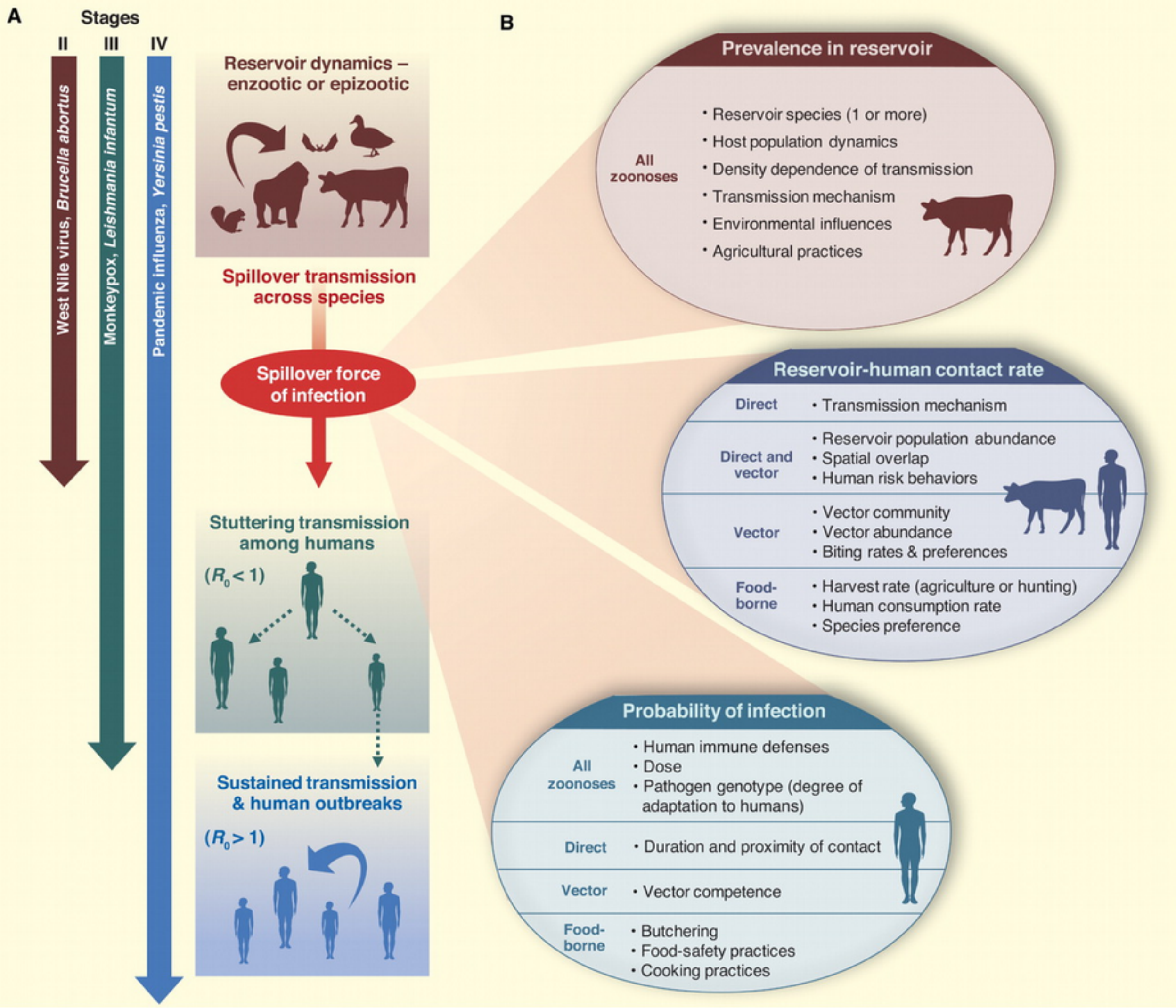
emerging infectious disease

30 Nov 2023

emerging and re-emerging disease



basically, anything we're worried about

- encounter filter: changing patterns of reservoir host/vector distribution, human contact, …
- compatibility filter: changes via mutation, recombination, selection for resistance, …

Do we need to understand *everything*?

- reservoir ecology
- pathogen biology
- human-reservoir interactions

How do we understand? How do we predict?

Batrachochytrium dendrobatidis

- 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?

