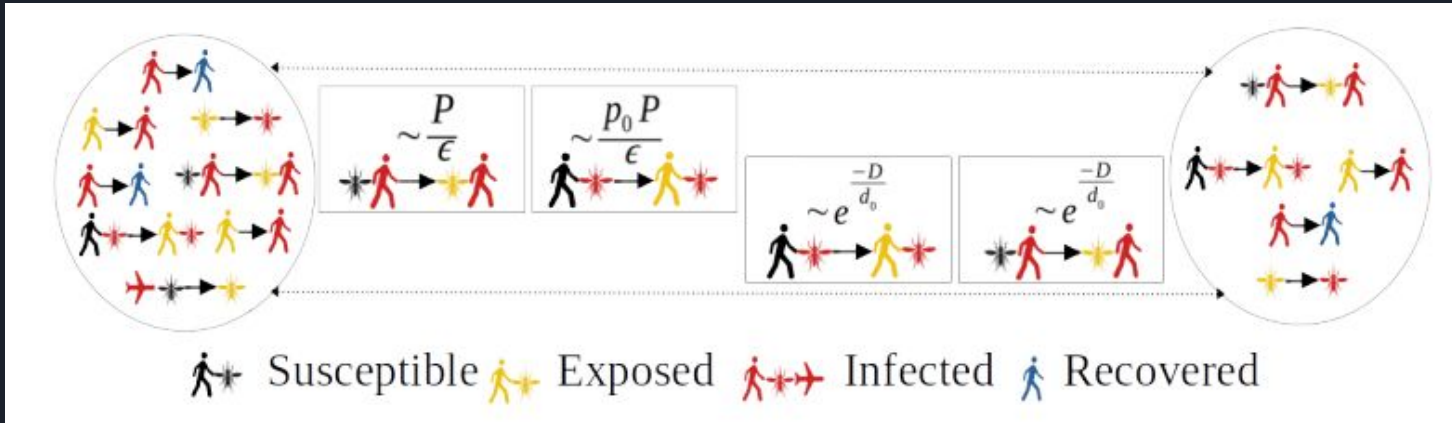# PRIN 2022 PNRR: Joint model of population dynamics and vector-borne diseases

...what I have done so far

Project overview

Our goal is to predict impact of vector-borne diseases in Italy in future decades

The disease model used is a classical SEIR model:

Project overview

Epidemic dynamics follow the SEIR model in each spatial patch, corresponding to Italy provinces

Interaction between different patches occurs via mobility of different agents (being vectors or hosts). This can happen in different ways:

- human (host) or human-mediated (vector) mobility
- autonomous vector-dispersal
- international airline traffic

Passengers coming from areas at risk of vector borne diseases are infectious hosts of SEIR model

Project overview

Mobility of hosts (humans) across decades can be estimated by computing human suitability for each area of interest

This is mostly related to **climatic variables (**temperature, precipitations) which also influence disease-related parameters such as transmission rates and expected life spans of vectors

To account for migration due to changes in human suitability, we use a generalized version of radiation model: **FERM**
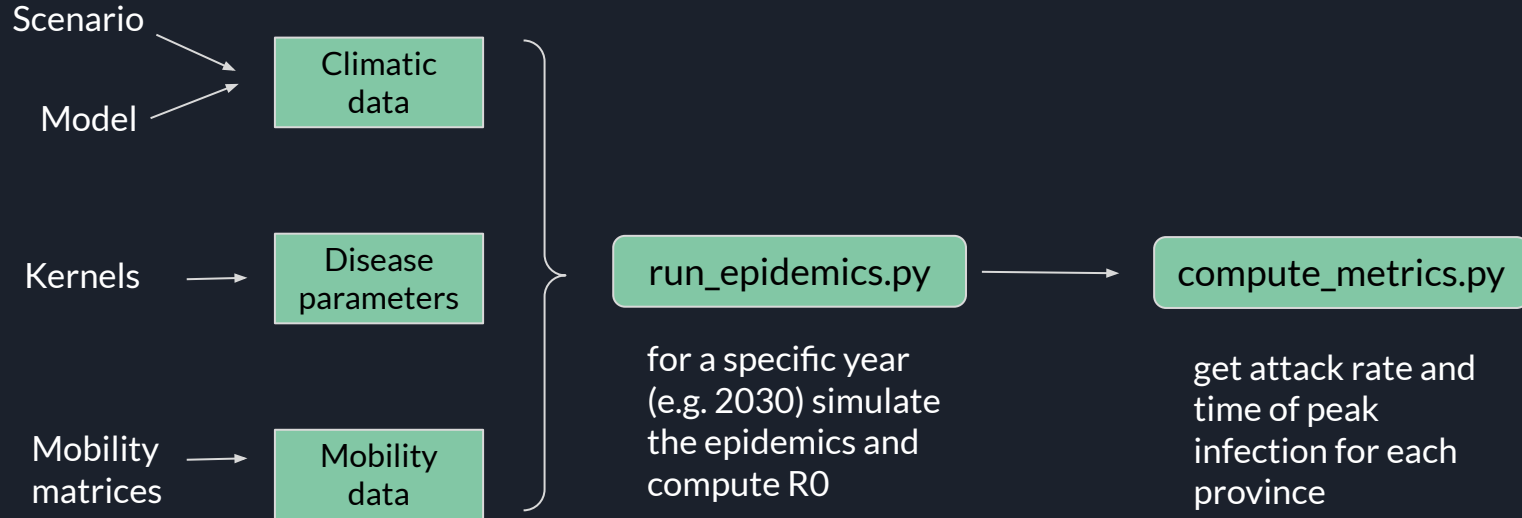
We have different models for climatic projections: ACCESS-CM2, MRI-ESM2-0, CESM2

