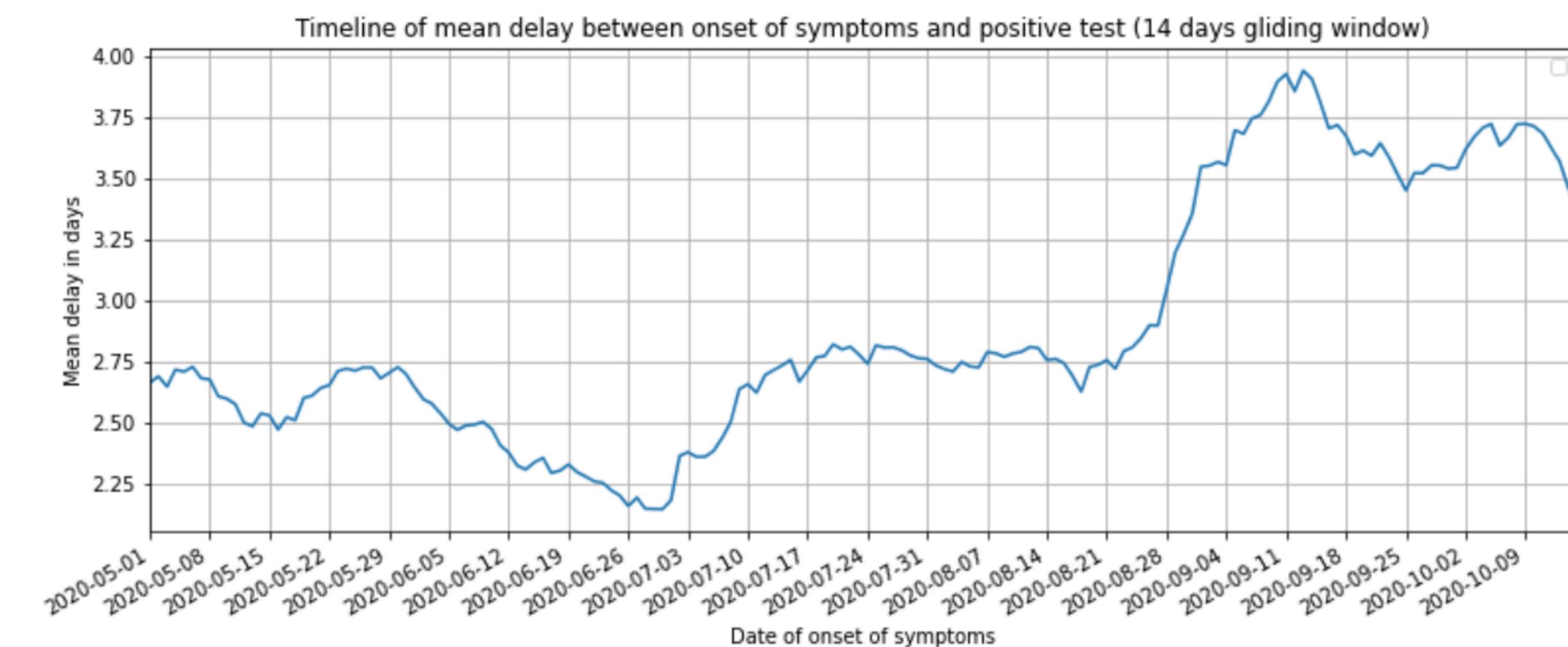
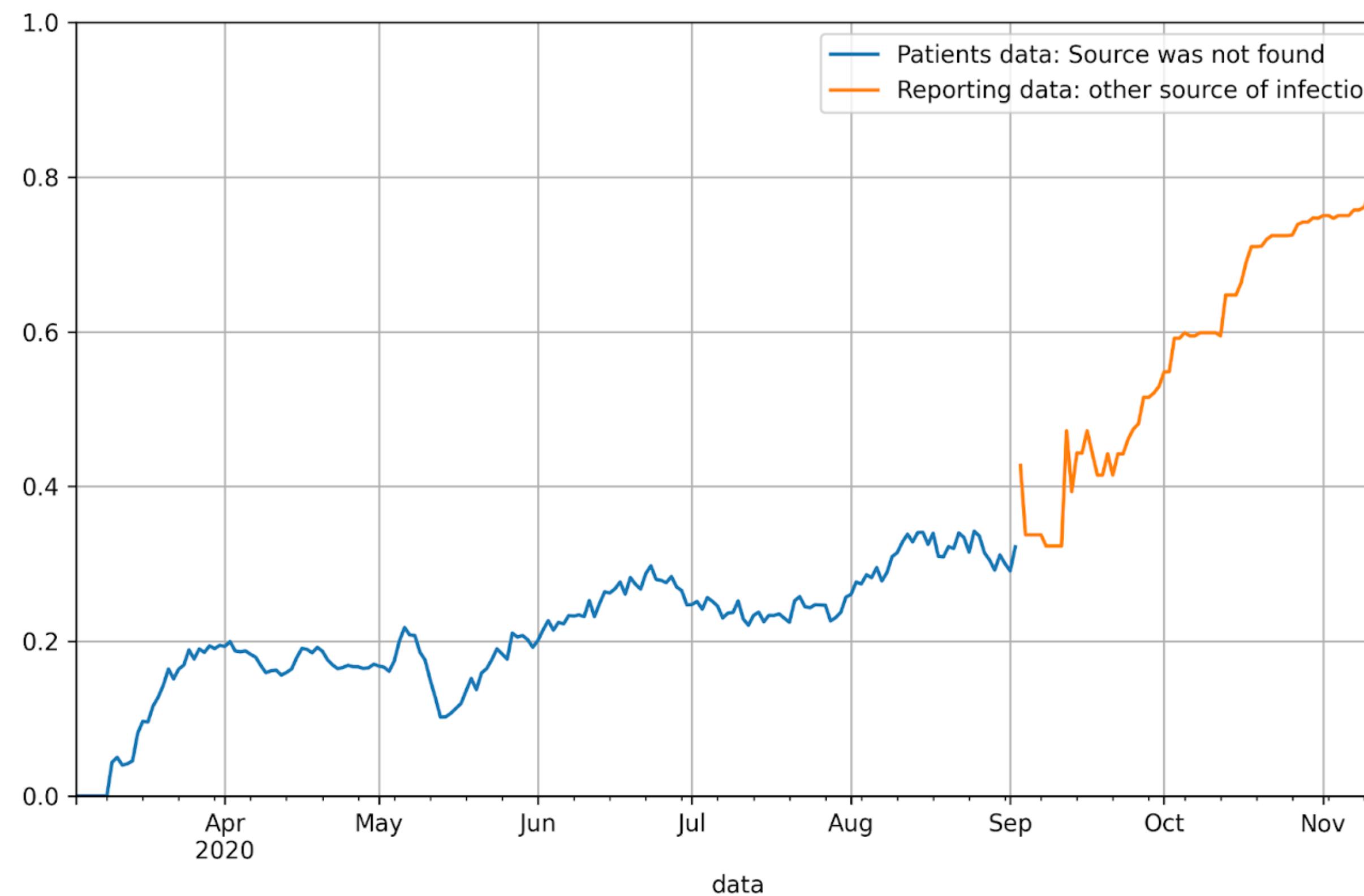


