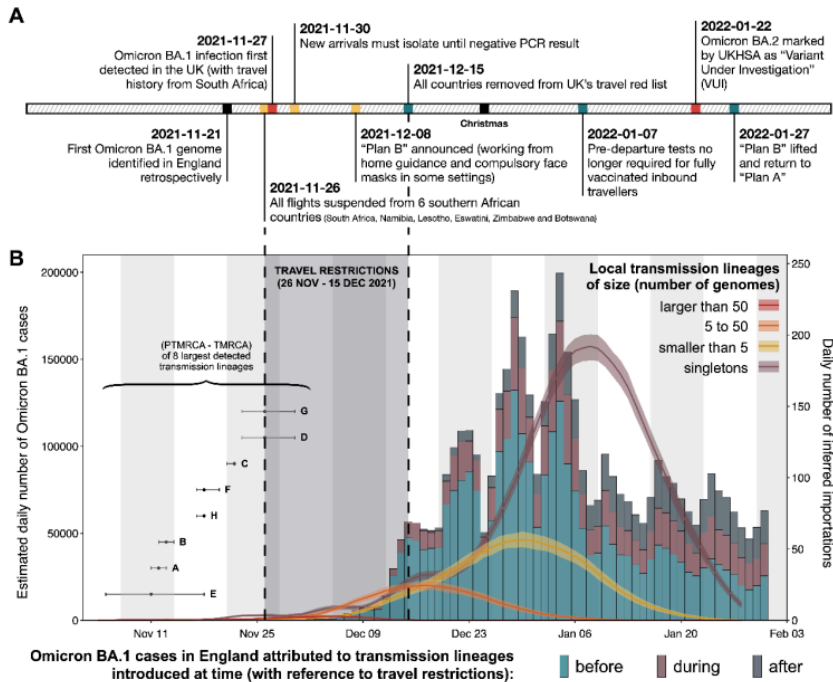


Chinazzi et al Science 2020



Clifford et al J Travel Med 2020

BA.1 importation and travel restrictions



Numerical findings

Pandemic flu PREPAREDNESS

Will travel restrictions control the international spread of pandemic influenza?

T Déirdre Hollingsworth, Neil M Ferguson & Roy M Anderson

OPEN ACCESS Freely available online

PLOS MEDICINE

Delaying the International Spread of Pandemic Influenza

Ben S. Cooper, Richard J. Pitman, W. John Edmunds, Nigel J. Gay

Statistics, Modelling, and Bioinformatics Department, Centre for Infections, Health Protection Agency, London, United Kingdom

Funding: This work was funded by the Health Protection Agency and, in part, by the EU SARSCONTROL project. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

ABSTRACT

Background

The recent emergence of hypervirulent subtypes of avian influenza has underlined the potentially devastating effects of pandemic influenza. Were such a virus to acquire the ability to spread efficiently between humans, control would almost certainly be hampered by limited

OPEN ACCESS Freely available online

PLOS MEDICINE

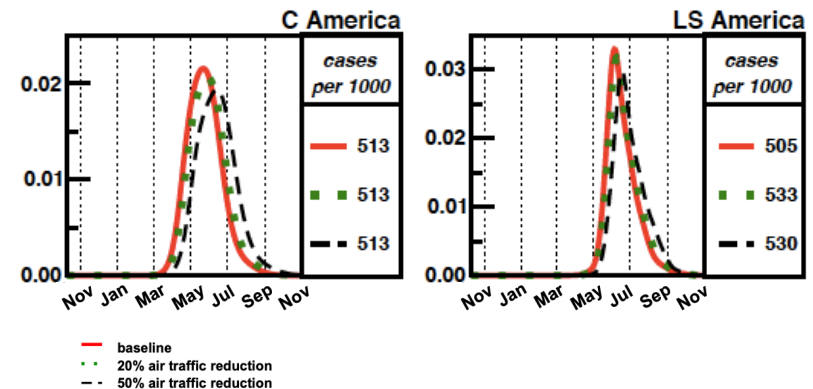
Modeling the Worldwide Spread of Pandemic Influenza: Baseline Case and Containment Interventions

Vittoria Colizza^{1,2}, Alain Barrat^{2,3}, Marc Barthelemy^{1,4}, Alain-Jacques Valleron^{5,6}, Alessandro Vespignani^{1,2*}

1 School of Informatics and Center for Biocomplexity, Indiana University, Bloomington, Indiana, United States of America, 2 Complex Networks Lagrange Laboratory, Institute for Scientific Interchange Foundation, Turin, Italy, 3 Unité Mixte de Recherche 8627, Centre National de la Recherche Scientifique, Université Paris-Sud, Orsay, France, 4 Commissariat à l'Energie Atomique, Direction Ile-de-France, Centre d'Etudes de Bruyères Le Châtel, Bruyères Le Châtel, France, 5 Unité de Recherche en Épidémiologie, Systèmes d'Information et Modélisation, Institut National de la Santé et de la Recherche Médicale, Unité Mixte de Recherche 707, Université Pierre et Marie Curie, Paris, France, 6 Hôpital Saint-Antoine, Assistance Publique-Hôpitaux de Paris, Paris, France

Funding: AB and AV are partially funded by the European

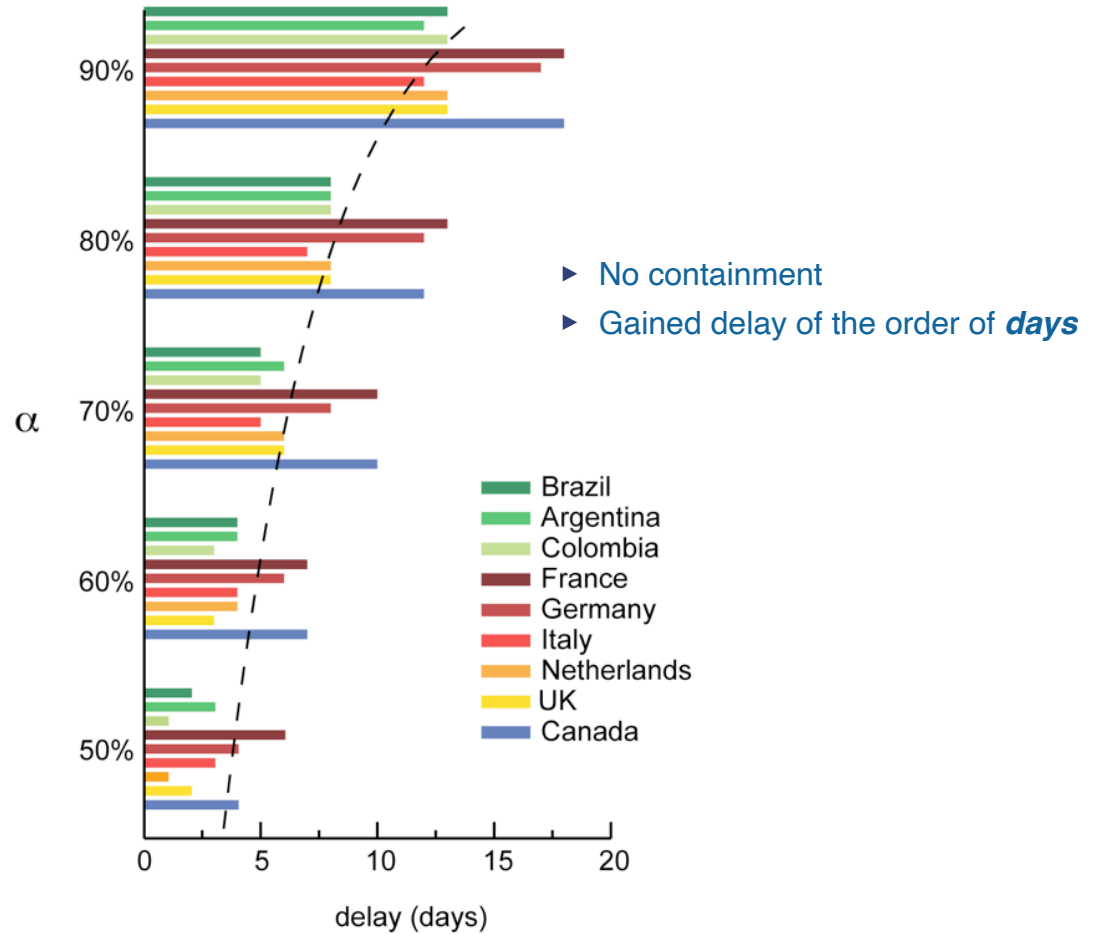
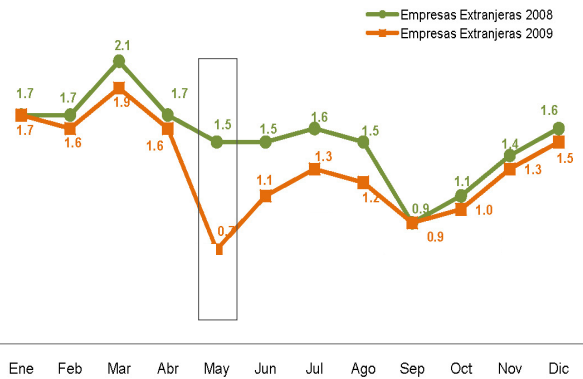
ABSTRACT



