Multispecies diseases

Two different approaches for spatial epidemics models

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Multi-species on different patches

$$S'_{ip} = d_{ip}(N_{ip} - S_{ip}) + v_{ip}R_{ip} - \sum_{j=1}^{s} \beta_{ijp}S_{ip}\frac{I_{jp}}{N_{jp}} + \sum_{q=1}^{n} m_{ipq}S_{iq} - \Gamma_{ip}S_{ip}$$

$$E'_{ip} = \sum_{j=1}^{s} \beta_{ijp}S_{ip}\frac{I_{jp}}{N_{jp}} - (d_{ip} + \varepsilon_{ip})E_{ip} + \sum_{q=1}^{n} m_{ipq}E_{iq} - \Gamma_{ip}E_{ip}$$

$$I'_{ip} = \varepsilon_{ip}E_{ip} - (d_{ip} + \gamma_{ip})I_{ip} + \sum_{q=1}^{n} m_{ipq}I_{iq} - \Gamma_{ip}I_{ip}$$

$$R'_{ip} = \gamma_{ip}I_{ip} - (d_{ip} + v_{ip})R_{ip} + \sum_{q=1}^{n} m_{ipq}R_{iq} - \Gamma_{ip}R_{ip}$$

$$\Gamma_{ip} = \sum_{q=1}^{n} m_{iqp}.$$

SEERS compartmental model with s species (i) on n patches (p).

Migration between patches, m_{pq} gives the movement from patch q to p.

From J. Arino et al, 2005

Mobility matrix

$$N'_{ip} = \sum_{q=1}^{n} m_{ipq} N_{iq} - \Gamma_{ip} N_{ip} \quad \Gamma_{ip} = \sum_{q=1}^{n} m_{iqp} \quad \longrightarrow \quad N'_i = M_i N_i$$

Dynamics of population of species i

We can build the matrix M as $M_i = \widehat{M}_i - D_i$, with $\widehat{M}_i = [m_{ipq}]$ and D_i has Γ_{ip} on the diagonal (p,p).
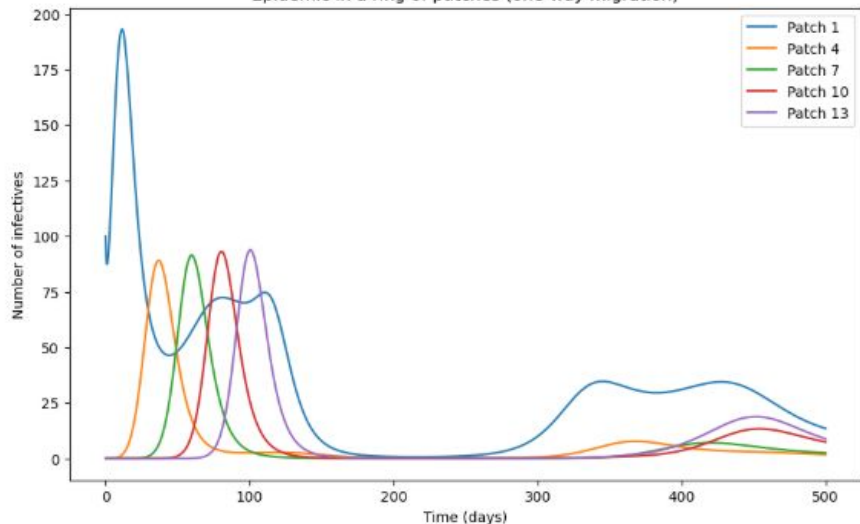
After some manipulations, we can build the matrices G,B,C,A to get the following result

Theorem 2.1. *For model* (2.3) *with s species and n patches,*

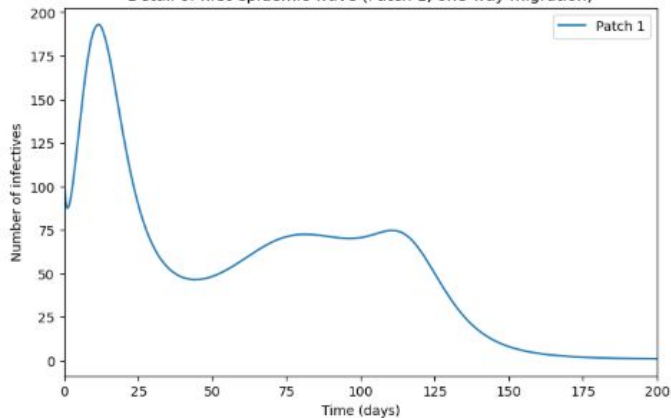$$\mathcal{R}_0 = \rho(GB^{-1}CA^{-1})$$

where ρ denotes the spectral radius. If $\mathcal{R}_0 < 1$, then the DFE is globally asymptotically stable, if $\mathcal{R}_0 > 1$ then the DFE is unstable.

Epidemic in a ring of patches (one-way migration)

Detail of first epidemic wave (Patch 1, one-way migration)

Ring of patches + one-way migration

- Each patch is placed in a ring and migration only occurs to the next patch (with the last patch looping back to the first).

- The secondary peaks we see in the second (and first) plot are the 'periodicity' of the migration. The first wave loops all the way back to patch 1, and since the migration brings in new susceptibles it reignites the epidemic.

Ring of patches + two-way migration

- Same as last time, but this time migration is allowed to both of the closest patches for any particular patch.

- Because of symmetry, the epidemic doesn't spread as much, the inflow of new susceptibles is hampered by the spreading of infectious on both sides.

Epidemic in a ring of patches (two-way migration)
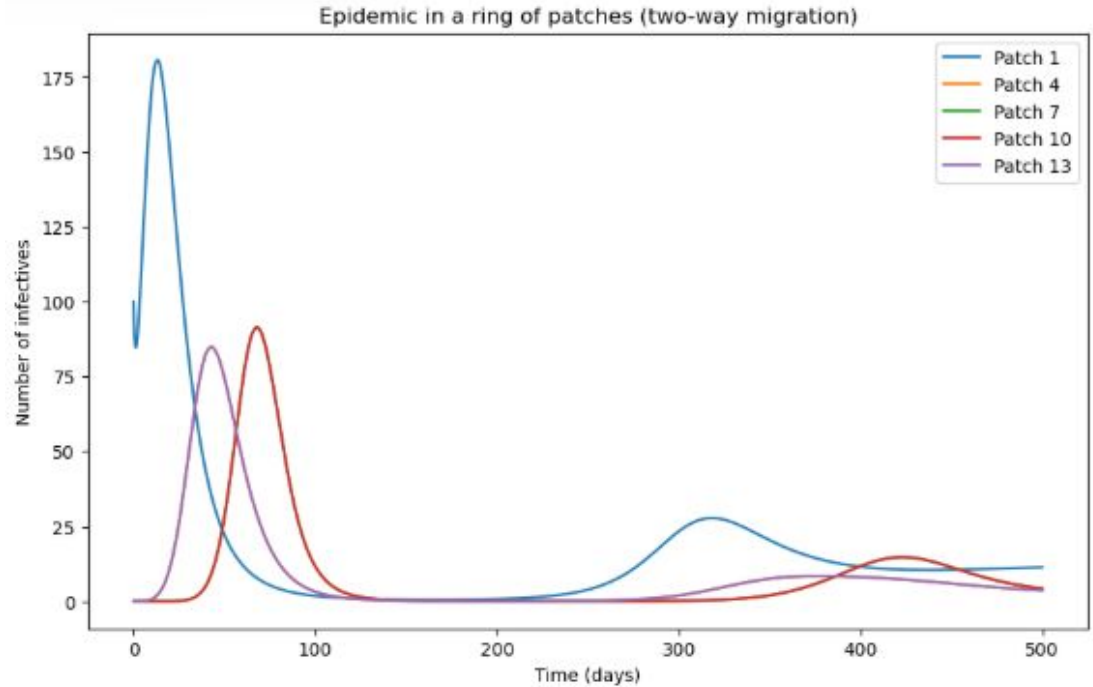
Effects of quarantine