Very confusing …

- declines occurred in pristine areas (probably not anthropogenic?)
- some species decline in the absence of Bd
- some species stable in the presence of Bd
- **tipping point hypothesis**: in populations all the time, but something happened to increase virulence/reduce tolerance or resistance (≈ compatibility filter)
    - climate change/El Niño ?
    - ultraviolet radiation?
    - pesticides?
    - combination (species × temperature × U/V × pesticide × …)? (Pounds et al., 2006; Rohr et al., 2008; Rohr & Raffel, 2010)
- **novel pathogen hypothesis**: mutation/speciation + dispersal
    - detection in historical specimens: CA/bullfrog, Brazil …
    - genomics (challenging!)
    - Asian sampling

Fisher & Garner (2020)

effects of climate change

- warming
    - 'good' or 'bad' for pathogens?
    - vector biology
        - extended range
        - higher activity?
        - e.g. Mordecai et al. (2020): shift from *Anopheles gambiae* to *Aedes aegypti*, malaria to arboviruses (dengue, chikungunya etc.)
- changes in seasonality, hydrological cycles
- local landscape change
    - hydrology
    - suburbanization and reforestation: Lyme disease
    - deforestation
        - MacDonald & Mordecai (2019): deforestation increases malaria, but malaria decreases deforestation
- changes in reservoir communities

effects of biodiversity change: dilution effect (Keesing & Ostfeld, 2021)

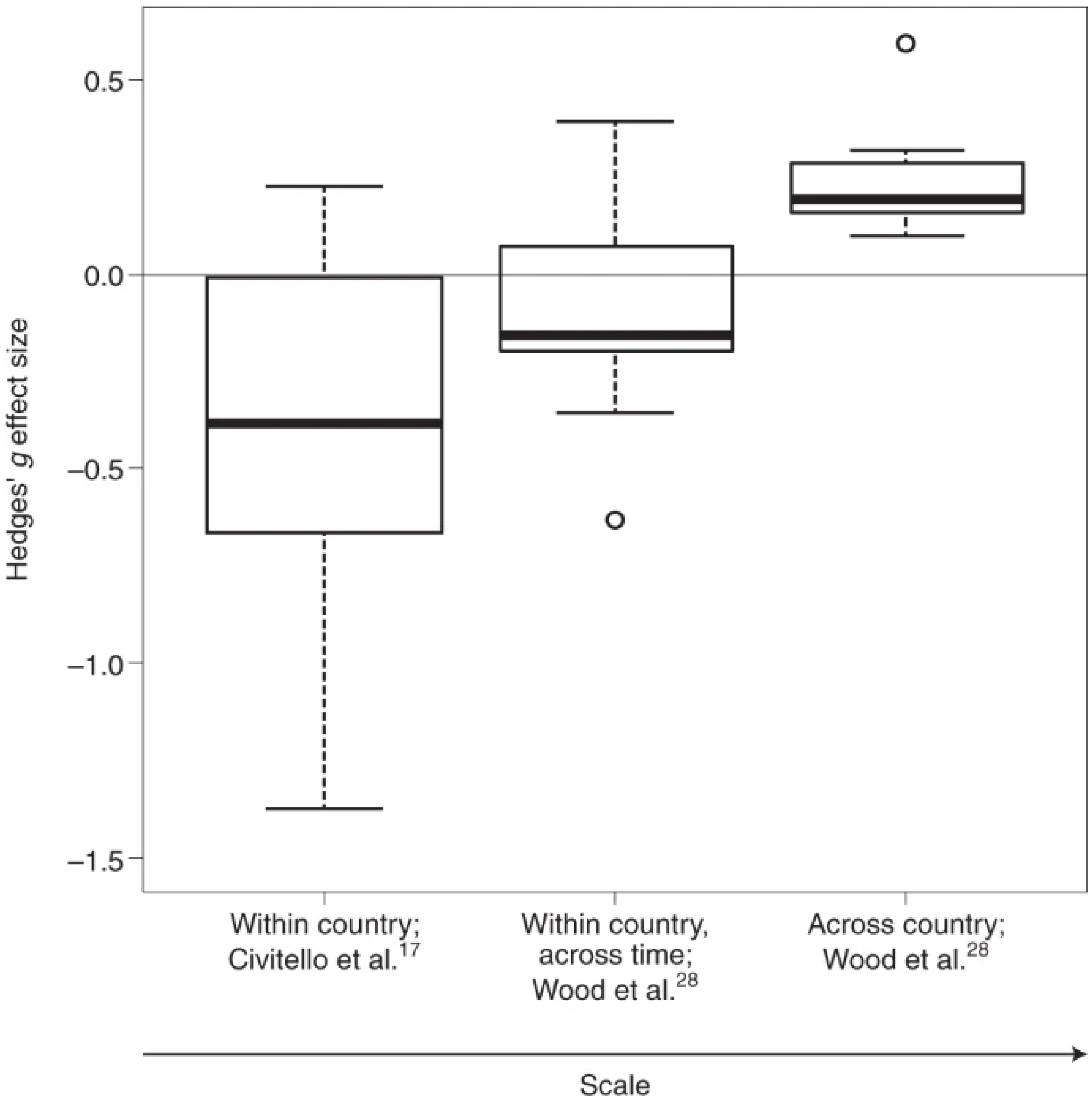
- does increased biodiversity decrease disease?
- variation in reservoir competence
- high-quality hosts decrease with increasing biodiversity

