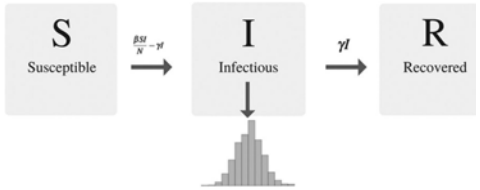
One Health surveillance for emerging infectious diseases



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Pathways to emergence

Evolutionary trajectory

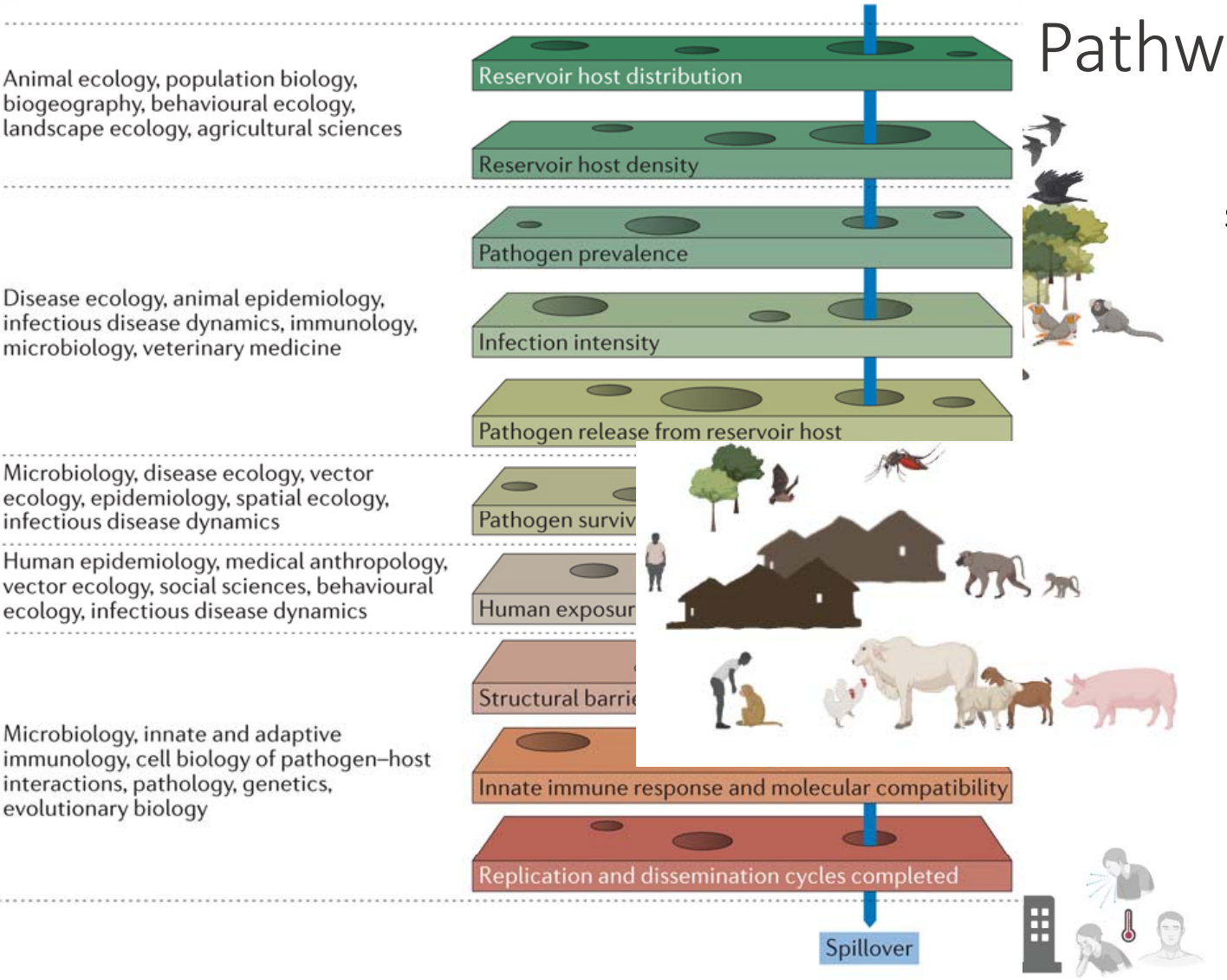
Stage 1: Wildlife reservoirs only

Stage 2: Primary Spillover

Stage 3: Short outbreaks

Stage 4: Prolonged outbreaks

Stage 5: Sustained human to human transmission



Plowright et al. 2017, Sokolow et al 2019

Where to look for Flaviviruses in Wildlife?

Predicting regions with high diversity of wildlife hosts

MENU

nature COMMUNICATIONS

Article | OPEN | Published: 21 December 2018

Predicting wildlife reservoirs and global vulnerability to zoonotic *Flaviviruses*

Pranav S. Pandit, Megan M. Doyle, Katrina M. Smart, Cristin C. W. Young, Gaylen W. Drape & Christine K. Johnson

Nature Communications **9**, Article number: 5425 (2018) | Download Citation

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Global distribution of *Flaviviruses*

