

Visualization of Spatiotemporal Disease Dynamics Using Compartment Models

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Overview

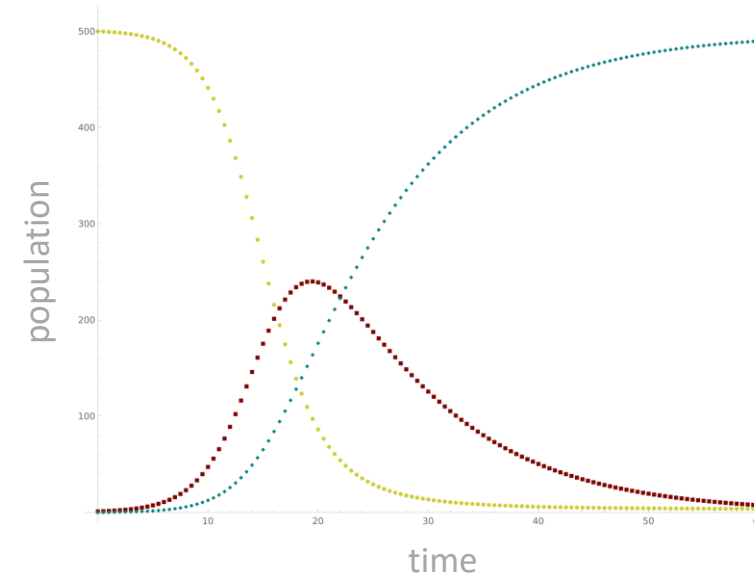
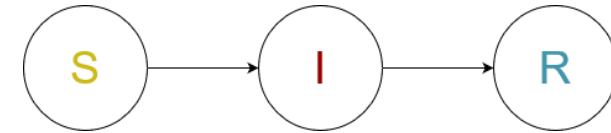
- Motivation for disease modeling
- Background information
- SEIRD compartment model
- Spatial SEIRD compartment model
- Results and evaluation

Motivation

- Modeling disease dynamics helps characterize the behavior of a disease
 - Duration of an epidemic
 - Total numbers of infections and deaths
 - Critical immunization threshold
- Modeling disease dynamics assists in the evaluation of preventive measures
 - Quarantines
 - Travel restrictions
 - Contact restrictions
 - Vaccination target groups

Compartment Models

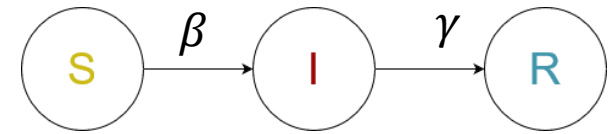
- Mathematical modeling technique for infectious diseases
- Originated in the early 20th century
- Idea:
 - Population is divided into labeled compartments (e.g., SIR model contains **S**usceptible, **I**nfectious, **R**ecovered)
 - People can transfer from one compartment to another at a given time rate
- Models are formulated with ordinary differential equations (stochastic or deterministic)
- Many variations of compartment types and parameters possible



The SIR model with **Susceptible**, **Infectious** and **Recovered** compartments [\[1\]](#).

Models Parameters

- Transmission rate β : probability of disease transmission times the average number of contacts per person per time unit
- Recovery rate γ : rate at which a infected person becomes non-infectious
- Reproductive number R : average number of secondary cases produced by one infected individual [\[2\]](#)
 - $R \approx \beta/\gamma$
 - $R > 1$: The disease can spread in the population
 - $R < 1$: The disease cannot spread in the population
- Basic reproductive number R_0 = assumes a population of susceptible individuals (stays constant)
- Effective reproduction number R_e : population of susceptible and non-susceptible individuals (can vary)



Flow chart of the SIR model

Related Work

- Keisuke-Kondo: “Simulating the impacts of interregional mobility restriction on the spatial spread of COVID-19 in Japan” [\[3\]](#)
- Interregional mobility added to standard SEIR model (Susceptible, Exposed, Infected, Recovered)
- Interregional mobility modelled with an Origin-Destination (OD) matrix using location data from mobile devices
- Assumption:
 - People commute from their residential region to a different region during the day
 - The disease can be transferred from the residential region to the region occupied during the day
 - The disease can be transferred from the region occupied during the day to the residential region

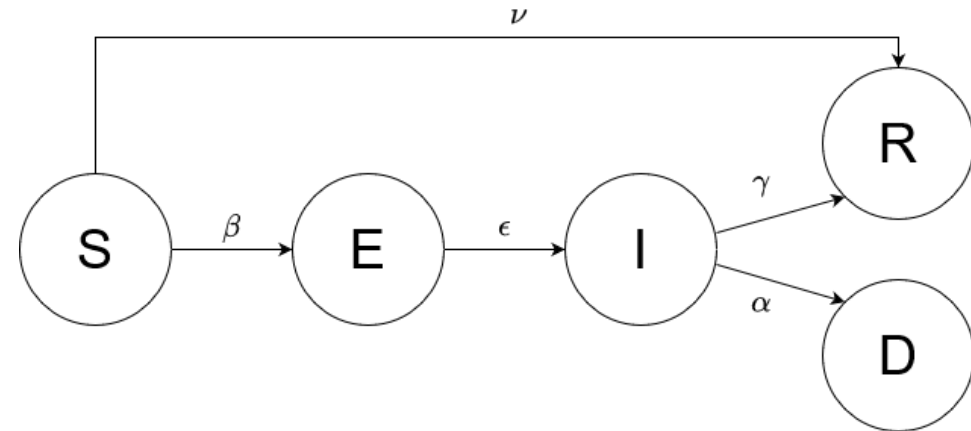
Implemented SEIRD Model

- Population N is divided into the compartments:

- S - Susceptible (not yet infected)
- E - Exposed (infected, not yet infectious)
- I - Infected
- R - Recovered
- D - Dead (virus induced deaths)
- (V - Vaccinated)

- Parameters:

- β = transmission rate
- ϵ = incubation rate
- γ = recovery rate
- α = virus induced death rate
- ν = vaccination rate