Quarantine a certain strip of patches from a to b. Define two factors r_{int} and r_{ext}, both between 0 and 1, representing the reduction of migration. r_{int} is for migrations within the quarantined patches, r_{ext} for migrations from and to the quarantined patches to the non-quarantined.

We can define the efficacy as 1-r for both and calculate the quarantine reproduction number as in theorem 2.1, reducing the rates in m_{iqp} by the factor r.

Effects of quarantine

```
One-way internal quarantine (patch 7):
 r_factor  avg_total_I  min_avg_patch  max_avg_patch       Rq
    1.000     112.8261         4.0541        25.0071 2.5265
    0.500     111.9945         3.8680        23.3052 2.5265
    0.100     108.9380         2.2522        25.5754 2.5265
    0.001     106.1554         0.0635        58.2401 2.5265
    0.000      97.9587         0.0000        58.8917 1.9996

One-way external quarantine (patch 1):
 r_factor  avg_total_I  min_avg_patch  max_avg_patch       Rq
    1.000     112.8261         4.0541        25.0071 2.5265
    0.500     113.9397         3.5628        31.6745 2.7472
    0.100     116.7969         2.5572        39.6996 2.9461
    0.001     106.6633         0.4487        64.5119 2.9988
    0.000       9.8743         0.0000         9.8743 2.9993
```
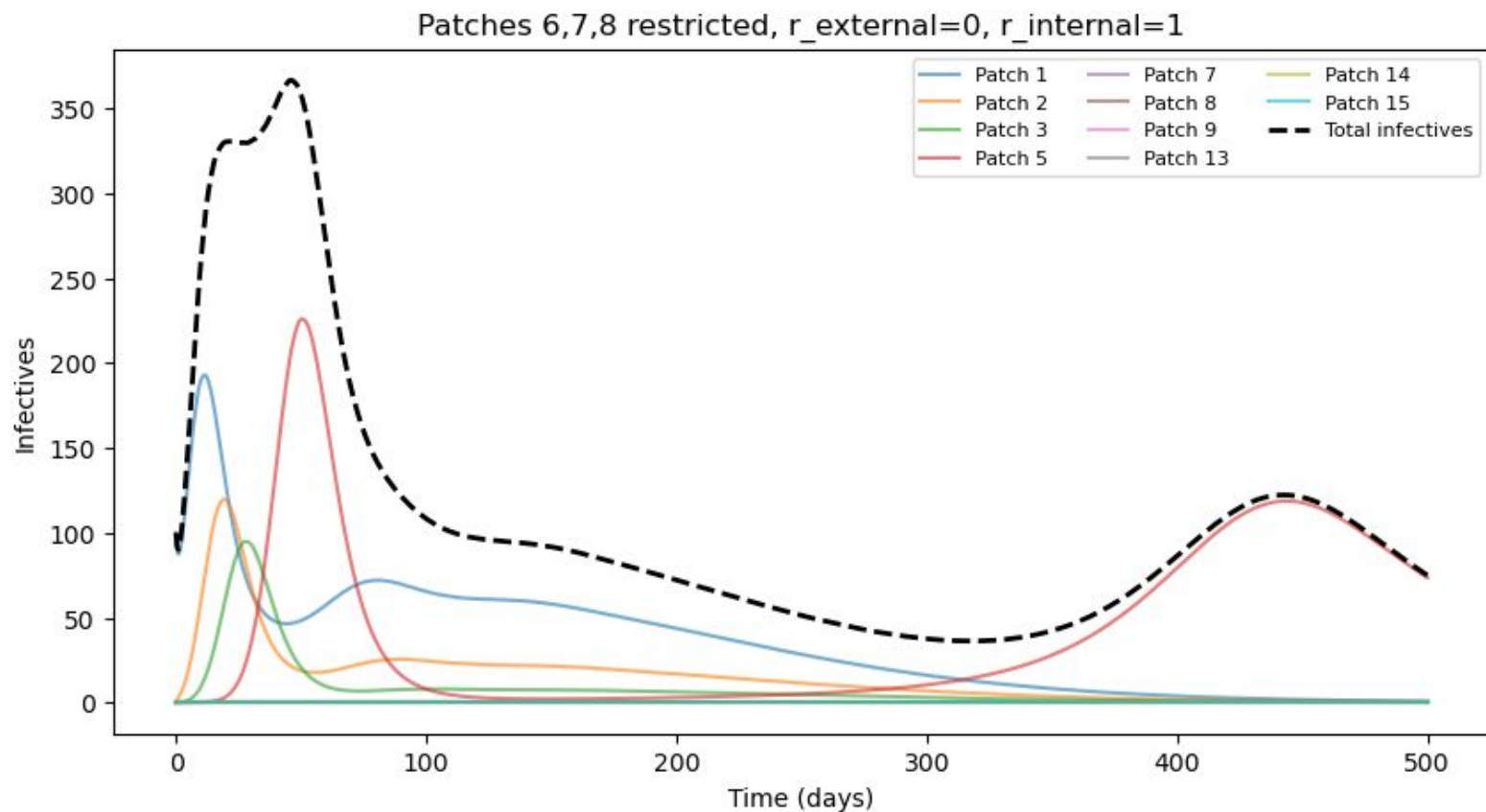
- The number of infected is quite high despite 100% quarantine efficacy

- For perfect quarantine, the infected are kept in patch 1, it doesn't spread

Effects of quarantine

Patches 6,7,8 restricted, r_external=0, r_internal=1

Rift Valley Fever

→Mostly asymptomatic in humans, but can sometimes cause dengue-like symptoms, eye disease, encepalitis, hemorrhagic fever or death.

