

Supplementary material

Methods for Figure 2

We generated figure 2 with a spatially structured susceptible-exposed-infectious-recovered (SEIR) model that incorporated realistic features such as seasonal, density-dependent births and demographic stochasticity (for full details see [1]). We implemented the models in R [2]. We assumed that the host was structured as a metapopulation of b local populations and that the state of the metapopulation was described by seven vectors, N , S , E , I , $I_{\text{super-high}}$, $I_{\text{super-long}}$, and R , each of length b , with a daily time-step. N is local population size, $I_{\text{super-high}}$ are super shedders, and $I_{\text{super-long}}$ are super-long-shedders. To consistently display results in two or three dimensions, we simulated dynamics within a linear array of host populations.

Pathogen transmission β_{ij} from individuals in patch j to individuals in patch i declines exponentially (Hanski, 1999), $\beta_{ij} = \beta e^{-cD_{ij}}$ (1), where D_{ij} is the distance between the two populations and c is a constant that is inversely related to the connectivity between populations. Pathogen transmission within a local population β_{ii} is β . We used a Nicholson-Bailey approach [3] to model the number of surviving susceptible hosts. The force of infection on individuals of subpopulation i is $\text{force}H_i = \sum_j \beta_{ij} I_j$; $S_i \leftarrow S_i \exp(-\text{force}H_i)$. We modeled births, deaths, recoveries, and transmissions as binomial random variables.

Methods for Figure 3

We produced an extrapolated grid of 10 locations and 12 months to represent a hypothetical spatial gradient (e.g., latitude, temperature, urbanization) over the annual cycle. We used the *spatstat* package in R to generate a random realization of a binomial point process [4]. Our random realization generated a small number of points ($n=6$) within this grid using the `runifpoint()` function and then computed the kernel smoothed intensity using the `density.ppp()` function. We note the spatial and temporal dependencies of infection dynamics violate the assumption of independence for random points generated from a binomial point process; however, this simple simulation serves as only a heuristic tool to illustrate the variation in inference from different spatiotemporal sampling designs. In a supplementary file, we have provided R code for this simple simulation and to generate figure 3.

References

- [1] Plowright, R. K., Foley, P., Field, H. E., Dobson, A. P., Foley, J. E., Eby, P. & Daszak, P. 2011 Urban habituation, ecological connectivity and epidemic dampening: the emergence of Hendra virus from flying foxes (*Pteropus spp.*). *Proceedings. Biological sciences / The Royal Society* **278**, 3703-3712. (DOI:10.1098/rspb.2011.0522).
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- [3] Nicholson, A. J. & Bailey, V. A. 1935 The balance of animal populations. Part I. *Proceedings of the Zoological Society of London* **105**, 551-598.
- [4] Baddeley, A., Rubak, E. & Turner, R. 2015 *Spatial point patterns: methodology and applications with R*, CRC Press.