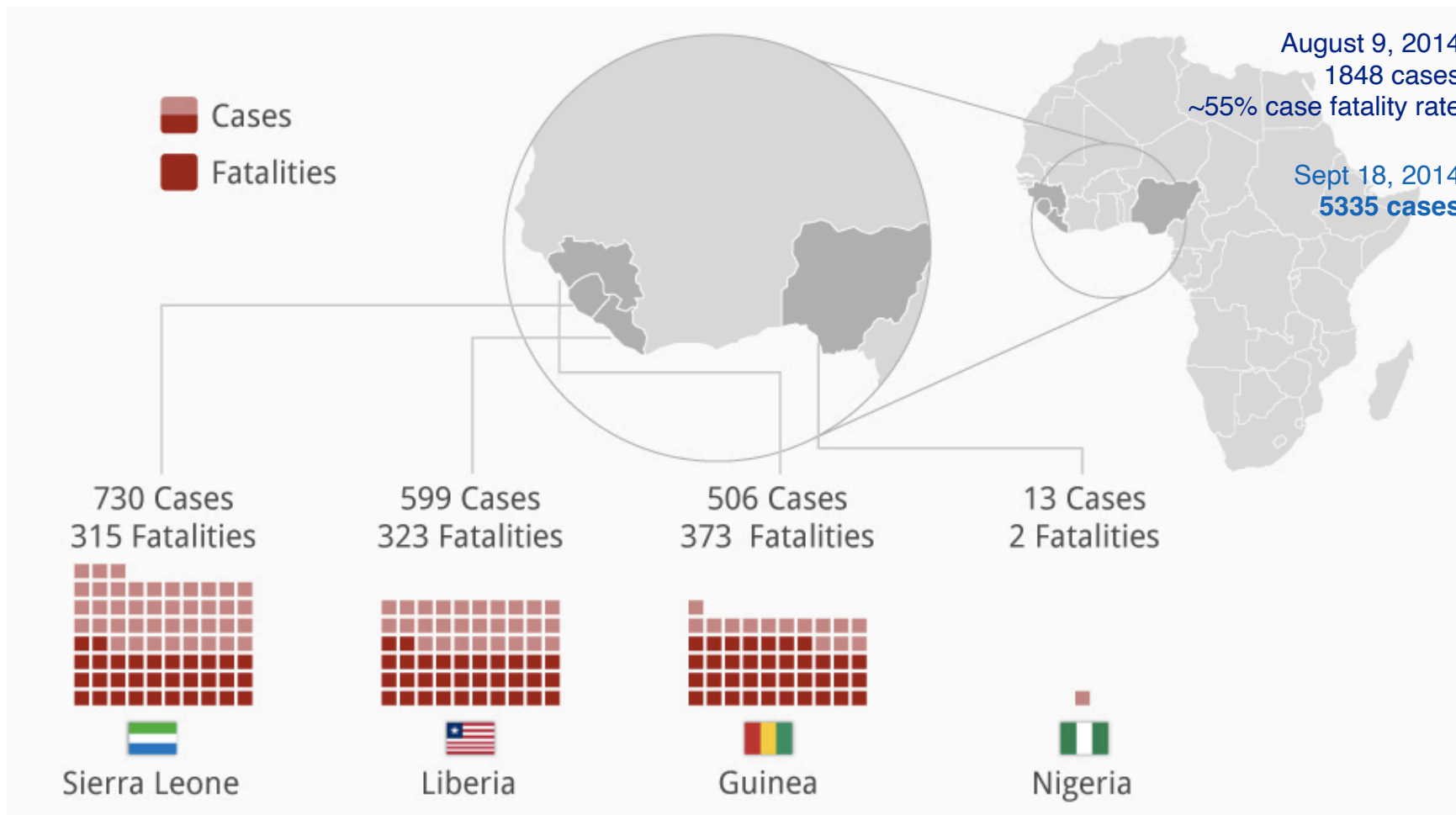
Travel restrictions as a non-medical intervention measure for a pandemic with $R_0 = 1.9$ starting in Hanoi in October

2009 H1N1 pandemic

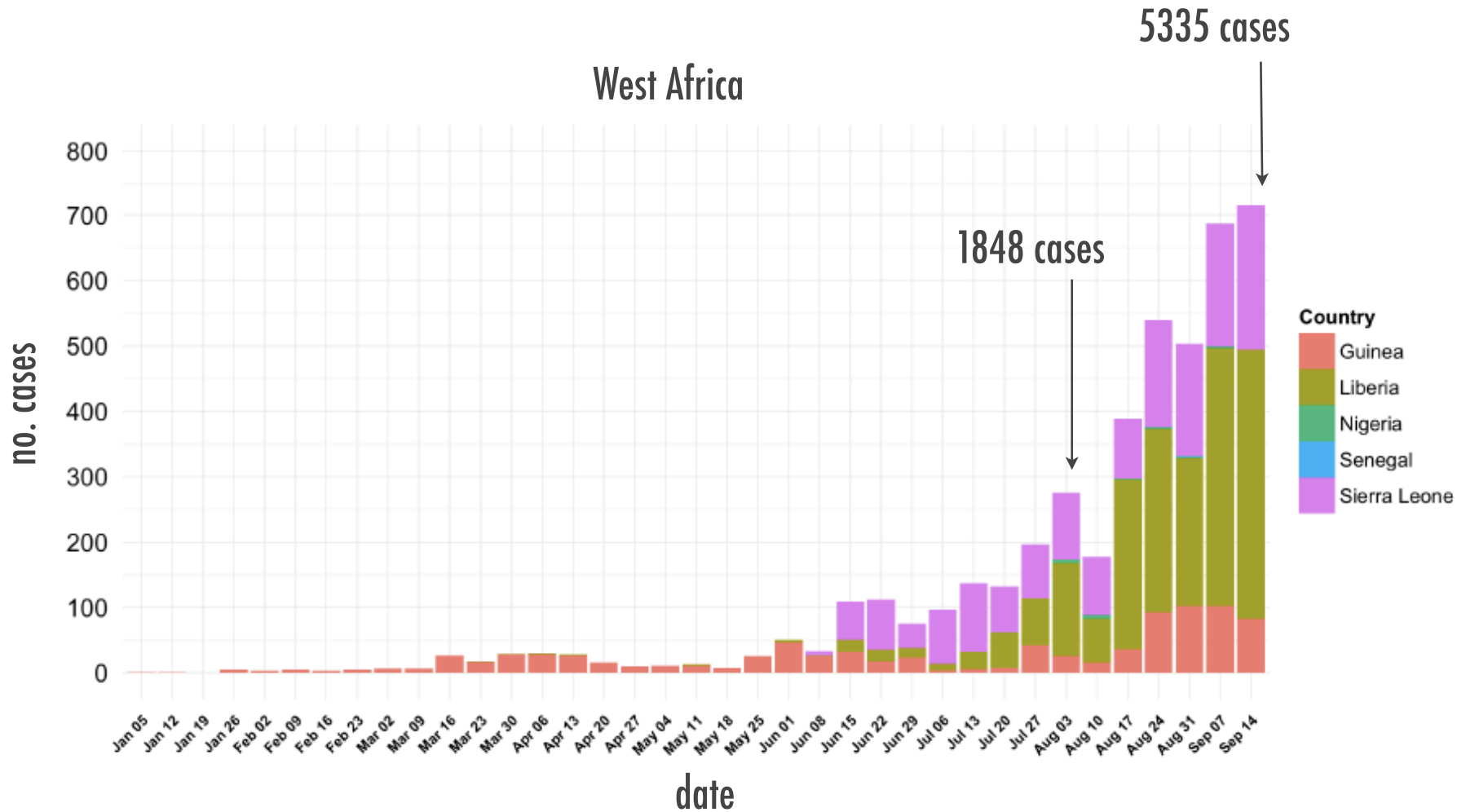
Pasajeros transportados en operación regular internacional
2008-2009
(millones)



