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² Susceptible host dynamics explain pathogen resilience to
³ perturbations

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⁶ Abstract

⁷ Major priority for epidemiological research in the time of anthropogenic change is un-
⁸ derstanding how infectious disease dynamics respond to perturbations. Interventions
⁹ to slow the spread of SARS-CoV-2 significantly disrupted the transmission of other
¹⁰ human pathogens. As interventions lifted, whether and when respiratory pathogens
¹¹ would eventually return to their pre-pandemic dynamics remains to be answered. We
¹² develop a framework for estimating pathogen resilience based on how fast epidemic
¹³ patterns return to their pre-pandemic, endemic dynamics. Our analysis suggests
¹⁴ that some pathogens may have settled to endemic cycles that are different from their
¹⁵ pre-pandemic patterns. Finally, we show that the replenishment rate of the suscep-
¹⁶ tible pool is a key determinant of pathogen resilience. Our framework offers a novel
¹⁷ perspective to characterizing the dynamics of endemic pathogens and their responses
¹⁸ to SARS-CoV-2 interventions. **[SWP: Need to emphasize broader implications.]**

19 Non-pharmaceutical interventions (NPIs) to slow the spread of SARS-CoV-2 disrupted
 20 the transmission of other human respiratory pathogens, adding uncertainties to their future epidemic dynamics and the overall public health burden [1].
 21 As NPIs lifted, large heterogeneities in outbreak dynamics were observed across
 22 different pathogens in different countries, with some pathogens exhibiting earlier
 23 resurgences than others [2, 3, 4]. Heterogeneities in the overall reduction in trans-
 24 mission and the timing of re-emergence likely reflect differences in NPI patterns,
 25 pathogen characteristics, immigration/importation from other countries, and pre-
 26 NPI pathogen dynamics [5]. Therefore, comparing the differential impact of the
 27 pandemic NPIs across pathogens can provide unique opportunities to learn about
 28 underlying pathogen characteristics, such as their transmissibility or duration of im-
 29 munity, from heterogeneities in re-emergence patterns [6].

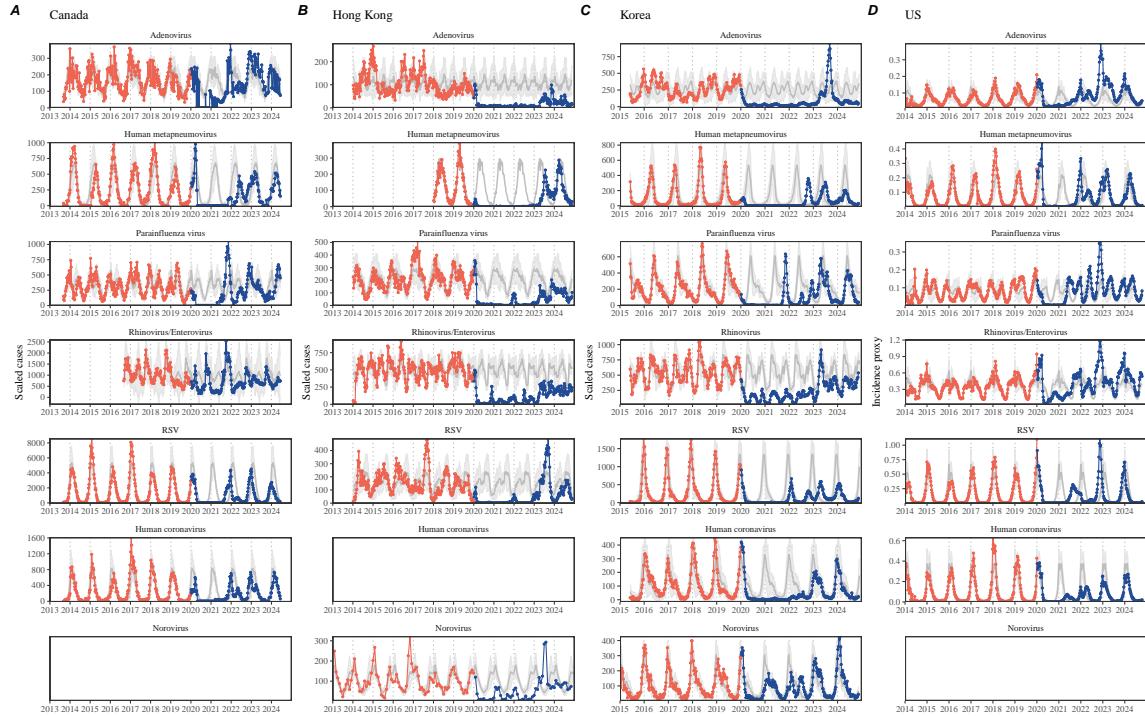


Figure 1: Observed heterogeneity in responses to pandemic NPIs across respiratory pathogens and norovirus in (A) Canada, (B) Hong Kong, (C) Korea, and (D) US. Red points and lines represent data before 2020. Blue points and lines represent data since 2020. Gray lines and shaded regions represent the mean seasonal patterns and corresponding 95% confidence intervals around the mean. Mean seasonal patterns were calculated by aggregating cases before 2020 into 52 weekly bins and taking the average in each week. Cases were scaled to account for changes in testing patterns (Materials and Methods).

31 Even though more than five years have passed since the emergence of SARS-CoV-
 32 2, we still observe persistent changes in pathogen dynamics following the pandemic

33 NPIs: for example, compared to pre-pandemic, seasonal patterns, human metapneu-
34 movirus in Korea seem to circulate at lower levels, whereas RSV in Korea seem to
35 exhibit different seasonality (Figure 1). These observations suggest a possibility for
36 a fundamental change in pathogen dynamics following the pandemic NPIs, which
37 can be driven by permanent shift in either human behavior or population-level im-
38 munity [7, 8]. The possibility of a long-lasting impact of the pandemic NPIs pose an
39 important question for future infectious disease dynamics: can we predict whether
40 and when other respiratory pathogens will eventually return to their pre-pandemic
41 dynamics? **[SWP: You suggested: I would say something about the dynamics of**
42 **these pathogens not being well understood, but I've since rewritten the most of intro**
43 **and I'm not sure where I would fit this. If you have any suggestions, let me know...]**

44 So far, the majority of epidemiological analyses of respiratory pathogens in the
45 context of the pandemic NPIs have focused on characterizing the timing of rebound
46 [1, 9, 5]. Instead, we seek to characterize how fast a pathogen returns to its pre-
47 pandemic dynamics. These two concepts have subtle but important differences: for
48 example, it took more than 3 years for human metapneumovirus to rebound in Hong
49 Kong but the observed epidemic patterns in 2024 are similar to pre-pandemic seasonal
50 means, suggesting a rapid return to pre-pandemic dynamics following a perturbation
51 (Figure 1). Measuring this rate of return is particularly useful because it allows us
52 to quantify the ecological resilience of a host-pathogen system [10, 11, 12, 13].

53 In this study, we lay out theoretical and statistical approaches to characterizing
54 the resilience of a host-pathogen system based on how fast the system recovers from
55 perturbation. We begin by laying out a few representative scenarios that capture the
56 potential impact of NPIs on endemic pathogen dynamics and illustrate how resilience
57 can be measured by comparing the pre- and post-pandemic dynamics of susceptible
58 and infected hosts. In practice, information on susceptible hosts is often unavail-
59 able, making this theoretical approach infeasible. Instead, we utilize a mathematical
60 technique to reconstruct empirical attractors from the data [14], which allows us to
61 measure the rate at which the host-pathogen system approaches this empirical attrac-
62 tor after a perturbation; this rate corresponds to the resilience of the host-pathogen
63 system. We use this method to analyze pathogen surveillance data for respiratory
64 and non-respiratory pathogens from Canada, Hong Kong, Korea, and US. Finally,
65 we show that susceptible host dynamics explain variation in pathogen resilience.

66 Conceptual introduction to pathogen resilience

67 In classical ecological literature, resilience of an ecological system is measured by
68 the rate at which the system returns to its reference state following a perturbation
69 [10, 11, 12, 13]. This rate corresponds to the largest real part of the eigenvalues of
70 the linearized system near equilibrium—here, we refer to this value as the *intrinsic*
71 resilience of the system, which represents the expected rate of return from perturbed
72 states. In practice, we rarely know the true model describing population-level dy-

73 namics of common respiratory pathogens, limiting our ability to infer the intrinsic
74 resilience of a system. Instead, we can still measure the *empirical* resilience of a
75 host-pathogen system by looking at how fast the system returns to the pre-pandemic,
76 endemic dynamics after interventions are lifted.

77 As an example, we begin with a simple Susceptible-Infected-Recovered-Susceptible
78 (SIRS) model with seasonally forced transmission and demography (i.e., birth and
79 death). The SIRS model is the simplest model that allows for waning of immunity
80 and is commonly used for modeling the dynamics of respiratory pathogens [15]. First,
81 consider an intervention that reduce transmission by 50% for 6 months starting in
82 2020, which causes epidemic patterns to deviate from its original stable annual cycle
83 for a short period of time and eventually come back (Figure 2A). To measure the
84 resilience of this system empirically, we first need to be able to measure the dis-
85 tance from its pre-pandemic attractor. There are many ways we can measure the
86 distance from the attractor, but for illustrative purposes, we choose one of the most
87 parsimonious approach: that is, we look at how the susceptible (S) and infected (I)
88 populations change over time and measure the distance on the SI phase plane (Figure
89 2B). In this simple case, the locally estimated scatterplot smoothing (LOESS) fit in-
90 dicates that the distance from the attractor decreases exponentially (linearly on a log
91 scale) on average (Figure 2C). Furthermore, the overall rate of return approximates
92 the intrinsic resilience of the seasonally unforced system (Figure 2C).

