Mathematical modeling and simulation for the diffusion of an epidemic of classical swine fever within and between farms

Diego de Pereda

Benjamin Ivorra

Ángel Manuel Ramos

momat

GOBIERNO DE ESPAÑA

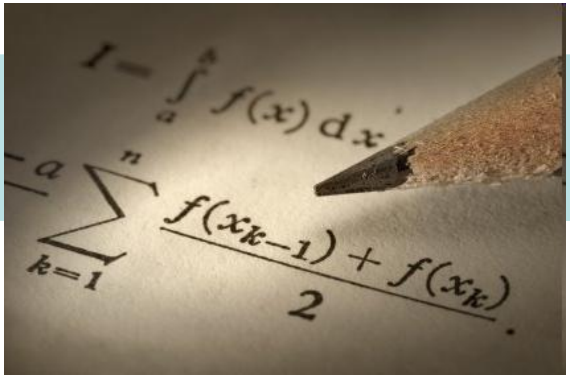
MINISTERIO DE MEDIO AMBIENTE Y MEDIO RURAL Y MARINO

Outlines

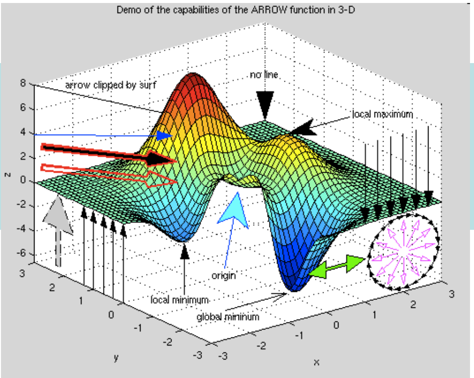
Introduction to epidemiology

- Basic concepts

Mathematical modeling



- SIR models



Numerical simulations

- Application to Classical Swine Fever

Introduction to epidemiology

Definition and objectives

DEFINITION:

Epidemiology consist on the study of spread patterns and associated risk factors of the diseases of humans or animals

The main objectives are:

Describe the **distribution**

Indentify **risk** factors

Prevention and **control**

Historical evolution

Historically, epidemics had a great impact on populations, causing demographic changes

Nowadays, some epidemics are persistent (HIV, malaria, tuberculosis, flu, …)

Historical evolution

Some important achievements:

Daniel Bernouilli (1760): First “statistical” model for smallpox virus variolation

William Heaton (1906): Discrete time model to explain the recurrence of measles

Ronald Ross (1911): PDE model to study the link between malaria and mosquitoes

Differences between diseases

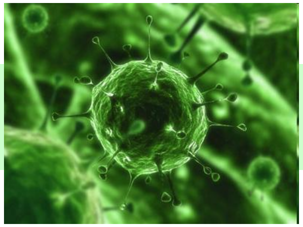
Ways of **transmission**:

Between humans or animals (flu)

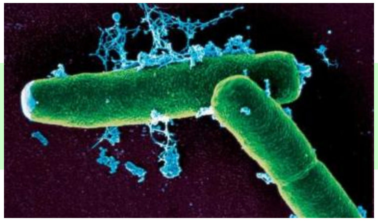
By the **environment** (cholera)

By **vectors**, such as insects (malaria)

Infectious **agents** (for instance):



Virus. Possible immunity



Bacteria. No immunity

Possible states

S **Susceptible**
Sane individuals and susceptible of being infected

E **Infected**
Infected individuals in latent phase, can't infect others

I **Infectious**
Infected individuals that can infect others

C **Clinical signs**
Infectious individuals with clear clinical signs of disease

R **Resistant**
Individuals with immunity to the disease

Population density distribution

$$S + E + I + C + R = 1$$

Basic reproduction number (R_0)

DEFINITION:

R_0 is the expected number of secondary cases produced by a single infection in a completely susceptible population

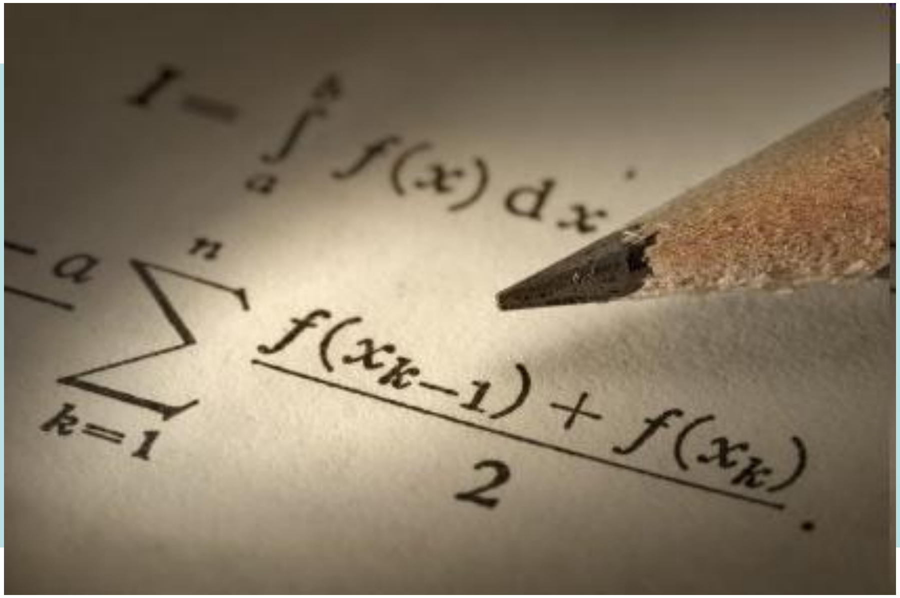
If $R_0 \leq 1$ then infection will **disappear** from population

If $R_0 > 1$ then infection **can be endemic**

$$R_0 = \int_0^{\infty} b(a)F(a)da$$

b(a) is the average **number of infected** individuals that an infectious will produce per unit time when infected for a total time *a*
F(a) is the probability that a newly infected individual **remains infectious** for at least time *a*

Mathematical modeling



Deterministic SIR models

New infectious individuals depends on density of susceptible S and infectious I states

Permanent resistant state R in virus infections (S+I+R=1)