Flow chart of the SEIRD model

Implemented SEIRD Model

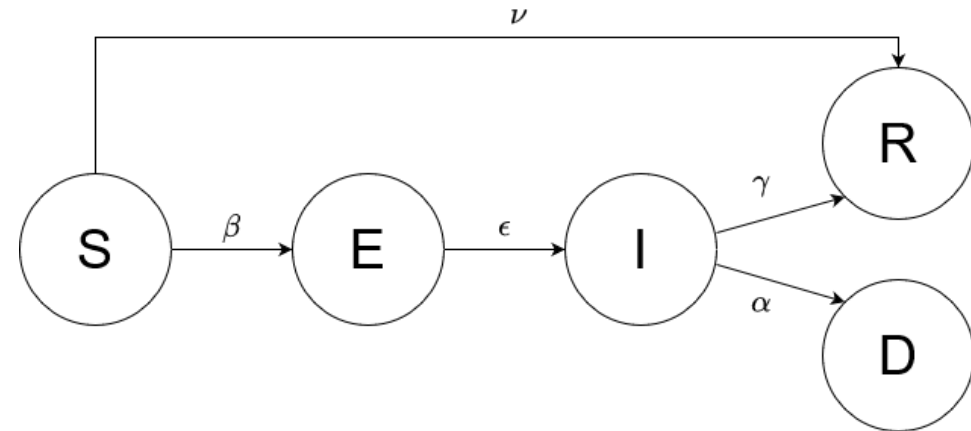
$$\frac{dS(t)}{dt} = -\nu S(t) - \beta S(t)I(t)/N$$

$$\frac{dE(t)}{dt} = \beta S(t)I(t)/N - \epsilon E(t)$$

$$\frac{dI(t)}{dt} = \epsilon E(t) - (\gamma + \alpha)I(t)$$

$$\frac{dR(t)}{dt} = \nu S(t) + \gamma I(t)$$

$$\frac{dD(t)}{dt} = \alpha I(t)$$



Flow chart of the SEIRD model

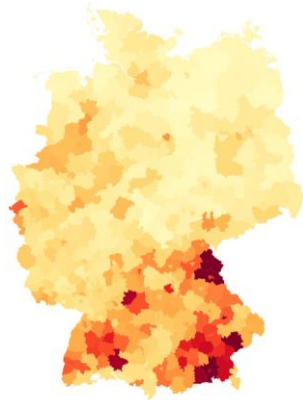
Parameters:

- N = population, β = transmission rate, ϵ = incubation rate, γ = recovery rate, α = virus induced death rate, ν = vaccination rate

Spatial SEIRD Model



Spatial resolution
on national level



Spatial resolution
on district level [\[4\]](#)

- Each district is modeled with its own SEIRD model
- Spatial disease spread between districts is enabled through the commuting population
- Commuting modeled with an origin-destination matrix
- The state of a district is influenced by the current situation within the district, the current situation of neighboring districts and the inflow and outflow of people between these districts.

Origin-Destination Matrix

$$\pi^h = \begin{bmatrix} \pi_{1,1}^h & \pi_{1,2}^h & \cdots & \pi_{1,m}^h \\ \pi_{2,1}^h & \pi_{2,2}^h & \cdots & \pi_{2,m}^h \\ \vdots & \vdots & \ddots & \vdots \\ \pi_{m,1}^h & \pi_{m,2}^h & \cdots & \pi_{m,m}^h \end{bmatrix}$$

- $h \in S, E, I, R$
- $\pi_{i,j}$ - probability for traveling from region i to region j
- $\pi^S = \pi^E = \pi^R$ (unrestricted travel)
- $\pi^I =$ identity matrix I (restricted travel)
- Commuting data taken from the Bundesagentur Für Arbeit, 2021 statistics [\[5\]](#)
- Commuting data for each district was restricted to a 150 km radius

Mobility Flow

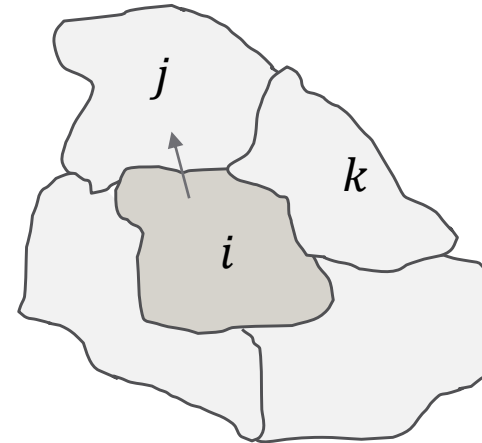
- Mobility flow from region i to region j at time t :

$$S_{ij}(t) = \pi_{ij}^S S_i(t)$$

$$E_{ij}(t) = \pi_{ij}^E E_i(t)$$

$$I_{ij}(t) = \pi_{ij}^I I_i(t)$$

$$R_{ij}(t) = \pi_{ij}^R R_i(t)$$



Total Daytime Inflow

- Daytime values for region i at time t :

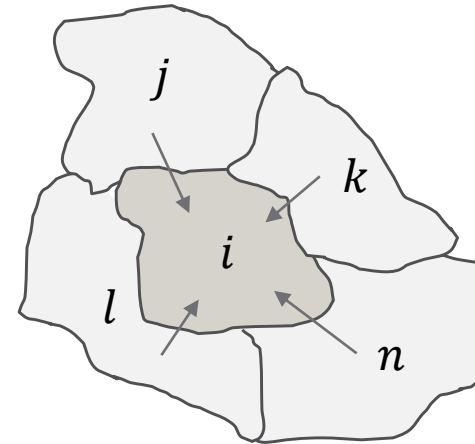
$$\tilde{S}_i(t) = \sum_{k=1}^m S_{ki}(t)$$

$$\tilde{E}_i(t) = \sum_{k=1}^m E_{ki}(t)$$

$$\tilde{I}_i(t) = \sum_{k=1}^m I_{ki}(t)$$

$$\tilde{R}_i(t) = \sum_{k=1}^m R_{ki}(t)$$

- m = number of districts
- Individuals from region j who commute to region i are exposed to the infection risk of region i during the daytime



Complete Model

$$\frac{dS_i(t)}{dt} = -\nu S_i(t) - \beta \sum_{k=1}^m \frac{\tilde{I}_k(t)}{\tilde{N}_k(t)} S_{ik}(t)$$

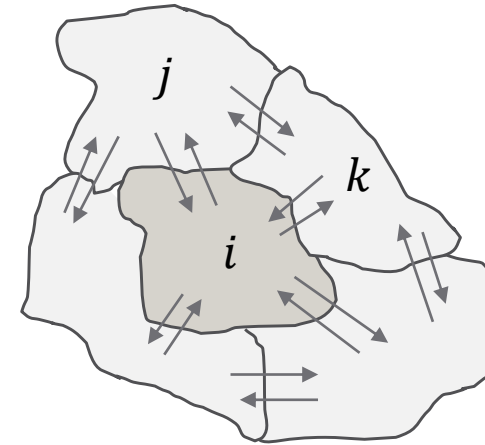
$$\frac{dE_i(t)}{dt} = \beta \sum_{k=1}^m \frac{\tilde{I}_k(t)}{\tilde{N}_k(t)} S_{ik}(t) - \epsilon E_i(t)$$

$$\frac{dI_i(t)}{dt} = \epsilon E_i(t) - (\gamma + \alpha) I_i(t)$$

$$\frac{dR_i(t)}{dt} = \nu S_i(t) + \gamma I_i(t)$$

$$\frac{dD_i(t)}{dt} = \alpha I_i(t)$$

$$\tilde{N}_i = \tilde{S}_i + \tilde{E}_i + \tilde{I}_i + \tilde{R}_i = \text{daytime population of region } i$$



