

*Prepare, Predict, Prevent: Creating Objectivity in Infectious
Disease Risk Assessment using Big Data Approaches*

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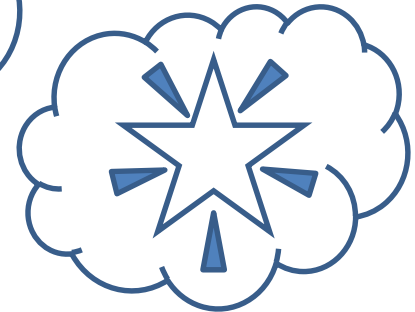
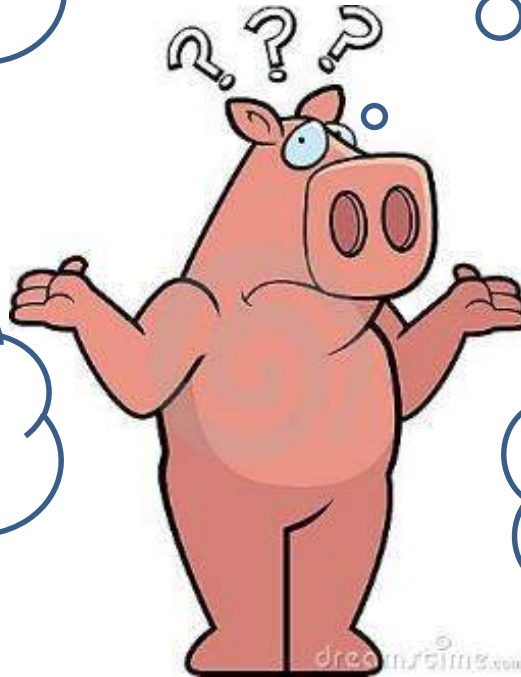
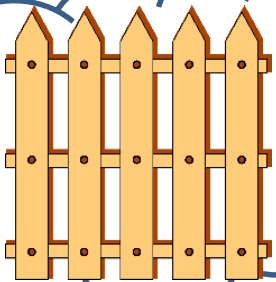
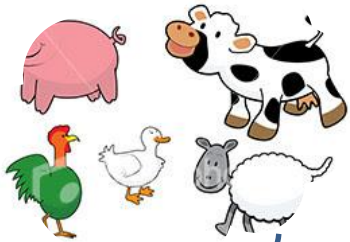


Risk Assessments Provide...

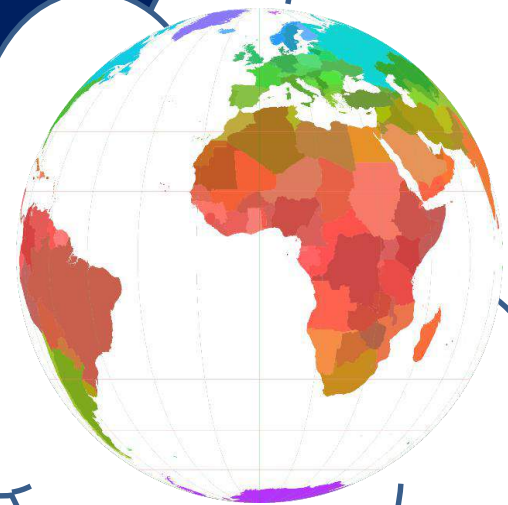
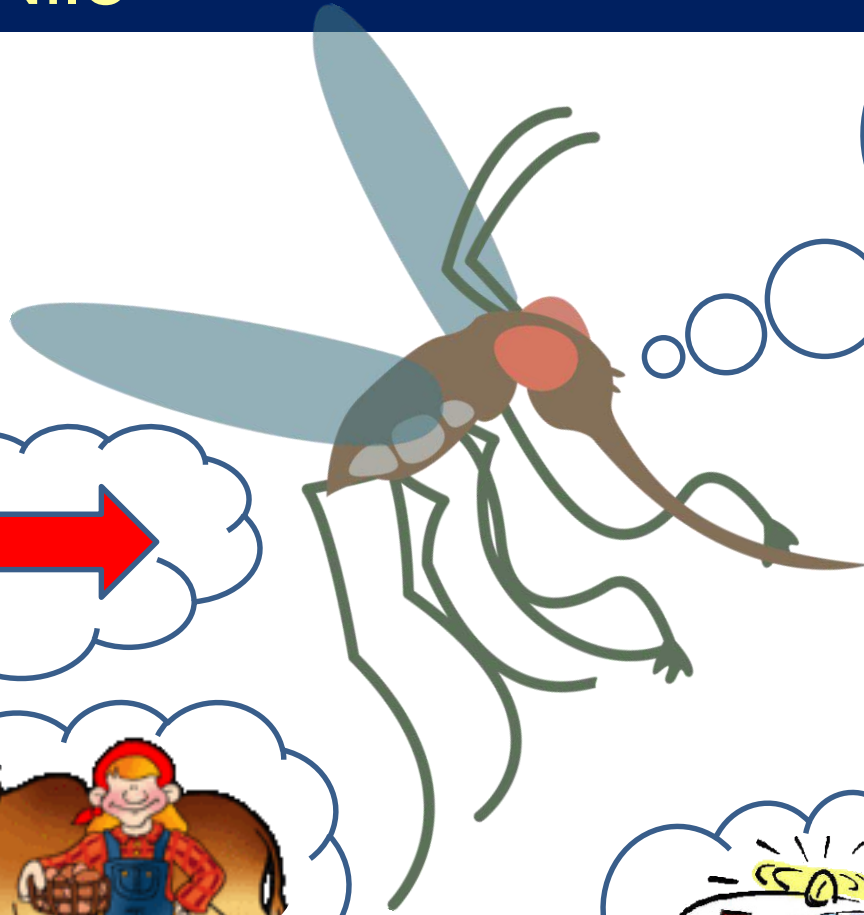


Prepare, Predict, Prevent: Schmallenberg Virus

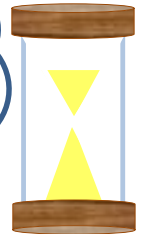
Where has
Schmallenberg
come from?