And different scenarios of greenhouse gases emission: SSP1-2.6 (optimistic), SSP2.4-5 (realistic), SSP5.8-5 (pessimistic)

We mostly want results for DENV, but the pipeline is easily extendable to CHIKV and ZIKA
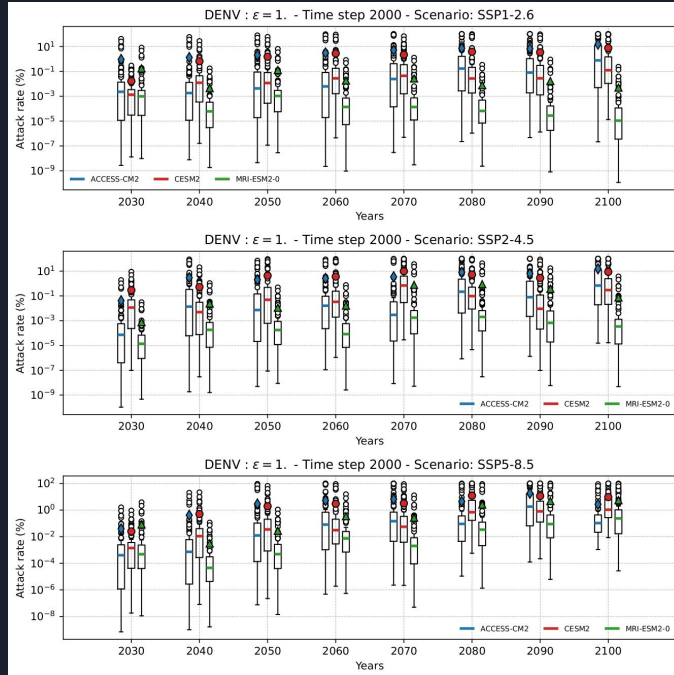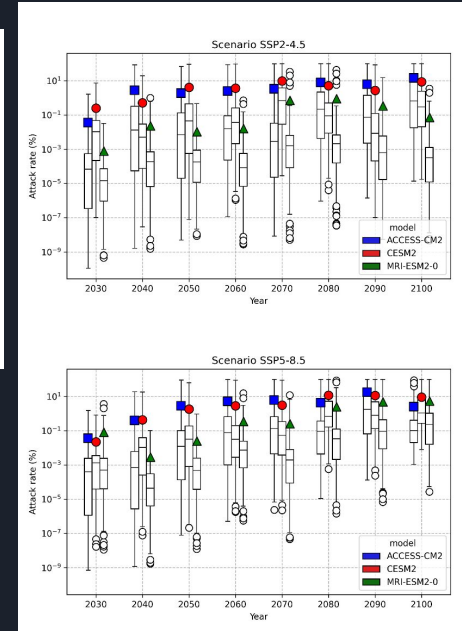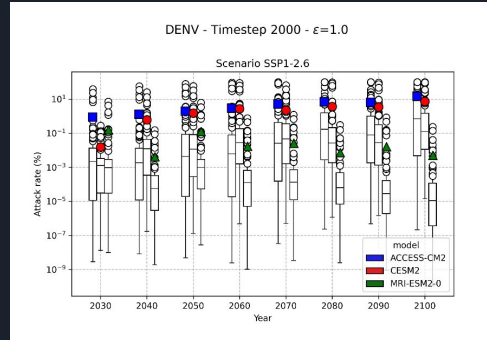
The pipeline

