The MOCOS COVID - 19 model

Epidemic models on networks (agent based models)

- agents with individual properties

- agent type dependent contact structure

- random, individual progression of disease

- time and process dependent change of environment

- Targetet complex counter-measures (NPI's e.g. contact tracing

Output MOCOS model group

Forecasts

- Short time forecast < 4 weeks
- Scenario forecast: several months

Effect of intervention scenarios

- Non-pharmaceutical interventions: testing, contact tracing, contact restrictions, quarantine
- Vaccination

Structural insights

- Identifying structural socio-economic risk factors
- Impact and estimation of key medical parameters
- Epidemic thresholds
- Mathematical analysis

Epidemic takes place on network of contacts

one needs:

- a network $G(V, E)$ on which process takes place

    - note: the infection process might change the network

- specification of the states of infection:

    -
$$\left\{ \begin{array}{c} 0 \triangleq \text{ susceptible (noninfected)} \\ 1 \triangleq \text{infected (sub-states } 1a, 1b\ldots), 2 \triangleq \text{recovered, immune,..} \end{array} \right\}$$

- state can also be a continuos variable e.g. the infectivity changes continuously over time (example HIV)
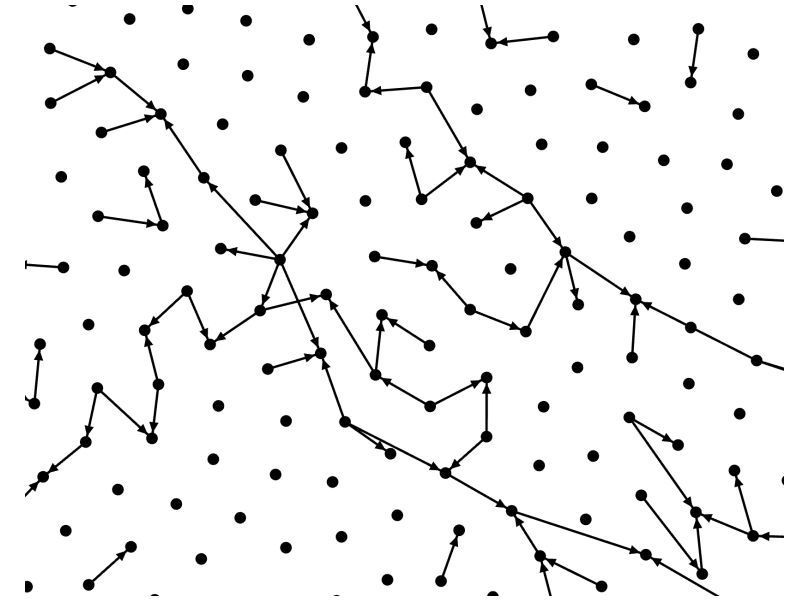
Infection graph is a subgraph of the contact graph

Epidemic models on networks (agent based models)

- types $x \in S$,

- infection states of individuals $\chi(i, t, x_i) \in A$

- contacts: $\kappa(x_i, y_j)$ defines probability of contact between individual i and j

- transmission probability (depending on infection states of individuals)

- both state and contacts could be time dependent

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

#102564

#102565

#102563

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

MOCOS – MOdelling COronavirus Spread

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

number of generated potential infections

Sampling random value from Poisson distribution — Poisson intensity	→	Random selection of newly infected from specific subgroups	→	Allocating random time of offspring infections

Break-down

Poisson intensity **=** Random time of being infectious **✕** Basic intensity of specific type of contacts (can be dynamic and/or set on individual level) **✕** (Optional) Sampling from Powerlaw distribution (To model superspreaders)
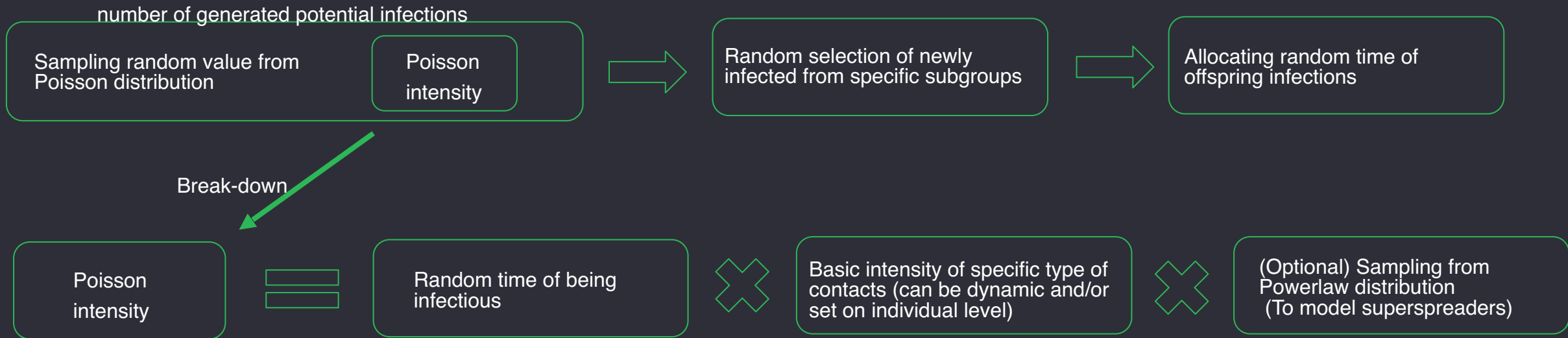
Infrastructure: Wroclaw Supercomputing and Networking Center (WCSS)

- 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

MOCOS – MOdelling COronavirus Spread
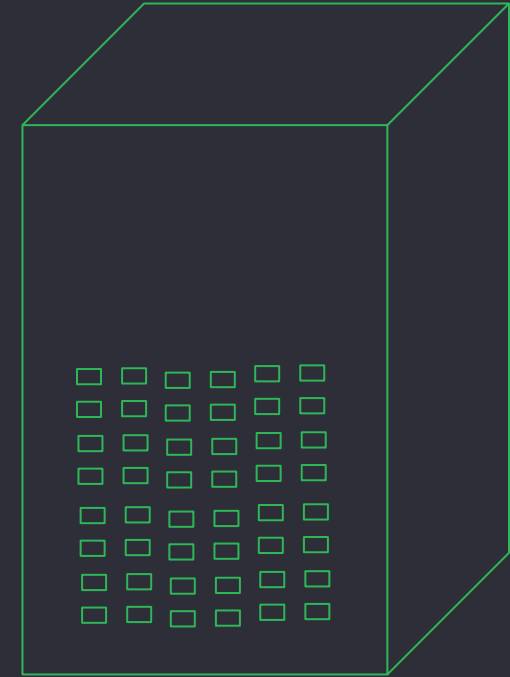
Infrastructure: Wroclaw Supercomputing and Networking Center (WCSS)

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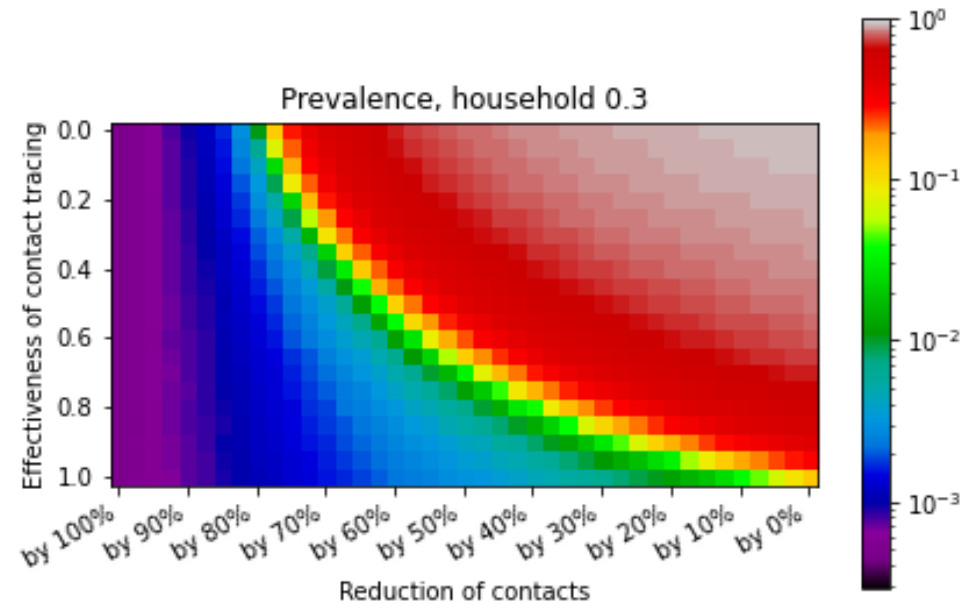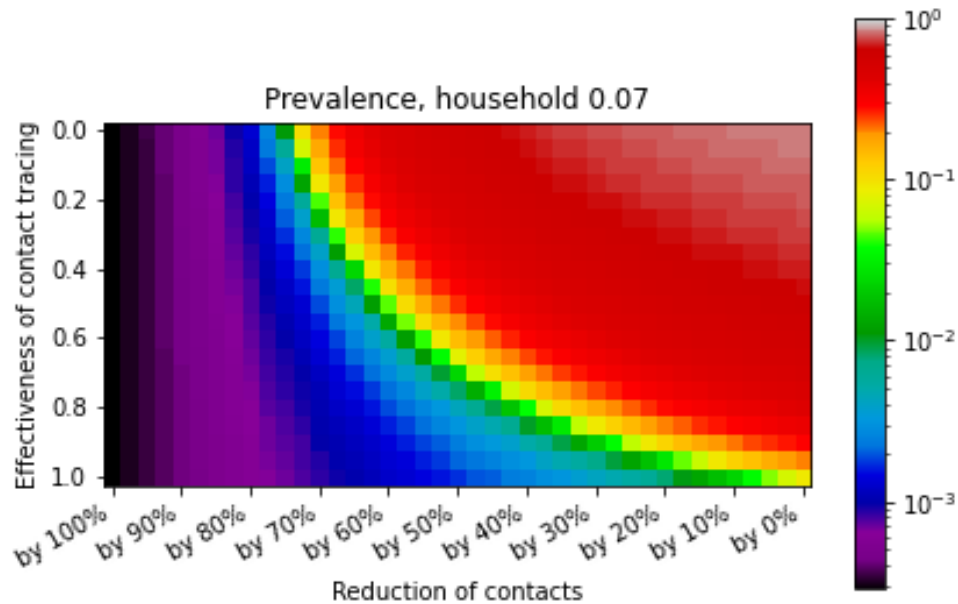
Similar heat map as before but for more efficient testing (q'=0.6 instead of 0.3)