93 Alternatively, NPIs can have a lasting impact on the pathogen dynamics; as an
94 example, we consider a scenario in which a 10% reduction in transmission persists
95 even after the NPIs are lifted (Figure 2D–F). In such cases in practice, we can-
96 not know whether the pathogen will return to its original cycle or a different cycle
97 until many years have passed, and we cannot measure the distance to the new un-
98 known attractor that the system might eventually approach. Nonetheless, we can
99 still measure the distance from the pre-pandemic attractor and ask how the distance
100 changes over time (Figure 2E). The LOESS fit suggests that the distance from the
101 pre-pandemic attractor will initially decrease exponentially on average (equivalently,
102 linearly on a log scale) and eventually plateau (Figure 2F). Here, a permanent 10%
103 reduction in transmission rate slows the system, which causes the distance from the
104 pre-pandemic attractor initially to decrease at a slower rate (Figure 2F) than it would
105 have otherwise (Figure 2C) before plateauing at a fixed distance between the two
106 attractors. This example shows that resilience is not necessarily an intrinsic prop-
107 erty of a specific pathogen. Instead, pathogen resilience is a property of a specific
108 attractor that a host-pathogen system approaches, which depends on both pathogen
109 and host characteristics.

110 Finally, transient phenomena can further complicate the picture (Figure 2G–I).
111 For example, a stage-structured model initially exhibits a stable annual cycle, but
112 perturbations from a 10% reduction in transmission for 6 months cause the epidemic
113 to shift to biennial cycles (Figure 2G). The system eventually approaches the original
114 pre-pandemic attractor (Figure 2H), suggesting that this biennial cycle is a transient
115 phenomenon. The LOESS fit indicates that the distance from the attractor initially

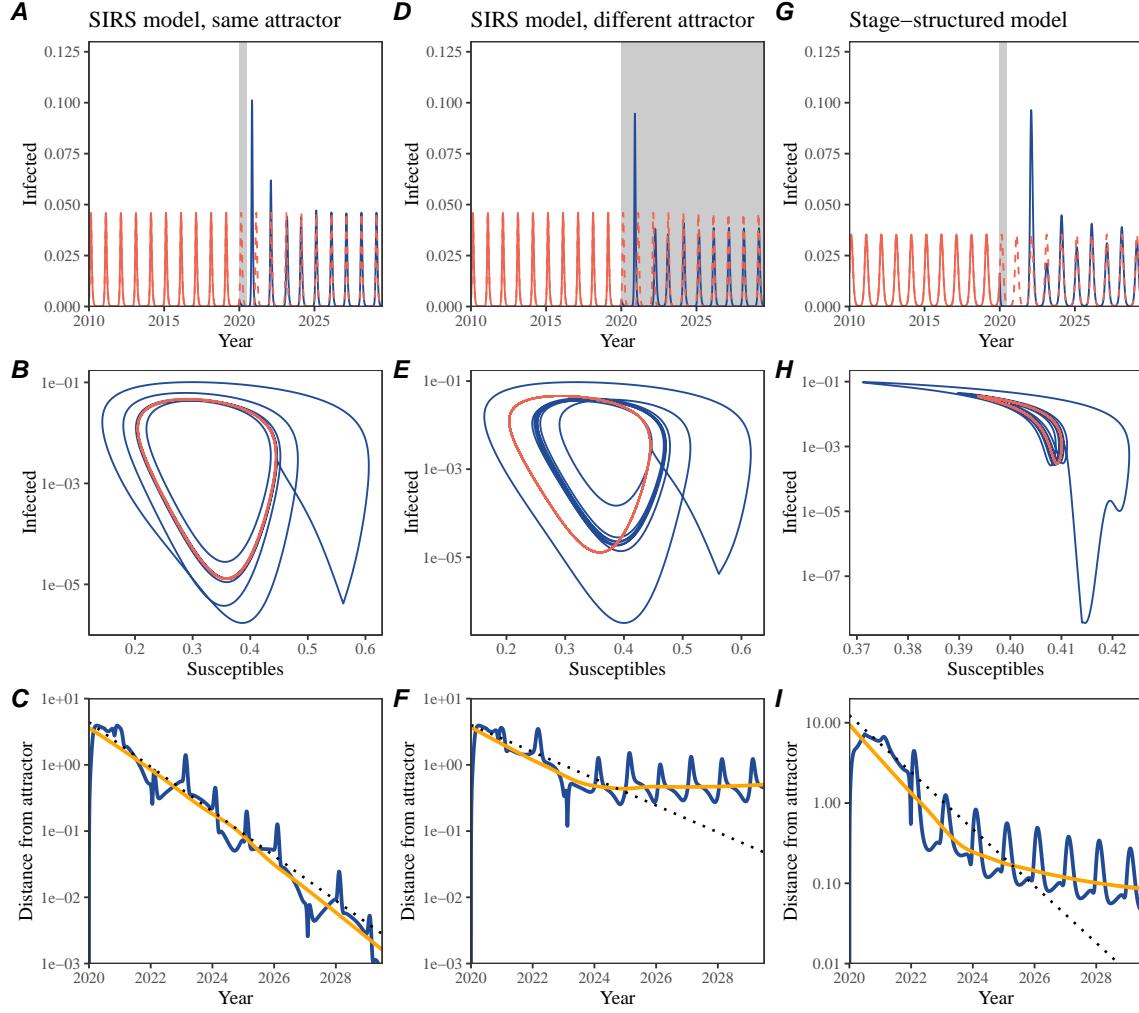


Figure 2: A simple method to measure pathogen resilience following NPIs across different scenarios. (A, D, G) Simulated epidemic trajectories across various models. Red and blue solid lines represent epidemic dynamics before and after interventions are introduced, respectively. Red dashed lines represent counterfactual epidemic dynamics in the absence of interventions. Gray regions indicate the duration of interventions. (B, E, H) Phase plane representation of the time series in panels A, D, and G alongside the corresponding susceptible host dynamics. Red and blue solid lines represent epidemic trajectories on an SI phase plane before and after interventions are introduced, respectively. (C, F, I) Changes in logged distance from the attractor over time. Blue lines represent the logged distance from the attractor. Orange lines represent the locally estimated scatterplot smoothing (LOESS) fits to the logged distance from the attractor. Dotted lines show the intrinsic resilience of the seasonally unforced system.

116 decreases exponentially at a rate that is consistent with the intrinsic resilience of

117 the seasonally unforced stage-structured system, but the rate of decrease decelerates
118 with the damped oscillations (Figure 2I). This behavior is also referred to as a ghost
119 attractor, which causes long transient dynamics and slow transitions [16]. Strong
120 seasonal forcing in transmission can also lead to transient phenomena for a simple
121 SIRS model, causing a slow return to pre-perturbation dynamics (Supplementary
122 Figure S1).

123 This empirical approach allows us to measure the resilience of a two-strain host-
124 pathogen system even when we have incomplete observation of the infection dynam-
125 ics. Simulations from a simple two-strain system illustrate that separate analyses of
126 individual strain dynamics (e.g., RSV A vs B) and a joint analysis of total infections
127 (e.g., total RSV infections) yield identical resilience estimates (Supplementary Fig-
128 ure S2, 3). This is expected because the dynamics of two strains (or two pathogens)
129 around the attractor in a coupled system are described by the same set of eigen-
130 values and eigenvectors, meaning that both strains should exhibit identical rates of
131 returns following a perturbation. Analogous to a single system, strong seasonal forc-
132 ing in transmission can cause the system to slow down through transient phenomena
133 (Supplementary Figure S4).

134 These observations indicate three possibilities. First, we can directly estimate the
135 empirical resilience of a host-pathogen system by measuring the rate at which the
136 system approaches an attractor, provided that we have a way to quantify the distance
137 from the attractor. The empirical approach to estimating pathogen resilience is
138 particularly convenient because it does not require us to know the true underlying
139 model; estimating the intrinsic resilience from fitting misspecified models can lead
140 to biased estimates (Supplementary Figure S5). Second, resilience estimates allow
141 us to make phenomenological predictions about the dynamics of a host-pathogen
142 system following a perturbation. Assuming that the distance from the attractor will
143 decrease exponentially over time, we can obtain a ballpark estimate for when the
144 system will reach an attractor; this prediction necessarily assumes that there won't
145 be permanent changes in pathogen dynamics (Figure 2F) or a long-term transient
146 phenomenon (Figure 2I). Finally, a change in the rate of an exponential decrease in
147 the distance from the attractor can provide information about whether the system
148 has reached an alternative attractor, or a ghost attractor, that is different from the
149 original, pre-pandemic attractor. These alternative attractors may reflect continued
150 perturbations from permanent changes in transmission patterns as well as changes in
151 immune landscapes. There will be periods of time when it is difficult to tell whether
152 pathogen dynamics are still diverging from its original attractor or have begun to
153 converge to an attractor; now that several years have passed since NPIs have been
154 lifted, we expect many respiratory pathogens to have had sufficient time to begin
155 returning to their post-NPI attractors.

156 **Inferring pathogen resilience from real data**

157 Based on these observations, we now lay out our approach to estimating pathogen
158 resilience from real data (Figure 3). We then test this approach against simulations
159 and apply it to real data.