Beginning of Part II

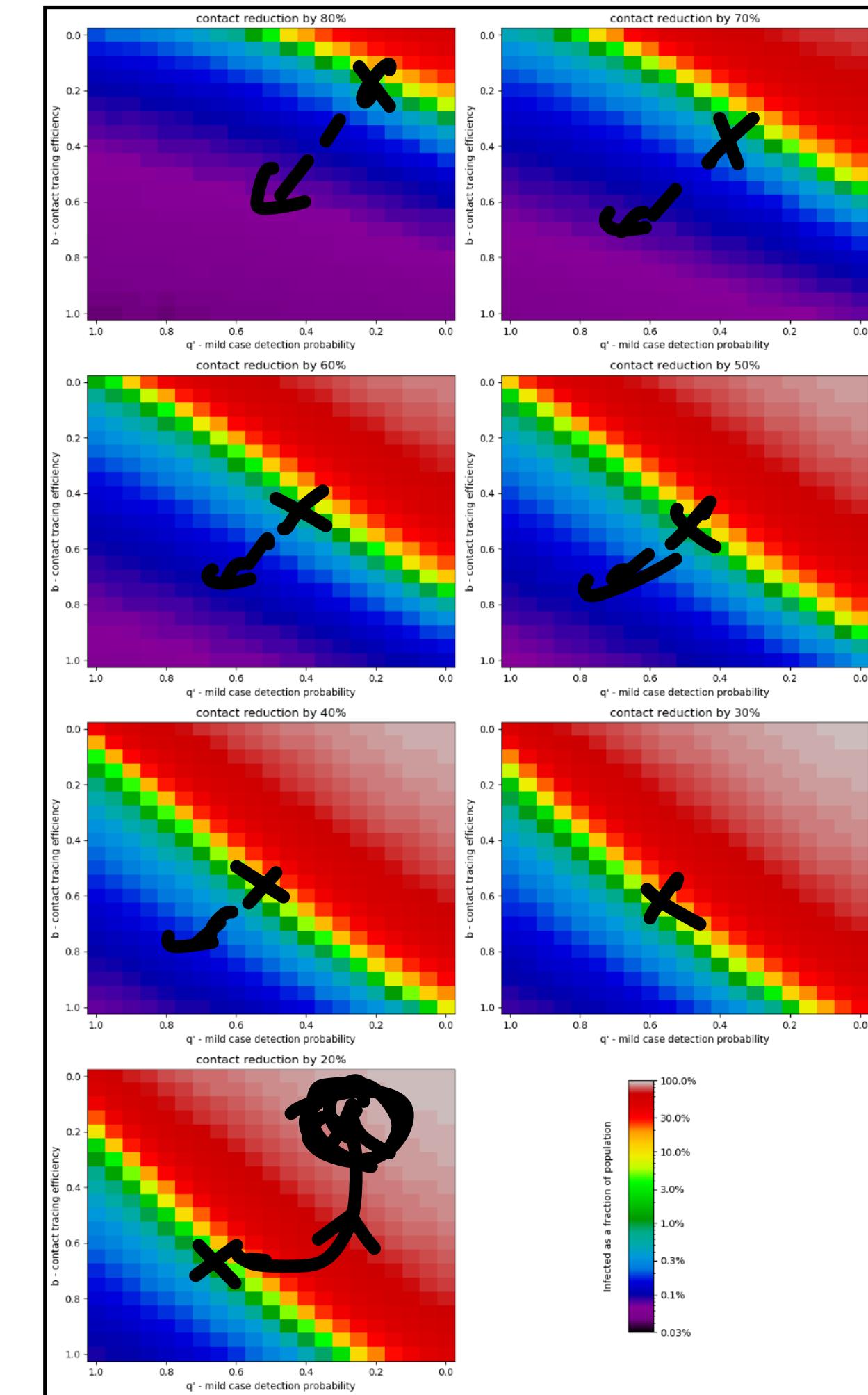
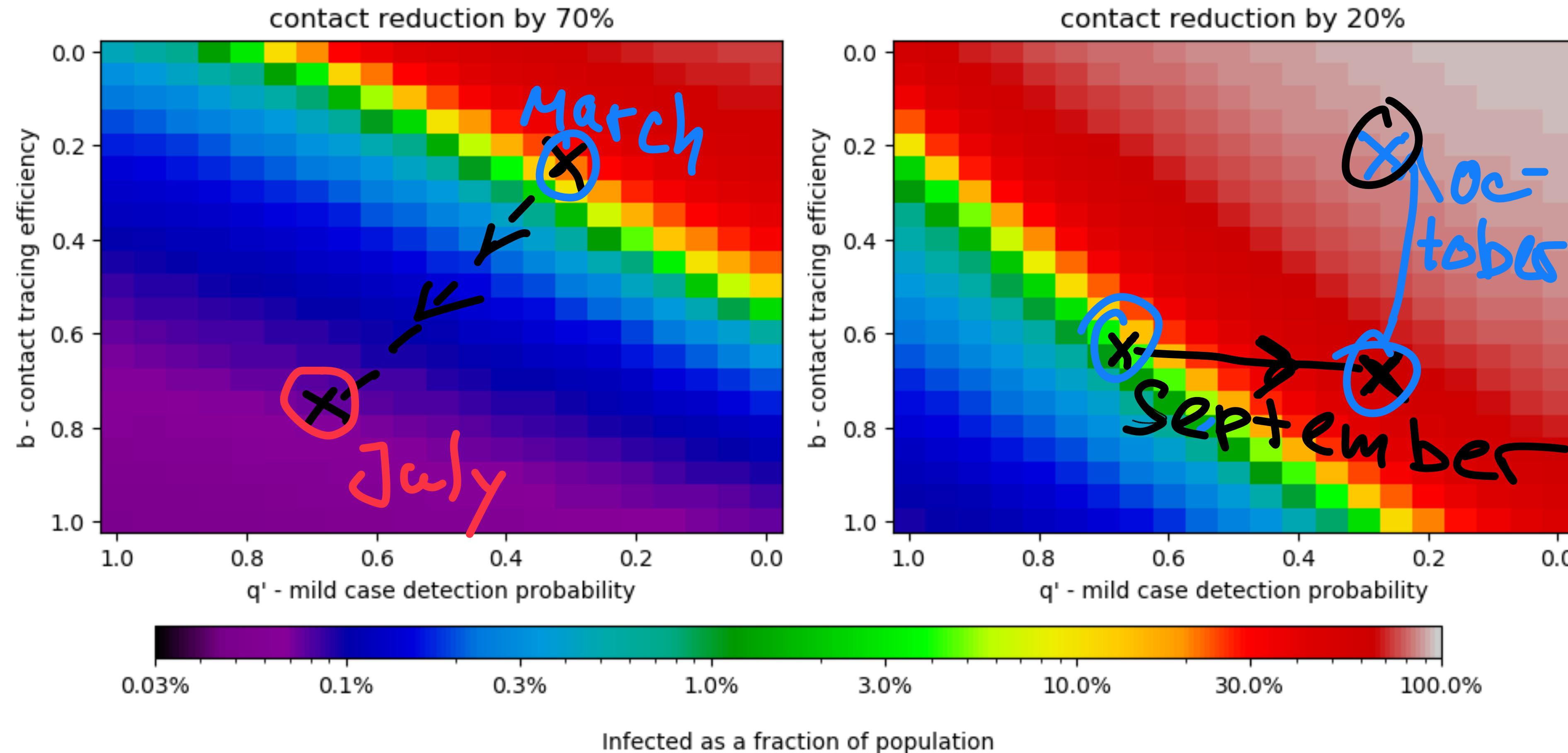
Some problems related to policy advice

- Sometimes fundamental lack of basic epidemiological understanding
- “Wrong” requests and “wrong “ decisions
- Wishful thinking (“we are different”, “this time is different”)
- Decision delay till “last moment”
- No proper risk prevention strategy (selective bias to more optimistic scenarios)
- Experts overly confident
- Lack of good data
- Non-transparent decision structures
- Impact of public opinion