2014 WA Ebola outbreak

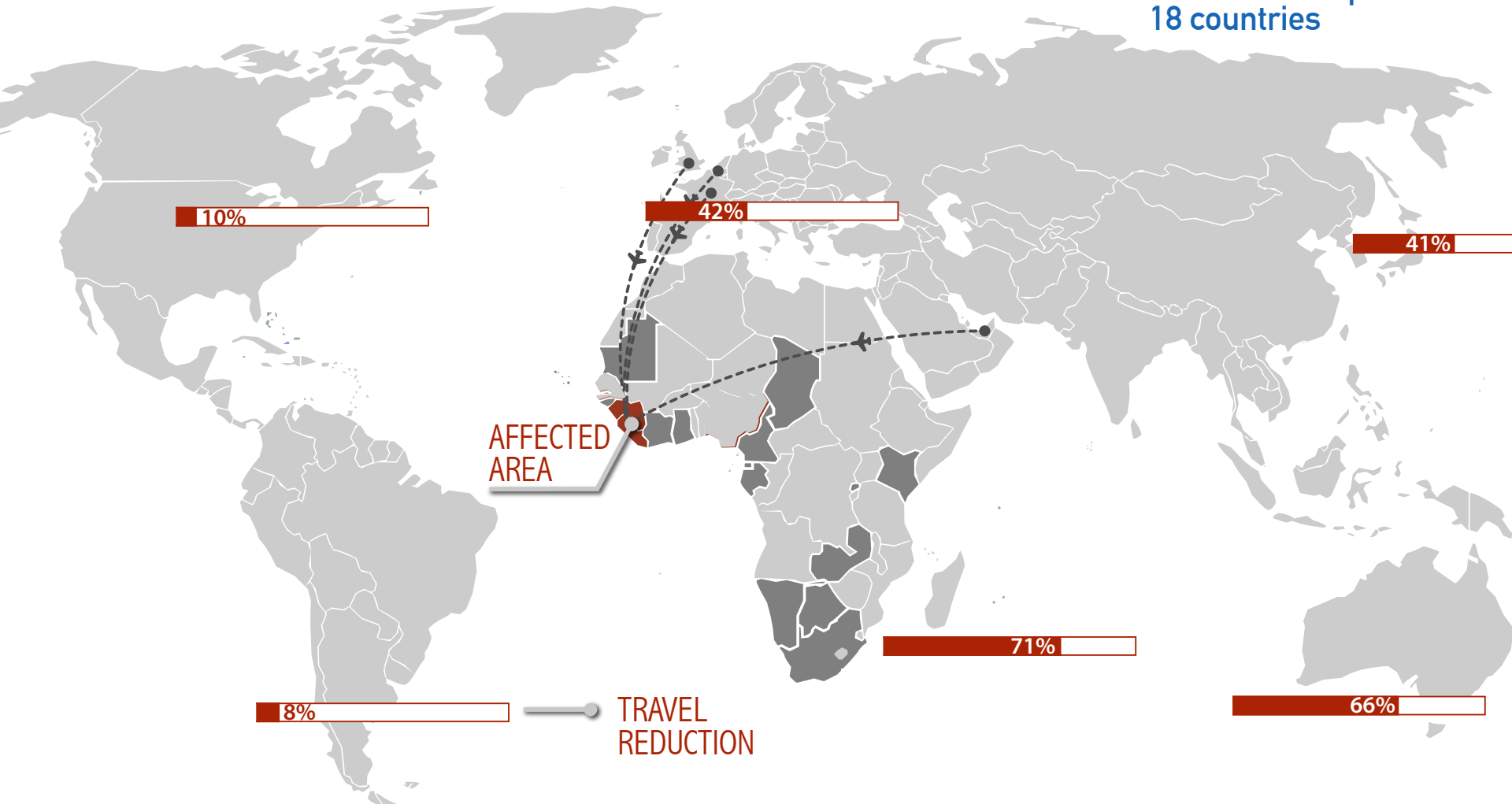


2014 WA Ebola outbreak

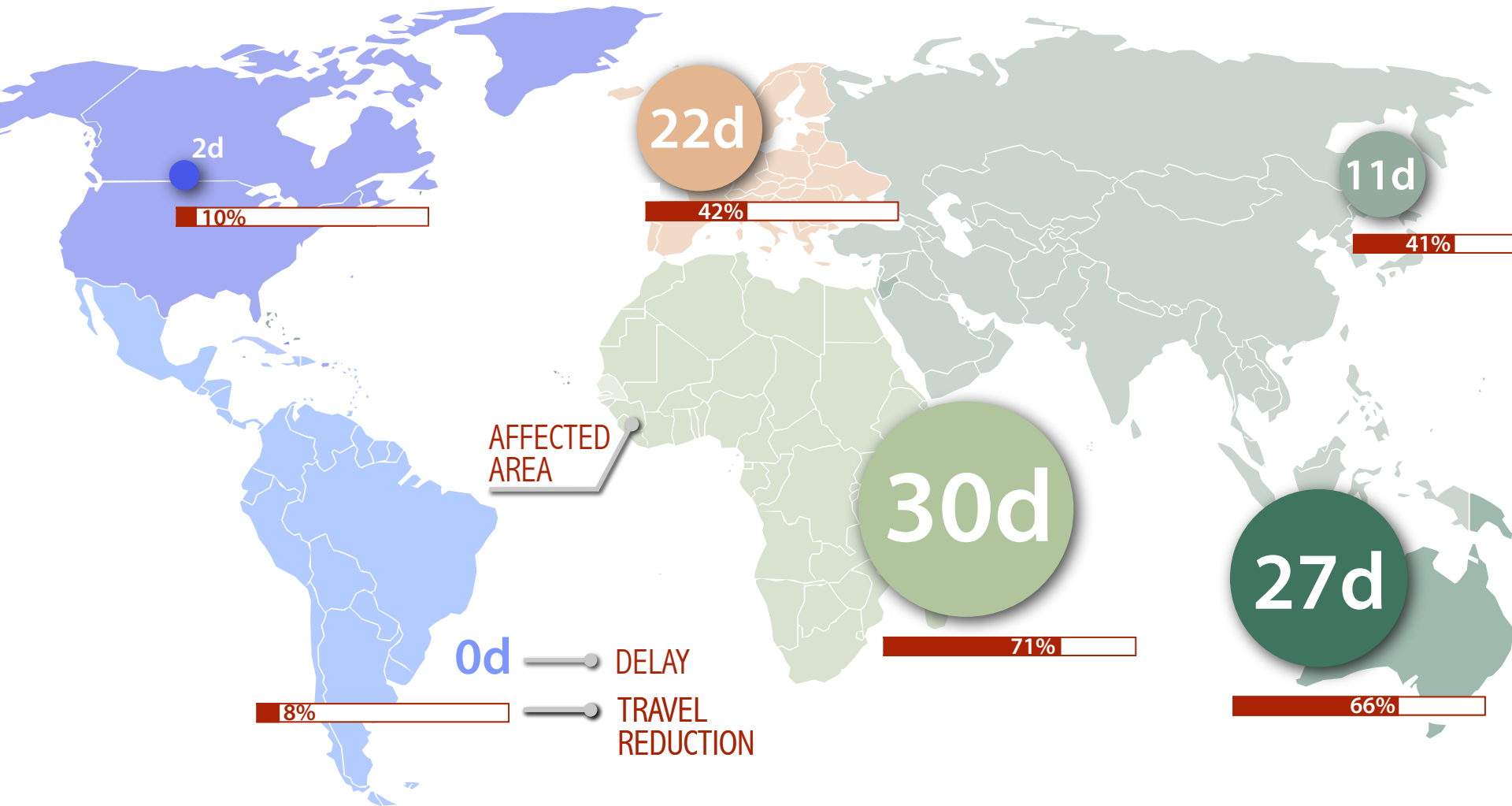


Reaction

11 airline companies
18 countries



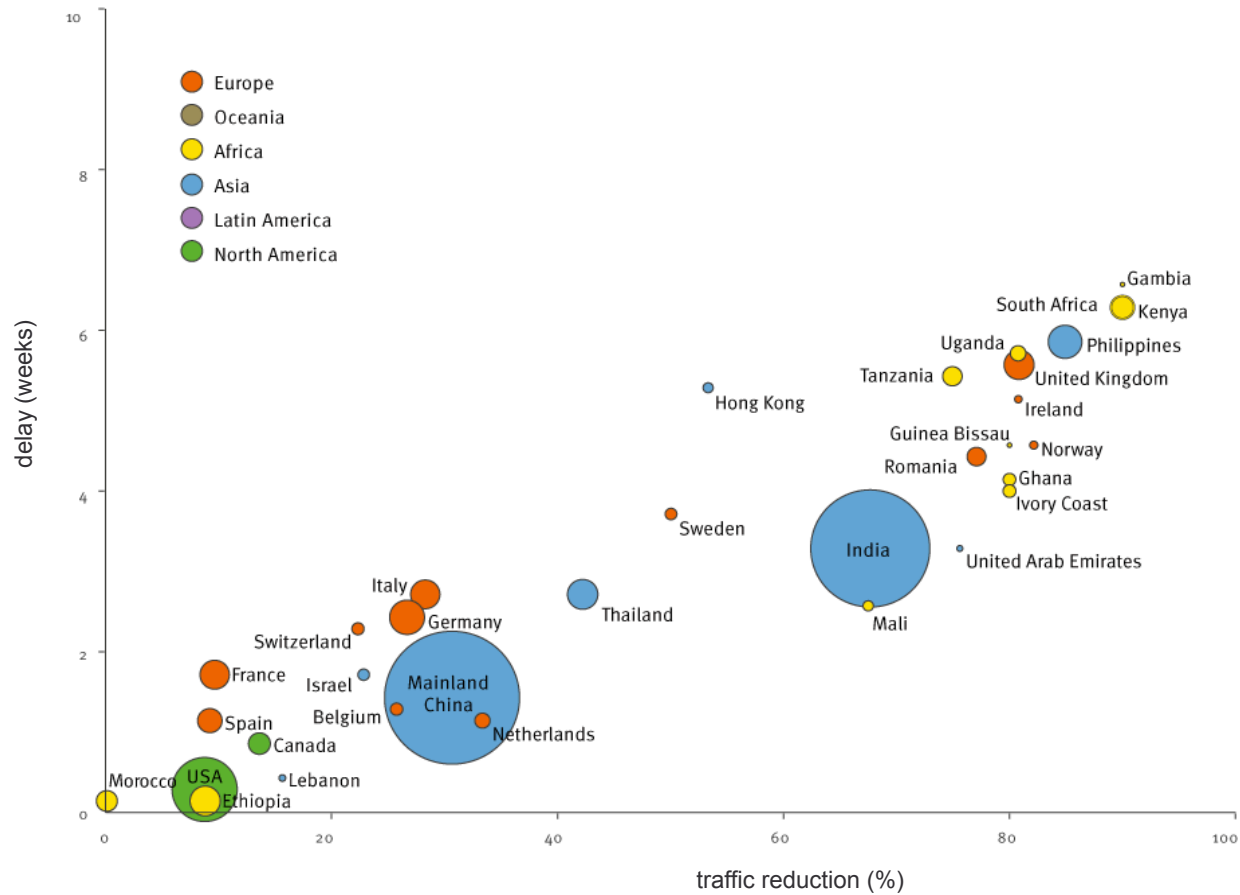
Model predictions



Model predictions

FIGURE 1

Modelled effect of travel restrictions on the risk of Ebola case importation for individual countries