Prevalence, household 0.07

Peak vs population, household 0.07

Prevalence, household 0.3

Peak vs population, household 0.3
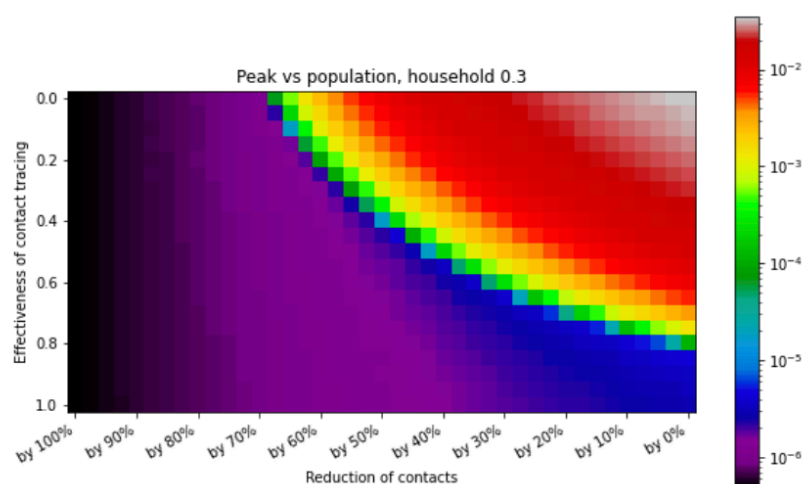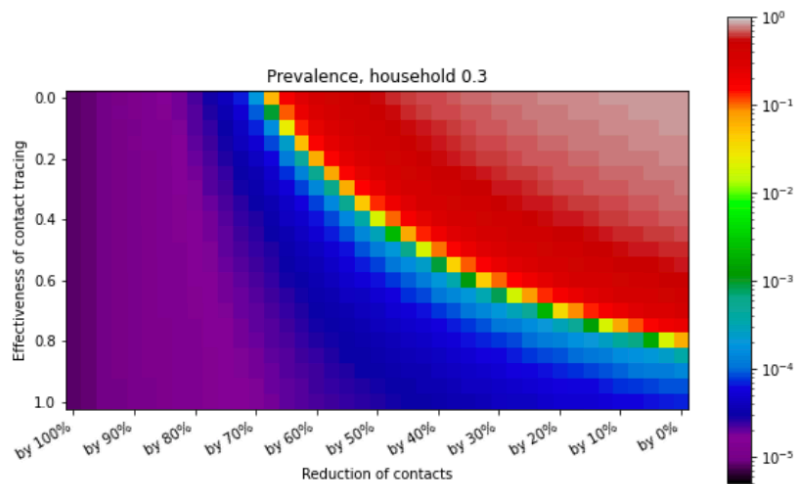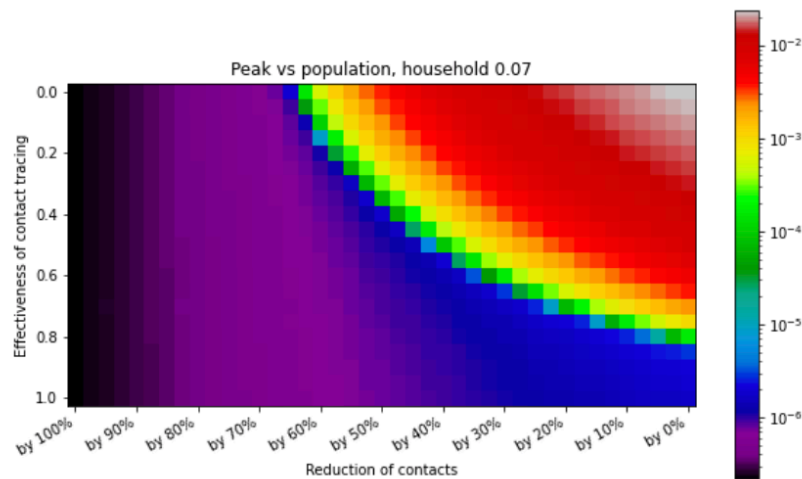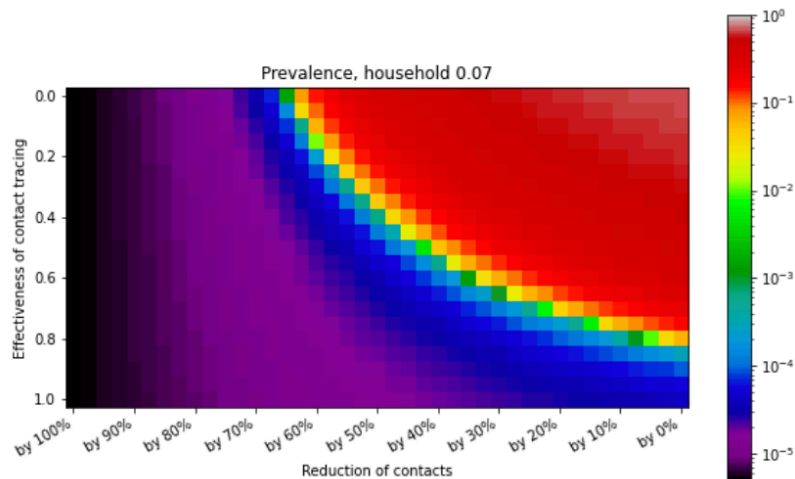
The inner part of the melon is the dangerous regime : R>1