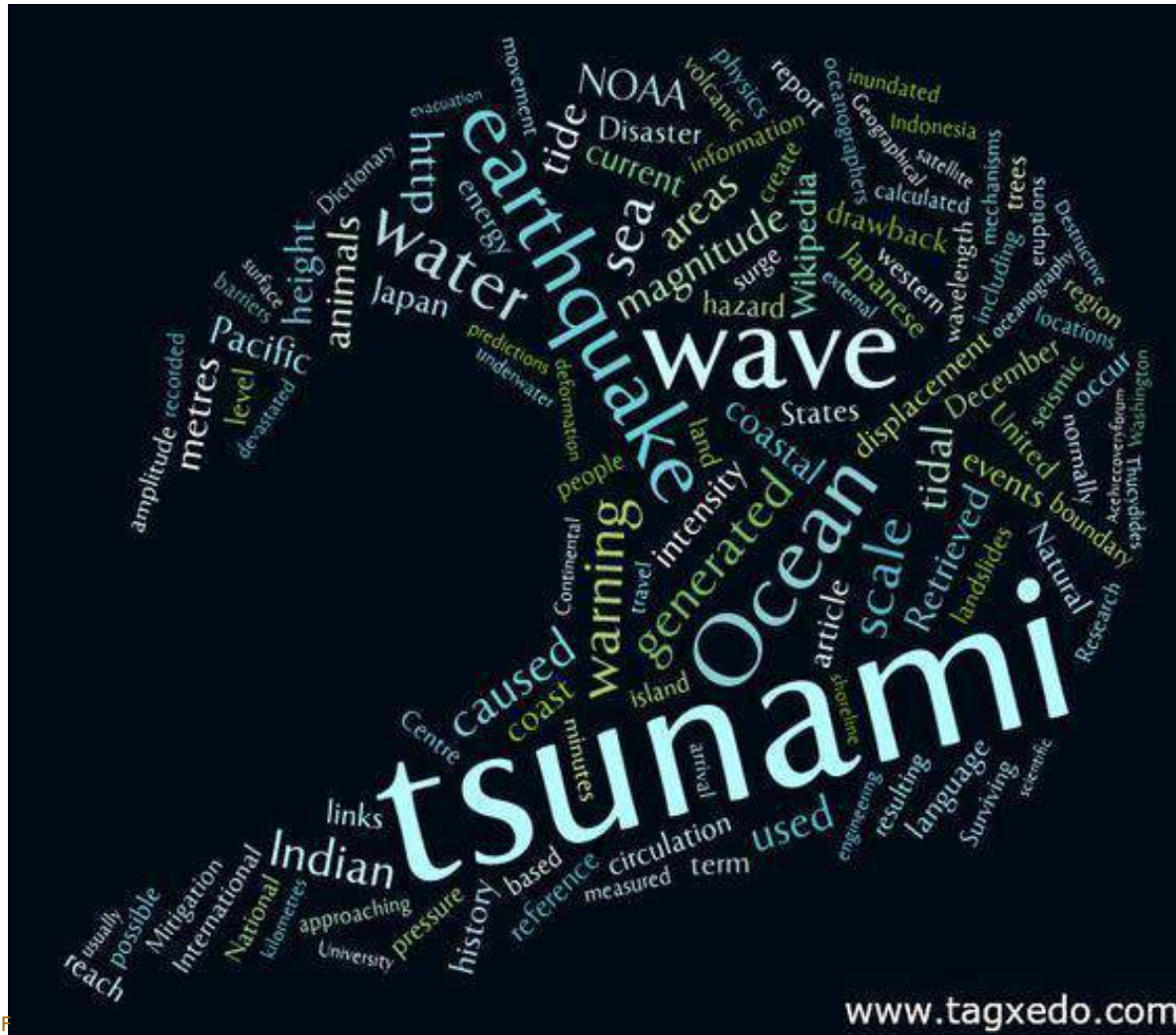
Prepare, Predict, Prevent: West Nile



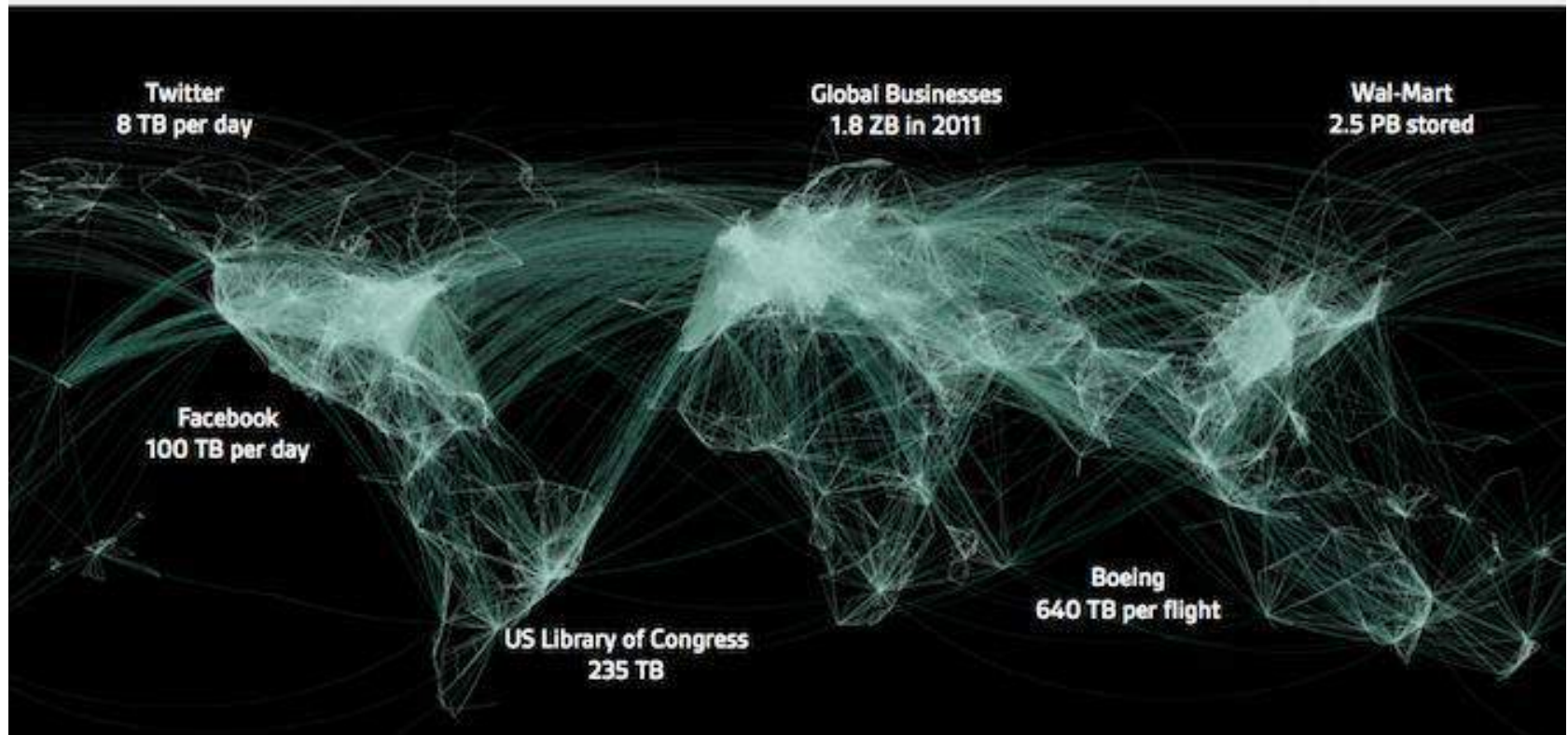
$\Sigma \alpha \beta \theta \lambda$



Studying the Dynamics of Systems...

