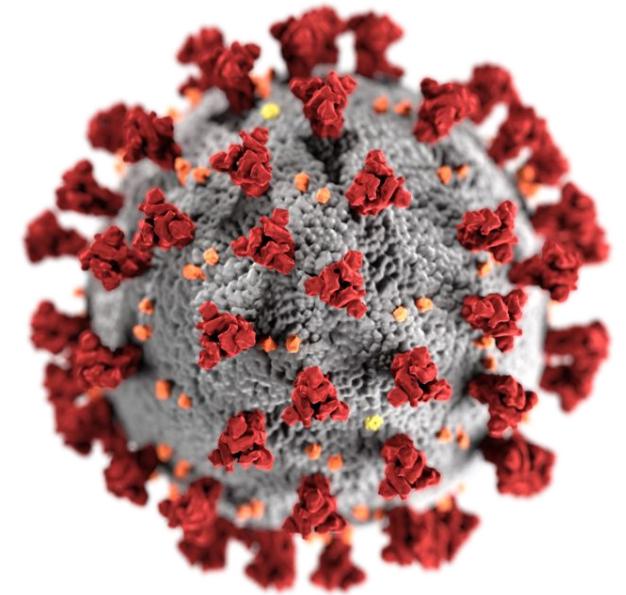


New questions on epidemic spreading suggested by the COVID-19 pandemic



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Vicenç Mut Postdoctoral Fellow



EXCELENCIA
MARÍA
DE MAEZTU
2023 - 2027

3rd January 2024
Department of Mathematics, National University
of Kaohsiung (Taiwan)

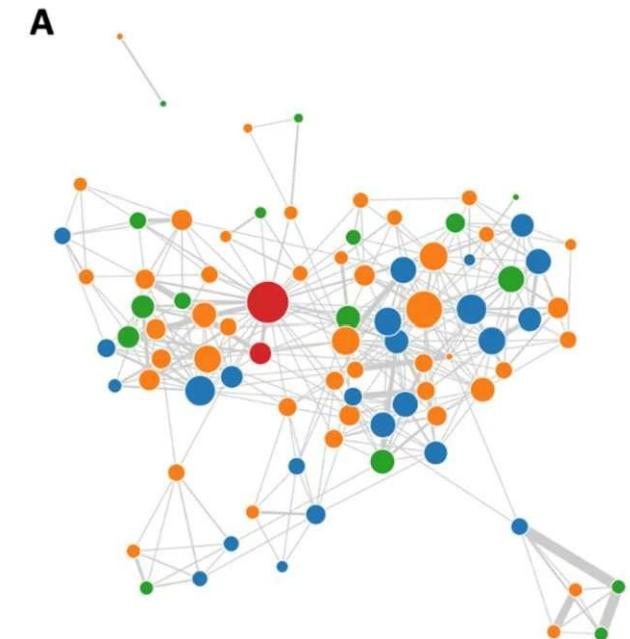
Once upon a time (20/09/2018) ...

“My cousin was looking forward to his holidays, year after year, and as he was taking several flights towards his final destination, he got sick on the dreamt holidays. He thought that he was unlucky, but he did not know about disease spreading dynamics”

Jorge P. Rodríguez

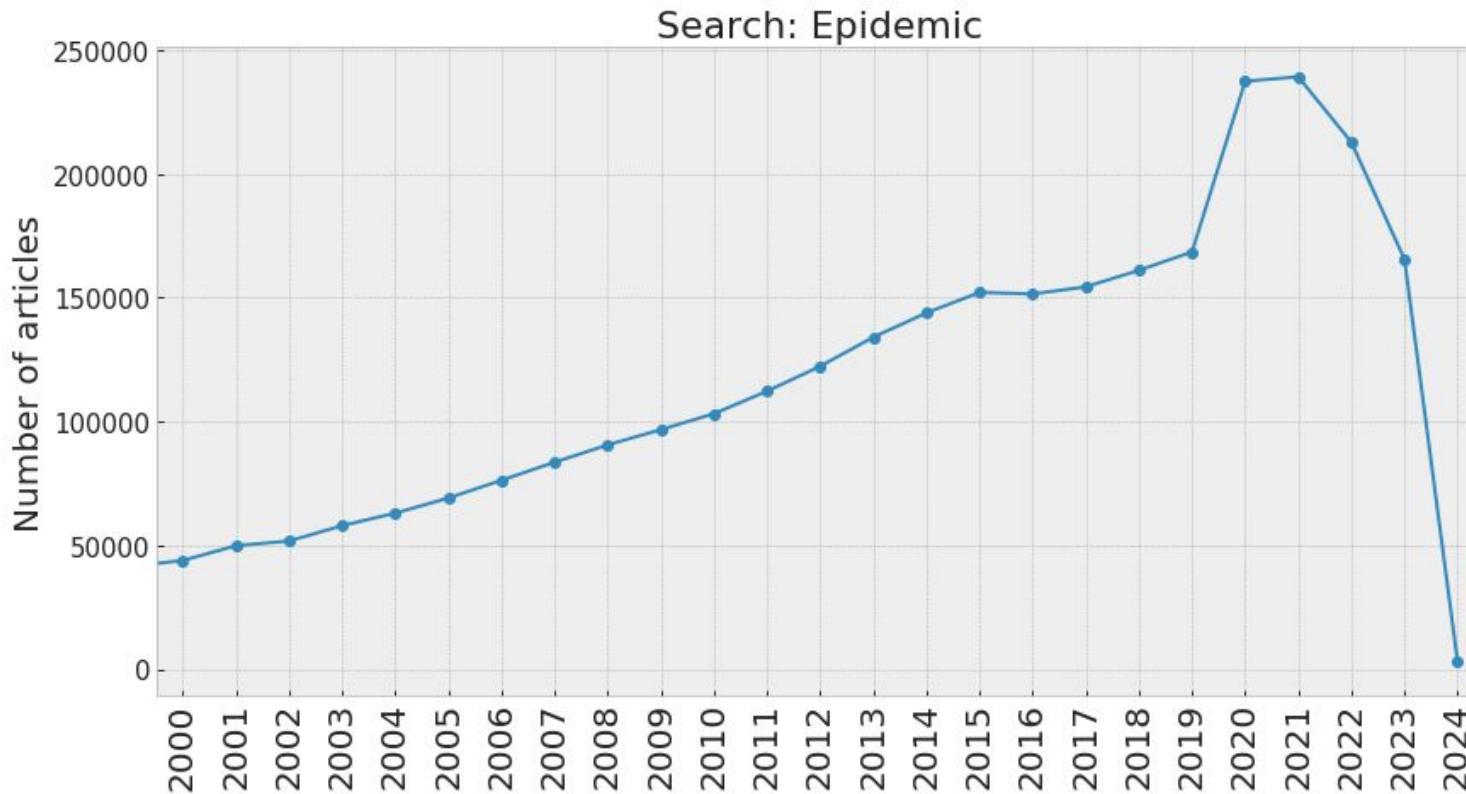
Useful approaches in the past to understand spreading:

- Temporal network dynamics (example: SocioPatterns)
- Intervention strategies (example: school closure)
- Interaction between awareness and spreading dynamics using multilayer approaches



Ozella et al. (EPJ Data Science, 2021)

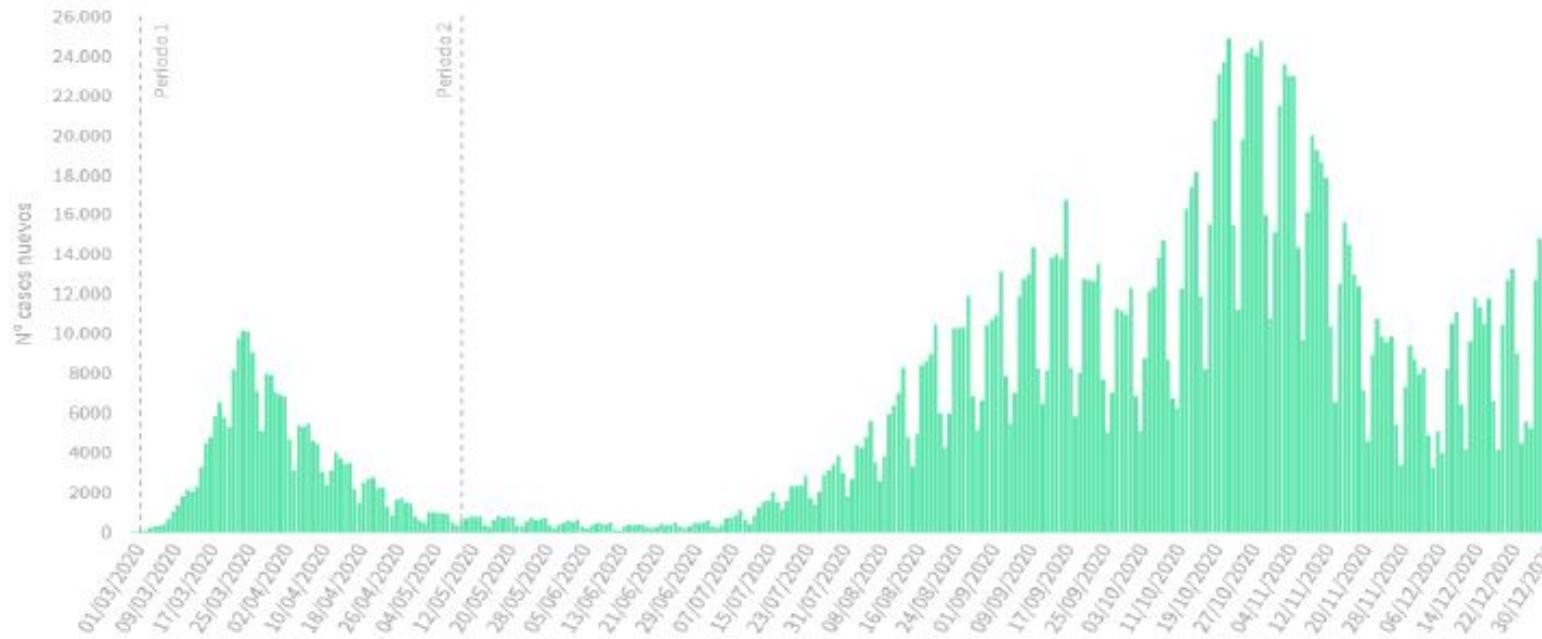
Scientific literature on epidemic spreading proliferated from 2020



Data from PubMed,
own visualization

Abundance + COVID-19 disruptions: slow-down in handling, harder for experts

1. Analysis of the first wave and prediction of subsequent waves



Source: Centre for Health Alert and Emergencies, Ministry of Health (Spain)

- **Isolation experiment:** national lockdown implied closure of passenger airports and ports' traffic only in Balearic Islands
- **Low impact** of first wave (seroprevalence study reported 2.3% on May 2020)
- Population N= 1.1 M, agent-based models are suitable
- Availability of **commuting data** from 2011 Census