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

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Tracing versus testing for 50% restriction and 40% vaccination (British variant)
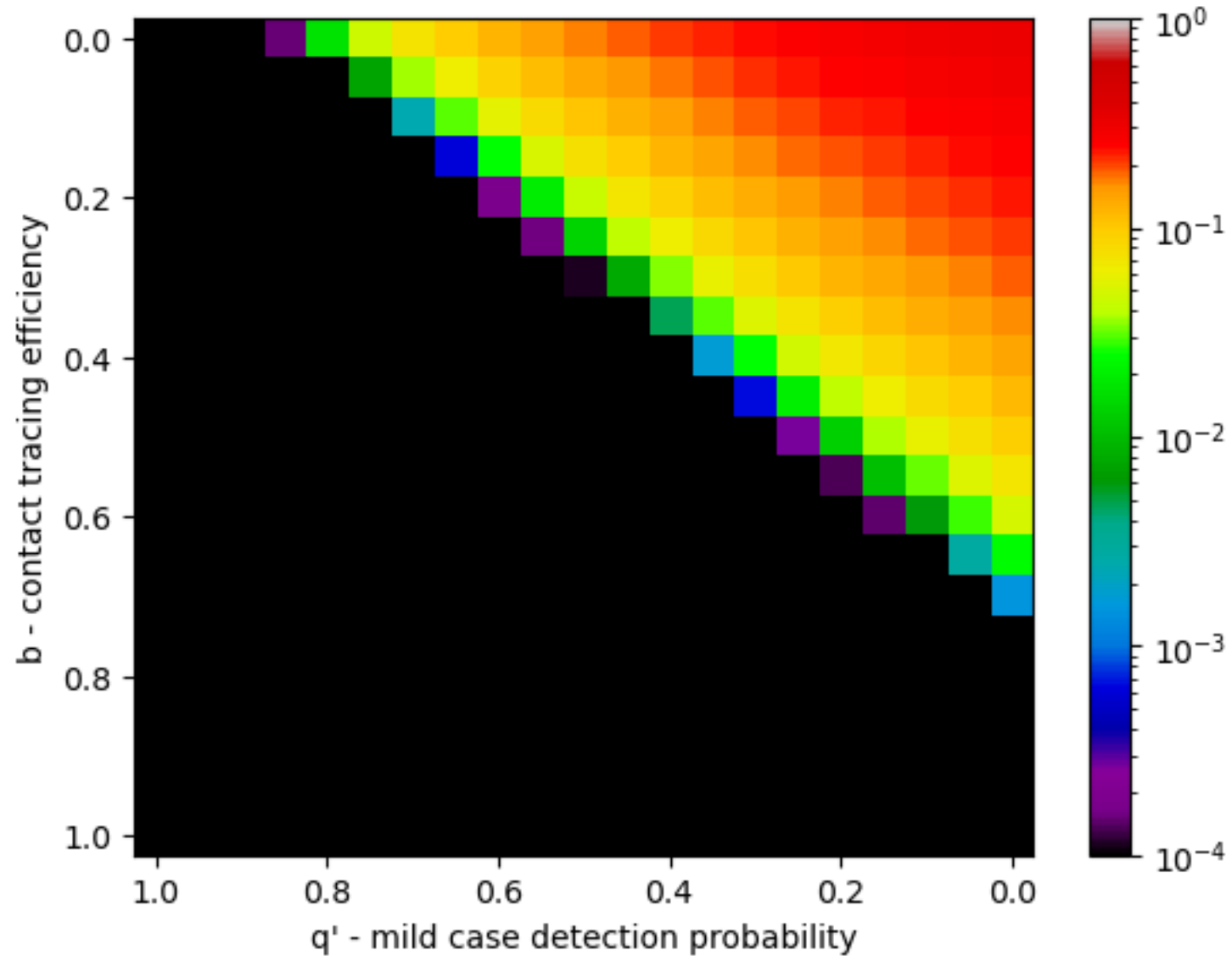
Epidemic thresholds for tracing versus testing for different levels of restriction and 40% vaccination (British variant)
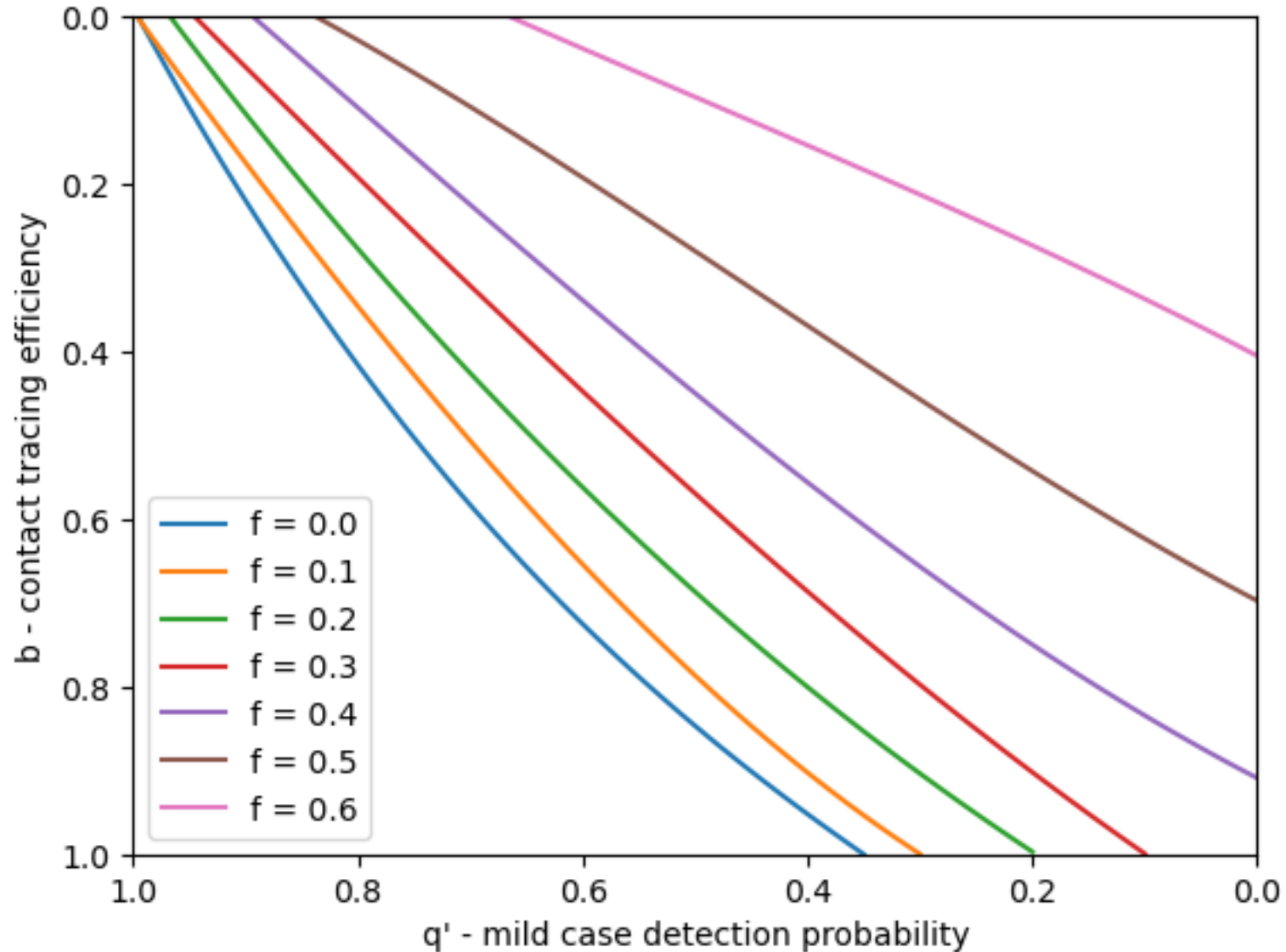
Output: localisation within heat maps
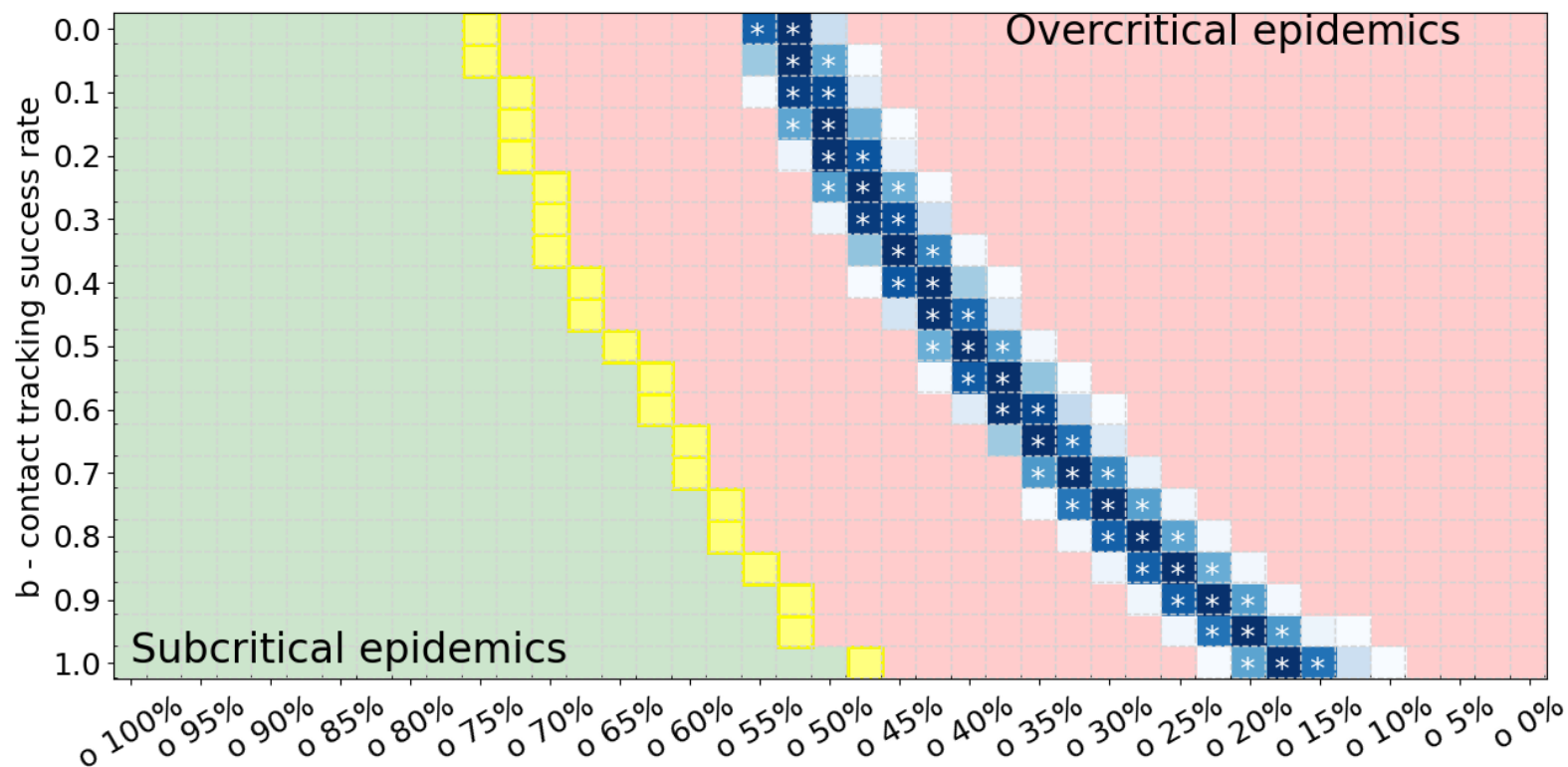
A: strong lockdown