Back to the maths...



Scalia-Tomba et al. Math Biosci 2008
Gautreau et al. JTB 2008

Back to the maths...

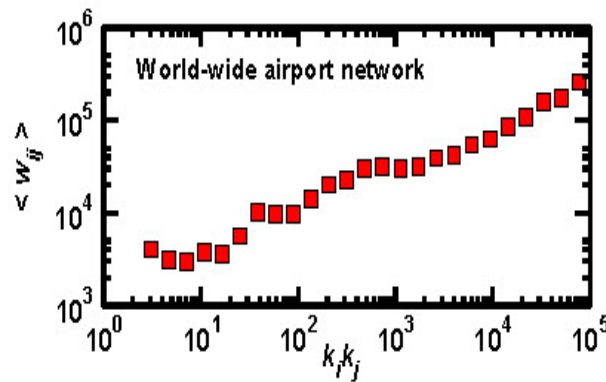
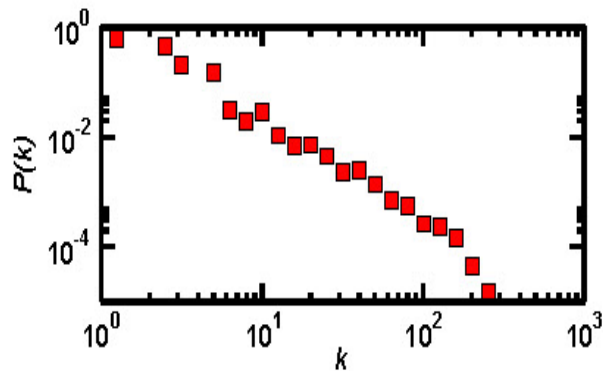
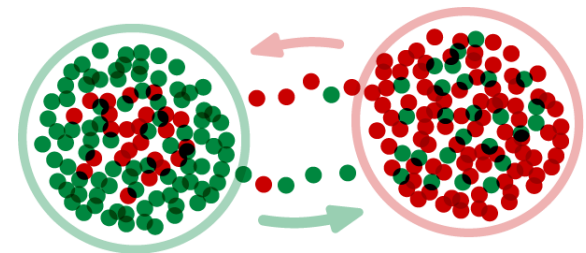
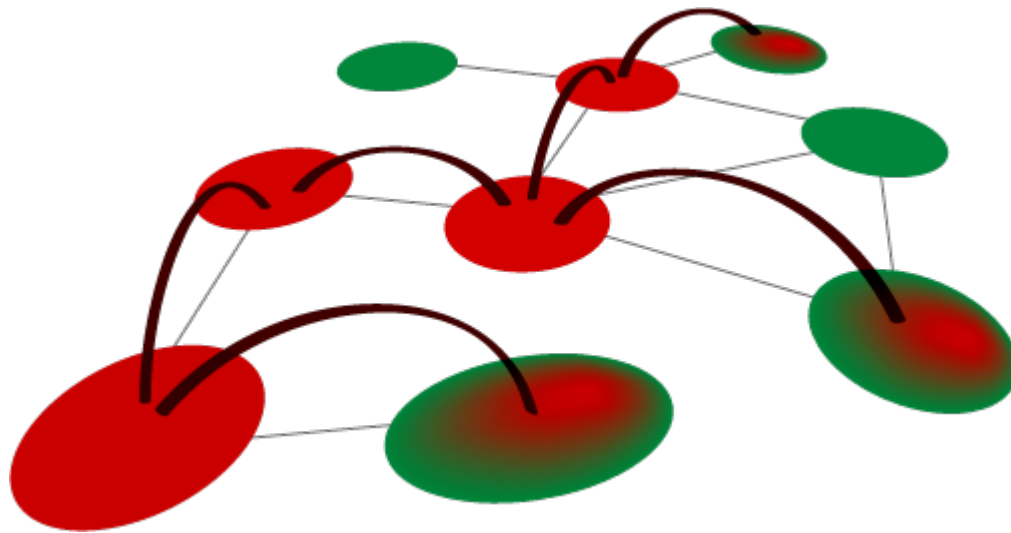


1



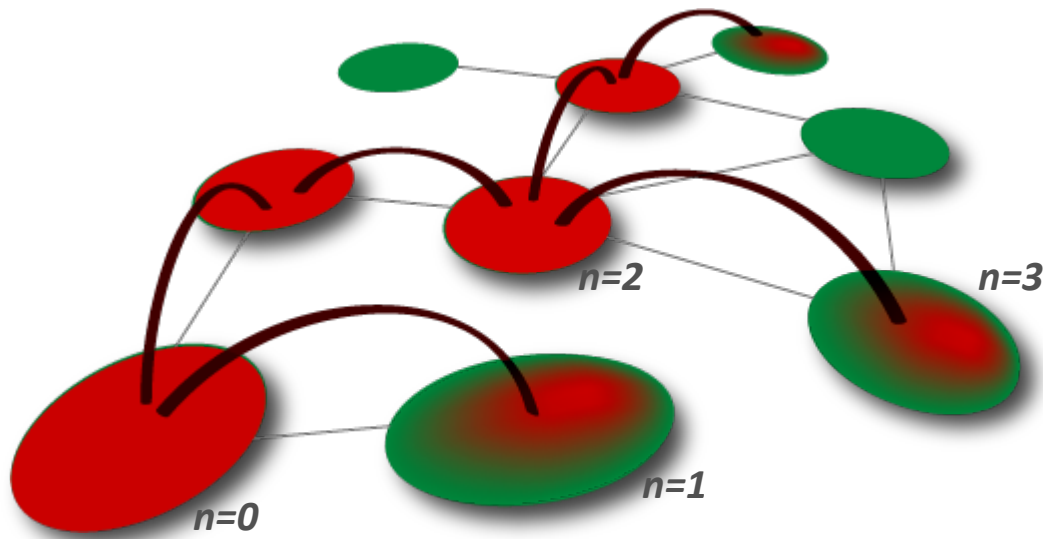
But is there a
threshold effect?