Our working pipeline is so structured:

Scenario

Model

Kernels

Mobility matrices

| Climatic data |
| Disease parameters |
| Mobility data |

run_epidemics.py

for a specific year (e.g. 2030) simulate the epidemics and compute R0

compute_metrics.py

get attack rate and time of peak infection for each province

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What I have done 1: recreating Paolo's plot

To get in touch with the pipeline I tried replicating Paolo's plot. It is a boxplot showing the attack rate over the years in different configurations of models and scenarios (but fixed ε). Logscale on y axis makes it easier to read:

Paolo's:

Mine:

WIHD 2: automating the pipeline

Paolo provided comprehensive code snippets for the run of epidemics and metrics computation given a selection of parameters:
(disease, net type, timestamp, scenario, model, year, ε)

I thought it was better for me to click one button and run all desired configuration, so I wrote a code snippet for running across all combinations of parameters once. The code automatically checks if results already exist for the specified configuration, otherwise it computes it

```
# Lists of parameters to test
models = ["CESM2", "ACCESS-CM2", "MRI-ESM2-0"]  # put your models here
years = [2030, 2040, 2050] #, 2060, 2070, 2080, 2090, 2100]  # put your years here
scenarios = ["SSP1-2.6", "SSP2-4.5","SSP5-8.5"]
epsilons = ["0.1","1.0","10.0"]
```

```
>>> Running: /home/luca3/Desktop/PoD/coding_env/bin/python /home/luca3/Desktop/PoD/stage/joint-model-parma-tobe-arc
hived/joint-model-parma-tobe-archived/run_epidemics_main.py --disease DENV --netType provinces --timeStep 2000 --da
y_to_stamp=123 --model CESM2 --year 2030 --scenario SSP1-2.6 --epsilon 0.0417
|                                                                              | Elapsed: 00:04
[INFO] Results already exist at /home/luca3/Desktop/PoD/stage/joint-model-parma-tobe-archived/joint-model-parma-tob
e-archived/luca_runs/DENV_provinces_2000_2030_SSP1-2.6_CESM2_0.0417, skipping run.
|                                                                              | Elapsed: 00:06
✅ Finished successfully
```

WIHD 3: exploring ε influence

Before attempting any run, I tried to give a naif interpretation of ε and what to expect when changing it

It is described in vademecum as the parameter that "informs on the relative velocity between disease and mobility"

In practice, ε handles the fraction of hosts that contribute to disease spreading in their own patch. This is obtained by

$$\frac{1}{1+\frac{1}{\epsilon}}$$

which tends to 0 as ε tends to 0
and to 1 when ε tends to ∞

So basically I expect the spread of the disease to be faster and more impactful as ε grows

