

# The coevolutionary mosaic of bat betacoronavirus emergence risk

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Pathogen evolution is one of the least predictable components of disease emergence, particularly in nature. Here, building on principles established by the geographic mosaic theory of coevolution, we develop a quantitative, spatially-explicit framework for mapping the evolutionary risk of viral emergence. Driven by interest in diseases like SARS, MERS, and COVID-19, we examine the global biogeography of bat-origin betacoronaviruses, and find that coevolutionary principles suggest geographies of risk that are distinct from the hotspots and coldspots of host richness. Further, our framework helps explain patterns like a unique pool of merbecoviruses in the Neotropics, a recently-discovered lineage of divergent nobecoviruses in Madagascar, and—most importantly—hotspots of diversification in southeast Asia, sub-Saharan Africa, and the Middle East that correspond to the site of previous zoonotic emergence events. Our framework may help identify hotspots of future risk that have also been previously overlooked, like west Africa and the Indian subcontinent, and may more broadly help researchers understand how host ecology shapes the evolution and diversity of pandemic threats.

1 Disease emergence is complex, and is driven not only by animal-human contact, but also by the  
2 underlying evolutionary dynamics in viral reservoirs.<sup>Plowright2017PatZoo?</sup> Although host richness is often  
3 used as a superficial proxy for spillover risk,<sup>Anthony2017GloPat?, Ruiz-Aravena2022EcoEvo?, Sanchez2022Strategy?</sup> these  
4 approaches oversimplify the relevant interspecific heterogeneity in immunology, behavior, and other  
5 traits, and therefore overlook unique host pools that allow for the rapid evolution of highly divergent  
6 viruses.<sup>Agosta2010HowSpe?</sup> In the case of generalist pathogens like betacoronaviruses, there is conceptual  
7 and empirical support to the idea that these community-level mechanisms are even more  
8 important,<sup>Power2004PatSpi?</sup> particularly given that cross-species transmission may, as a rule, structure viral  
9 evolution more than co-divergence with hosts.<sup>Geoghegan2017ComAna?</sup> This creates a disconnect between  
10 coevolutionary theory and most existing ecological frameworks for mapping spillover risk.

11 The geographic mosaic theory of coevolution (GMTC) attempts to explicitly connect microevolutionary  
12 dynamics to the macroecology and biogeography of symbiotic interactions.<sup>Thompson2005GeoMos?</sup> The GMTC  
13 posits that coevolutionary processes among pairs<sup>Thompson1994CoePro?</sup> or complexes<sup>Janzen1980WheIt?</sup> of  
14 species are structured in space by the rippling effects of abiotic conditions onto evolutionary mechanisms,  
15 giving rise to fragmented systems with different ecologies over large spatial extents.<sup>Price2002MacThe?</sup> The  
16 GMTC predicts a spatial fragmentation of coevolutionary dynamics under the joint action of three  
17 processes:<sup>Gomulkiewicz2007DosDon?</sup> coevolutionary hot- and coldspots, which appear when the intensity of  
18 *interaction* (in terms of reciprocal fitness consequences) varies spatially; selection mosaics, wherein the  
19 intensity of *selection* varies across space, driven by both the biotic complexity of the community (locally  
20 diverse hosts and viruses are more biotically complex) and the local favorability of the  
21 environment;<sup>Thrall2007CoeSym?</sup> and trait remixing, which occurs when coevolutionary dynamics change  
22 when community-level *functional traits* change through meta-community dynamics.

23 Here, we apply the GMTC to explore and explain the global biogeography of betacoronaviruses, the group  
24 that includes SARS-CoV, MERS-CoV, and SARS-CoV-2. In their bat reservoirs, coronaviruses evolve  
25 through a mix of host jumps, recombination among disparate lineages, and, to a lesser degree,  
26 co-divergence with their hosts—<sup>Anthony2017GloPat?</sup> a mix of mechanisms that creates a complex and  
27 nonlinear relationship between host diversity and viral emergence. Working from a recently published  
28 database of bat hosts of betacoronaviruses, we test whether spatial structure in bat-betacoronavirus  
29 coevolution is identifiable at a global scale. Aiming to explain these patterns, we develop a generalized  
30 framework for applying the GMTC to host-virus interactions, with a specific emphasis on the potential to

31 create independent coevolutionary dynamics (and therefore spatial fragmentation in risk) through  
32 heterogeneity. We develop a trivariate risk assessment system that connects each GMTC mechanism to a  
33 quantifiable aspect of host-virus interactions: (i) viral sharing rates in host communities, representing the  
34 strength of potential interaction between viruses and any one host (i.e., places where viruses undergo  
35 constant host switching may be coevolutionary coldspots); (ii) the phylogenetic diversity of hosts, as a  
36 proxy for variation in the immunological mechanisms that antagonize viruses (i.e., the selection mosaic);  
37 and (iii) the local uniqueness of the bat community, representing the potential for viruses to be exposed to  
38 novel host traits (e.g., variation in receptor sequences). Together, we argue that these can be used to  
39 identify and map the evolutionary drivers that—in conjunction with transmission processes (e.g., viral  
40 prevalence in reservoirs and animal-human contact rates)—determine disease emergence risk.

## 41 Results and Discussion

### 42 Bat and betacoronavirus biogeography are broadly consistent

43 Most previous work has assumed that the presence or richness of key groups of bat hosts are predictive of  
44 coronavirus diversity.<sup>Anthony2017GloPat?, Ruiz-Aravena2022EcoEvo?</sup> Projecting bat and betacoronavirus  
45 phylogeny over space (fig. 1), we find support for the idea that bat community assembly is directly  
46 responsible for a global mosaic of viral evolution. The distinct groupings (represented by different colors,  
47 symbolizing positions in a subspace formed by the first two phylogenetic principal components) are  
48 essentially equivalent between the two groups, and can be coarsely delineated as (1) south and southeast  
49 Asia; (2) east Asia (including northern China), west Asia, and the Mediterranean coast; (3) Eurasia above  
50 a northing of 40; and (4) Africa and Latin America. In some cases, this diverges from expectations about  
51 coronavirus biogeography: for example, previous work has rarely flagged India as a region of interest, but  
52 for both bats and betacoronaviruses, the subcontinent falls into the same regions as the southeast Asian  
53 peninsula (and indeed, the region is home to known bat hosts of multiple betacoronavirus subgenera,  
54 including nobecoviruses, sarbecoviruses, and merbecoviruses).<sup>Ruiz-Aravena2022EcoEvo?</sup>

55 [Figure 1 about here.]