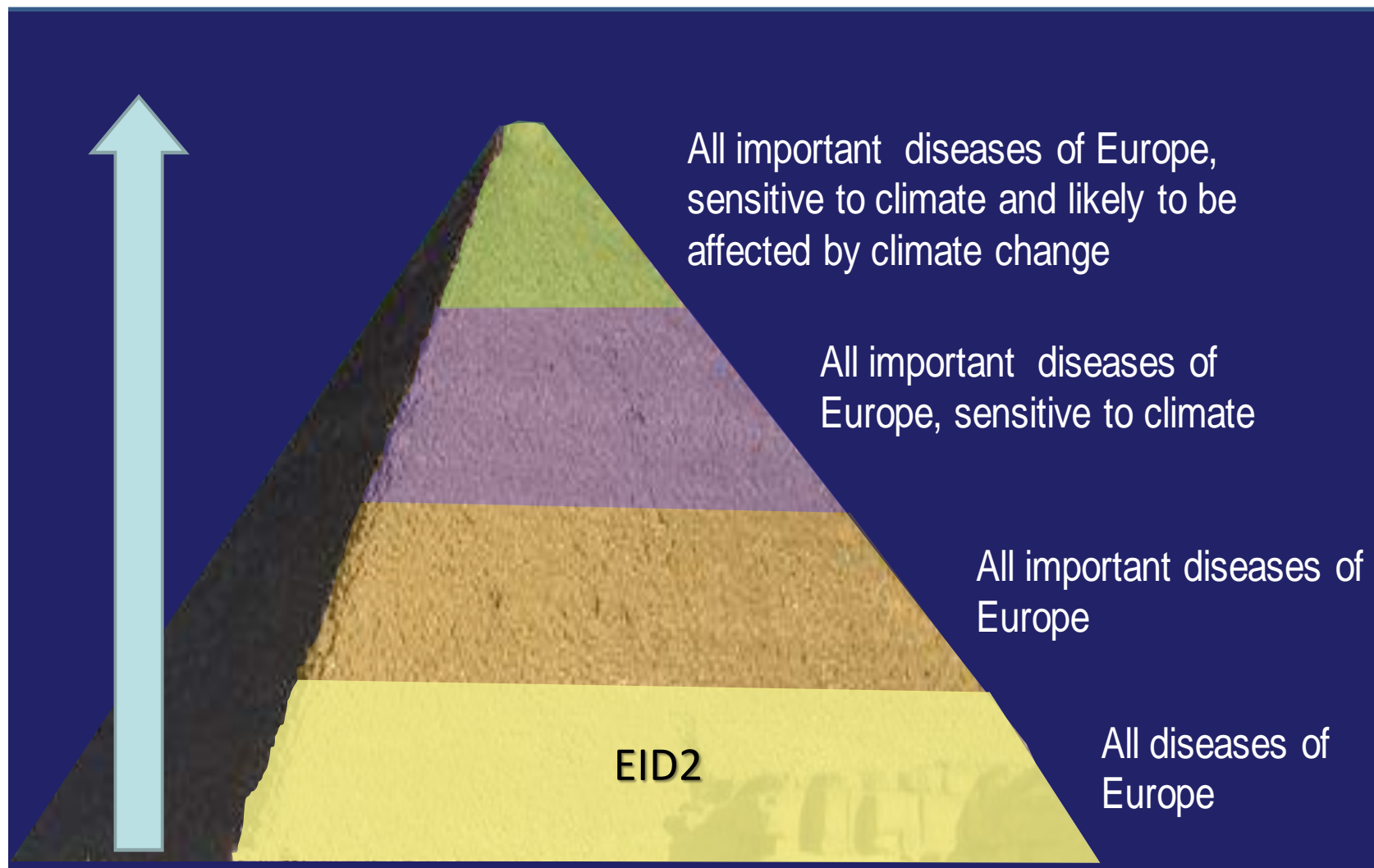


A Tidal Wave of Data



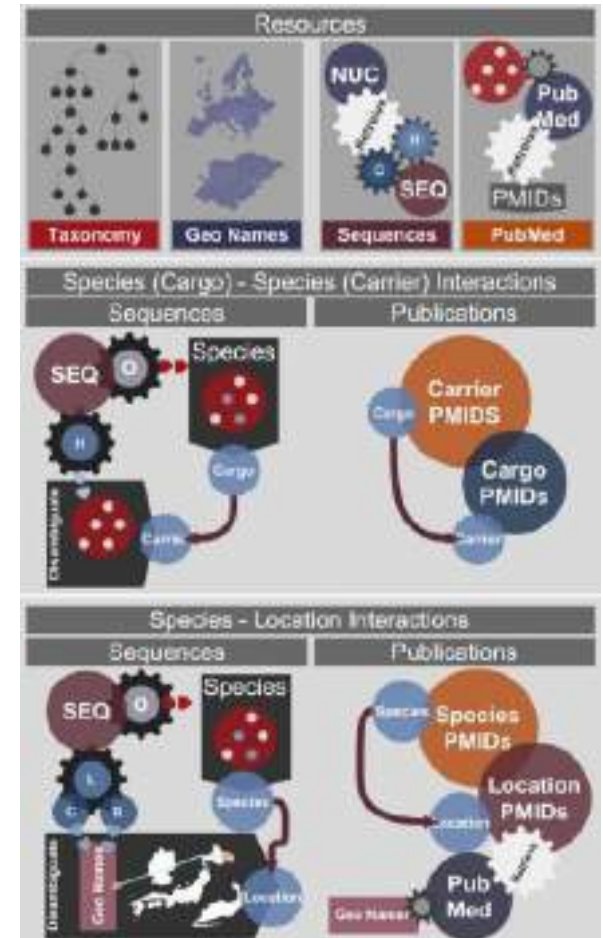
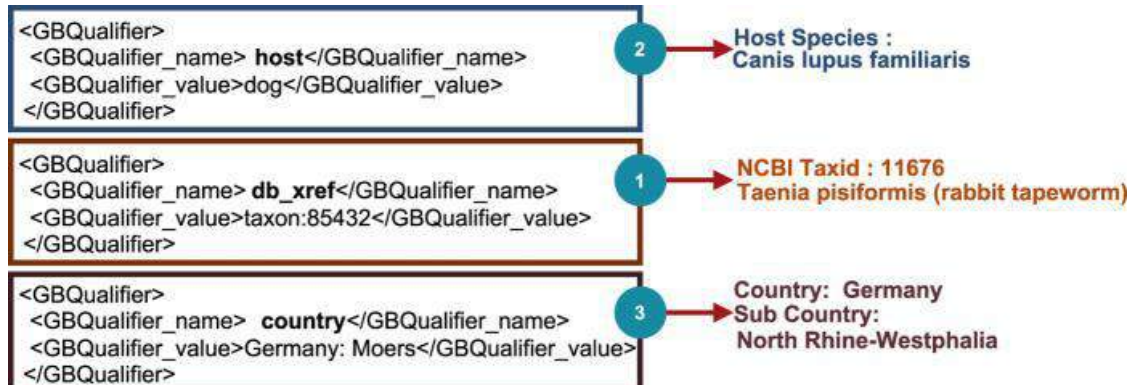
ERA-NET Health & Climate in Europe (ENHanCE)

- How realistic is the threat to human & animal health from climate change's effects on infectious diseases?
- Will most diseases respond to climate change or just a few?
- Will there be a net increase or decrease in disease burden?
- Is it possible that the diseases 'that matter most' are the least likely to respond to climate change?