Infectious individuals remain 1/α days until becoming resistant

$$S \xrightarrow{\beta SI} I \xrightarrow{\alpha I} R$$

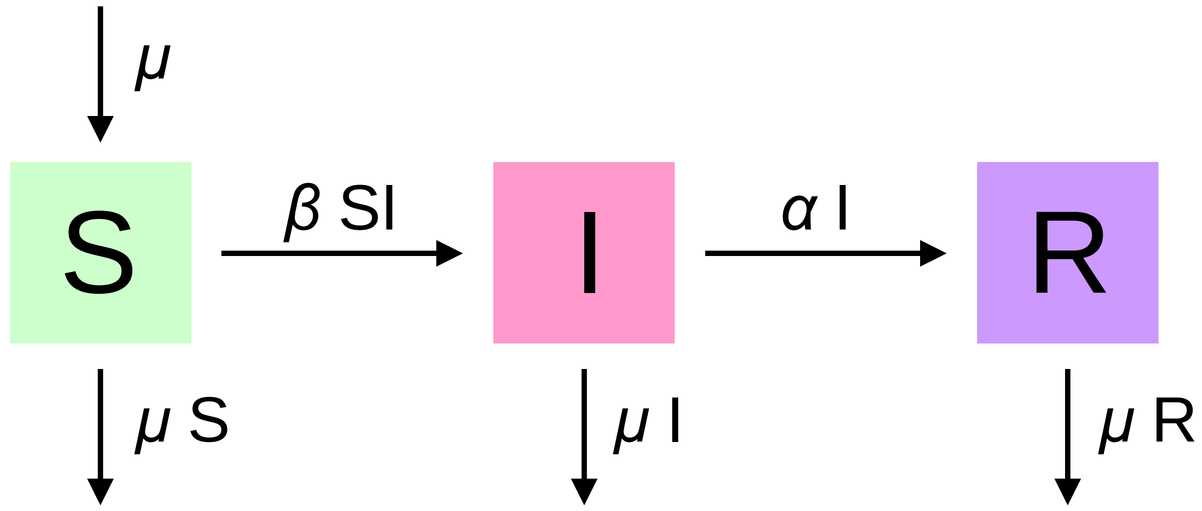
$$S' = -\beta SI$$
$$I' = \beta SI - \alpha I$$
$$R' = \alpha I$$

$$R_0 = \frac{\beta}{\alpha}$$

SIR models: Natural death

Individuals have a life expectancy of $1/\mu$ days

Total population is constant (#births = #deaths)



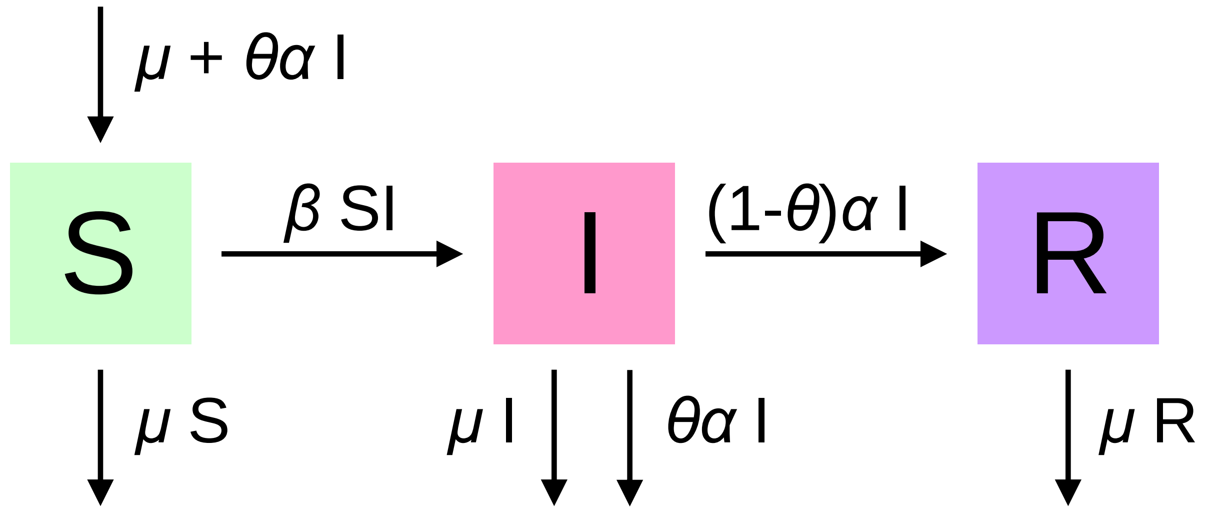
$$S' = -\beta SI + \mu (1-S)$$
$$I' = \beta SI - \alpha I - \mu I$$
$$R' = \alpha I - \mu R$$

$$R_0 = \frac{\beta}{\alpha + \mu}$$

SIR models: Disease death

A proportion θ of individuals that left infectious state I, die because of the disease

Total population stills constant (#births = #deaths)



$$S' = -\beta SI + \mu (1-S) + \theta\alpha I$$
$$I' = \beta SI - \alpha I - \mu I$$
$$R' = (1-\theta)\alpha I - \mu R$$

$$R_0 = \frac{\beta}{\alpha + \mu}$$

R_0 value study

R_0 value

$$F(a) = e^{-\theta\alpha a - (1-\theta)\alpha a - \mu a} = e^{-(\alpha+\mu)a}$$

Prob. remains infectious

$$b(a) = \beta$$

Infected pigs per unit of time

And apply formula $R_0 = \dfrac{\beta}{\alpha+\mu}$

Steady states

$$\begin{pmatrix} 1 & 0 & 0 \end{pmatrix}$$

All sane (unstable if $R_0>1$)

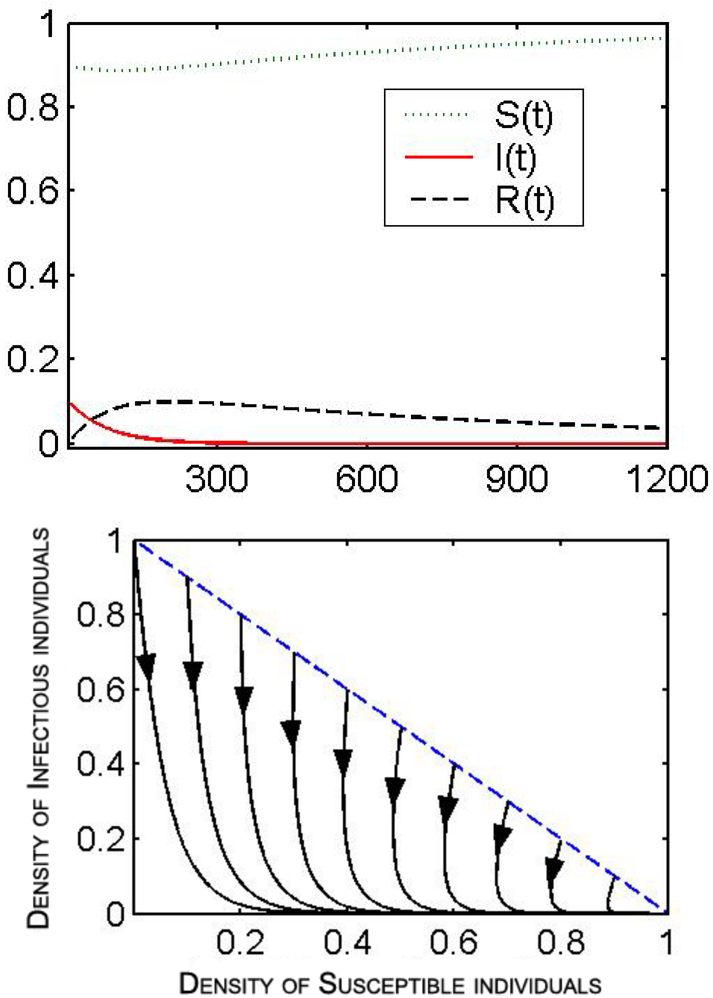
$$\begin{pmatrix} \dfrac{\alpha+\mu}{\beta} & \dfrac{\mu(\beta-\alpha-\mu)}{\beta(\mu+(1-\theta)\alpha)} & \dfrac{(1-\theta)\alpha(\beta-\alpha-\mu)}{\beta(\mu+(1-\theta)\alpha)} \end{pmatrix}$$