160 So far, we focused on simple examples that assume a constant transmission re-
161 duction. However, in practice, the impact of NPIs on pathogen transmission is likely
162 more complex (Figure 3A), reflecting introduction and relaxation of various NPI
163 strategies. In some cases, strong NPIs can even lead to a local fadeout, requiring im-
164 migration from another location for epidemic re-emergence. These complexities can
165 lead to longer delays between the introduction of NPIs and pathogen re-emergence as
166 well as temporal variation in outbreak sizes (Figure 3B): in this example, continued
167 transmission reduction from NPIs limits the size of the first outbreak in 2021 fol-
168 lowing the emergence, allowing for a larger outbreak in 2022 when NPIs are further
169 relaxed.

170 Previously, we relied on the dynamics of susceptible and infected hosts to com-
171 pute the distance from the attractor (Figure 2), but information on susceptible hosts
172 is rarely available in practice. In addition, uncertainties in case counts due to obser-
173 vation error as well as multiannual cycles in the observed epidemic dynamics (e.g.,
174 adenovirus circulation patterns in Hong Kong and Korea) add challenges to defin-
175 ing pre-pandemic attractors, which limits our ability to measure the distance from
176 the attractor. To address these challenges, we can reconstruct an empirical attrac-
177 tor by utilizing Takens' theorem [14], which states that an attractor of a nonlinear
178 multidimensional system can be mapped onto a delayed embedding (Materials and
179 Methods). For example, we can use delayed logged values of pre-pandemic cases $C(t)$
180 (Figure 3C) to reconstruct the attractor:

$$\langle \log(C(t) + 1), \log(C(t - \tau) + 1), \dots, \log(C(t - (M - 1)\tau) + 1) \rangle, \quad (1)$$

181 where the delay τ and embedding dimension M are determined based on autocor-
182 relations and false nearest neighbors, respectively [17, 18]. We can then apply the
183 same delay and embedding dimensions to the entire time series to determine the
184 position on a multi-dimensional state space (Figure 3D), which allows us to mea-
185 sure the nearest neighbor distance between the current state of the system and the
186 empirical pre-pandemic attractor (Figure 3E). In theory, we can now quantify how
187 fast this distance decreases by fitting a linear regression on a log scale, where the
188 slope of the linear regression corresponds to pathogen resilience. However, resulting
189 estimates of pathogen resilience can be sensitive to choices about embedding delays
190 and dimensions; for example, using longer delays and higher dimensions tends to
191 smooth out temporal variations in the distance from the attractor (Supplementary
192 Figure S6).

193 Complex changes in the distance from the attractor suggest that estimating
194 pathogen resilience from linear regression will be particularly sensitive to our choice
195 of fitting windows for the regression (Figure 3E). Therefore, before we tried estimat-

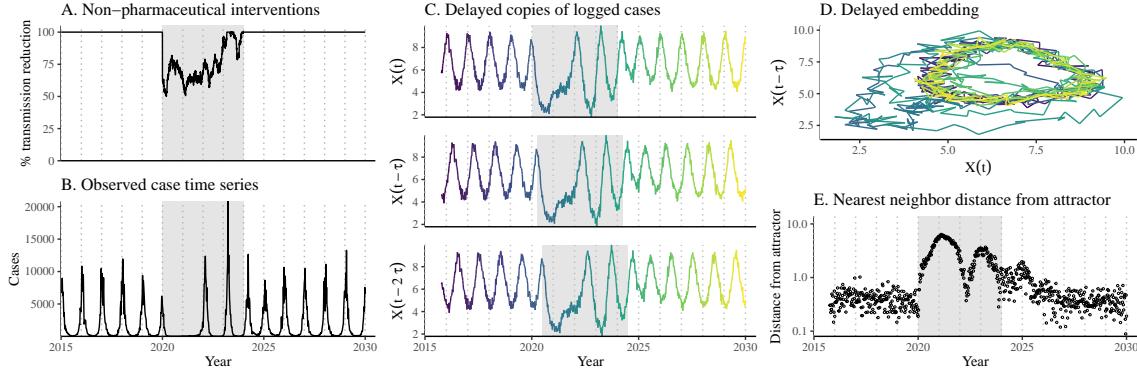


Figure 3: **A schematic diagram explaining the inference of pathogen resilience from synthetic data.** (A) A realistic example of simulated NPIs, represented by a relative reduction in transmission. (B) The impact of the synthetic NPI on epidemic dynamics simulated using a SIRS model with demographic stochasticity. (C) Generating delayed copies of the logged time series allows us to obtain an embedding. (D) Two dimensional representation of an embedding. (E) Delayed embedding allows us to calculate the nearest neighbor distance from the empirical attractor, which is determined based on the pre-pandemic time series. This distance time series can be used to infer pathogen resilience after choosing an appropriate window for linear regression.

ing resilience from real data, we explored an automated window selection criterion for linear regression and test it against randomized, stochastic simulations across a wide range of realistic NPI shape; in doing so, we also explored optimal choices for embedding dimensions and evaluated our choices for fitting window parameters and embedding dimensions by quantifying correlation coefficients between the estimated resilience and the intrinsic resilience of a seasonally unforced system (Materials and Methods). Overall, we find large variation in estimation performances with correlation coefficient ranging from 0.21 to 0.61 (Supplementary Figure S7). In almost all cases, the automated window selection approach outperformed a naive approach that uses the entire time series, starting from the peak distance (Supplementary Figure S7).

Based on the best performing window selection criteria and embedding dimension, we applied this approach to pathogen surveillance data presented in Figure 1 (Materials and Methods). For each time series, we applied Takens' theorem independently to reconstruct the empirical attractor and obtained the corresponding time series of distances from attractors (Supplementary Figure S8). Then, we use the automated window selection criterion to fit a linear regression and estimate the empirical resilience for each pathogen in each country (Supplementary Figure S8); the window selection criterion gave poor regression window for three cases (norovirus in Hong Kong and Korea and Rhinovirus/Enterovirus in the US), leading to unrealistically low resilience estimates, and so we used ad-hoc regression windows instead

217 (Supplementary Figure S9; Materials and Methods).

218 For all pathogens we consider, resilience estimates fall between 0.4/year and
219 1.8/year (Figure 4A). We estimate the mean resilience of common respiratory pathogens
220 to be 0.99/year (95% CI: 0.80/year–1.18/year). As a reference, this is \approx 7.5 times
221 higher than the intrinsic resilience of pre-vaccination measles in England and Wales
222 (\approx 0.13/year). Finally, resilience estimates for norovirus are comparable to those of
223 common respiratory pathogens: 1.44/year (95%CI: 1.01/year–1.87/year) for Hong
224 Kong and 1.07/year (95%CI: 0.86/year–1.29/year) for Korea. Based on a simple
225 ANOVA test, we do not find significant differences in resilience estimates across
226 countries ($p = 0.25$) or pathogens ($p = 0.68$).

227 [SWP: You suggested “I think we probably need to spell out a bit more that
228 long-term changes in the transmission rate (or some other parameter) mean the at-
229 tractor is permanently different and the distance should remain nonzero” and I think
230 we’ve done that enough early on with current revisions so I don’t feel like we need
231 to do it again here. Let me know what you think.] Using resilience estimates, we
232 now predict when each pathogen would hypothetically return to their pre-pandemic
233 dynamics, assuming no long-term change in the attractor. Specifically, we extend
234 our linear regression fits to distance-from-attractor time series and ask when the pre-
235 dicted regression line will cross a threshold value; since we relied on nearest neighbor
236 distances, pre-pandemic distances are always greater than zero (Figure 3E), meaning
237 that we can use the mean of pre-pandemic distances as our threshold. We predict
238 that a return to pre-pandemic cycles would be imminent for most pathogens (Figure
239 4B). We also predict that many pathogens should have already returned to their pre-
240 pandemic dynamics by the end of 2024, but these predictions contradict some of the
241 observed pathogen dynamics. For example, we predict that both human metapneu-
242 movirus and RSV in Korea should have returned to their attractors by now, but the
243 magnitude and timing of recent epidemics are different from pre-pandemic patterns
244 (Figure 1). These observations suggest the possibility that some common respiratory
245 pathogens may have converged to different attractors.

246 In Supplementary Materials, we also consider using a lower threshold for the false
247 nearest neighbor approach when determining the embedding dimension; this gives a
248 higher embedding dimension. As explained earlier (Supplementary Figure S6), this
249 gives a smoother distance-from-attractor time series (compare Supplementary Figure
250 S10 with S8); this also requires us to use longer time series, which prevents us from
251 estimating resilience for some pathogens. Overall, resulting estimates of pathogen
252 resilience with higher embedding dimensions still mostly fall between 0.3/year and
253 2.1/year (Supplementary Figure S11). A direct comparison between two approaches
254 (i.e., original estimate vs using higher dimensions) shows a strong consistency in
255 resilience estimates (Supplementary Figure S12).