ENHanCED Infectious Diseases (EID2) database

www.zoonosis.ac.uk/eid2



[illegible]

Name

accipiter cooperii

accipiter gentilis

aedes albopictus

aedes cinereus

aedes vexans

aegyptius monachus

agelaius phoeniceus

anas querquedula

anopheles messeae

anopheles subpictus

anser anser

anser sp.

aquila chrysaetos

argynnis pandora

athene noctua

bonasa umbellus

branta canadensis

bubo virginianus

bubulcus ibis

buteo jamaicensis

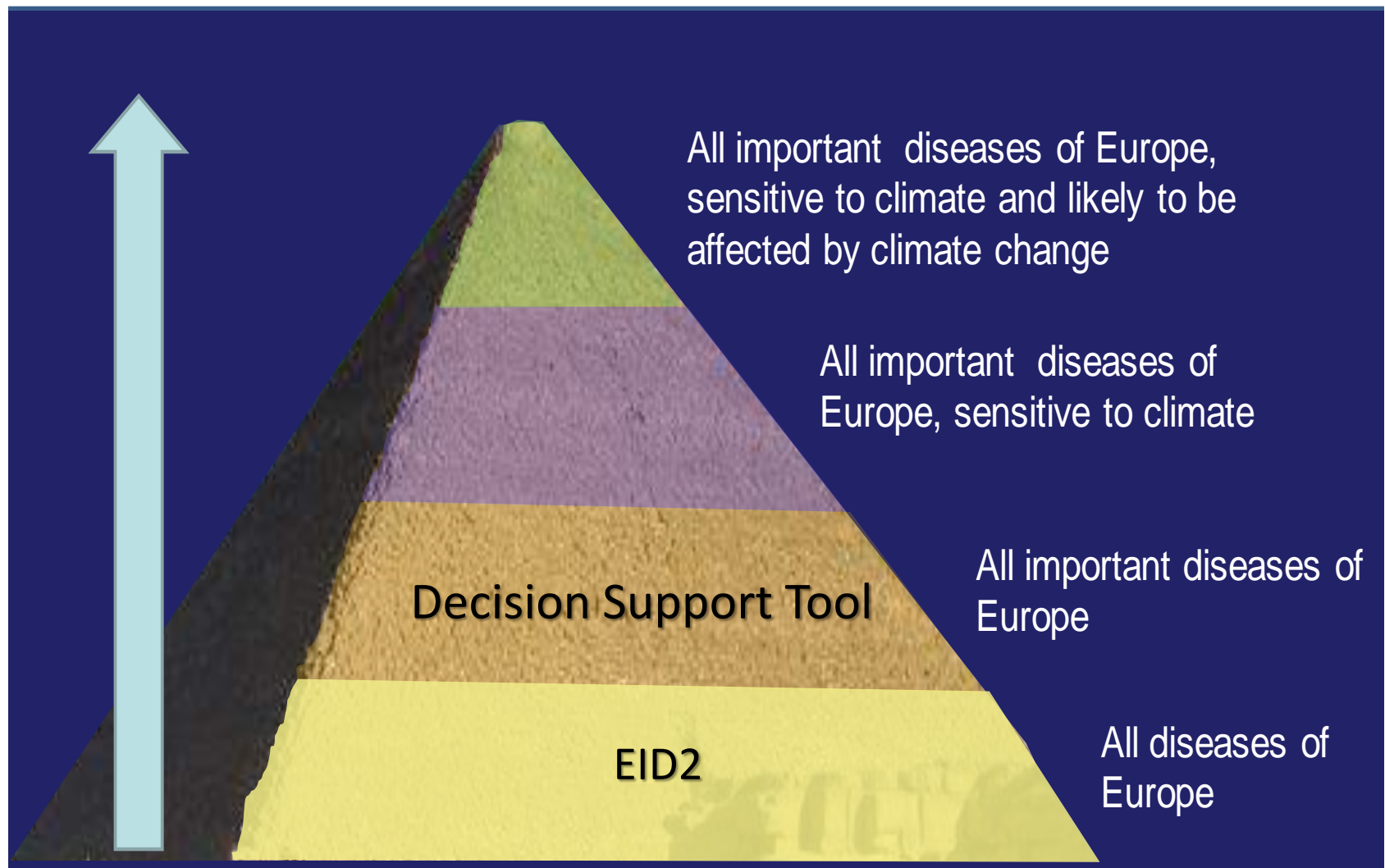
buteo lineatus

butorides virescens

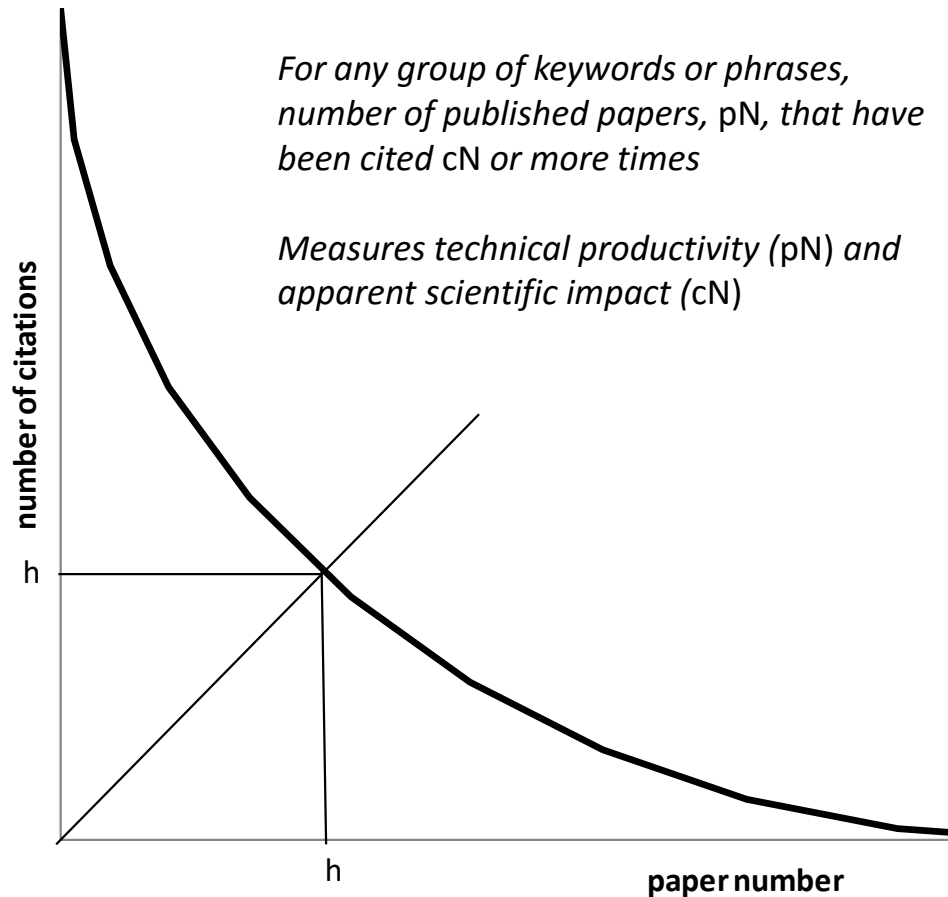
canis lupus familiaris

carios capensis





Which pathogens/diseases have greatest impact?