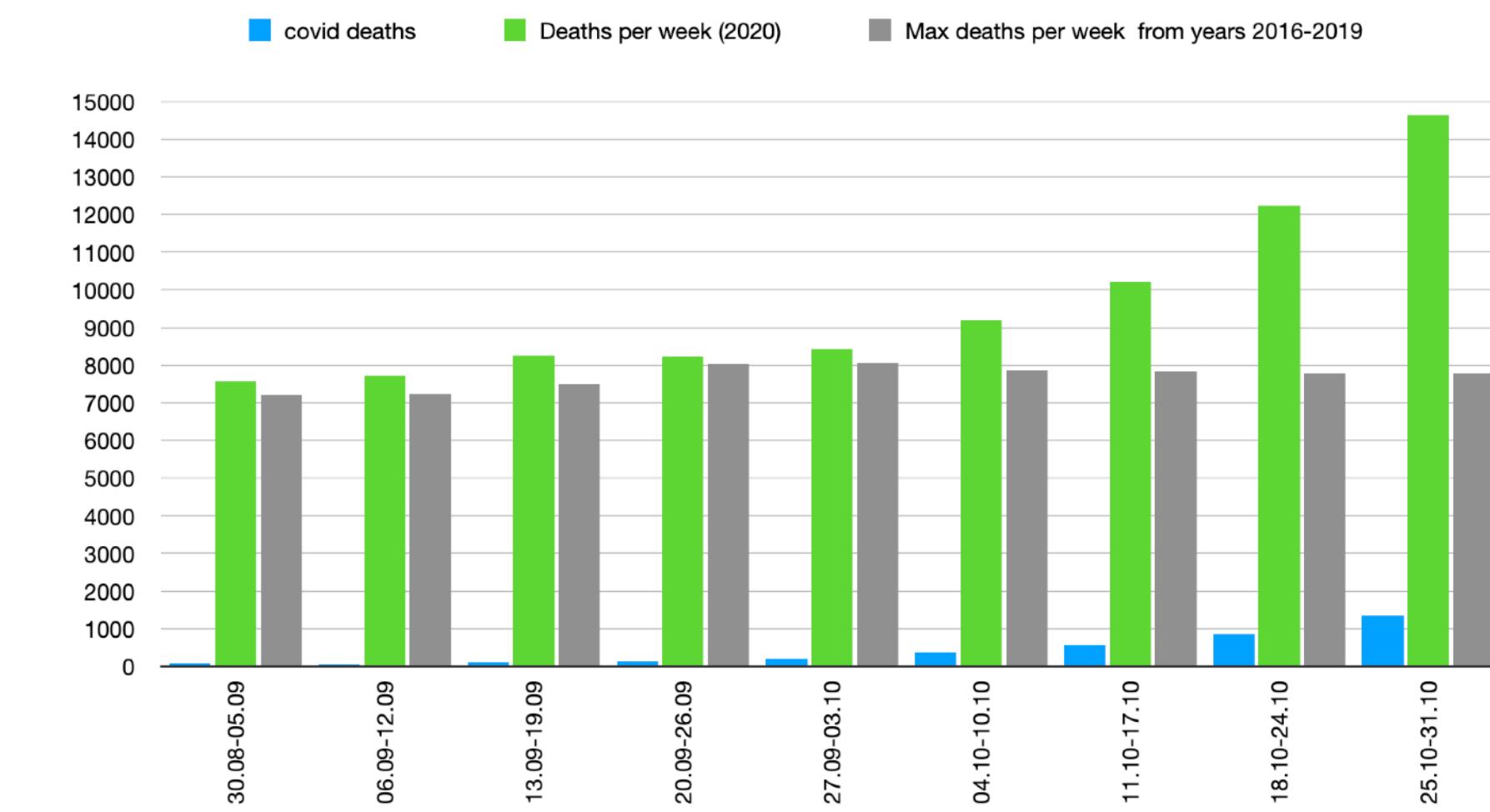
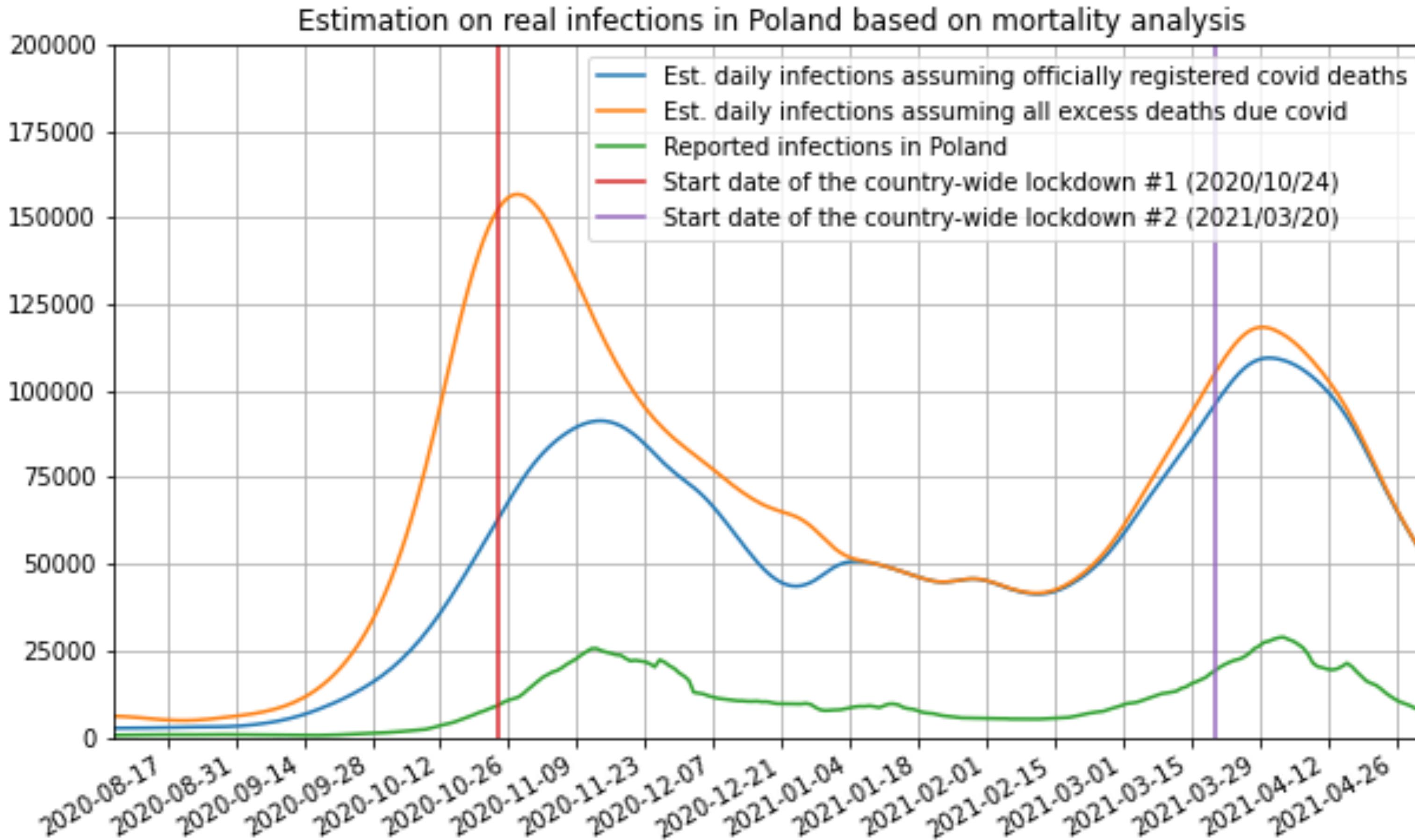
Efficient contact tracing and quick detection of cases is crucial: what happened in September 2020?



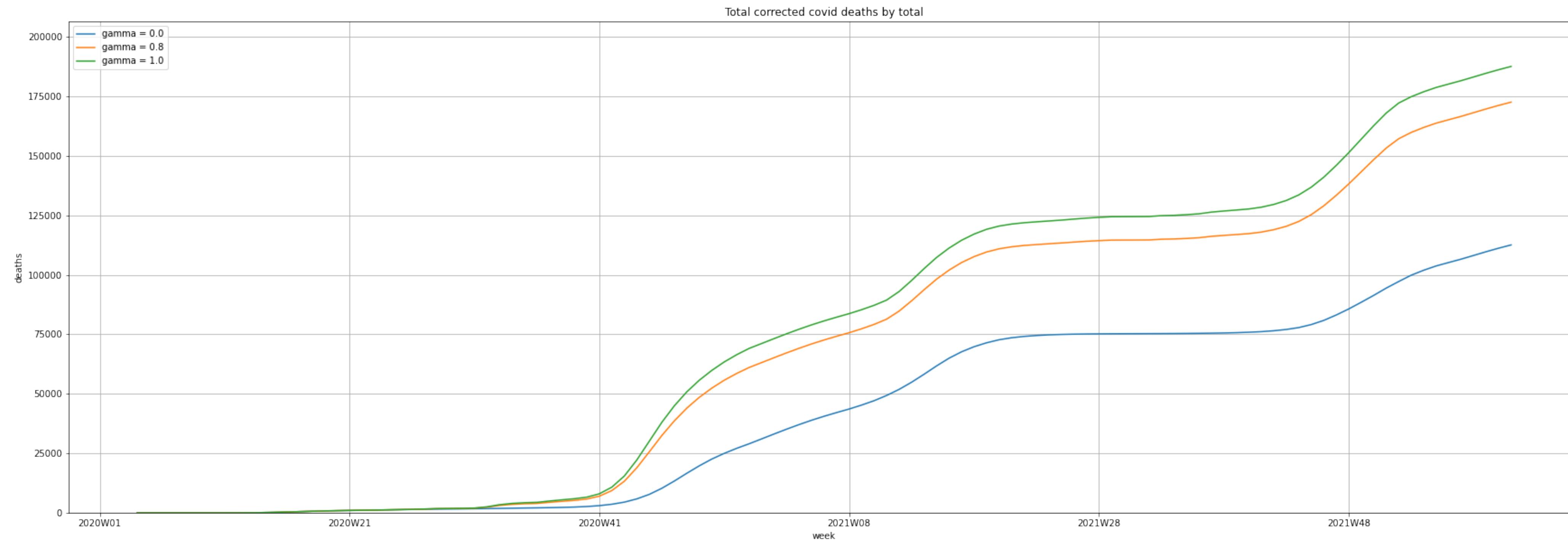
Testing probability versus tracking detection probability (for several fixed contact reduction f) :
 The localisation of Poland over time within the heat map