56 Overall, these results suggest that the boundaries of bat and betacoronavirus biogeographic regions are  
57 broadly consistent at a global scale; perfect matching between the biogeographic regions would have

58 indicated that the signal of virus distribution is fully predicted by bat hosts ranges. Areas for which the  
59 biogeographic regions for bats and betacoronaviruses differ are primarily (i) southeast Asia and southern  
60 China, and (ii) the Arabian peninsula, which are both regions where zoonotic transmission has been  
61 documented (potentially driving a unique level of viral sampling effort that generates these patterns).  
62 These spatially limited mismatches notwithstanding, the large level of congruence may be surprising,  
63 given that cross-species transmission may play a stronger role in coronavirus diversification than  
64 cospeciation—[Anthony2017GloPat?](#) a property that would theoretically allow for substantial broad divergence  
65 in their biogeography. However, host jumps at the family level or higher are relatively rare and significant  
66 events in coronavirus evolutionary history; [Anthony2017GloPat?](#), [Latinne2020OriCro?](#) as a result, the mosaic of  
67 betacoronavirus phylogeny is assembled from a set of overlapping smaller coevolutionary systems,  
68 superimposed in space and filtered by the importance of different subgroups in local host communities.  
69 For example, the most speciose and cosmopolitan family of bats, the vesper bats (Vespertilionidae), are  
70 considered the primary hosts of the subgenus *Merbecovirus* (MERS-like  
71 viruses); [Latinne2020OriCro?](#), [Ruiz-Aravena2022EcoEvo?](#) but in the Americas, where merbecoviruses are the only  
72 lineage present, they have only been found in other bat taxa (e.g., Molossidae,  
73 Phyllostomidae). [Anthony2013CorBat?](#), [Goes2013NovBat?](#), [Goes2016GenDiv?](#), [Brandao2008CorDet?](#) At the coarsest scale,  
74 these heterogeneities are lost, and betacoronavirus biogeography tracks the deep rifts in bat evolutionary  
75 history—but within broad regions, the component coevolutionary systems may have very different  
76 dynamics.

## 77 **Hotspots of bat and betacoronavirus biodiversity are distinct**

78 Bats, the second most diverse group of mammals, are found worldwide; gradients in their species  
79 richness generally track broader patterns of mammal diversity, [Tanalgo2022Mapping?](#) with a striking  
80 Neotropical hotspot (especially in the Amazon basin) and a secondary hotspot centered in Indochina.  
81 These hotspots of bat diversity are generally presumed to be hotspots of viral adaptive radiation, and  
82 therefore areas of concern for human health. [Anthony2017GloPat?](#), [Olival2017HosVir?](#) However, the hotspots of  
83 known bat betacoronavirus hosts show a distinct pattern, with primary hotspots (both in terms of area and  
84 higher values) of host richness situated in southeast Asia, parts of southern Europe, and to a lesser extent  
85 parts of Africa in the -25-0 range of latitudes (fig. 2; top). Although hundreds of species likely host  
86 undiscovered betacoronaviruses, machine learning predictions have suggested that these undiscovered

87 reservoirs should follow the same diversity gradient. Becker2022OptPre? In principle, these hotspots of  
88 locally-diverse, virus-rich bat communities should drive more adaptive diversification in their viruses.

89 [Figure 2 about here.]

90 However, we find that the global pattern of betacoronavirus phylogenetic distinctiveness is quite distinct  
91 from both bat host richness and phylogenetic distinctiveness (fig. 2; bottom). In contrast to the sparsity of  
92 Neotropical betacoronavirus hosts, South and Central America have the most evolutionary distinct hosts  
93 and viruses, followed by secondary hotspots in southeast Asia and the Rift Valley region have mostly  
94 distinct viruses. Some degree of sampling bias may contribute to these patterns: for example, the  
95 Neotropics are one of the places where the fewest bat betacoronavirus sequences have been  
96 generated, Worobey2022HuaMar?, Temmam2022BatCor?, Boni2020EvoOri? resulting in a sparser phylogenetic tree, and  
97 artificially inflating distinctiveness; conversely, disproportionate research effort in eastern  
98 China Cohen2022SamStr? may have led to a more complete inventory of the local diversity of coronaviruses,  
99 again inflating these metrics relative to underlying patterns. Even accounting for these potential biases,  
100 though, there is obvious heterogeneity in betacoronavirus evolutionary distinctiveness that is distinct from  
101 overall bat diversity.

102 Overall, these patterns recapitulate the evolutionary history of both the order Chiroptera and the genus  
103 *Betacoronavirus*. Horseshoe bats (Rhinolophidae) include the reservoirs of the SARS-like viruses  
104 (subgenus *Sarbecovirus*), the group of pandemic threats that have been of the greatest interest to  
105 researchers Latinne2020OriCro? (and so have been sampled most intensively). Cohen2022SamStr? The hotspots of  
106 host richness and viral diversity in southeast Asia—both of which are disproportionately high,  
107 considering the global landscape of bat species richness—are almost entirely driven by viral adaptive  
108 radiation through host switching within this clade Becker2022OptPre?, Ruiz-Aravena2022EcoEvo?. In contrast, the  
109 Neotropical hotspot of viral distinctiveness is driven by isolation by host vicariance. Out of the four main  
110 groups of betacoronaviruses, only merbecoviruses have been found in animals in the Americas—an  
111 introduction that is generally presumed to be ancient. Ruiz-Aravena2022EcoEvo?, Olival2020PosRev? While  
112 comparatively understudied, New World merbecoviruses have been found in the ghost-faced bats  
113 (Mormoopidae), Neotropical leaf-nosed bats (Phyllostomidae), and free-tailed bats  
114 (Molossidae). Anthony2013CorBat?, Goes2013NovBat?, Goes2016GenDiv?, Brandao2008CorDet? The former two groups and  
115 a clade of the latter are endemic to the Neotropics, while the explosive adaptive radiations of the

116 phyllostomids are responsible for the hotspot of bat diversity in the Amazon.<sup>Ammerman2012FirMol?</sup> Together,  
117 these clades of New World bats play host to a distinct regime of betacoronavirus coevolution.

118 Our approach is potentially limited by sampling bias: key hotspots identified by our model have, indeed,  
119 been sampled intensely following major zoonotic emergence events. In these areas, more betacoronavirus  
120 hosts will have been discovered, leading to higher overall diversity and potentially higher sharing.

121 Similarly, hotspots of evolutionary uniqueness - as in the Arabian peninsula - could reflect much broader  
122 lineages that have only been sampled in focal areas for public health. While the discovery of new branches  
123 of bat-betacoronavirus coevolution is certainly likely, and might change some of the observed patterns, our  
124 framework is likely to be fairly robust: the 126 hosts in our study capture nearly 10% of global bat diversity,  
125 and the underlying evolutionary patterns they represent are much less sensitive to new information than  
126 any inferences about viral evolution.

## 127 **Coevolutionary regimes structure evolutionary potential for zoonotic emergence**

128 The existence of well-defined cophylogenetic regions suggests that the bat-betacoronavirus system is  
129 spatially fragmented enough to create divergent coevolutionary trajectories; in turn, this coevolutionary  
130 mosaic may alter the risk of zoonotic emergence. These ideas are, respectively, supported by the existence  
131 of hotspots of viral uniqueness and the diverse origins of human betacoronaviruses. Together, this  
132 framework points to a predictable relationship between host community structure and coevolutionary  
133 pressure: phylogeographic structure in bat hosts (and their diverse immune strategies)<sup>Banerjee2020NovIns?</sup>  
134 creates a landscape of selective pressure; the trajectory of viruses' coevolutionary response is, in turn,  
135 constrained by their opportunities for either specialization or diversification through host jumps and  
136 recombination.