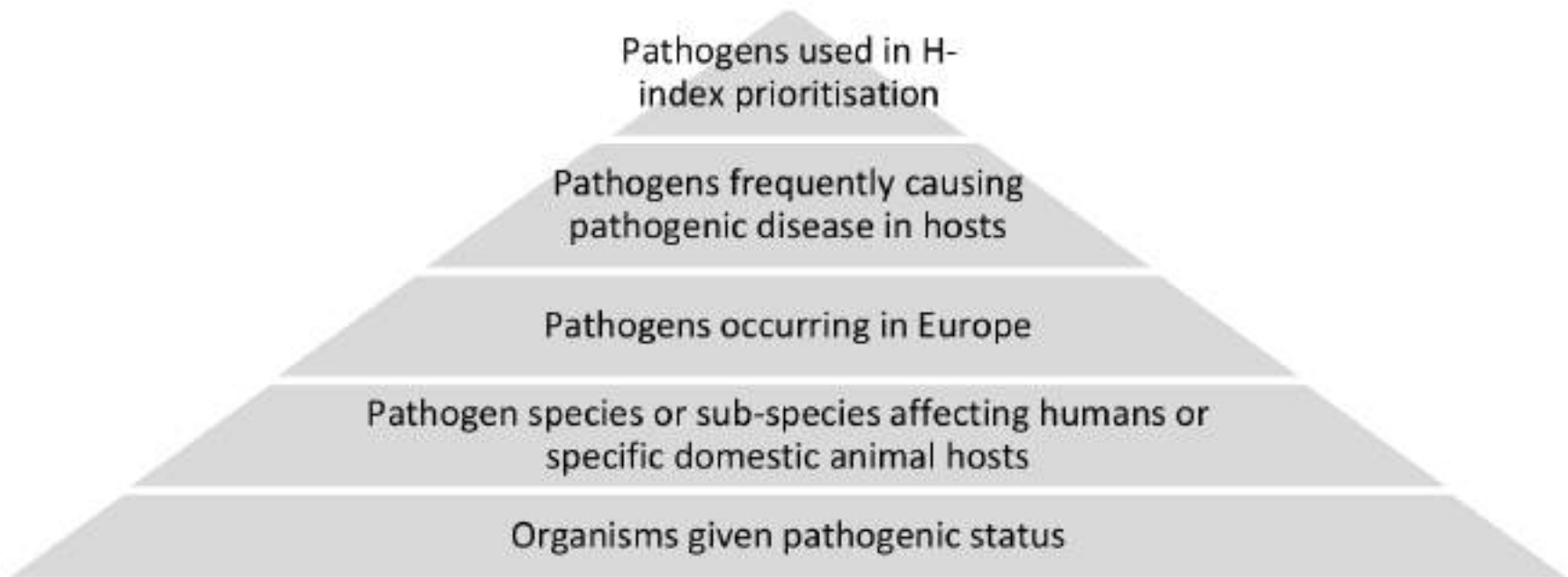


Use the (Hirsch-) H-index to assess

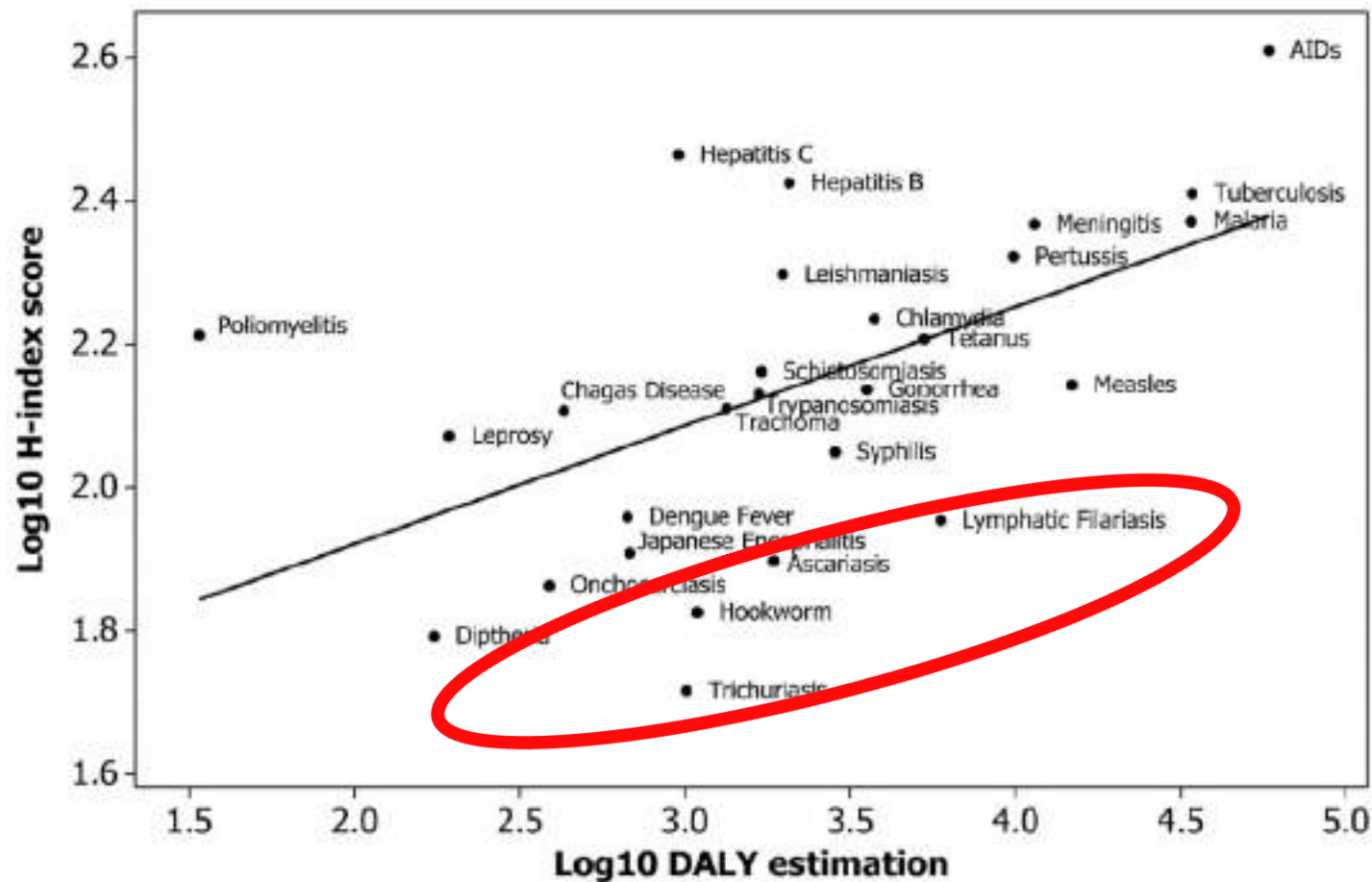
Searches run in WoS

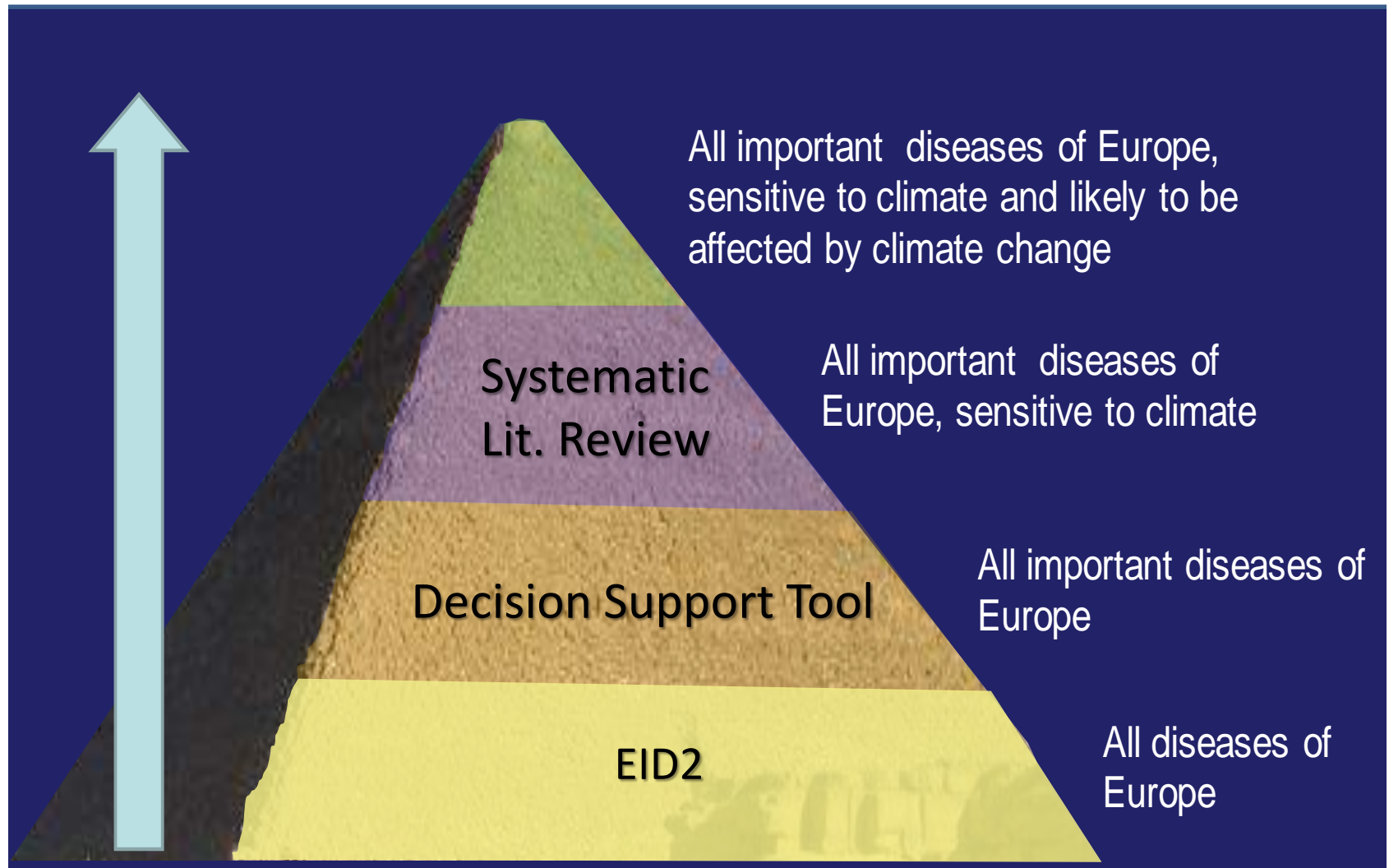
Correlation between H-index scores & other bibliographic indexes

- SCOPUS - $P < 0.001$
- Google Scholar - $P < 0.001$



Which pathogens/diseases have greatest impact?





	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	Where	where	review results.Organism	review results.Keyw	catgroup	Impact	JoTitle	review	PMID	truecd	dosere	abstrac	Article	Studyty	Effec	eviden
1	Where	where	review results.Organism	review results.Keyw	catgroup	Impact	JoTitle	review	PMID	truecd	dosere	abstrac	Article	Studyty	Effec	eviden