→ In animals such as sheep, cattle and goats it can cause waves of abortion and high rates of neonatal deaths.

Rift Valley Fever in the Comoros Archipelago

- deterministic, discrete-time, age-structured SEIR metapopulation model
- Within patch dynamics are SEIR with 10 distinct age groups.
- Patches are connected by explicit livestock movement of the youngest age group.
- Bayesian inference of parameters.

a Between island model
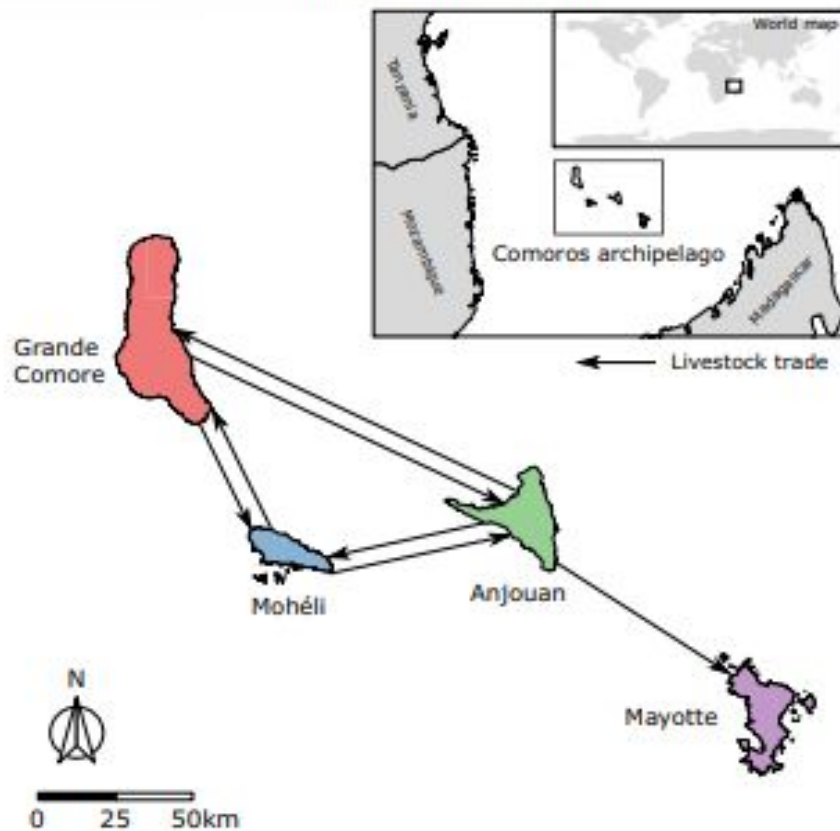
b Within-island model

W. Tennant et al, 2021
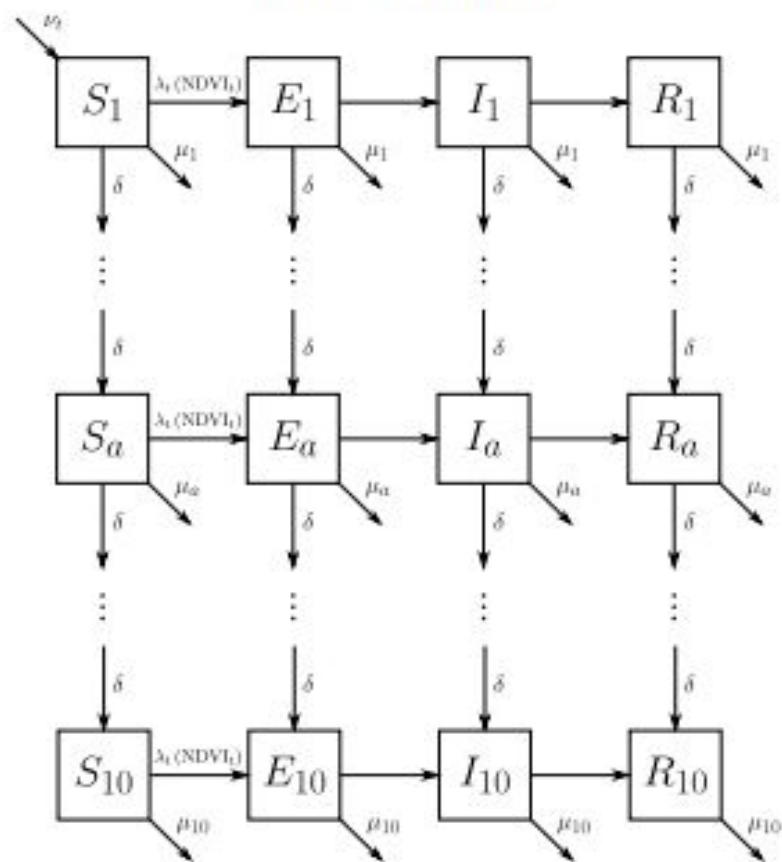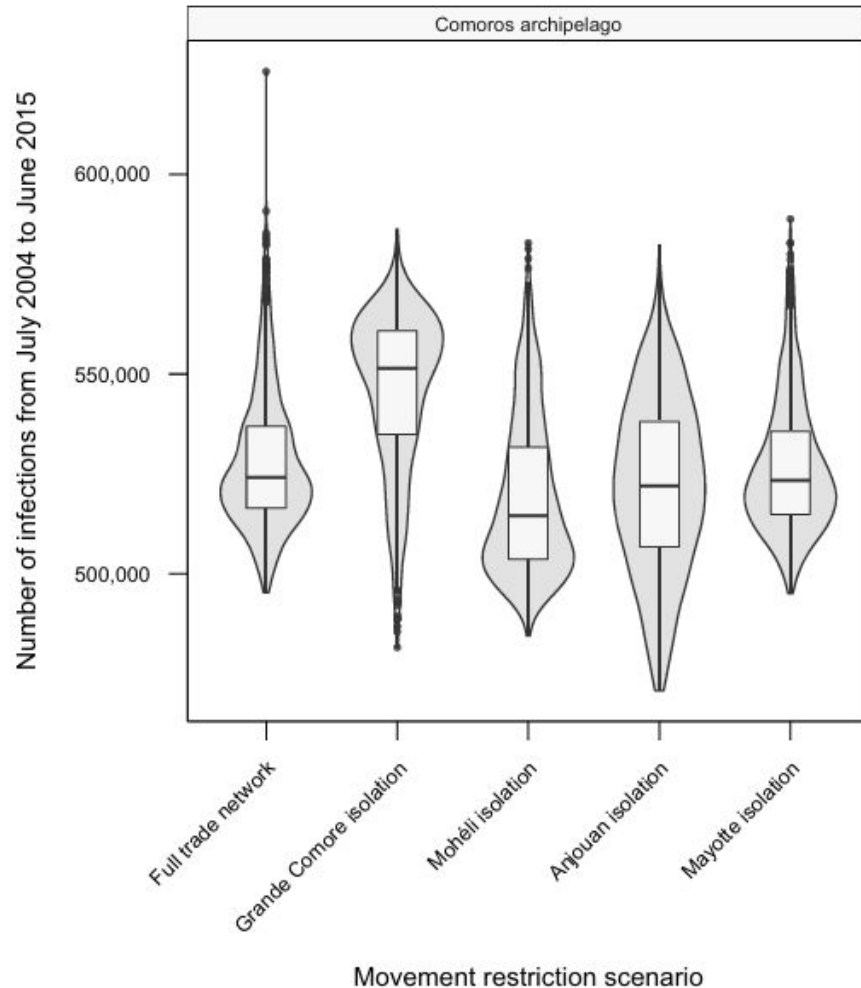
Surprisingly, isolating islands increases the overall number of infections in the archipelago.

