Using climate models to project the future distributions of climate-sensitive infectious diseases

Prof. Matthew Baylis
Liverpool University Climate and Infectious Diseases of Animals
Department of Epidemiology and Population Health
Institute of Infection and Global Health, University of Liverpool
matthew.baylis@liv.ac.uk

UNIVERSITY OF LIVERPOOL

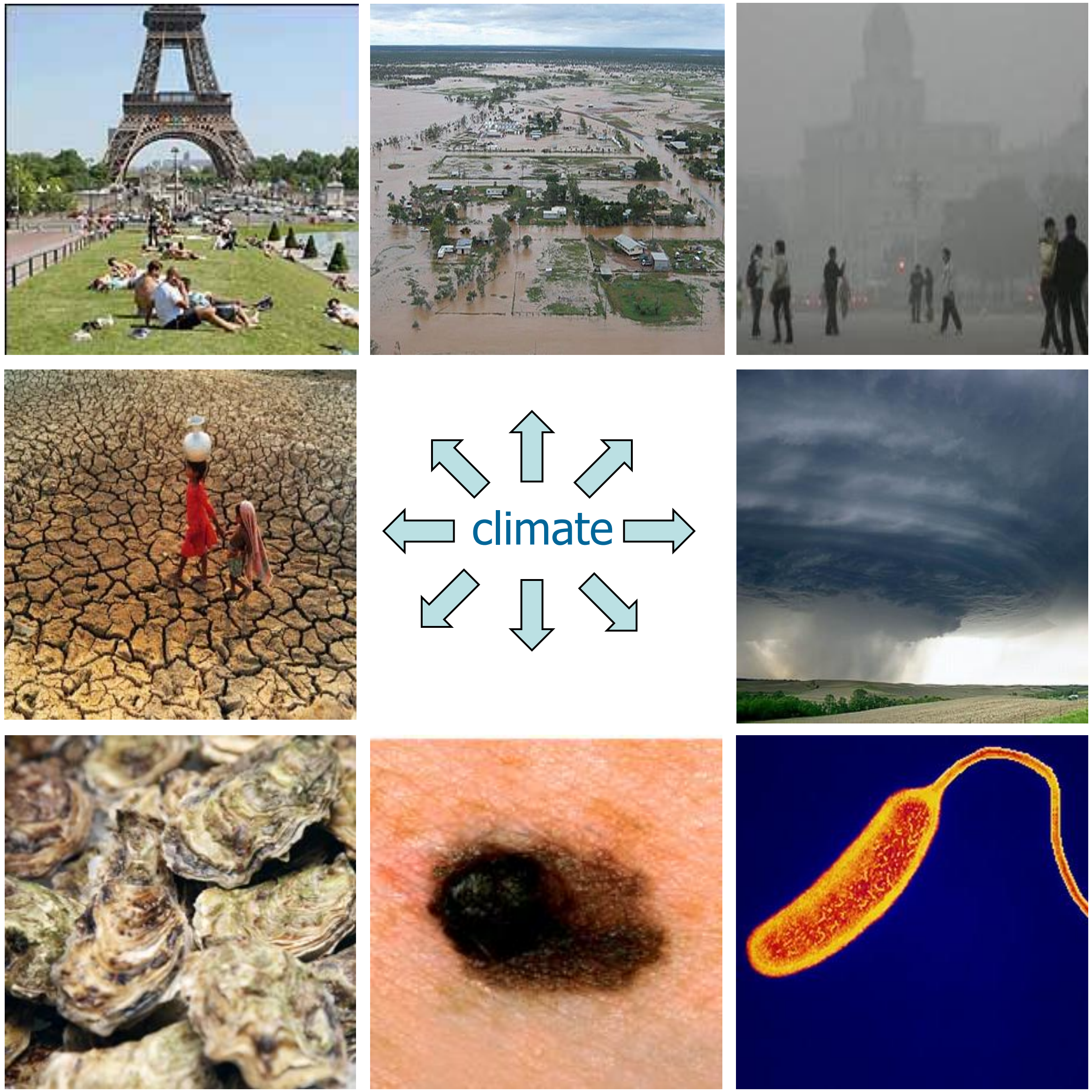
LUCINDA

Climate & climate change impacts on health

5,671

7,637

~800,000



185

13,650

300

~65,000

~2,000,000

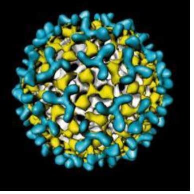
Climate and Infectious disease

Climate may affect:

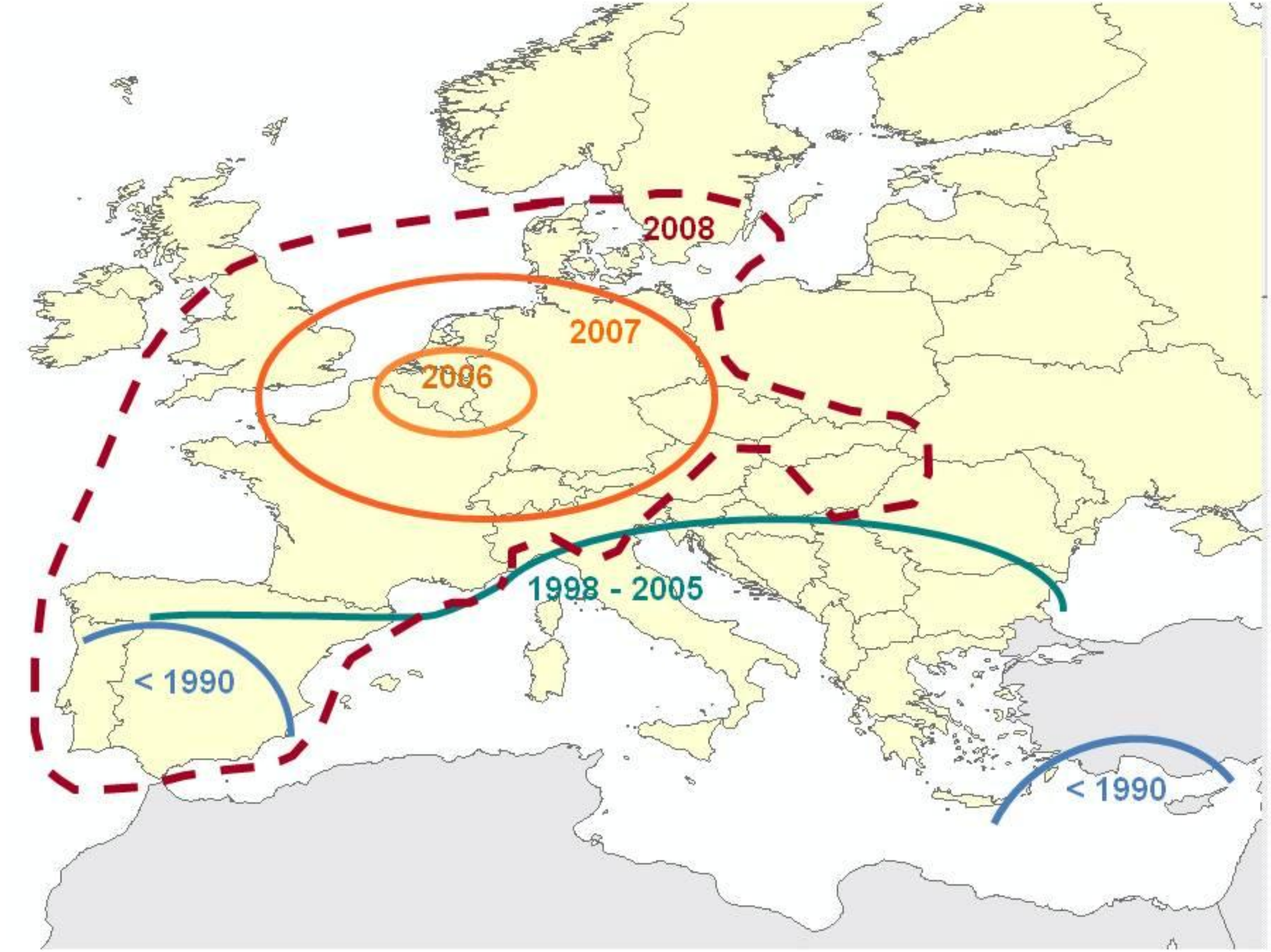
- Spatial distribution of outbreaks: *where?*
- Timing of disease outbreaks: *when?*
- Frequency of disease outbreaks: *how often?*
- Intensity or severity of outbreaks: *how bad?*

Via effects on

- Pathogens: *if free-living or outside of host*
- Hosts: *eg, immunity*
- Vectors: *eg mosquitoes, ticks etc*
- Dynamics: *eg contact rates*
- Indirect effects: *effects on other disease drivers*