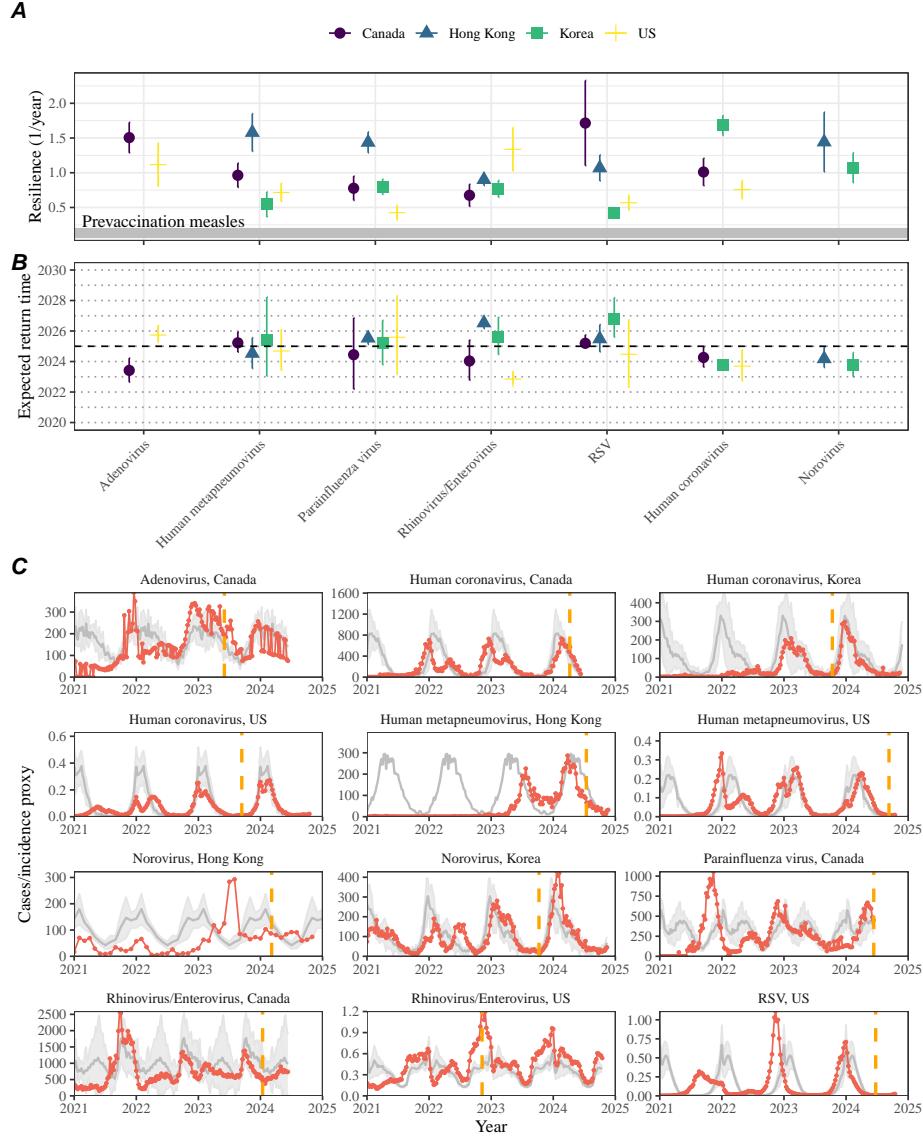


Figure 4: Summary of resilience estimates and predictions for return time. (A) Estimated pathogen resilience. The gray horizontal line represents the intrinsic resilience of pre-vaccination measles dynamics. (B) Predicted timing of when each pathogen will return to their pre-pandemic cycles. The dashed line in panel B indicates the end of 2024 (current observation time). Error bars represent 95% confidence intervals. (C) Observed dynamics for pathogen that are predicted to have returned before the end of 2024. Red points and lines represent data before 2020. Gray lines and shaded regions represent the mean seasonal patterns and corresponding 95% confidence intervals around the mean, previously shown in Figure 1. Orange vertical lines represent the predicted timing of return.

256 **Susceptible host dynamics explain variation in pathogen
257 resilience**

258 So far, we focused on quantifying pathogen resilience from the observed patterns of
259 pathogen re-emergence following NPIs. But what factors determine how resilient a
260 host-pathogen system is? Here, we use the SIRS model to show that susceptible host
261 dynamics are the key determinants of pathogen resilience. To do so, we vary the
262 basic reproduction number \mathcal{R}_0 , which represents the average number of secondary
263 infections caused by a newly infected individual in a fully susceptible population,
264 and the duration of immunity and compute intrinsic resilience for each parameter.

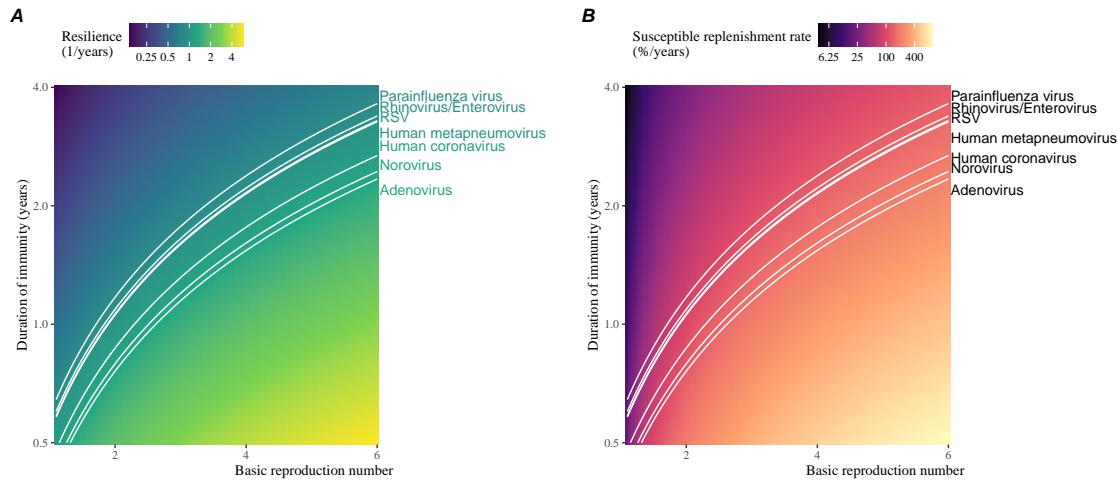


Figure 5: **Linking pathogen resilience to epidemiological parameters and susceptible host dynamics.** (A) The heat map represents intrinsic resilience as a function of the basic reproduction number \mathcal{R}_0 and the duration of immunity. (B) The heat map represents per-capita susceptible replenishment rate as a function of the basic reproduction number \mathcal{R}_0 and the duration of immunity. The standard SIRS model is used to compute intrinsic resilience and per-capita susceptible replenishment rate. Lines correspond to a set of parameters that are consistent with mean resilience estimates for each pathogen. Pathogens are ranked based on their mean resilience estimates, averaged across different countries.

265 We find an increase in \mathcal{R}_0 and a decrease in duration of immunity correspond
266 to an increase in pathogen resilience (Figure 5A). These variations can be under-
267 stood in terms of the susceptible host dynamics, where faster per-capita susceptible
268 replenishment rate causes the system to be more resilient (Figure 5B). This rate can
269 be expressed as a ratio between absolute rate at which new susceptibles enter the
270 population and the equilibrium number of susceptible individuals in the population,
271 \bar{S} . Therefore, both higher \mathcal{R}_0 and shorter duration of immunity can drive faster
272 per-capita susceptible replenishment rate (Figure 5B), especially because higher \mathcal{R}_0

273 leads to lower \bar{S} .

274 Finally, we can rank different pathogens based on the average values of empirical
275 resilience computed previously, which allows us to determine a set of parameters that
276 are consistent with the estimated resilience (Figure 5A). Across all pathogens we
277 consider, except for bocavirus and norovirus, we estimate that the average duration
278 of immunity is likely to be short (< 6 years) across a plausible range of \mathcal{R}_0 . These
279 rankings further allow us to map each pathogen onto a set of SIRS parameters that
280 are consistent with its empirical resilience (Figure 5A) and obtain a plausible range
281 of susceptible replenishment rates for each pathogen (Figure 5B). However, we note
282 that there is no one-to-one correspondence between susceptible replenishment rates
283 and pathogen resilience, leading to a wide uncertainty in the estimates for susceptible
284 replenishment rates (Figure 5B).

285 **Pathogen resilience determines sensitivity to stochastic perturbations**

287 **Discussion**

288 The pandemic NPIs have caused major disruptions to circulation patterns of both
289 respiratory and non-respiratory pathogens, adding challenges to predicting their future
290 dynamics [1, 2, 3, 4]. However, these NPIs offer large-scale natural experiments
291 for understanding how different pathogens respond to perturbations. In this study,
292 we show that pathogen re-emergence patterns following NPIs can be characterized
293 through the lens of ecological resilience. We show that variation in pathogen resilience
294 can be explained by the differences in susceptible host dynamics, where faster replenish-
295 ment of the susceptible pool corresponds to a more resilient host-pathogen system.
296 Finally, we show that pathogen resilience also determines the sensitivity to stochastic
297 perturbations, which in turn determines the persistence of a host-pathogen system.

298 Traditionally, ecological resilience measures how fast a system returns to a reference
299 state following a perturbation [10, 11, 12, 13]. In the context of respiratory
300 pathogens, resilience measures how fast epidemics return to their endemic cycles
301 after NPIs are lifted.

302 We use an attractor reconstruction approach to quantify how distance from the
303 attractor changes over time for each pathogen [14]. We show that the resilience of
304 a host-pathogen system can be estimated by fitting a linear regression to a logged
305 distance-from-attractor time series. Overall, we estimate that the resilience for most
306 common respiratory pathogens ranges between 0.4/year and 1.8/year, which is 3–14
307 times more resilient than prevaccination measles, indicating potential challenges in
308 controlling common respiratory pathogens.

309 Our framework allows us to make phenomenological predictions about when each
310 pathogen will return to their endemic cycles. The ability to predict future epidemic
311 patterns from resilience estimates offers a new paradigm for epidemic forecasting.

312 While this approach cannot predict the exact timing of outbreaks or epidemic pat-
313 terns, it is nonetheless useful for predicting when epidemics will settle down to regular
314 cycles after a large perturbation, such as pandemic NPIs.