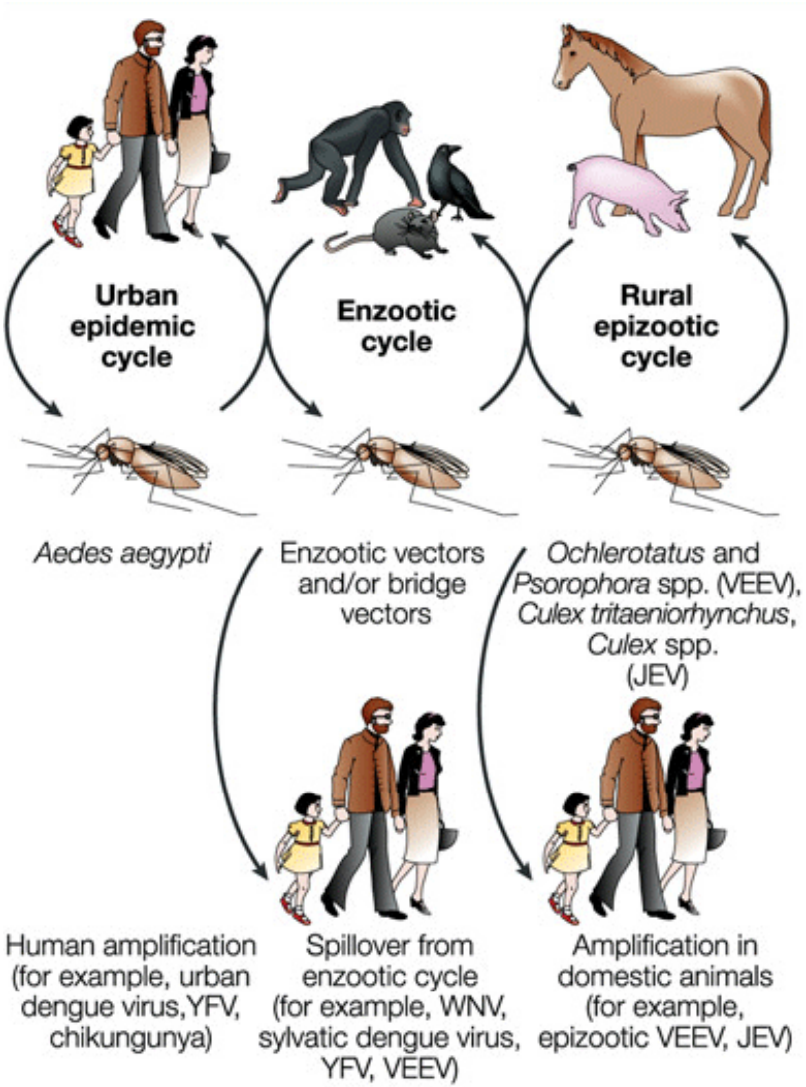
- Mostly vector borne
  - Mosquitoes and Ticks
- Endemic in regions of the World : JEV, DENV
- Emerging in new regions: Zika, WNV
- Threat to vulnerable populations
  - New World Primates: Yellow fever
  - Yellow-billed Magpie: West Nile virus

Why we need to know wildlife hosts of Flaviviruses?

- Wildlife hosts promote viral evolution
- Potential zoonotic sources of recurring epidemics

- Difficult to detect positive species
  - Logistics of sampling species from remote habitats
  - Short shedding periods

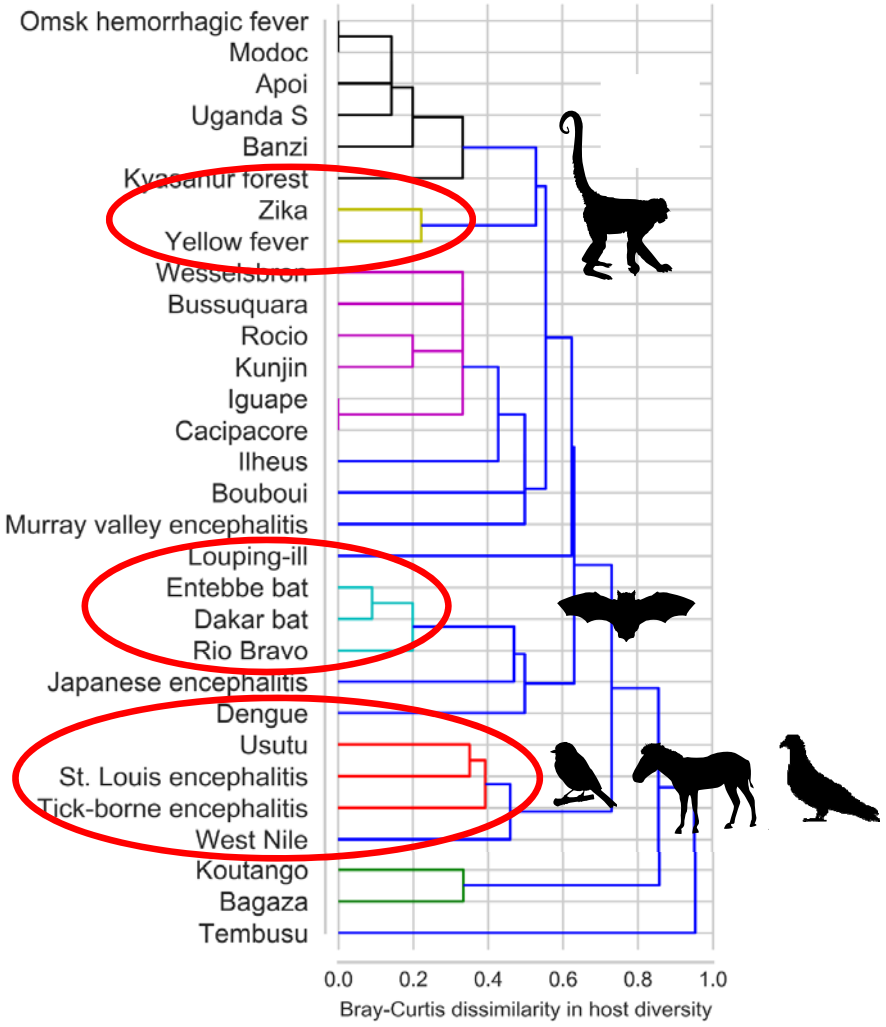
- Can we predict unknown hosts by looking at known hosts?