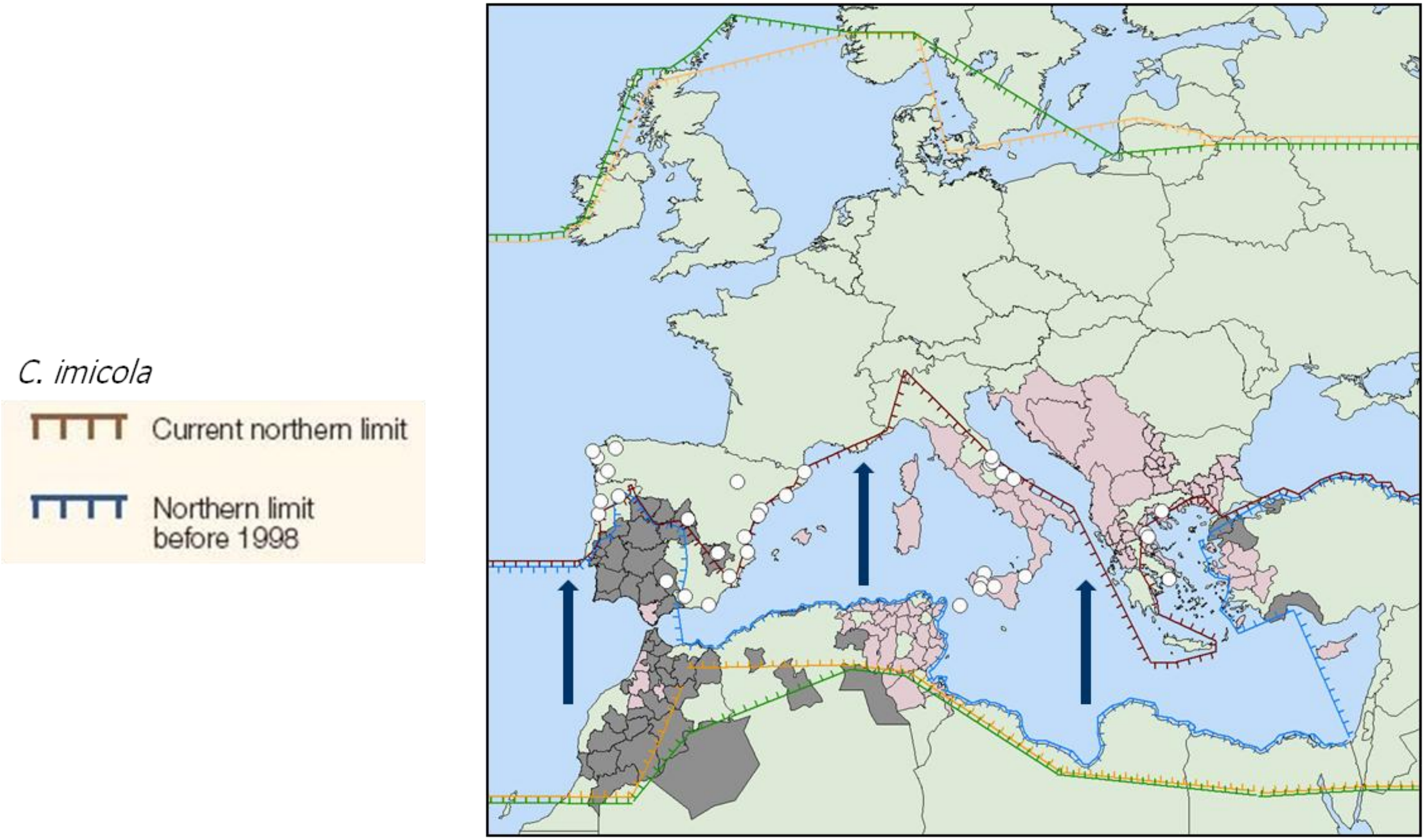


History of bluetongue (BT) in Europe



Factors underlying BT's emergence

- Spread of *C. imicola* across Mediterranean basin, and to north
- Transmission of BT viruses by indigenous *Culicoides* spp (*C. obsoletus*).



Purse B.V. *et al.* 2005

The need to link disease models to climate

Has it warmed enough........
Has it warmed too much.....
} to explain the observed emergence of BT?

We need a model that:

- quantifies the expected amount of disease for a given climate; or
- quantifies the expected change in amount of disease for a given change in climate.

We can develop:

- a climate-driven model of disease spread
- a climate-driven model of disease risk

Disease models: the basic reproductive ratio, R_0

R_0:

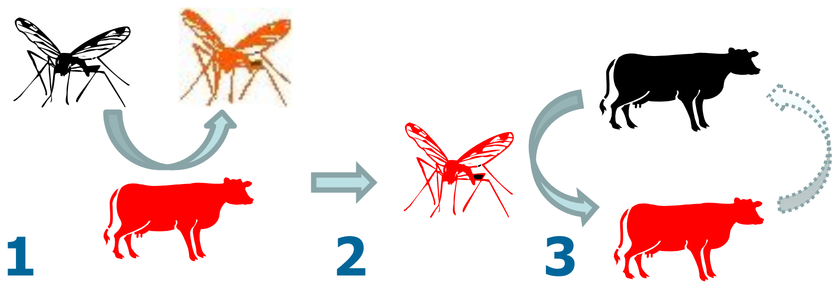
- Defined as the average number of individuals infected by a single infected individual during its entire infectious period in a population which is entirely susceptible;
- Described as ‘one of the foremost and most valuable ideas that mathematical thinking has brought to epidemic theory’*;
- There is an important threshold:
  - If $R_0 < 1$, infection will be cleared from the population
  - If $R_0 > 1$, the pathogen can invade the population
- The magnitude of R_0 indicates the risk of an epidemic arising from the introduction of a pathogen into a susceptible population;
- The proportion of a population that must be vaccinated to protect a population is $1 - 1/R_0$;
- To control a disease outbreak, we need only reduce R_0 to below 1; maths will do the rest.

* Heesterbeek & Dietz, 1996)

Examples of R_0 for a variety of diseases

Disease	**Transmission**	**R0**
Influenza	Airborne droplet	2-3
SARS	Airborne droplet	2-5
HIV/AIDS	Sexual contact	2-5
Mumps	Airborne droplet	4-7
Rubella	Airborne droplet	5-7
Polio	Faecal-oral	5-7
Smallpox	Social contact	5-7
Diphtheria	Saliva	6-7
Pertussis	Airborne droplet	12-17
Measles	Airborne	12–18
Dengue	Vector-borne	4-8
Malaria	Vector-borne	1-3000 (median 115)

Modelling R0 for bluetongue



$$R0 = \frac{m\, a^2\, b\, p^n}{-r \ln(p)}$$

m: ratio vectors to host
a: biting rate
b: vector competence
p: daily survival rate
n: extrinsic incubation period
r:1/duration of viraemia in host

1

Duration of viraemia in host (1/r)
Ratio vector/host (m)
Biting rate (a)

2

Competence (c)
Survival (p) during the
Length of extrinsic incubation cycle (n)

3

Survival (p)
Biting rate (a)

Mapping of BT's past, present and future R_0

Two host species

$$R0 = \frac{b\beta a^2}{p}\left(\frac{n}{p+n}\right)\left(\frac{m_C\phi^2}{r_C+d_C}+\frac{m_S(1-\phi)^2}{r_S+d_S}\right)$$

(Gubbins 2007)

AIM: assess spatial & temporal variations in BT R0 under climate change scenarios

r:1/duration of viraemia in host (C,S)
d: disease induced mortality rate (C,S)
b: Prob. transmission of vector to host
β: Prob. transmission of host to vector
→ Constant in time and space

Φ: proportion of bites on each host species
→ Constant in time, varying in space

m: ratio vectors to host (C: cattle, S: sheep)
n: 1/extrinsic incubation period
a: biting rate
p: vector mortality rate
→ Varying in time and space

Feeding preferences

r:1/duration of viraemia in host (C,S)

d: disease induced mortality rate (C,S)

b: Prob. transmission of vector to host

β: Prob. transmission of host to vector

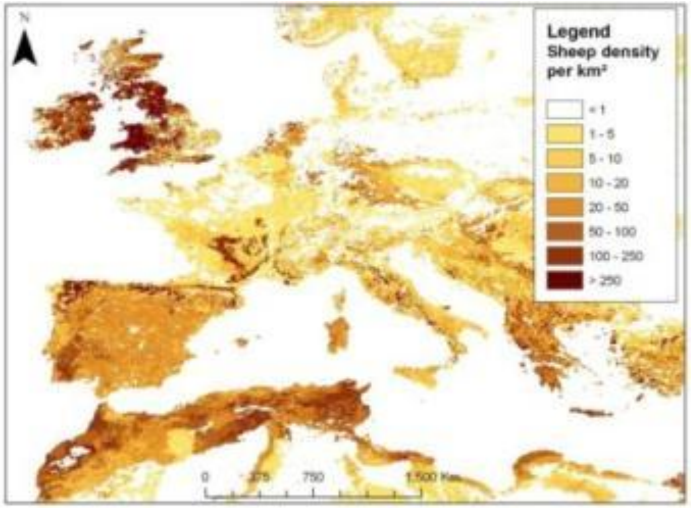
Φ: proportion of bites on each host species