Stable endemic solution

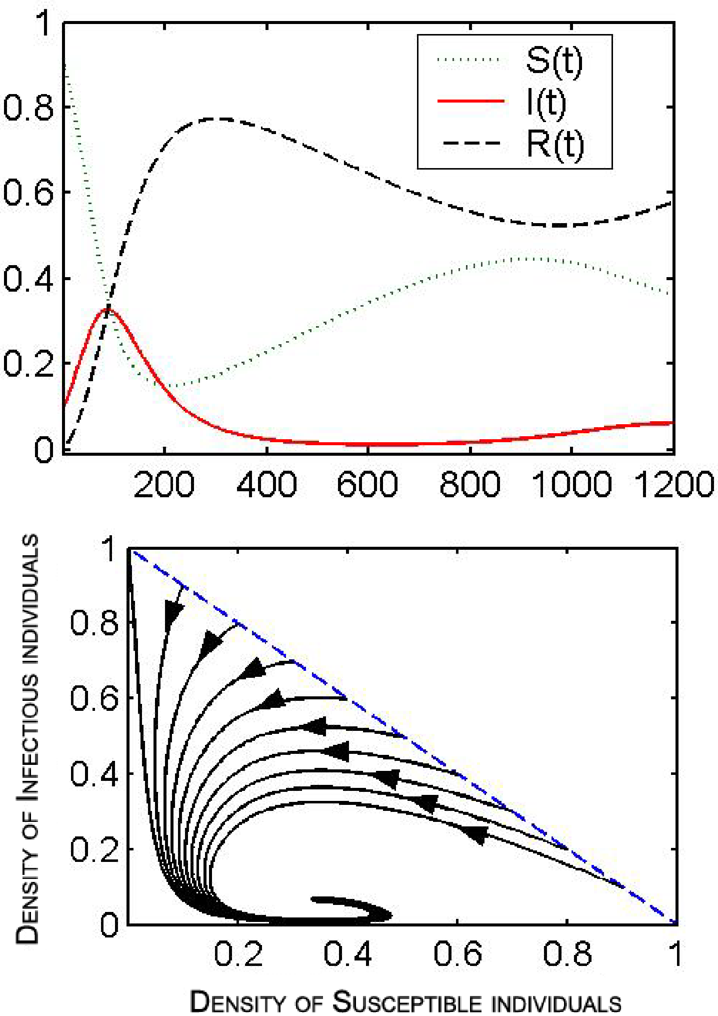
All states must be positive $\Rightarrow$ $(\beta-\alpha-\mu)>0$ $\Rightarrow$ $R_0 > 1$

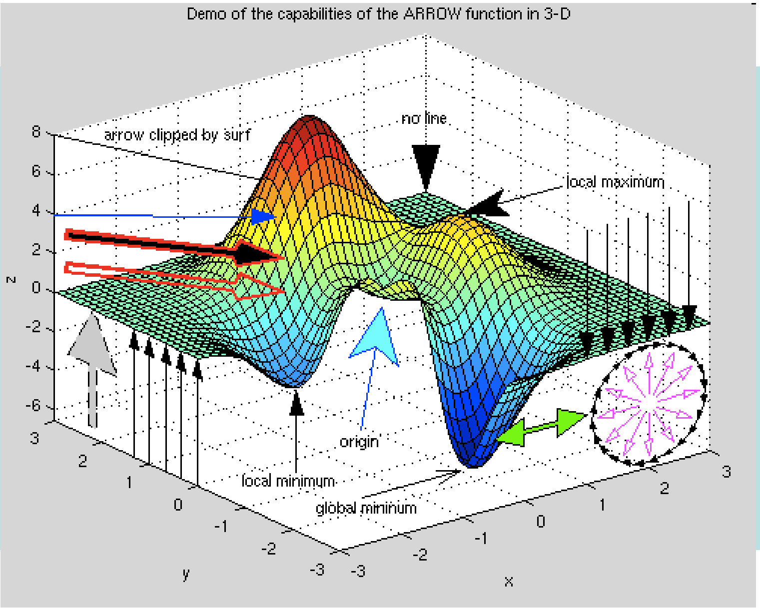
Evolution depending on R_0

$R_0 \leq 1$



$R_0 > 1$

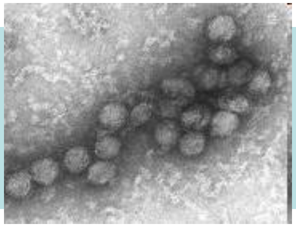




Numerical simulations

Classical swine fever (CSF)

What it is:



Highly **contagious viral** disease caused by *Flaviviridae Pestivirus*

Affects domestic and wild **pigs**

Consequences:

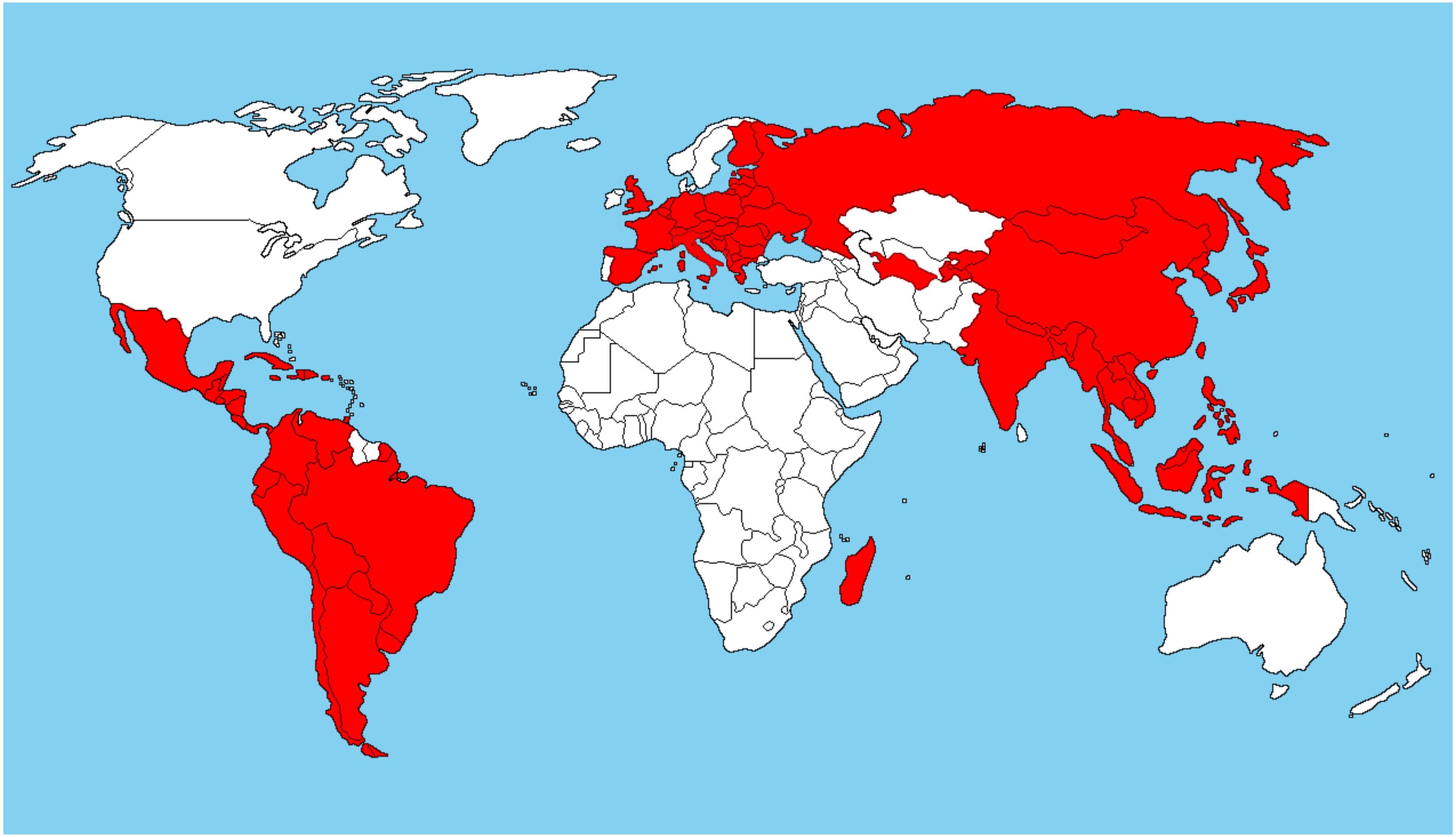
Symptoms: fever, hemorrhages, ...