Wildlife Hosts

140 mammal species (Out of 5536)

277 avian species (Out of 10424)

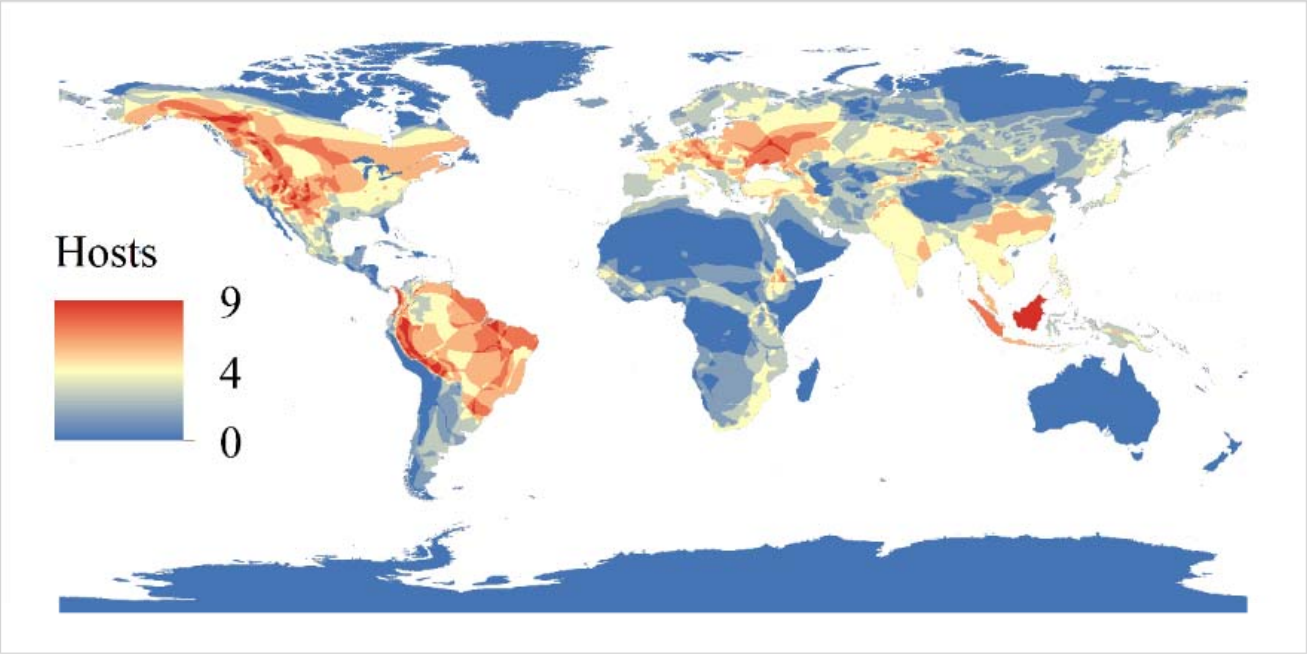


Mosquitoes	Number of viruses
Aedes aegypti	7
Culex pipiens	6
Culex annulirostris	6
Aedes albopictus	5
Culex tritaeniorhynchus	5
Culex perfuscus	5
Aedes vexans	5
Culex quinquefasciatus	5
Aedes africanus	5

Ticks	Number of viruses
Dermacentor marginatus	3
Dermacentor silvarum	3
Hyalomma marginatum	3
Amblyomma variegatum	2
Rhipicephalus muhsamae	2
Ornithodoros capensis	2
Ixodes ricinus	2
Haemaphysalis longicornis	2
Haemaphysalis concinna	2
Haemagogus lucifer	2

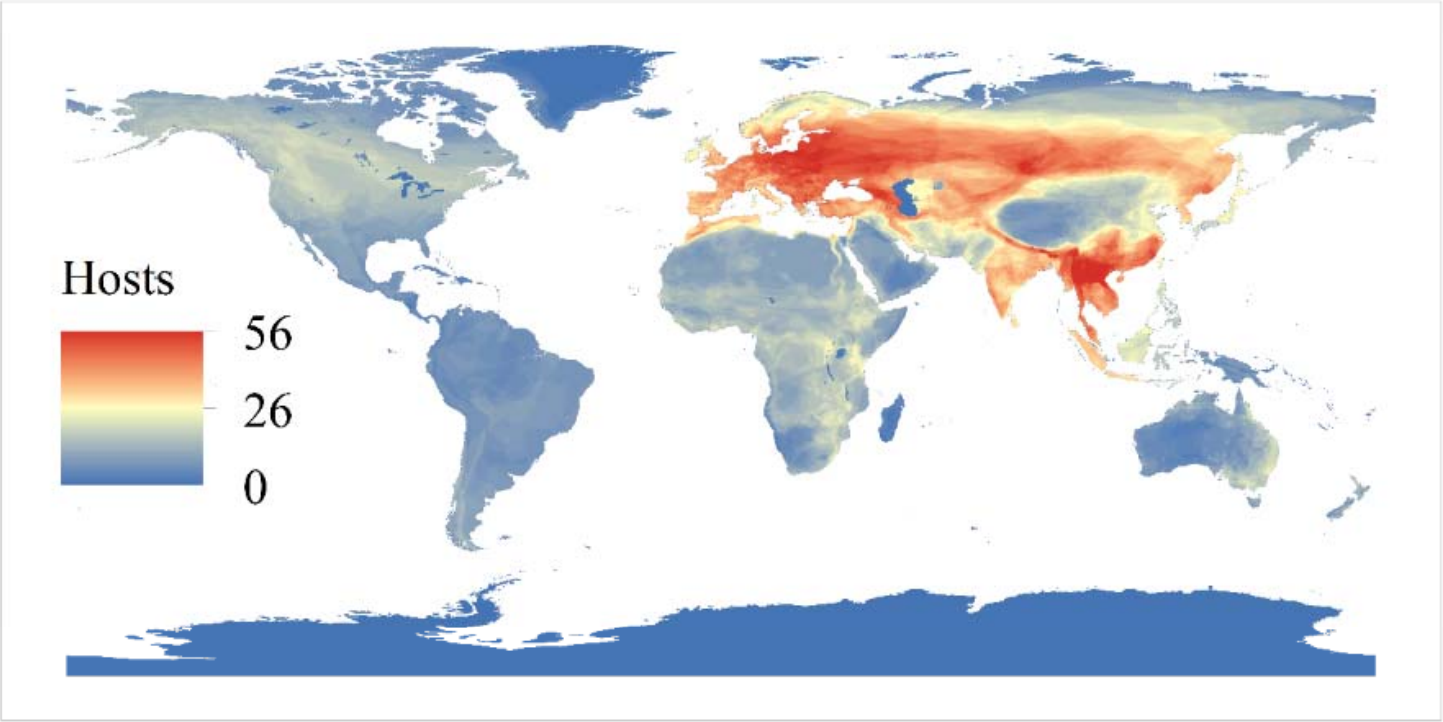
Distribution of Predicted Hosts

Yellow fever virus and Zika virus



Distribution of Predicted Hosts

Japanese encephalitis virus



Targeted surveillance of wildlife

Viruses	Number of predicted hosts	Known hosts
Yellow fever, Zika	112	14
West Nile, St. louis, Usutu	708	254
Dengue	173	23
Japanese encephalitis	408	20