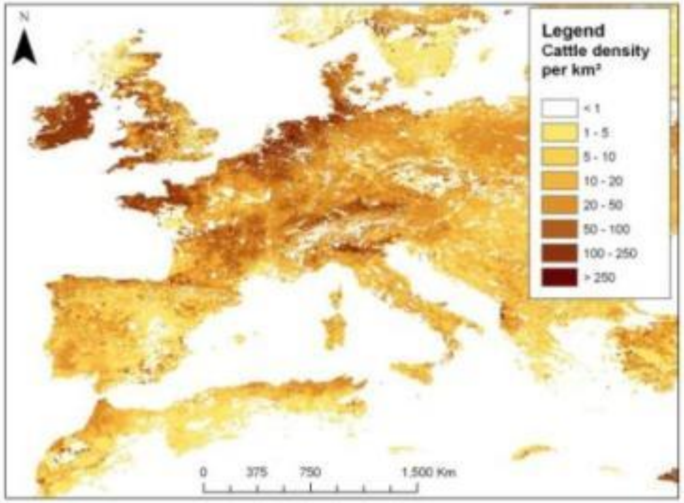
m: ratio vectors to host (C: cattle, S: sheep)

a: biting rate

p: vector mortality rate

n: 1/extrinsic incubation period



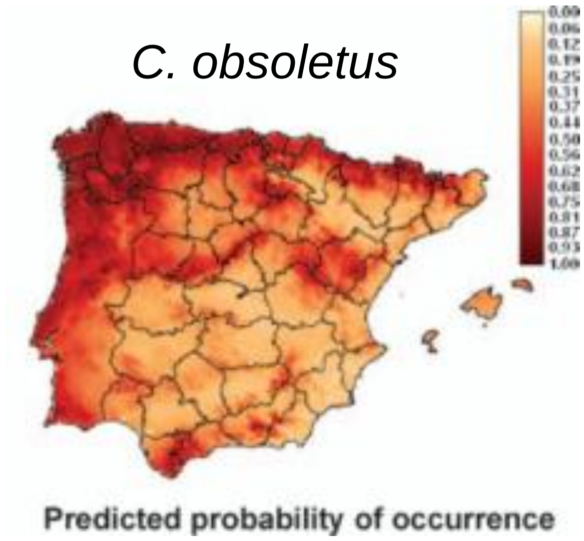


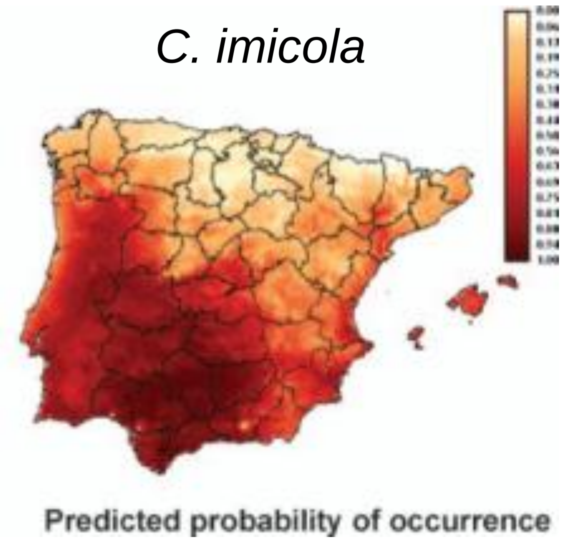
FAO: data set of livestock densities

Vector and host densities

r:1/duration of viraemia in host (C,S)
d: disease induced mortality rate (C,S)
b: Prob. transmission of vector to host
β: Prob. transmission of host to vector
Φ: proportion of bites on each host species
m: ratio vectors to host (C: cattle, S: sheep)
a: biting rate
p: vector mortality rate
n: 1/extrinsic incubation period

Models driven largely by temperature and precipitation variables





Virus transmission variables

Lab or field studies:

r:1/duration of viraemia in host (C,S)

d: disease induced mortality rate (C,S)

b: Prob. transmission of vector to host

β: Prob. transmission of host to vector

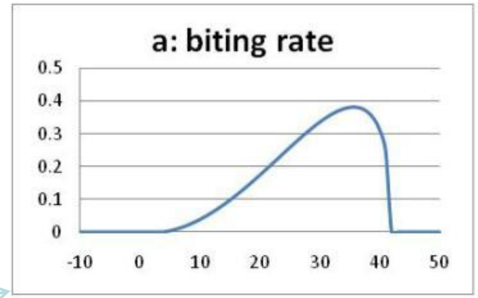
Φ: proportion of bites on each host species

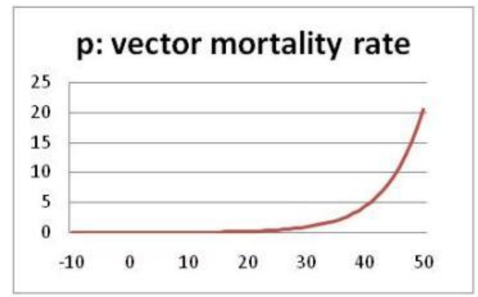
m: ratio vectors to host (C: cattle, S: sheep)