Model Assumptions

- Only considers movement of commuting workers
- No movement across international borders
- No virus mutations
- No population growth
- Recovered and vaccinated people are assumed to have total immunity

Implementation and Visualization

- SEIRD model solved with the Python SciPy Library (Adams method for integration)
- Data wrangling
 - Geo data (geojson data of Germany on district level)
 - Covid-19 data from the Robert Koch Institute (ArcGIS REST Api [\[6\]](#))
- Animation with Plotly graphing library for data visualization [\[7\]](#)

Comparison with RKI Data

- Timeseries data from the Robert Koch Institute (RKI) starting on the date 10.11.2020 (second covid wave in Germany)

- Initial model values given by:

$$D_i(t) = T_i(t)$$

$$R_i(t) = P_i(t - \gamma^{-1}) - D_i(t)$$

$$I_i(t) = P_i(t) - R_i(t) - D_i(t)$$

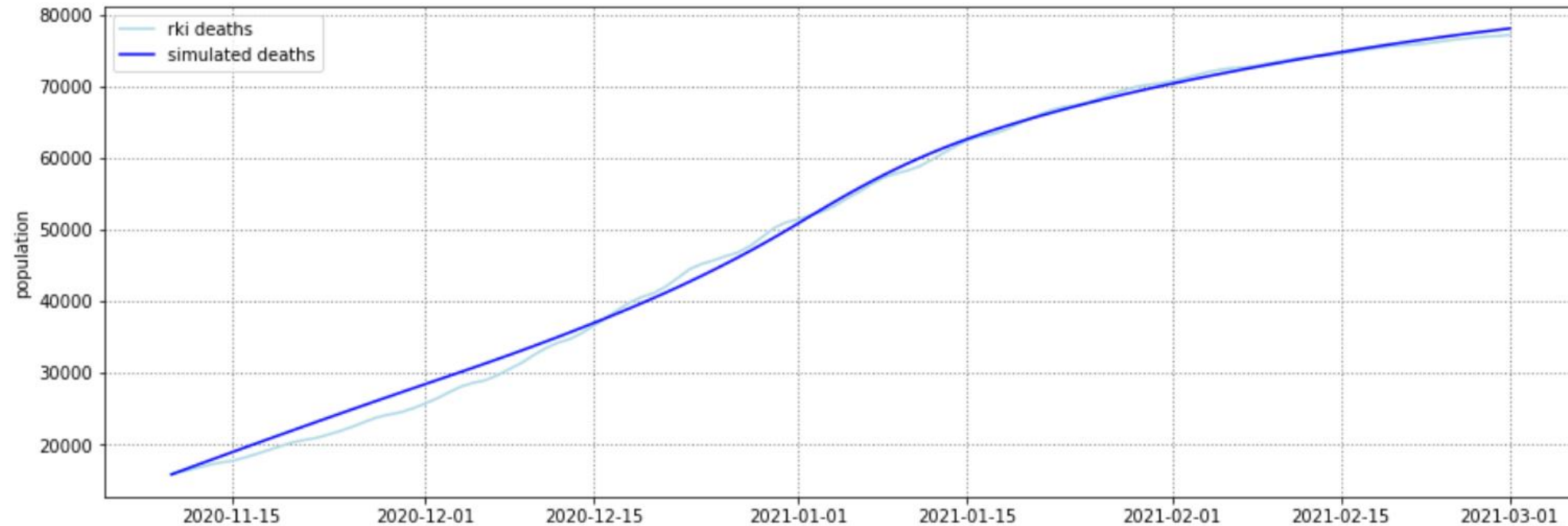
$$E_i(t) = P_i(t + \epsilon^{-1}) - P_i(t)$$

$$S_i(t) = N_i - E_i(t) - I_i(t) - R_i(t) - D_i(t)$$

- With

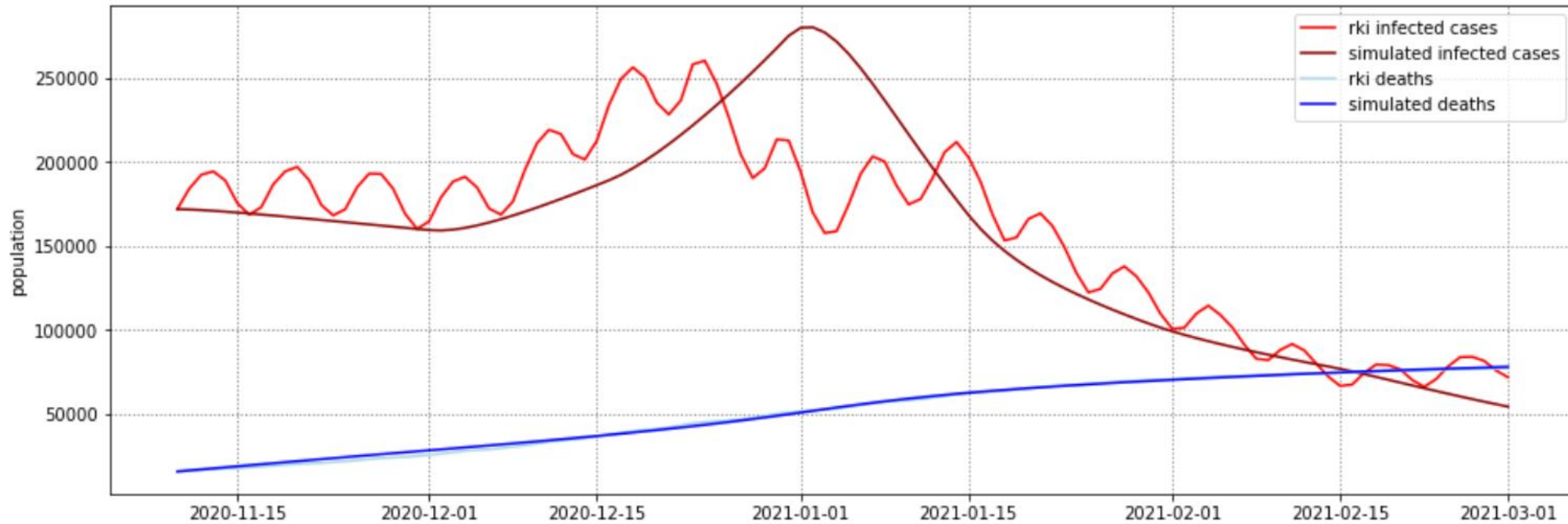
- $T_i(t)$ = cumulative deaths reported in region i up until day t
- $P_i(t)$ = cumulative positive cases reported in region i up until day t
- γ^{-1} = infectious period in days
- ϵ^{-1} = incubation period in days