Wildlife surveillance for early detection of wildlife health events

Unusual wildlife events that increase pathogen release from wildlife hosts

PROCEEDINGS B

royalsocietypublishing.org/journal/rspb

Research

Cite this article: Kelly TR *et al.* 2021 Early detection of wildlife morbidity and mortality through an event-based surveillance system. *Proc. R. Soc. B* **288**: 20210974.
https://doi.org/10.1098/rspb.2021.0974

Early detection of wildlife morbidity and mortality through an event-based surveillance system

Terra R. Kelly[1,†], Pranav S. Pandit[2,†], Nicole Carion[3], Devin F. Dombrowski[4], Krysta H. Rogers[3], Stella C. McMillin[3], Deana L. Clifford[3], Anthony Riberi[5], Michael H. Ziccardi[1], Erica L. Donnelly-Greenan[6] and Christine K. Johnson[2]

[1]Karen C. Drayer Wildlife Health Center and [2]EpiCenter for Disease Dynamics, One Health Institute, School of Veterinary Medicine, University of California, Davis, CA, USA
[3]Wildlife Health Laboratory, California Department of Fish and Wildlife, Rancho Cordova, CA, USA
[4]The Wild Neighbors Database Project, Middletown, CA, USA
[5]Y3TI, Lafayette, CA, USA
[6]Moss Landing Marine Laboratories/BeachCOMBERS Program, San Jose State University, CA, USA

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Wildlife Investigations Lab

Wild Neighbors Database Project

Y3TI

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Wildlife rehabilitation centers as wildlife health indicators

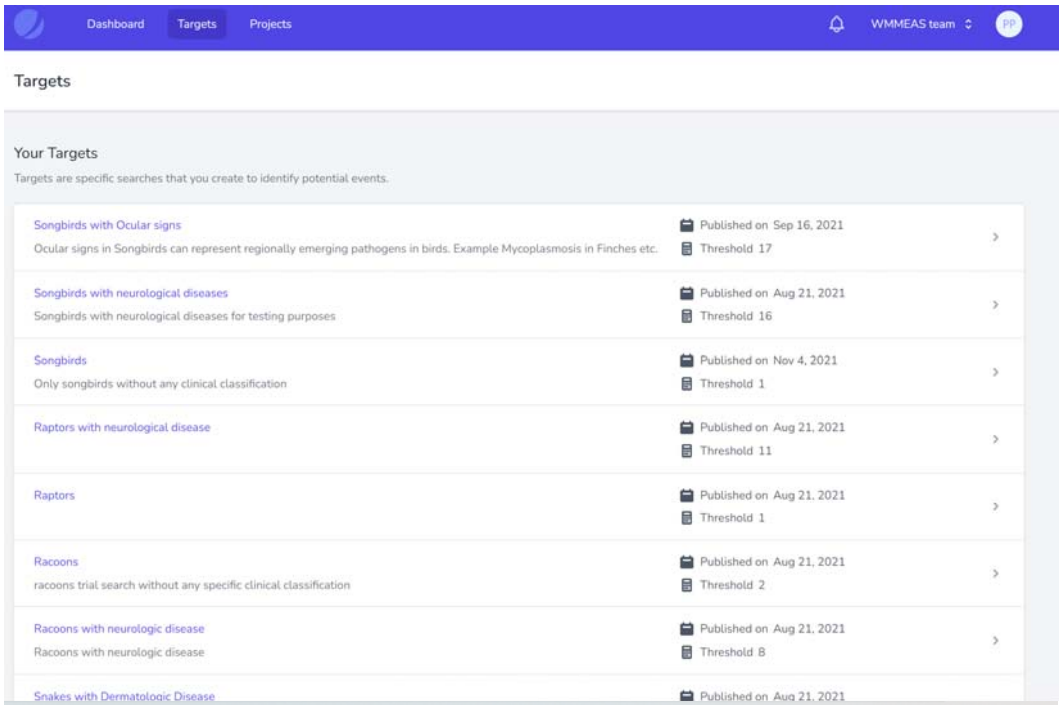
- Rehabilitation Centers assimilate large amounts of data
- Uniquely poised to advance knowledge of threats to wildlife health and populations

- Intelligent surveillance system is essential to:
  - Assimilate and process large amounts of data
  - Identify spatio-temporal trends in wildlife admissions
  - Provide real-time information on wildlife health events

Wildlife Morbidity and Mortality Event Alert System (WMMEAS)

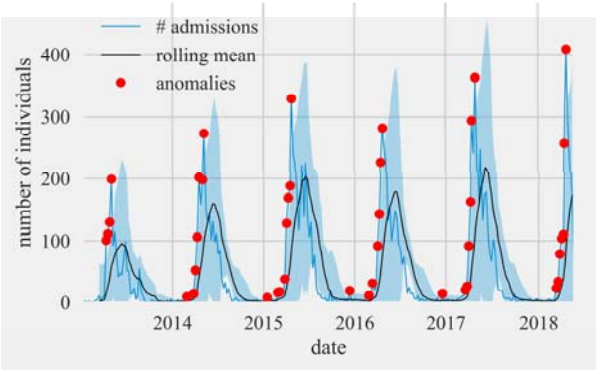
- Runs parallel to the Wildlife Rehabilitation Database (WRMD)
- California wide : 30 participating centers participate data real-time

Wildlife Morbidity and Mortality Event Alert System (WMMEAS)