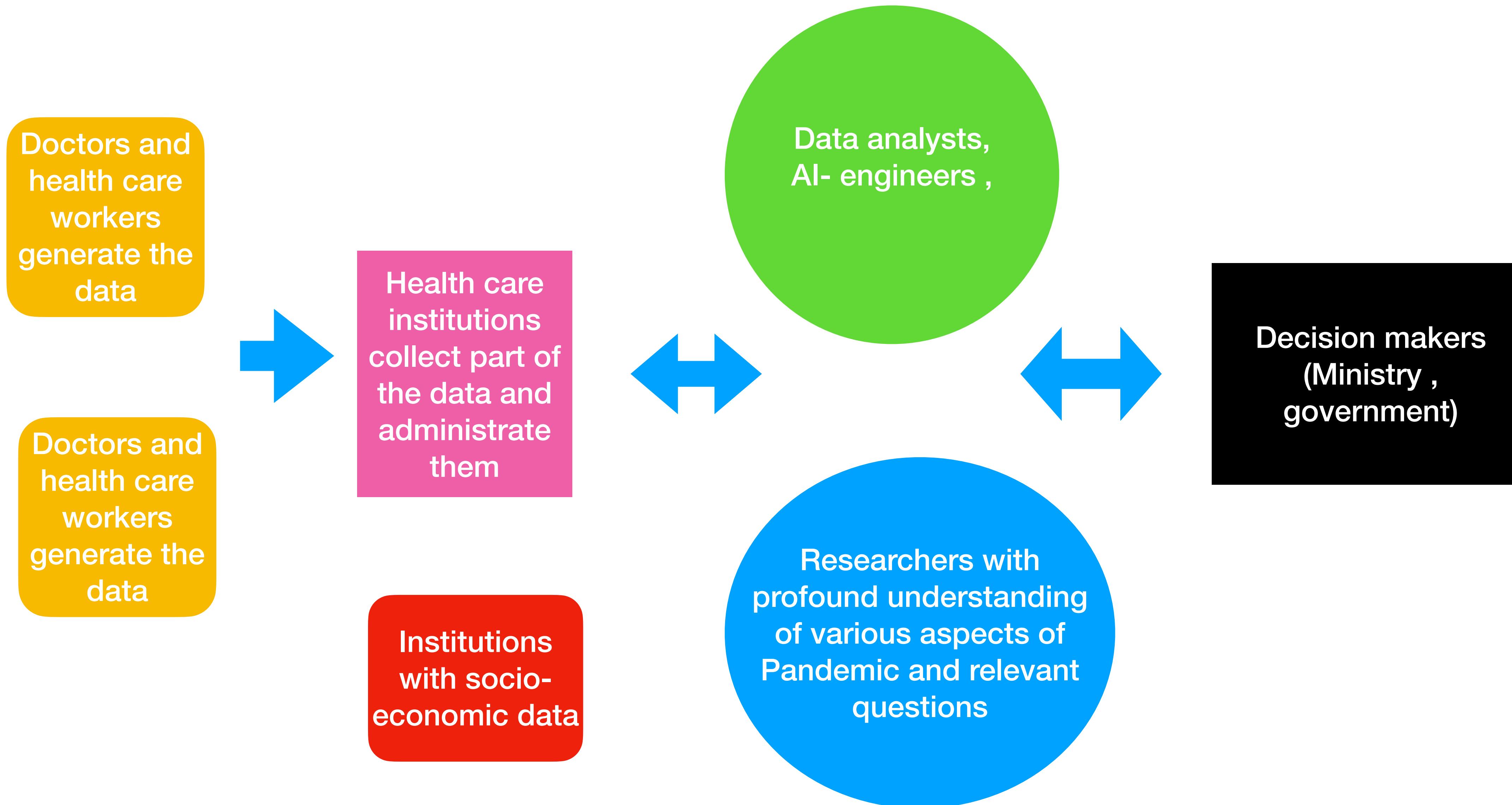
Bad data bad decisions



Excess death Poland



Not much harmony between the players



At the end of the day everybody has only small data

And therefore we still know very little about

- Infectivity and detailed transmission dynamics
- Fraction of asymptomatic cases
- Infection fatality rate for different age groups
- Infection relevant contact structure

MOCOS model in a pill

- Event driven microsimulation model of COVID 19 epidemics
- Continuous-time distributions of disease progression
(developing symptoms, self-quarantine)
- Disease progression on the synthetic population based on available statistical data
- Random and varied structure of intra-household and out-household contacts
- Assessing social intervention measures:
quarantine, targeted testing, contact tracing, contact reduction, contact tracking app
- Extendable and adjustable to specific scenarios.

Input parameters

- Population with basic features: age, gender, household assignment
- Special features: social competence, workplace, high-risk profession, (comorbidity , region assignment, geolocation)

There is no hard limit on population size

- VM with 32GB RAM can simulate pandemics on Poland – size population)
- Configuration JSON specifying kernel intensities, initial conditions, detection delays, path to the generated population file
- Disease progression distributions

Example attributes:

- ▶ Basic features:
 - ▶ Agent id: 102564
 - ▶ Age: 23 yo
 - ▶ Gender: male
 - ▶ Household: id 410256
(Living with 4 other household members: 47 yo female, 42 yo male, 19 yo female, 15 yo female)
- ▶ (Optional) Other features:
 - ▶ Social competence: friendly (factor 3.32)
 - ▶ Workplace: id 5 (coworking with 20 other people with ids: [...])
 - ▶ High-risk profession: No
 - ▶ Comorbidity diseases: No
 - ▶ Smoking status: No
 - ▶ Region assignment: Pomerania
 - ▶ Geolocation: 54.372158, 18.638306



More technically about events

Event structure

- Time (4 bytes)
- subject_id (4 bytes)
- source_id (4 bytes)
- event_kind (1 byte)
- event_sub_kind (1 byte)

Types of events

- Contact
(Infection contact through one of kernels)
- Disease Progression
 - Become Infectious
 - Mild Symptoms
 - Severe Symptoms
 - Recovery
 - Death
- Home Treatment
- Hospitalization
- Detection
- Quarantine extension
- Tracking

Precomputing disease progression times to optimize the simulation

- For each person in the sample population, following random delay times are calculated in advance:
 - T0 – incubation time
 - T1 – developing mild symptoms/contact with healthcare
 - T2 – developing severe symptoms/hospitalization
 - T^* - death time realized with death probability correlated with age
 - TR – recovery time according to WHO

Above delay times will be realized under the condition that the infection will happen for a specific person

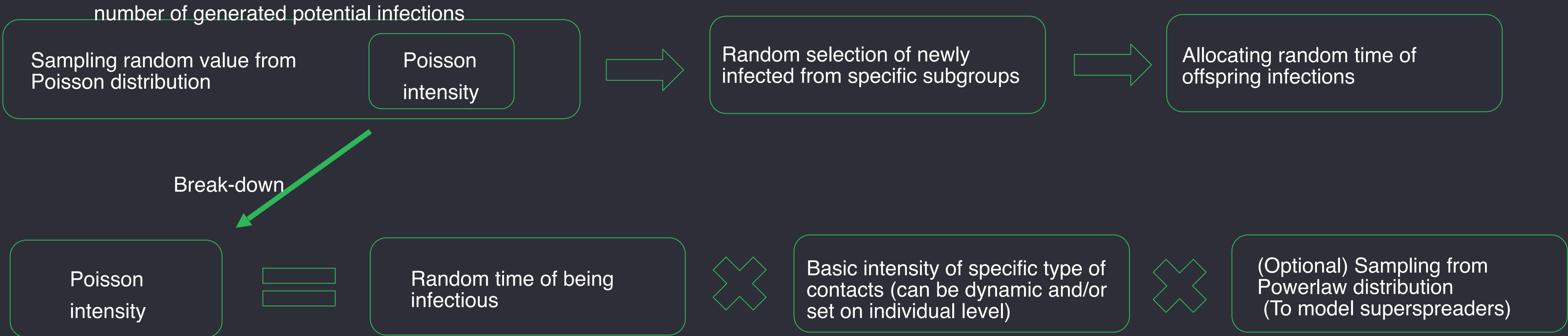
Overview of kernels

We model potential infections as easy-to-interpretable stochastical kernels that are generating induced infection-contact networks during the simulation

- ▶ Household kernel (modelling in-household contacts)
- ▶ Sporadic contact kernel (e.g. contacts via shopping or in public transport)
- ▶ Friendship kernel (modelling contacts within a group of friends or out- household family)
- ▶ Hospital kernel (modelling contacts in hospitals)
- ▶ Age dependent kernel (e.g. contacts in schools)
- ▶ Workplace kernel
- ▶ Geographical kernel (taking into account distance dependence of contact structure)