B: soft lockdown

C: actual lokdown

* : actual localisation
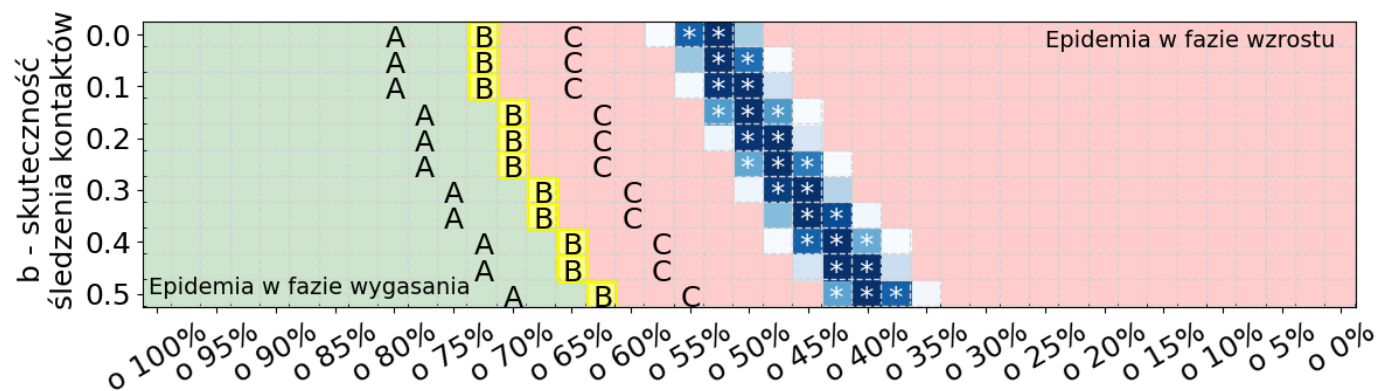
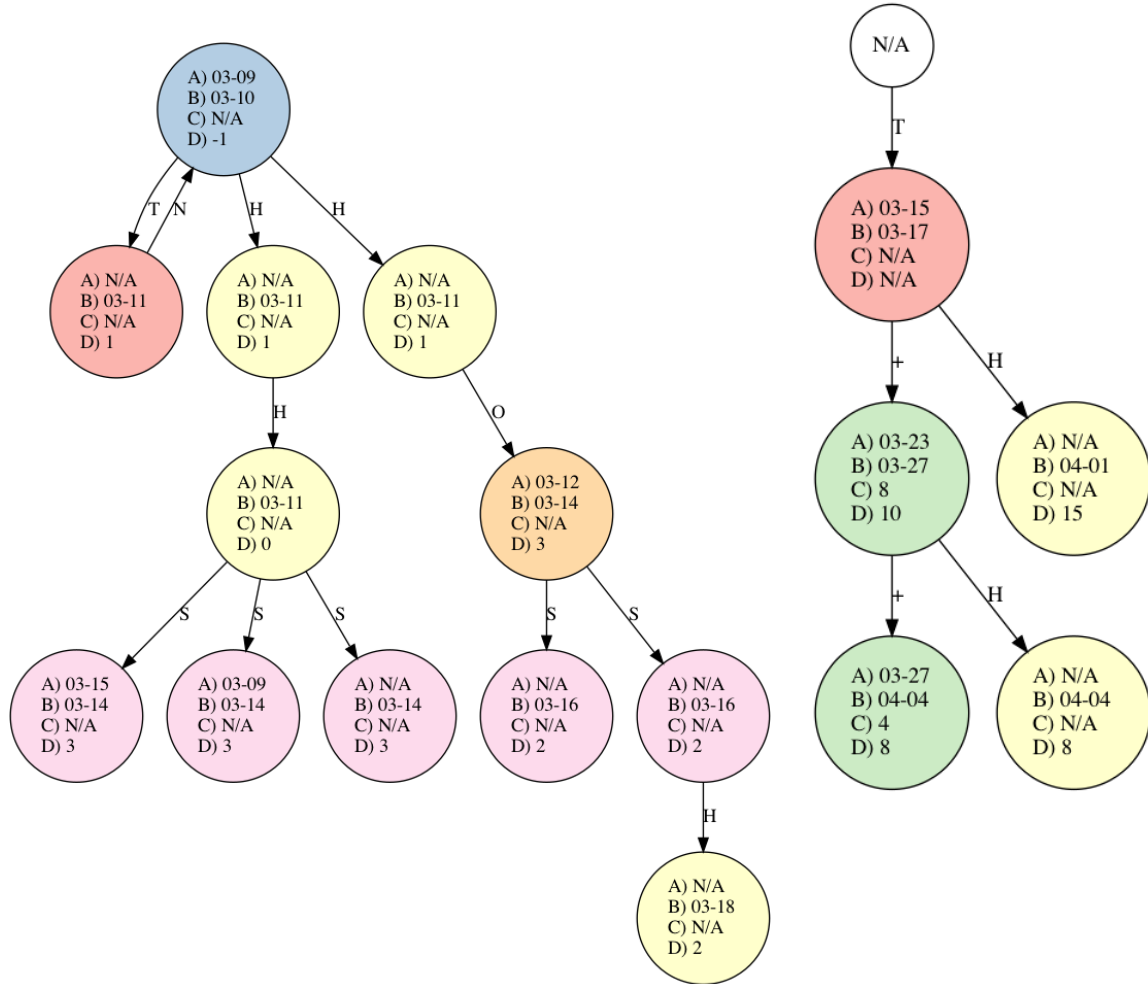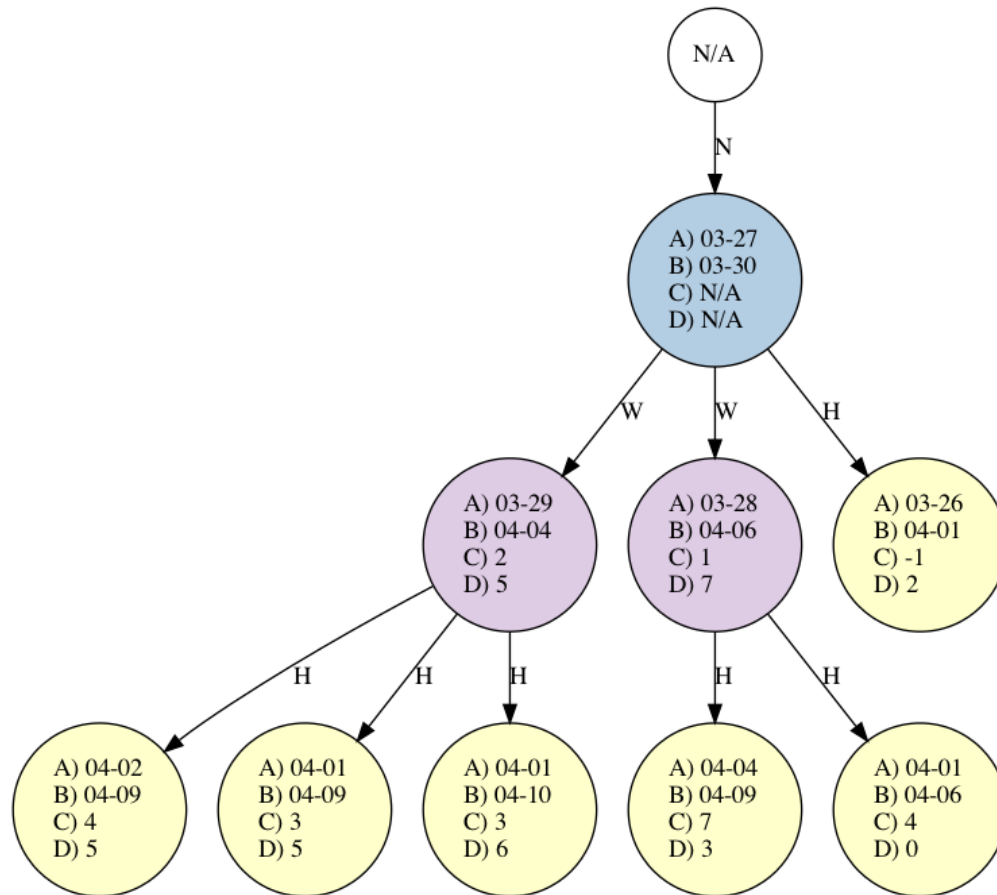# Output: forecasts as weighted ensemble of sample paths
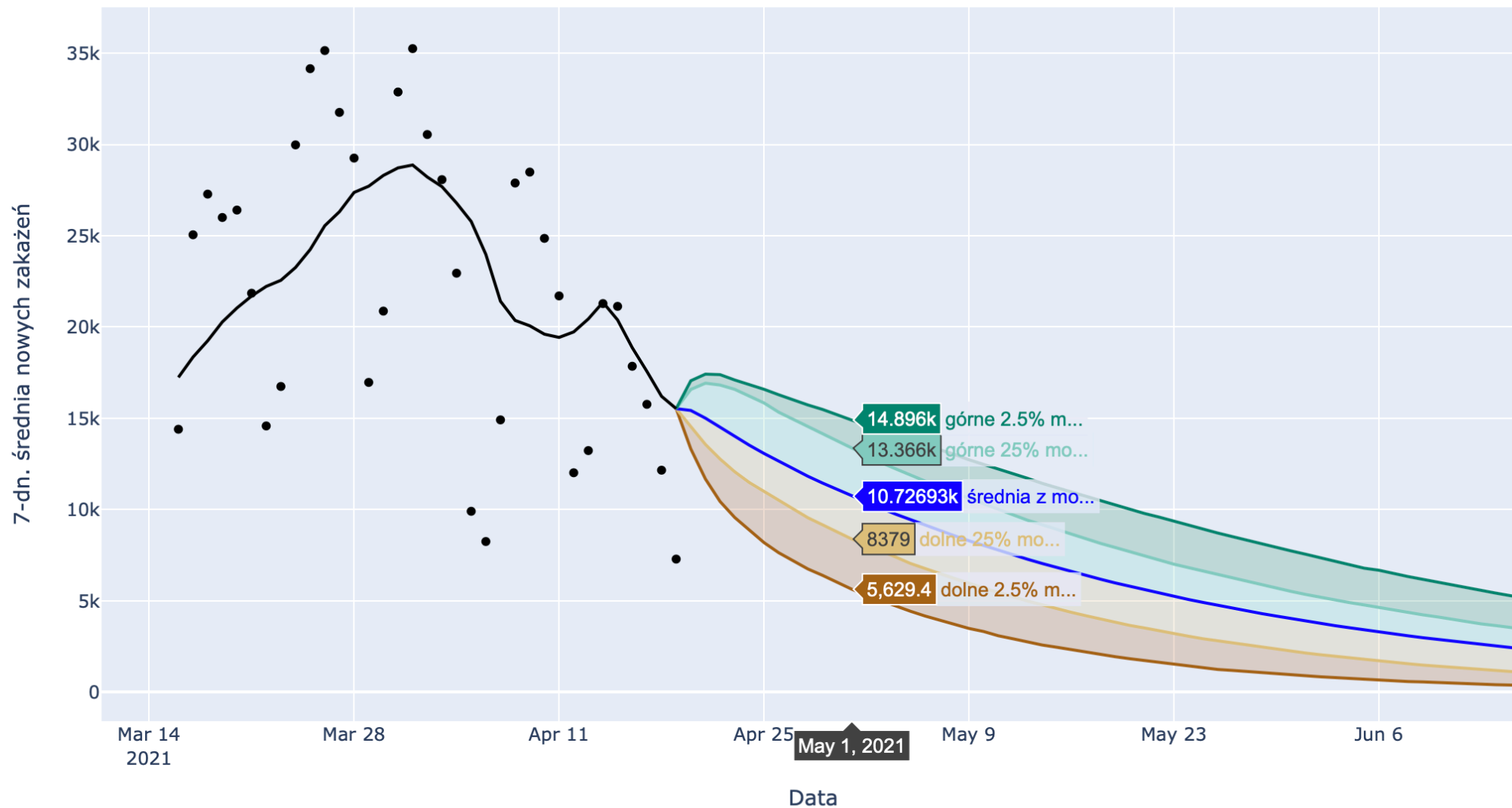
Testing success rate q', tracking probabilities b, delay