WIHD 3: exploring ε influence

As expected increasing ε leads the attack rate to increase. This trend seems to be consistent across all scenarios and models
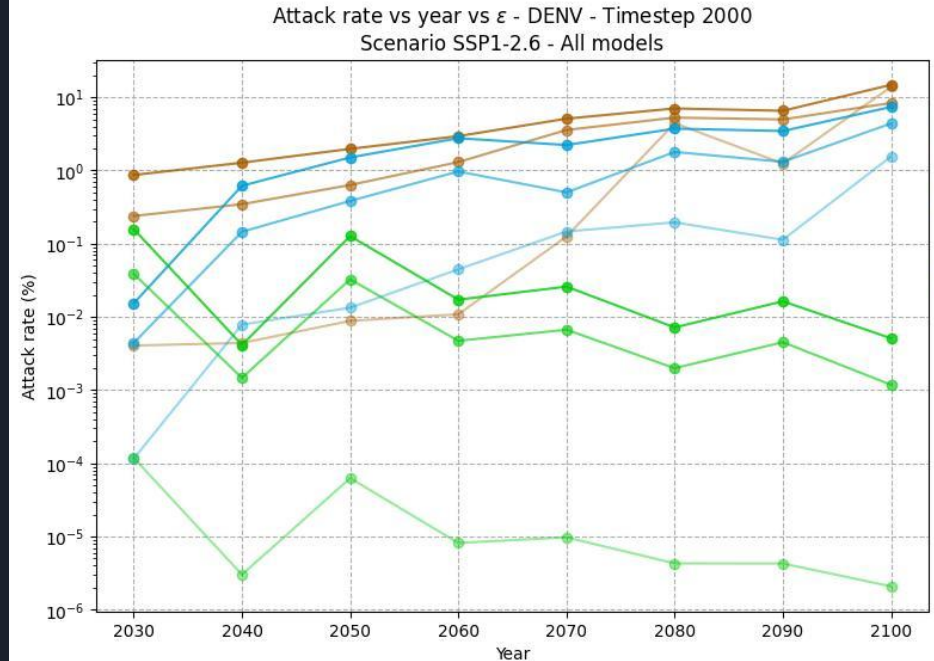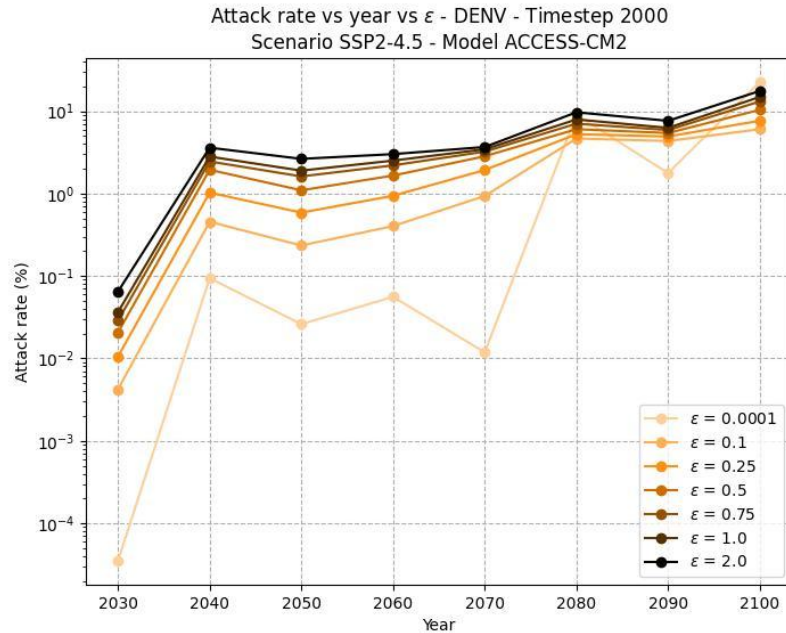
WIHD 4: exploring ε deeply