137 Based on the geographic mosaic theory of coevolution, we developed a trivariate map of coevolutionary  
138 pressure (fig. 3): (1) *host phylogenetic diversity*: a high diversity of evolutionary histories should expose  
139 viruses to more variation in host immune traits; (2) *host community uniqueness*: exposure to greater host  
140 trait heterogeneity can drive viral diversification, and coevolving with more unique host communities  
141 should create more unique branches of viral evolution; and (3) propensity for *viral sharing*: frequent  
142 cross-species transmission may act as a buffer on selective pressure, while lower rates of exchange may  
143 enable more simultaneous trajectories of viral specialization to coexist within a given community. We

144 combine global maps of all three to generate a map of coevolutionary regimes, where close colors  
145 represent similar risks, and paler pixels represent overall higher risk (see Methods). We find that these  
146 regions do not neatly overlap with those defined in fig. 1 or fig. 2, reinforcing the notion that local-scale  
147 coevolutionary mosaics can form within cophylogenetic regions.

148 [Figure 3 about here.]

149 The greatest evolutionary potential for zoonotic emergence exists where pathogen pools have a high  
150 genetic diversity and high propensity for cross-species transmission. In our framework, emergence risk is  
151 therefore maximized under higher phylogenetic diversity (viruses are exposed to different host clades),  
152 higher host uniqueness (viruses are experiencing novel, heterogeneous host traits combinations), and low  
153 to medium viral sharing (host-virus pairs can coevolve independently, but divergent viruses may still have  
154 opportunities for recombination). In fig. 3, this corresponds to yellow areas (dynamics dominated by low  
155 viral sharing, with equal contributions of selection mosaics and trait remixing; southeast Asia, and the  
156 Indian sub-continent), green-yellow areas (dynamics with low viral sharing but dominated by the  
157 selection mosaic effect of host diversity; sub-Saharan Africa), and red-yellow areas (dynamics with low  
158 viral sharing but dominated by trait remixing in host communities; the Middle East). Translating this axis  
159 of variation back into a univariate risk map (fig. 4) highlights that this evolutionary landscape has a  
160 striking correspondence to regions where zoonotic betacoronaviruses have previously emerged. Our  
161 findings align with predictions regarding the spatial location of cross-species transmission. These  
162 locations not only pose a potential risk of viral jumps that could endanger human health but also provide  
163 valuable information for monitoring wildlife health. This could guide us to determine where and what  
164 measures to implement for effectively monitoring wildlife and human betacoronavirus outbreaks before  
165 they escalate to critical levels. Nevertheless, there are actually very few documented cases of emergence  
166 events, and similarities could be some degree of coincidental.

167 Compared to approaches that map emergence risk based only on the number of known bat hosts of  
168 betacoronaviruses, our framework suggests regions where high viral sharing dominates coevolutionary  
169 dynamics—such as Latin America, or Eurasia above a northing of 30—would pose less of a relative risk of  
170 zoonotic emergence. Nevertheless, areas of high host uniqueness coupled with high viral sharing  
171 (red-to-pink in fig. 3) could create hotspots facilitated by viral codivergence. Our framework identifies  
172 Madagascar, where most bat species are endemic following evolutionary divergence from sister species in

173 both African and Asian continents, Shi2014DeeDiv? as one such hotspot; interestingly, a recent  
174 study Kettenburg2022FulGen? reported a novel and highly divergent lineage of nobecoviruses from  
175 Madagascar-endemic pteropid bat species (*Pteropus rufus* and *Rousettus madagascariensis*), again  
176 supporting the predictive power of the coevolutionary framework.

177 [Figure 4 about here.]

## 178 Human landscapes filter the geography of emergence risk

179 The relationship between the underlying pathogen pool and emergence risk is mediated by both  
180 human-wildlife interfaces (the probability of spillover) and opportunities for onward horizontal  
181 transmission (the probability that spillovers become epidemics) Plowright2017PatZoo?. It must be noted that  
182 the assessment of risk based on the GMTC mechanisms does not account for human presence; for this  
183 reason, it represents “potential” level of risk, which must be re-evaluated in the light of human presence.  
184 As a proxy for both, we finally overlaid the risk component from the composite map (see above) with the  
185 proportion of built land, as a proxy for a mix of habitat disturbance, potential for bat synanthropy or  
186 contact with bridge hosts like livestock, Rulli2021LanCha?, Cui2019OriEvo? and human population density and  
187 connectivity Plowright2017PatZoo?, Muylaert2022PreFut?, Hassell2017UrbDis? (fig. 5). Accounting for these factors,  
188 most of South America and Europe are at comparatively lower risk, as—although densely  
189 populated—settlements tend to be in areas with lower potential risk. Conversely, regions like Malaysia and  
190 the northern coast of Australia have a high evolutionary risk component, but should represent a relatively  
191 lower effective risk due to low human density. However, southeast Asia, the Indian subcontinent, and  
192 scattered hotspots in sub-Saharan Africa are at high risk due to the overlap between human populations  
193 and natural opportunities for cross-species transmission of betacoronaviruses.

194 [Figure 5 about here.]

195 Reassuringly, these predictions correspond to the geographic origins of the three bat-origin coronaviruses  
196 that have recently emerged in human populations. While available information puts the spillover of  
197 SARS-CoV-2 in a live animal market in Wuhan, China, the ultimate origin of the virus is almost certainly  
198 in a divergent lineage of sarbecoviruses from Indochina that was poorly characterized prior to the  
199 pandemic. Worobey2022HuaMar?, Temmam2022BatCor?, Boni2020EvoOri? Similarly, the SARS-CoV outbreak began in

200 Guangdong province in 2002, reaching humans through small carnivore bridge hosts, but was eventually  
201 traced back to a set of likely progenitor viruses found in cave-dwelling horseshoe bats in Yunnan  
202 province; <sup>Hu2017DisRic?</sup> nearby, antibody evidence has indicated human exposure to SARS-like  
203 viruses. <sup>Wang2018SerEvi?</sup> MERS-CoV was first detected in Jordan, but is widespread in camels in East Africa  
204 and the Middle East, and may have reached its bridge host decades earlier than originally  
205 supposed; <sup>Muller2014MerCor?</sup> as a result, the geography of the original bat-to-camel transmission is still  
206 widely regarded as uncertain. All of these are broadly consistent with the risk factors we identify. Notably,  
207 India and west Africa are additional hotspots that have yet to experience the emergence of a bat  
208 coronavirus into human populations, but may still be at risk—particularly given known gaps in bat  
209 surveillance, <sup>Cohen2022SamStr?</sup> and a dense population in both regions with global connectivity. In any of  
210 these regions, surveillance on viral reservoirs can be paired with targeted monitoring of high-risk human  
211 populations (i.e., those with regular wildlife contact) <sup>Xu2004EpiClu?</sup> for maximum impact.