315 Our analyses suggest a possibility that several pathogens may have converged
316 to different endemic cycles compared to their pre-pandemic epidemic patterns. Key
317 examples include human metapnuemovirus, RSV, and bocavirus in Korea as well as
318 RSV in Hong Kong. These changes may reflect changes in surveillance or actual shift
319 in the dynamics, caused by permanent changes in behavior or population-level immu-
320 nity. While it seems unlikely that permanent changes in behavior would only affect a
321 few pathogens and not others, we cannot rule out this possibility given heterogeneity
322 in the age of infection across different respiratory pathogens [SWP: CITE]. A shift
323 in population-level immunity is plausible, as the emergence of SARS-CoV-2 and ex-
324 tinction of influenza B/Yamagata likely caused major changes in immune landscapes;
325 interactions among co-circulating pathogens, such as cross immunity between RSV
326 and HMPV [19], may have also contributed to changes in population-level immu-
327 nity. However, we currently do not know how immunity, or lack thereof, from these
328 pathogens would affect infection from other pathogens. Future studies should use
329 detailed mechanistic models, coupled with behavioral and immunological data, to
330 test these hypotheses and better understand post-pandemic dynamics of endemic
331 pathogens.

332 We show that susceptible host dynamics shape pathogen resilience, where faster
333 replenishment of the susceptible population causes the pathogen to be more resilient.
334 For simplicity, we focus on waning immunity and birth as the main drivers of the
335 susceptible host dynamics but other mechanisms can also contribute to the replen-
336 ishment of the susceptible population. In particular, pathogen evolution, especially
337 the emergence of antigenically novel strains, can cause effective waning of immunity
338 in the population; therefore, we hypothesize that faster rates of antigenic evolution
339 can also cause a pathogen to be more resilient. Future studies should explore the
340 relationship between the rate of evolution and resilience for antigenically evolving
341 pathogens.

342 Quantifying pathogen resilience also offers novel approaches to validating population-
343 level epidemiological models. So far, most of model validation in infectious disease
344 ecology is based on the ability of a model to reproduce the observed epidemic dy-
345 namics and to predict future dynamics [20, 19, 21, 22, 23]. However, many models
346 can perform similarly under these criteria. For example, two major RSV models
347 have been proposed to explain biennial epidemic patterns: (1) a stage- and age-
348 structured model that allows disease severity to vary with number of past infections
349 and age of infection [21] and (2) a pathogen-interaction model that accounts for cross
350 immunity between RSV and human metapnuemovirus [19]. Since both models can
351 accurately reproduce the observed epidemic patterns, standard criteria for model
352 validation do not allow us to distinguish between these two models from population-
353 level data alone. Instead, it would be possible to measure the empirical resilience of
354 each model by simulating various perturbations and compare them to estimates of

355 empirical resilience from data, using pandemic NPIs as an opportunity.

356 There are several limitations to our work. First, we did not extensively explore
357 other approaches to reconstructing the attractor. Recent studies showed that more
358 sophisticated approaches, such as using non-uniform embedding, can provide more
359 robust reconstruction for noisy data [18]. In the context of causal inference, choices
360 about embedding can have major impact on the resulting inference [24]. Our re-
361 silience estimates are likely overly confident given a lack of uncertainties in attractor
362 reconstruction as well as the simplicity of our statistical framework. Short pre-
363 pandemic time series also contribute to the crudeness of our estimates. Nonetheless,
364 as illustrated in our sensitivity analyses (Supplementary Figure S6, S10–S12), infer-
365 ences about pathogen resilience in our SIRS model appear to be robust to decisions
366 about embedding lags and dimensions—this is because tracking the rate at which
367 the system approaches the attractor is likely a much simpler problem than making
368 inferences about causal directionality. Our qualitative prediction that common res-
369 piratory pathogens are more resilient than prevaccination measles is also likely to be
370 robust to these predictions, given how rapid many respiratory pathogens returned to
371 their original cycles following pandemic NPIs.

372 Predicting the impact of anthropogenic changes on infectious disease dynamics
373 is a fundamental aim of infectious disease research in a rapidly changing world. Our
374 study illustrates that quantifying pathogen resilience can help us understand how
375 infectious disease pathogens respond to major perturbations caused by NPIs. More
376 broadly, a detailed understanding of the determinants of pathogen resilience may
377 offer unique insights into pathogen persistence and controllability.

378 Materials and Methods

379 Data

380 We gathered time series on respiratory infections from Canada, Hong Kong, Korea,
381 and United States (US). As a reference, we also included time series data on norovirus
382 infections for available countries—in contrast to respiratory pathogens, we expect
383 gastrointestinal viruses, such as norovirus, to be differently affected by pandemic
384 NPIs. For all time series, we rounded every year to 52 weeks by taking the average
385 number of cases and tests between the 52nd and 53rd week. We also rescale all time
386 series to account for changes in testing patterns, which are then used for the actual
387 analysis.

388 Weekly time series of respiratory infection cases in Canada comes from the Res-
389piratory Virus Detection Surveillance System, which collect data from select labo-
390ratories across Canada. We extracted the data from <https://www.canada.ca/en/public-health/services/surveillance/respiratory-virus-detections-canada.html>. To account for an increase in testing from 2013 to 2024, we calculate a 2 year
391 moving average for the number of tests for each pathogen, which we use as a proxy
392 for testing effort. Then, we divide the smoothed testing patterns by the smoothed
393

395 value at the final week such that the testing effort has a maximum of 1. We then
396 divide weekly cases by the testing effort to obtain a scaled case time series. A similar
397 approach was used earlier for the analysis of RSV time series in the US [21].

398 Weekly time series of respiratory infection cases in Hong Kong comes from the
399 Centre for Health Protection, Department of Health. We extract the data from
400 <https://www.chp.gov.hk/en/statistics/data/10/641/642/2274.html>. We also
401 apply the same scaling procedure to the time series as we did for Canada. For Hong
402 Kong, we only adjust for testing efforts up to the end of 2019 because there was a
403 major reduction in testing for common respiratory pathogens since 2020.

404 Weekly time series of acute respiratory infection cases in Korea comes from Ko-
405 rea Disease Control and Prevention Agency. We extract the data from <https://dportal.kdca.go.kr/pot/is/st/ari.do>. While we do not have information on
406 testing, the reported number of respiratory infections consistently increased from
407 2013 to the end of 2019, which we interpreted as changes in testing patterns. Since
408 we do not have testing numbers, we used the weekly sum of all acute respiratory vi-
409 ral infection cases as a proxy for testing, which were further smoothed with moving
410 averaged and scaled to have a maximum of 1. For Korea, we also only adjust for
411 testing efforts up to the end of 2019.

412 Finally, weekly time series of respiratory infection cases in the US comes from
413 the National Respiratory and Enteric Virus Surveillance System. In the US, there
414 has been a large increase in testing against some respiratory pathogens, especially
415 RSV, which could not be corrected for through simple scaling. Instead, we derive an
416 incidence proxy by multiplying the test positivity with influenza-like illness positivity,
417 which is taken from <https://gis.cdc.gov/grasp/fluview/fluportaldashboard.html>. This method of estimating an incidence proxy has been recently applied in
418 the analysis of seasonal coronaviruses [7] and *Mycoplasma pneumoniae* infections [4].
419 Detailed assumptions and justifications are provided in [25].

422 Estimating pathogen resilience

423 In order to measure pathogen resilience from surveillance data, we first reconstruct
424 the empirical pre-pandemic attractor of the system using Takens' embedding theorem
425 [14]. Specifically, for a given pathogen, we take the pre-pandemic (before 2020)
426 case time series $C(t)$ and reconstruct the attractor using delayed embedding with a
427 uniform delay of τ and dimension M :

$$X_{\tau,m}(t) = \langle \log(C(t) + 1), \log(C(t - \tau) + 1), \dots, \log(C(t - (M - 1)\tau) + 1) \rangle. \quad (2)$$

428 Here, the delay τ is determined by calculating the autocorrelation of the logged pre-
429 pandemic time series and asking when the autocorrelation crosses 0 for the first time
430 [18]; a typical delay for an annual outbreak is around 13 weeks.

431 Then, for a given delay τ , we determine the embedding dimension M using the
432 false nearest neighbors approach [17, 18]. To do so, we start with an embedding
433 dimension e and construct a set of points $A_{\tau,e} = \{X_{\tau,e}(t) | t < 2020\}$. Then, for

434 each point $X_{\tau,e}(t)$, we determine the nearest neighbor from the set $A_{\tau,e}$, which we
 435 denote $X_{\tau,e}(t_{nn})$ for $t \neq t_{nn}$. Then, if the distance between these two points on
 436 $e+1$ dimension, $D_{\tau,e+1}(t) = \|X_{\tau,e+1}(t_{nn}) - X_{\tau,e+1}(t)\|_2$, is larger than their distance
 437 on e dimension, $D_{\tau,e}(t) = \|X_{\tau,e}(t_{nn}) - X_{\tau,e}(t)\|_2$, these two points are deemed to
 438 be false nearest neighbors; specifically, we use a threshold R for the ratio between
 439 two distances $D_{\tau,e+1}(t)/D_{\tau,e}(t)$ to determine false nearest neighbors. In the main
 440 text, we determine the embedding dimension based on the first dimension without
 441 any false nearest neighbors for $R = 10$. In Supplementary Materials, we impose
 442 $R = 5$ to select for higher dimensions. Once we determine the embedding lag τ
 443 and dimension M , we apply the embedding to the entire time series and calculate
 444 the nearest neighbor distance against the attractor $A_{\tau,M}$ to obtain a time series of
 445 distance from the attractor $D_{\tau,M}(t)$.