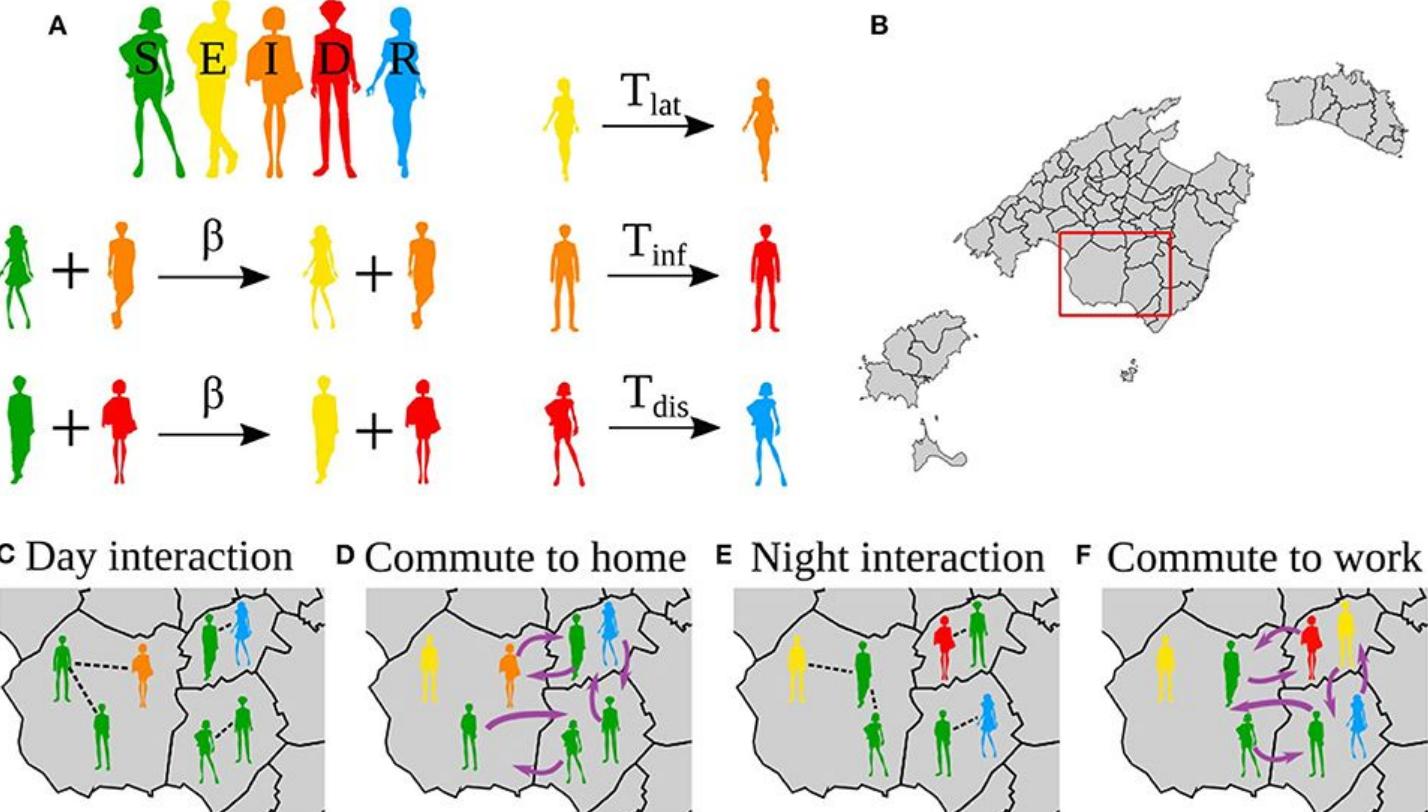


- Metapopulation model between 67 municipalities

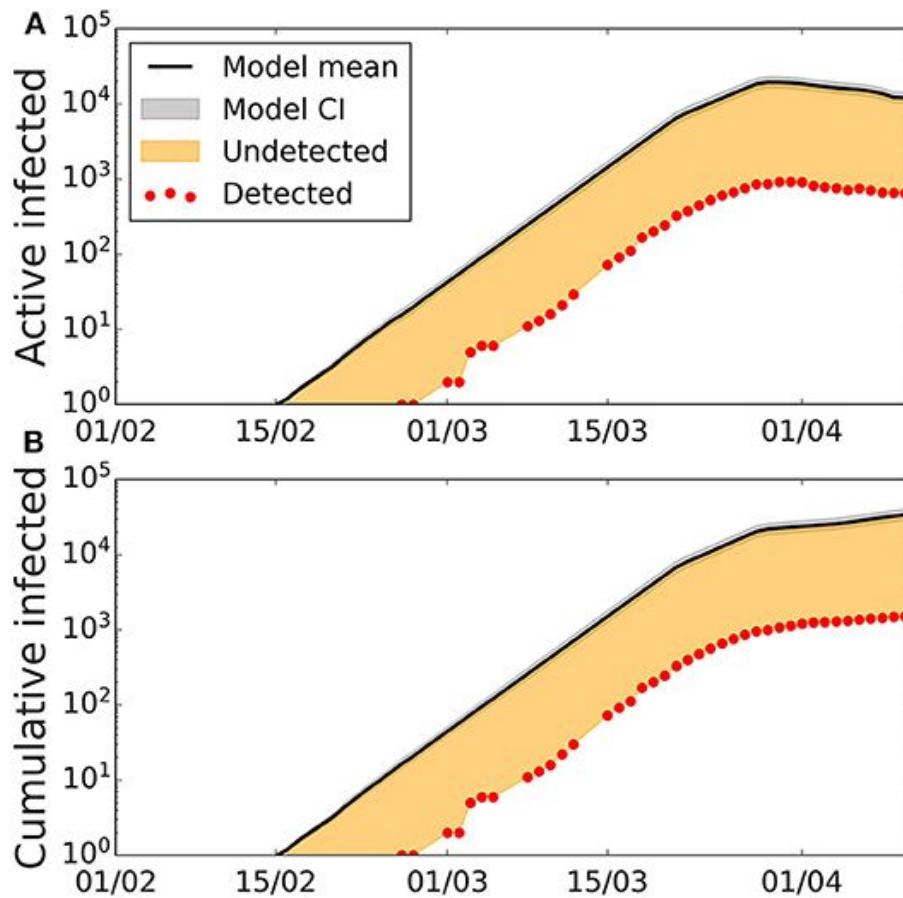
- Distinguishable agents:
any agent always performs the same trip,
previous approaches chose travellers randomly.
Ideal for recurrent mobility

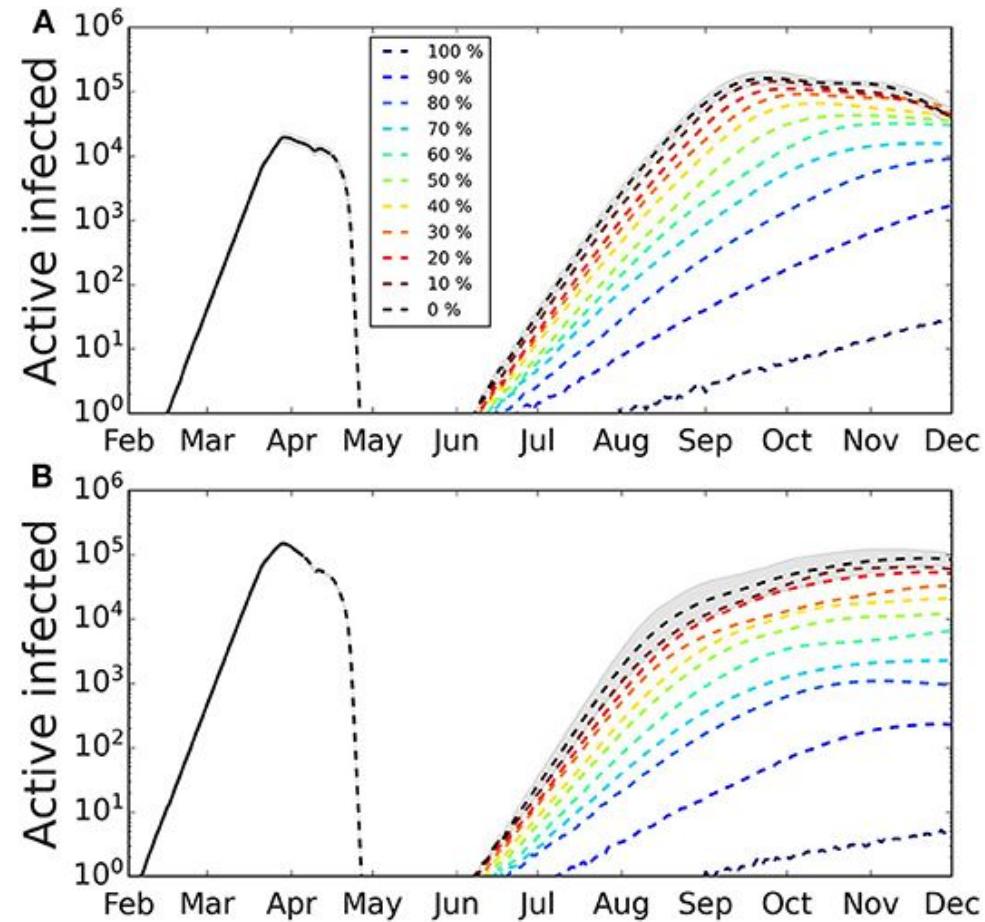
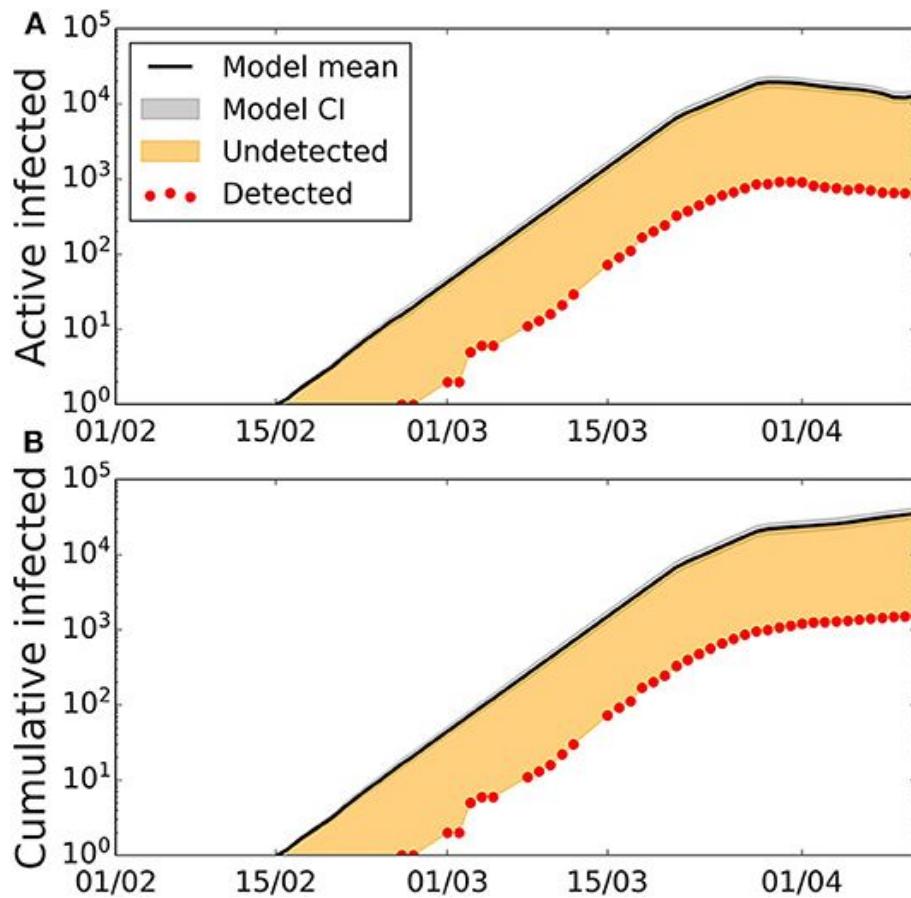
- Estimate T_{lat} , T_{inf} and T_{dis} from changes in the curves