High disease **mortality**

Severe **economical** consequences

CSF world distribution

Reports of Classical Swine Fever since 1990



Our scenario

Our **data** on farms (provided by province of Segovia)

Geographical **Situation**

Sanitary group

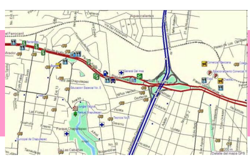
Type of production

Integration group

Number of pigs

Movement of pigs

Ways of **transmission**:



Local spread

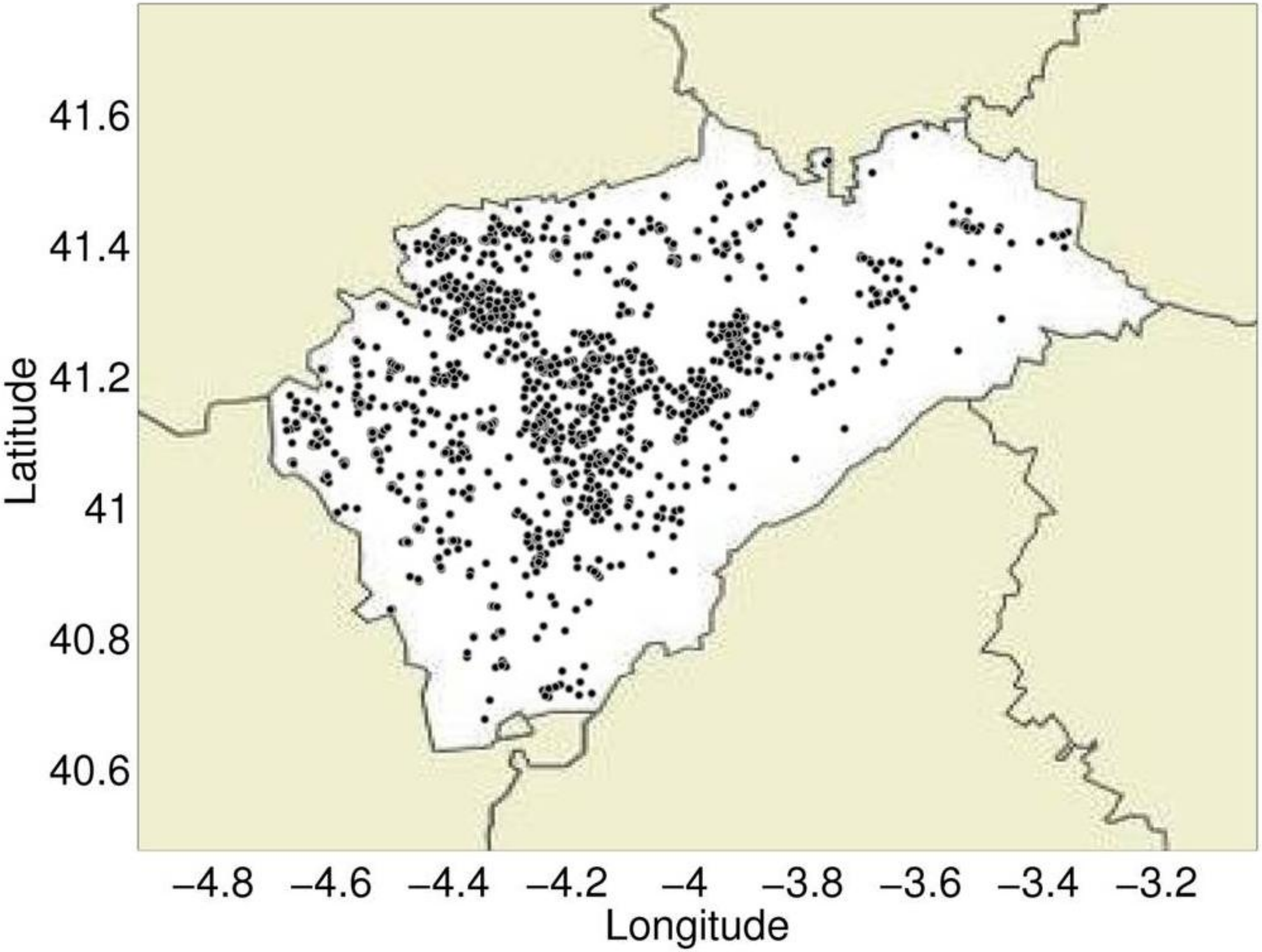
Sanitary spread

Direct **contact** within a farm

Integration spread

Movement of pigs

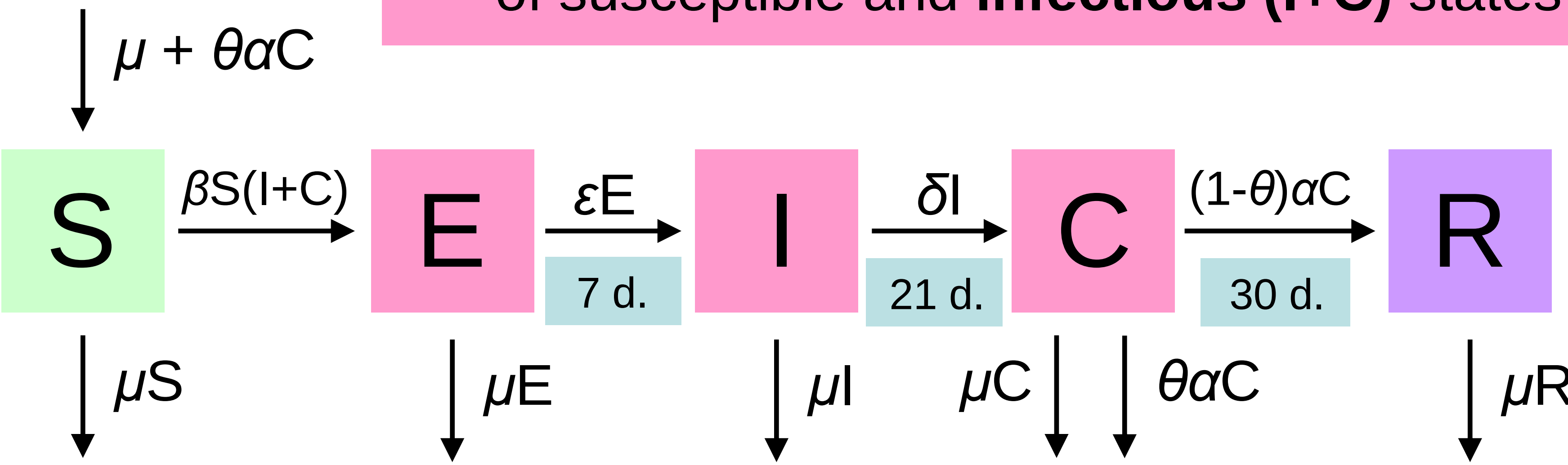
Farm distribution



SEICR farm model

One SEICR model **for each farm**

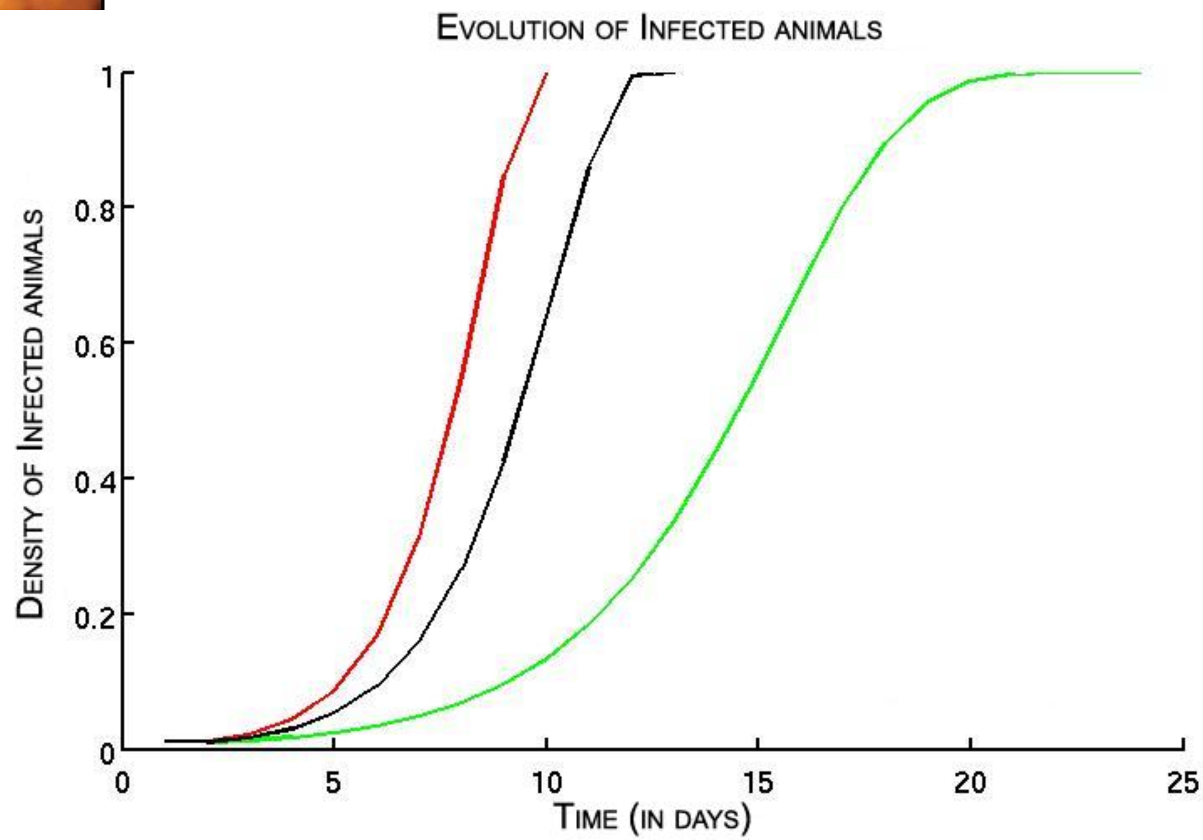
New infected individuals depends on density of susceptible and **infectious (I+C)** states



$$
\begin{aligned}
S' &= -\beta S(I+C) + \mu(1-S) + \theta\alpha C \\
E' &= \beta S(I+C) - \varepsilon E - \mu E \\
I' &= \varepsilon E - \delta I - \mu I \\
C' &= \delta I - (1-\theta)\alpha C - \mu C - \theta\alpha C \\
R' &= (1-\theta)\alpha C - \mu R
\end{aligned}
$$

CSF spread within a farm

Quick spread within the farm



Value of *β*:

1.85

8.52

5.18

Type of farm:

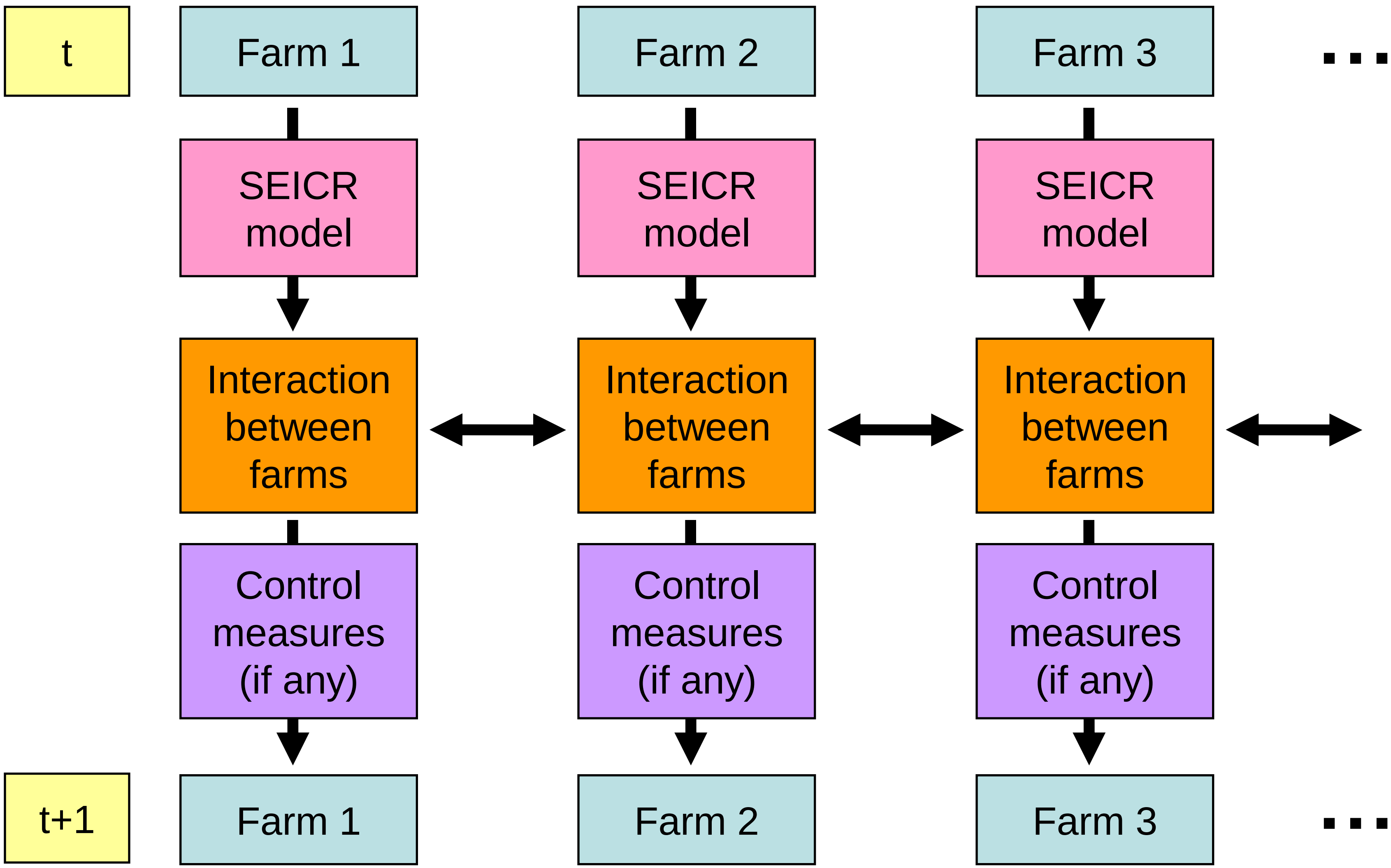
Fattening (young)

Farrowing (old)

Farrow-to-finish (mix)

Hybrid model algorithm

Differential equations model with **discrete time**



Movement of pigs

Way of **transmission**:

When infected pigs are **translated**, epidemic spreads to destination farm

Our **data** on pig movements (provided by the province of Segovia)

Movements between Segovia’s farms in 2008

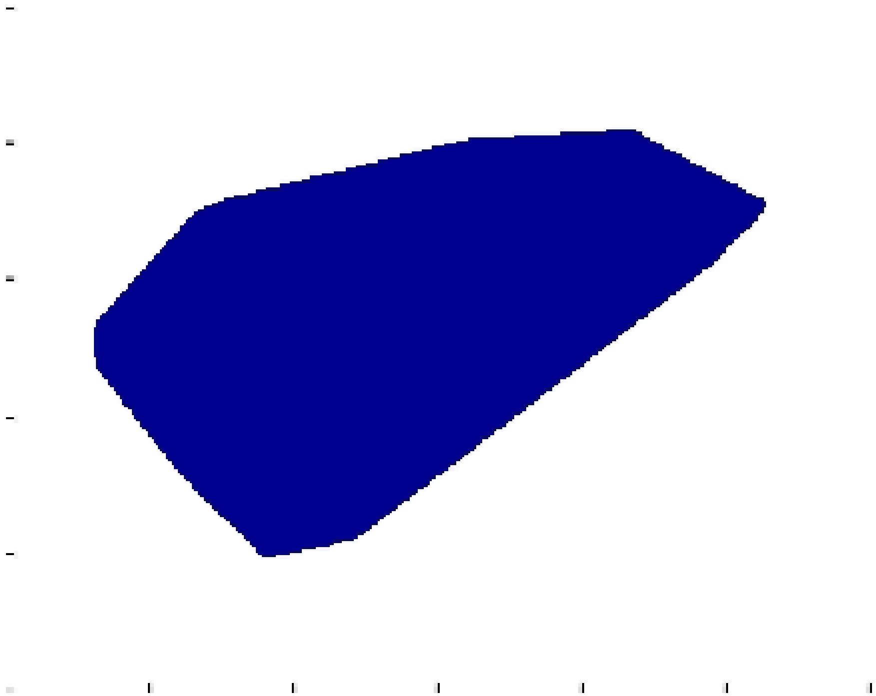
Origen and destination farms

Quantity of moved

Date of movement

We run a one-year simulation repeating these movements

Movement of pigs



Sanitary and Integration groups

Ways of **transmission**:

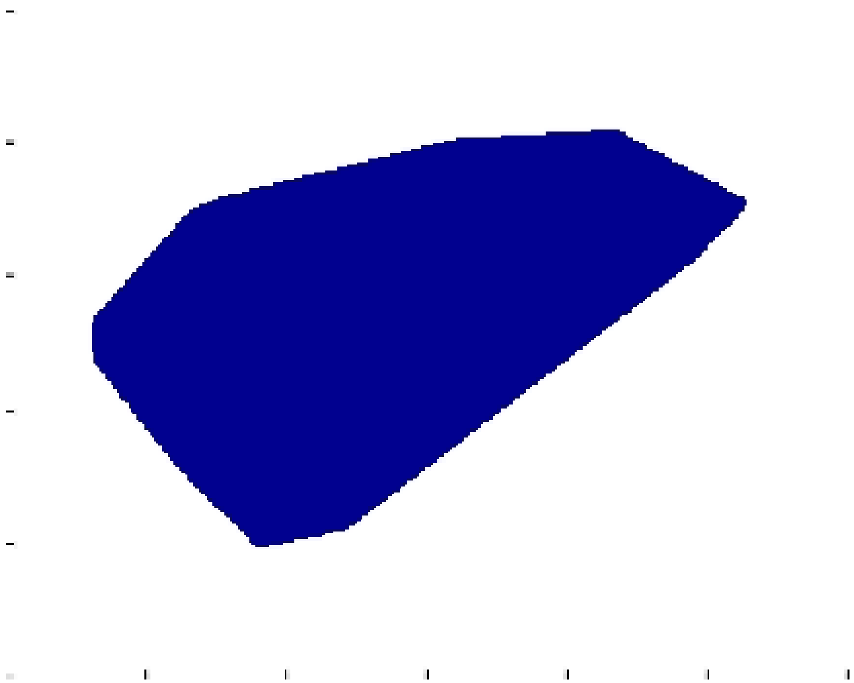
Contact with infected trucks or infected fomites (food, materials, …)

Farms with same sanitary or integration group are susceptible to spread epidemic between each other