Comparison with RKI Data



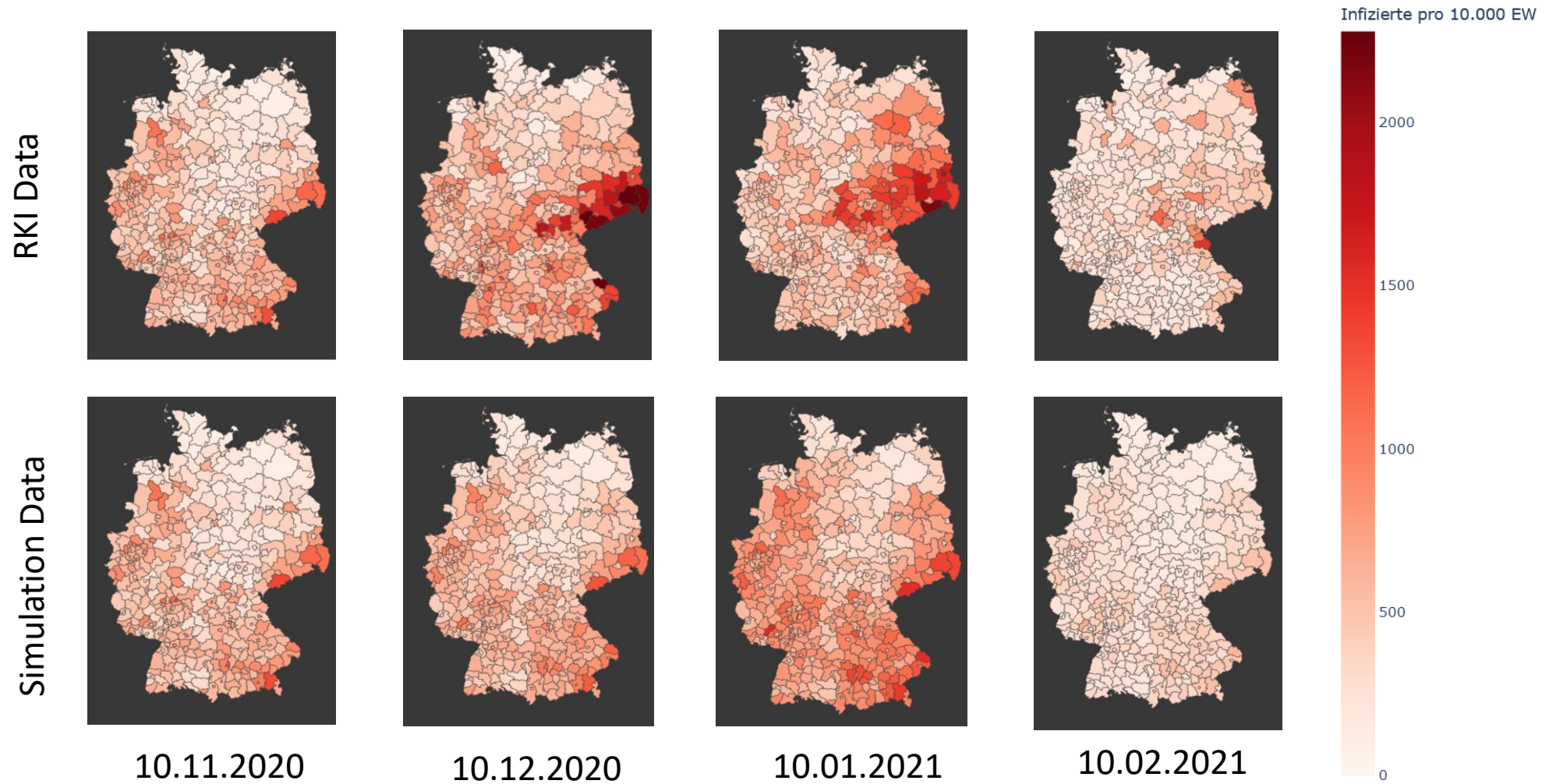
Model fitted to the national death curve. Parameters: $R_0 = 3.4$, $\epsilon = \frac{1}{5.22}$, $\gamma = \frac{1}{10}$, $\beta = 0.34$, $\alpha = 0.0036$

Comparison with RKI Data



Model fitted to the national death curve. Parameters: $R_0 = 3.4$, $\epsilon = \frac{1}{5.22}$, $\gamma = \frac{1}{10}$, $\beta = 0.34$, $\alpha = 0.0036$

