

Relations between pathogens, hosts and environment: joining up the dots

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

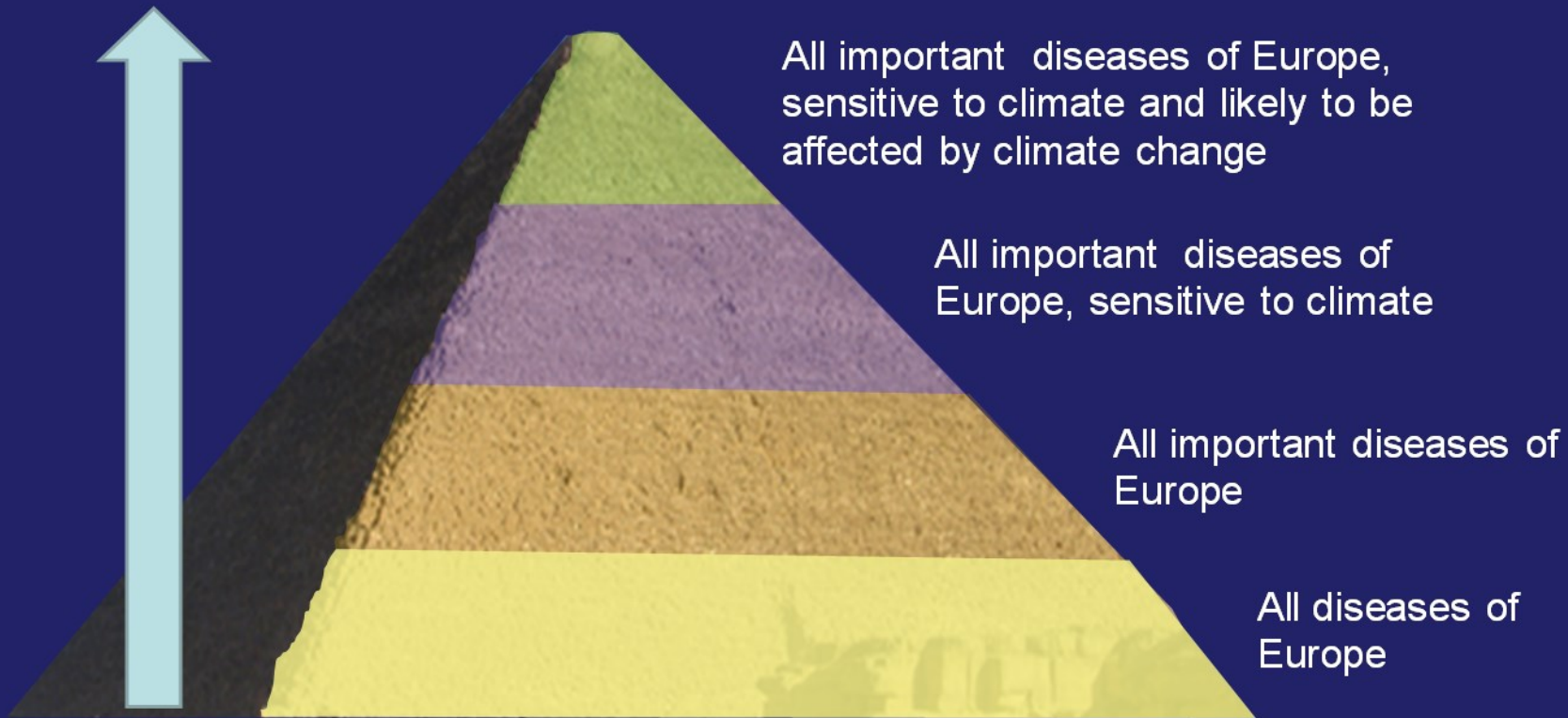


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SOURCES OF NOVEL PATHOGENS

Bottom-up approach

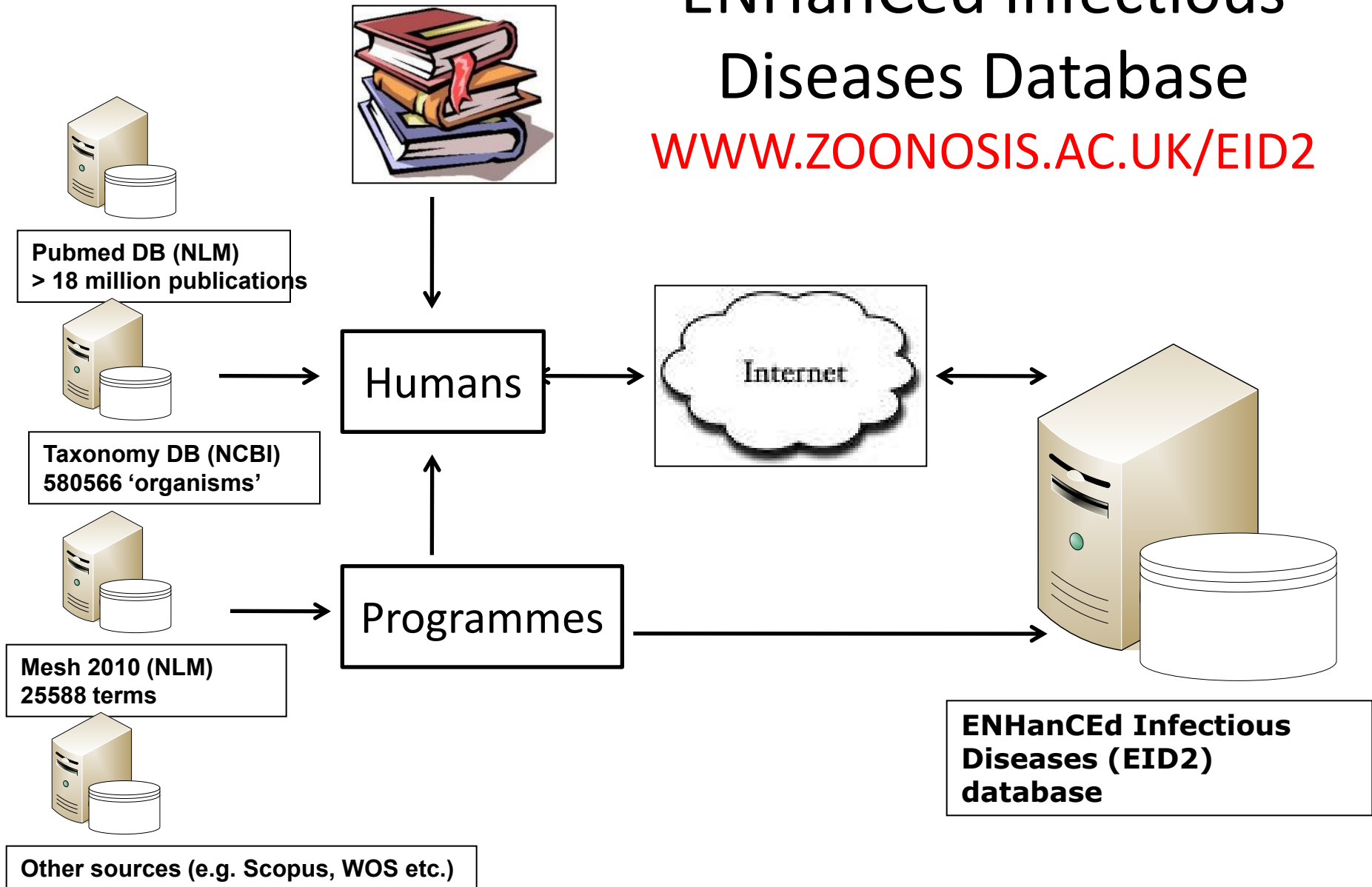


ERANET ENVHEALTH PROJECT - *ENHANCE*



ENHanCed Infectious Diseases Database

WWW.ZOONOSIS.AC.UK/EID2



Data mining from NCBI

LOCUS GU591166 6979 bp cRNA linear VRL 03-MAY-2010
DEFINITION La Crosse virus isolate Dallas/TX/2009 segment L, complete sequence.
ACCESSION GU591166
VERSION GU591166.1 GI:295387991
KEYWORDS
SOURCE La Crosse virus
ORGANISM La Crosse virus
Viruses; ssRNA negative-strand viruses; Bunyaviridae; Orthobunyavirus.
REFERENCE 1 (bases 1 to 6979)
