VOCAB:

* Zoonose- disease that travels from animals to humans. This article mostly focused on viruses. When something is a zoonose, it is called zoonotic
* Taxa/taxon- group or species with similar characteristics. EX: mammals are a taxon
* Richness- number of unique viral species for a given host, including those that may have potential to infect humans
* Sympatry- areas where two species habitats overlap. (EX: racoons and humans have strong sympatry in cities)
* Phylogenetic host breadth- used to describe the zoonotic viruses. Basically says how much the hosts range in terms of relatedness. Higher breadth means the virus can infect hosts that are really unrelated.
* The majority of human emerging infectious diseases originated in animals, with viruses mostly from wild mammals.
* Pandemic surveillance programs try to understand patterns of this crossover to see if they can prevent it
* Data Analysis:
  + Generalized additive models (GAMs)- used to rank and identify host-specific predators and the total number of zoonotic viruses in mammals
  + Best fit model- used on total viral richness per wild mammal species. Best model explained 82% of deviance.
  + pairwise patristic distances
* Models used to determine viral richness and sharing:
  + Factors that influence richness
  + Identify and rank the traits that make some species more likely hosts of zoonoses than other
  + Identify and rank viral traits that increase likelihood of mammalian viruses to become zoonotic
* Hypothesis: “We hypothesize that the number of viruses a given mammal species shares with humans decreases with phylogenetic distance from humans and increases with opportunity for human contact.” Basically what this means is things that are less related to humans (IE a rat compared to a chimp) are less likely to carry zoonotic viruses. Second part is that wild animals that are never in contact with humans are less likely to be zoonotic than animals always in contact with humans.
  + Distance part of hypothesis is true, even when they removed reverse zoonoses (AKA disease going from human to animal)
* Results of this study:
  + found that the number of total viruses that infect a given species and the proportion likely to have originated from animals is predictable
  + found which taxa (think groups of species) and which geographic areas are missing viruses or diseases, which allows for further surveillance
  + urbanization increase the rate of zoonotic spillover, as does increasing human population density
  + Bats, primates, and rodents had highest proportion of zoonotic viruses compared to other mammal groups
  + Bats, rodents, primates, even-toed ungulates, and odd-toed ungulates had higher than expected viral richness. These are good ones to surveil in the future.
  + Richness mostly depends on:
    - Research effort
    - Sympatry
    - Host geographic range
    - Extended Data Figure 2 is really helpful. It shows the viruses on the Y axis and the mammalian families on the X and shows how many viruses each host has. Shows the richness
* Figure 4 seems to show the data you guys are looking for (especially a and b)
* Extended Data Figure 3 also looks helpful. Idk how the data is organized but this puts it into geographical context. Compares the observed viral richness, the predicted viral richness, observed zoonotic richness, and predicted zoonotic richness.