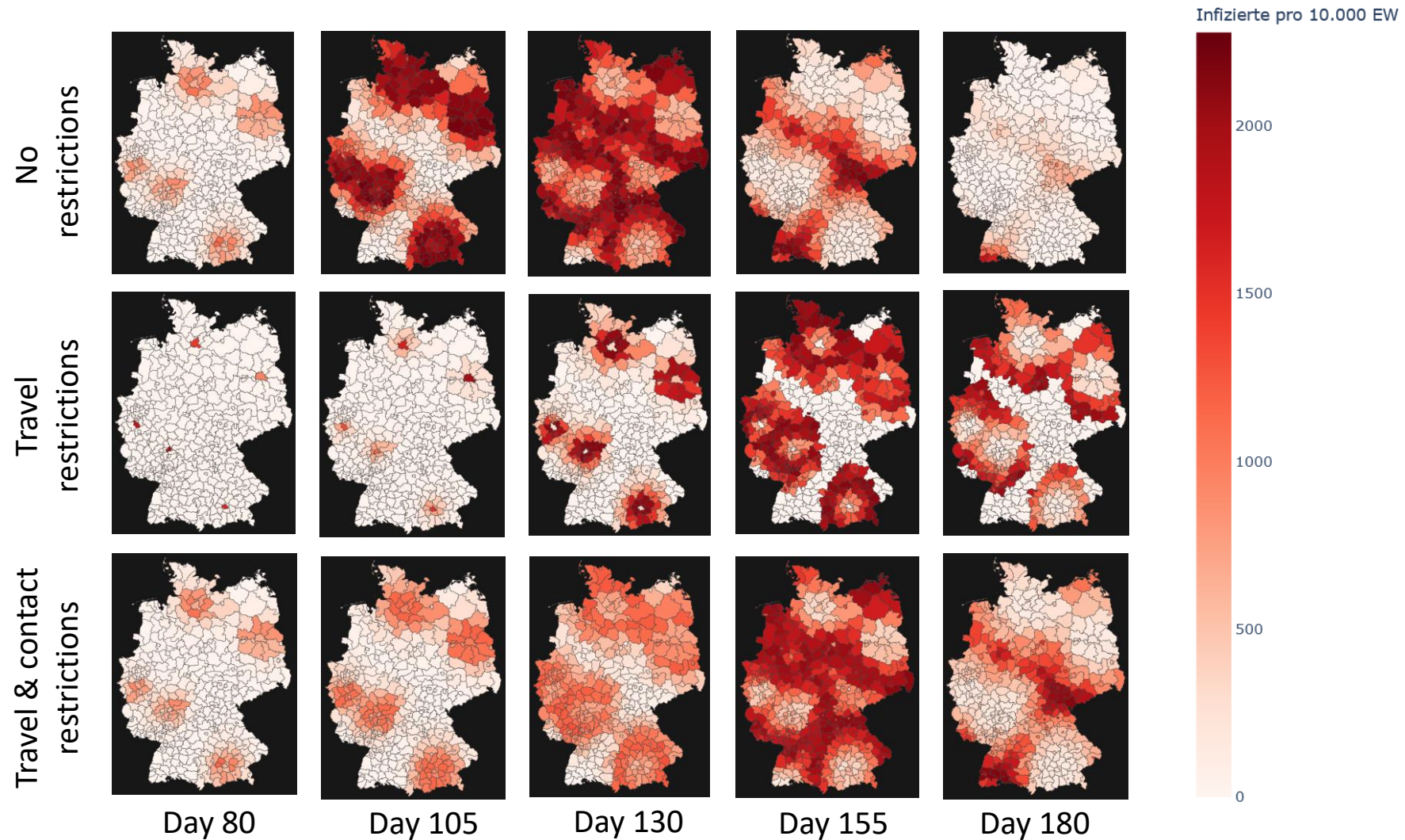
Comparison with RKI Data



Simulation: Outbreak in Five Cities

- Starting points: Berlin, Hamburg, München, Köln, Frankfurt
- Starting values:
 - E: 100
 - I: 50
 - Runtime: 180 days
 - R_0 : 3.4
- Scenarios:
 - No restrictions
 - Early travel restrictions (OD-Matrix = I on day 2)
 - Hard lockdown: three-week travel and contact restrictions starting on day 90 (OD-Matrix = I and $R_e = 0.8$)