AUTHORS Lambert,A.J., Blair,C.D., D'Anton,M., Ewing,W., Harborth,M., Seiferth,R., Xiang,J. and Lanciotti,R.S.
TITLE La Crosse virus in Aedes albopictus mosquitoes, Texas, USA, 2009
JOURNAL Emerging Infect. Dis. 16 (5), 856-858 (2010)
PUBMED [20409384](#)
REFERENCE 2 (bases 1 to 6979)
AUTHORS Lambert,A.J., Blair,C.D., D'Anton,M., Ewing,W., Harborth,M., Seiferth,R., Xiang,J. and Lanciotti,R.S.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-2010) DVBLD, CDC, Rampart Road, Fort Collins, CO 80522, USA
COMMENT GenBank Accession Numbers GU561164-GU591166 represent the complete genome of La Crosse virus isolate Dallas/TX/2009.
FEATURES
source Location/Qualifiers
1..6979
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la crosse virus
- united states

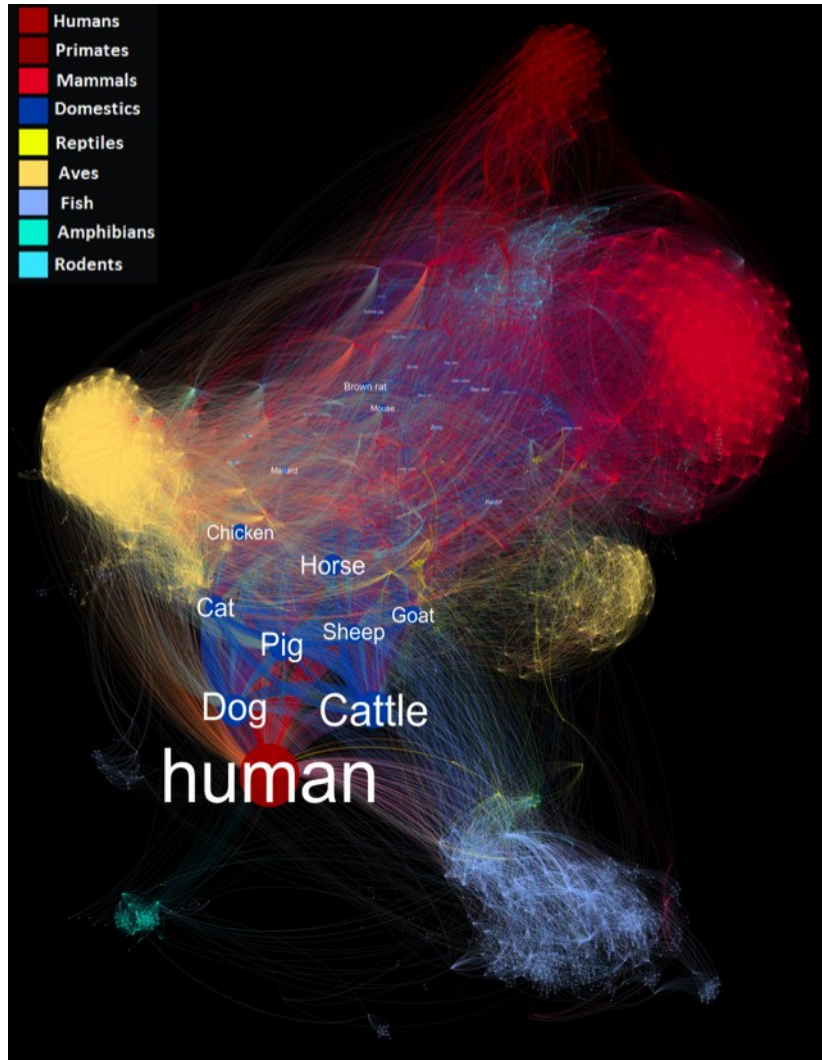
aedes
albopictus -
united states

la crosse virus
- aedes
albopictus

Big Data!