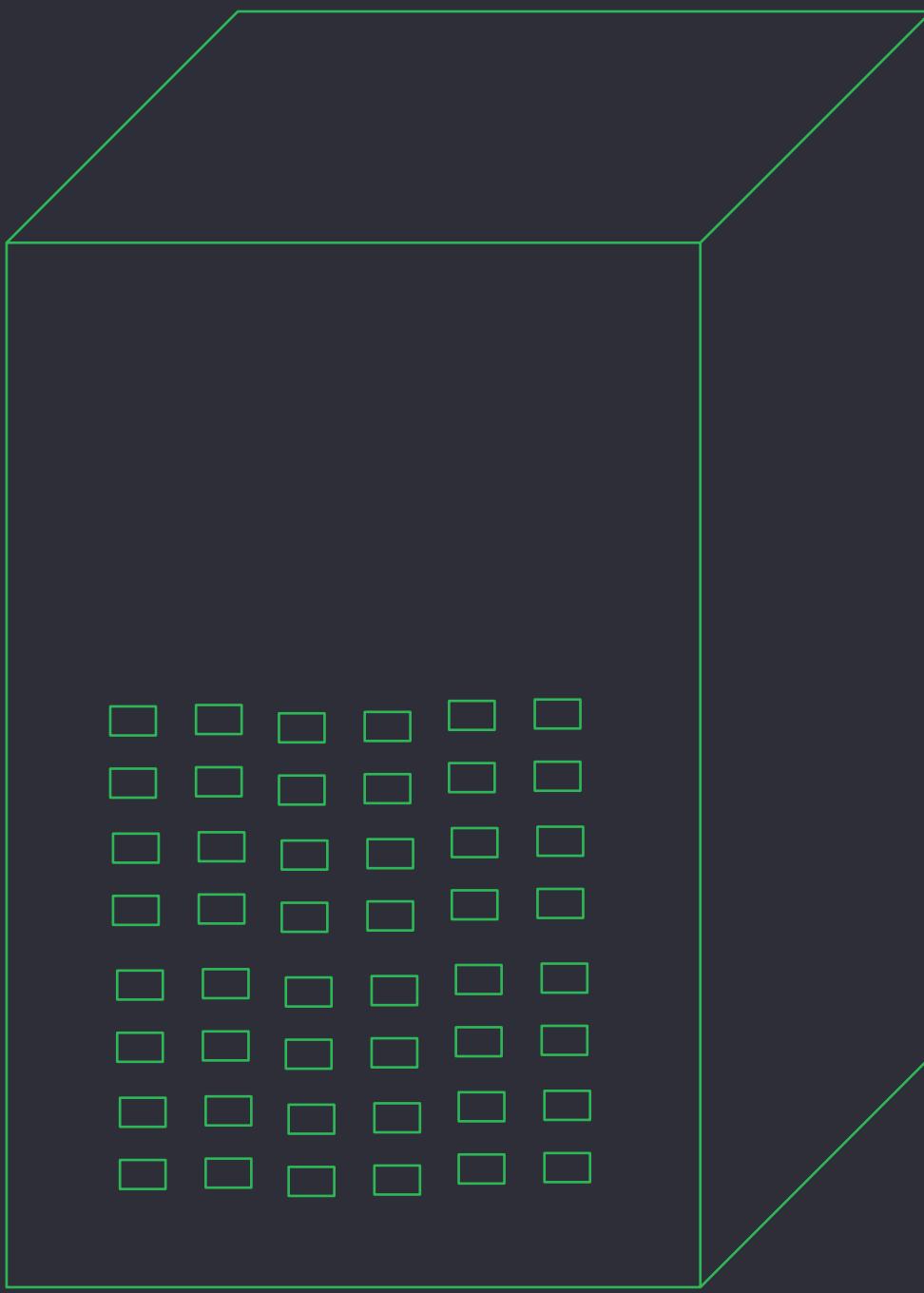
Kernels as a way of describing local spread of the epidemics

We model potential infections as easy-to-interpretable stochastical kernels that are generating induced infection-contact networks during the simulation



Infrastructure: Wroclaw Supercomputing and Networking Center (WCSS)

- Cluster BEM: 860 TFLOPS, 74.6GB memory, 1600 Intel Xeon processors with ~22k cores
- Running tasks through global queue manager PBS
 - WCSS team has created a dedicated priority queue “*-q covid-19*” exclusively for our team



Infrastructure: Wrocław Supercomputing and Networking Center (WCSS)

- Resources of typical task

generating 100 trajectories for single set of parameters

- Simulation for Wrocław – 1CPU, 4GB memory, processing time up to 15min, artifacts up to 500MB
- Simulation for Poland – 1CPU, 32GB memory, processing time up to 16h, artifacts up to 32GB

- Typical experiment

861 tasks – 2d “grid” evaluating each combination of two parameters

e.g. probability of contact tracking & probability of detecting mild cases

- Full artifacts from a single typical experiment weigh up to 7TB – require postprocessing on-site

Output from the model

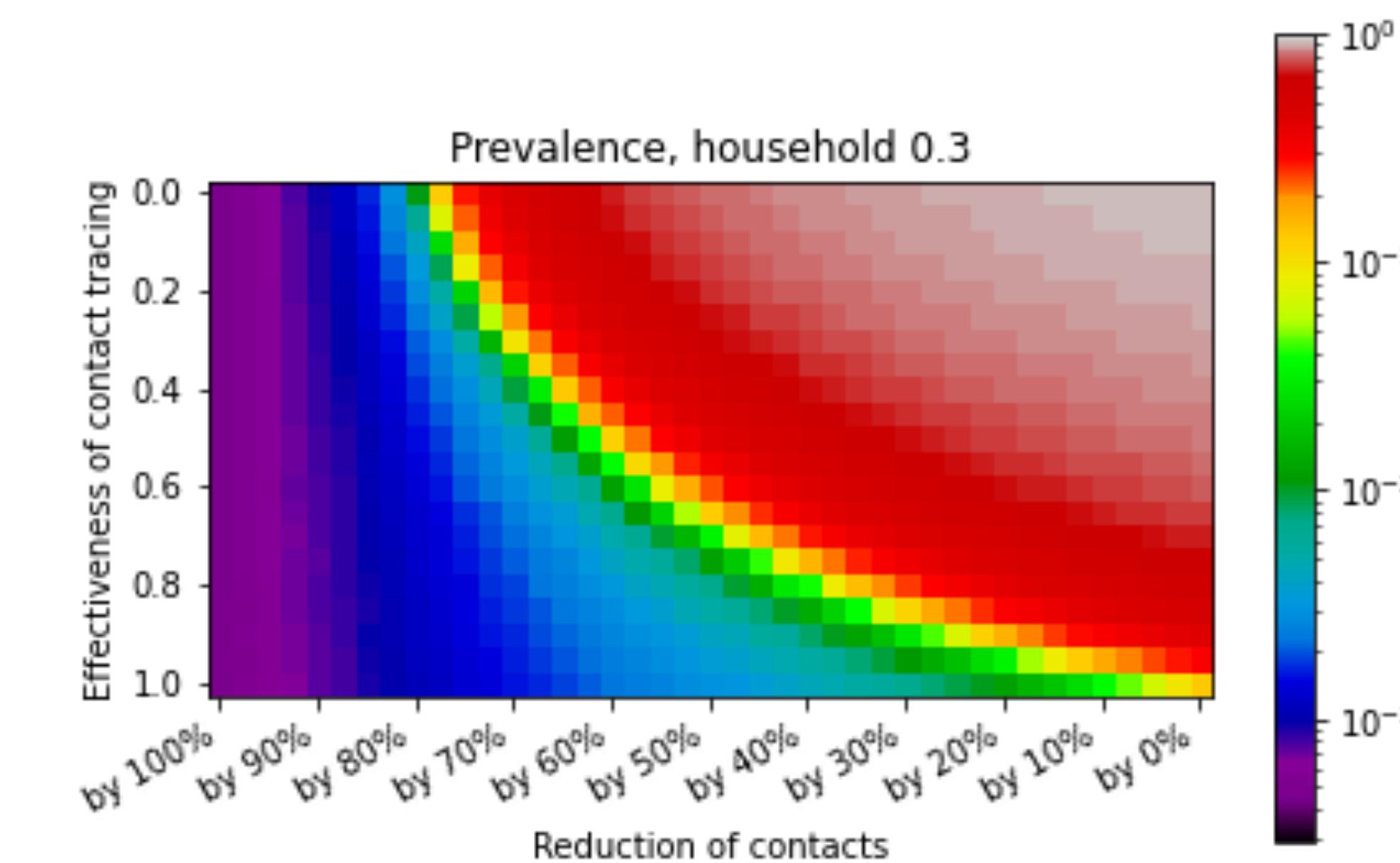
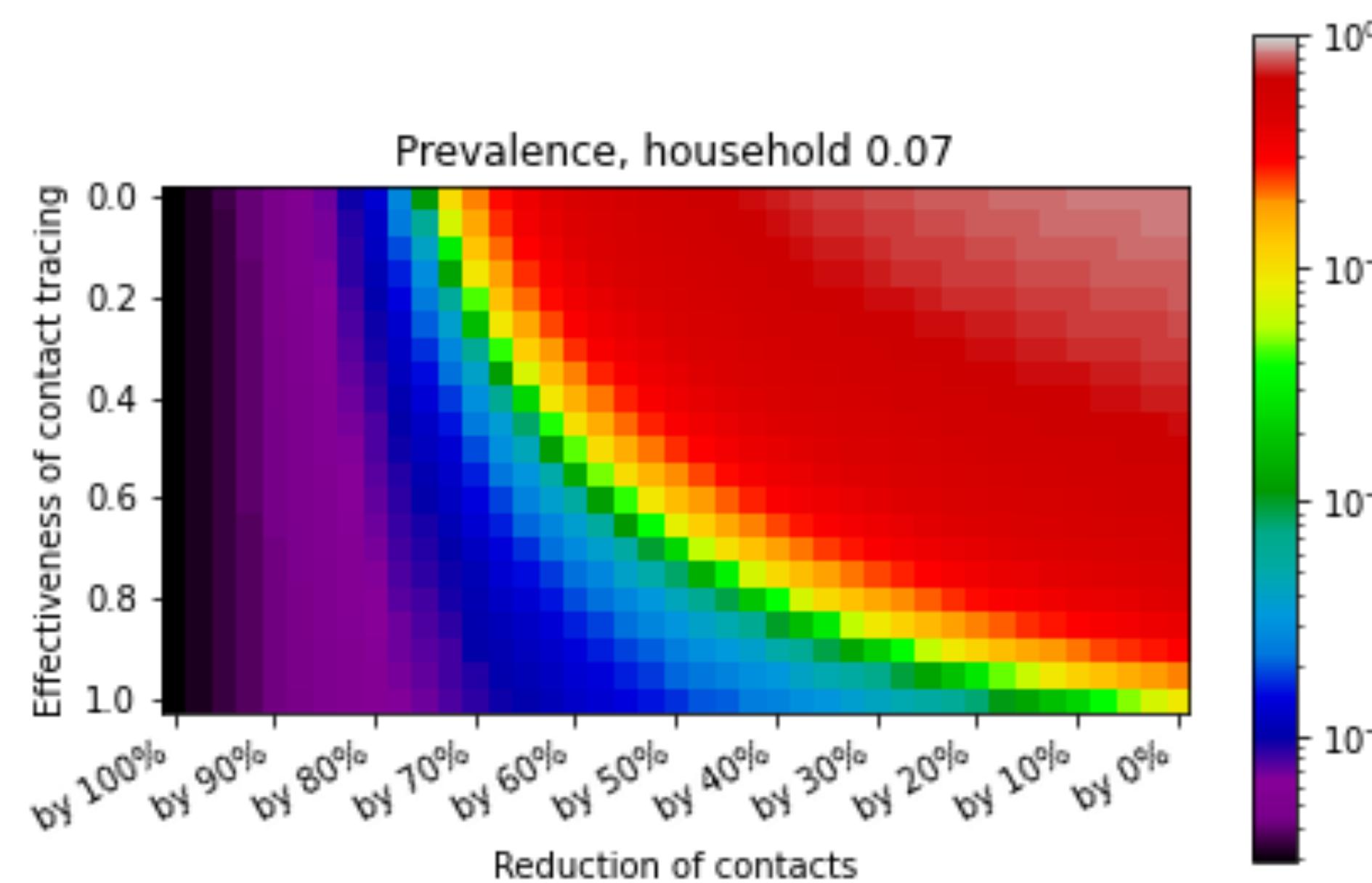
- Trajectories: infections, detections, number of hospitalized, number of active cases, number of quarantined (Possibility to fit stochastic trajectories with observed data)
- Age or gender specific trajectories or histograms,
- Disease progressions and outcome,
- Whether specific ICU limit was surpassed within a specific timeframe,
- Confidence intervals for number of reported cases or daily deaths
- The full forest of infections to recreate infection clusters along with infection ways (names of clusters)