## 212 Conclusion

213 Bats emerged around 64 million years ago, and are one of the most diverse mammalian orders, with more  
214 than 1,400 estimated species. <sup>Peixoto2018SynEco?, Simmons2020BatSpe?</sup> They exhibit a broad variety of habitat use,  
215 behaviour, and feeding strategies, putting them at key positions in the delivery and provisioning of several  
216 ecosystem services, tied to important ecosystem-derived benefits to humans. <sup>Kasso2013EcoEco?</sup> Over  
217 two-thirds of bats are known to be either obligate or facultative insectivores, therefore actively  
218 contributing for agricultural pest control, <sup>Voigt2016BatAnt?, Williams-Guillen2008BatLim?</sup> and vectors of pathogens  
219 that put a risk on human health; <sup>Gonsalves2013MosCon?, Gonsalves2013MosInf?</sup> some other species are essential  
220 links in many seed-dispersal networks. <sup>Mello2011MisPar?</sup> However, many of these species face a high risk of  
221 extinction, particularly given persecution and killings that sometimes follows from messaging about their  
222 role in disease emergence. Areas where bats, viruses, and humans co-occur are not always hotspots of risk  
223 for human health; as such, developing more precise ways to map zoonotic hazards can help bats and  
224 humans coexist safely, and support the conservation of these important and unique animals.  
  
225 Here, we propose a simple framework with broad explanatory power that helps contextualize discoveries  
226 like highly divergent nobecoviruses in Madagascar and the once-neglected adaptive radiation of  
227 sarbecoviruses in the Indochinese peninsula. In doing so, it advances ecological theory beyond the current

228 state of the art for global maps of emergence risk. For example, previous studies that have used host  
229 richness as a proxy have predicted a high diversity of unsampled bat viruses,<sup>Olival2017HosVir?</sup> bat  
230 coronaviruses,<sup>Anthony2017GloPat?</sup> and even specifically betacoronaviruses<sup>Becker2022OptPre?</sup> in both the  
231 Amazon and southeast Asia. While we find that both regions are characterized by unique and diverse  
232 communities of both hosts and viruses, our framework is able to identify key differences between the two  
233 systems. We find that the merbecovirus complex in Latin America has been a unique branch of evolution  
234 separate from the rest of the global pool, but with limited potential for viral diversification—a finding that  
235 is supported by previous work indicating a higher rate of codivergence in Latin  
236 America.<sup>Anthony2017GloPat?,Caraballo2022CroTra?</sup> In contrast, in southeast Asia, host richness and viral  
237 distinctiveness are high but sharing is low; this suggests a different type of evolutionary dynamics that  
238 could generate high local diversity of viruses through host switching and viral recombination (see  
239 e.g.,<sup>Latinne2020OriCro?</sup> as well as the discovery of recombinant viruses with genetic material from both the  
240 SARS-CoV and SARS-CoV-2 branches of the Sarbecovirus lineage).<sup>Wu2021ComSur?</sup> Both of these regions are  
241 priority areas for sampling, especially given predictions that they contain many bat hosts of undiscovered  
242 betacoronaviruses.<sup>Becker2022OptPre?,Cohen2022SamStr?</sup> However, both the evolutionary and ecological aspects  
243 of emergence risk are higher in southeast Asia—a fact that will only become more relevant, as bats track  
244 shifting climates and exchange viruses with other species, creating a hotspot of elevated cross-species  
245 transmission unique to the region.<sup>Carlson2022CliCha?,Muylaert2022PreFut?</sup>

246 Our trivariate additive mapping of components of risk (fig. 3) aims to elicit the complexity of spatial  
247 cross-species transmission risk beyond the mere presence or absence of the pathogen host in a specific  
248 location. By considering coevolutionary factors such as viral sharing and host uniqueness, we suggest  
249 insights that can aid in identifying potential locations for surveillance of betacoronavirus circulation and  
250 assessing the risk of cross-species transmission to other mammals. In communities characterized by  
251 diverse but unique host populations, with limited viral sharing between them, we could encounter viruses  
252 that specialize in targeting the immune system of specific hosts. This implies a low likelihood of infecting  
253 novel hosts but, once locally introduced into a new host (either a new species, or an immunologically  
254 naïve population), the specialized virus could spread relatively easily due to encountering little immune  
255 resistance (CITE PLOWRIGHT). With the right combination of viral traits, such as low disease-induced  
256 mortality or high transmission rate, this could lead to successfully spread within the new host community.  
257 However, while high adaptation to a specific host can be advantageous, it may also lead to maladaptation

258 when the pathogen encounters a new unsuitable host, potentially resulting in its extinction.

259 Plowright RK, Foley P, Field HE, Dobson AP, Foley JE, Eby P, Daszak P. Urban habituation,  
260 ecological connectivity and epidemic dampening: the emergence of Hendra virus from flying  
261 foxes (*Pteropus* spp.). Proceedings of the Royal Society B: Biological Sciences. 2011 Dec  
262 22;278(1725):3703-12.

263 Bats—and the spillover of their viruses—are also sensitive to anthropogenic factors others than climate  
264 change, including deforestation and other kinds of habitat loss, increased stress, and greater contact with  
265 potential bridge hosts like domesticated

266 species. <sup>Alves2018GeoVar?, Treitler2016EffLoc?, Rulli2021LanCha?, Mendenhall2014PreBio?</sup> This represents a challenge for  
267 both conservation strategies and pandemic prevention, <sup>Amman2011InvRoI?</sup> but identifying areas at risk, and  
268 protecting the health of bats and ecosystems within those zones, can be a win-win intervention for  
269 both. <sup>Hopkins2021HowIde?, Plowright2021LanUse?, OHHLEP2022OneHea?</sup> As we scale these predictions down in space  
270 to finer spatial resolutions to guide public health actions,<sup>1</sup> the incorporation of human activity predictors  
271 will become more importyant.<sup>2</sup>

272 **Acknowledgements:** We acknowledge that this study was conducted on land within the traditional  
273 unceded territory of the Saint Lawrence Iroquoian, Anishinabewaki, Mohawk, Huron-Wendat, and  
274 Omàmiwininiwak nations. This work was supported by funding to the Viral Emergence Research  
275 Initiative (VERENA) consortium including NSF BII 2021909 and a grant from Institut de Valorisation des  
276 Données (IVADO). This research was enabled in part by support provided by Calcul Québec  
277 ([www.calculquebec.ca](http://www.calculquebec.ca)) and Compute Canada ([www.computecanada.ca](http://www.computecanada.ca)). NF is funded by the NSERC  
278 BIOS<sup>2</sup> CREATE program. TP and NF are funded by the Courtois Foundation. RLM was supported by  
279 Bryce Carmine and Anne Carmine (née Percival), through the Massey University Foundation. DJB was  
280 supported by the National Institute of General Medical Sciences of the National Institutes of Health  
281 (P20GM134973).

282 **Methods**

283 **Known *Betacoronavirus* hosts**

284 We downloaded the data on bats hosts of *Betacoronavirus* from  
285 <https://www.viralemergence.org/betacov> on Apr. 2022, Becker2022OptPre? and filtered it to “known”  
286 hosts (established before the emergence of SARS-CoV-2) and “novel” hosts (confirmed through sampling  
287 and competence assays since the initial data collection). The original database was assembled by a  
288 combination of data mining and literature surveys, including automated alerts on the “bats” and  
289 “coronavirus” keywords to identify novel empirical evidence of bats-betacoronaviruses associations; this  
290 yielded a total of 126 known hosts, 47 of which were novel hosts. This host-virus list of interactions was  
291 obtained through a comprehensive aggregation of GenBank data as well as systematic literature  
292 searches, Becker2022OptPre?, Cohen2022SamStr? such that we have high confidence in its fitness for the purpose  
293 of inference at a large spatial scale.