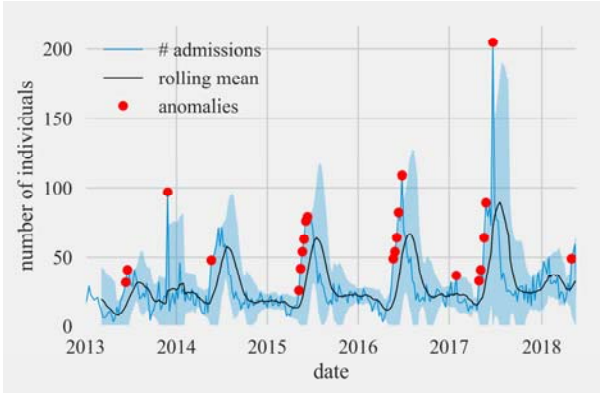


https://www.wmmeas.health/

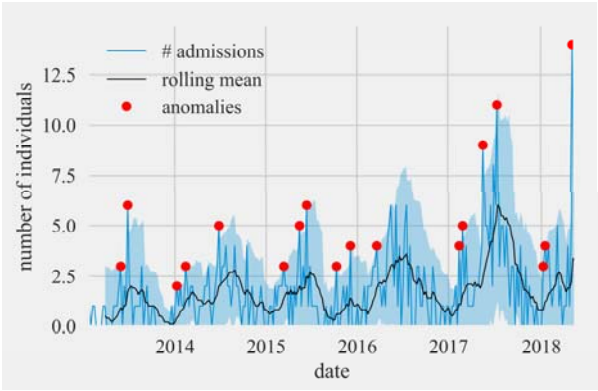
Mallard: all cases



Accipitridae: all cases

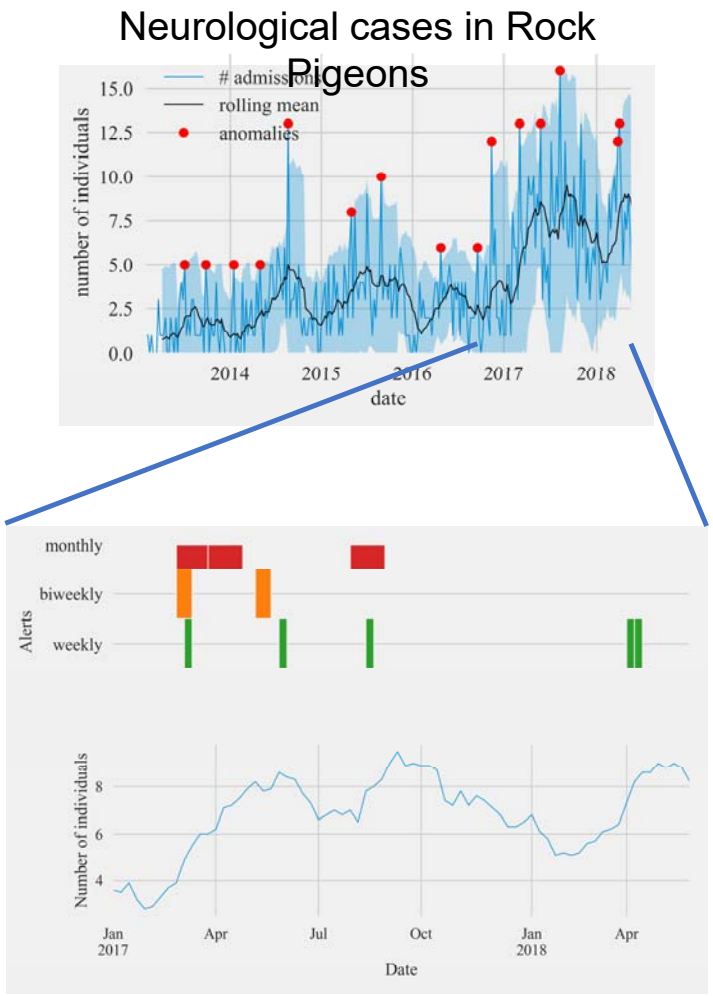


Striped Skunk: Neurological cases



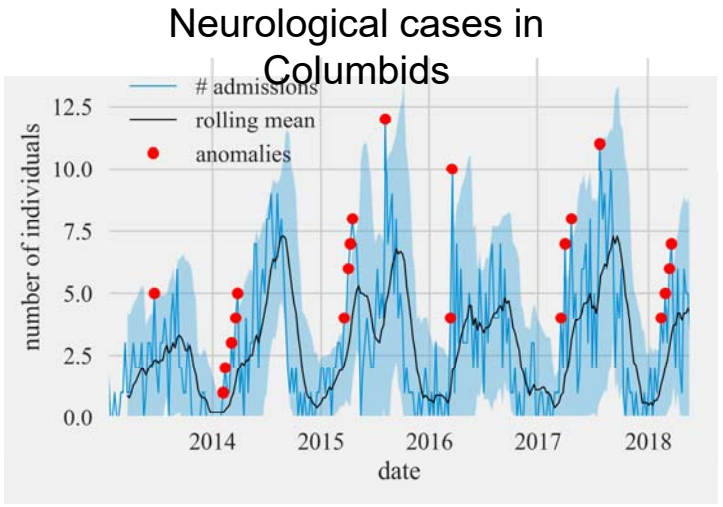
Outbreak investigation
Neurological cases in Rock Pigeon