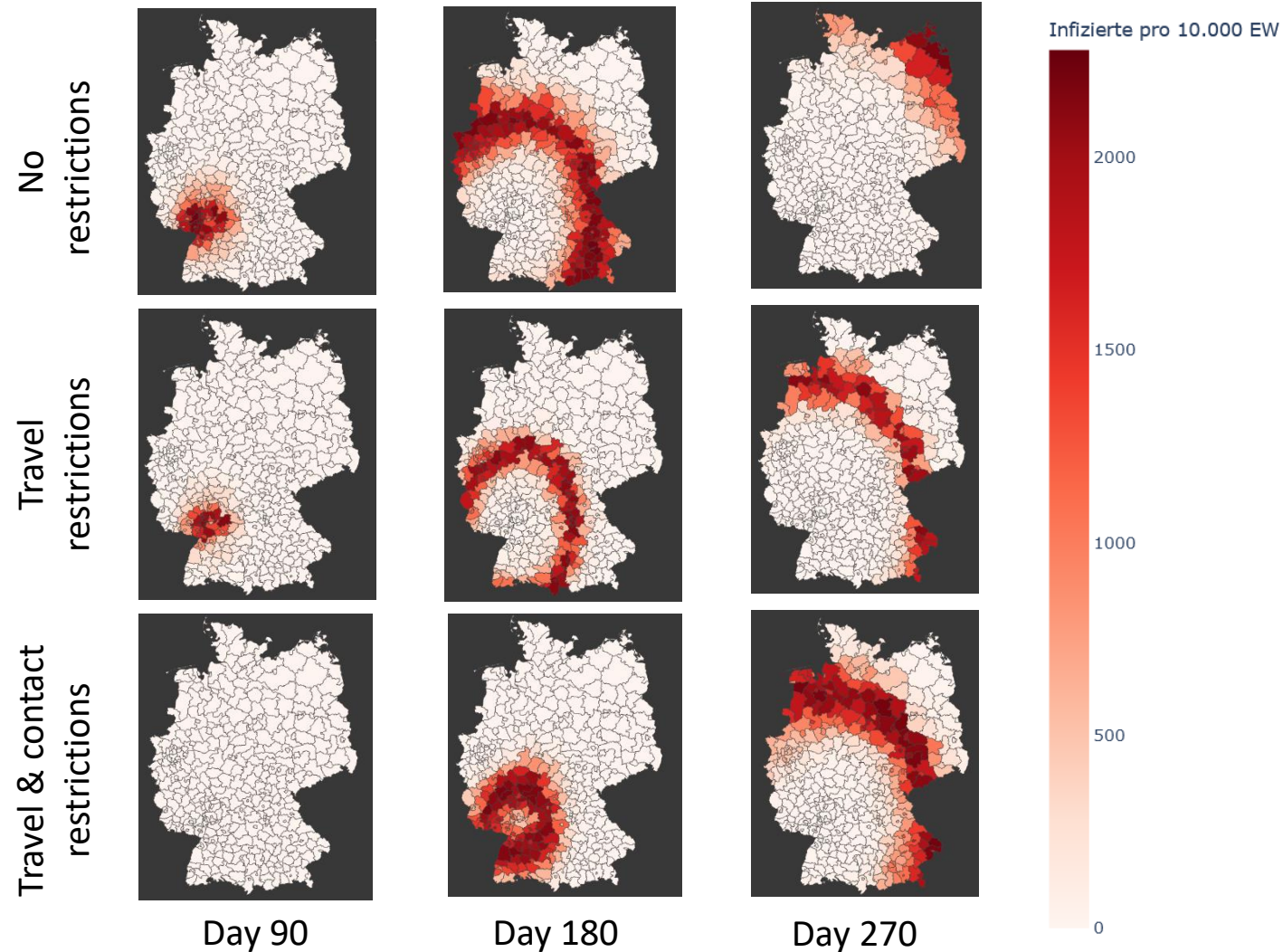
Simulation: Outbreak in Five Cities



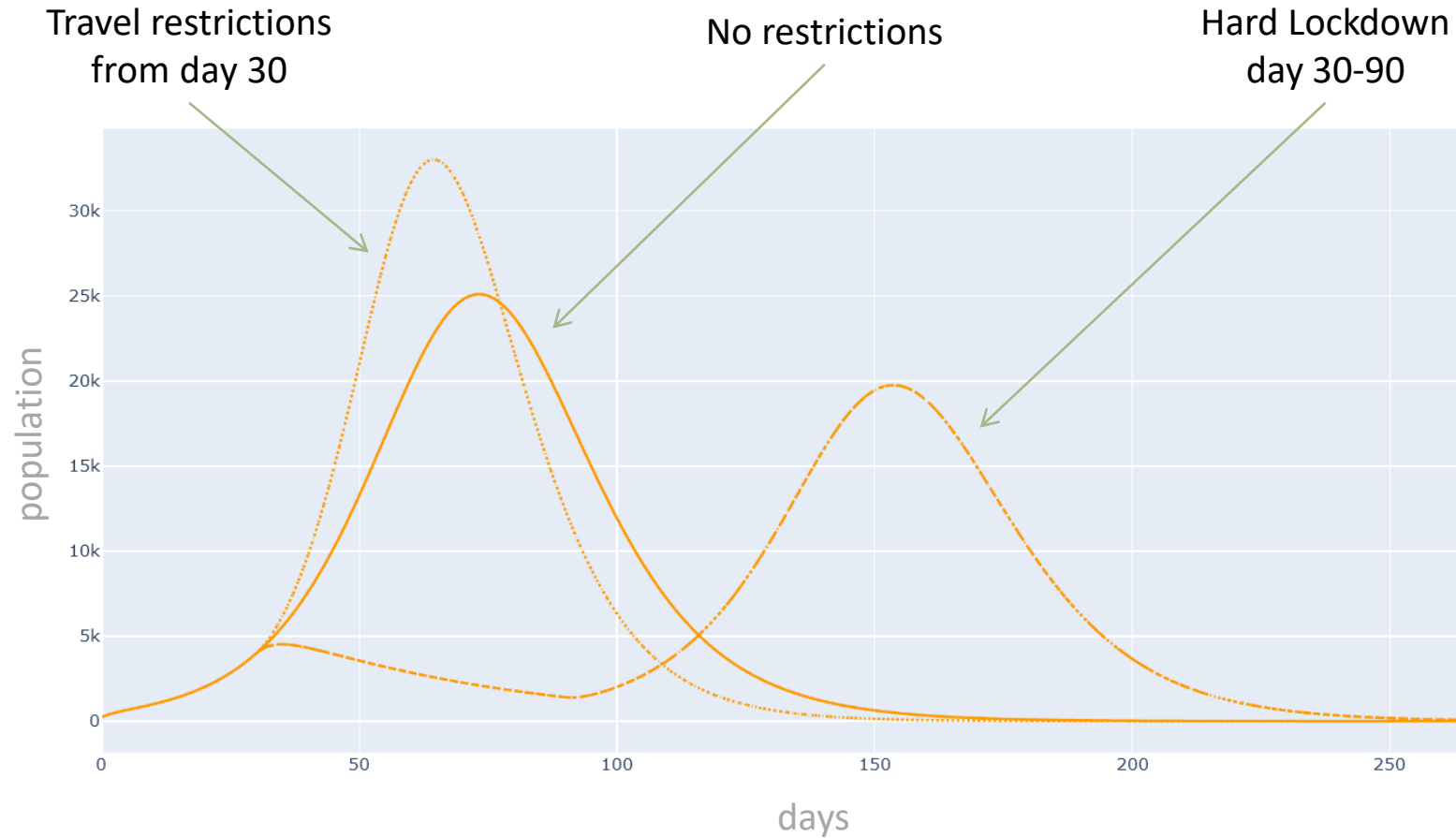
Simulation: Outbreak in Heidelberg

- Starting point: Heidelberg
- Starting values:
 - E: 800
 - I: 250
 - Runtime: 360 days
 - R_0 : 3.4
- Scenarios:
 - No restrictions
 - Travel restrictions from day 30 (OD-Matrix = I)
 - Hard lockdown: travel and contact restrictions from day 30 - 90 (OD-Matrix = I and $R_e = 0.8$)