294 **Bat occurrences**

295 We downloaded the rangemap of every current bat species that was classified as an empirically  
296 documented host of *Betacoronavirus* from the previous step, according to recent IUCN data. IUCN2021IucRed?  
297 The IUCN data have been assembled to support wildlife conservation efforts, and therefore we do not  
298 expect that they are biased by wildlife disease sampling efforts or priority. The range maps were  
299 subsequently rasterized using the rasterize function from GDAL RouaultEven2022GdaOgr? at a resolution of  
300 approximately 100kmx100km at the equator. For every pixel in the resulting raster where at least one bat  
301 host of *Betacoronavirus* was present, we extract the species pool (list of all known bat hosts), which was  
302 used to calculate the following risk assessment components: bat phylogenetic diversity, bat compositional  
303 uniqueness, and predicted viral sharing risk.

304 **Bat phylogenetic diversity**

305 For every pixel, we measured Faith’s Phylogenetic Diversity Faith1992ConEva? based on a recent synthetic tree  
306 with robust time calibration, covering about 6000 mammalian species. Upham2019InfMam? Faith’s PD  
307 measures the sum of unique branches from an arbitrary root to a set of tips, and comparatively larger

308 values indicate a more phylogenetic diverse species pool. We measured phylogenetic diversity starting  
309 from the root of the entire tree (and not from Chiroptera); this bears no consequences on the resulting  
310 values, since all branches leading up to Chiroptera are only counted once per species pool, and (as we  
311 explain when describing the assembly of the composite risk map), all individual risk components are  
312 ranged in [0,1]. This measure incorporates a richness component, which we chose not to correct for; the  
313 interpretation of the phylogenetic diversity is therefore a weighted species richness, that accounts for  
314 phylogenetic over/under-dispersal in some places.

### 315 **Bat compositional uniqueness**

316 For every species pool, we measured its Local Contribution to Beta-Diversity;<sup>Legendre2013BetDiv?</sup> LCBD  
317 works from a species-data matrix (traditionally noted as **Y**), where species are rows and sites are columns,  
318 and a value of 1 indicates occurrence. We extracted the Y matrix assuming that every pixel represents a  
319 unique location, and following best practices<sup>Legendre2019SpaTem?</sup> transformed it using Hellinger's distance  
320 to account for unequal bat richness at different pixels. The correction of raw community data is  
321 particularly important for two reasons: first, it prevents the artifact of richer sites having higher  
322 importance; second, it removes the effect of overall species richness, which is already incorporated in the  
323 phylogenetic diversity component. High values of LCBD indicate that the pixel has a community that is on  
324 average more dissimilar in species composition than what is expected knowing the entire matrix, i.e. a  
325 more unique community. Recent results by<sup>Dansereau2022EvaEco?</sup> shows that LCBD measures are robust with  
326 regards to spatial scale, and are therefore applicable at the global scale.

### 327 **Viral sharing between hosts**

328 For all bat hosts of *Betacoronavirus*, we extracted their predicted viral sharing network, generated from a  
329 previously published generalized additive mixed model of virus sharing by a tensor function of  
330 phylogenetic distance and geographic range overlap across mammals.<sup>Albery2020PreGlo?</sup> This network stores  
331 pairwise values of viral community similarity, measured for all hosts (to maintain consistency with the  
332 phylogenetic diversity measure) across all viruses; therefore, we consider that it accounts for some overall  
333 similarity in the way hosts deal with viruses, and not only betacoronaviruses. There is empirical evidence  
334 that capacity for cross-species transmission even between divergent species is generally high,<sup>3</sup> especially

335 for beta-coronaviruses.<sup>4</sup> To project viral sharing values into a single value for every pixel, we averaged the  
336 pairwise scores. High values of the average sharing propensity means that this specific extant bat  
337 assemblage is likely to be proficient at exchanging viruses.

### 338 Composite risk map

339 To visualize the aggregated risk at the global scale, we combine the three individual risk components  
340 (phylogenetic diversity, compositional uniqueness, and viral sharing) using an additive color  
341 model. [Seekell2018GeoLak?](#) In this approach, every risk component gets assigned a component in the RGB  
342 color model (phylogenetic diversity is green, compositional uniqueness is red, and viral sharing is blue).  
343 In order to achieve a valid RGB measure, all components are re-scaled to the [0,1] interval, so that a pixel  
344 with no sharing, no phylogenetic diversity, and no compositional uniqueness is black, and a pixel with  
345 maximal values for each is white. This additive model conveys both the intensity of the overall risk, but  
346 also the nature of the risk as colors diverge towards combinations of values for three risk components. Out  
347 of the possible combinations, the most risky in terms of rapid diversification and spillover potential is high  
348 phylogenetic diversity and low viral sharing, [Gomulkiewicz2000HotSpo?](#) in that this allows multiple  
349 independent host-virus coevolutionary dynamics to take place in the same location. In the colorimetric  
350 space, this correspond to yellow – because the HSV space is more amenable to calculations for feature  
351 extraction, [Keke2010StuSki?](#) we measured the risk level by calculating the angular distance of the hue of each  
352 pixel to a reference value of 60 (yellow), and weighted this risk level by the value component. Specifically,  
353 given a pixel with colorimetric coordinates  $(h, s, v)$ , its ranged weighted risk value is

$$v \times \left[ 1 - \frac{|\text{atan}(\cos(\text{rad}(h)), \sin(\text{rad}(h))) - X|}{2\pi} \right],$$

354 where  $X$  is  $\text{atan}(\cos(\text{rad}(60)), \sin(\text{rad}(60)))$ , a constant approximately equal to 0.5235.

### 355 Viral phyogeography and evolutionary diversification

356 To next represent phyogeography of betacoronaviruses in bats, we aggregated and analyzed  
357 betacoronavirus sequence data. We used the following query to pull all *Betacoronavirus* sequence data  
358 from the GenBank Nucleotide database except SARS-CoV-2; (“Betacoronavirus”[Organism] OR

359 betacoronavirus[All Fields]) NOT (“Severe acute respiratory syndrome coronavirus 2”[Organism] OR  
360 sars-cov-2[All Fields]). We added a single representative sequence for SARS-CoV-2 and manually curated  
361 to remove sequences without the RNA-dependent RNA polymerase (RdRp) sequence or that contained  
362 words indicating recombinant or laboratory strains including “patent”, “mutant”, “GFP”, and  
363 “recombinant”. We filtered over-represented taxa including betacoronavirus 1, hCoV-OC43, Middle East  
364 respiratory syndrome coronavirus, Murine hepatitis virus, and hCoV-HKU1. Curated betacoronavirus  
365 RdRp sequences were then aligned using MAFFT<sup>Katoh2013MafMul?</sup> v1.4.0 (Algorithm FFT-NS-2, Scoring  
366 matrix 200PAM / k=2, gap open penalty 1.53m offset value 0.123) and a maximum likelihood tree  
367 reconstructed in IQ-TREE<sup>Nguyen2015IqtFas?</sup> v1.6.12 with ModelFinder<sup>Kalyaanamoorthy2017ModFas?</sup> ultrafast  
368 bootstrap approximation<sup>Hoang2018UfbImp?</sup> with a general time reversible model with empirical base  
369 frequencies and the 5-discrete-rate-category FreeRate model of nucleotide substitution (GTR+F+R5).