- 224,751 species in NCBI taxonomy database
- 39,238,061 sequences in NCBI nucleotide sequence database
- 19,717,726 sequences linked to 171,967 species
- 2,706,620 had Host tag
- 6,714,520 had Country tag
- 6,473,167 publications in PubMed database
- 6,028,487 linked to 7,463 species

Pathogen network



Home > Data Descriptors > Data Descriptor

SCIENTIFIC DATA | DATA DESCRIPTOR OPEN

Database of host-pathogen and related species interactions, and their global distribution

Maya Wardeh, Claire Risley, Marie Kirsty McIntyre, Christian Setzkorn & Matthew Baylis

[Affiliations](#) | [Contributions](#) | [Corresponding authors](#)

Scientific Data 2, Article number: 150049 (2015) | doi:10.1038/sdata.2015.49
Received 29 May 2015 | Accepted 05 August 2015 | Published online 15 September 2015

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Abstract

[Abstract](#) • [Background & Summary](#) • [Methods](#) • [Data Records](#) • [Technical Validation](#) • [Additional Information](#) • [References](#) • [Data Citations](#) • [Acknowledgements](#) • [Author Information](#)

Interactions between species, particularly where one is likely to be a pathogen of the other, as well as the geographical distribution of species, have been systematically extracted from various web-based, free-access sources, and assembled with the accompanying evidence into a single database. The database attempts to answer questions such as what are all the pathogens of a host, and what are all the hosts of a pathogen, what are all the countries where a pathogen was found, and what are all the pathogens found in a country. Two datasets were extracted from the database, focussing on species interactions and species distribution, based on evidence published between 1950–2012. The quality of their evidence was checked and verified against well-known, alternative, datasets of pathogens infecting humans, domestic animals and wild mammals. The presented datasets provide a valuable resource for researchers of infectious diseases of humans and animals, including zoonoses.

Online attention



Altmetric score (what's this?)

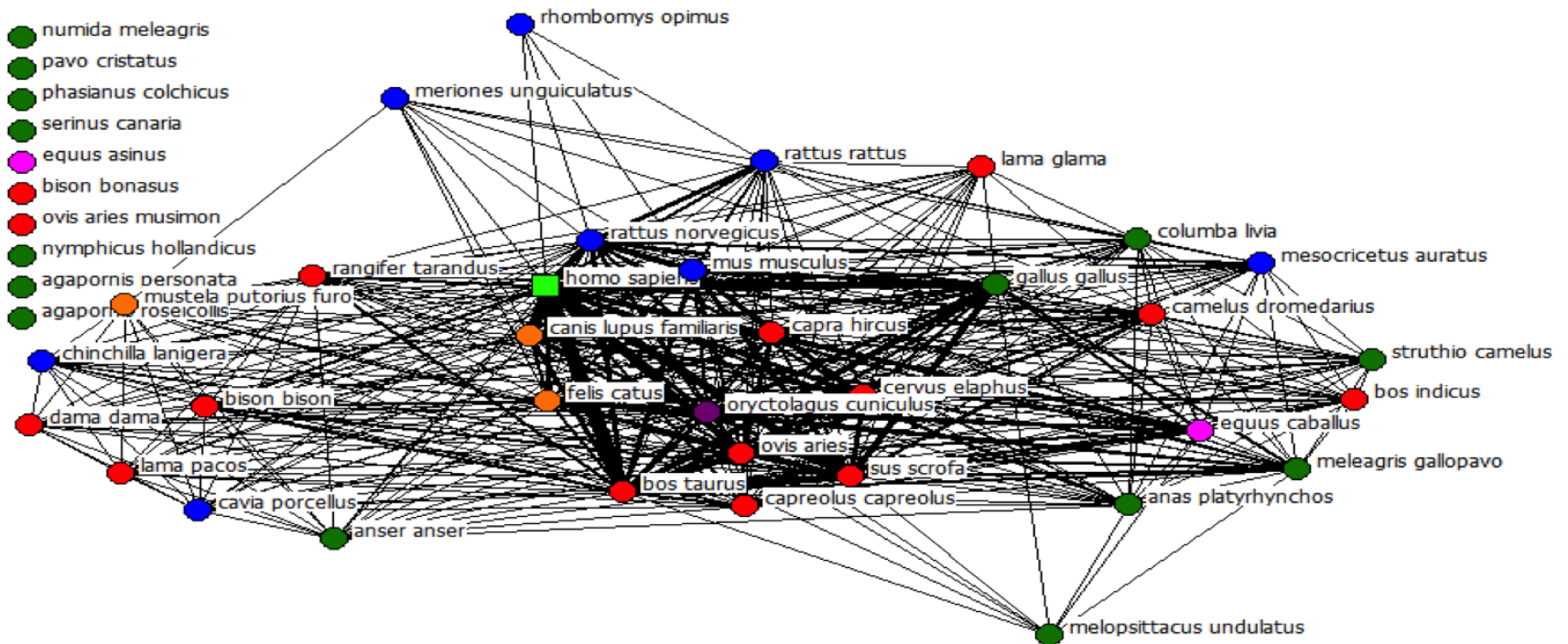
- Tweeted by 239
- Blogged by 2
- On 4 Facebook pages
- Mentioned in 1 Google+ posts
- Picked up by 3 news outlets
- 3 Reddit
- 2 readers on Mendeley
- 1 readers on Citeulike

This Altmetric score means that the article is:

- in the 99th percentile (ranked 637th) of the 122,315 tracked articles of a similar age in all journals
- in the 93rd percentile (ranked 1st) of the 15 tracked articles of a similar age in *Scientific Data*