- Monthly, biweekly, and weekly alerts
  - Neurological cases in *Columba livia*



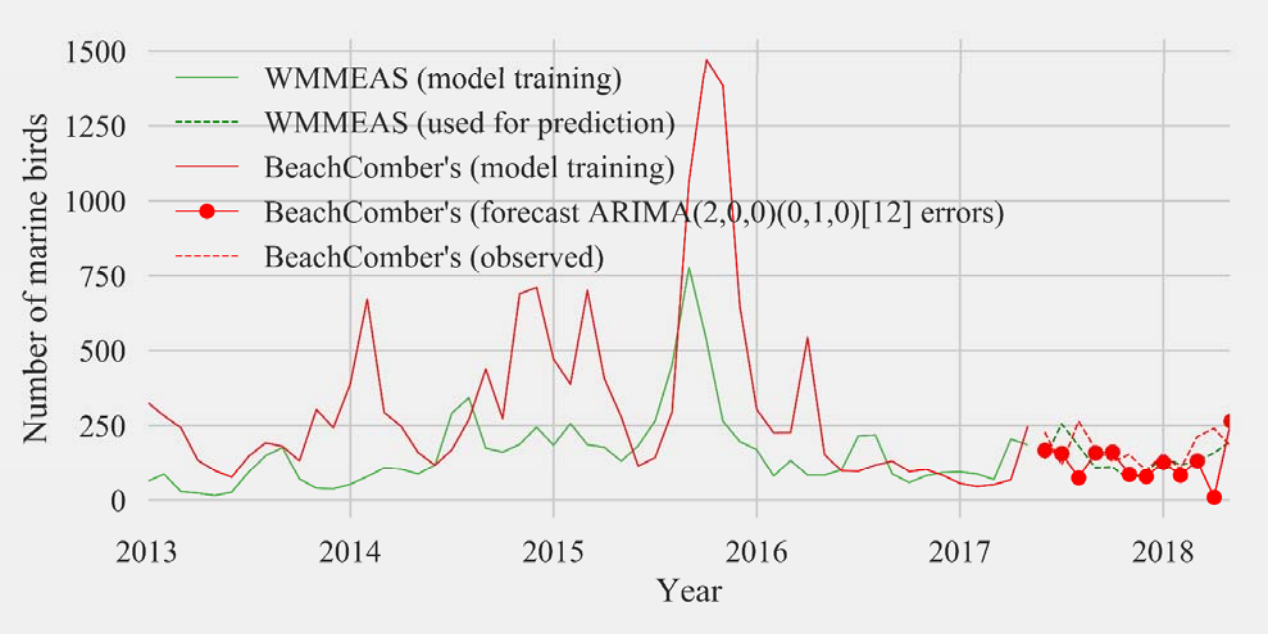
Pigeon Paramyxovirus Type 1 (PPMV-1) outbreak in Columbids

- PPMV-1 Outbreak in 2017 in Columbids
- Detected in various Doves and Pigeons
- Pathogen of concern, can spillover to native wildlife



Early indication of health events

- Comparison with **strandings observed in independent surveillance system**.
- SARIMAX model
- WMMEAS (lag of first order) is significantly associated with the marine birds stranding observed in the BEACHCOMBERS data ($p > 0.001$)



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Zoonotic transmission risk of novel viruses

Evolutionary trajectory of
novel viruses

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ARTICLE

Predicting the potential for zoonotic transmission and host associations for novel viruses

Pranav Pandit, Simon Anthony, Tracey Goldstein, Kevin Olival, Megan Doyle, Nicole Gardner, Brian Bird, Woutrina Smith, David Wolking, Kristen Gilardi, Corina Monagin, Terra Kelly, Marcela Uhart, Jonathan Epstein, Catherine Machalaba, Melinda Rostal, Patrick Dawson, Emily Hagan, Ava Sullivan, Hongying Li, Aleksei Chmura, Alice Latinne, Christian Lange, Tammie O'Rourke, Sarah Olson, Lucy Keatts, A. Patricia Mendoza, Alberto Perez, Catia Dejuste de Paula, Dawn Zimmerman, Marc Valitutto, Matthew LeBreton, David McIver, Ariful Islam, Veasna Duong, Moctar Mouiche, Zheng-Li Shi, Prime Mulembakani, Charles Kumakamba, Mohamed Ali, Nigatu Kebede, Ubald Tamoufe, Samuel Bel-Nono, Alpha Camara, Joko Pamungkas, Julien Kalpy Coulibaly, Ehab Abu-Basha, Joseph Kamau, Soubanh Silithammavong, James Desmond, Tom Hughes, Enkhtuvshin Shiilegdamba, Ohnmar Aung, Dibesh Karmacharya, Julius Nziza,

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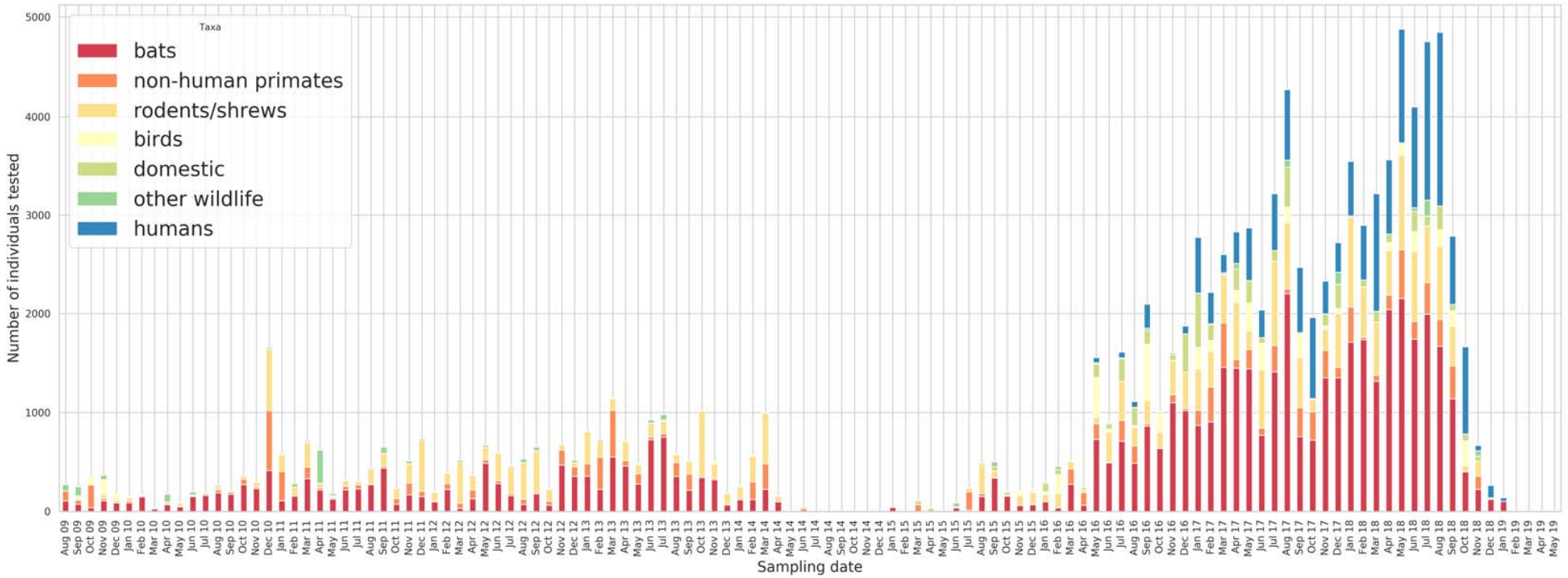
Risk-based Surveillance of Wildlife

- Influenza viruses
- Coronaviruses
- Paramyxoviruses
- Filoviruses
- Flaviviruses

STRENGTHENED laboratory systems and zoonotic disease detection capabilities in over 60 labs around the world.