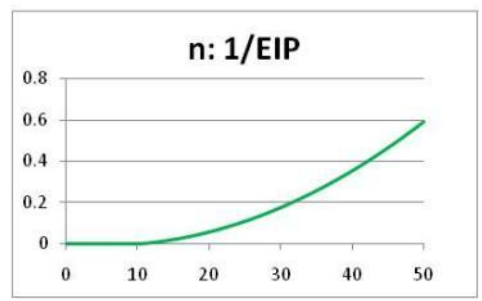
a: biting rate

p: vector mortality rate

n: 1/extrinsic incubation period







Temperature

Past and future climate

EU ENSEMBLES project

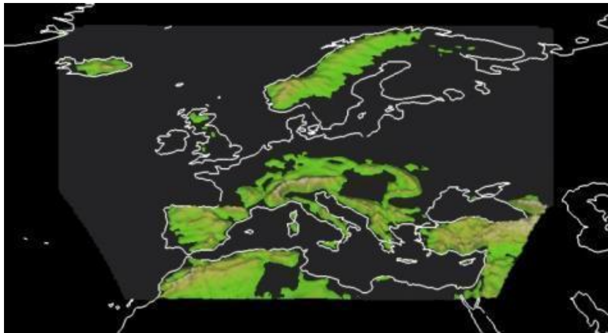
Developing a quality controlled, high resolution prediction system for climate change for Europe.

Three datasets used:

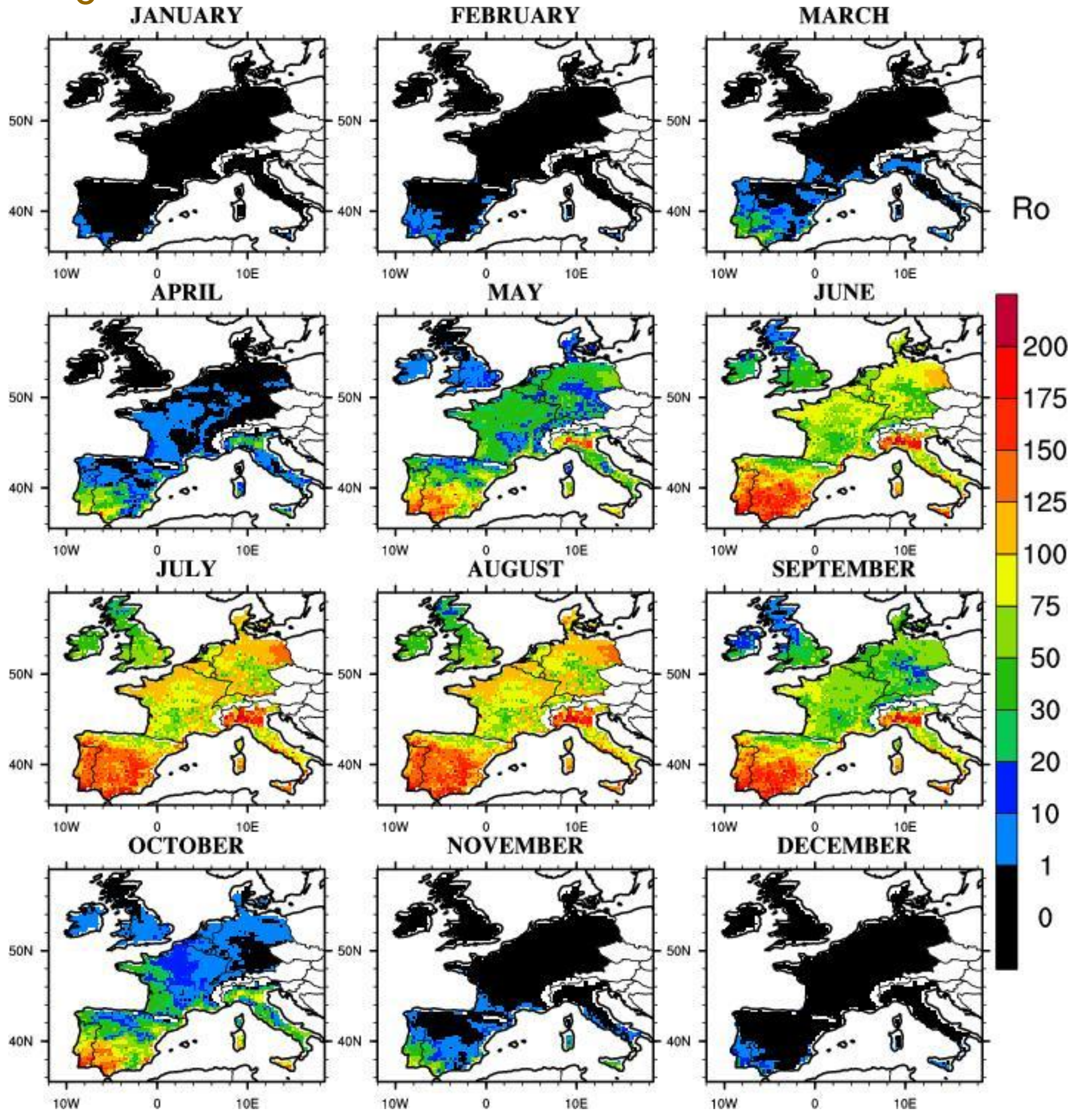
1960-2006: a newly available, high resolution (25 km) observed climate dataset: *European Climatic Assessment and Dataset program*.

1961 – 2000: Simulated Control experiment (*SimCTL*); 11 Regional Climate Model simulations. With external forcing, and forced at boundary by ERA-40

1961 – 2050: Simulated SRESA1B (*SimA1B*); 11 RCMs; forced at boundary by GCM and SRESA1B emission scenario