Within islands restrictions have a stronger impact on the reduction of infections, both on the island as on the archipelago.
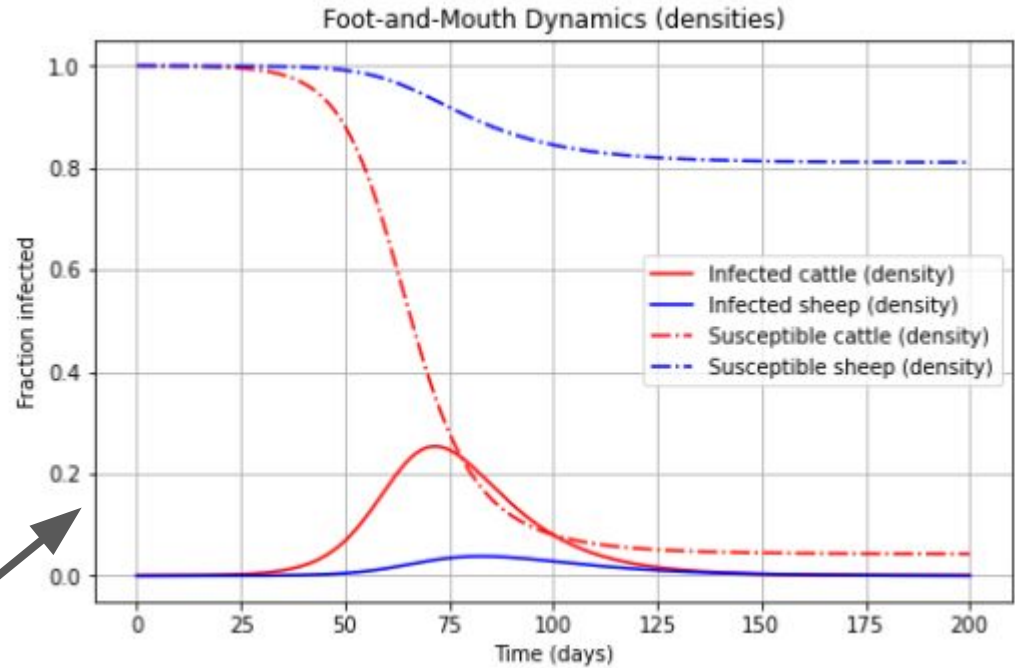
FOOT-AND-MOUTH DISEASE

Causes fever and blisters in the mouth and hoof, resulting in lameness and lower milk/meat production.

- Efforts to model/predict requires understanding of the interplay between species.

Transmission matrix between cattle and sheep

$$\beta = b \begin{pmatrix} 27 & 15 \\ 1.8 & 1 \end{pmatrix}$$

We can see that cattle are the propagators of the disease. In the absence of cattle the reproduction rate in sheep is just 0.4; control measures (vaccination/culling) should therefore target cattle.

Foot-and-Mouth Dynamics (densities)

- Infected cattle (density)
- Infected sheep (density)
- Susceptible cattle (density)
- Susceptible sheep (density)

Two questions:
1) Is the epidemic 'under control'
2) Whether additional targeted culling would lead to a reduction in total loss of livestock.

THREE MODELS USED FOR 2001 FOOT-AND MOUTH EPIDEMIC

1) InterSpread

The first model used for FMD 2001. We initially seed with the known location of all farms + livestock as listed in the latest census. Transmission is dependent on distances between farms and number/type of livestock. Other mechanisms can be either very simple or *very* complex. The vast number of mechanisms is both a strength and a weakness.

2) Cambridge-Edinburgh model

An explicit spatial model. We seed all farms identical to InterSpread. Transmission is simply modelled as susceptibility multiplied by infectivities.

Infection rate for farm j

$$= \text{Susceptibility}^j \times \sum_{\text{infectious farms } i} \text{Infectivity}^i \times K(d_{ij}),$$

where

$$\text{Susceptibility}^j = \sum_s N_s^j S_s \quad \text{Infectivity}^i = \sum_s N_s^i T_s.$$