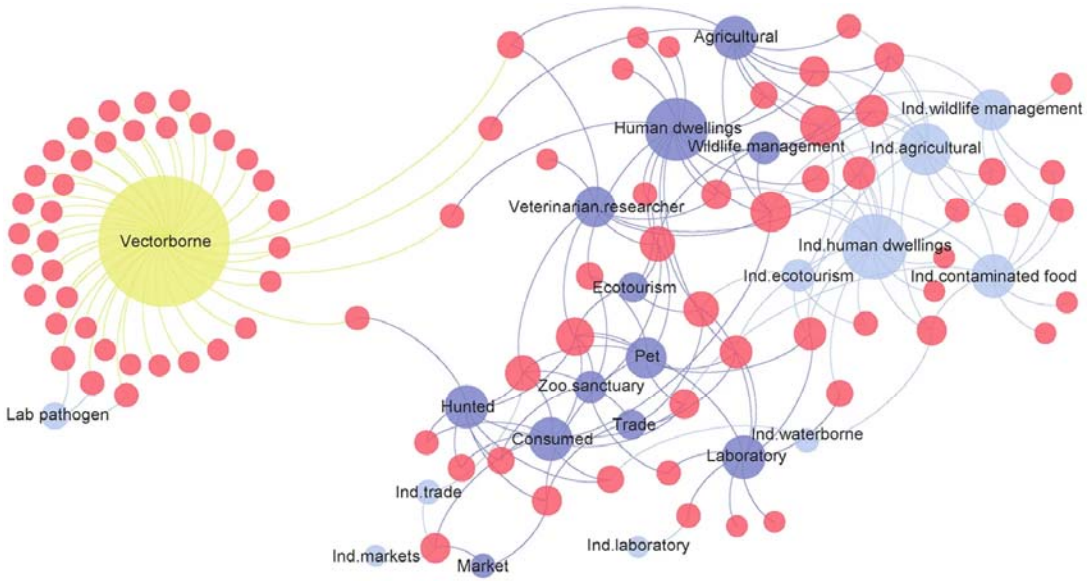
931 NOVEL **218** KNOWN

DETECTED over 1,100 unique viruses, including zoonotic diseases of public health concern such as Bombali ebolavirus, Zaire ebolavirus, Marburg virus, and MERS- and SARS-like coronaviruses.



Network Based Approach for understanding zoonotic risk

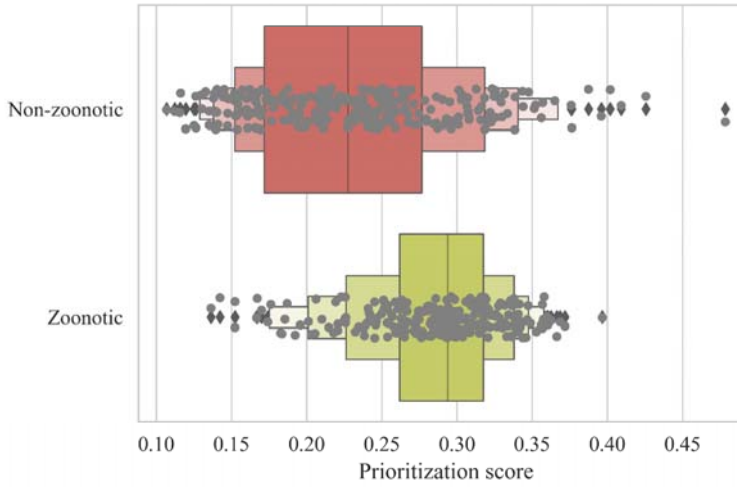
- For data driven quantification of zoonotic risk and to prioritize viruses for further in-vivo characterization
    - Grange et al (2021) presented an opinion-based ranking of novel viruses.
- Host-virus networks behave similar to social networks and missing links can help understand zoonotic potential of viruses.



