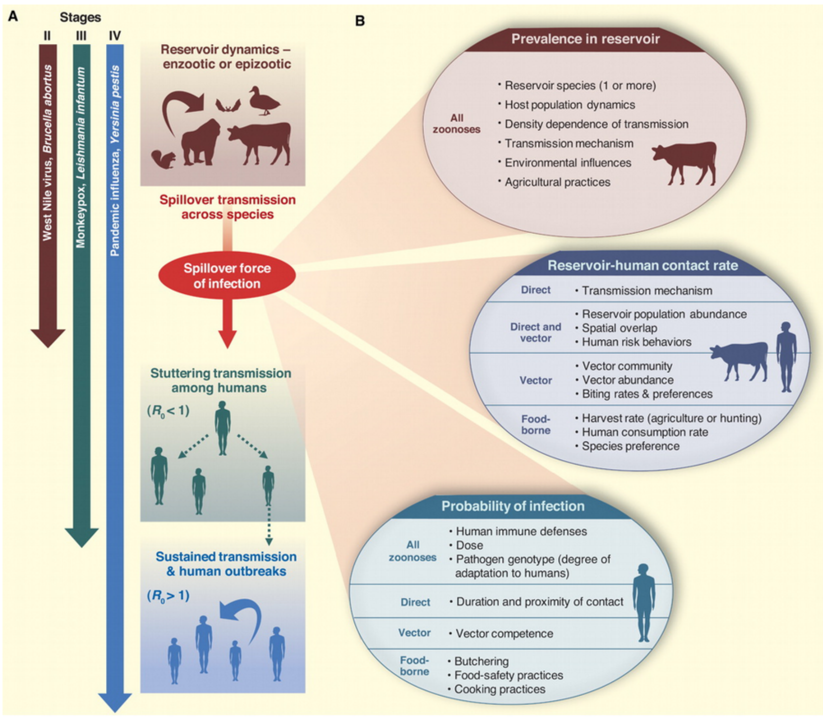
emerging infectious disease

3 April 2022

emerging and re-emerging disease



basically, anything we're worried about

- new mutations
- change in environment
- resistant strains
- species jumps (encounter and compatibility: changes via recombination, mutation)

Do we need to understand *everything*?

- reservoir ecology
- pathogen biology
- human-reservoir interactions

How do we understand? How do we predict?

Batrachochytrium dendrobatidis

Reminders

- fungal pathogen

  - most other chytrids are saprophytes, plant pathogens
  - *B. salamandrivorans*: salamander pathogen (more restricted)

- first discoved in poison dart frogs
- caused die-offs in E Australia, Central America, Colorado, California . . .
- association with high altitude?
- occurred in pristine areas (probably not anthropogenic?)
- pathogenesis via screwed-up osmoregulation

Very confusing . . .

- some species decline in the absence of Bd
- some species stable in the presence of Bd (Bd may have been there all along?)
- susceptibility:
  - ability to bask
  - antimicrobial peptides

tipping point hypothesis: in populations all the time, but something happened to increase virulence/reduce tolerance or resistance

- climate change/El Niño ?
- ultraviolet radiation?
- cooler temperatures? (basking etc.)
- pesticides?
- combination (species × temperature × U/V × pesticide × . . .)
- Pounds et al. (2006): "chytrid-thermal-optimum hypothesis"
- Rohr et al. (2008): "numerous other variables, including regional banana and beer production, were better predictors of these extinctions"
- Rohr & Raffel (2010)

novel pathogen hypothesis: mutation/speciation + dispersal

- "Out of Africa" hypothesis
- earlier/broader detection in historical specimens: CA/bullfrog, Brazil . . .
- genomics (challenging!)
- Asian sampling