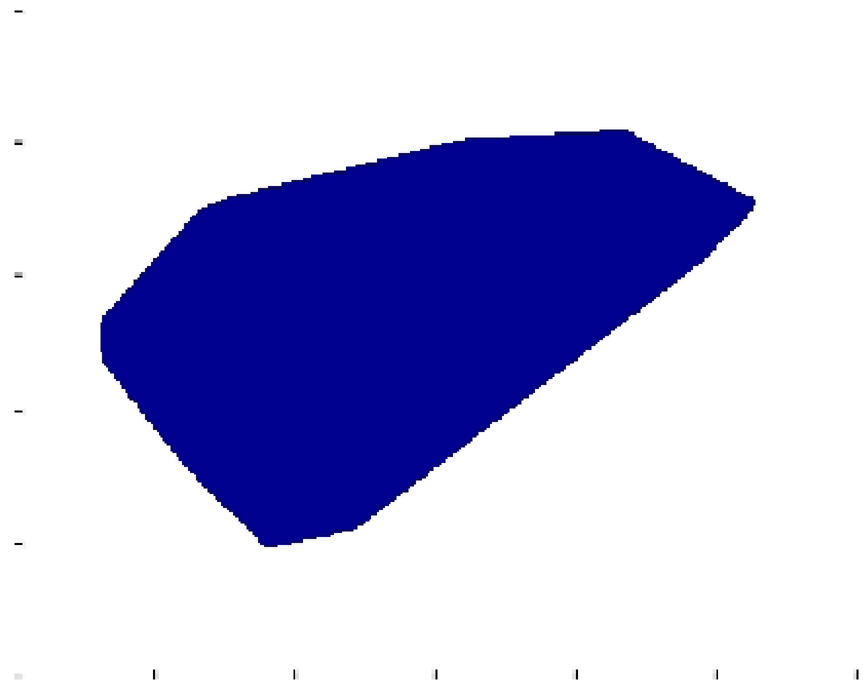
Daily rates of infection are 0.0068 for Integration and 0.0065 for Sanitary

Sanitary and Integration groups

Sanitary



Integration

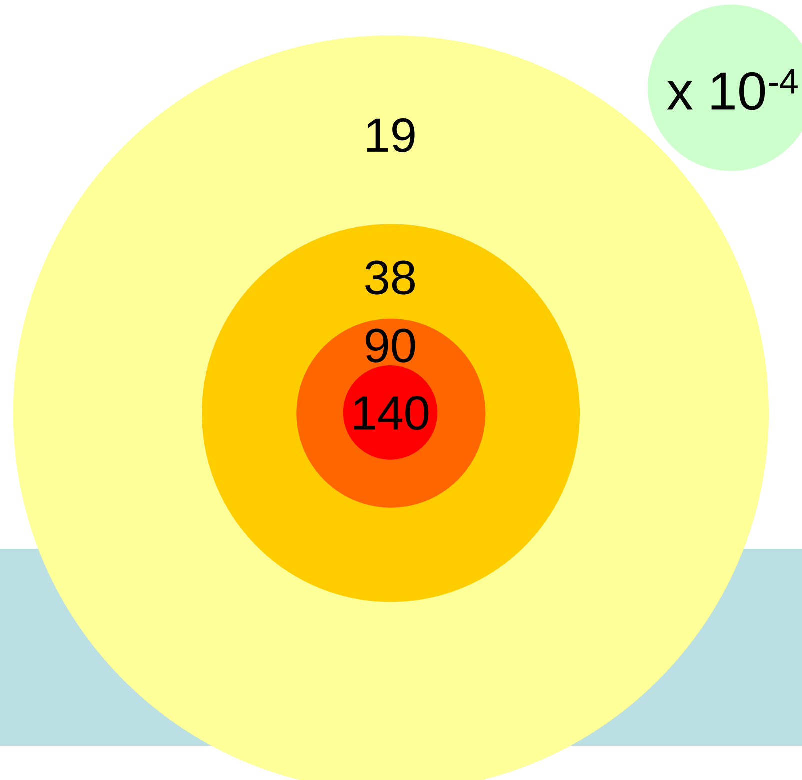


Local spread

Ways of **transmission**:

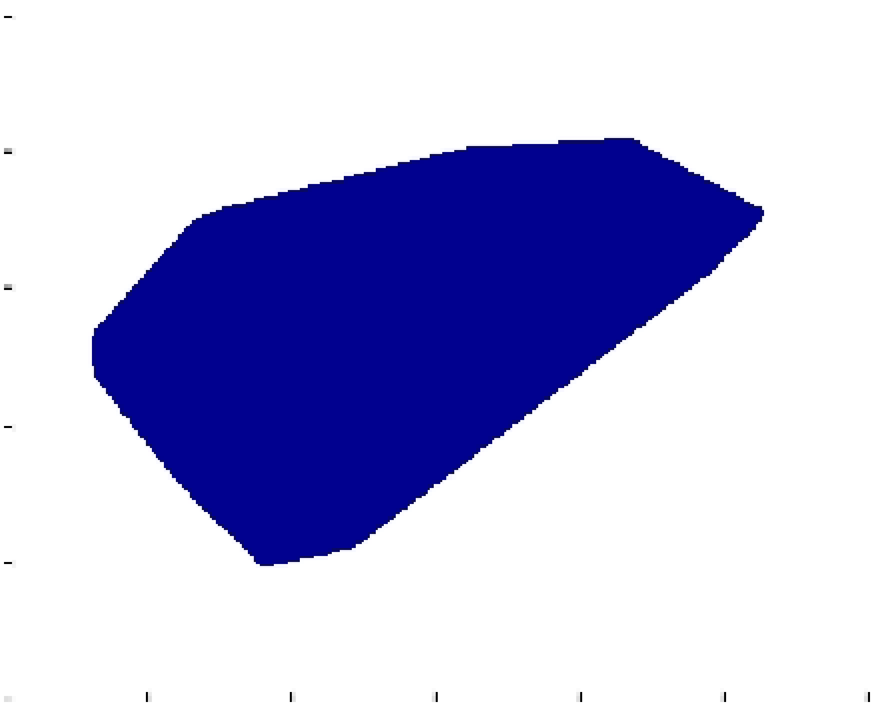
Airborne spread or fomits

Daily rate of infection depends on the distance between farms

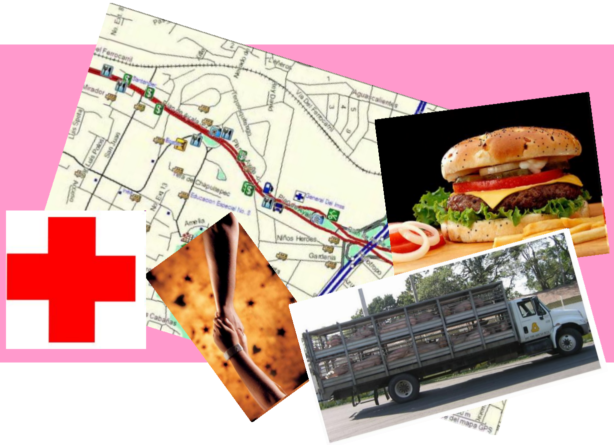


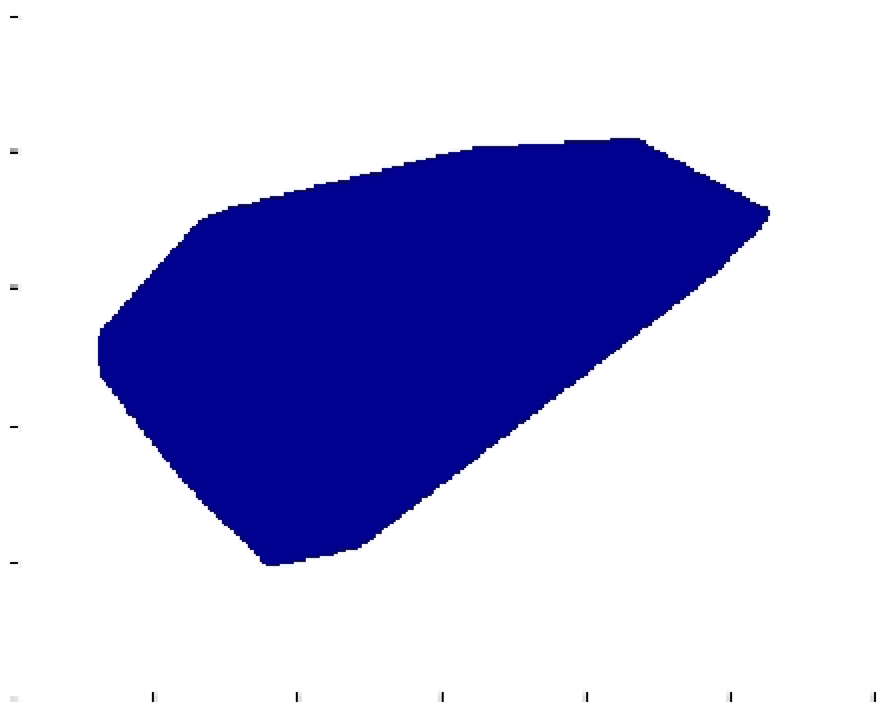
Radius: 250m 1000m 500m 2000m

Local spread



Considering all risk factors





Control measures

Infected farm is **depopulated**: all animals are sacrificed

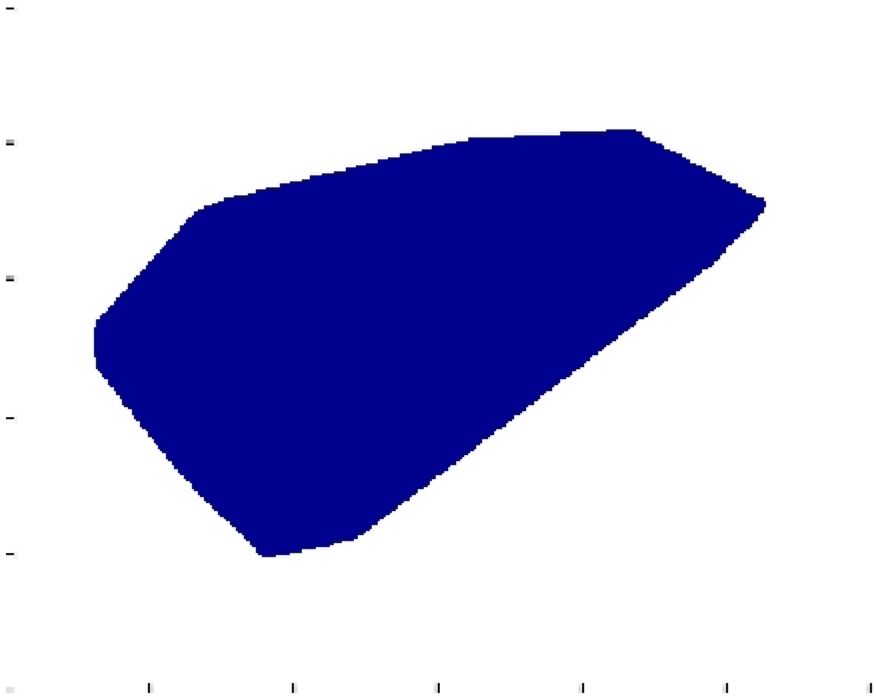
Quarantine during 90 days: Incoming and out-coming **movements are limited**

Detection of infection:

We consider than an infected farm is detected when there is, at least, one pig with clinical signs

$$C * N > 1$$