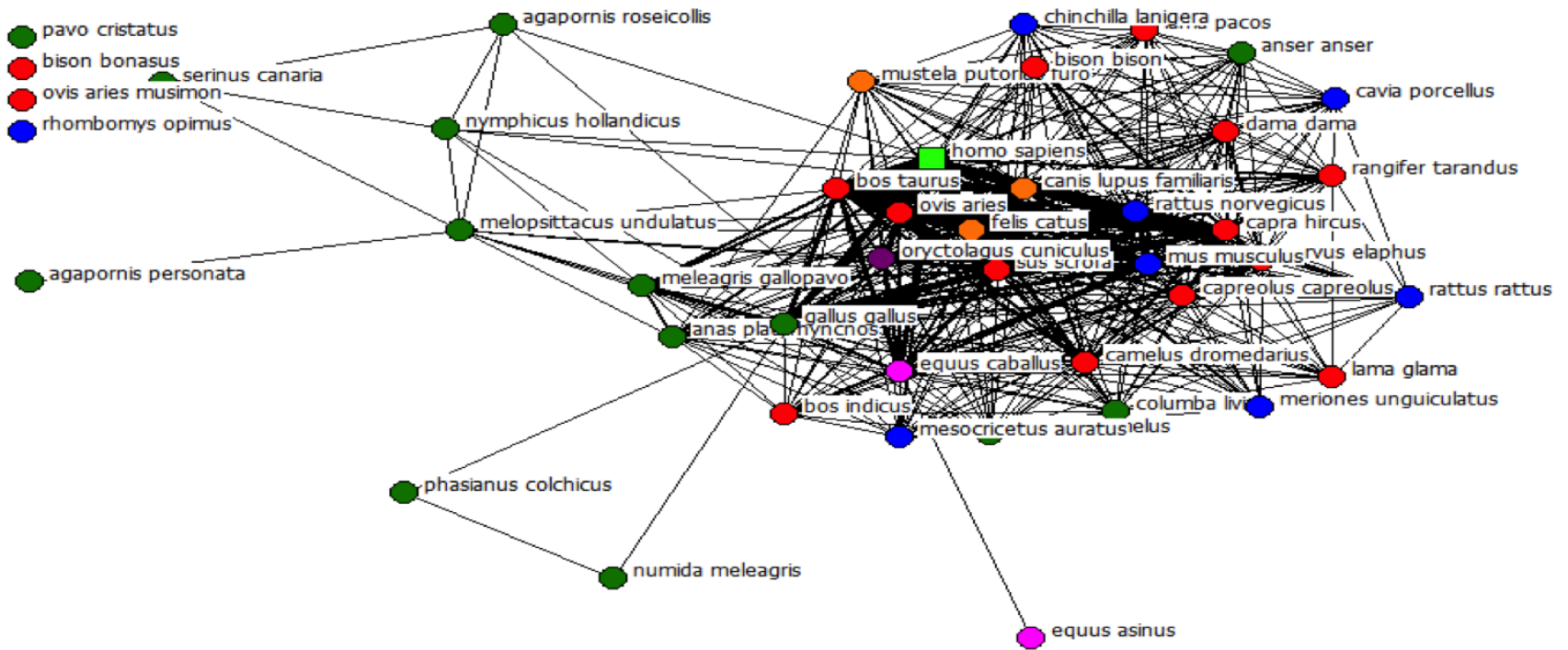
Scientific Data 2, Article number: 150049 (2015) doi:10.1038/sdata.2015.4