times D and R* (out-household reproduction number) can be estimated from linked patient data
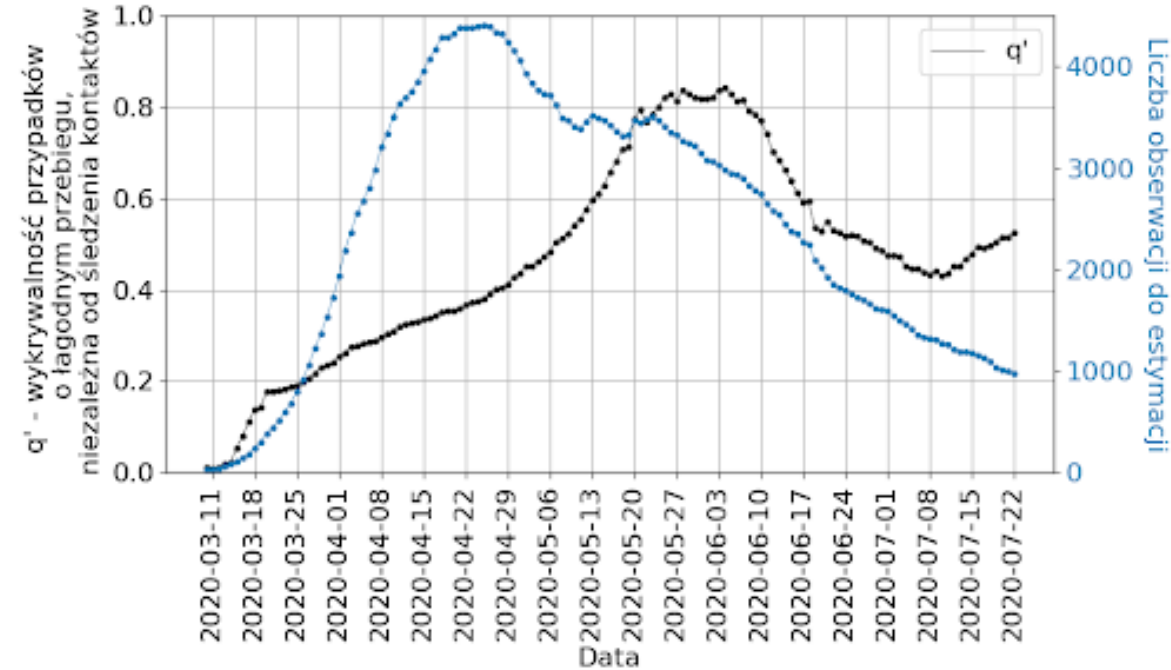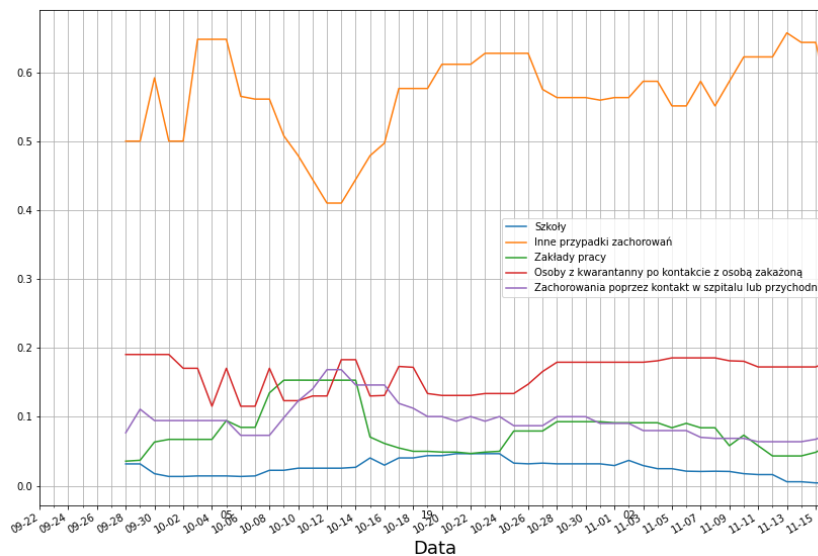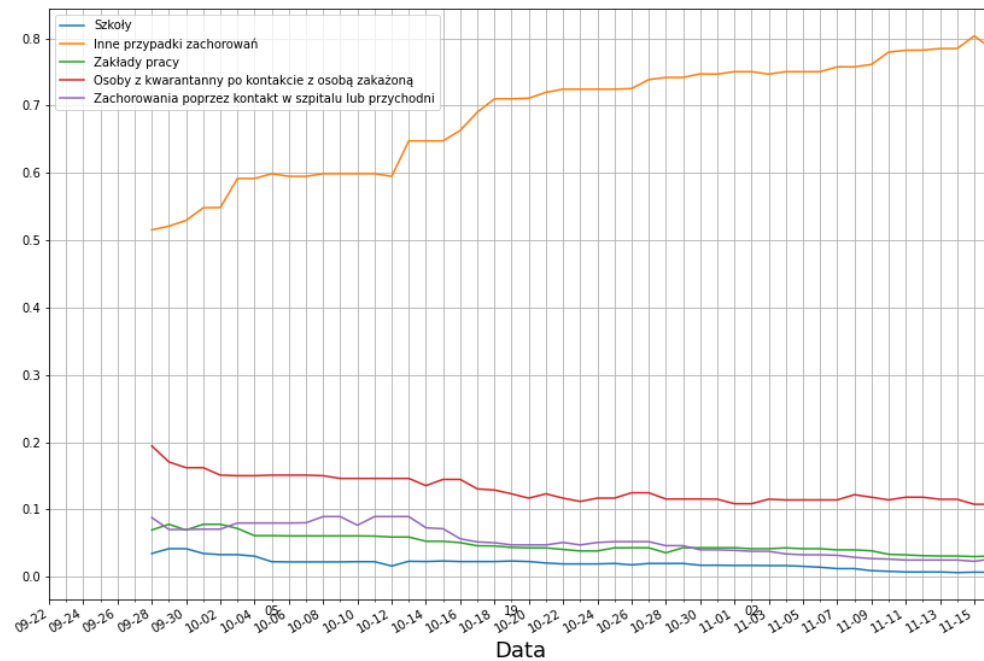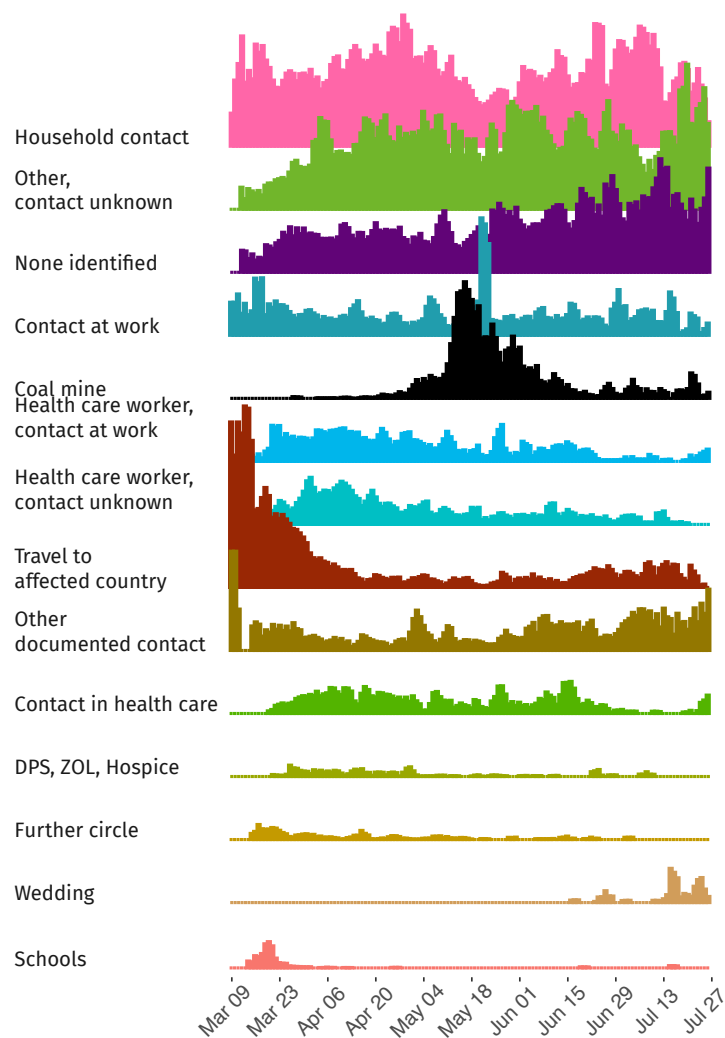
Problems with data: assignment of link structure can be wrong, missing data