3) Imperial model

Strongly based on traditional SIR dynamics. Ignores farm-types - only differentiates between local and long-range transmissions. Captures local clustering with SIR ODEs that assume farms can weakly couple over long distances but strongly couple with a limited number of local connections.
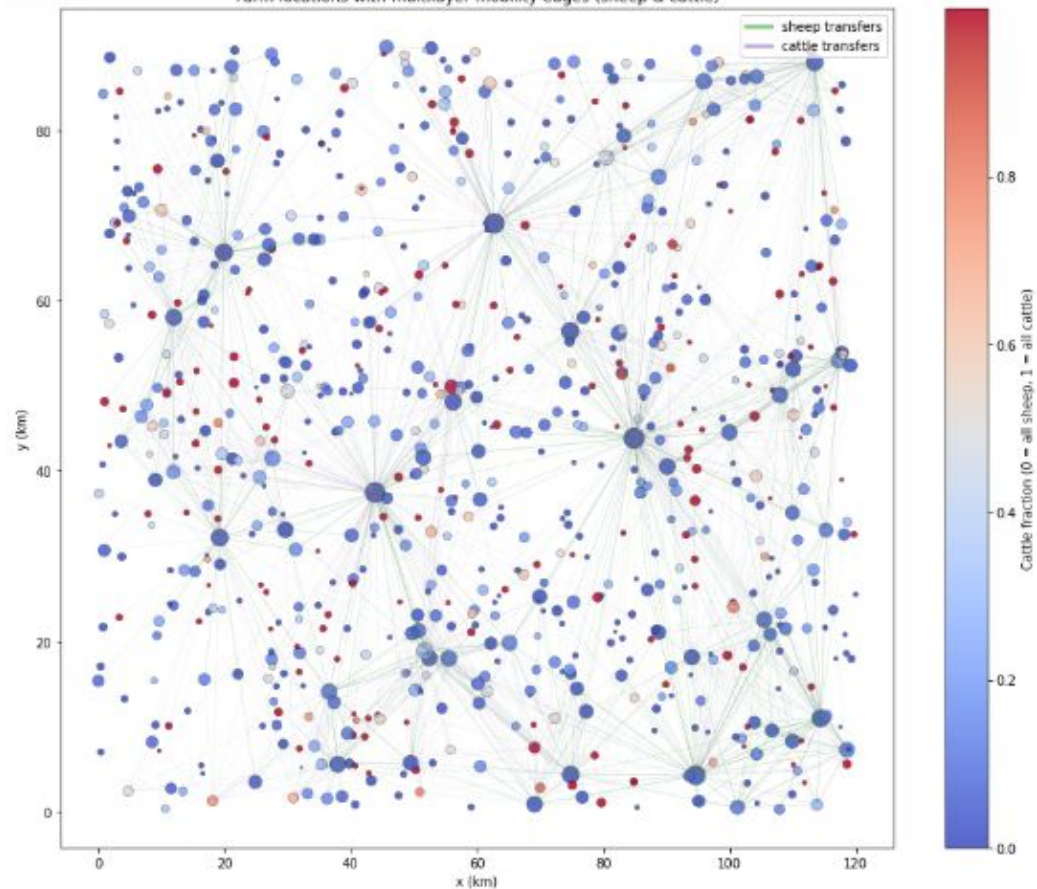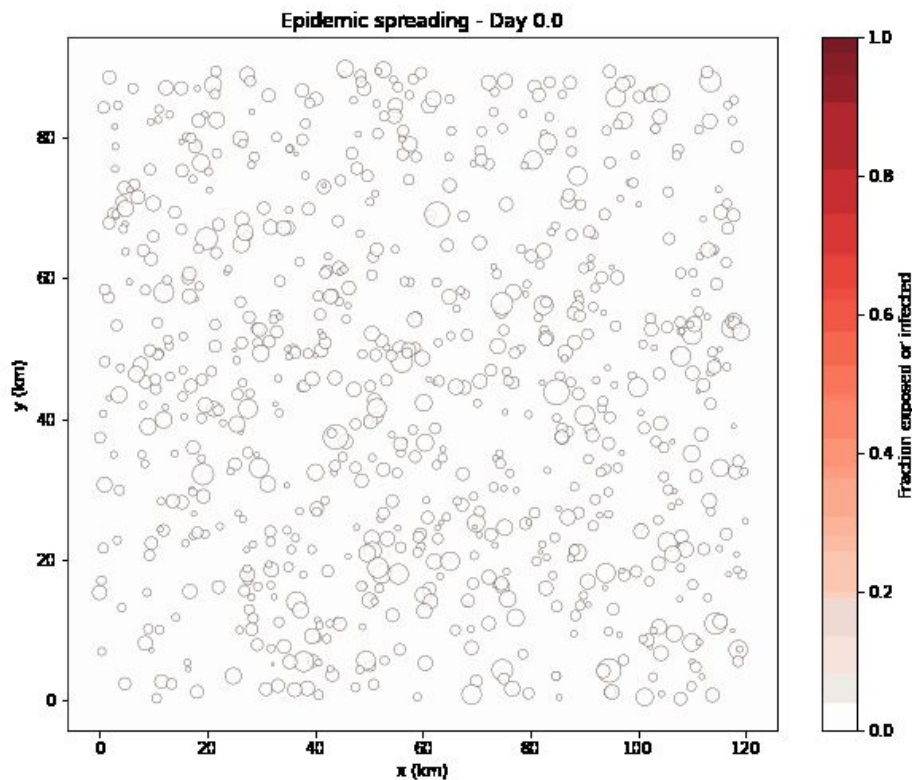
Farm sizes and species composition
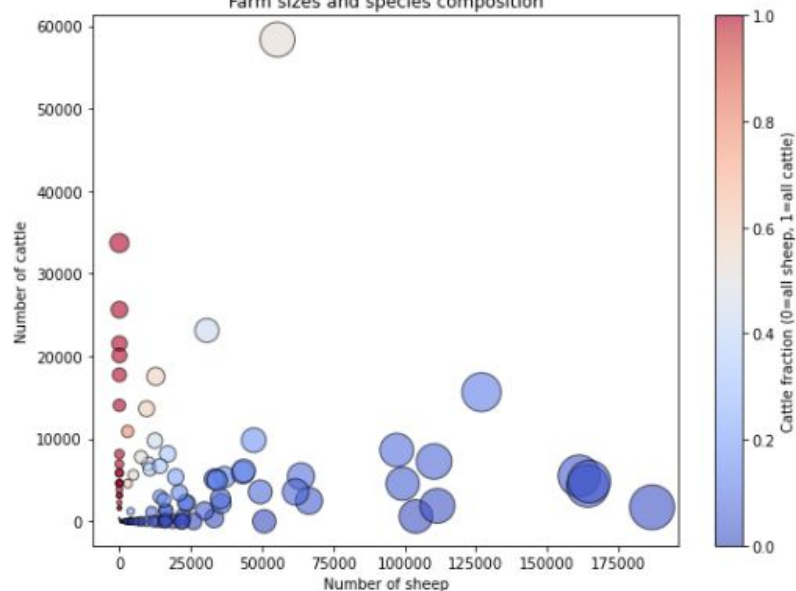
	farm_id	type	sheep	cattle
0	0	mixed	47103	9826
1	1	sheep_only	998	0
2	2	cattle_only	0	1625
3	3	mixed	33239	373
4	4	sheep_only	13469	0

Totals: 2640000 sheep, 512001 cattle

Farm locations with multilayer mobility edges (sheep & cattle)

Epidemic spreading - Day 0.0

MODEL FOUR: Spread of foot-and-mouth disease in a spatial network of different farms