monkeypox

climate change

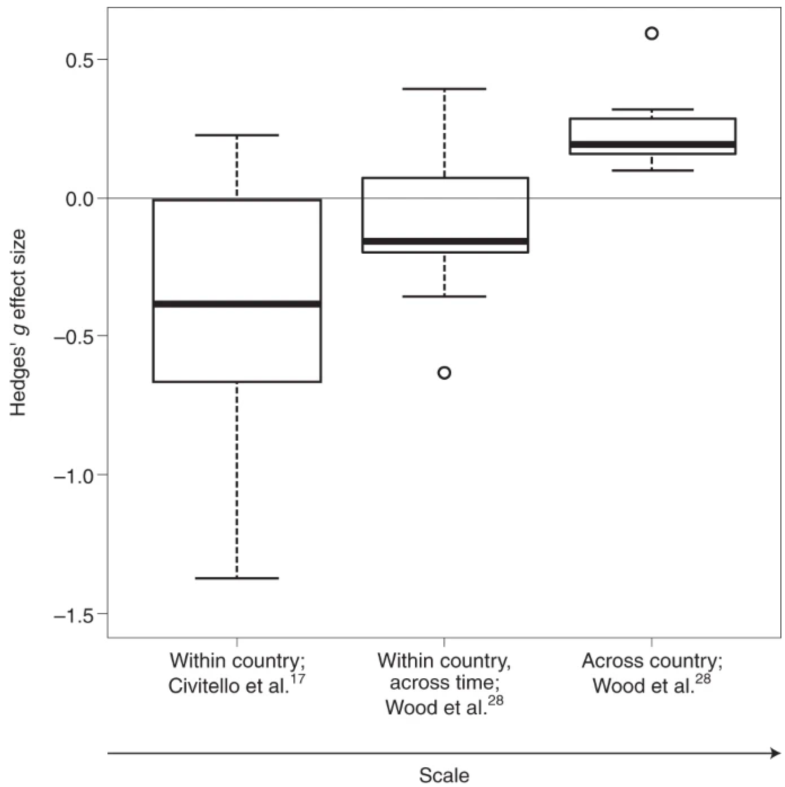
- warming
  - 'good' or 'bad' for pathogens?
  - vector biology
    * extended range
    * higher activity?
- changes in seasonality, hydrological cycles
- local landscape change
  - hydrology
  - land cover (Lyme disease)
  - forest cover
- changes in reservoir communities

dilution effect (Keesing & Ostfeld, 2021)

- does increased biodiversity decrease disease?
- variation in reservoir competence
- high-quality hosts decrease with increasing biodiversity
  - encounter reduction; host regulation; vector preferences

Kain & Bolker (2019)
Rohr et al. (2020)

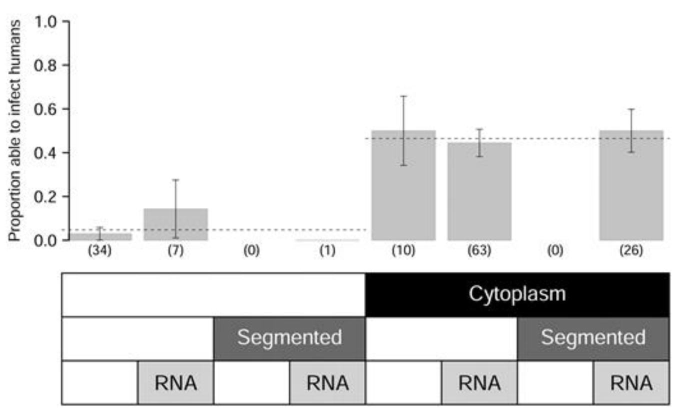
Fig. 4: Hedges' *g* effect sizes.