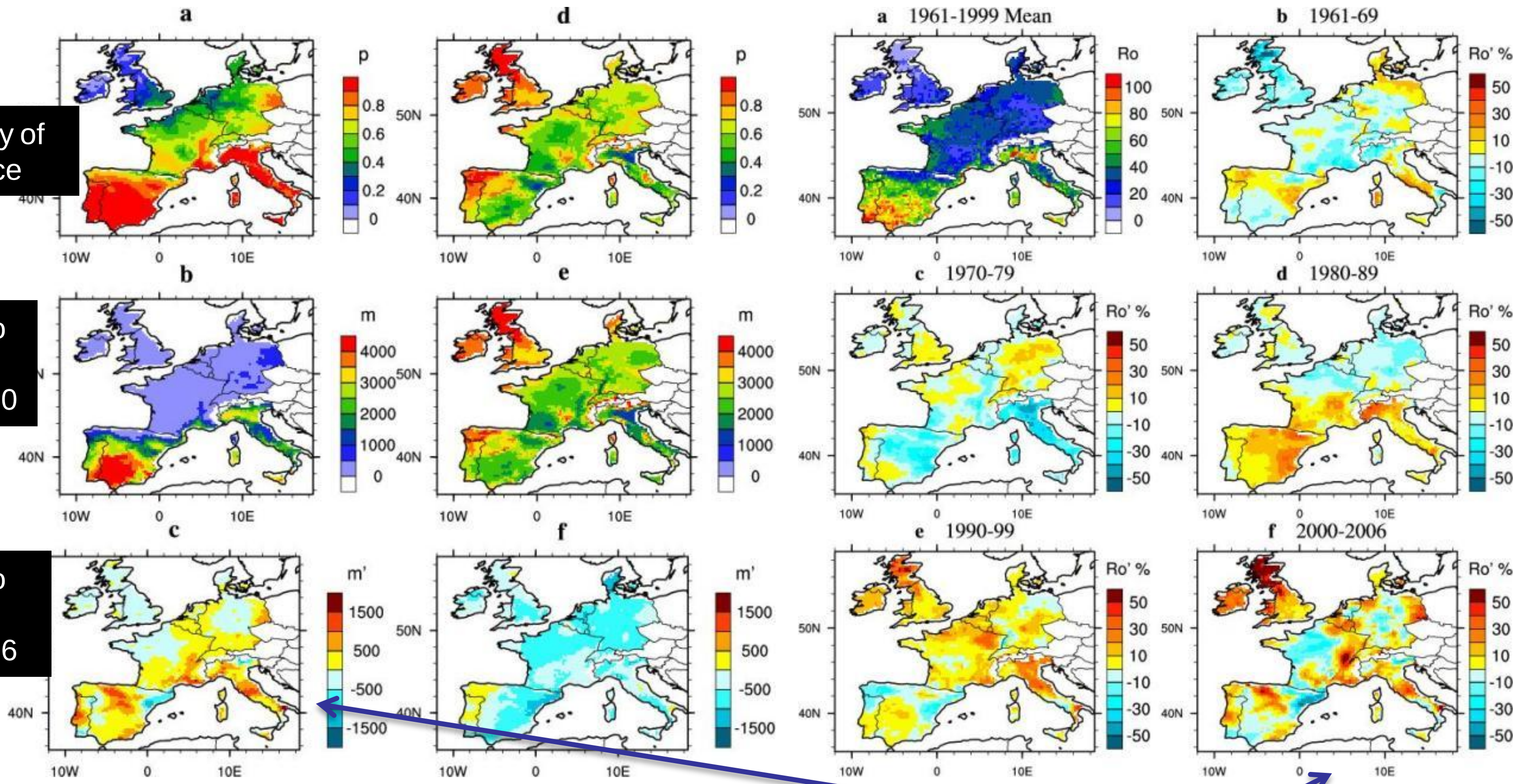
Seasonal R_0



JANUARY
FEBRUARY
MARCH
APRIL
MAY
JUNE
JULY
AUGUST
SEPTEMBER
OCTOBER
NOVEMBER
DECEMBER
50N
40N
10W
0
10E
Ro
200
175
150
125
100
75
50
30
20
10
1
0