Farm locations with multilayer mobility edges (sheep & cattle)
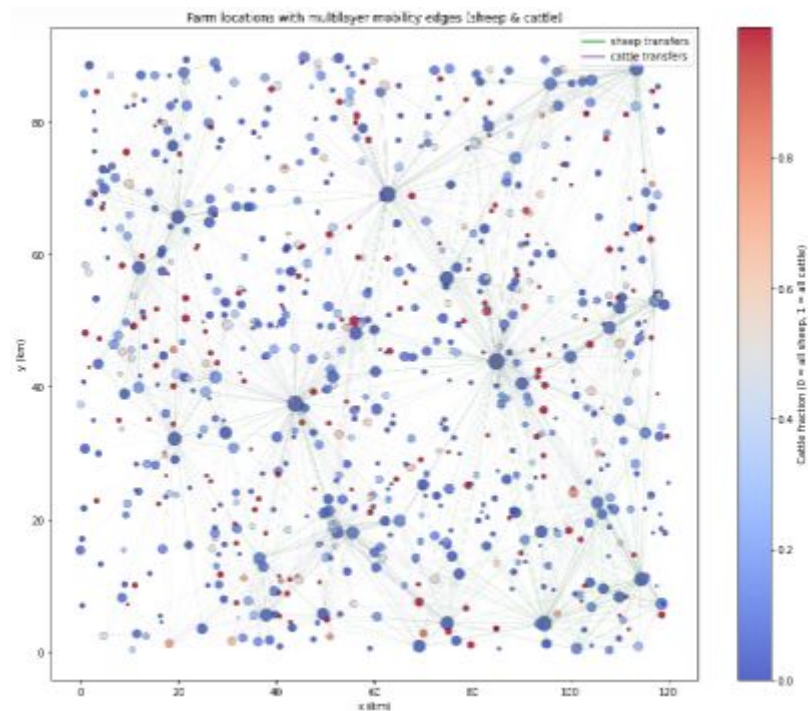
In the last slide the dynamics were randomly spreading sheep-only, cattle-only and mixed farms throughout the plot with transmission inversely proportional to distance.

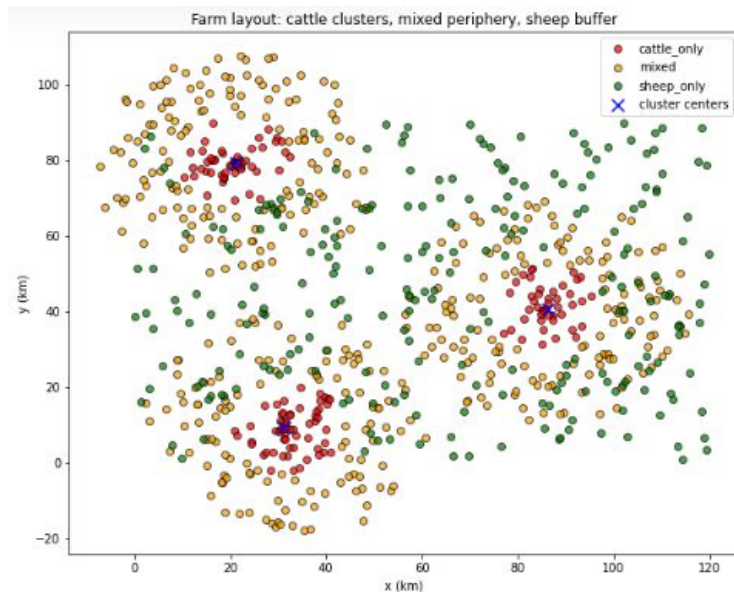**NEXT QUESTION**: if we can place the farms in a way that limits the spread of disease

CATTLE FARMS:
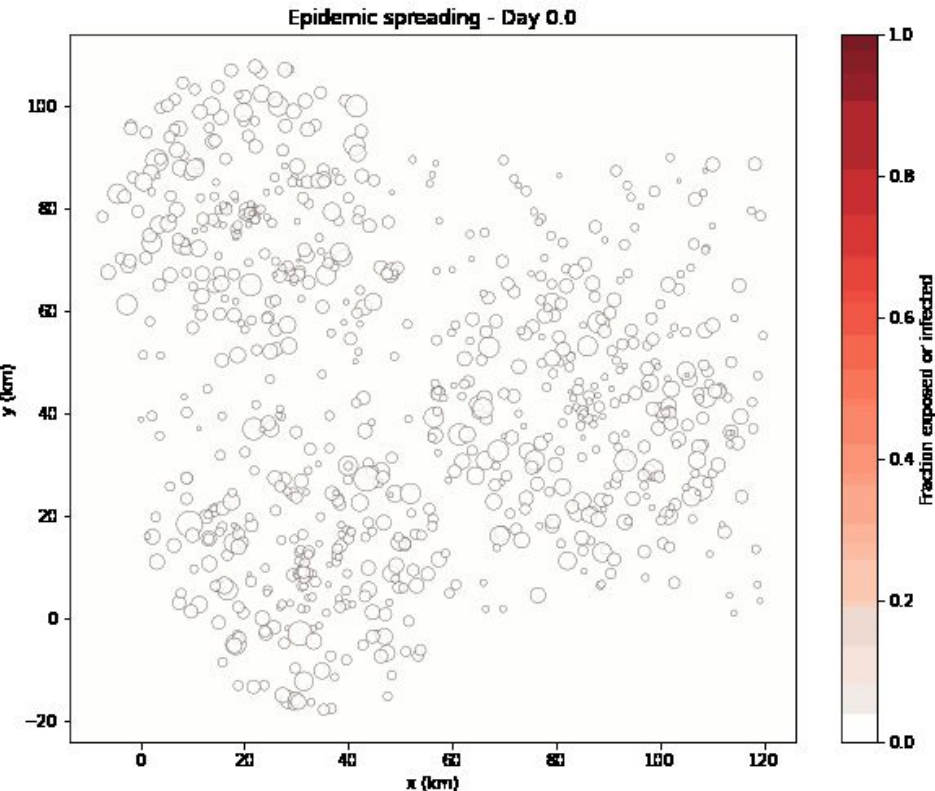Placed in clusters, with each cluster greatly separated from each other.

MIXED FARMS:
Placed around the cattle farm clusters as a buffer.

SHEEP FARMS:
Placed in between the clusters as they seem to be insulators for the epidemic spread.

Farm layout: cattle clusters, mixed periphery, sheep buffer

- cattle_only
- mixed
- sheep_only
- cluster centers

Epidemic spreading - Day 0.0

Strangely, it appears that the mixed farms actually spread the disease *faster* than the cattle farms

```python
# destination preference by farm type for this species
dest_weights = np.zeros(n)
for i, t in enumerate(df['type'].values):
    if species == 'sheep':
        if t == 'sheep_only':
            dest_weights[i] = dest_pref_same
        elif t == 'mixed':
            dest_weights[i] = dest_pref_mixed
        else:  # cattle_only
            dest_weights[i] = dest_pref_other
    elif species == 'cattle':
        if t == 'cattle_only':
            dest_weights[i] = dest_pref_same
        elif t == 'mixed':
            dest_weights[i] = dest_pref_mixed
        else:
            dest_weights[i] = dest_pref_other
    else:
        raise ValueError("species must be 'sheep' or 'cattle'")

dest_total = (df['sheep'] + df['cattle']).values
```

```python
size_attr = np.power(dest_total + 1.0, dest_size_power)
dest_attr = dest_weights * size_attr
```