- **Whole time to detect the cluster took 11 days**
- **Order of in- household links is often doubtful**

Estimation of
tracking probabilities

Likelihood heatmap of coronavirus dynamics on Poland 22/05/2020 (Assuming q'=0.3)

Good knowledge of sources of infections is key for targeted social distancing and
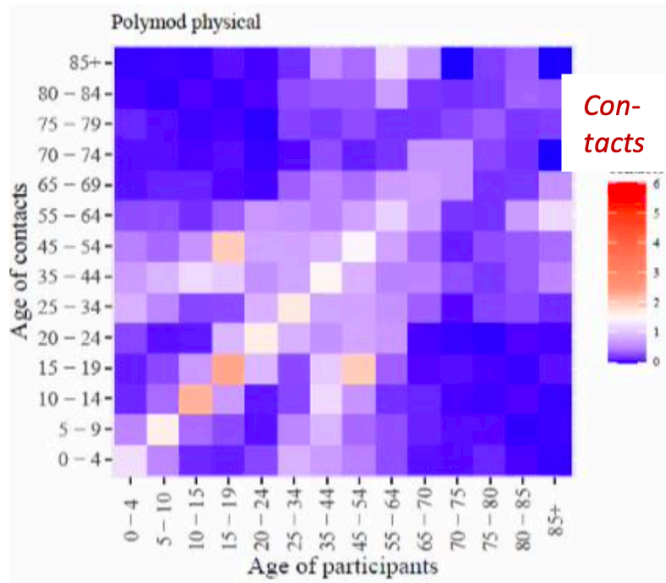

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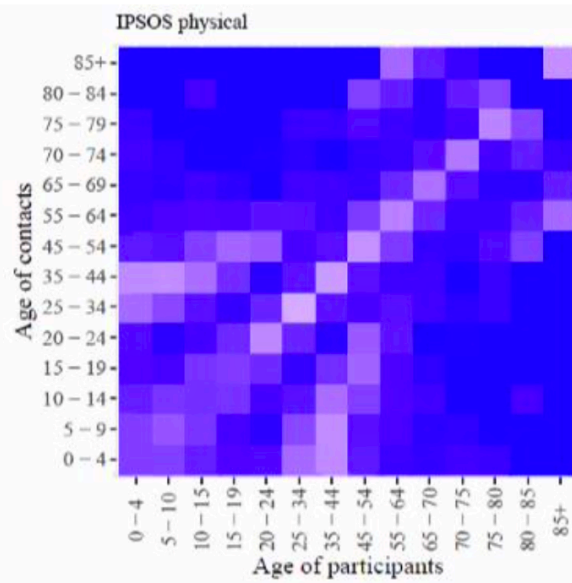# Behavioural Questionaire: Contact Matrices

(Veronika Jäger, Münster)

ALL PHYSICAL CONTACTS

*Before lock down*   *During Lock down*

Required: Time-series of Contacts, age-stratified

**Example shown**: Effects of 1st Lock-down

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)

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Household structure plays significant role in epidemics spreading