446 From a time series of distances from the attractor, we estimate pathogen resilience
 447 by fitting a linear regression to an appropriate window. To automatically select
 448 the fitting window, we begin by smoothing the distance time series using locally
 449 estimated scatterplot smoothing (LOESS) to obtain $\hat{D}_{\tau,M}(t)$, where the smoothing
 450 is performed on a log scale and exponentiated afterwards. Then, we determine
 451 threshold values (T_{start} and T_{end}) for the smoothed distances and choose the fitting
 452 window based on when $\hat{D}_{\tau,M}(t)$ crosses these threshold values for the first time.
 453 These thresholds are determined by first calculating maximum distance,

$$\max \hat{D} = \max \hat{D}_{\tau,M}(t), \quad (3)$$

454 and mean pre-pandemic distance,

$$\hat{D}_{\text{mean}} = \frac{1}{N_{t < 2020}} \sum_{t < 2020} \hat{D}_{\tau,M}(t), \quad (4)$$

455 as a reference, and then dividing their ratios into 10 equal bins:

$$T_{\text{start}} = \hat{D}_{\text{mean}} \times \left(\frac{\max \hat{D}}{\hat{D}_{\text{mean}}} \right)^{9/10} \quad (5)$$

$$T_{\text{end}} = \hat{D}_{\text{mean}} \times \left(\frac{\max \hat{D}}{\hat{D}_{\text{mean}}} \right)^{1/10} \quad (6)$$

456 This allows us to discard the initial period during which the distance increases (from
 457 the introduction of intervention measures) and the final period during which the
 458 distance plateaus (as the system reaches an attractor). The fitting window is deter-
 459 mined based on when the smoothed distance $\hat{D}_{\tau,M}(t)$ crosses these threshold values
 460 for the first time; then, we fit a linear regression to logged (unsmoothed) distances
 461 $\log D_{\tau,M}(t)$ using that window.

462 **Mathematical modeling**

463 Throughout the paper, we use a series of mathematical models to illustrate the con-
 464 cept of pathogen resilience and to understand the determinants of pathogen resilience.
 465 In general, the intrinsic resilience for a given system is given by the largest real part
 466 of the eigenvalues of the linearized system at endemic equilibrium. Here, we focus on
 467 the SIRS model with demography and present the details of other models in Supple-
 468 mentary Materials. The SIRS (Susceptible-Infected-Recovered-Susceptible) model is
 469 the simplest model that allows for waning of immunity, where recovered (immune)
 470 individuals are assumed to become fully susceptible after an average of $1/\delta$ time pe-
 471 riod. The dynamics of the SIRS model is described by the following set of differential
 472 equations:

$$\frac{dS}{dt} = \mu - \beta(t)SI - \mu S + \delta R \quad (7)$$

$$\frac{dI}{dt} = \beta(t)SI - (\gamma + \mu)I \quad (8)$$

$$\frac{dR}{dt} = \gamma I - (\delta + \mu)R \quad (9)$$

$$(10)$$

473 where μ represents the birth/death rate, $\beta(t)$ represents the time-varying trans-
 474 mission rate, and γ represents the recovery rate. The basic reproduction number
 475 $\mathcal{R}_0(t) = \beta(t)/(\gamma + \mu)$ is defined as the average number of secondary infections that
 476 a single infected individual would cause in a fully susceptible population at time t
 477 and measures the intrinsic transmissibility of a pathogen.

478 When we first introduce the idea of pathogen resilience (Figure 2), we impose
 479 sinusoidal changes to the transmission rate to account for seasonal transmission:

$$\beta(t) = b_1(1 + \theta \cos(2\pi(t - \phi)))\alpha(t), \quad (11)$$

480 where b_1 represents the baseline transmission rate, θ represents the seasonal am-
 481 plitude, and ϕ represents the seasonal offset term. Here, we also introduce an ex-
 482 tra multiplicative term $\alpha(t)$ to account for the impact of pandemic NPIs, where
 483 $\alpha(t) < 1$ indicates transmission reduction. Figure 2A and 2B are generated assum-
 484 ing $b_1 = 3 \times (365/7 + 1/50)/\text{years}$, $\theta = 0.2$, $\phi = 0$, $\mu = 1/50/\text{years}$, $\gamma = 365/7/\text{years}$,
 485 and $\delta = 1/2/\text{years}$. In Figure 2A, we impose a 50% transmission reduction for 6
 486 months from 2020:

$$\alpha(t) = \begin{cases} 0.5 & 2020 \leq t < 2020.5 \\ 1 & \text{otherwise} \end{cases} \quad (12)$$

487 In Figure 2B, we impose a 50% transmission reduction for 6 months from 2020 and
 488 a permanent 10% reduction onward:

$$\alpha(t) = \begin{cases} 1 & t < 2020 \\ 0.5 & 2020 \leq t < 2020.5 \\ 0.9 & 2020.5 \leq t \end{cases} \quad (13)$$

489 In both scenarios, we simulate the SIRS model from the following initial conditions
490 ($S(0) = 1/\mathcal{R}_0$, $I(0) = 1 \times 10^{-6}$, and $R(0) = 1 - S(0) - I(0)$) from 1900 until 2030.

491 To measure the empirical resilience of the SIR model (Figure 2C and 2F), we
492 compute the normalized distance between post-intervention susceptible and logged
493 infected proportions and their corresponding pre-intervention values at the same time
494 of year:

$$\sqrt{\left(\frac{S(t) - S_{\text{pre}}(t)}{\sigma_S}\right)^2 + \left(\frac{\log I(t) - \log I_{\text{pre}}(t)}{\sigma_{\log I}}\right)^2}, \quad (14)$$

495 where σ_S and $\sigma_{\log I}$ represent the standard deviation in the pre-intervention suscep-
496 tible and logged infected proportions. We normalize the differences in susceptible
497 and logged infected proportions to allow both quantities to equally contribute to the
498 changes in distance from the attractor. We used logged prevalence, instead of abso-
499 lute prevalence, in order to capture epidemic dynamics in deep troughs during the
500 intervention period. In Supplementary Materials, we also compare how the degree
501 of seasonal transmission affects empirical resilience by varying θ from 0 to 0.4; when
502 we assume no seasonality ($\theta = 0$), we do not normalize the distance because the
503 standard deviation of pre-intervention dynamics are zero.

504 Finally, we use the SIRS model to understand how underlying epidemiological
505 parameters affect pathogen resilience and link this relationship to underlying sus-
506 ceptible host dynamics. For the simple SIRS model without seasonal transmission
507 ($\theta = 0$), the intrinsic resilience corresponds to

$$-\frac{\text{Re}(\lambda)}{2} = \frac{\delta + \beta I^* + \mu}{2}. \quad (15)$$

508 Here, I^* represents the prevalence at endemic equilibrium:

$$I^* = \frac{(\delta + \mu)(\beta - (\gamma + \mu))}{\beta(\delta + \gamma + \mu)}. \quad (16)$$

509 The susceptible replenishment rate is given by

$$S_{\text{replenish}} = \frac{\mu + \delta R}{S^*}, \quad (17)$$

510 where $S^* = 1/\mathcal{R}_0$ represents the equilibrium proportion of susceptible individuals.
511 We vary the basic reproduction number \mathcal{R}_0 between 1.1 to 6 and the average duration
512 of immunity $1/\delta$ between 2 to 80 years, and compute these two quantities. In doing
513 so, we fix all other parameters: $\mu = 1/80/\text{years}$ and $\gamma = 365/7/\text{years}$.

514 Data availability

515 Funding

516 **Supplementary Text**

517 **Resilience of a stage-structured system.**

518 In Figure 2G–I, we use a more realistic, stage-structured model to illustrate how
 519 transient phenomena can cause the system to slow down. Specifically, we use the
 520 stage-structured RSV model proposed by [21], which assumes that subsequent rein-
 521 fections cause an individual to become less susceptible and transmissible than previ-
 522 ous infections. The model dynamics can be described as follows:

$$\frac{dM}{dt} = \mu - (\omega + \mu)M \quad (S1)$$

$$\frac{dS_0}{dt} = \omega M - (\lambda(t) + \mu)S_0 \quad (S2)$$

$$\frac{dI_1}{dt} = \lambda(t)S_0 - (\gamma_1 + \mu)I_1 \quad (S3)$$

$$\frac{dS_1}{dt} = \gamma_1 I_1 - (\sigma_1 \lambda(t) + \mu)S_1 \quad (S4)$$

$$\frac{dI_2}{dt} = \sigma_1 \lambda(t)S_1 - (\gamma_2 + \mu)I_2 \quad (S5)$$

$$\frac{dS_2}{dt} = \gamma_2 I_2 - (\sigma_2 \lambda(t) + \mu)S_2 \quad (S6)$$

$$\frac{dI_3}{dt} = \sigma_2 \lambda(t)S_2 - (\gamma_3 + \mu)I_3 \quad (S7)$$

$$\frac{dS_3}{dt} = \gamma_3 I_3 - (\sigma_3 \lambda(t) + \mu)S_3 + \gamma_4 I_4 \quad (S8)$$

$$\frac{dI_4}{dt} = \sigma_3 \lambda(t)S_3 - (\gamma_4 + \mu)I_4 \quad (S9)$$

(S10)