370 We first tested the hypothesis that hotspots of viral diversification would track hotspots of bat  
371 diversification. To do so, we plotted the number of known bat hosts (specifically only those included in the  
372 phylogeny, so there was a 1:1 correspondence between data sources) against the “mean evolutionary  
373 distinctiveness” of the associated viruses. To calculate this, we derived the fair proportions evolutionary  
374 distinctiveness<sup>Isaac2007MamEdg?</sup> for each of the viruses in the tree, then averaged these at the bat species  
375 level, projected these values onto their geographic distributions, and averaged across every bat found in a  
376 given pixel. As such, this can be thought of as a map of the mean evolutionary distinctiveness of the  
377 known viral community believed to be associated with a particular subset of bats present.

### 378 Co-distribution of hosts and viral hotspots

379 Subsequently, we tested the hypothesis that the biogeography of bat betacoronaviruses should track the  
380 biogeography of their hosts. To test this idea, we loosely adapted a method  
381 from, <sup>Kreft2007GloPat?,Kreft2010FraDel?</sup> who proposed a phylogenetic method for the delineation of animal  
382 biogeographic regions. In their original method, a distance matrix - where each row or column represents  
383 a geographic raster’s grid cell, and the dissimilarity values are the “beta diversity similarity” of their  
384 community assemble - undergoes non-metric multidimensional scaling (NMDS); the first two axes of the  
385 NMDS are projected geographically using a four-color bivariate map. Here, we build on this idea with an  
386 entirely novel methodology. First, we measure the phylogenetic distance between the different viruses in  
387 the betacoronaviruses tree by using the cophenetic function in ape;<sup>Paradis2019ApeEnv?</sup> subsequently, we take

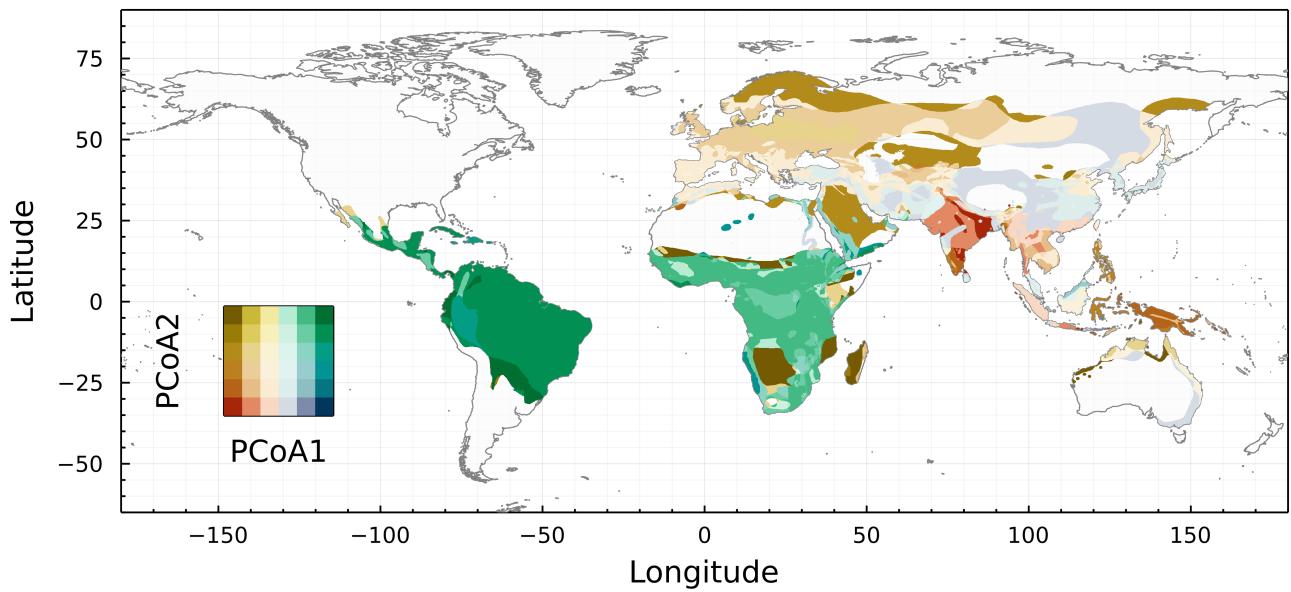
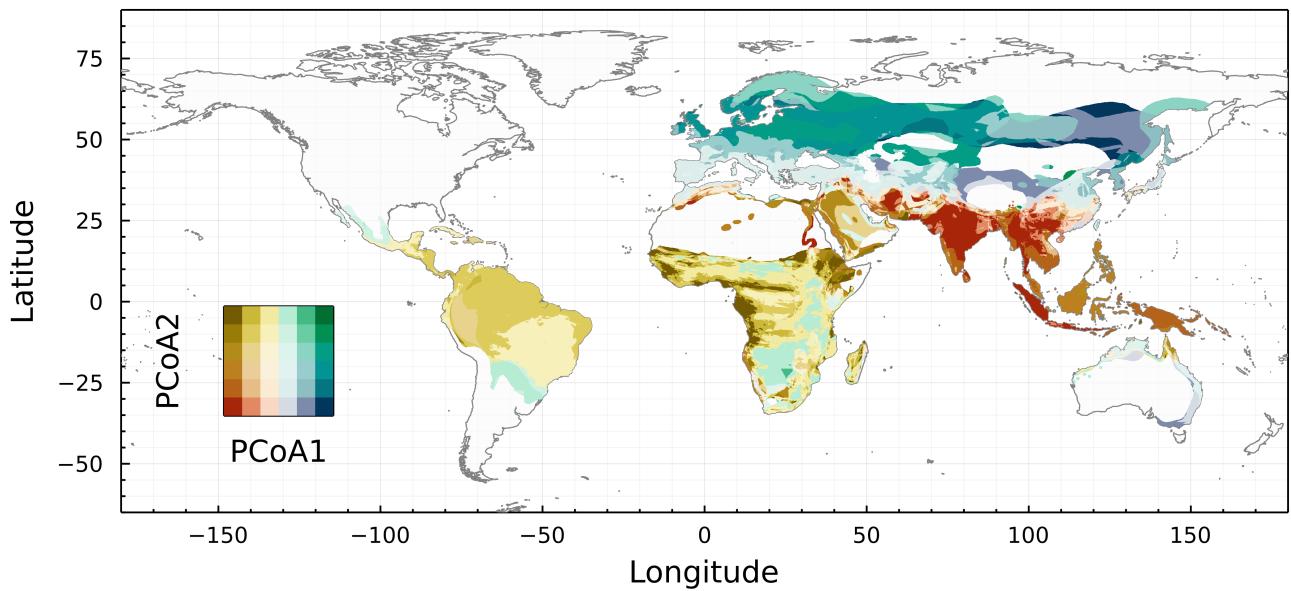
388 a principal components analysis of that distance matrix (readily interchangeable for NMDS in this case) to  
389 project the viral tree into an n-dimensional space. We then take the first two principal components and, as  
390 with the evolutionary distinctiveness analysis, aggregated these to a mean host value and projected them  
391 using a four-color bivariate map.

392 **Data availability statement**

393 The code to reproduce these analyses, as well as the data (with the exception of the IUCN rangemaps,  
394 which must be downloaded from their website) are available in the [viralemergence/betamap](#) repository  
395 on GitHub.