Metapopulation theory



$$P(k) \sim k^{-\gamma}$$
$$w_{ij} \sim (k_i k_j)^\theta$$

Metapopulation theory



branching process

$$D_k^0, D_k^1, \dots$$

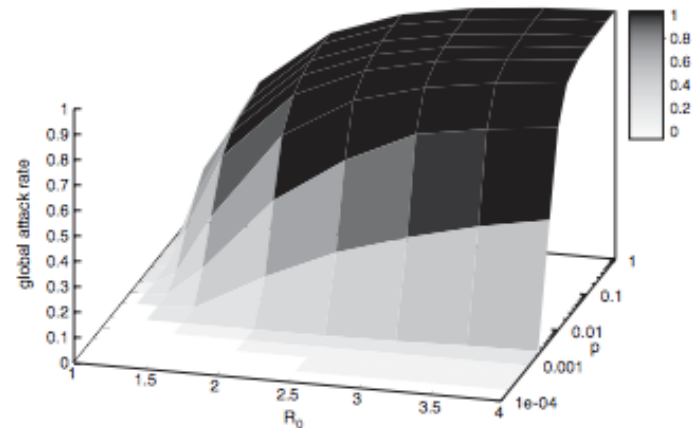
#**infected** patches of degree k at generation $n=0, 1, \dots$

$$P(k) \sim k^{-\gamma}$$

$$d_{kk'} \sim p(kk')^\theta$$

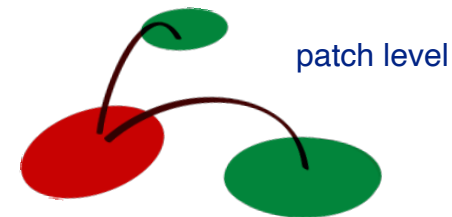
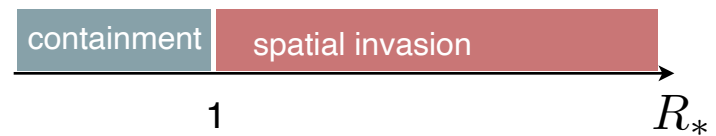
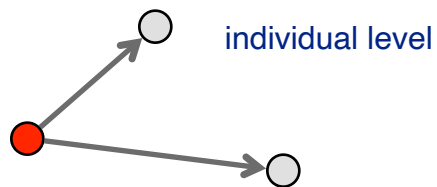
$$D_k^n = \sum_{k'} D_{k'}^{n-1} \overbrace{(k' - 1)}^{\text{possible paths of infection}} \underbrace{\left[1 - \left(\frac{1}{R_0} \right)^{\lambda_{k'k}} \right]}_{\text{from micro to macro}} \overbrace{P(k|k')}^{\text{connection } k'-k} \underbrace{\left(1 - \frac{D_k^{n-1}}{V_k} \right)}_{\text{probability of finding uninfected patch}}$$

Global invasion threshold



R_0

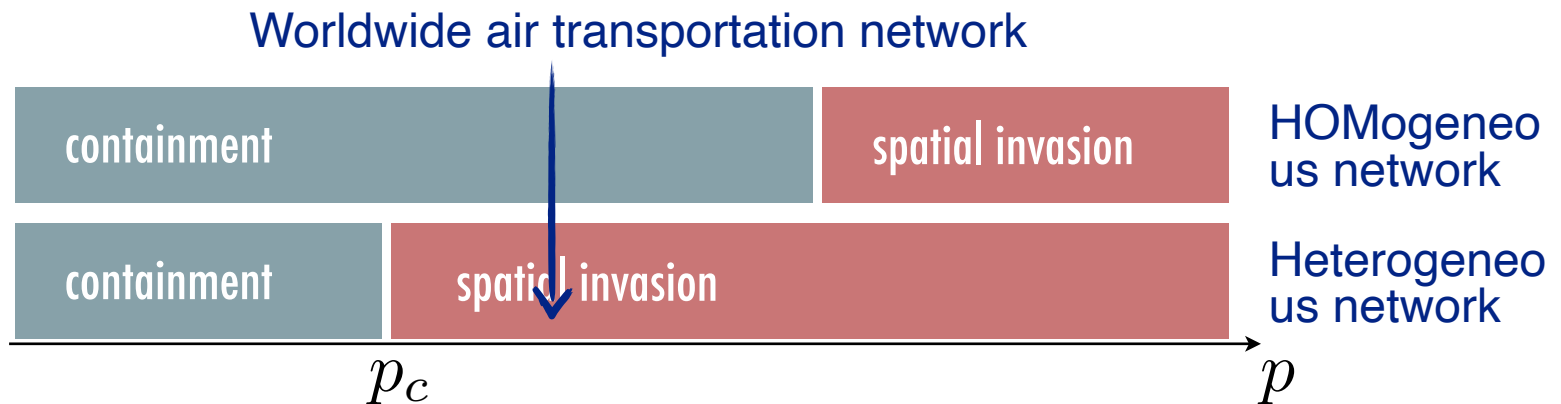
$$R_* = (R_0 - 1) \frac{\langle k^{2+2\theta} \rangle - \langle k^{1+2\theta} \rangle}{\langle k^{1+\theta} \rangle^2} \frac{p \bar{N} \alpha}{\mu} > 1$$



Mobility threshold

$$R_* = \underbrace{\frac{2(R_0 - 1)^2}{\mu R_0^2}}_{\text{disease}} \cdot \underbrace{\frac{\langle k^{2+2\theta} \rangle - \langle k^{1+2\theta} \rangle}{\langle k^{1+\theta} \rangle^2}}_{\text{population contacts}} \underbrace{p \bar{N}}_{\text{mobility}} > 1$$

$$p > \frac{1}{\bar{N}} \frac{\langle k^{1+\theta} \rangle^2}{\langle k^{2+2\theta} \rangle - \langle k^{1+2\theta} \rangle} \cdot \frac{\mu R_0^2}{2(R_0 - 1)^2}$$



Back to the maths...



1

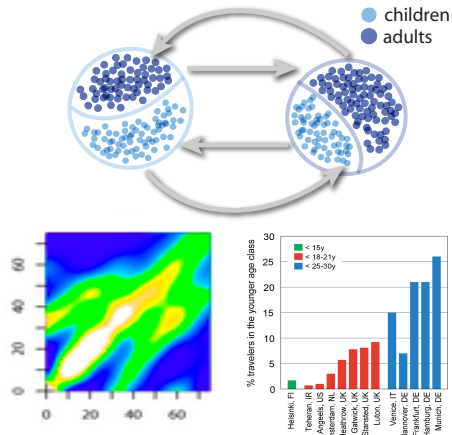
2



containment | invasion
 ↑ reality
 travel

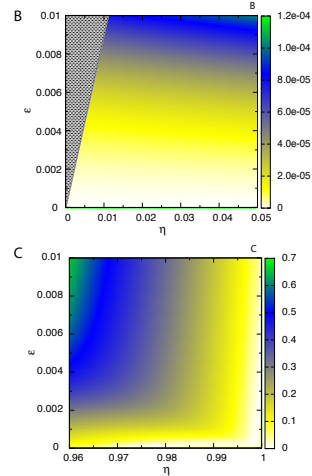
Colizza et al PRL (2007),
 Nat Phys (2007), JTB (2008).

age structure



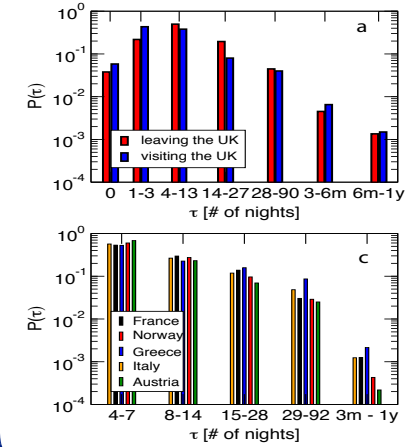
Apolloni et al BMC Inf Dis 2013

social structure

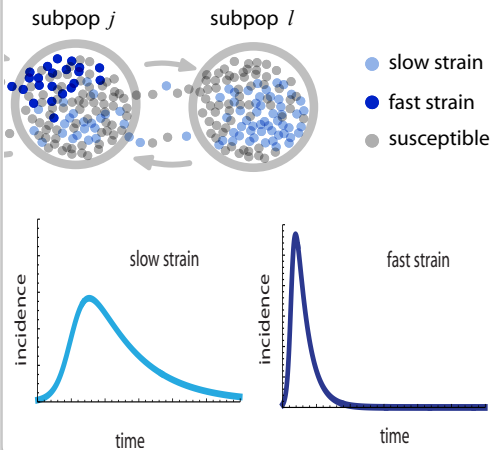


Apolloni et al Theor Bio Medical Model 2014 Poletto et al JTB 2013

memory, length of stay

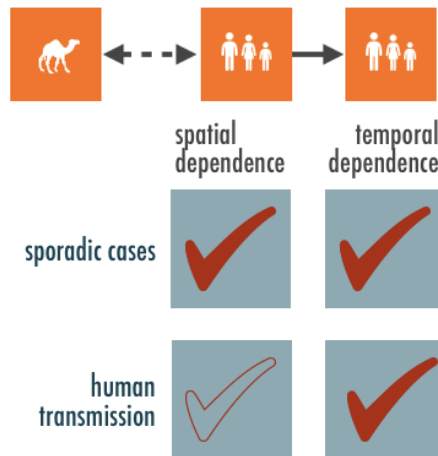


multi-strain (flu)



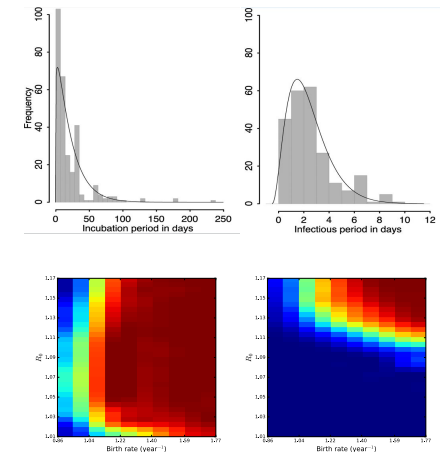
Poletto et al. PLOS Comp Biol 2013

multi-transmission (MERS)