Model outputs

Vectors **R0**



Probability of occurrence

Vectors to hosts: 1961-2000

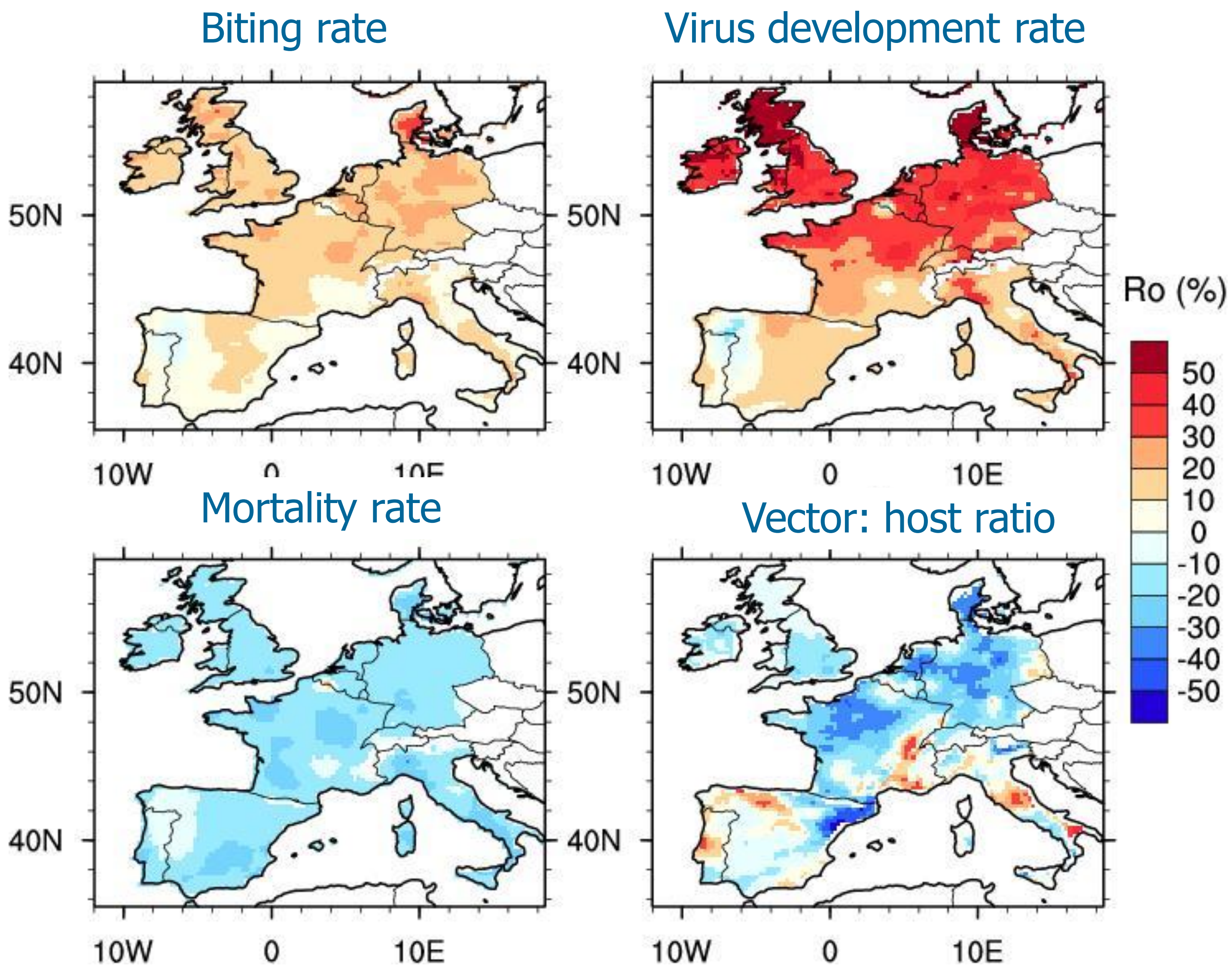
Vectors to hosts: 2001-2006

C. imicola

C. obsoletus

South: change in R0 driven by C. imicola density
North: change in R0 driven by temperature

