**Mammal virus diversity estimates are unreliable at species levels**

Gibb R., Albery G. …, Carlson C.

**Abstract**

Recent years have seen a proliferation of research aimed at assessing species-level zoonotic risk, often intended to identify putative reservoir hosts of unknown or emerging viral pathogens of public health concern. These studies often heavily leverage currently catalogued data on wildlife virus diversity, which represents only a tiny fraction of the true viral diversity in nature, and which is structured by systematic biases in research effort across space, time and taxa. These biases and their relationship to changes in viral discovery effort over time are poorly quantified, with potentially severe consequences for the accuracy of [studies using them]. Here, we compile a comprehensive global database of catalogued mammal host-virus associations and their

We fit virus discovery curves

**Introduction**

**Methods**

**Results & Discussion**

**References**

Wille – How accurately can we assess zoonotic risk? https://www.biorxiv.org/content/10.1101/2020.08.17.254961v1.abstract

Carlson – Global estimates of mammal virus diversity

Woolhouse 2008 – Temporal trends in the discovery of human viruses

Clarkson – How many human pathogens are there in Laos?

Olival – Host and virus traits predict zoonotic spillover

Han – Rodent reservoirs

Albery – Host sharing networks