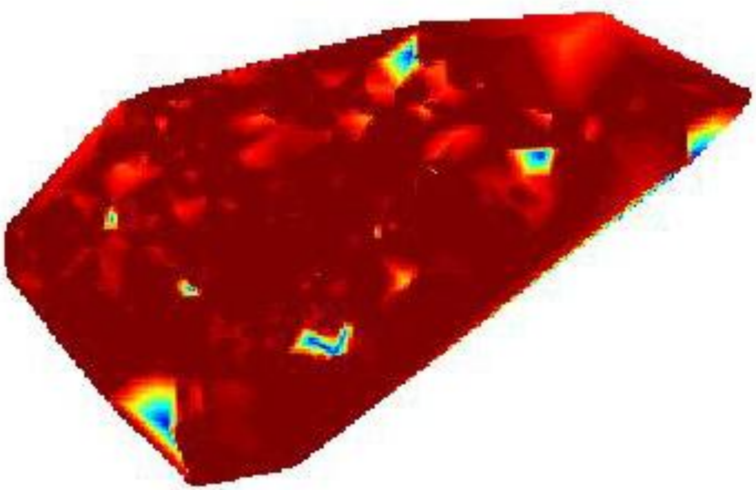
Control measures

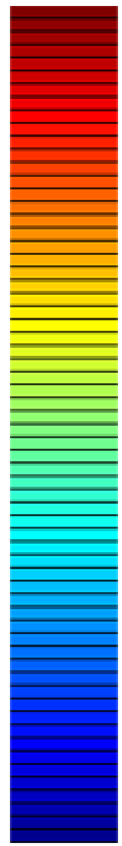


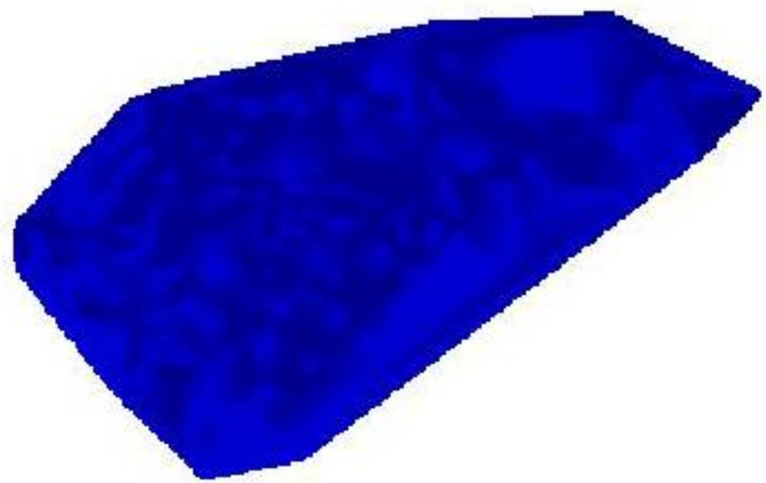
Control measures

No control measures

With control measures







Conclusions

Conclusions

Work done:

Mathematical modeling and analysis of a CSF epidemic

Simulations with real data

Results:

Infection **spreads quickly** within and between farms

Local spread is the most relevant risk factor

Control measures are essentials

In a **future**:

Try other **control measures**

Compute $\mathbf{R_0}$ **value** for this hybrid model

Quantify **economical** consequences


That's All Folks