- Calibrate β weekly to account for changes in mobility



Eguíluz et al. (Front. Medicine, 2020)





Available on medRxiv from May 08, 2020

Eguíluz et al. (Front. Medicine, 2020)

2. Digital twins of cities to reproduce contacts and inform epidemic spreading models



AIM: To reproduce human contacts in cities to inform spreading models

Global data

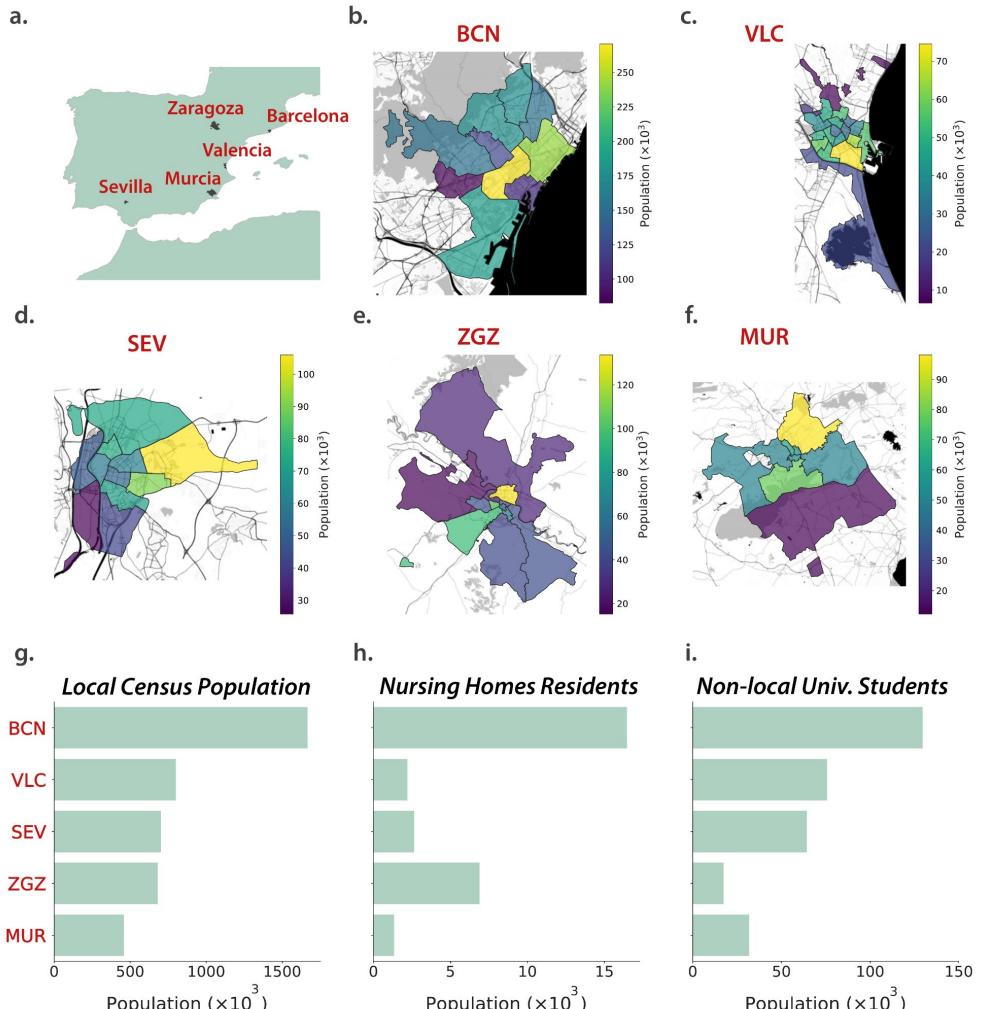
National data

Regional data
(17 autonomous regions!)