523 where M represents the proportion of individuals who are maternally immune; S_i
 524 represents the proportion of individuals who are susceptible after i prior infections; I_i
 525 represents the proportion of individuals who are currently (re)-infected with their i -th
 526 infection; μ represents the birth and death rates; $1/\omega$ represents the mean duration
 527 of maternal immunity; $1/\gamma_i$ represents the mean duration of infection; $\lambda(t)$ represents
 528 the force of infection; and σ_i represents the reduction in susceptibility for the i -th
 529 reinfection. The force of infection is modeled using a sinusoidal function:

$$\beta(t) = b_1(1 + \theta \cos(2\pi(t - \phi)))\alpha(t) \quad (S11)$$

$$\lambda(t) = \beta(I_1 + \rho_1 I_2 + \rho_2(I_3 + I_4)), \quad (S12)$$

530 where b_1 represents the baseline transmission rate; θ represents the seasonal ampli-
 531 tude; ϕ represents the seasonal offset term; $\alpha(t)$ represents the intervention effect;
 532 and ρ_i represents the impact of immunity on transmission reduction. We use the

533 following parameters to simulate the impact of interventions on epidemic dynam-
 534 ics [21]: $b_1 = 9 \times (365/10 + 1/80)/\text{years}$, $\theta = 0.2$, $\phi = -0.1$, $\omega = 365/112/\text{years}$,
 535 $\gamma_1 = 365/10/\text{years}$, $\gamma_2 = 365/7/\text{years}$, $\gamma_3 = 365/5/\text{years}$, $\sigma_1 = 0.76$, $\sigma_2 = 0.6$,
 536 $\sigma_3 = 0.4$, $\rho_1 = 0.75$, $\rho_2 = 0.51$, and $\mu = 1/80/\text{years}$. We assume a 50% transmission
 537 reduction for 6 months from 2020:

$$\alpha(t) = \begin{cases} 0.5 & 2020 \leq t < 2020.5 \\ 1 & \text{otherwise} \end{cases} \quad (\text{S13})$$

538 The model is simulated from 1900 to 2030 using the following initial conditions:
 539 $M = 0$, $S_0 = 1/\mathcal{R}_0 - I_1$, $I_1 = 1 \times 10^{-6}$, $S_1 = 1 - 1/\mathcal{R}_0$, $I_2 = 0$, $S_2 = 0$, $I_3 = 0$,
 540 $S_3 = 0$, and $I_4 = 0$. For the phase plane analysis (Figure 2H) and distance analysis
 541 (Figure 2I), we rely on the average susceptibility,

$$\bar{S} = S_0 + \sigma_1 S_1 + \sigma_2 S_2 + \sigma_3 S_3, \quad (\text{S14})$$

542 and total prevalence,

$$I_{\text{total}} = I_1 + I_2 + I_3 + I_4. \quad (\text{S15})$$

543 These quantities are used to compute the normalized distance from the attractor, as
 544 described in the main text.

545 Resilience of a multistrain system.

546 We use a simple two-strain model to show that a multistrain host-pathogen system
 547 that is coupled through cross immunity can be described by a single resilience value.
 548 The model dynamics can be described as follows [19]:

$$\frac{dS}{dt} = \mu - \mu S - (\lambda_1 + \lambda_2)S + \rho_1 R_1 + \rho_2 R_2 \quad (\text{S16})$$

$$\frac{dI_1}{dt} = \lambda_1 S - (\gamma_1 + \mu)I_1 \quad (\text{S17})$$

$$\frac{dI_2}{dt} = \lambda_2 S - (\gamma_2 + \mu)I_2 \quad (\text{S18})$$

$$\frac{dR_1}{dt} = \gamma_1 I_1 - \lambda_2 \epsilon_{21} R_1 - \rho_1 R_1 + \rho_2 R - \mu R_1 \quad (\text{S19})$$

$$\frac{dR_2}{dt} = \gamma_2 I_2 - \lambda_1 \epsilon_{12} R_2 - \rho_2 R_2 + \rho_1 R - \mu R_2 \quad (\text{S20})$$

$$\frac{dJ_1}{dt} = \lambda_1 \epsilon_{12} R_2 - (\gamma_1 + \mu)J_1 \quad (\text{S21})$$

$$\frac{dJ_2}{dt} = \lambda_2 \epsilon_{21} R_1 - (\gamma_2 + \mu)J_2 \quad (\text{S22})$$

$$\frac{dR}{dt} = \gamma_1 J_1 + \gamma_2 J_2 - \rho_1 R - \rho_2 R - \mu R \quad (\text{S23})$$

549 where S represents the proportion of individuals who are fully susceptible to infections
 550 by both strains; I_1 represents the proportion of individuals who are infected
 551 with strain 1 without prior immunity; I_2 represents the proportion of individuals who
 552 are infected with strain 2 without prior immunity; R_1 represents the proportion of
 553 individuals who are fully immune against strain 1 and partially susceptible to rein-
 554 fection by strain 2; R_2 represents the proportion of individuals who are fully immune
 555 against strain 2 and partially susceptible to reinfection by strain 1; J_1 represents the
 556 proportion of individuals who are infected with strain 1 with prior immunity against
 557 strain 2; J_2 represents the proportion of individuals who are infected with strain
 558 2 with prior immunity against strain 1; R represents the proportion of individuals
 559 who are immune to infections from both strains; μ represents the birth/death rate;
 560 λ_1 and λ_2 represent the force of infection from strains 1 and 2, respectively; ρ_1 and
 561 ρ_2 represent the waning immunity rate; γ_1 and γ_2 represent the recovery rate; ϵ_{21}
 562 and ϵ_{12} represent the susceptibility to reinfection with strains 2 and 1, respectively,
 563 given prior immunity from infection with strains 1 and 2, respectively. The force of
 564 infection is modeled as follows:

$$\beta_1 = b_1(1 + \theta_1 \sin(2\pi(t - \phi_1)))\alpha(t) \quad (\text{S24})$$

$$\beta_2 = b_2(1 + \theta_2 \sin(2\pi(t - \phi_2)))\alpha(t) \quad (\text{S25})$$

$$\lambda_1 = \beta_1(I_1 + J_1) \quad (\text{S26})$$

$$\lambda_2 = \beta_2(I_2 + J_2) \quad (\text{S27})$$

565 In Supplementary Figures S2–S4, we assume the following parameters: $b_1 = 2 \times$
 566 52/years, $b_2 = 4 \times 52/\text{years}$, $\phi_1 = \phi_2 = 0$, $\epsilon_{12} = 0.9$, $\epsilon_{21} = 0.5$, $\gamma_1 = \gamma_2 = 52/\text{years}$,
 567 $\rho_1 = \rho_2 = 1/\text{years}$, and $\mu = 1/70/\text{years}$. For all simulations, we assume a 50%
 568 transmission reduction for 6 months from 2020:

$$\alpha(t) = \begin{cases} 0.5 & 2020 \leq t < 2020.5 \\ 1 & \text{otherwise} \end{cases} \quad (\text{S28})$$

569 The seasonal amplitude θ is varied from 0 to 0.4. All simulations were ran from 1900
 570 to 2030 with following initial conditions: $S(0) = 1 - 2 \times 10^{-6}$, $I_1(0) = 1 \times 10^{-6}$,
 571 $I_2(0) = 1 \times 10^{-6}$, $R_1(0) = 0$, $R_2(0) = 0$, $J_1(0) = 0$, $J_2(0) = 0$, and $R(0) = 0$.

572 We consider three scenarios for measuring pathogen resilience: (1) we only have
 573 information about strain 1, (2) we only have information about strain 2, and (3)
 574 we are unable to distinguish between strains. In the first two scenarios (see panels
 575 A–C for strain 1 and panels D–F for strain 2), we consider the dynamics of average
 576 susceptibility for each strain and total prevalence:

$$\bar{S}_1 = S + \epsilon_{12}R_2 \quad (\text{S29})$$

$$\hat{I}_1 = I_1 + J_1 \quad (\text{S30})$$

$$\bar{S}_2 = S + \epsilon_{21}R_1 \quad (\text{S31})$$

$$\hat{I}_2 = I_2 + J_2 \quad (\text{S32})$$

577 In the third scenario (panels G–I), we consider the dynamics of total susceptible and
578 infected populations:

$$\hat{S} = S + R_2 + R_1 \quad (\text{S33})$$

$$\hat{I} = I_1 + J_1 + I_2 + J_2 \quad (\text{S34})$$

579 These quantities are used to compute the normalized distance from the attractor, as
580 described in the main text.

581 Estimating intrinsic resilience using mechanistic model

582 We tested whether we can reliably estimate the intrinsic resilience of a system by fit-
583 ting a mechanistic model. Specifically, we simulated case time series from stochastic
584 SIRS and two-strain models and fitted a simple, deterministic SIRS model using a
585 Bayesian framework.