Output: structural heat maps (Poland)

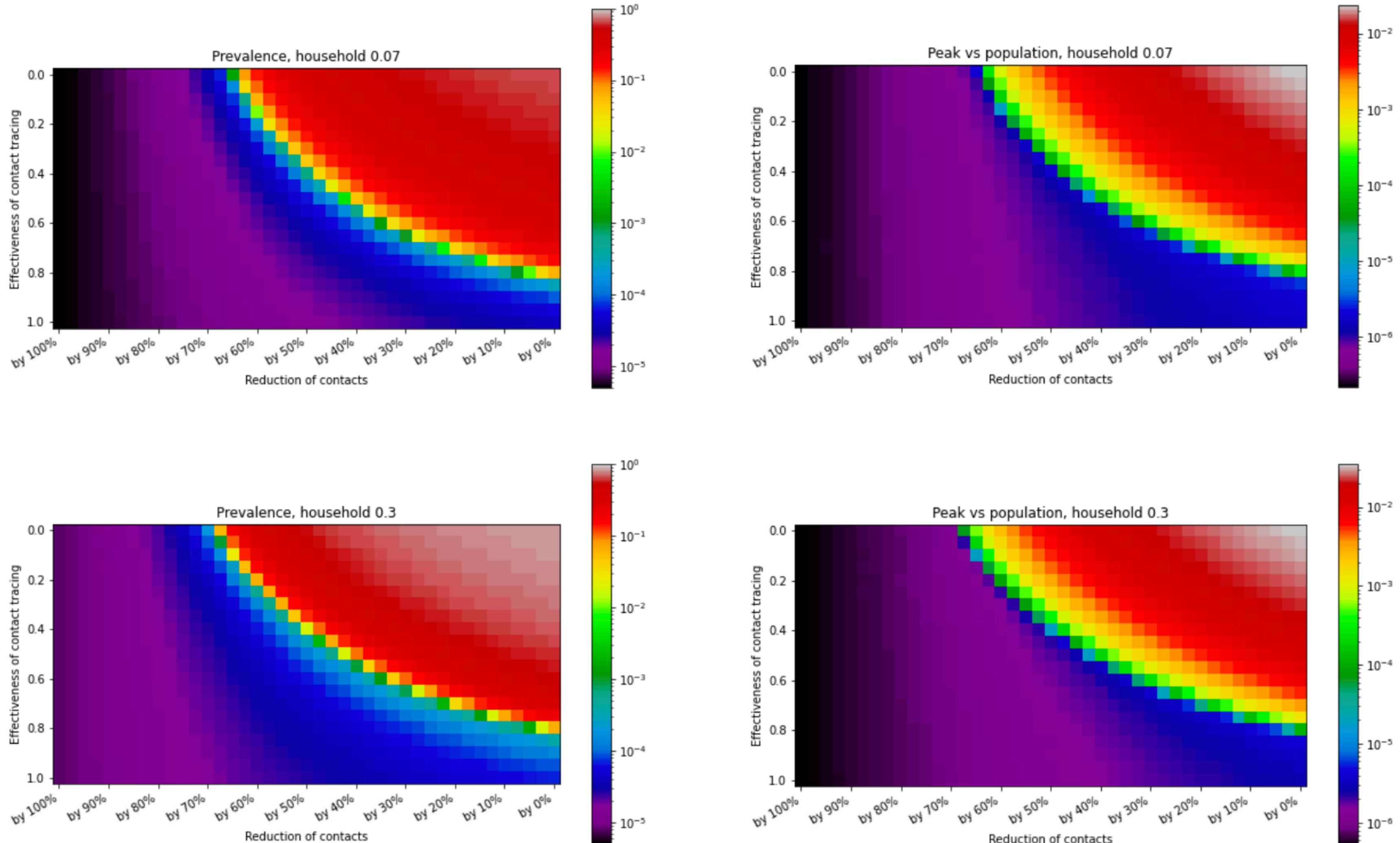
Heatmaps show epidemic outcomes (the color) as function of parameters relevant in controlling epidemics

Key parameters are :

- f : degree of contact reduction
- q' : probability to uncover mild cases
- b : success probability in contact tracing
- D : time delays for testing and tracing