396 **References**

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**Figure 1: Bat and betacoronavirus biogeographic regions.** Phylogeography of bats (top) and viruses (bottom) is categorized based on analysis of bat distributions paired with bat or virus phylogeny. The different colors show tendencies to separate alongside the first two components of a PCoA. Note that the PCoA for the bats and viruses are independent, and so cannot be compared directly – that being said, the regions can be compared across maps.

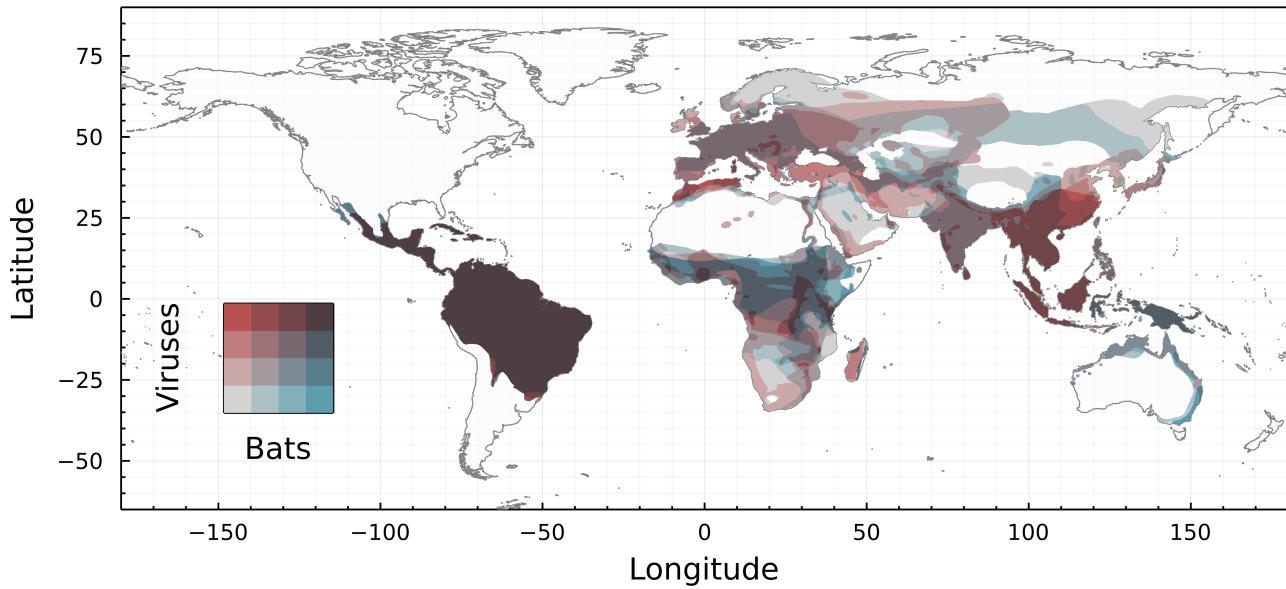
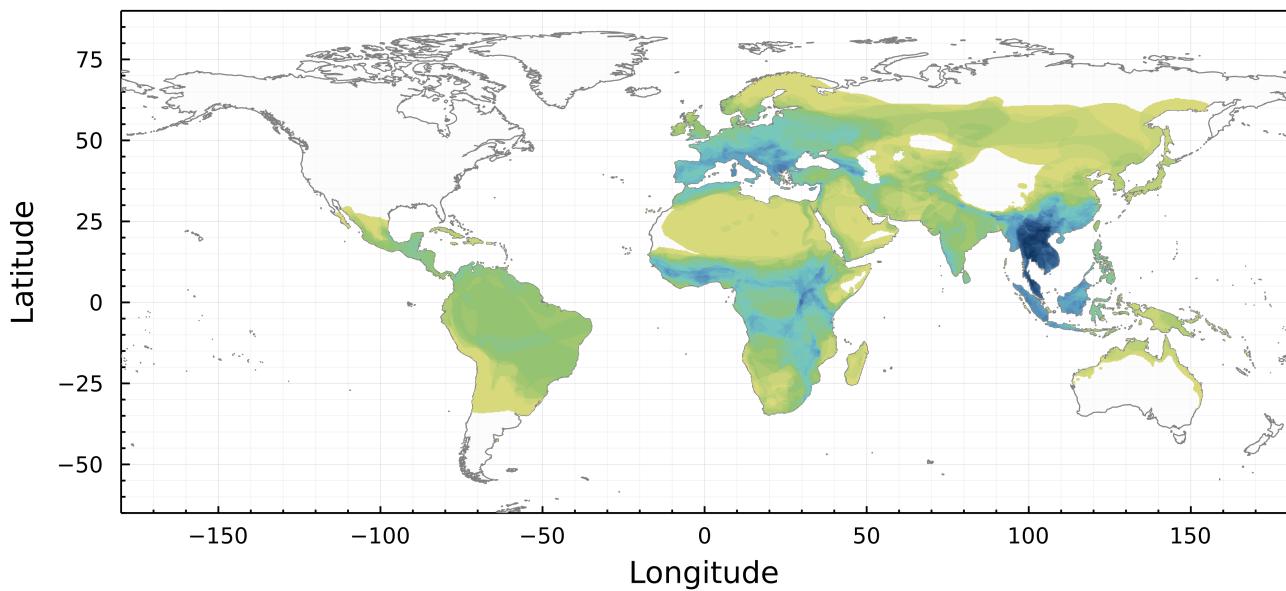
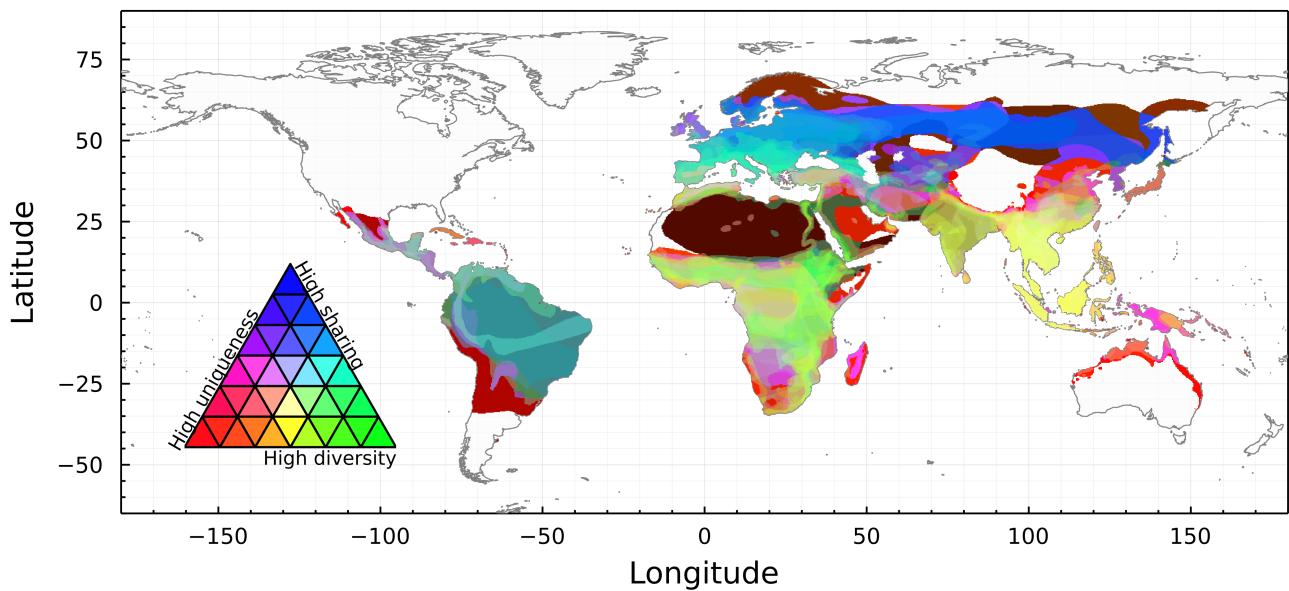