Sensitivity analysis

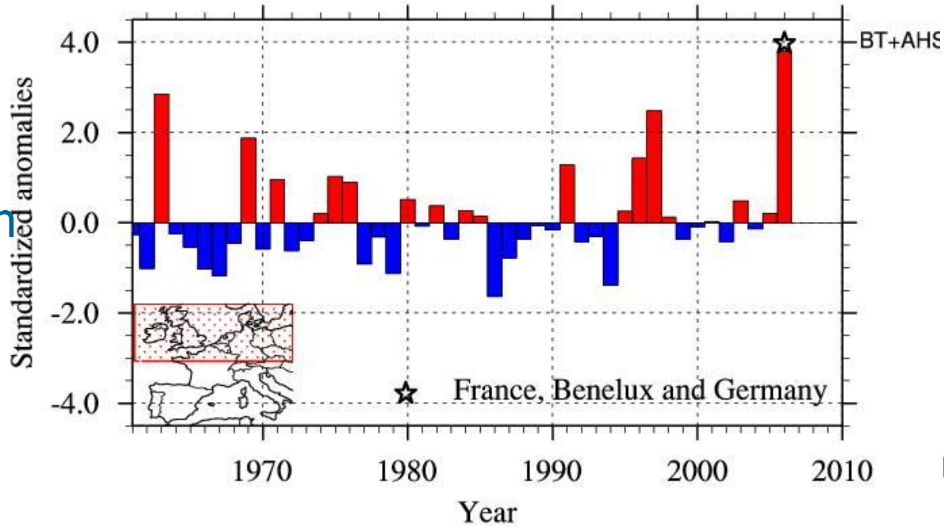


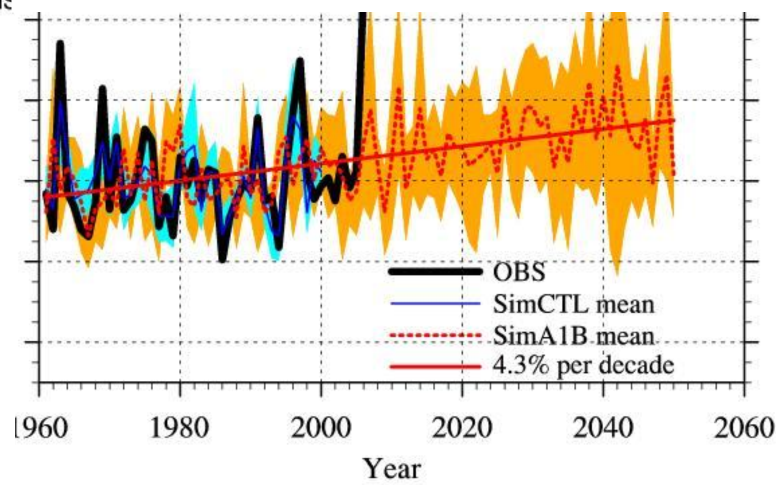
Past and future trends in R_0

Forced by E-OBS

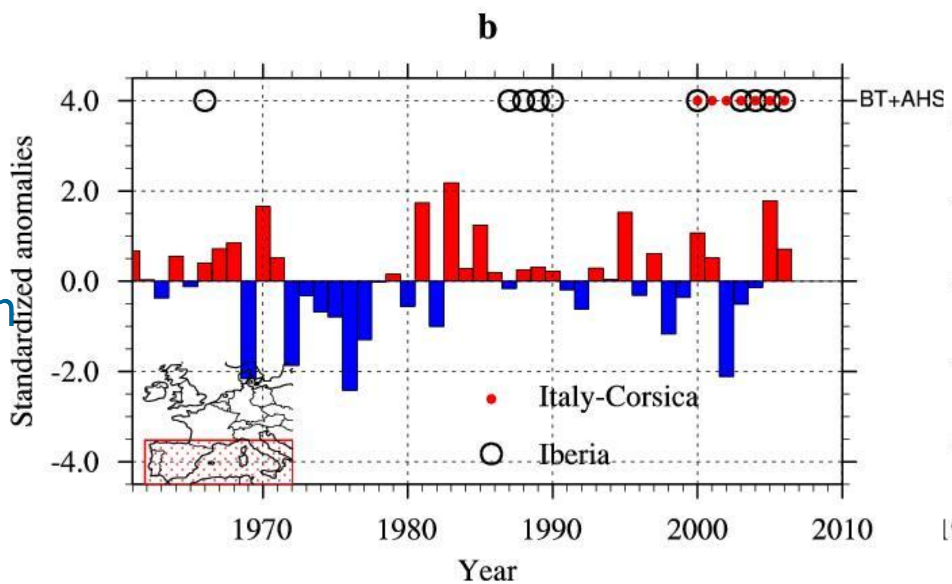
Forced by E-OBS, SimCTL & SimA1B

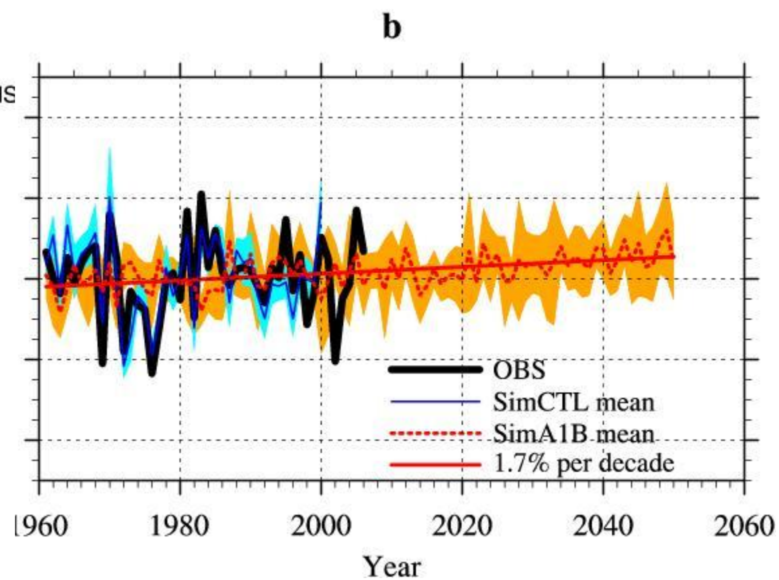
North-western Europe



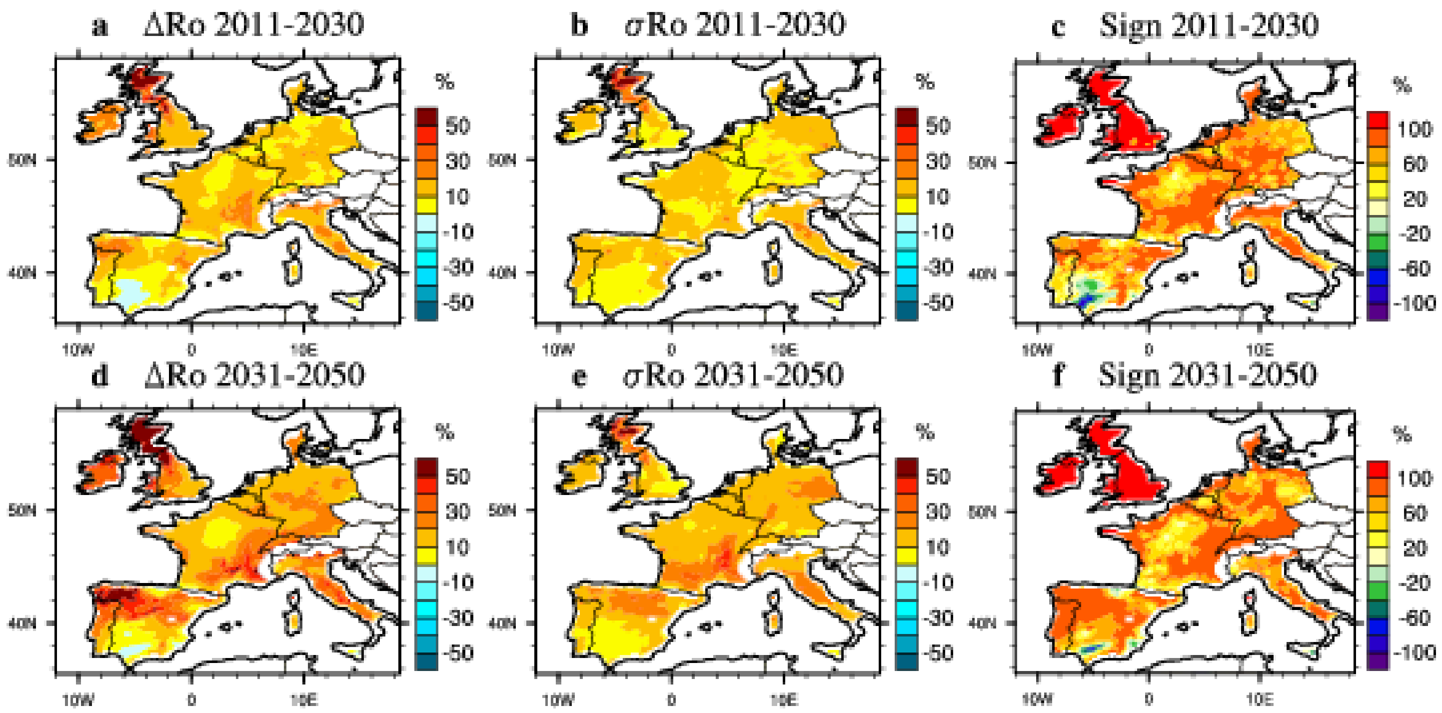


South-western Europe





Simulated regional R0 changes



% change in R0 Multimodel spread Sign consistency

Conclusions

Bluetongue has emerged dramatically in Europe over the last 12 years;

Driving variation in R_0 using high resolution climate data allows the influence of climate on changing disease risk to be examined;

Many aspects of BT's emergence agree in space and time with model outputs, lending support to the belief that bluetongue's dramatic emergence is attributable to recent climate change.

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