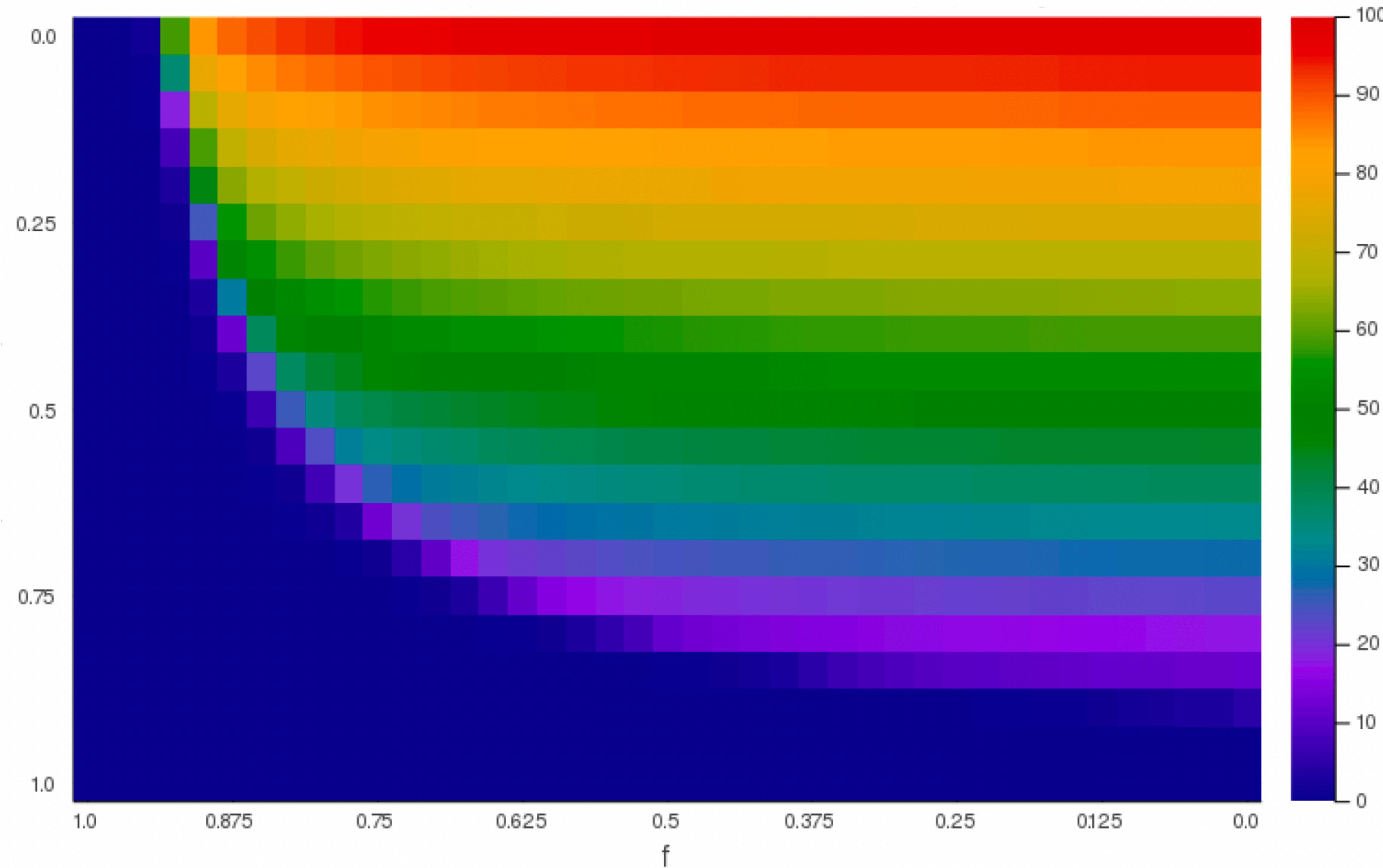
Similar heat map as before but for more efficient testing ($q'=0.6$ instead of 0.3)



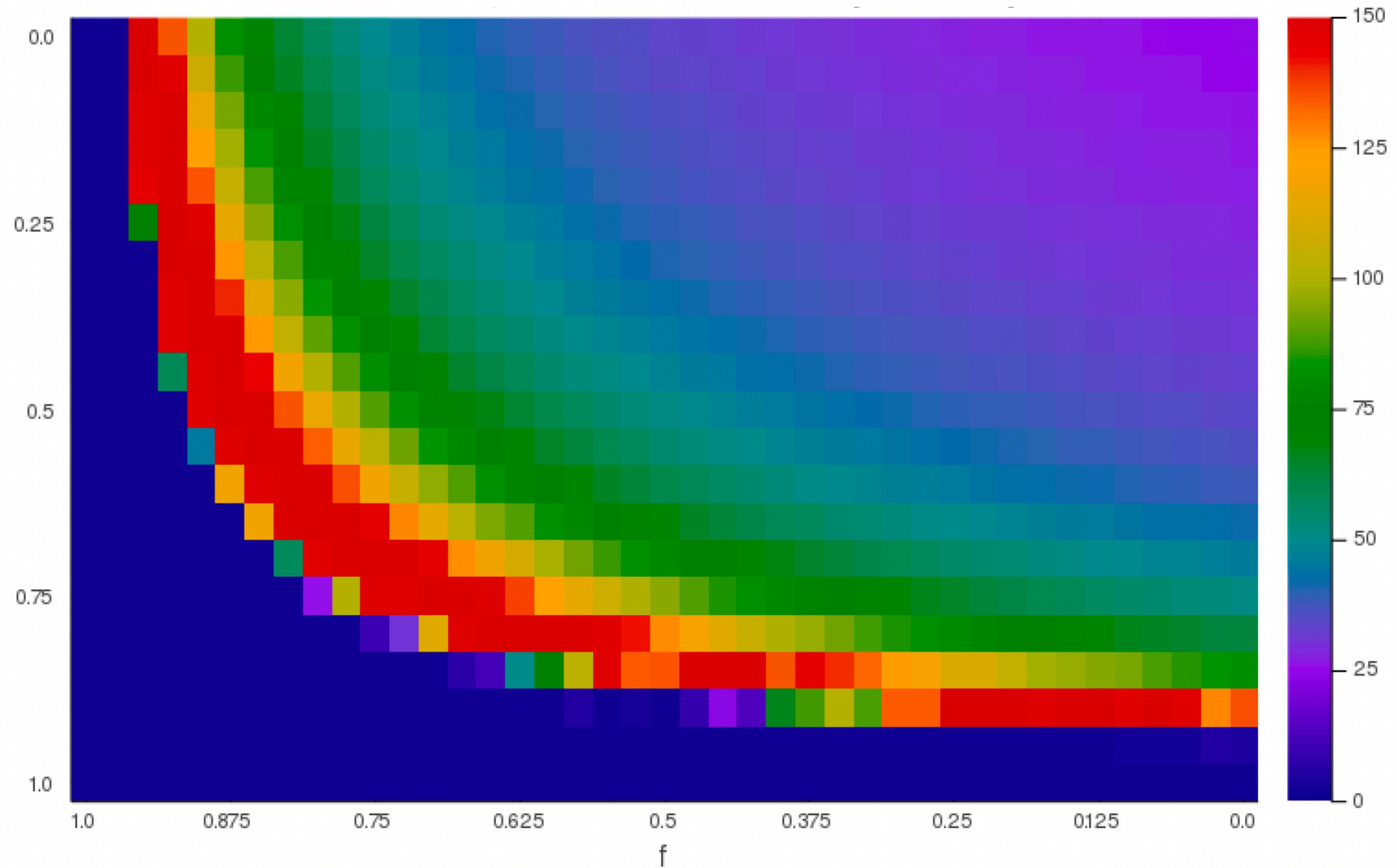
The inner part of the melon is the dangerous regime : $R>1$

The outside of the melon is the subcritical regime: $R<1$

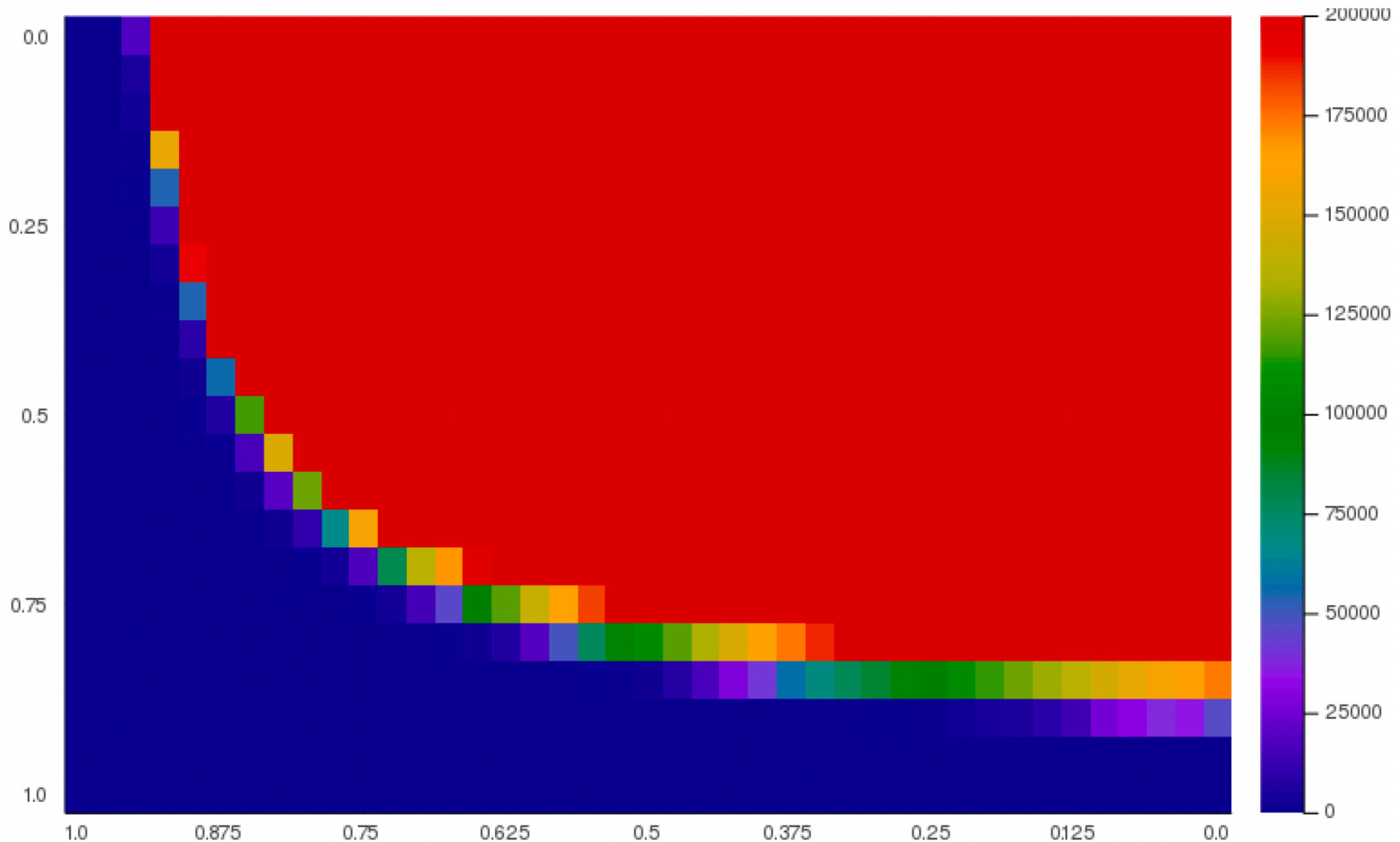
Immunisation versus restrictions heat map for omicron: prevalence