Now I wanted to see what happened by only adjusting **ε** while keeping all other parameters constant. When I plotted results using logscale on x and y, I was surprised:
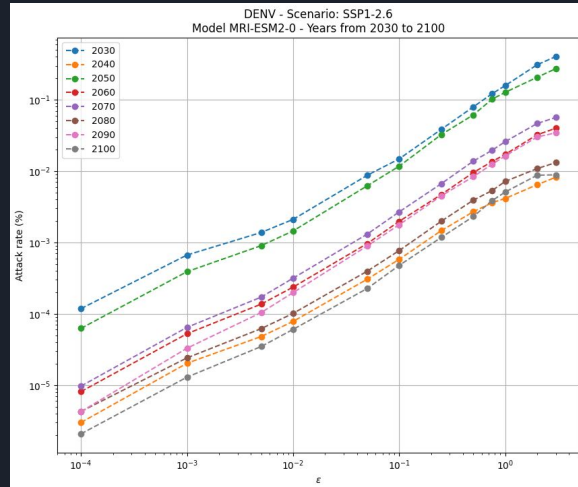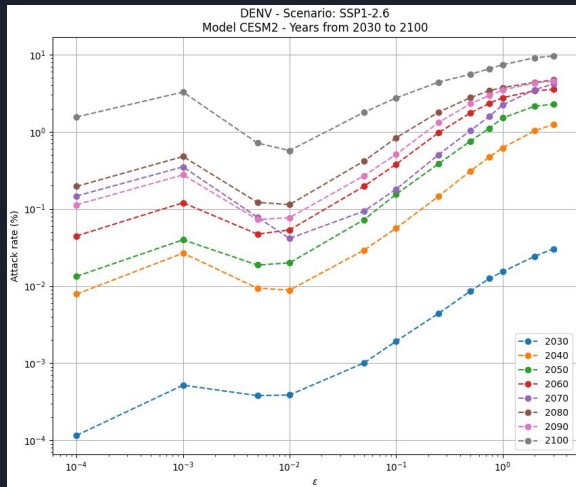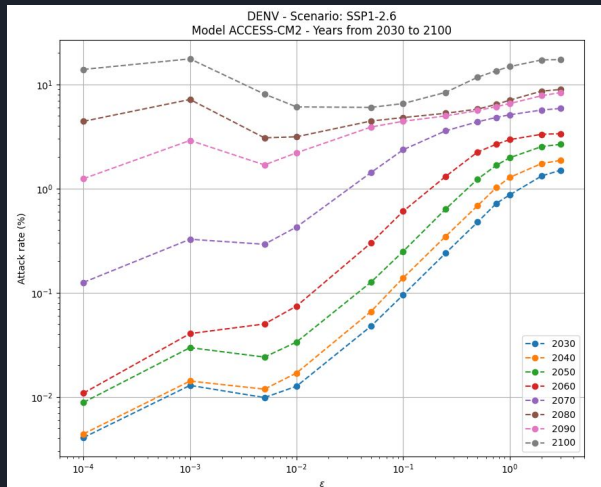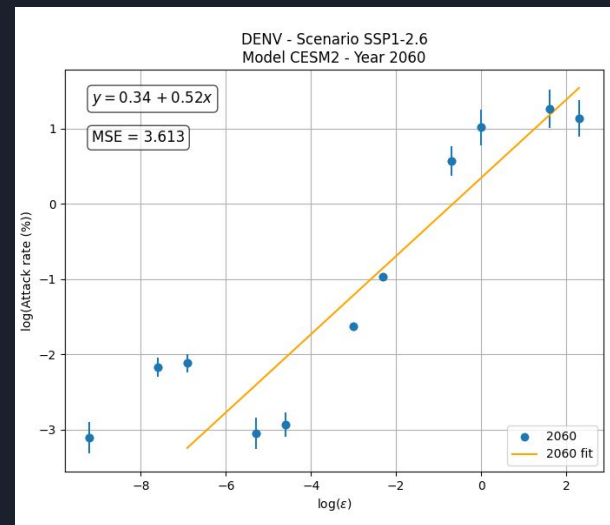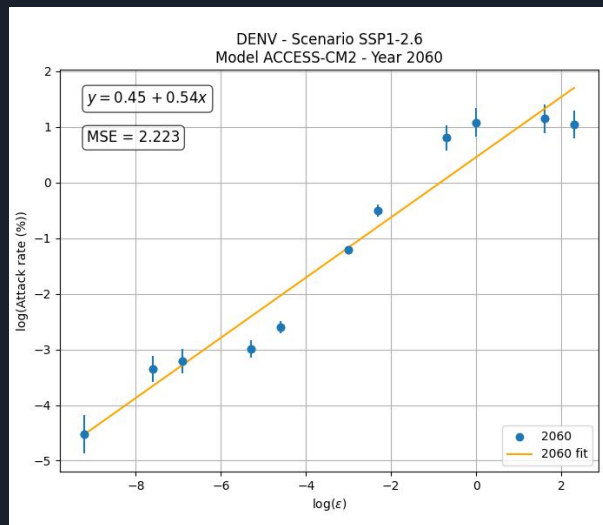
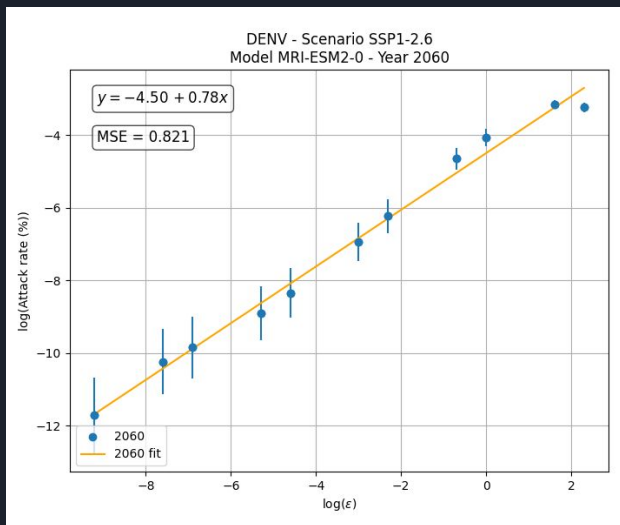

The relation is almost linear in for specific ε ranges, depending on the scenario-model combination

Could there be a power law?