2	Phil	abstract	acinetobacter baumannii	flood	Extreme weather	1.51	Current m	2001	11381332	n	n					
3	Phil	abstract	acinetobacter baumannii	humid	Moisture	NULL	Acta medi	2009	20034329							

Automated searches

Climate driver terms n=190 x pathogens n=157

Combinations n=29830

~27 000 rows describing climate driver term x pathogen

Examined ~5000 rows for evidence

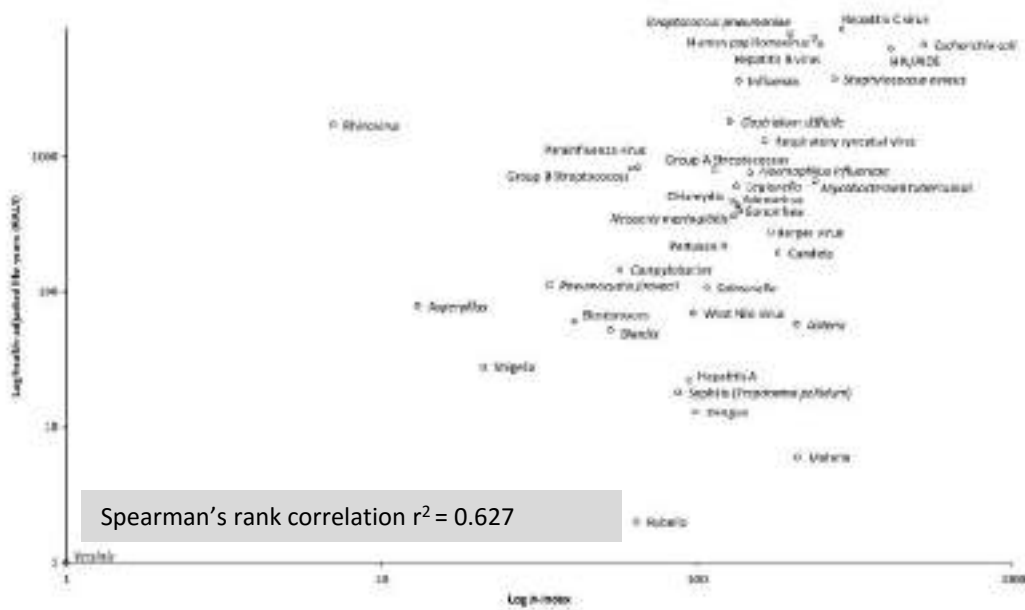
Stratified by:

- pathogen
- climate driver

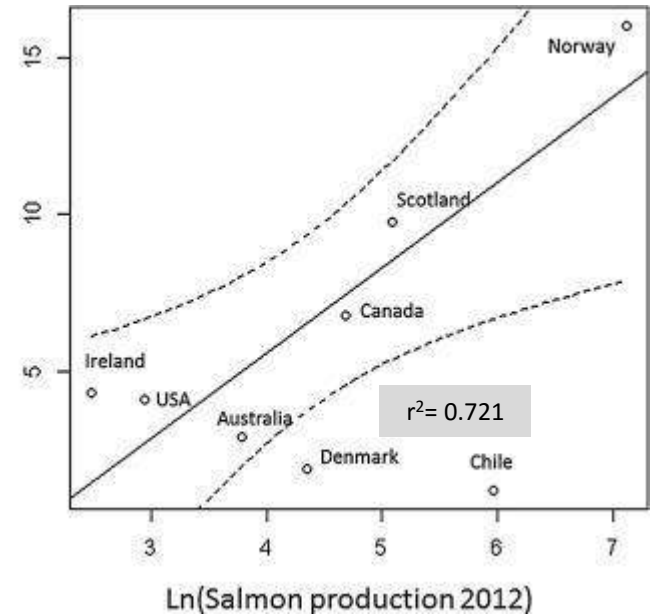
Prioritised according to:

- impact factor
- year of publication

Which Pathogens/Diseases Have Greatest Impact in N America & Salmon?!