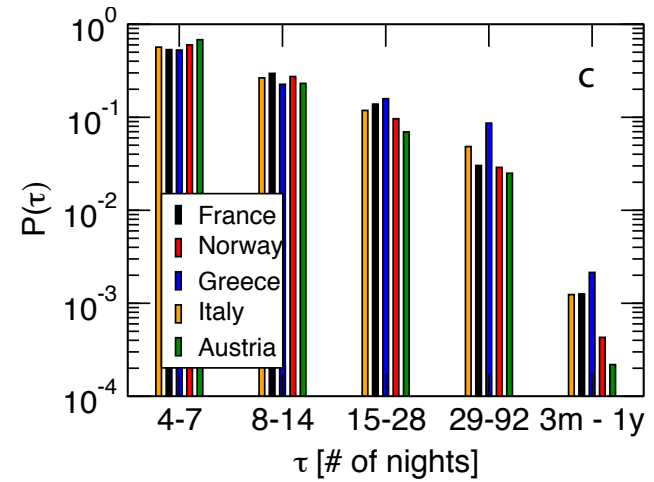
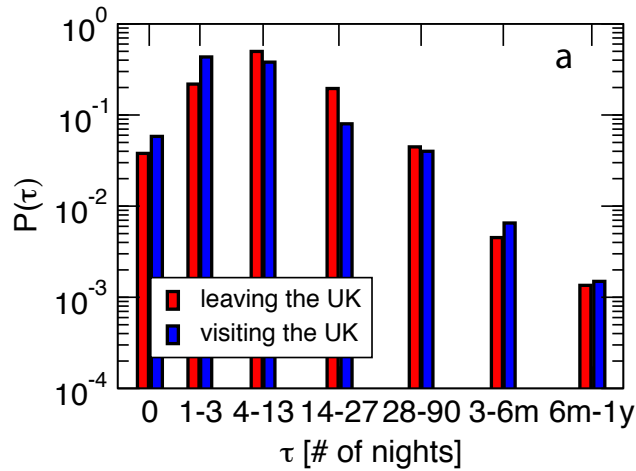
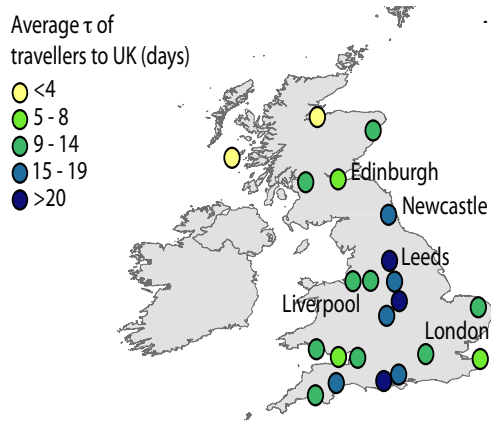
Poletto et al BMC Inf Dis 2016

non-exp disease stages



Colombi et al. PLOS Negl Trop Dis 2020

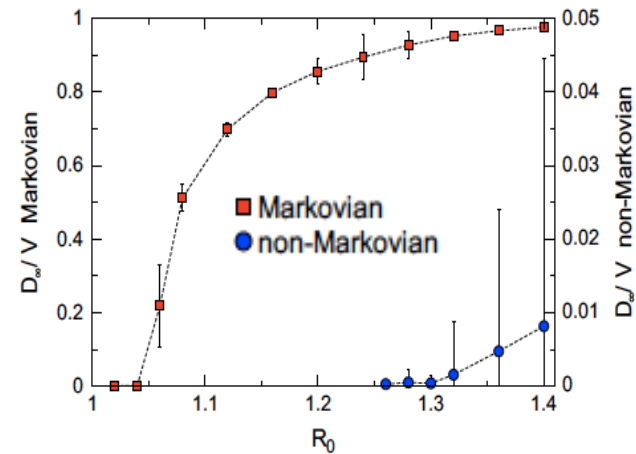
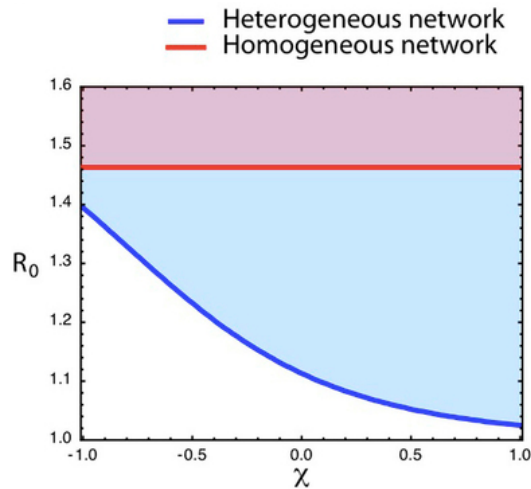
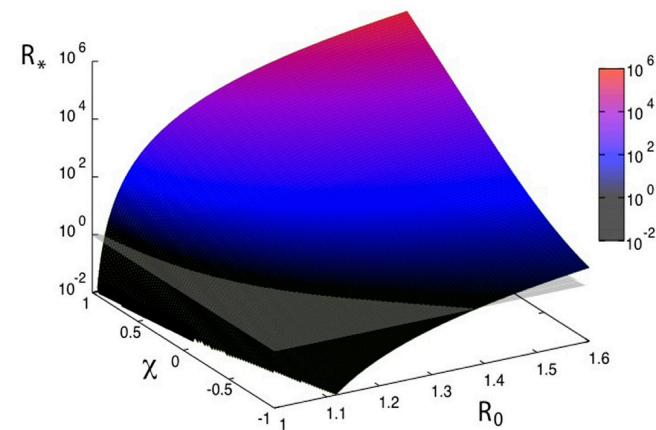
Heterogeneous length of stay



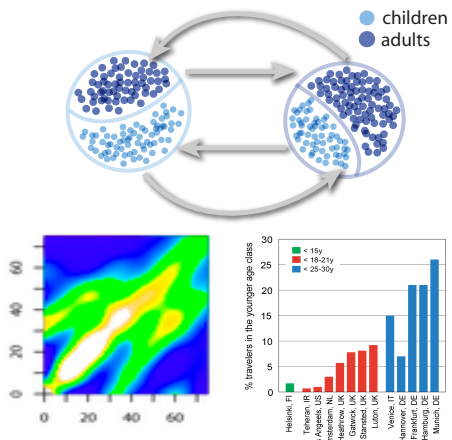
$$\tau_k \sim k^\chi, \quad \chi \begin{cases} > 0 & \text{enhancing role of hubs} \\ < 0 & \text{suppressing role of hubs} \end{cases}$$

Global invasion threshold

$$R_* = \frac{2(R_0 - 1)^2}{R_0^2} \sigma \bar{N} \bar{\tau} \frac{\Lambda(\{P(k)\}, \sigma, \bar{\tau}, \bar{N})}{\langle k \rangle \langle k^\phi \rangle \langle k^\chi \rangle}$$

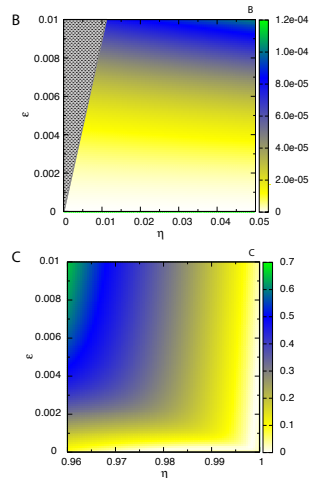


age structure



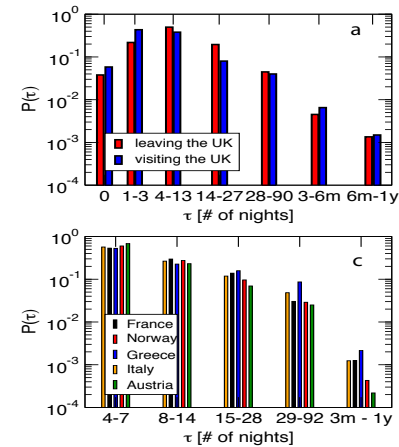
Apolloni et al BMC Inf Dis 2013

social structure

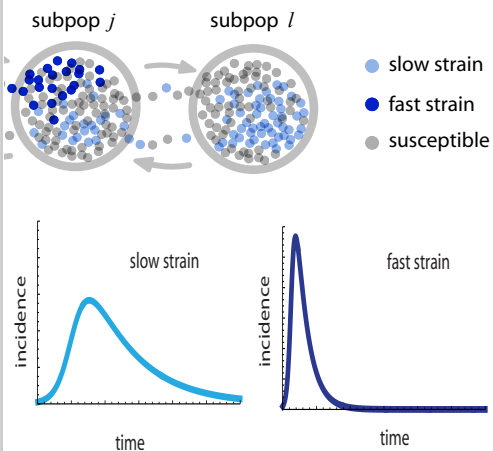


Apolloni et al Theor Bio Medical Model 2014 Poletto et al JTB 2013

memory, length of stay

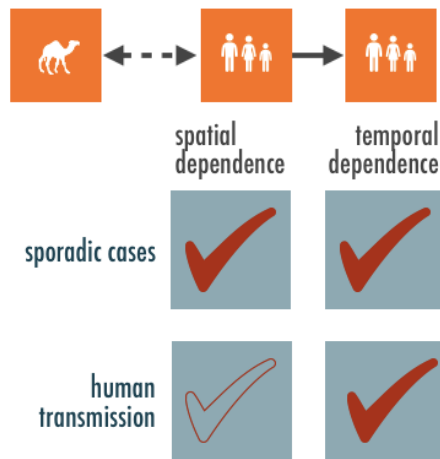


multi-strain (flu)