+ exponential decay due to distance

NEXT QUESTION: The effect of culling cattle on the number of infecteds

- **0-50%:** We see the same dynamics, but as more cattle are culled the weaker the epidemic becomes
- **75%:** The epidemic dies off immediately, with sheep falling and cattle infections never rising above 22.
- **100%:** There are no cattle - this effectively shows the dynamics of a sheep-only farm with no mobility.
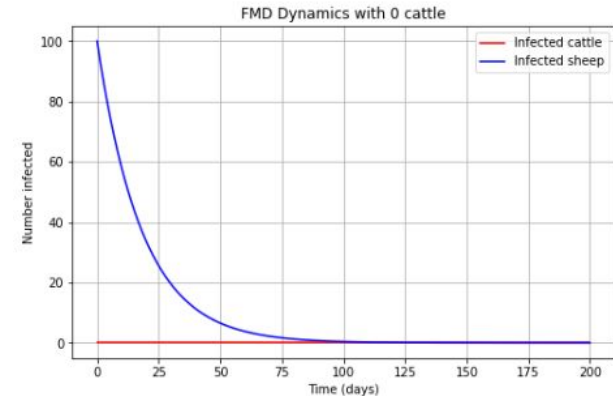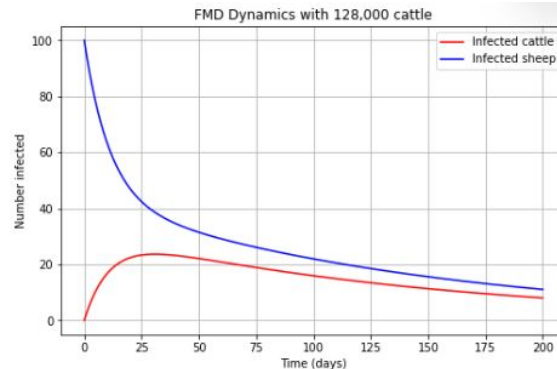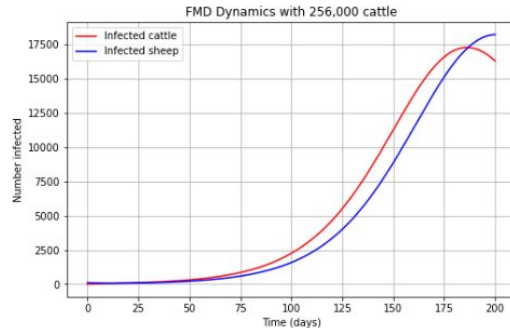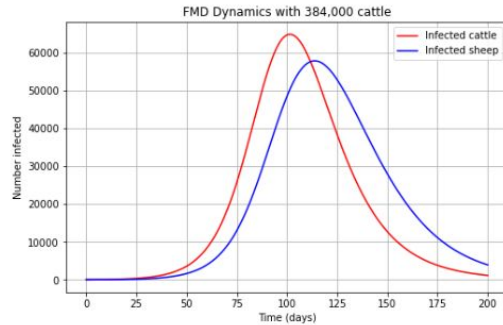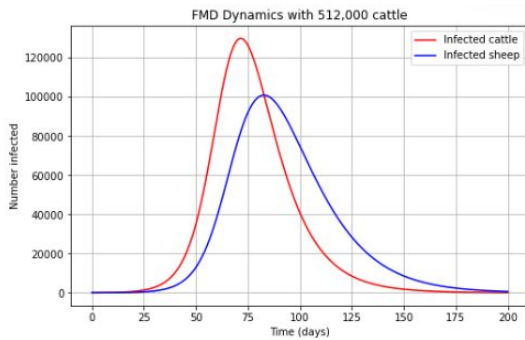
CULLING

Animals can either die from the infection or from culling. The culling percentage is coded by reducing N_c by that percentage. We see exponential decrease at first as infection deaths decrease, but we then see linear increase as culling deaths dominate.

culling vs disease deaths
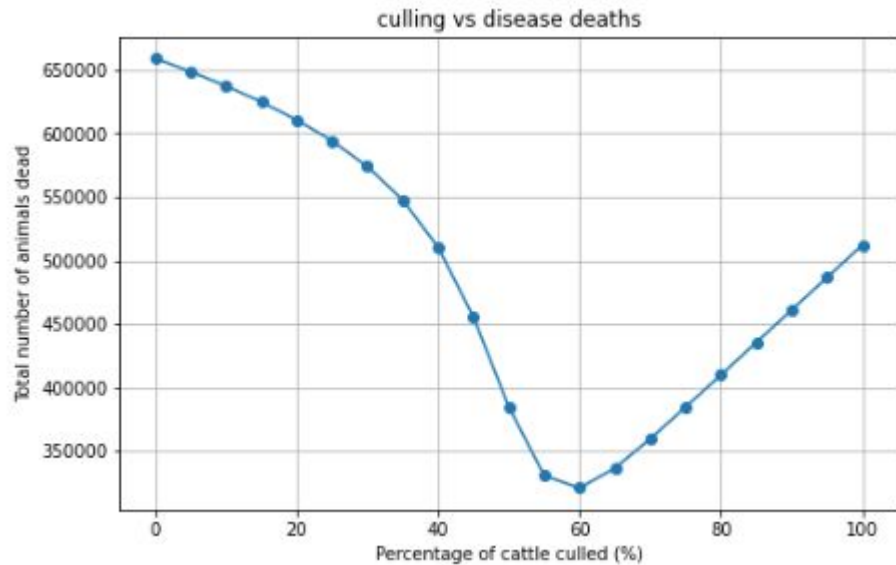
```
for f in fractions:
    Nc = int(f * N_c)
    t, (Sc, Ic, Rc, Ss, Is, Rs) = CullingCows(Nc)

    # Disease deaths: 3% of total infected
    total_infected_cattle = Rc[-1] / (1 - fatality_rate)
    total_infected_sheep  = Rs[-1] / (1 - fatality_rate)
    disease_deaths = fatality_rate * (total_infected_cattle + total_infected_sheep)

    # Culling deaths: difference from original cattle pop
    cull_deaths = N_c - Nc

    # Total deaths
    total_deaths.append(disease_deaths + cull_deaths)
    cull_percents.append(100 * (1 - f))
```

In the real life 2001 foot-and mouth disease epidemic over **6 million cattle** were culled in an attempt to slow the spread.

IMPOSING MOBILITY RESTRICTIONS

We set up one final model, where instead of considering animal populations we consider whole farms to be infected or not.