WIHD 5: fitting ε

The power-law hypothesis is generally accurate, but this depends on the combination of model and scenario

WIHD 6: questions on ε meaning

We must remember the nature of ε parameter: it influences the fraction of hosts that contribute to their own patch. Moreover, I tried to think about the meaning of "relative velocity" between mobility and disease related events

ε could then be seen as a dimensionless parameter that explains the difference in timescale of those events. Something such as:

$$\epsilon = \frac{\tau_{disease}}{\tau_{mobility}}$$ where for $\tau_{disease}$ I refer to the typical time span of a mobility event and $\tau_{mobility}$ refers instead to typical time spans of disease events

In this framework ε ranges vary depending on the type of mobility event considered:

- $\tau \in [10, 20]$ days for **epidemics** events
- $\tau \in [0.5, 1]$ day for **mobility** events (**daily commute**, contribute to own patch)
- $\tau \in [60, 120]$ days for **mobility** events (**migrations**, contribute to new patches)

I expect that the infections behave differently based on the type of chosen mobility events

WIHD 6: questions on ε meaning

So far I have considered only average values of attack rates (in %) in my analysis. But what about the distribution of attack rates across the provinces?I tried to plot some to have a rough idea of what is happening:
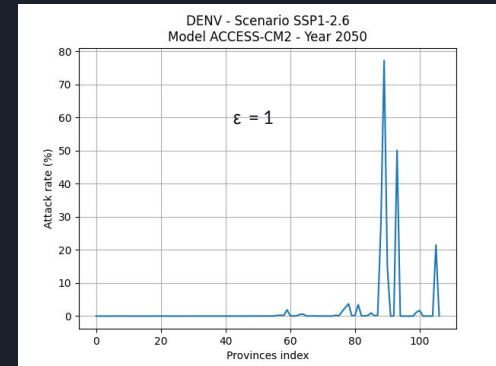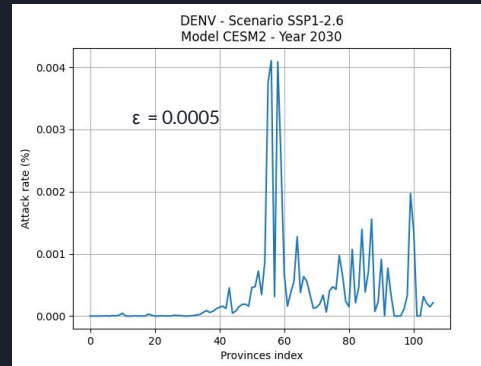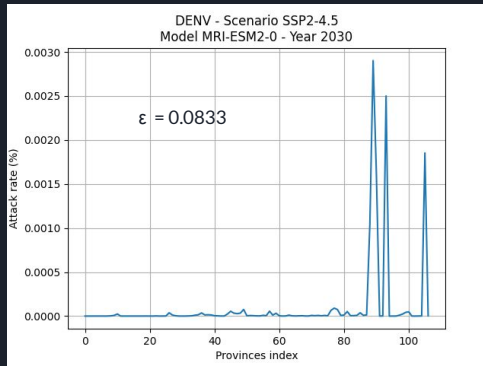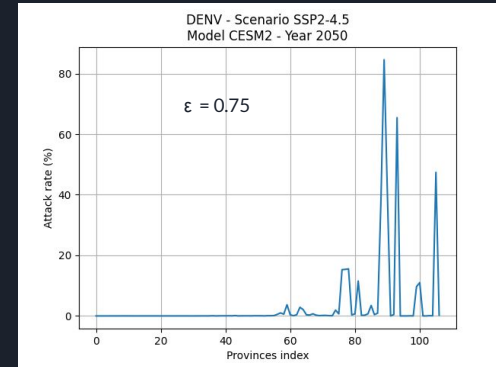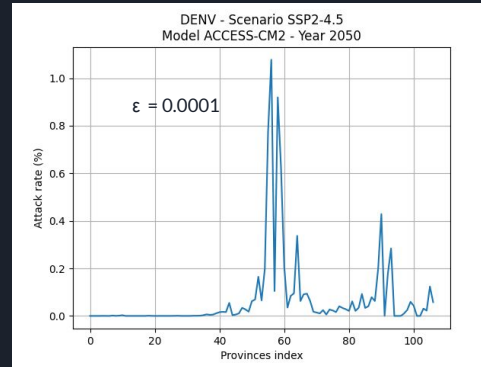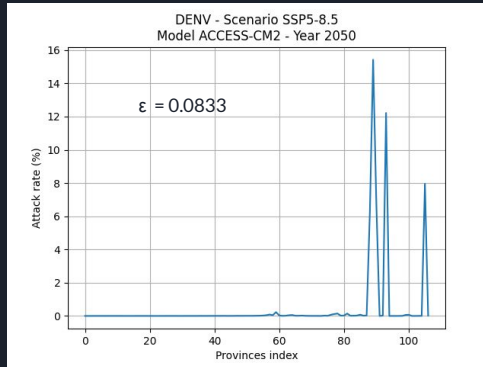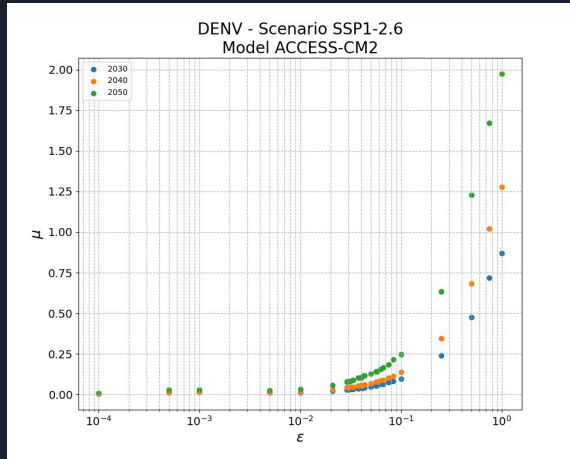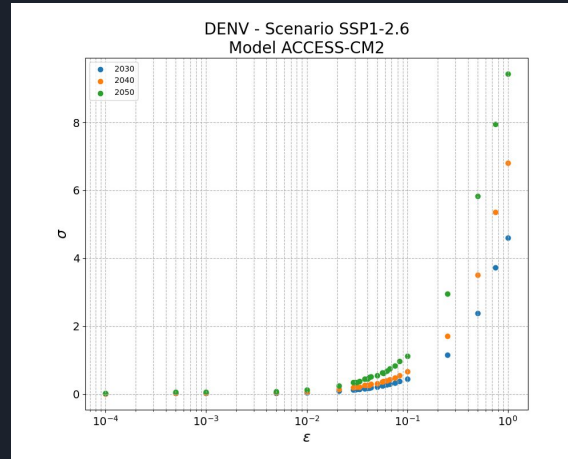
WIHD 6: questions on ε meaning