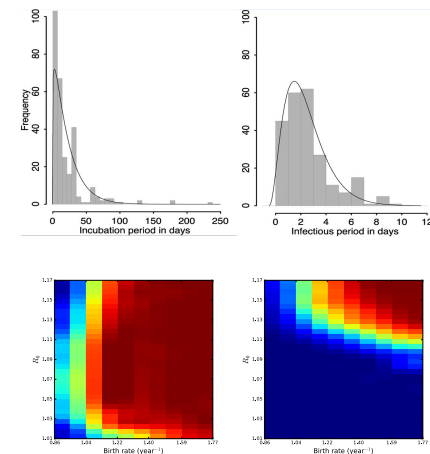
Poletto et al. PLOS Comp Biol 2013

multi-transmission (MERS)



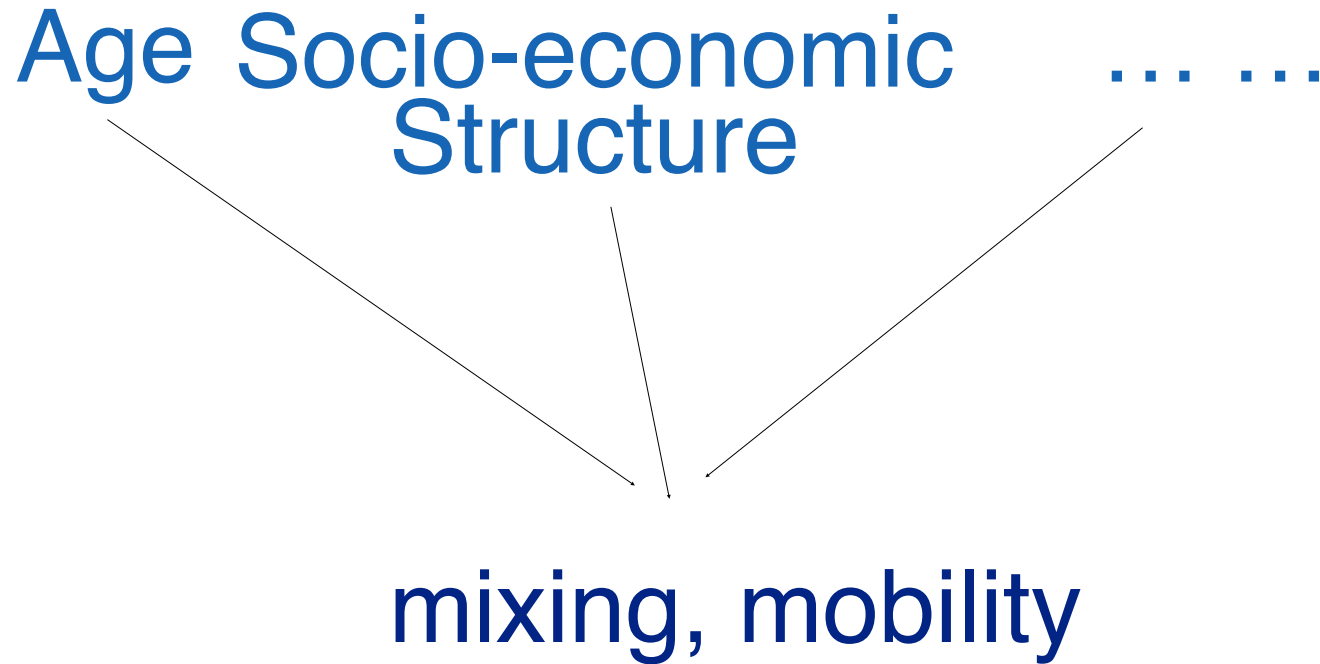
Poletto et al BMC Inf Dis 2016

non-exp disease stages



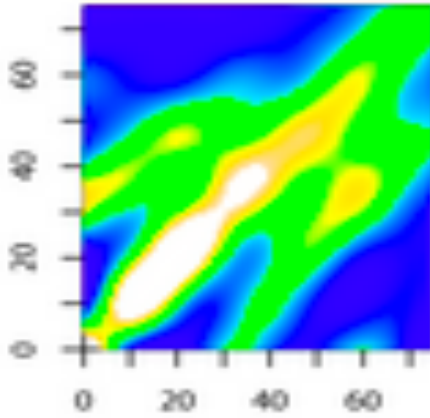
Colombi et al. PLOS Negl Trop Dis 2020

Patch population stratification



Age stratification

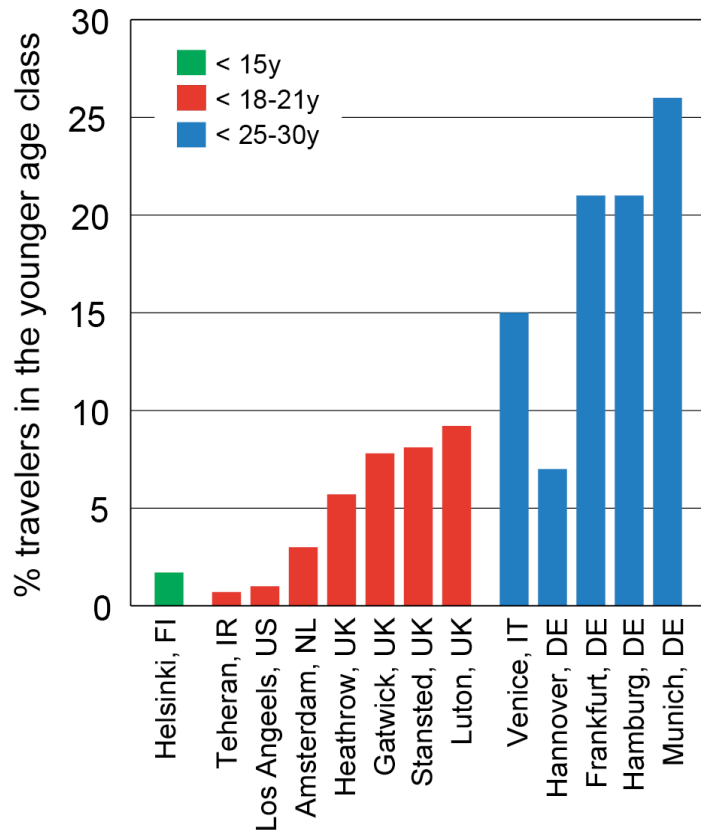
mixing



Mossong et al.
PLOS Med 2008

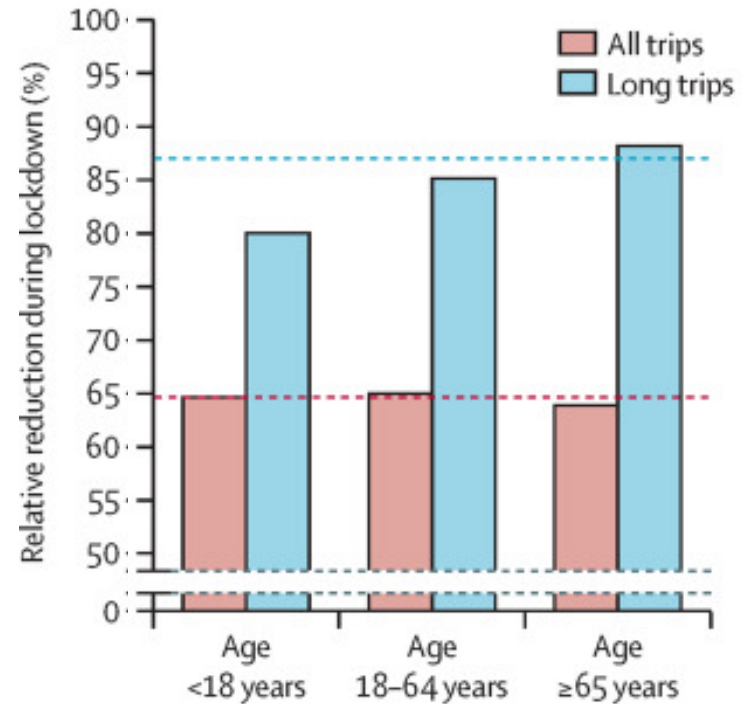
Age and mobility

Air travel DATA (reference)