Transmission routes environment



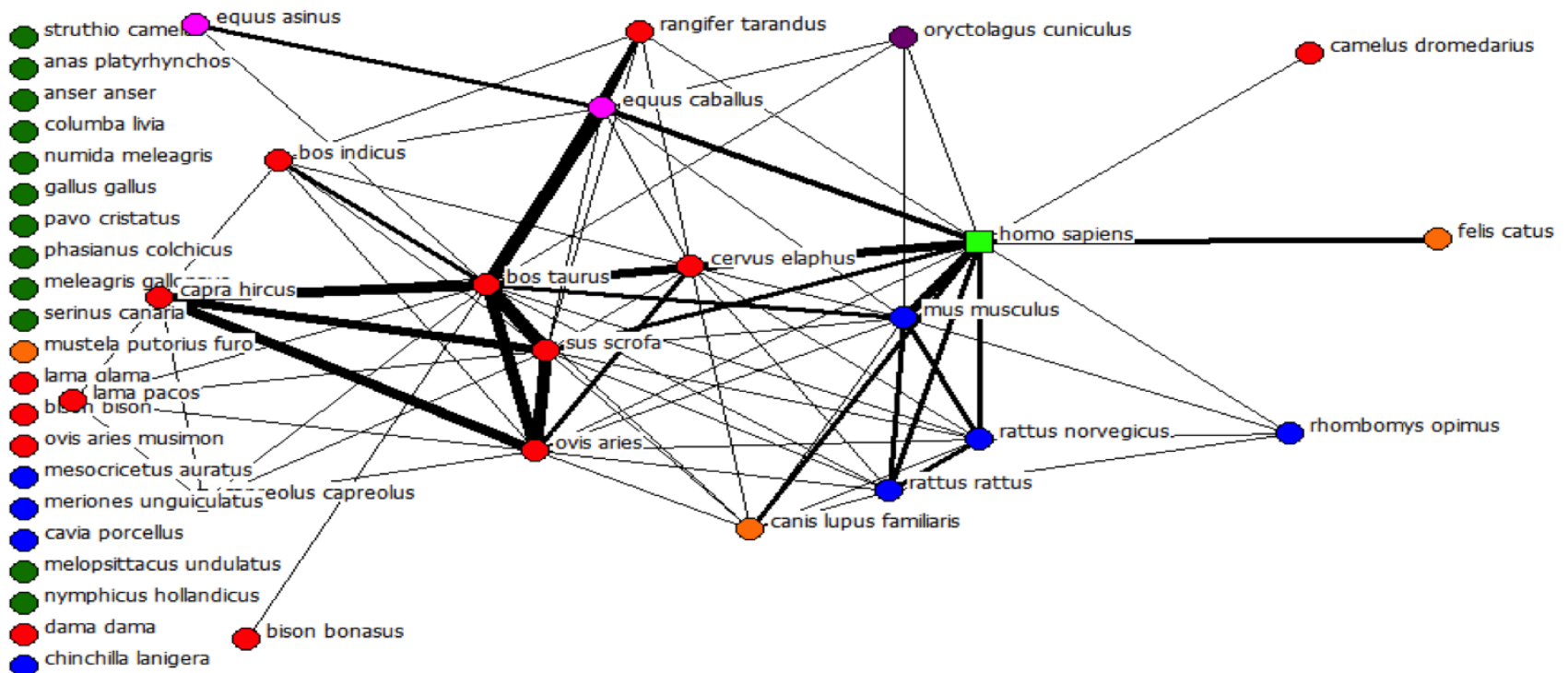
Transmission routes

ingestion

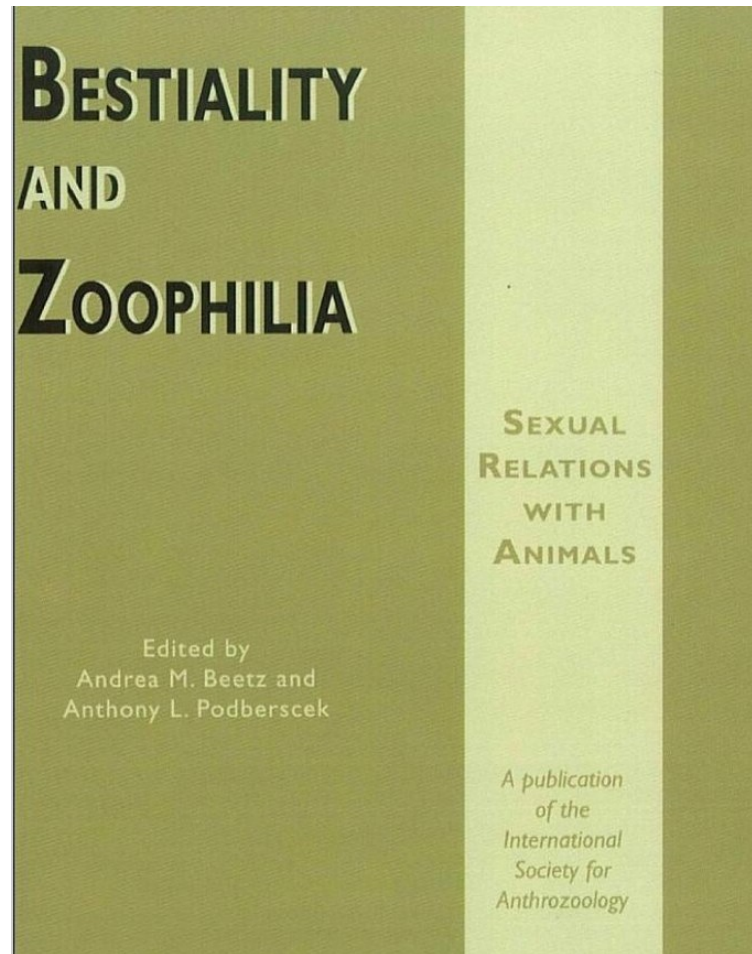


Transmission routes

sexual



It's a funny old world



Zoonotic pathogens

[1] 1,415 human pathogens, of which

868 (61%) HUMAN PATHOGENS ARE ZOOBOTIC

[2] 706 pathogens of livestock and 456 of domestic carnivores

LIVESTOCK PATHOGENS: 46% INFECT HUMANS [EID2, 40%]

DOMESTIC CARNIVORE PATHOGENS: 70% INFECT HUMANS [EID2, 65%]

EID2 finds 43% of livestock/carnivore pathogens to infect humans

[1] Taylor et al (2001). Phil Trans Roy Soc B, **356**, 983-989

[2] Cleaveland et al (2001). Phil Trans Roy Soc B, **356**, 991-999

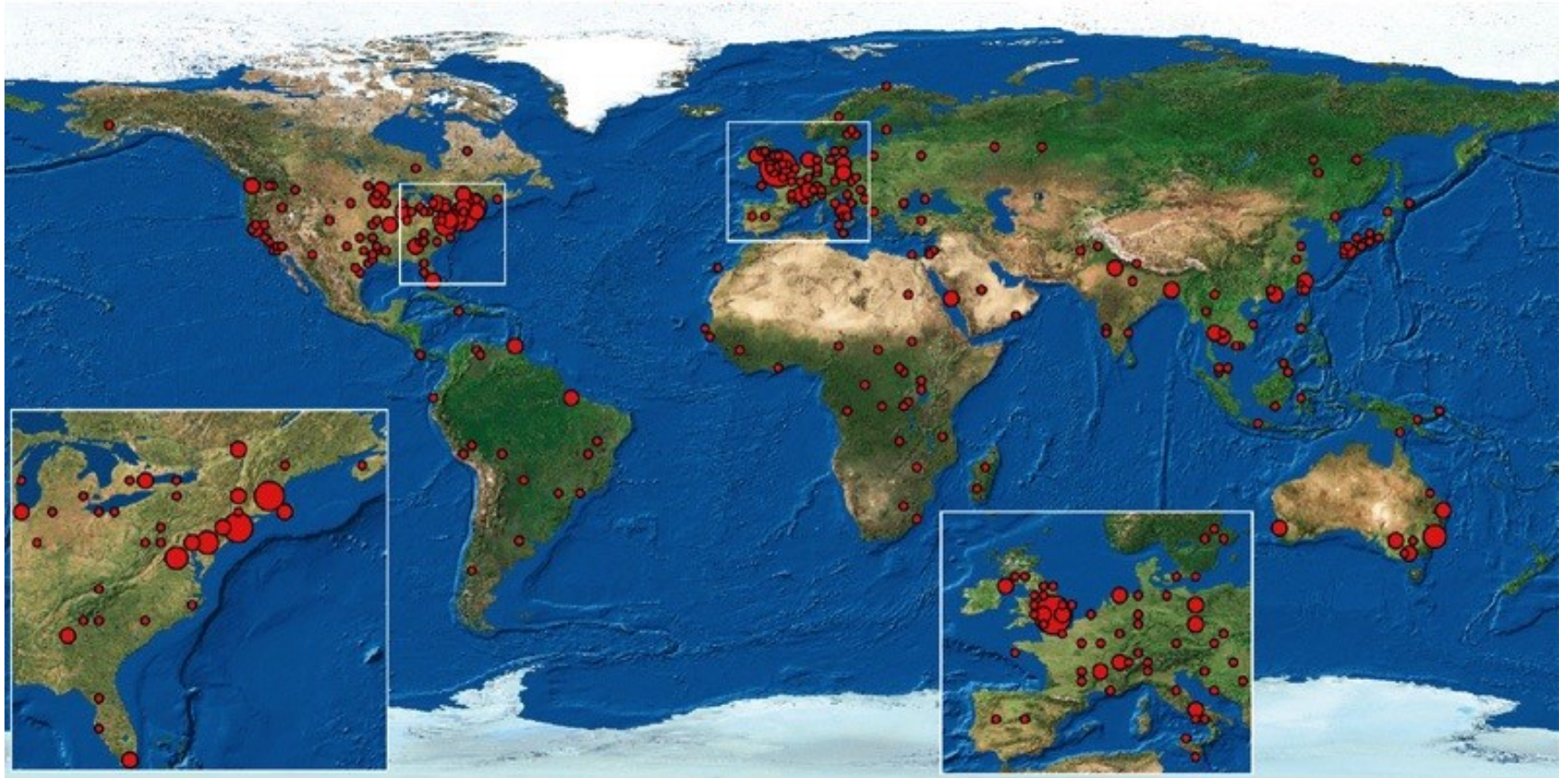


DRIVERS OF DISEASE EMERGENCE

Global richness

Map of geographic origins of EID events, 1940-2004 (Jones et al, 2008, Nature)