    - encounter reduction; host regulation; vector preferences

Kain & Bolker (2019)

Rohr et al. (2020)

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



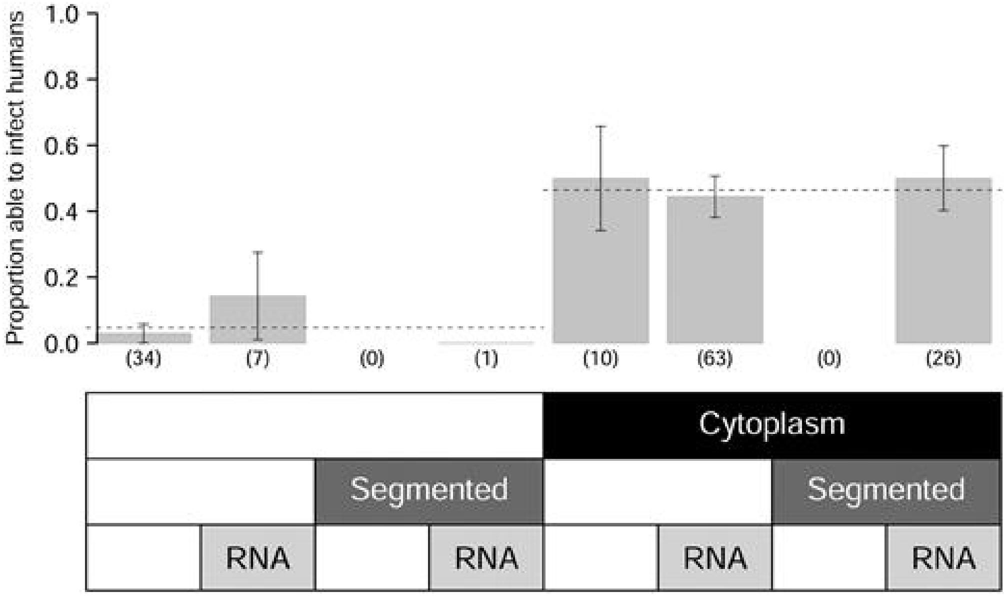
- Carlson et al. (2022): *higher* rodent diversity and climate anomalies drive plague spillover