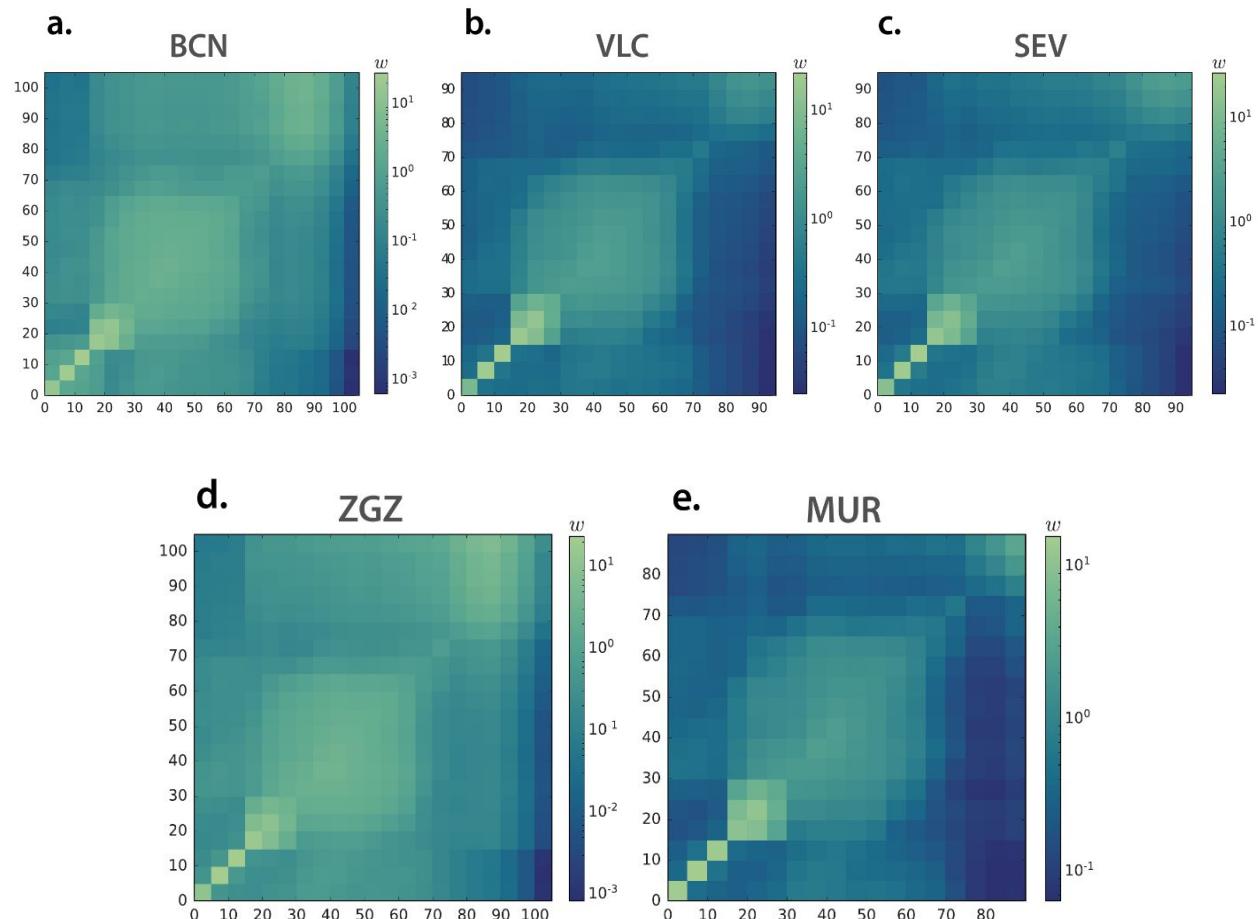
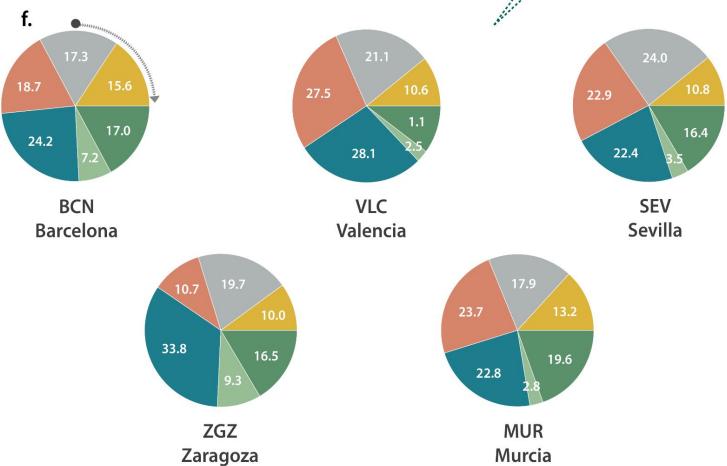
Local data



- 5 Spanish cities (municipalities): Barcelona, Valencia, Seville, Zaragoza and Murcia
- Information available at census district
- Demographic data (age, gender), household structure, school group sizes per level, university registered students...
- 6 interaction layers: households, schools, work, nursing homes, universities, community