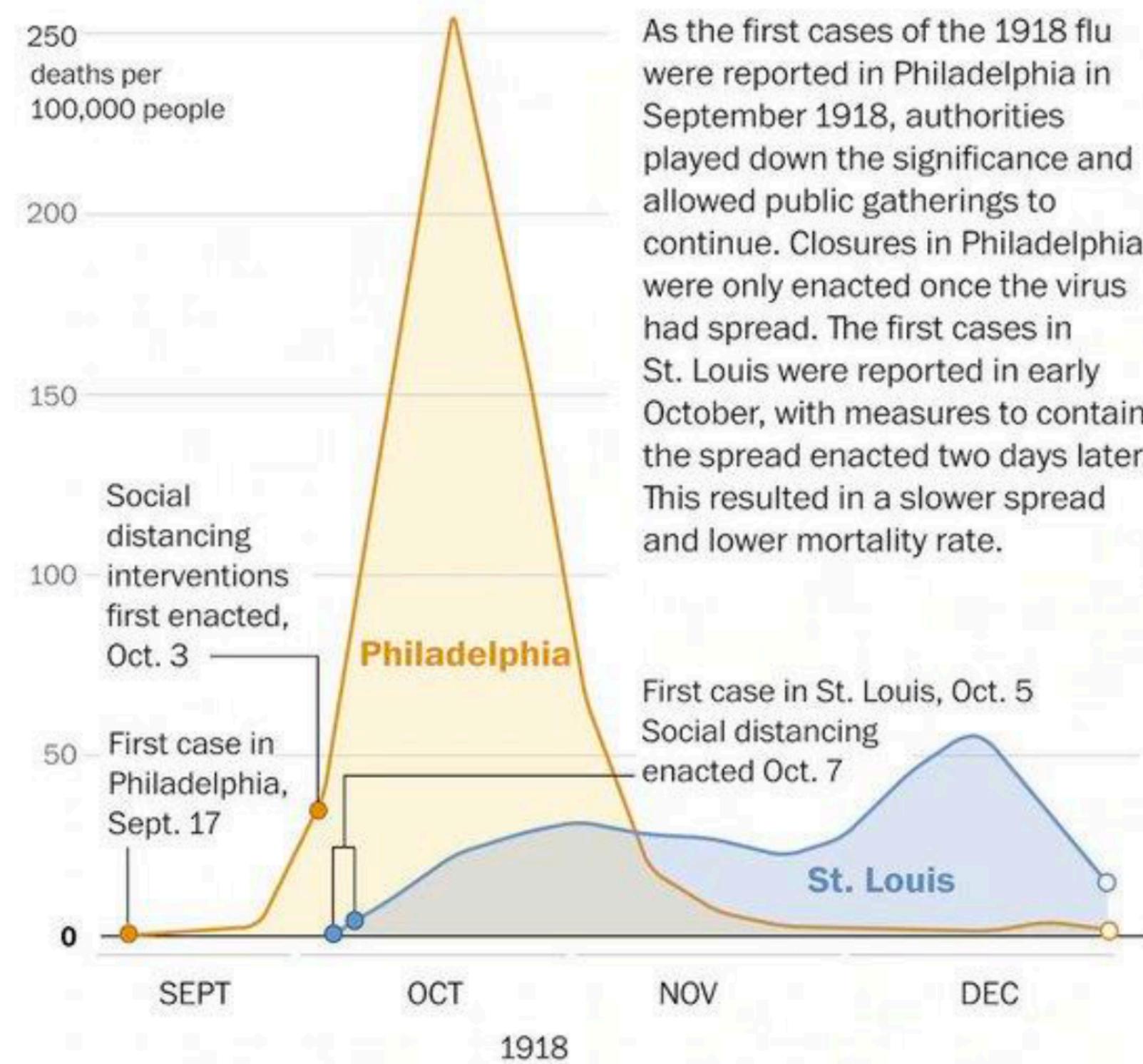
Immunisation versus restrictions heat map for omicron: time till max



Immunisation versus restrictions heat map for omicron: max cases



Effects of social distancing on 1918 flu deaths



Sources: "Public health interventions and epidemic intensity during the 1918 influenza pandemic" by Richard J. Hatchett, Carter E. Mecher, Marc Lipsitch, Proceedings of the National Academy of Sciences May, 2007. Data derived from "Public health interventions and epidemic intensity during the 1918 influenza pandemic" by Richard J. Hatchett, Carter E. Mecher, Marc Lipsitch, Proceedings of the National Academy of Sciences May, 2007.

TIM MEKO/THE WASHINGTON POST

During the 1918 Spanish Flu

- Philadelphia did not practice social distancing and badly suffered
- St Louis did implement social distancing early



1918



#abc7eyewitness

ANTI-MASK MEETING

TONIGHT (Saturday) JAN. 25

DREAMLAND RINK

To Protest Against the Unhealthy Mask Ordinance

Extracts will be read from State Board of Health Bulletin showing compulsory mask wearing to be a failure.

Eugene E. Schmitz and other interesting speakers.

Admission Free.

MOCOS group

- Simulations and illustrations based on the model and data analysis:
Marcin Bodych, Tomasz Ożański, Marek Bawiec, Ewa Szczurek
- MOCOS Wrocław: Barbara Adamik, Marek Bawiec, Viktor Bezborodov, Marcin Bodych, Tyll Krüger, Agata Migalska, Tomasz Ożański, Barbara Pabjan, Ewa Skubalska-Rafajłowicz, Ewaryst Rafajłowicz, Wojciech Rafajłowicz, Piotr Sobczyk, Piotr Szymański, Tyll Krüger
MOCOS Warszawa: Przemysław Biecek, Tomasz Cąkała, Anna Gamin, Krzysztof Gogolewski, Barbara Poszewecka, Daniel Rabczenko, Magdalena Rosińska, Michał Startek, Ewa Szczurek
- MOCOS Germany: Wolfgang Bock, Jan Pablo Burgard, Thomas Götze
- MOCOS Philippines: Johniel Babiera, Jinky B. Bornales, Randy L. Caga-anan, Dubhe Joy S. Carmen, Gabriel C. Engcong, Yashika Jayathunga, John Alfred M. Liwanag, Jennifer Joyce M. Montemayor, Ruth P. Serquiña, Dante Dinawanao

References

- MOCOS web page: www.mocos.pl
- MOCOS preprint “Mitigation and Heard immunity strategy for COVID-19 is like to fail “ (<https://www.medrxiv.org/content/10.1101/2020.03.25.20043109v1.full.pdf>)
- MOCOS code: <https://github.com/mocos-covid19>
- Random graph reference: Bollobas, B., Janson, S., & Riordan, O. (2007). The phase transition in inhomogeneous random graphs. *Random Structures & Algorithms* 31(1), 3-122
- COVID- 19 statistical data collections and visualisations:
<https://apps.health-atlas.de/covid-19-grapher/>
<https://www.worldometers.info/coronavirus/>
- US forecast hub: <https://github.com/reichlab/covid19-forecast-hub>