surveillance and prediction

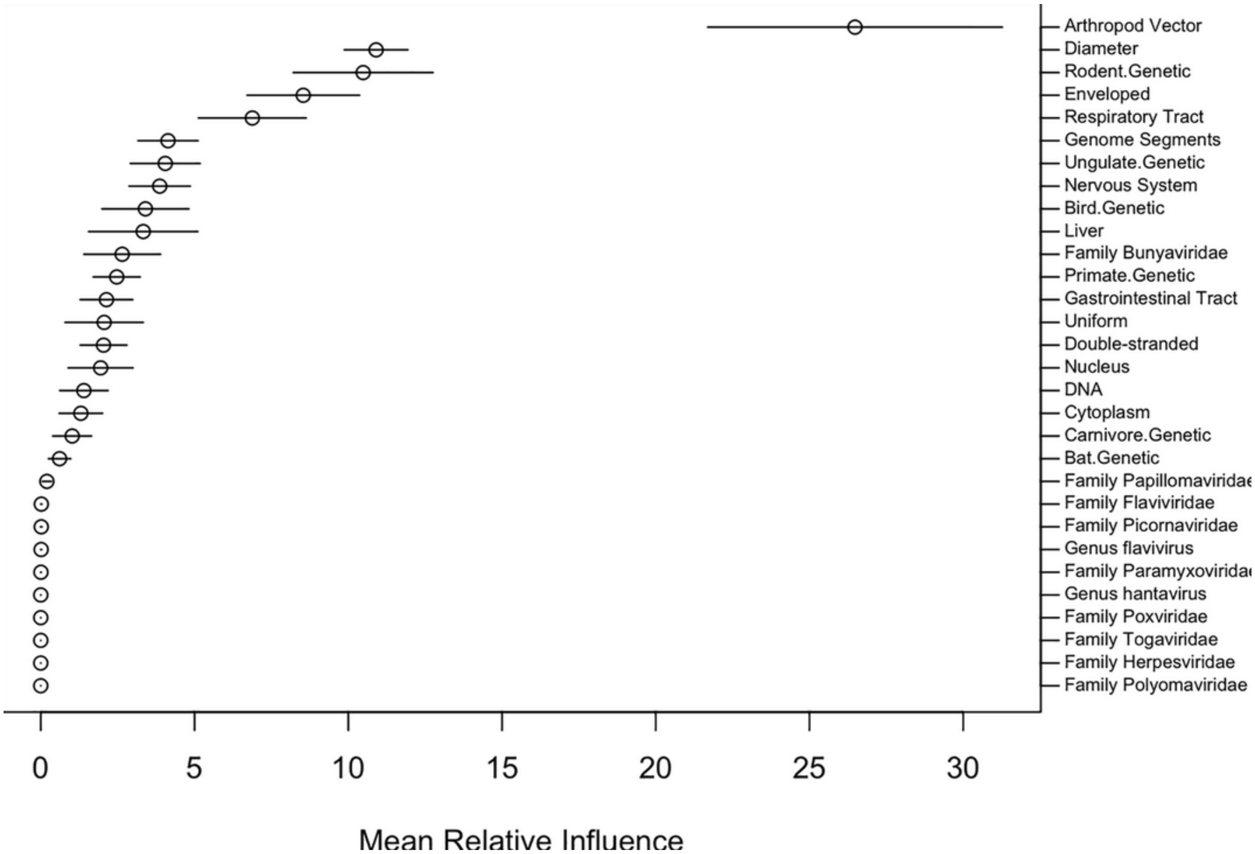
- which viruses will emerge, where, why?

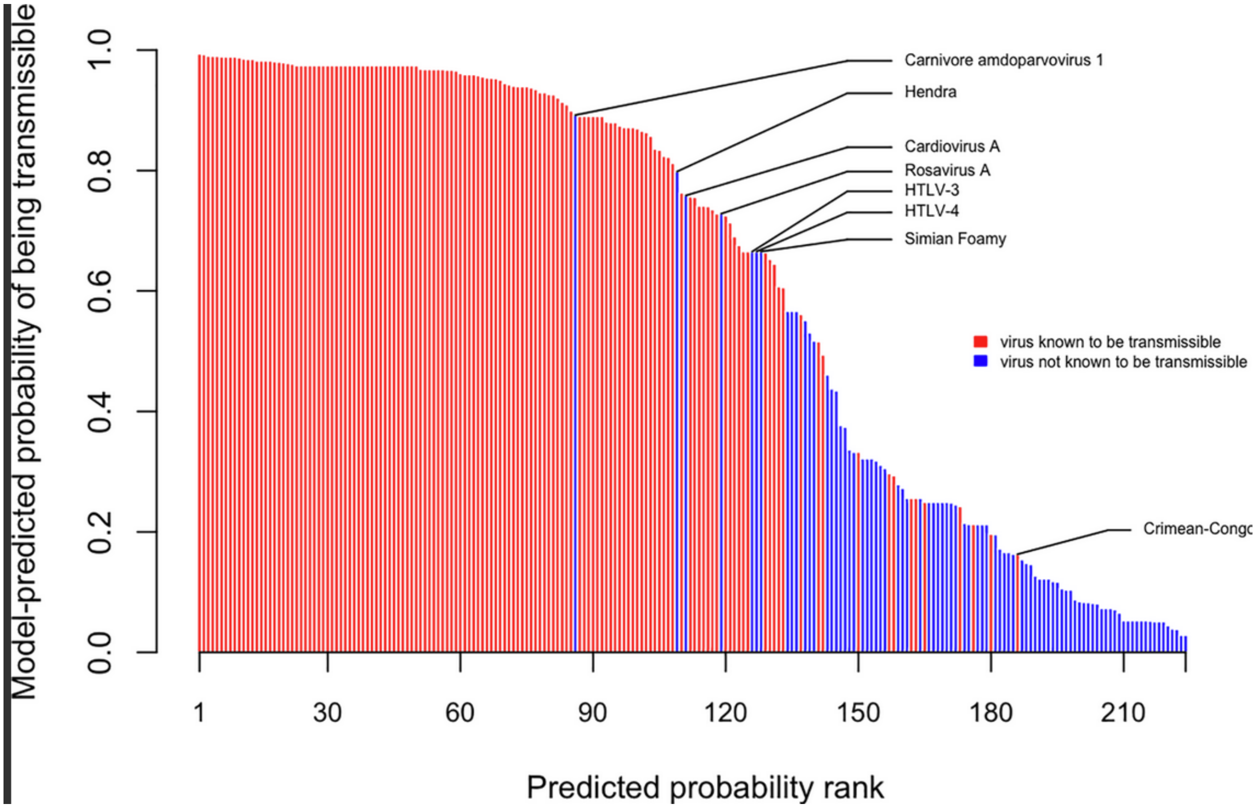
Pulliam & Dushoff (2009): predict zoonotic transmission of livestock viruses