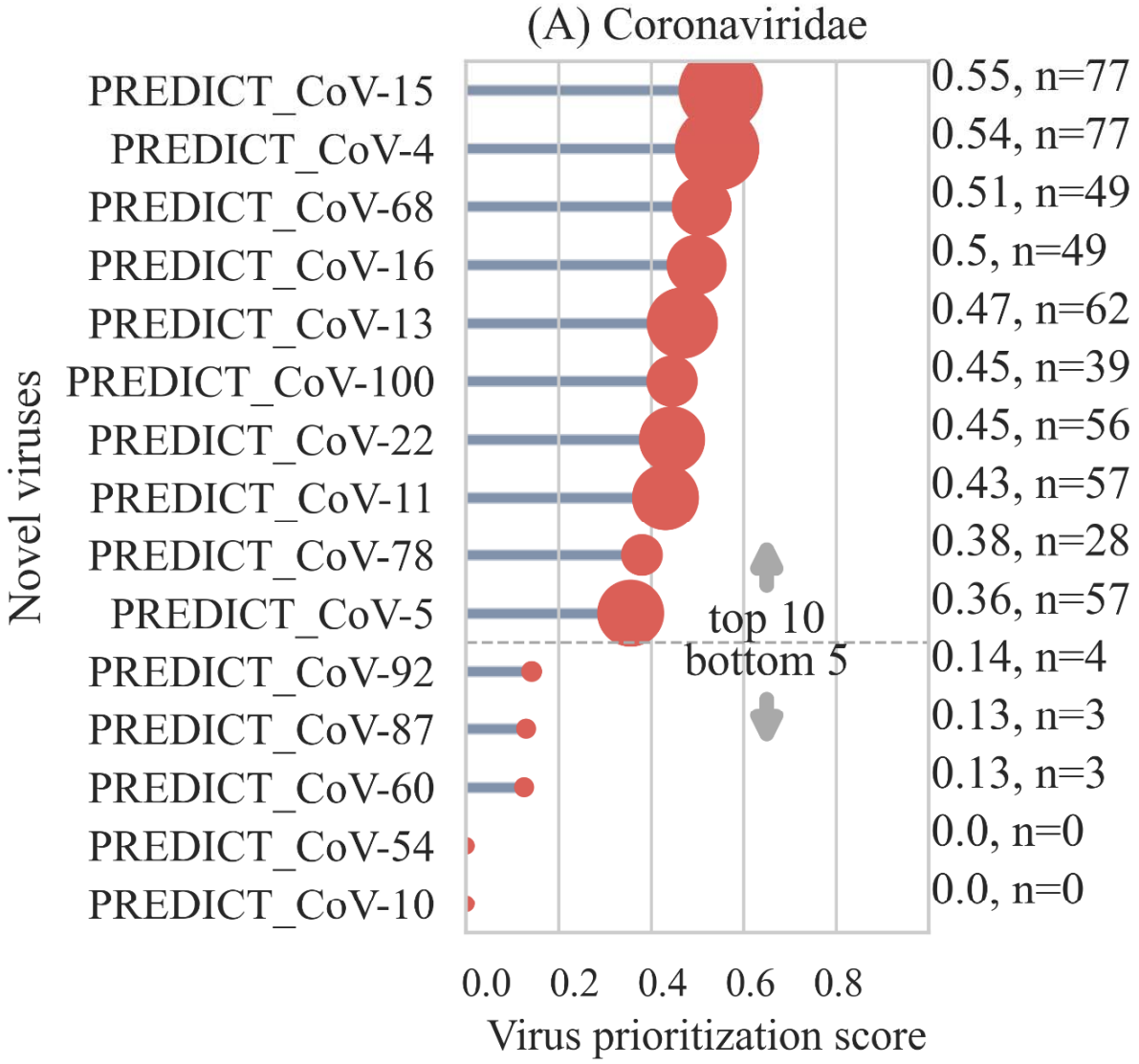
Quantifying zoonotic risk

Developed prioritization score:

- Number of predicted human links (support) and
- Average probability of links formed due to sharing human as host



Prioritization scores for known zoonotic and non-zoonotic viruses.



Key ecological insights in ecology of novel viruses

- Novel viruses are more host specific than previously recognized viruses
  - Longer tails of $G_{predicted}$ compared to G_C
  - Lower centrality measures for novel viruses compared to recognized viruses

- Novel coronaviruses predicted to infect a greater number of species novel viruses from other families.
  - Significantly higher predicted network centralities

- Prioritization score:
  - Data driven metric to quantify zoonotic risk for novel viruses.
  - Requires the data on hosts and virus families

Key animal-human interfaces for zoonotic transmission

Understanding human exposure

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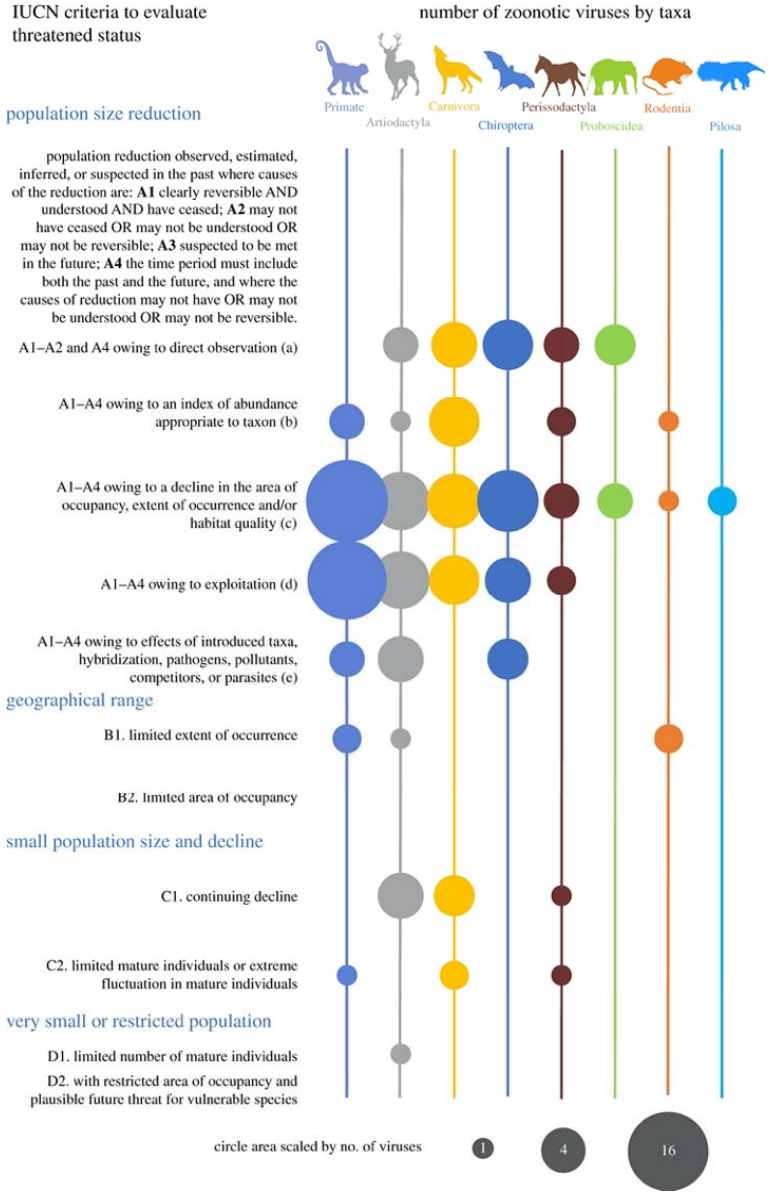
Key Animal-Human Interfaces



Johnson et al, 2020, Proc. Royal Soc. B

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