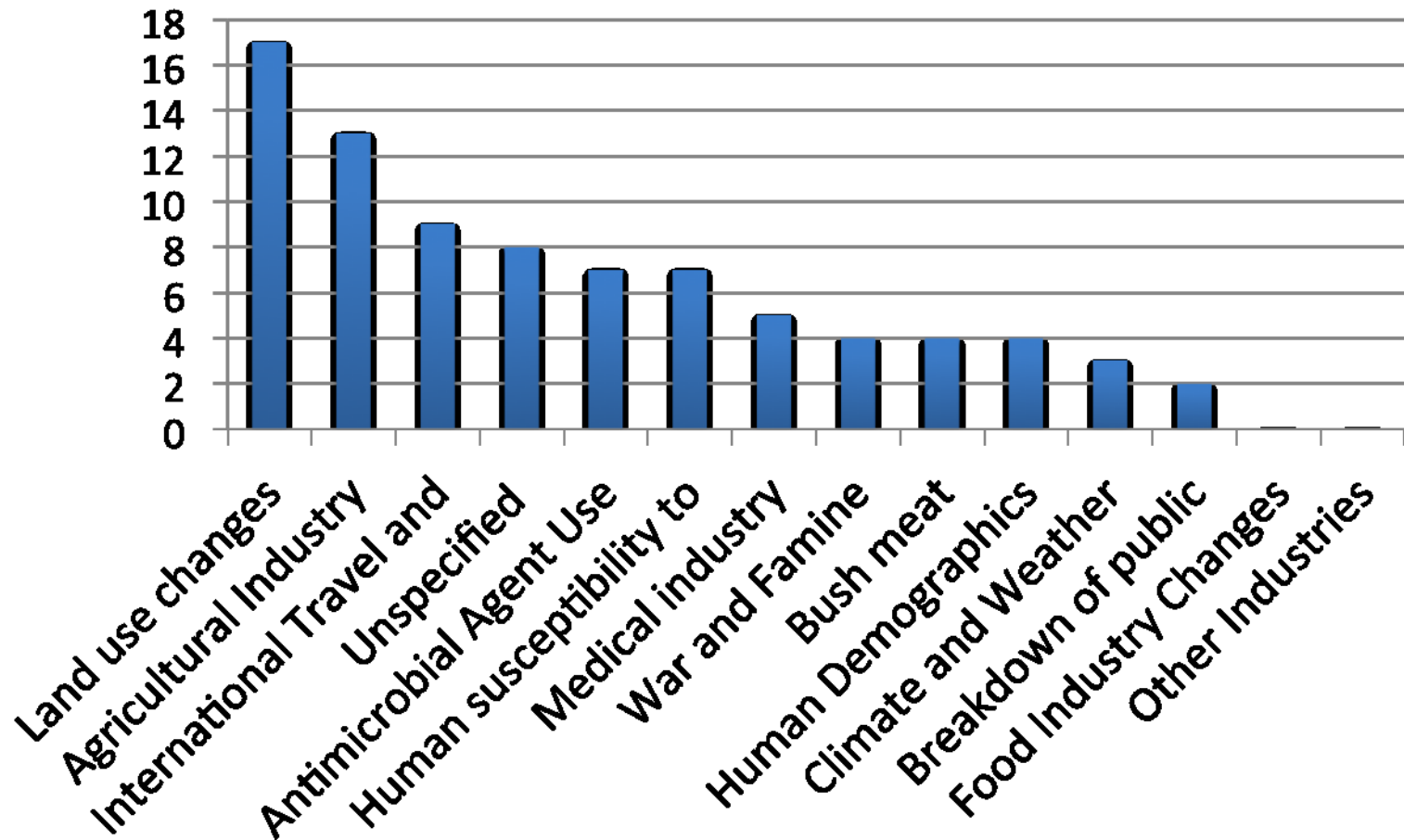
No. of EID events • 1 ● 2-3 ● 4-5 ● 6-7 ● 8-11



Drivers of [human viral] disease emergence

(Based on Jones *et al.*, 2008. *Nature*)

Number of viral diseases



Some drivers of animal virus re-emergence

Example	Drivers
Foot-and-mouth, 2001	Feeding food waste to pigs; delayed detection of index farm; Extensive animal movements; lack of standstills; no vaccination
Avian influenza, H5N1	Viral spread from wildlife to domestic animals; extensive mixing of poultry species; extensive movements of poultry; reassortment of viruses; bird migration
Chikungunya	Spread of insect vector; viral evolution; tourism & travel
Tick-borne encephalitis	Political change leading to Socioeconomic decline leading to Behavioural change; climate change?
Ebola	Viral dispersal in bats; bushmeat consumption; spread by health workers; slow response time
African swine fever	Global trade and travel; Feeding food waste to pigs; extensive animal movements
Bluetongue-8	Climate change, global transport of livestock/midges/viruses
Schmallenberg	Reassortment of viruses; global transport of livestock/midges/viruses