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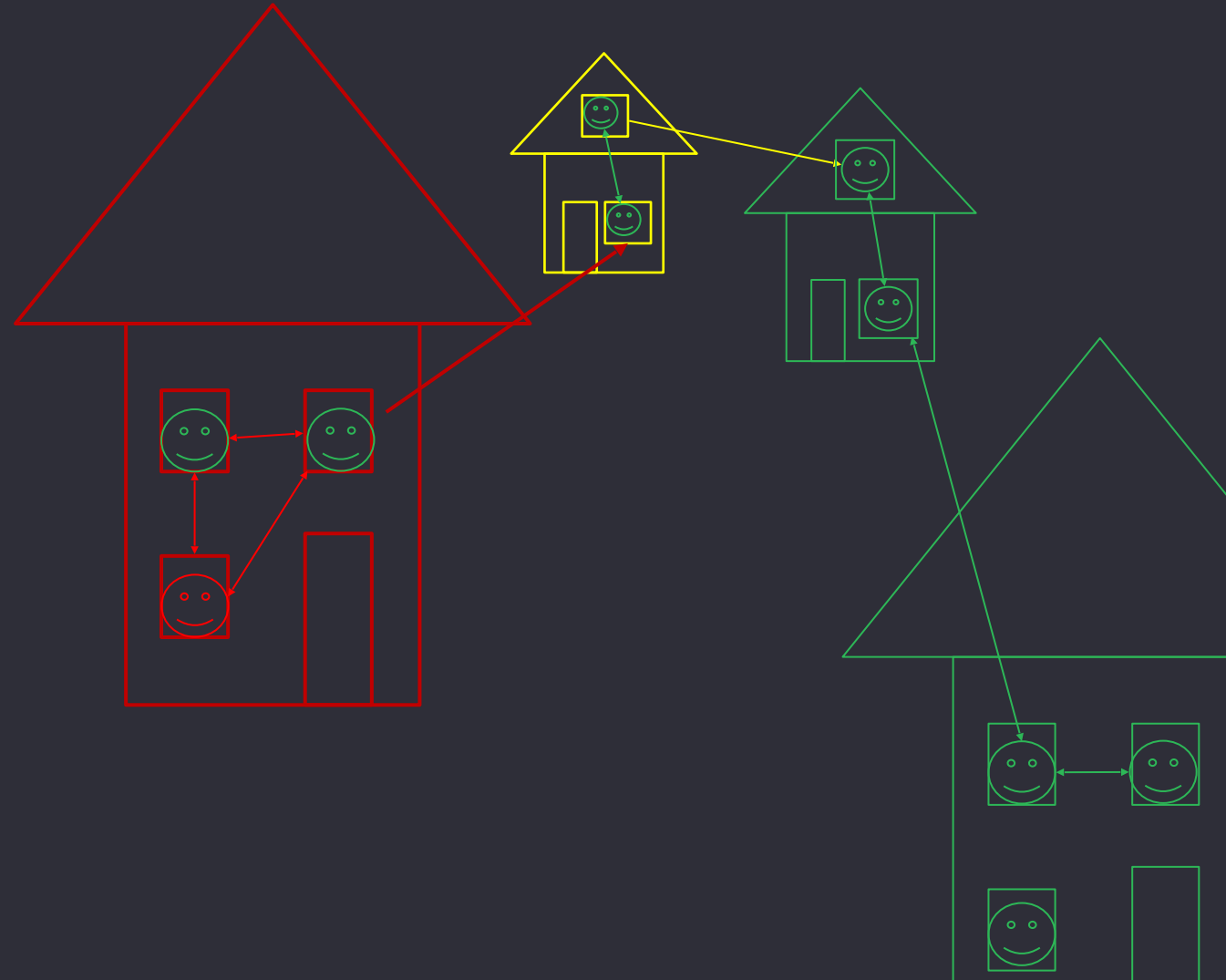
Structural insights: Households are a key factor for epidemic dynamics
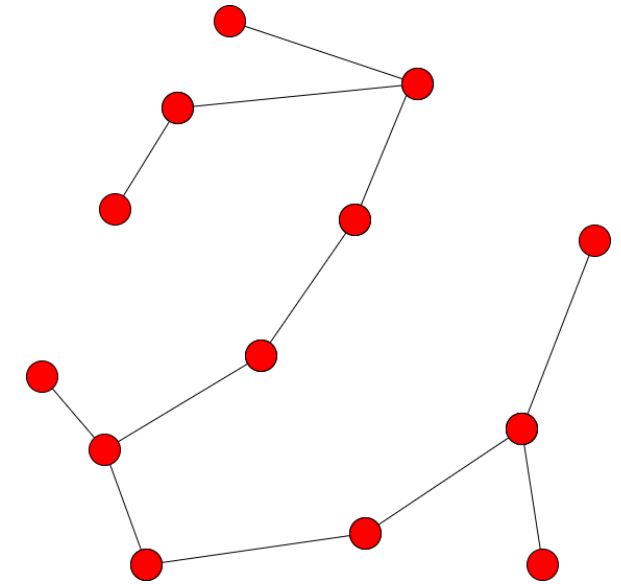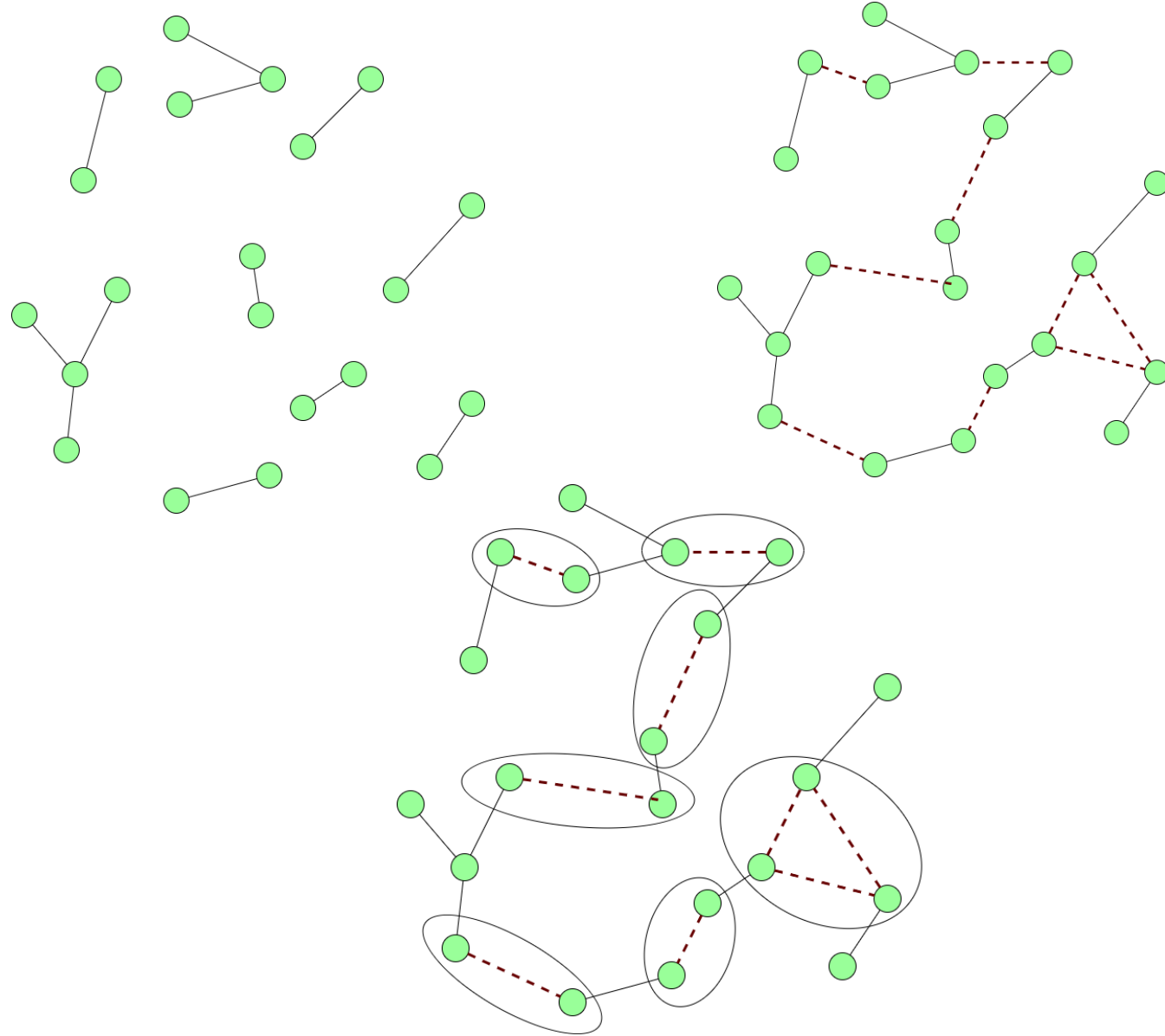
From network between individuals to network between households