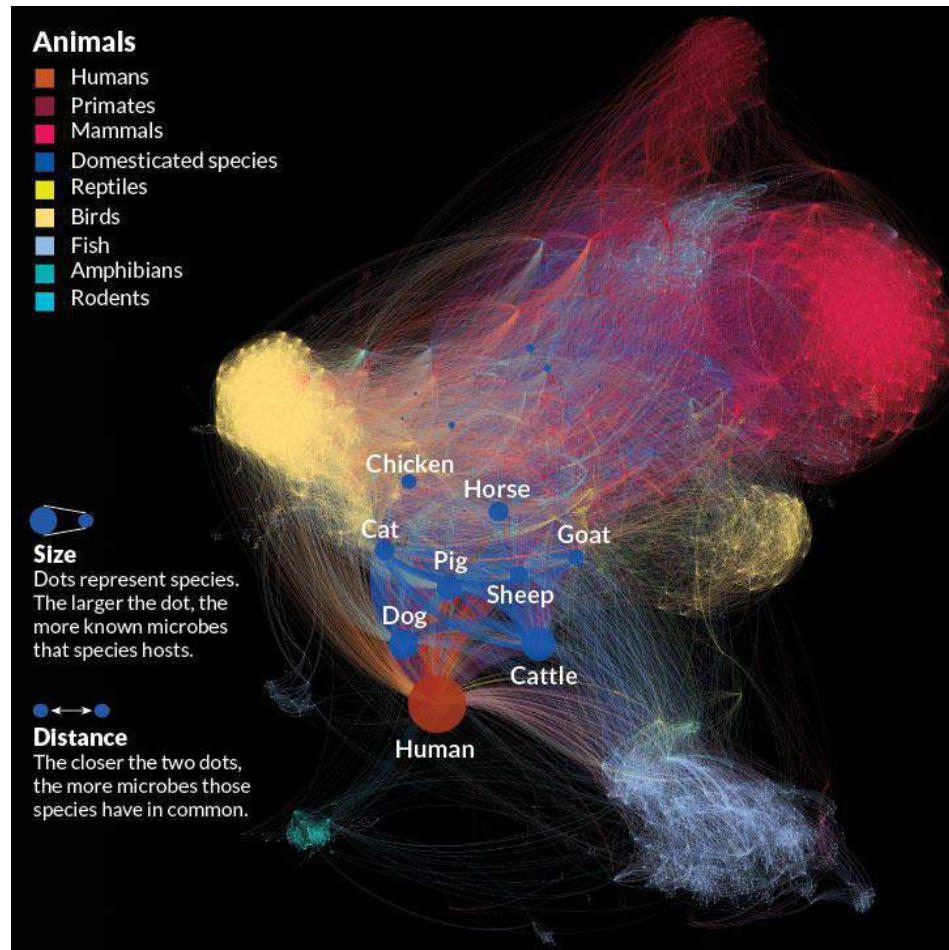


Cox et al. (2014) Trans Emerg Dis 63(1):79-91

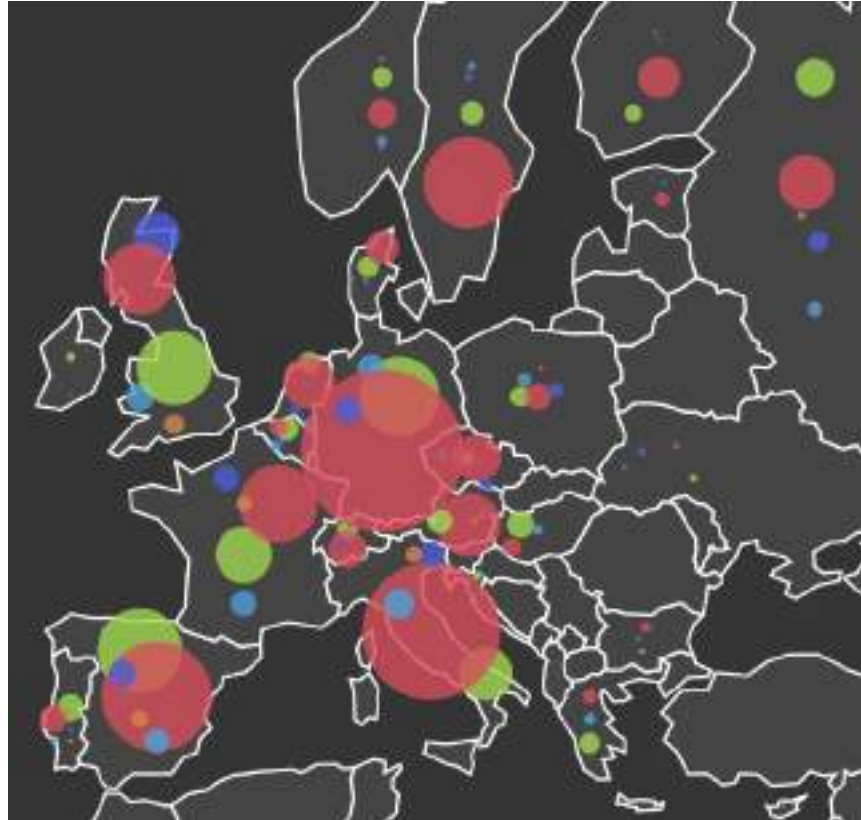


Murray et al. (2016)
Prev Vet Med 126:199-207

Which Host Groups are Most Important for Disease Transmission?



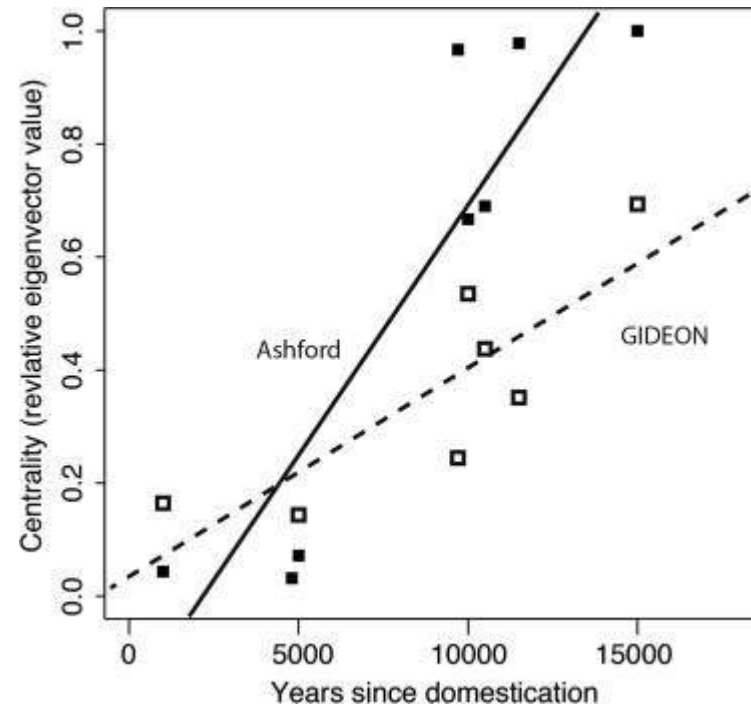
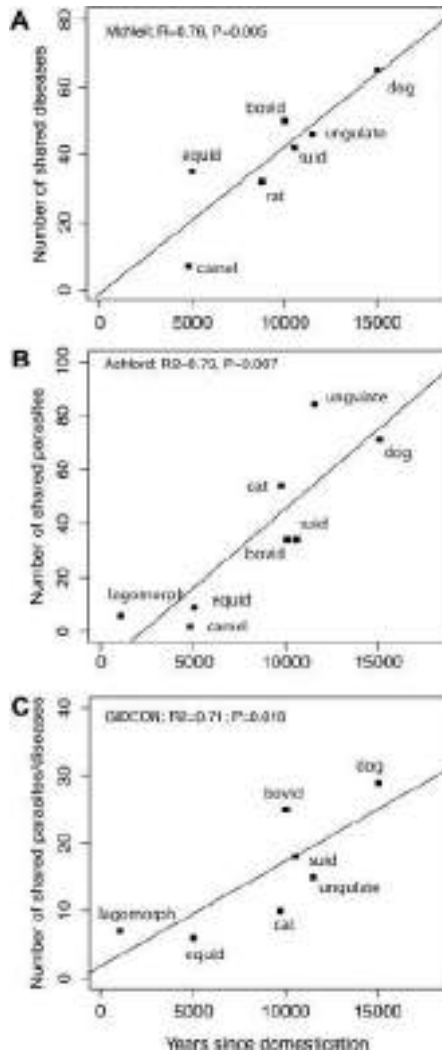
What Evidence do we Have for Pathogens in EU countries?