Fraction of contacts per layer



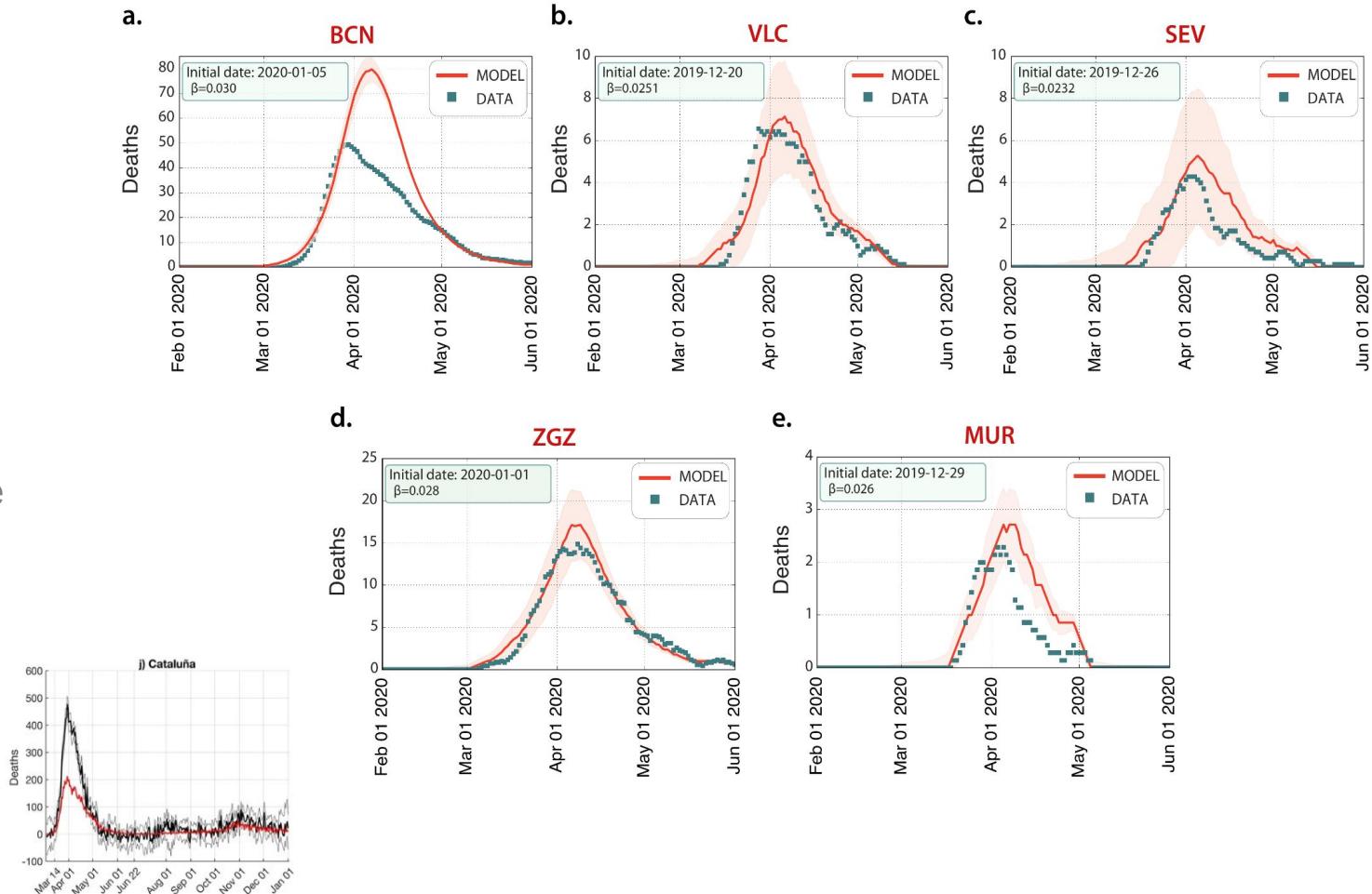
- COVASIM software, 1 initial seed

- State of alarm (14th March): stop school, university and community, reduce work to 20%

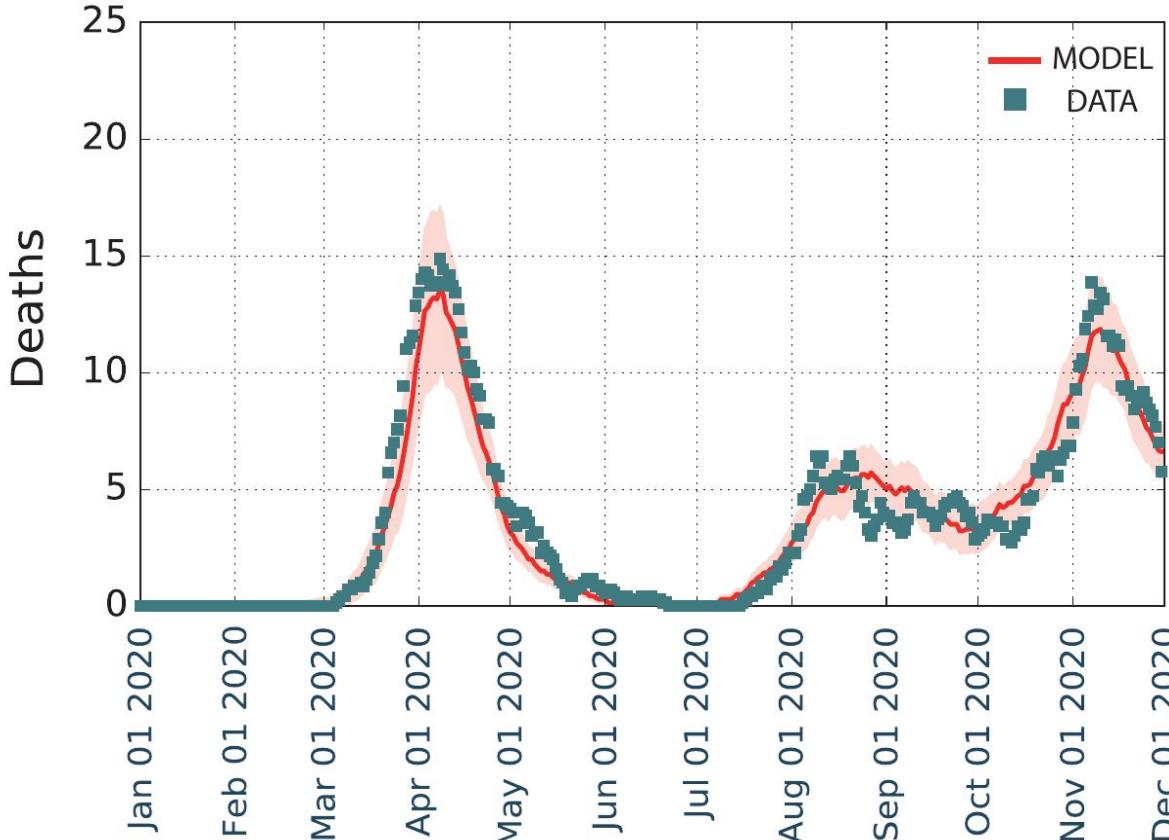
- We calibrate arrival date and infection rate β

- Agreement between observed and predicted deaths (excess at the beginning, Barcelona excess at peak)

- Seroprevalence



Results (2nd wave, Zaragoza) *



No variants: continue realizations from 1st wave (same β) lifting restrictions

Tests (prob per symptoms day):

15% until Sep

8% from Sep

Tracing:

40% until 19th Aug

45% 20th Aug-30th Sep

55% 1st Oct

Schools:

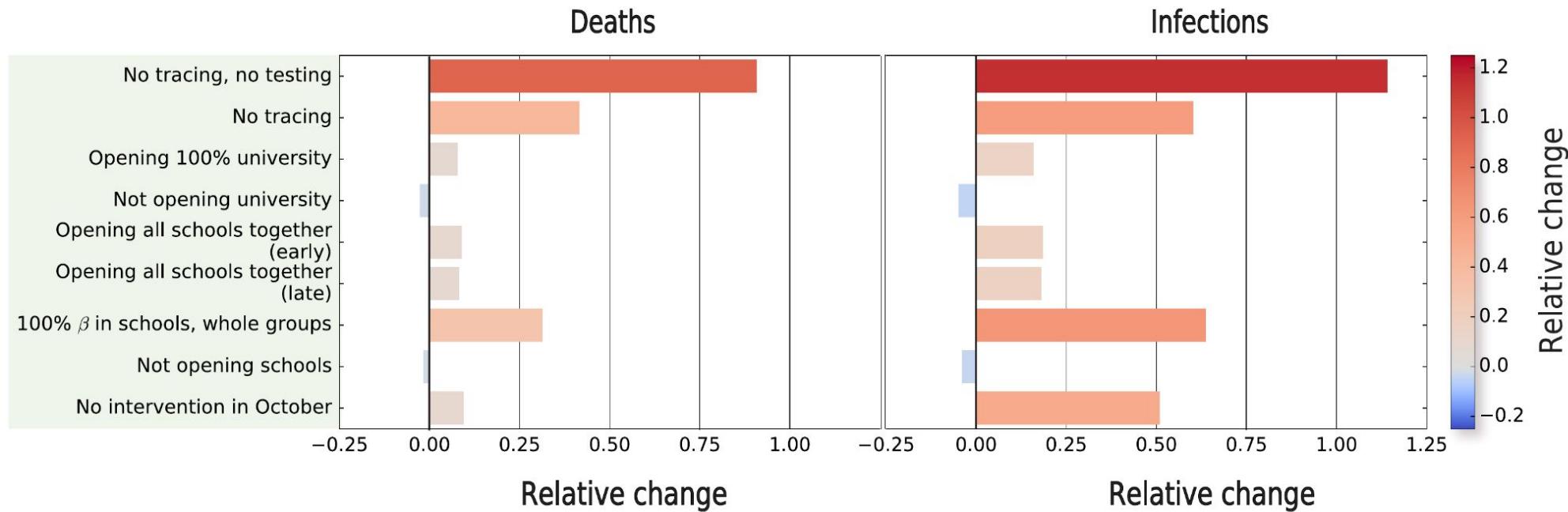
Progressive opening in Sep

Beta in school 60%

Small groups (25% contacts)

University:

Opened on 14th Sep (45%, 25% after 19th Oct)

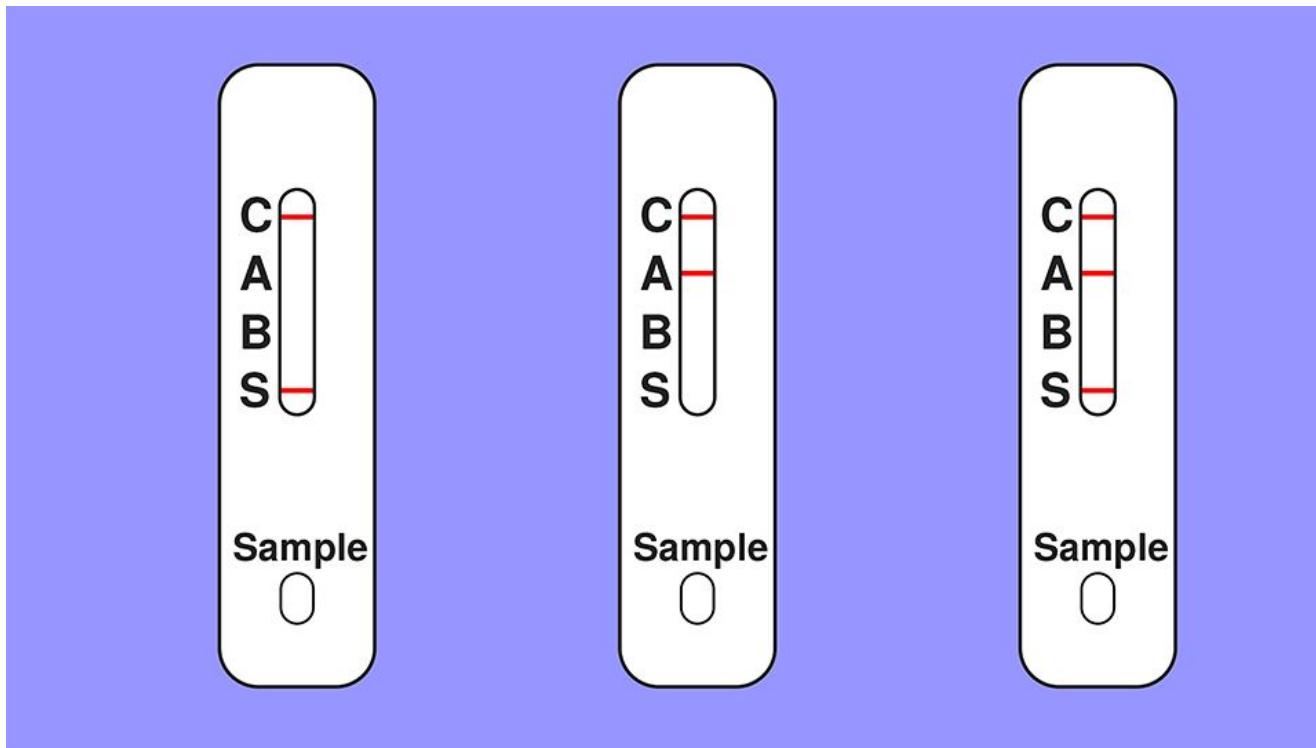


- Test-Trace-Isolation: best strategy for reducing deaths and infections.

- October interventions (State of Alarm): extension confirms second wave would have continued until middle of December, with impact on deaths similar to no tracing scenario.

Rodríguez, Aleta, Moreno (Front. Publ. Health, 2023)

3. Coupling between infectious diseases



Single infection

Susceptible - Infected - Recovered

$$\frac{ds}{dt} = -\beta si,$$

$$\frac{di}{dt} = \beta si - \mu i,$$

$$\frac{dr}{dt} = \mu i.$$

Solution at infinite time:

$$r_\infty = 1 - e^{-r_\infty \beta / \mu}$$

Non-zero stable solution if $R = \beta/\mu > 1$

Single infection

Susceptible - Infected - Recovered

Variable of interest: peak, $di/dt (t=t^\uparrow) = 0$

$$s^\uparrow = R^{-1},$$

$$i^\uparrow = 1 - R^{-1}(1 + \log R),$$

$$r^\uparrow = R^{-1} \log R,$$

i^\uparrow grows monotonically with R : $di^\uparrow/dR = \log R / R^2 > 0$

Two infections: 0 and 1

Susceptible individuals get infected with β_0 , β_1

If “touched” by the other disease, they get infected with $k_0\beta_0$, $k_1\beta_1$

$k_i = 1$: independent

$k_i > 1$: cooperative (co-infection)

$k_i < 1$: competitive (cross-immunity)

Two infections: 0 and 1

Susceptible individuals get infected with β_0, β_1 Infected recover with μ_0, μ_1

If “touched” by the other disease, they get infected with $k_0\beta_0, k_1\beta_1$

$k_i = 1$: independent

$k_i > 1$: cooperative (co-infection)

$k_i < 1$: competitive (cross-immunity)

9 different states, reduced to 5 differential equations

$$\frac{ds}{dt} = -\beta_0 s q_0 - \beta_1 s q_1,$$

$$\frac{dq_0}{dt} = \beta_0 s q_0 + k_0 \beta_0 q_0 t_1 - \mu_0 q_0,$$

$$\frac{dq_1}{dt} = \beta_1 s q_1 + k_1 \beta_1 q_1 t_0 - \mu_1 q_1,$$

$$\frac{dt_0}{dt} = \beta_0 q_0 s - k_1 \beta_1 q_1 t_0,$$

$$\frac{dt_1}{dt} = \beta_1 q_1 s - k_0 \beta_0 q_0 t_1,$$

Symmetric interaction, cooperative regime ($k_0 = k_1 = k = 1+\epsilon$)