Figure 2: **Bat and betacoronavirus diversity.** Top panel: relative diversity of known bat hosts of betacoronaviruses. This map shows that the region with the largest number of possible hosts is South-Eastern Asia. Bottom panel: congruence between the evolutionary distinctiveness of the hosts (grey to blue) and the viruses (grey to red).



**Figure 3: Trivariate additive mapping of the components of risk.** Viral sharing runs from yellow (low) to blue (high); host phylogenetic diversity runs from pink (low) to high (green); and host compositional uniqueness runs from cyan (low) to red (high). The GMTC suggests that the highest evolutionary potential for emergence exists in unique and diverse host communities with low viral sharing, *i.e.* pixels around yellow. All components within bat host ranges are scaled in brightness so that a pixel with no sharing, no phylogenetic diversity, and no compositional uniqueness would be black, and a pixel with maximal values for each would be white.

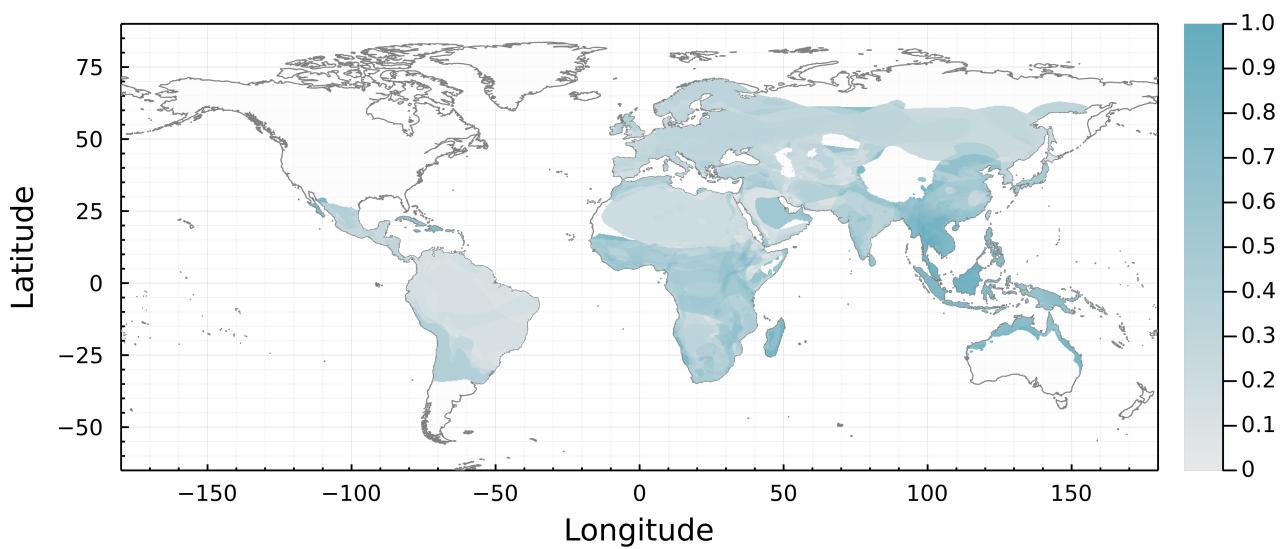


Figure 4: **Evolutionary potential for zoonotic emergence of bat-origin betacoronaviruses.** Risk is a composite measure of the color value and angular distance to the yellow hue in fig. 3 (see Methods).

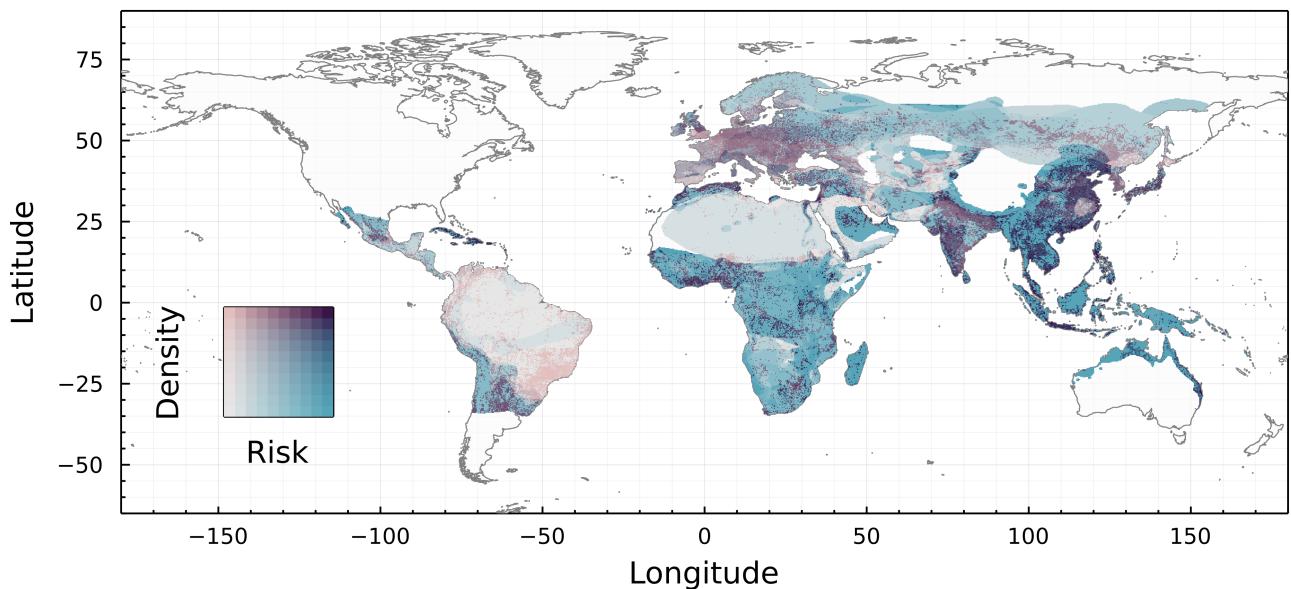


Figure 5: **Overlap between evolutionary potential and ecological opportunity for zoonotic emergence.** Overlap of the percent of each pixel occupied by urbanized structures, representing the degree of settlement, on the spillover risk map (where the risk comes only from wildlife, and ignores multi-hosts chains of transmissions including non-bats hosts). Darker pixels correspond to more risk, in that the GMTC-derived risk of fig. 4 is high *and* the pixel is densely occupied by human populations.