Simulation: Outbreak in Heidelberg

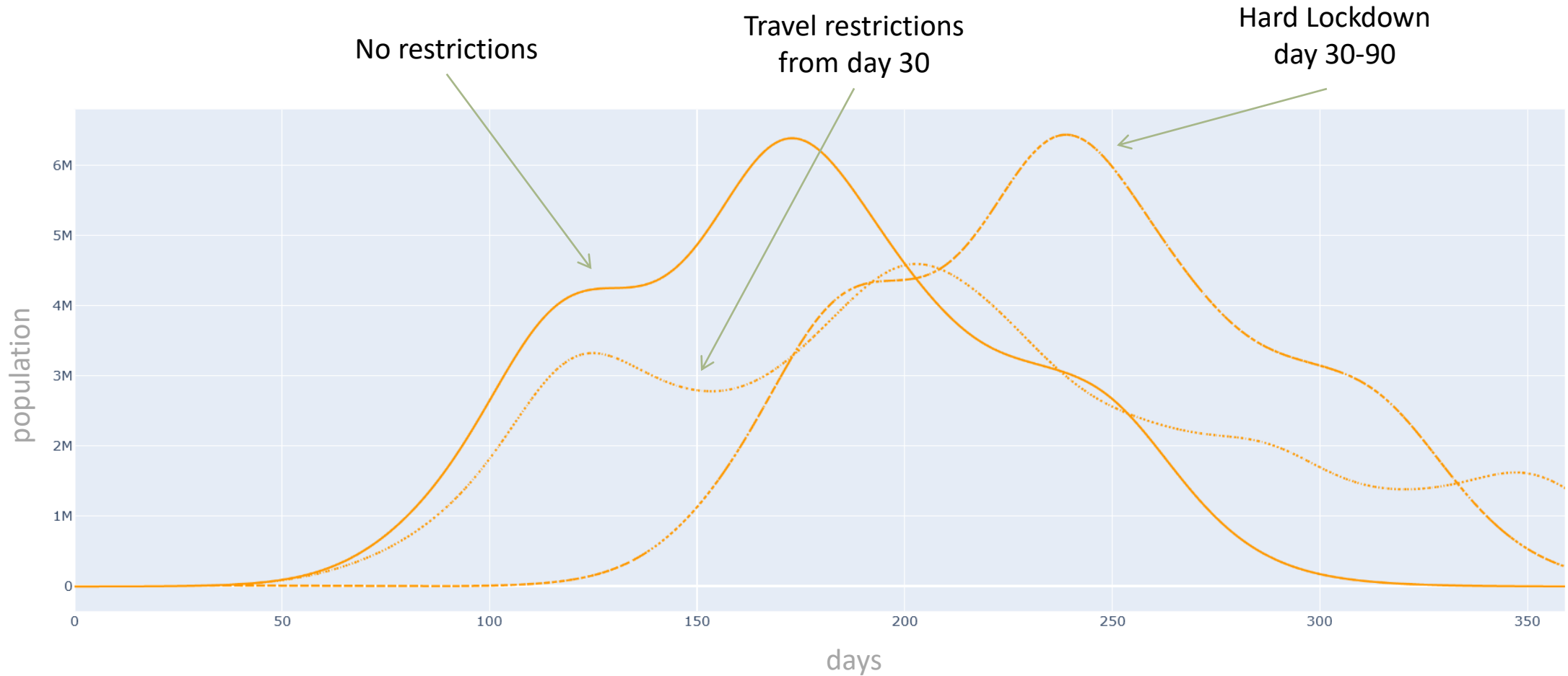


Simulation: Outbreak in Heidelberg



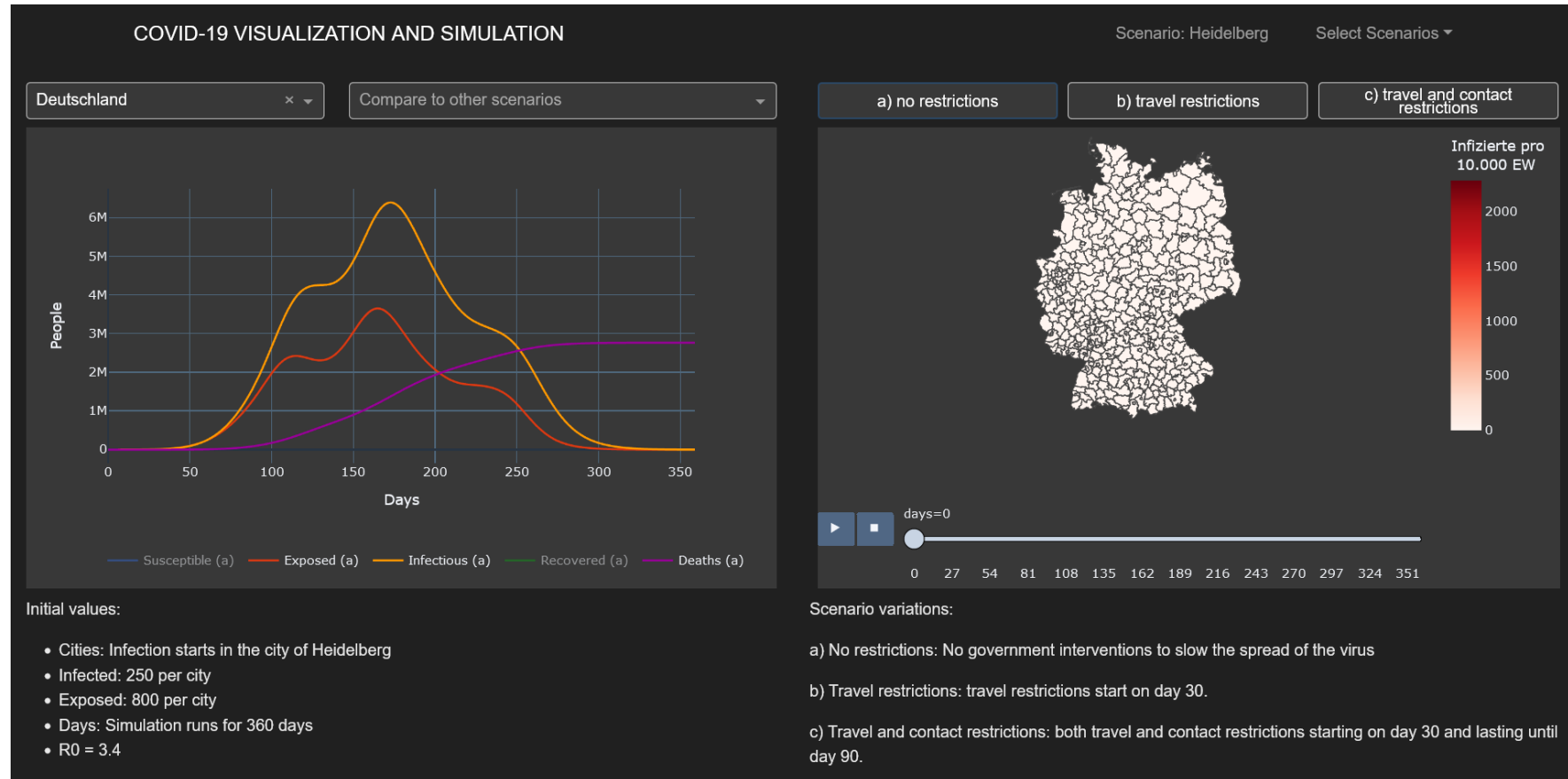
Number of infected people over time in Heidelberg