As seen previously the distribution and absolute values of attack rates are really dependent on the scenario, model and year chosen

I wanted to see how the distribution of attack rate over provinces changes with ε

μ vs ε   σ vs ε   σ/μ vs ε
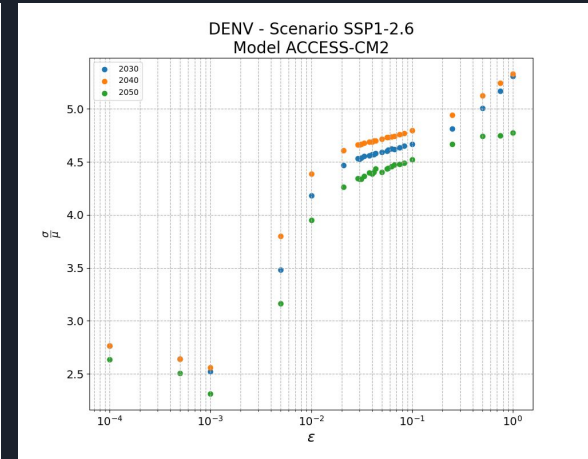
Trends show that both μ and σ **increase** with ε, leading to higher overall **prevalence** and **incidence**

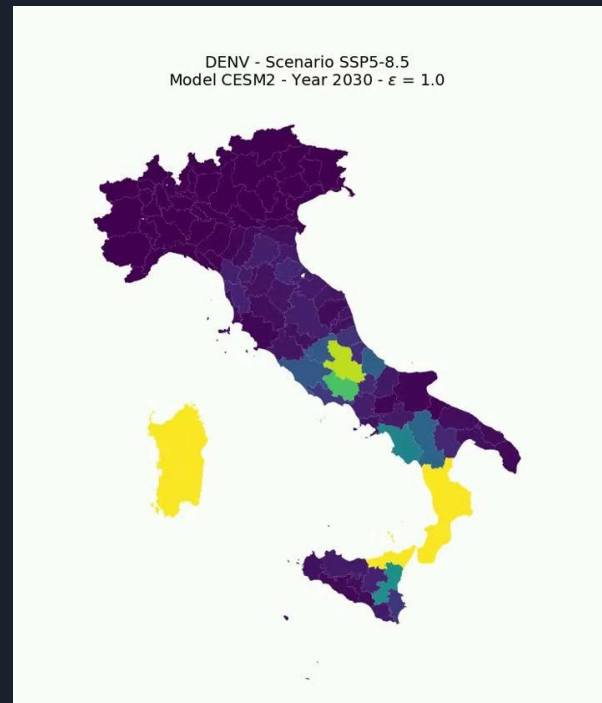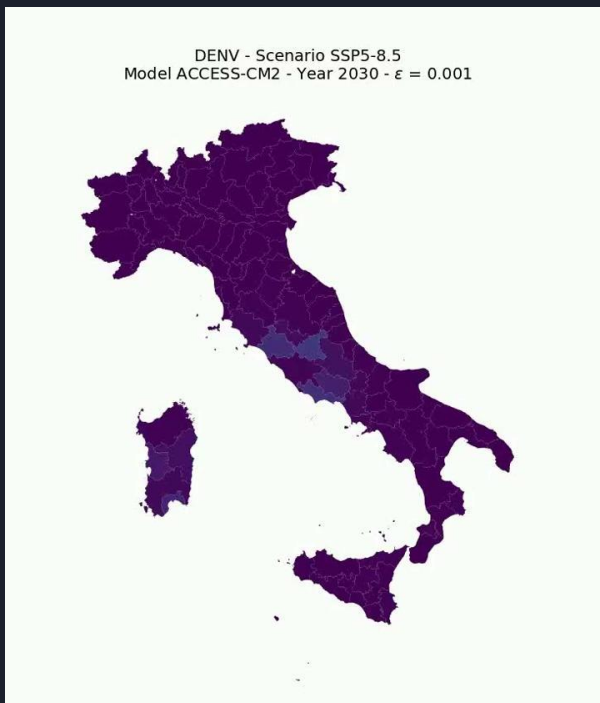Moreover, as ε grows, σ grows faster than μ, leading to higher **spatial heterogeneity**

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WIHD 6: questions on ε meaning

In addition to that, I wanted to explore what happens to the attack rate when fixing the parameters, but leaving ε free:

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WIHD 6: questions on ε meaning

And what happens when keeping ε to a fixed value and increasing the year:

Testing ε vs every combination

I now want to quantify the influence of ε on every combination. To do that, I took simulations for different ε values [0.1, 0.5, 1, 5, 10] for all combinations of model-scenario, and I computed the average maximum increase in attack rate across the years:

Scenario	Model	Average change in attack rate (%)
SSP1-2.6	ACCESS-CM2	12.1 ± 3.4
	CESM2	6.9 ± 2.9
	MRI-ESM2-0	0.2 ± 0.2
SSP2-4.5	ACCESS-CM2	13.2 ± 5.0
	CESM2	8.7 ± 3.3
	MRI-ESM2-0	0.8 ± 0.6
SSP5-8.5	ACCESS-CM2	15.6 ± 5.1
	CESM2	10.7 ± 3.3
	MRI-ESM2-0	5.3 ± 2.9

Final considerations

So far I have explored:
- exclusively DENV simulations
- all combinations of scenarios and models
- a rather comprehensive list of values for ε

From the plots and the seen results I took some considerations:
- as expected, increasing ε leads the epidemics to spread with higher prevalence and incidence
- effects of ε really depend on the model-scenario combination, with higher impact on **ACCESS** model and **SSP5** scenario
- the **power-law** hypothesis is realistic, but it validity strictly depends from the model-scenario combination and is valid only for specific ε ranges
- generally speaking, provinces with higher incidences are always the same across most combinations: these are the areas most subject to change in climate variables and that have airports

Thank you for your attention!