Farm Types:
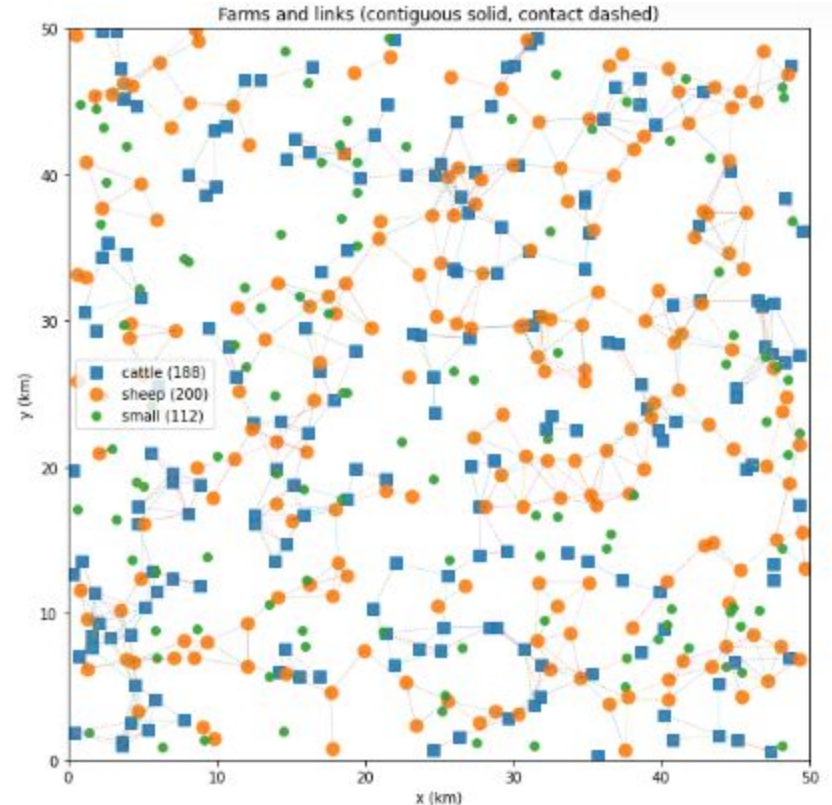Cattle, Sheep, Small

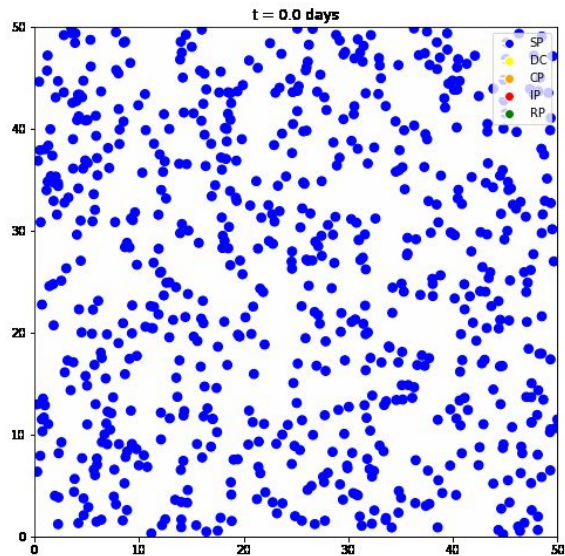**'Hidden' Compartments:**
SP_hid, IP_hid, RP_hid

Public Compartments:
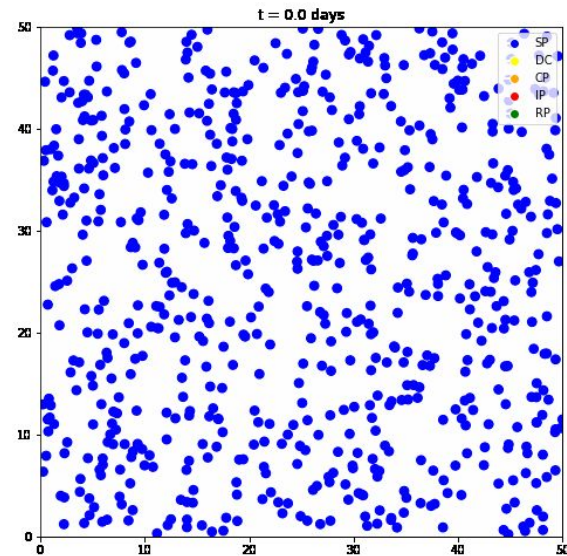SP, CP, DC, IP, RP

Connections between farms:
Contiguous, Contact, Long Distance

Farms and links (contiguous solid, contact dashed)

cattle (188)
sheep (200)
small (112)

# NO LONG DISTANCE JUMPING   WITH LONG DISTANCE JUMPING

MOBILITY RESTRICTIONS

We test for three different scenarios:

1) We cut all Contact/Long Distance edges to IPs.
2) We cut all Contact/Long Distance edges to IPs, DCs, and CPs.
3) We cut every single Contact/Long Distance edge right from the start

We leave Contiguous edges as these represent a connection between two farms that physically touch

Num farms = 1000
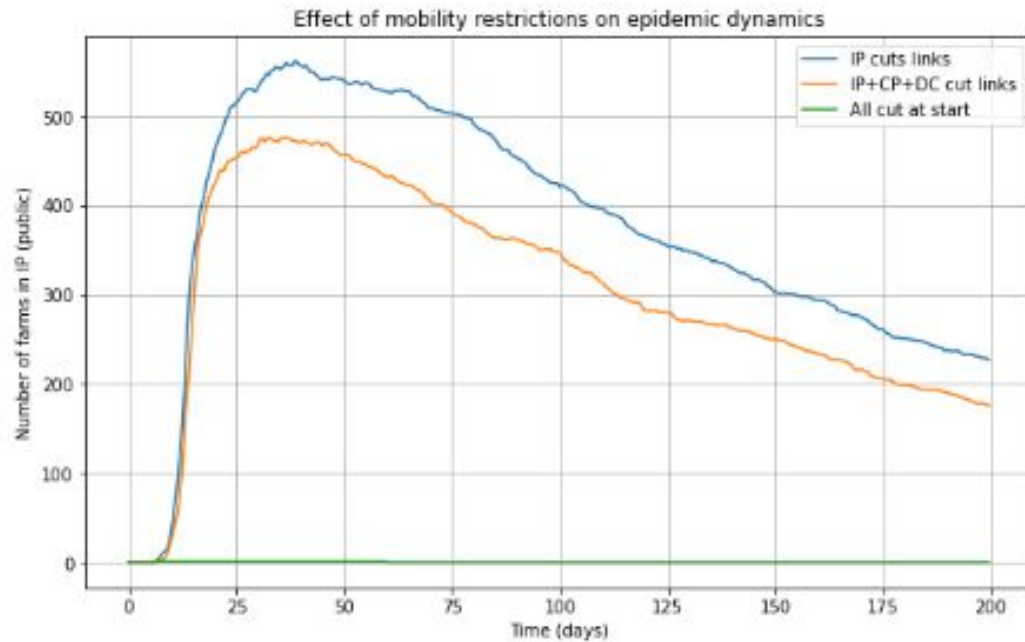
This is when response times = 1 day (was 1 week before) →