there is rarely a simple story with only one driver

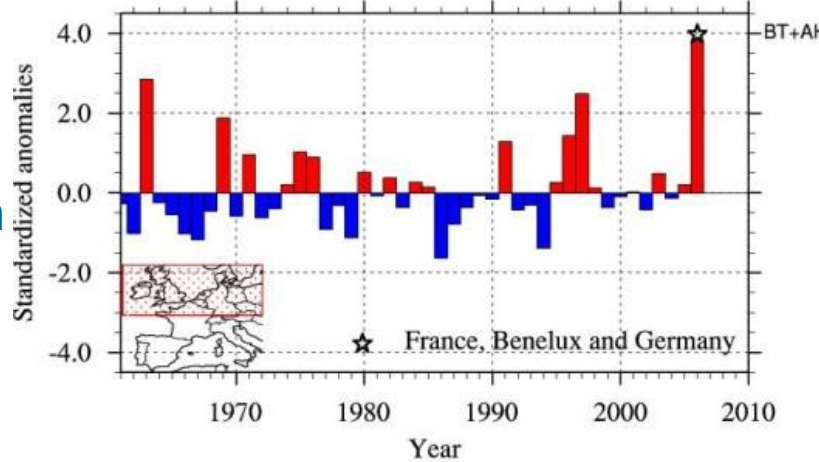
MODELLING SPREAD OF EMERGING PATHOGENS

Culicoides biting midges



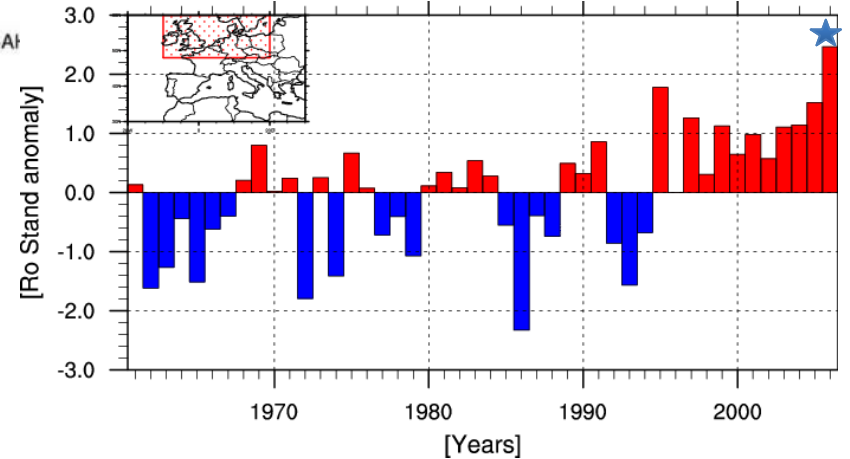
Past trends in R_0 - bluetongue

Full model (inc vector density)

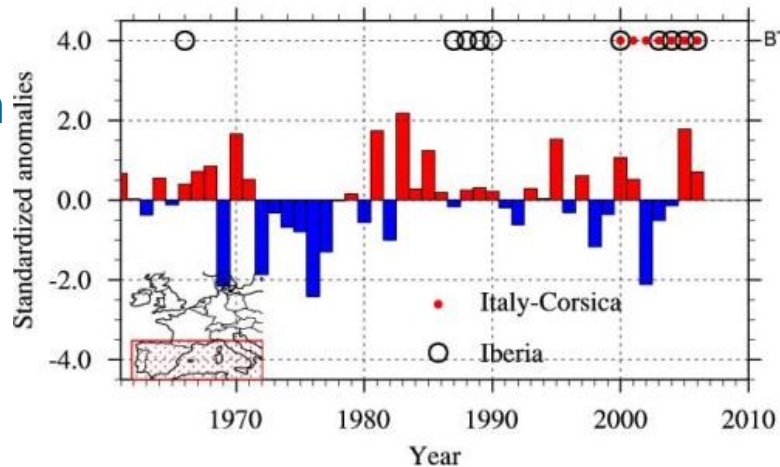


North-
western
Europe

Reduced model (only VC)

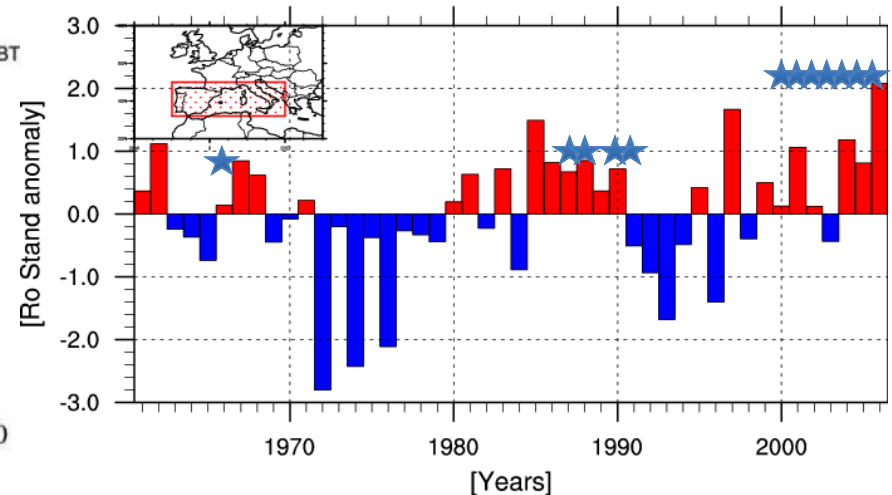


b

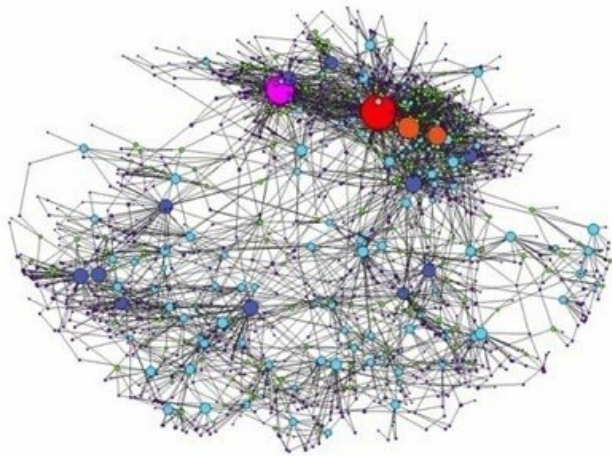


South-
western
Europe

Southern_Europe (ASO) lat=36/45 lon=-10/20



Spread of infection - networks



Infection spreads from farm-to-farm by three routes:

- **Movement of cattle**
 - Cattle Tracing Scheme, 2006
- **Movement of sheep**
 - Animal Movement Licensing Scheme, 2006
- **Dispersal of vectors**
 - Non-directional (and follows a kernel!)