Colours represent taxonomic groups

Size represents number of pathogen species

Does Animal Domestication Play a Role in the Development of Zoonoses?

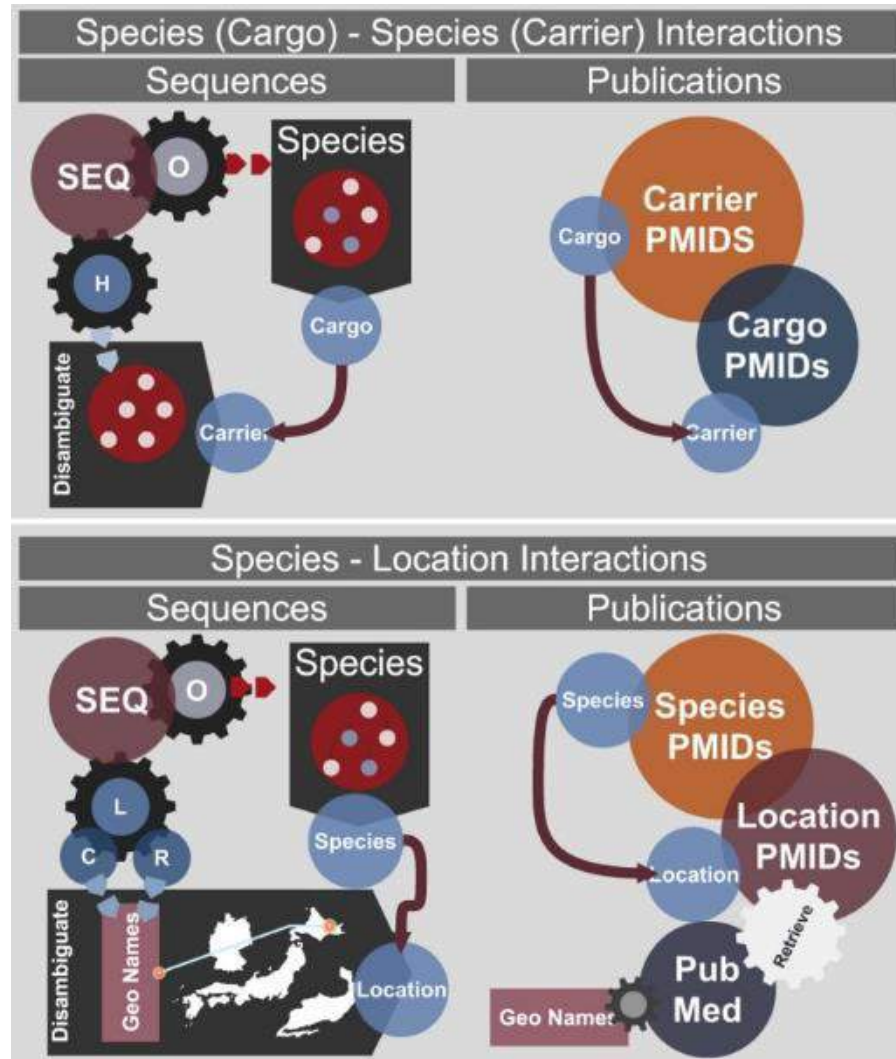


- Domestication time related to:
- number of shared pathogens
 - host network centrality

Challenges of Big Data Approaches

Accuracy of Incorporating Data

94.5% of carriers identified,
99.44% correctly



60% metadata with country contained additional location information which needed further geo-spatial assignment. 99.99% & 99.65% of countries & regions correctly identified, respectively

Wardeh et al. (2015) Scientific Data 2(150049)

95% of assumed pathogen-country interactions correct

McIntyre et al. (2014)
Prev Vet Med 116:
325–335

How Complete is EID2 Host-Pathogen Data Compared to Other Sources?



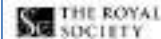
doi:10.1098/rstb.2001.0888

Risk factors for human disease emergence

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A comprehensive literature review identifies 1415 species of infectious organism known to be pathogenic to humans, including 217 viruses and prions, 538 bacteria and rickettsia, 307 fungi, 66 protozoa and 287 helminths. Out of these, 868 (61%) are zoonotic, that is, they can be transmitted between humans and animals, and 175 pathogenic species are associated with diseases considered to be 'emerging'. We test the hypothesis that zoonotic pathogens are more likely to be associated with emerging diseases than non-emerging ones. Out of the emerging pathogens, 132 (75%) are zoonotic, and overall, zoonotic pathogens are twice as likely to be associated with emerging diseases than non-zoonotic pathogens. However, the result varies among taxa, with protozoa and viruses particularly likely to emerge, and helminths particularly unlikely to do so, irrespective of their zoonotic status. No association between transmission route and emergence was found. This study represents the first quantitative analysis identifying risk factors for human disease emergence.



doi:10.1098/rstb.2001.0888

Diseases of humans and their domestic mammals: pathogen characteristics, host range and the risk of emergence

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Pathogens that can be transmitted between different host species are of fundamental interest and importance from public health, conservation and economic perspectives, yet systematic quantification of these pathogens is lacking. Here, pathogen characteristics, host range and risk factors determining disease emergence were analysed by constructing a database of disease-causing pathogens of human and domestic mammals. The database consisted of 345 pathogens causing disease in humans, 681 in livestock and 374 in domestic carnivores. Mobile pathogens were very prevalent among human pathogens (60.6%) and even more so among domestic mammal pathogens (livestock 72.1%, carnivores 90.0%). Pathogens able to infect human, domestic and wildlife hosts constituted a similar proportion of disease-causing pathogens for all three host groups. One hundred and ninety-six pathogens were associated with emerging diseases, 75 in humans, 29 in livestock and 12 in domestic carnivores. Across all three groups, helminths and fungi were relatively unlikely to emerge whereas viruses, particularly RNA viruses, were highly likely to emerge. The ability of a pathogen to infect multiple hosts, particularly both in other mammalian orders or wildlife, were also risk factors for emergence in human and livestock pathogens. There is clearly a need to understand the dynamics of infectious diseases to complex mammal communities in order to mitigate disease threats to public health, livestock communities and wildlife.

McIntyre et al. (2014) *Prev Vet Med* 116: 325–335

Wardeh et al. (2015) *Scientific Data* 2(150049)

Data quality & sharing challenges

Need to consider:

- information is presence-only
- spatial resolution
- temporal resolution
- efficiency of data collection
- specificity & sensitivity of methods
- choice of keyword/phrases
- quality of & evidence available within secondary sources
- comparison (or combination) with manual (primary data) methods
- institutional inertia to systems-based approaches

Contributors



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