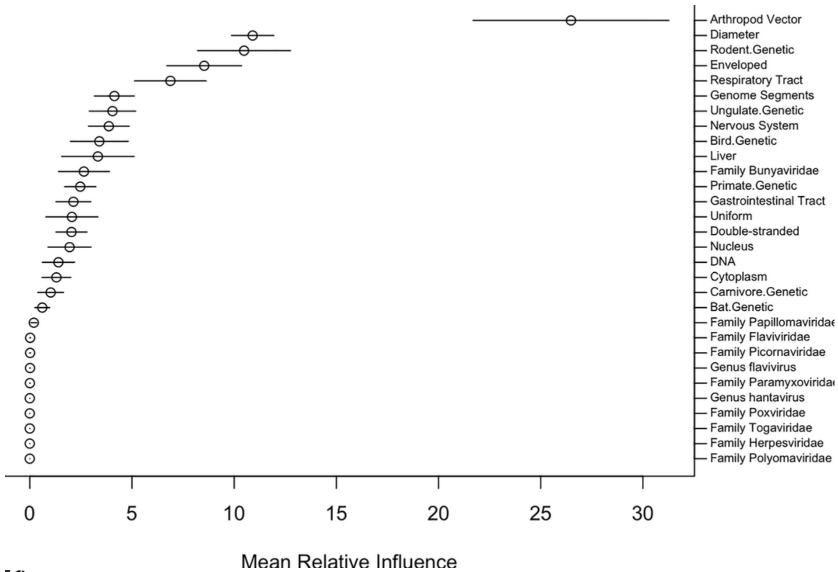
prediction

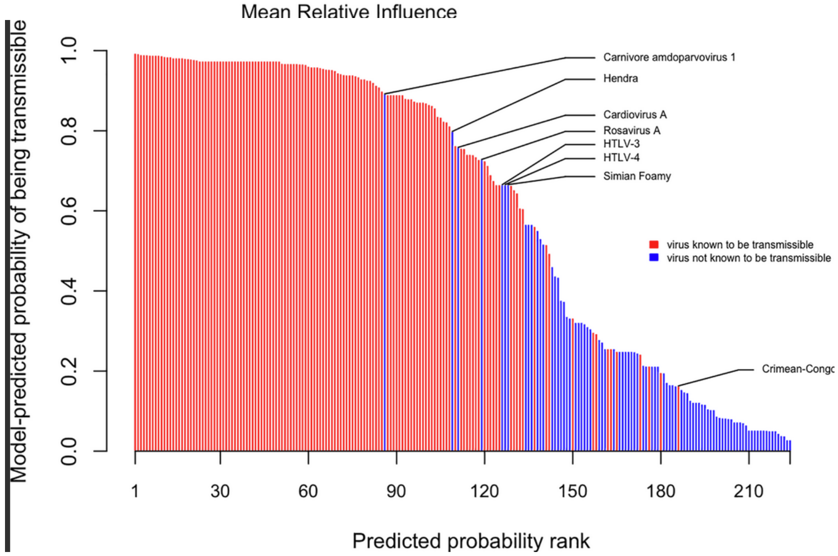
Pulliam & Dushoff (2009)

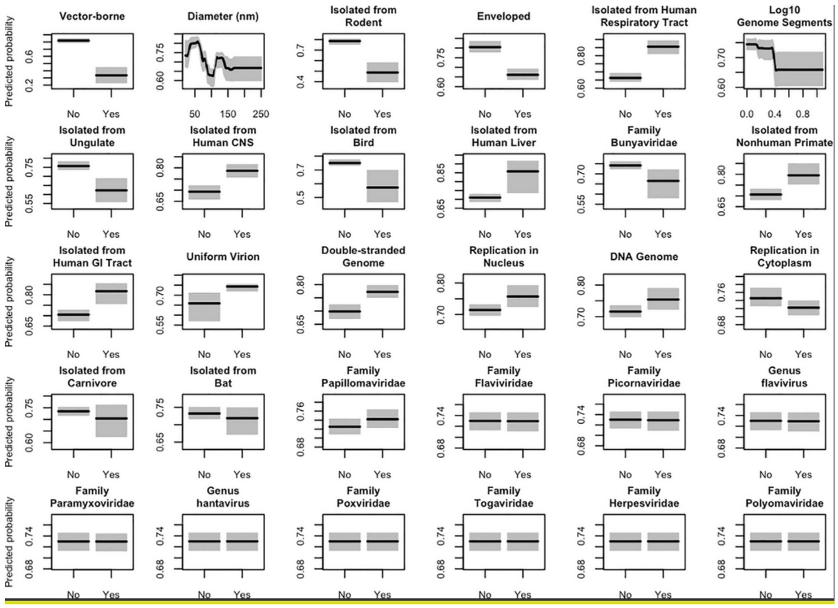
Figure 1.