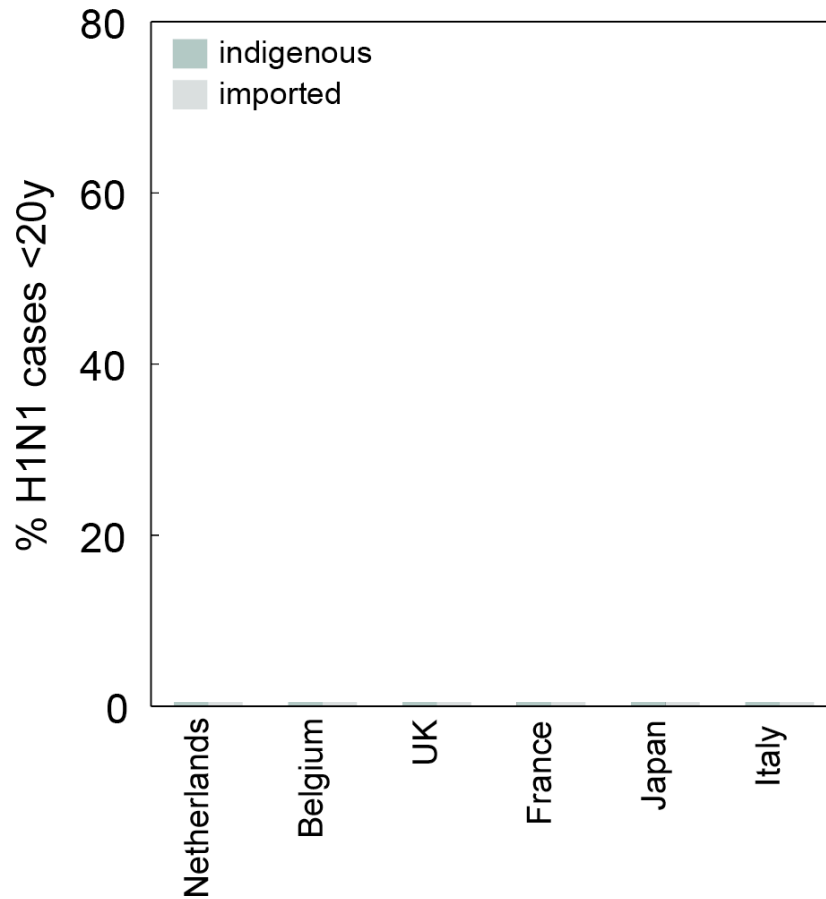
Apolloni et al. BMC Inf Dis 2013

Mobile phone data (1st covid lockdown)



Pullano et al. Lancet Digit Health 2020

Age and invasion/local transmission



initial stage of H1N1 pdm

Age and invasion/local transmission

School Holidays



School holidays

reduction of
human mobility
+ new destinations



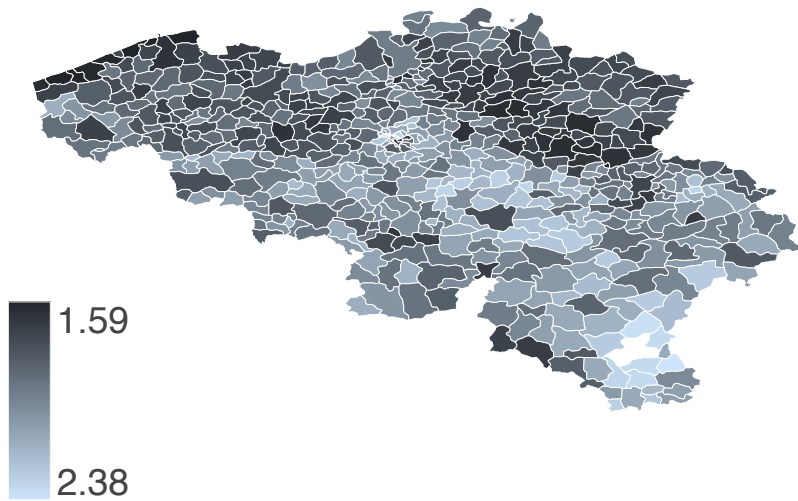
social mixing
change

Social mixing

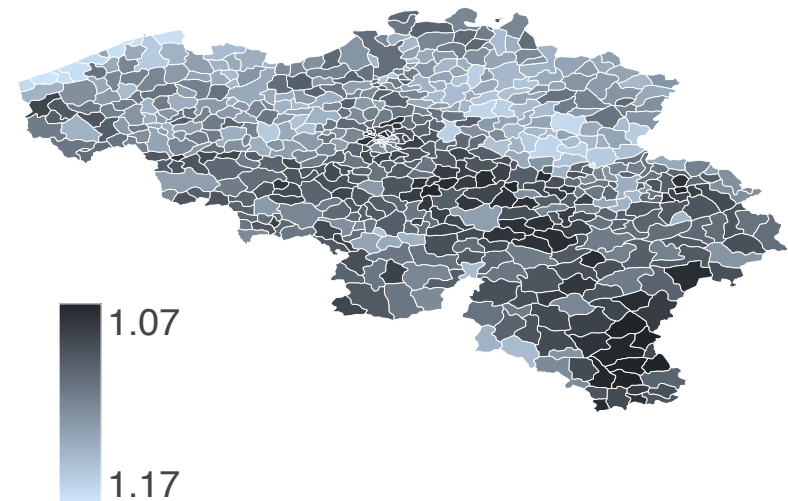


R_0 in space

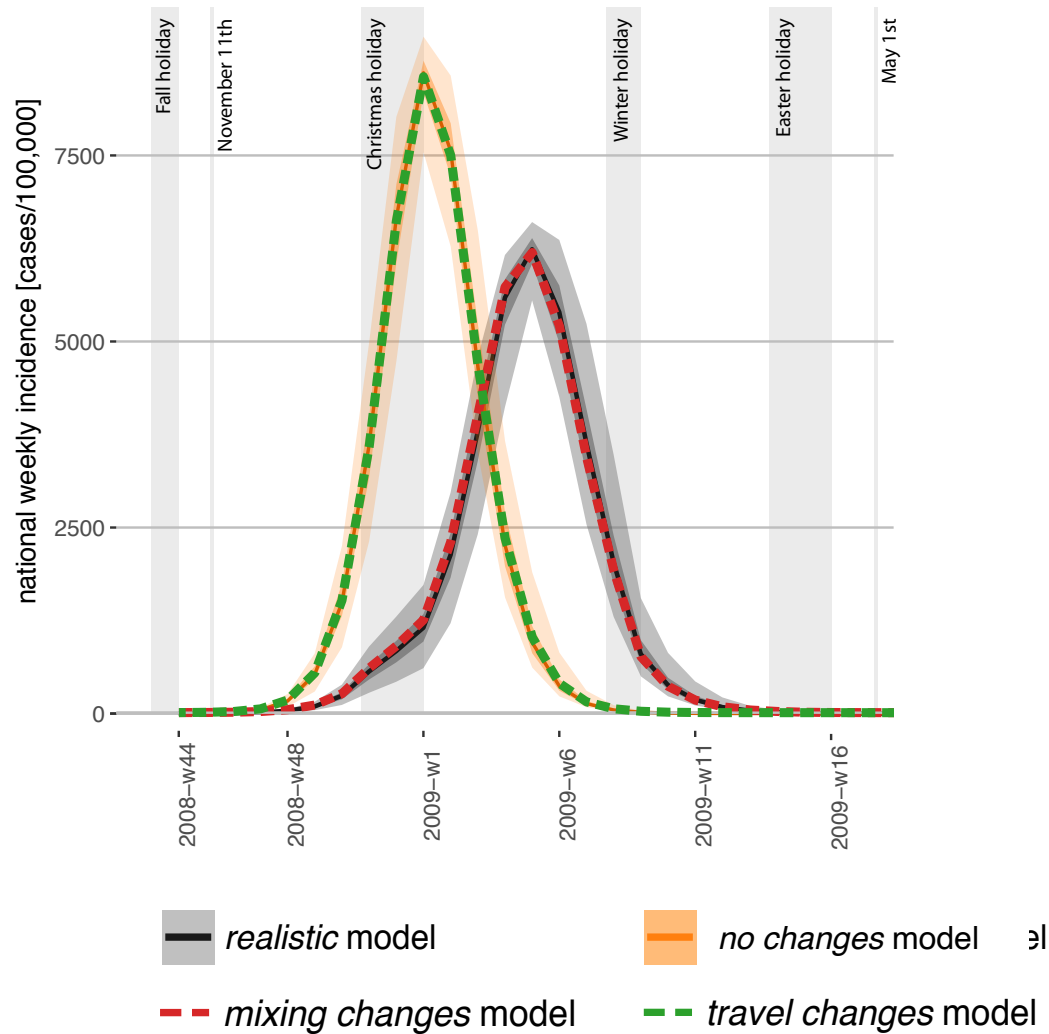
regular weekday



regular weekend



Impact of mobility vs. contacts



in the US:

- Ewing et al. 2017

travel restrictions:

- Cooper et al, 2006
- Epstein et al, 2007
- Hollingsworth et al, 2006
- Colizza et al, 2007
- Bajardi et al, 2011