Simulation: Outbreak in Heidelberg



Number of infected people over time in Germany

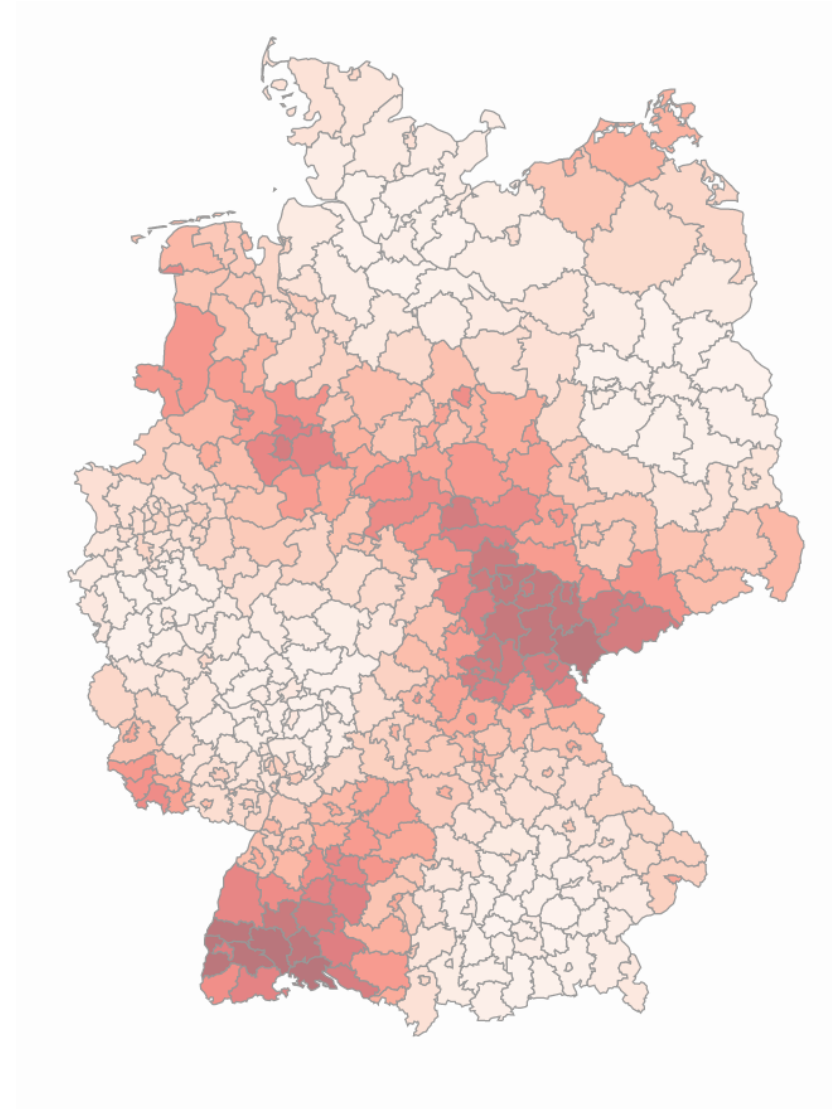
Dashboard



Dashboard implementation using Plotly and Dash applications

Conclusion

- Summary:
 - Implemented a spatial SEIRD model using commuting data between districts
 - Model can simulate disease spread with different starting points and intervention methods
 - Animation of disease spread for different scenarios
- Limitations:
 - Very simplified view of the disease spread (no demographics, seasonal variations or loss of immunity)
 - Parameters are global (no regional lockdowns)

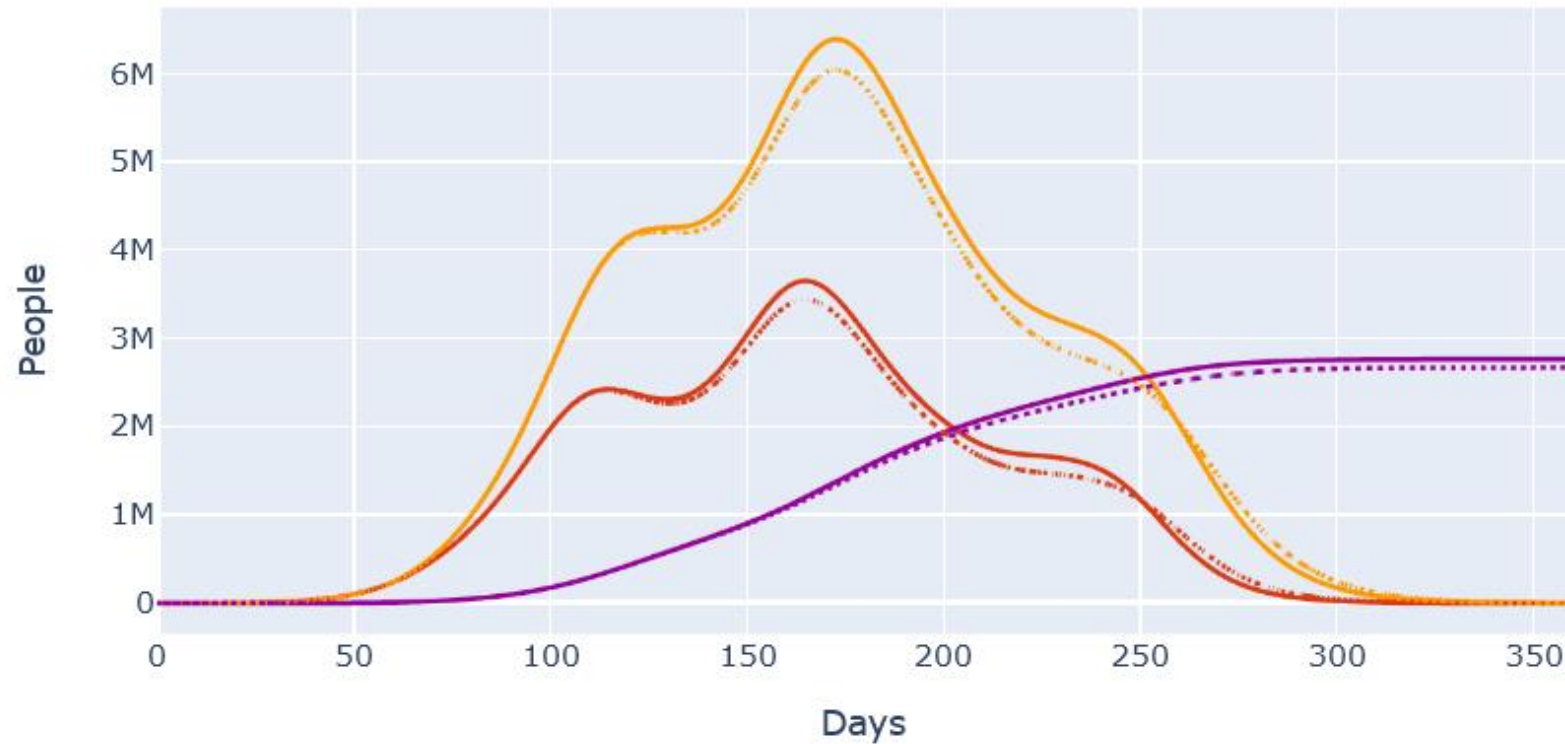


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- Schüler, Lennart. "Data Driven High Resolution Modeling and Spatial Analyses of the COVID-19 Pandemic in Germany." *PLOS ONE*, 18 Aug. 2021, <https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0254660> [4]
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- *Layer: Covid19_RKI_Sums (ID:0)*. services7.arcgis.com/mOBPykOjAyBO2ZKk/ArcGIS/rest/services/Covid19_RKI_Sums/FeatureServer/0. (viewed 08.10.2022). [6]
- *Plotly*. plotly.com/python. (viewed 08.10.2022) [7]

Scenario: Heidelberg with Vaccinations

- Vaccinations starting on day 100 with a low rate of 0.0004



Infected (yellow), exposed (red) and dead (purple) without vaccinations (line) and with vaccinations (dotted line)