Large households have catalytic effect on the spread because link probability between two households is proportional to the product of their sizes
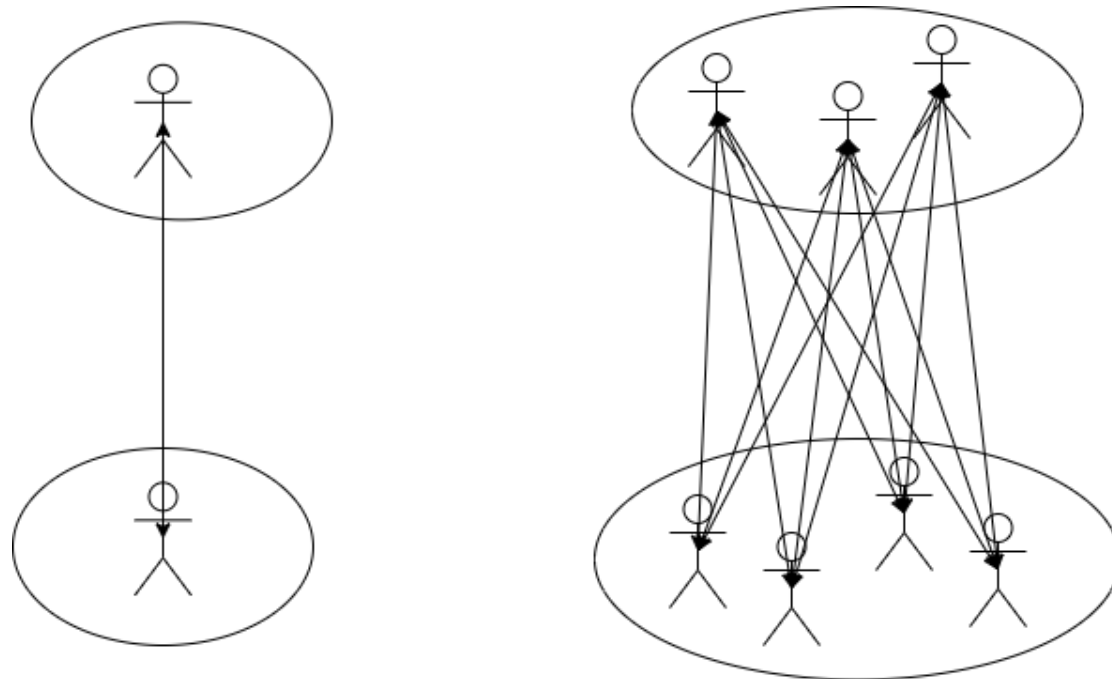
Household graphs : simple example of constant attack rate a

a_H

- household kernel defining the link structure between households of size x and size y :

$$\frac{c}{E}\left(1 + a_H\left(x - 1\right)\right) \cdot y \tag{2}$$

- Transfer operator:
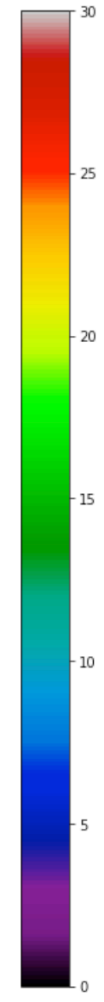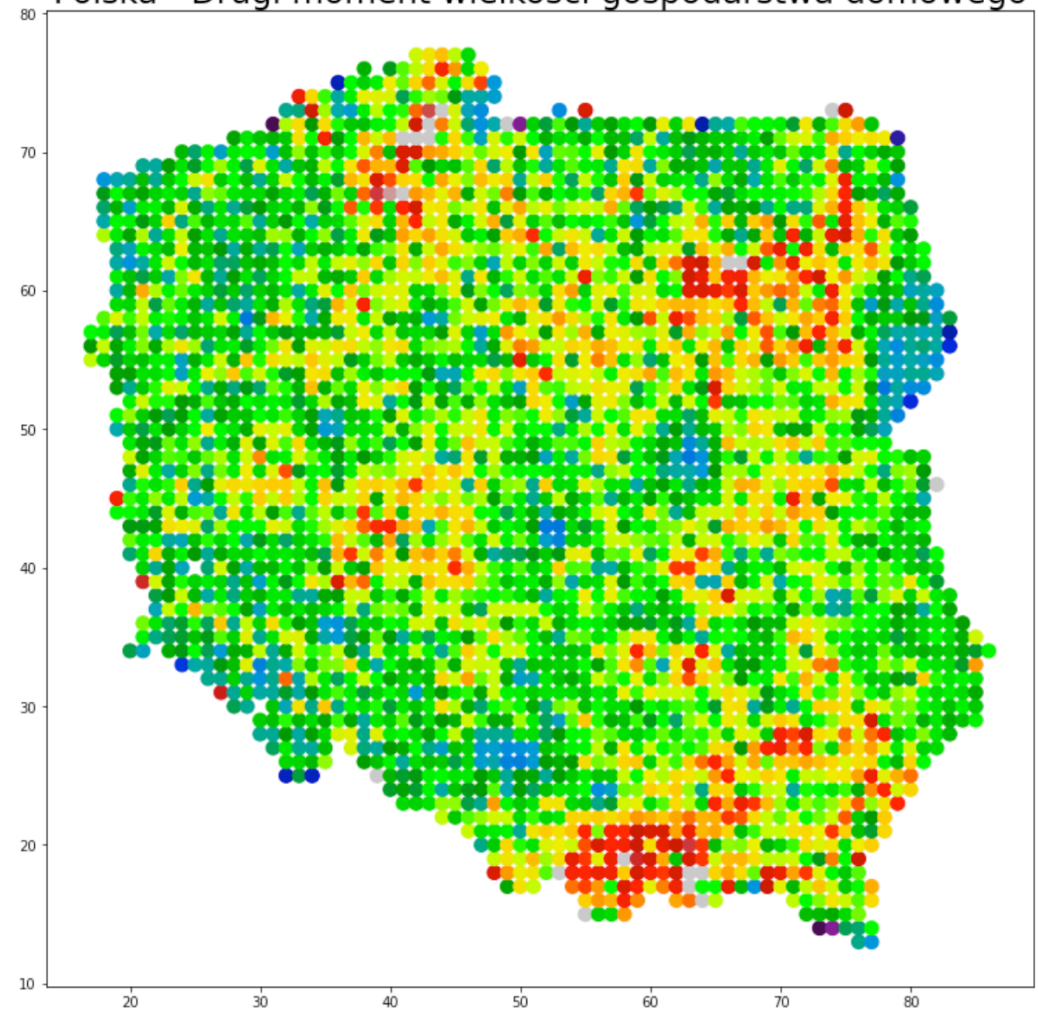- spectral norm of the associated household transfer operator is given by :

$$\frac{c}{E}\sum_{k \geq 1}\left(1 + a_H\left(k - 1\right)\right) \cdot k \cdot \eta\left(k\right) \tag{3}$$

$$= c\left(1 + a_H\left(\frac{m_2}{E} - 1\right)\right) ; \; m_2 \text{ second moment of } \eta \tag{4}$$
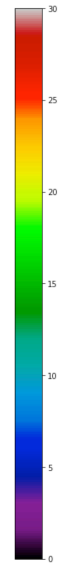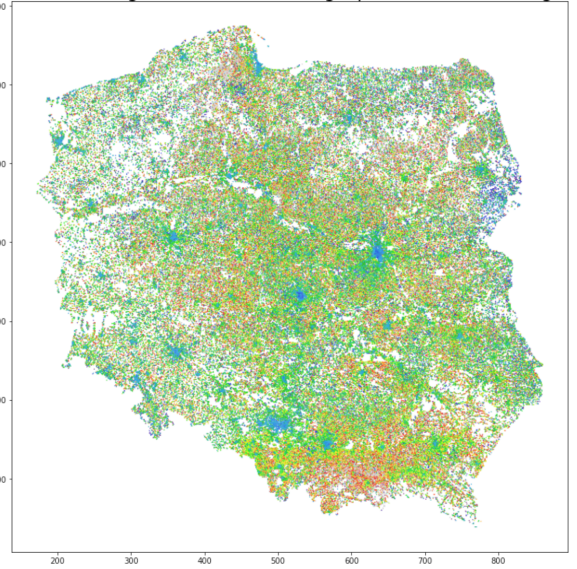
where $\eta\left(k\right)$ is the fraction of households of size k

- T is a rank one, non-symmetric linear operator

Polska - Drugi moment wielkości gospodarstwa domowego

References 1/2

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- Github repository https://github.com/MOCOS-COVID19

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  https://github.com/KITmetricslab/covid19-forecast-hub-de

- Forecast website https://kitmetricslab.github.io/forecasthub/forecast

- Bock, Wolfgang, et al. "Mitigation and herd immunity strategy for COVID-19 is likely to fail." medRxiv (2020).
  Available at: https://www.medrxiv.org/content/10.1101/2020.03.25.20043109v2.full

- Adamik, Barbara, et al. "Bounds on the total number of SARS-CoV-2 infections: The link between severeness rate, household attack rate and the number of undetected cases." (2020).
  Available at: https://www.researchgate.net/profile/Wolfgang-Bock-2/publication/343295720_Bounds_on_the_total_number_of_SARS-CoV-2_infections_The_link_between_severeness_rate_household_attack_rate_and_the_number_of_undetected_cases/links/5f21e28392851cd302c8764a/Bounds-on-the-total-number-of-SARS-CoV-2-infections-The-link-between-severeness-rate-household-attack-rate-and-the-number-of-undetected-cases.pdf

- Bracher, Johannes, et al. "Short-term forecasting of COVID-19 in Germany and Poland during the second wave–a preregistered study." *medRxiv* (2020).
  Available at: https://www.medrxiv.org/content/10.1101/2020.12.24.20248826v2

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