Consider $R_0 > R_1$

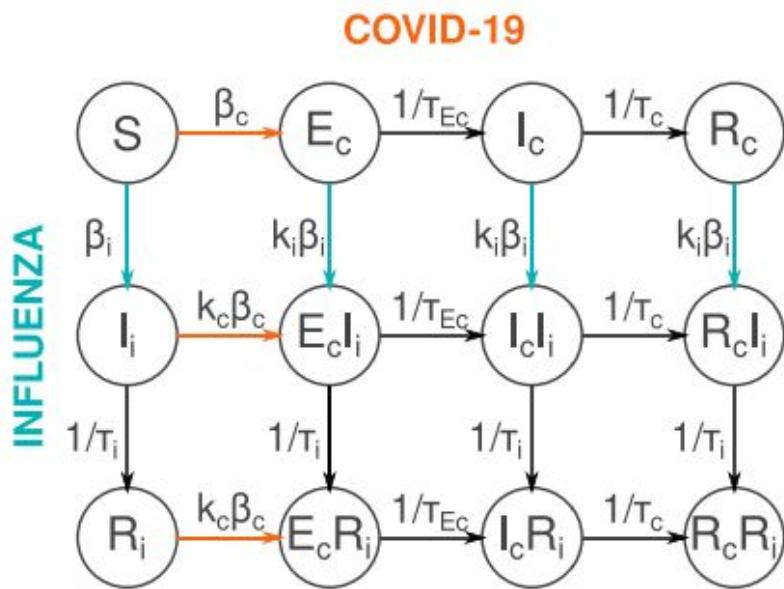
Initial synchronization for an initial seed of α infected in each infection:

$$\left. \frac{dq_0}{dq_1} \right|_{t=0} = \left. \frac{dq_0}{dq_1} \right|_{t=0,ni} + \epsilon \alpha \frac{\mu_0}{\mu_1} \frac{R_1 - R_0}{[R_1(1 - \alpha) - 1]^2},$$

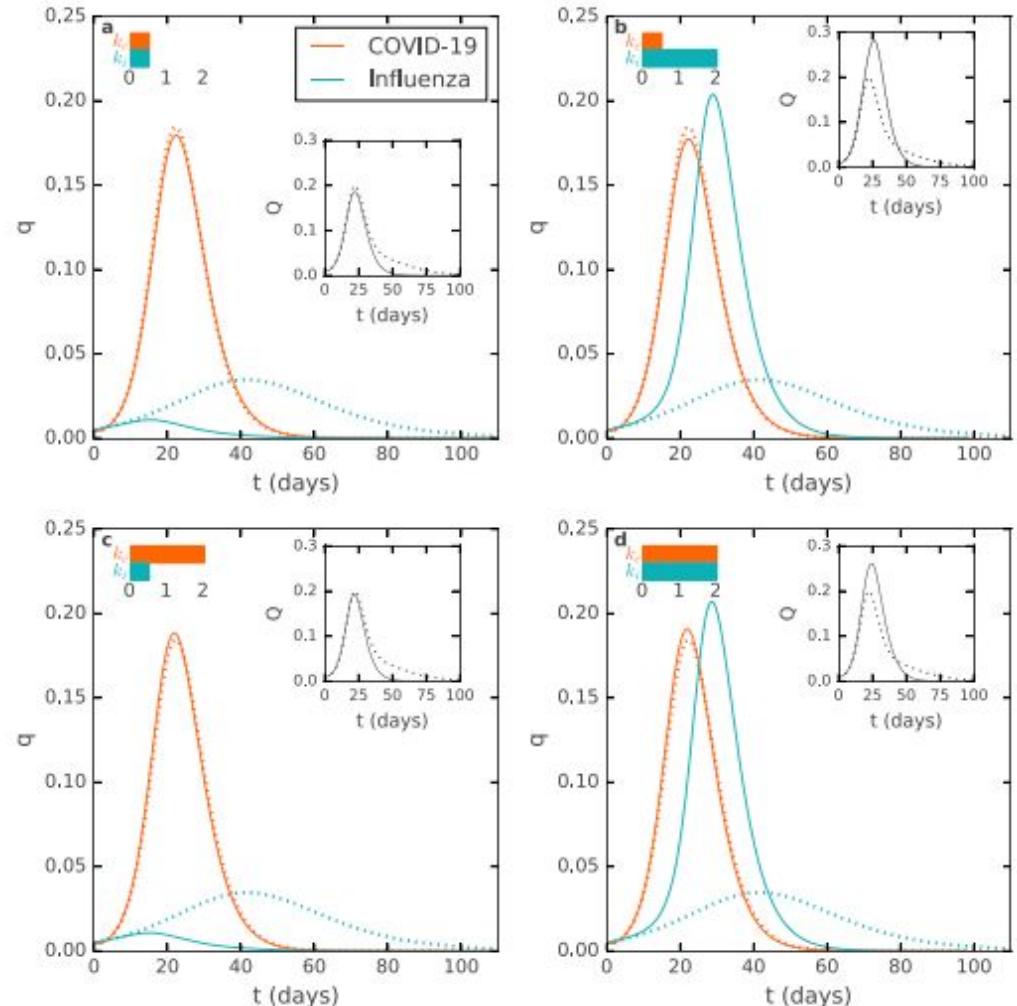
This implies that the initial growth tends to be more similar, and consequently the peaks, related to the effective basic reproductive ratios (remember single disease dynamics), will synchronize

This case represents **early synchronization**

In **competitive** scenarios, we show analytically the presence of **late synchronization**



Rodríguez & Eguíluz, Chaos (2023)





Contents lists available at [ScienceDirect](#)

Biological Conservation

Journal homepage: www.elsevier.com/locate/biocon



Global COVID-19 lockdown highlights humans as both threats and custodians of the environment



scientific reports



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Key epidemiological indicators and spatial autocorrelation patterns across five waves of COVID-19 in Catalonia

Francesc Belvis  , Alberto Aleta , Álvaro Padilla-Pozo  , Juan-M. Pericàs , Juan Fernández-Gracia , Jorge P. Rodríguez  , Víctor M. Eguiluz , Charles Novaes De Santana , Mireia Julià  , Joan Benach  & the COVID-SHINE group *

In preparation:
Integrating social determinants and machine learning to understand COVID-19 mortality in Catalonia, Spain

COVID-19 brought many lessons to epidemiology

1. Abrupt measurements (i.e., lockdown) facilitate quick control, but subsequent waves are very likely to occur
2. Digital twins are ideal for the design and test of non-pharmaceutical interventions. Need to work on data availability and standardization
3. Epidemic threshold is important, but solving real problems request other analysis, for example the peaks (maximum health-care demand)

COVID-19 brought many lessons to epidemiology

We have learnt, we have more powerful tools to fight pandemics, but we should focus our efforts on avoiding mistakes that led us to a highly risky system

Team



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謝謝！



jorgep.rodriguez

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G CONSELLERIA
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