Spread modelling

Blue = exposed

Red = infectious

Green = detected

Bluetongue

Farm infection status



day = 180: blue=exposed, red=infectious, green=detected

Schmallenberg

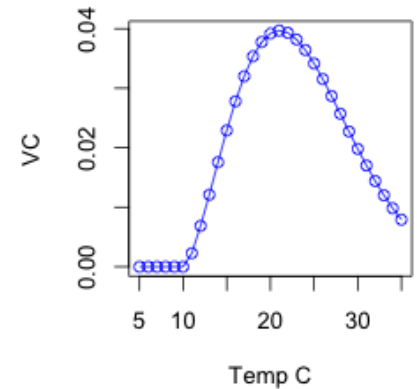
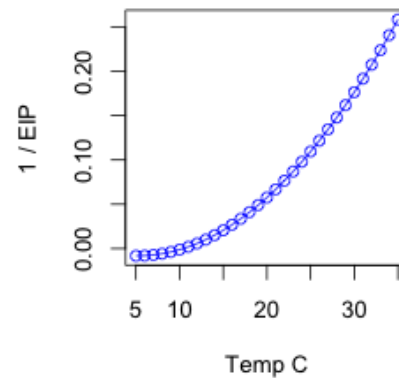
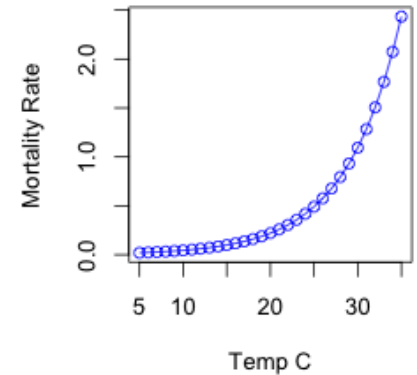
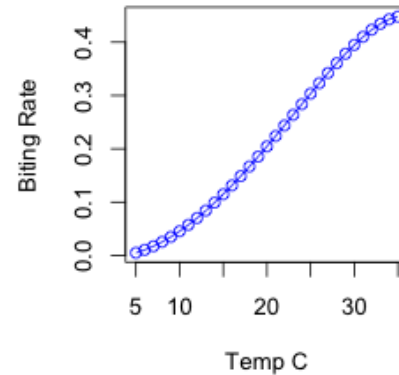
Farm infection status



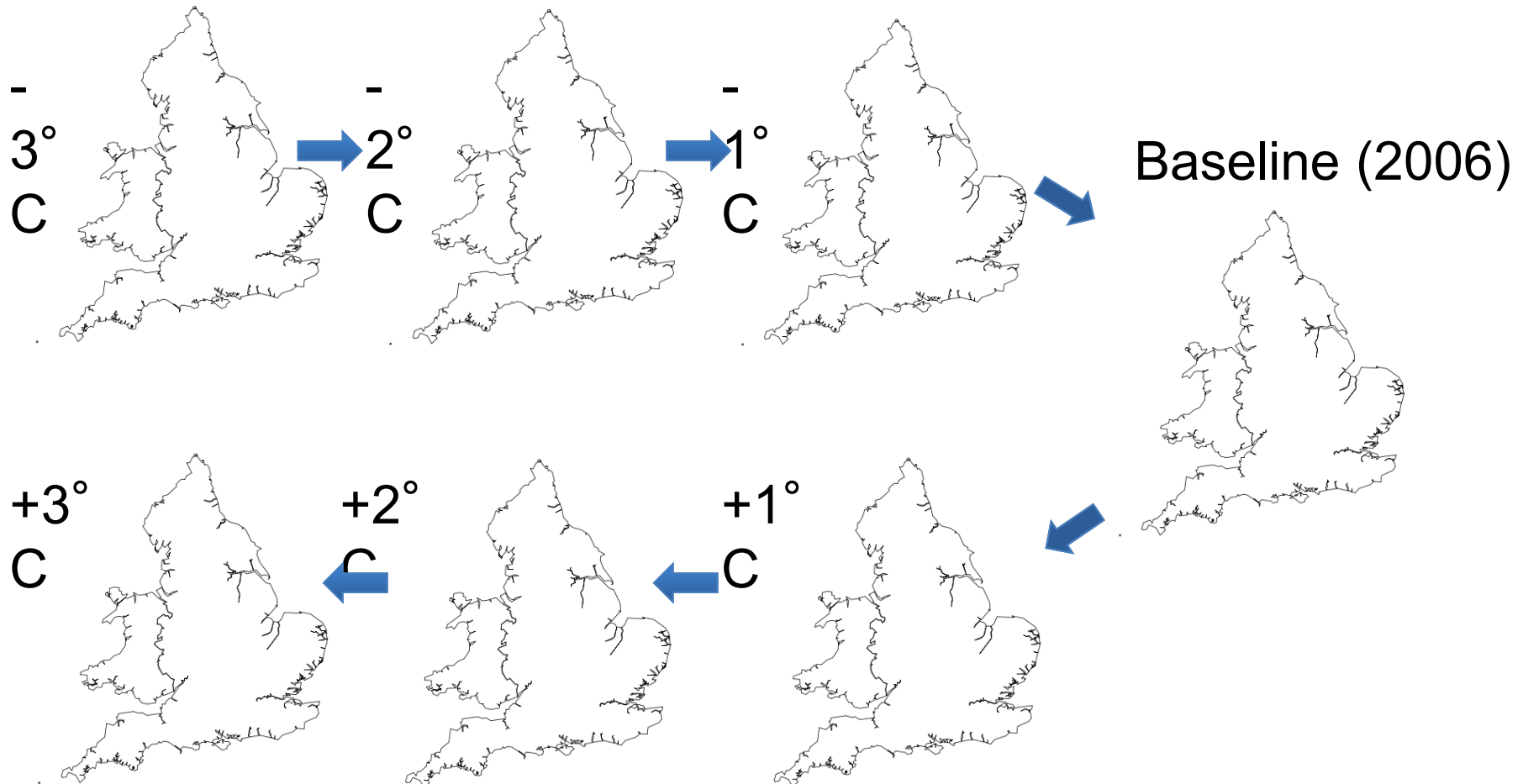
day = 180: blue=exposed, red=infectious, green=detected

Climate change and BT dynamics

- Model is climate sensitive
 - Temperature affects
 - vectorial capacity
 - vector seasonality



Simulating effect of temperature change



Conclusions

- Animals are a major source of human pathogens – but we have poor knowledge of the pathogens they harbour
- Big Data approaches can help identify new patterns
- Pathogen networks indicate that pathogens are shared with close relatives, co-habitants and predator/prey
- Many factors drive the emergence of new pathogens; climate change is one
- Climate change has driven the emergence of some vector-borne diseases, such as bluetongue
- Transmission models indicate that bluetongue outbreaks will be larger under warmer climates

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