Figure 1.

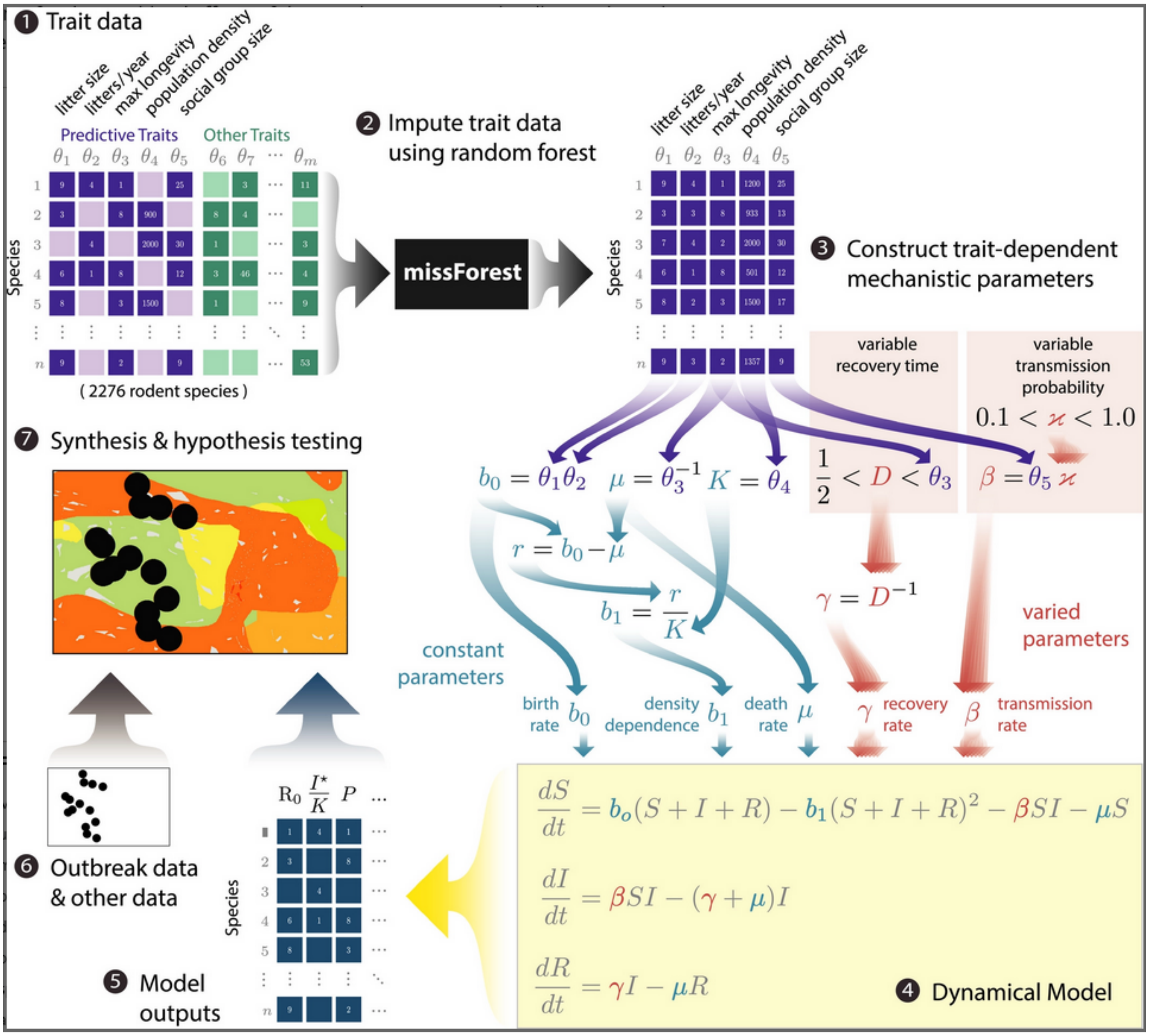


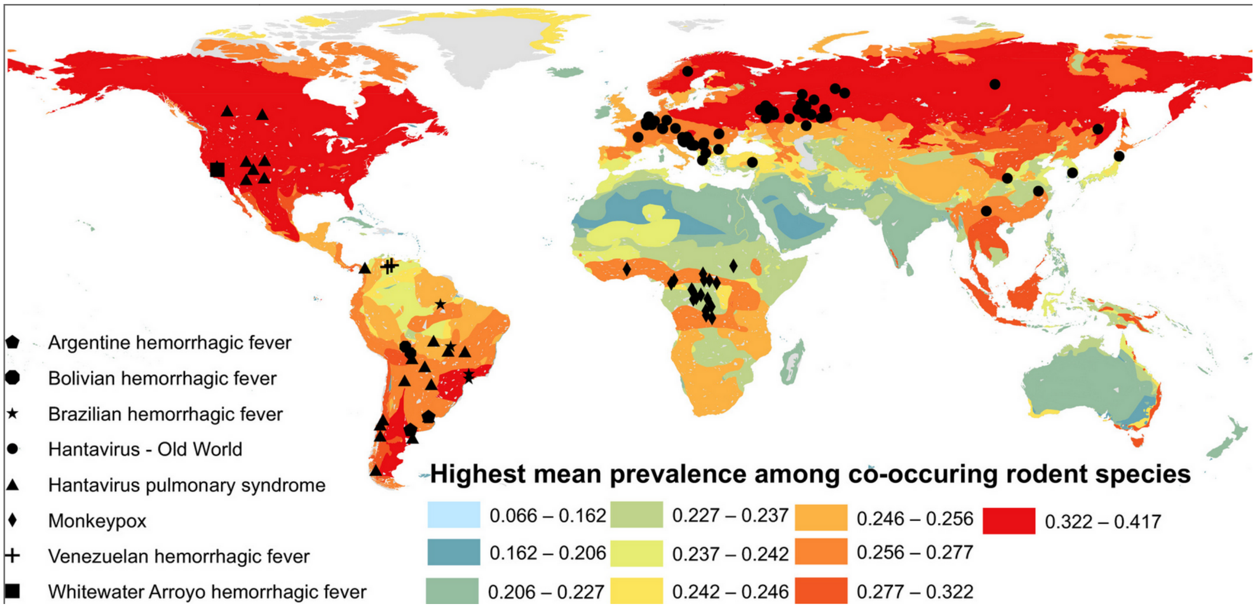
Walker et al. (2018): predict human transmission ability of zoonotic viruses





Han et al. (2020): model rodent life history


❶ Trait data
litter size
litters/year
max longevity
population density
social group size
Predictive Traits
Other Traits
θ_1 θ_2 θ_3 θ_4 θ_5 θ_6 θ_7 $\cdots$ θ_m
Species
(2276 rodent species)
❷ Impute trait data using random forest
missForest
❸ Construct trait-dependent mechanistic parameters
variable recovery time
variable transmission probability
$0.1 < \varkappa < 1.0$
$b_0 = \theta_1\theta_2$
$\mu = \theta_3^{-1}$
$K = \theta_4$
$\frac{1}{2} < D < \theta_3$
$\beta = \theta_5\,\varkappa$
$r = b_0 - \mu$
$b_1 = \frac{r}{K}$
$\gamma = D^{-1}$
constant parameters
varied parameters
birth rate b_0
density dependence b_1
death rate μ
γ recovery rate
β transmission rate
$\frac{dS}{dt} = b_o(S+I+R) - b_1(S+I+R)^2 - \beta SI - \mu S$
$\frac{dI}{dt} = \beta SI - (\gamma+\mu)I$
$\frac{dR}{dt} = \gamma I - \mu R$
❹ Dynamical Model
❺ Model outputs
R_0 $\frac{I^\star}{K}$ P ...
❻ Outbreak data & other data
❼ Synthesis & hypothesis testing



Evans et al. (2023): 2017-2020 sample: 12% of 693 individuals sampled in Myanmar were seropositive for sarbecovirus, more likely if they were loggers/hunters or had been exposed to bats …

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