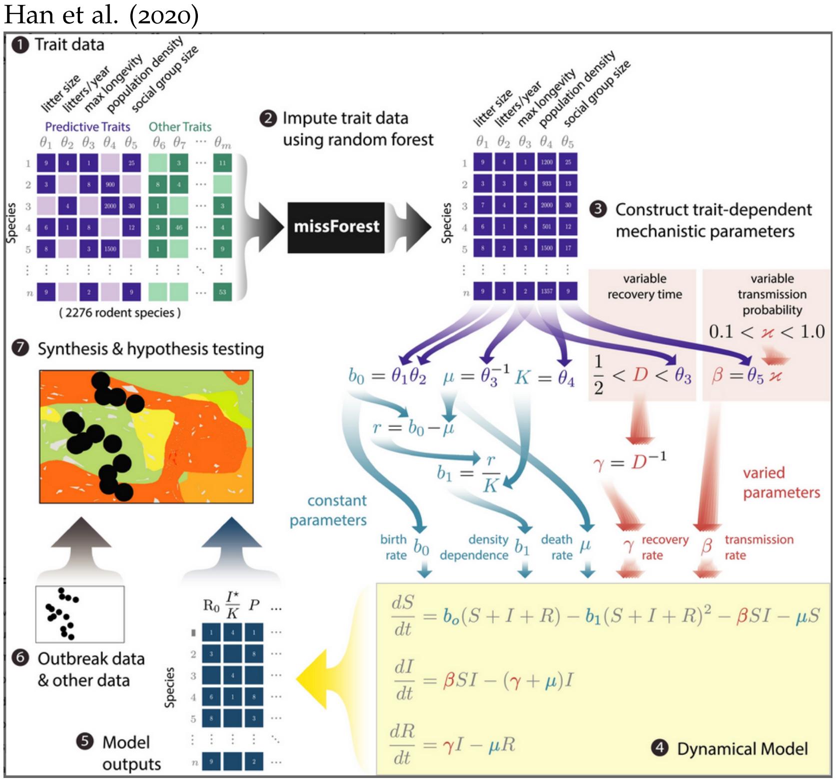
Walker et al. (2018)

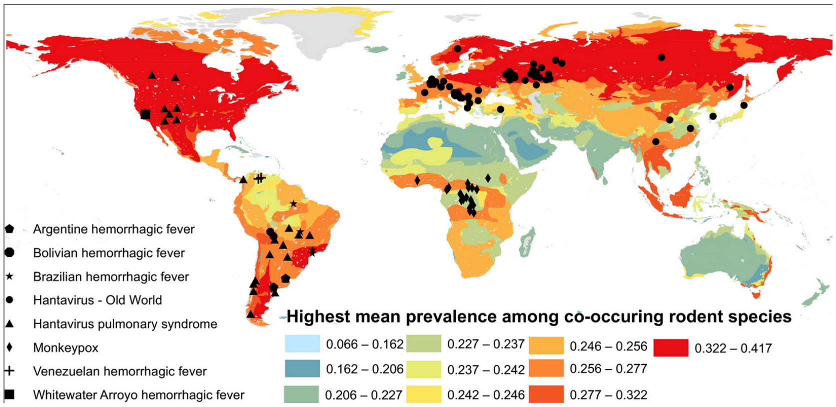

Arthropod Vector
Diameter
Rodent.Genetic
Enveloped
Respiratory Tract
Genome Segments
Ungulate.Genetic
Nervous System
Bird.Genetic
Liver
Family Bunyaviridae
Primate.Genetic
Gastrointestinal Tract
Uniform
Double-stranded
Nucleus
DNA
Cytoplasm
Carnivore.Genetic
Bat.Genetic
Family Papillomaviridae
Family Flaviviridae
Family Picornaviridae
Genus flavivirus
Family Paramyxoviridae
Genus hantavirus
Family Poxviridae
Family Togaviridae
Family Herpesviridae
Family Polyomaviridae
0
5
10
15
20
25
30
Mean Relative Influence


Model-predicted probability of being transmissible
0.0
0.2
0.4
0.6
0.8
1.0
Carnivore amdoparvovirus 1
Hendra
Cardiovirus A
Rosavirus A
HTLV-3
HTLV-4
Simian Foamy
virus known to be transmissible
virus not known to be transmissible
Crimean-Congo
1
30
60
90
120
150
180
210
Predicted probability rank



Han et al. (2020)





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