586 We simulated the models in discrete time, incorporating demographic stochastic-
587 ity:

$$\beta(t) = \mathcal{R}_0 \left(1 + \theta \cos \left(\frac{2\pi t}{364} \right) \right) \alpha(t)(1 - \exp(-\gamma)) \quad (\text{S35})$$

$$\text{FOI}(t) = \beta(t)I(t - \Delta t)/N \quad (\text{S36})$$

$$B(t) \sim \text{Poisson}(\mu N) \quad (\text{S37})$$

$$\Delta S(t) \sim \text{Binom}(S(t - \Delta t), 1 - \exp(-(\text{FOI}(t) + \mu)\Delta t)) \quad (\text{S38})$$

$$N_{SI}(t) \sim \text{Binom}\left(\Delta S(t), \frac{\text{FOI}(t)}{\text{FOI}(t) + \mu}\right) \quad (\text{S39})$$

$$\Delta I(t) \sim \text{Binom}(I(t - \Delta t), 1 - \exp(-(\gamma + \mu)\Delta t)) \quad (\text{S40})$$

$$N_{IR}(t) \sim \text{Binom}\left(\Delta I(t), \frac{\gamma}{\gamma + \mu}\right) \quad (\text{S41})$$

$$\Delta R(t) \sim \text{Binom}(R(t - \Delta t), 1 - \exp(-(\delta + \mu)\Delta t)) \quad (\text{S42})$$

$$N_{RS}(t) \sim \text{Binom}\left(\Delta R(t), \frac{\delta}{\delta + \mu}\right) \quad (\text{S43})$$

$$S(t) = S(t - \Delta t) + N_{RS}(t) + B(t) - \Delta S(t) \quad (\text{S44})$$

$$I(t) = I(t - \Delta t) + N_{SI}(t) - \Delta I(t) \quad (\text{S45})$$

$$R(t) = R(t - \Delta t) + N_{IR}(t) - \Delta R(t) \quad (\text{S46})$$

588 where FOI represent the force of infection; N_{ij} represent the number of individuals
589 moving from compartment i to j on a given day; and $B(t)$ represents the number
590 of new births. We simulate the model on a daily scale—assuming 364 days in a
591 year so that it can be evenly grouped into 52 weeks—with the following parameters:
592 $\mathcal{R}_0 = 3$, $\theta = 0.1$, $\gamma = 1/7/\text{days}$, $\delta = 1/(364 \times 2)/\text{days}$, $\mu = 1/(364 \times 50)/\text{days}$, and
593 $N = 1 \times 10^8$. The model is simulated from 1900 to 2030 assuming $S(0) = N/3$,

⁵⁹⁴ $I(0) = 100$, and $R(0) = N - S(0) - I(0)$. The observed incidence from the model is
⁵⁹⁵ then simulated as follows:

$$C(t) = \text{Beta-Binom}(N_{SI}(t), \rho, k), \quad (\text{S47})$$

⁵⁹⁶ where ρ represents the reporting probability and k represents the overdispersion pa-
⁵⁹⁷ rameter of beta-binomial distribution. Here, we use the beta-binomial distribution to
⁵⁹⁸ account for overdispersion in reporting. We assume $\rho = 0.002$ (i.e., 0.2% probability)
⁵⁹⁹ and $k = 1000$.

⁶⁰⁰ We used an analogous approach for the two-strain model:

$$\beta_1(t) = b_1 \left(1 + \theta_1 \cos \left(\frac{2\pi(t - \phi_1)}{364} \right) \right) \alpha(t) \quad (\text{S48})$$

$$\beta_2(t) = b_2 \left(1 + \theta_2 \cos \left(\frac{2\pi(t - \phi_2)}{364} \right) \right) \alpha(t) \quad (\text{S49})$$

$$\text{FOI}_1(t) = \beta_1(t)(I_1(t - \Delta t) + J_1(t - \Delta t))/N \quad (\text{S50})$$

$$\text{FOI}_2(t) = \beta_2(t)(I_2(t - \Delta t) + J_2(t - \Delta t))/N \quad (\text{S51})$$

$$B(t) \sim \text{Poisson}(\mu N) \quad (\text{S52})$$

$$\Delta S(t) \sim \text{Binom}(S(t - \Delta t), 1 - \exp(-(\text{FOI}_1(t) + \text{FOI}_2(t) + \mu)\Delta t)) \quad (\text{S53})$$

$$N_{SI_1}(t) \sim \text{Binom}\left(\Delta S(t), \frac{\text{FOI}_1(t)}{\text{FOI}_1(t) + \text{FOI}_2(t) + \mu}\right) \quad (\text{S54})$$

$$N_{SI_2}(t) \sim \text{Binom}\left(\Delta S(t), \frac{\text{FOI}_2(t)}{\text{FOI}_1(t) + \text{FOI}_2(t) + \mu}\right) \quad (\text{S55})$$

$$\Delta I_1(t) \sim \text{Binom}(I_1(t - \Delta t), 1 - \exp(-(\gamma_1 + \mu)\Delta t)) \quad (\text{S56})$$

$$N_{I_1 R_1}(t) \sim \text{Binom}\left(\Delta I_1(t), \frac{\gamma_1}{\gamma_1 + \mu}\right) \quad (\text{S57})$$

$$\Delta I_2(t) \sim \text{Binom}(I_2(t - \Delta t), 1 - \exp(-(\gamma_2 + \mu)\Delta t)) \quad (\text{S58})$$

$$N_{I_2 R_2}(t) \sim \text{Binom}\left(\Delta I_2(t), \frac{\gamma_2}{\gamma_2 + \mu}\right) \quad (\text{S59})$$

$$\Delta R_1(t) \sim \text{Binom}(R_1(t - \Delta t), 1 - \exp(-(\epsilon_{21}\text{FOI}_2(t) + \rho_1 + \mu)\Delta t)) \quad (\text{S60})$$

$$N_{R_1 S}(t) \sim \text{Binom}\left(\Delta R_1(t), \frac{\rho_1}{\epsilon_{21}\text{FOI}_2(t) + \rho_1 + \mu}\right) \quad (\text{S61})$$

$$N_{R_1 J_2}(t) \sim \text{Binom}\left(\Delta R_1(t), \frac{\epsilon_{21}\text{FOI}_2(t)}{\epsilon_{21}\text{FOI}_2(t) + \rho_1 + \mu}\right) \quad (\text{S62})$$

$$\Delta R_2(t) \sim \text{Binom}(R_2(t - \Delta t), 1 - \exp(-(\epsilon_{12}\text{FOI}_1(t) + \rho_2 + \mu)\Delta t)) \quad (\text{S63})$$

$$N_{R_2 S}(t) \sim \text{Binom}\left(\Delta R_2(t), \frac{\rho_2}{\epsilon_{12}\text{FOI}_1(t) + \rho_2 + \mu}\right) \quad (\text{S64})$$

$$N_{R_2 J_1}(t) \sim \text{Binom}\left(\Delta R_2(t), \frac{\epsilon_{12}\text{FOI}_1(t)}{\epsilon_{12}\text{FOI}_1(t) + \rho_2 + \mu}\right) \quad (\text{S65})$$

$$\Delta J_1(t) \sim \text{Binom}(J_1(t - \Delta t), 1 - \exp(-(\gamma_1 + \mu)\Delta t)) \quad (\text{S66})$$

$$N_{J_1R}(t) \sim \text{Binom}\left(\Delta J_1(t), \frac{\gamma_1}{\gamma_1 + \mu}\right) \quad (\text{S67})$$

$$\Delta J_2(t) \sim \text{Binom}(J_2(t - \Delta t), 1 - \exp(-(\gamma_2 + \mu)\Delta t)) \quad (\text{S68})$$

$$N_{J_2R}(t) \sim \text{Binom}\left(\Delta J_2(t), \frac{\gamma_2}{\gamma_2 + \mu}\right) \quad (\text{S69})$$

$$\Delta R(t) \sim \text{Binom}(R(t - \Delta t), 1 - \exp(-(\rho_1 + \rho_2 + \mu)\Delta t)) \quad (\text{S70})$$

$$N_{RR_1}(t) \sim \text{Binom}\left(\Delta R(t), \frac{\rho_1}{\rho_1 + \rho_2 + \mu}\right) \quad (\text{S71})$$

$$N_{RR_2}(t) \sim \text{Binom}\left(\Delta R(t), \frac{\rho_2}{\rho_1 + \rho_2 + \mu}\right) \quad (\text{S72})$$

$$S(t) = S(t - \Delta t) - \Delta S(t) + B(t) + N_{R_1S}(t) + N_{R_2S}(t) \quad (\text{S73})$$

$$I_1(t) = I_1(t - \Delta t) - \Delta I_1(t) + N_{SI_1}(t) \quad (\text{S74})$$

$$I_2(t) = I_2(t - \Delta t) - \Delta I_2(t) + N_{SI_2}(t) \quad (\text{S75})$$

$$R_1(t) = R_1(t - \Delta t) - \Delta R_1(t) + N_{I_1R_1}(t) + N_{RR_1}(t) \quad (\text{S76})$$

$$R_2(t) = R_2(t - \Delta t) - \Delta R_2(t) + N_{I_2R_2}(t) + N_{RR_2}(t) \quad (\text{S77})$$

$$J_1(t) = J_1(t - \Delta t) - \Delta J_1(t) + N_{R_2J_1}(t) \quad (\text{S78})$$

$$J_2(t) = J_2(t - \Delta t) - \Delta J_2(t) + N_{R_1J_2}(t) \quad (\text{S79})$$

$$R(t) = R(t - \Delta t) - \Delta R(t) + N_{J_1R}(t) + N_{J_2R}(t) \quad (\text{S80})$$

We simulate the model on a daily scale with previously estimated parameters for the RSV-HMPV interaction [19]: $b_1 = 1.7/\text{weeks}$, $b_2 = 1.95/\text{weeks}$, $\theta_1 = 0.4$, $\theta_2 = 0.3$, $\phi_1 = 0.005 \times 7/364$, $\phi_2 = 4.99 \times 7/364$, $\epsilon_{12} = 0.92$, $\epsilon_{21} = 0.45$, $\gamma_1 = 1/10/\text{days}$, $\gamma_2 = 1/10/\text{days}$, $\rho_1 = 1/364/\text{days}$, $\rho_2 = 1/364/\text{days}$, $\mu = 1/(70 \times 364)/\text{days}$, and $N = 1 \times 10^8$. The model is simulated from 1900 to 2030 assuming $S(0) = N - 200$, $I_1(0) = 100$, $I_2(0) = 100$, $R_1(0) = 0$, $R_2(0) = 0$, $J_1(0) = 0$, $J_2(0) = 0$, and $R(0) = 0$. The observed incidence for each strain is then simulated as follows:

$$C_1(t) = \text{Beta} - \text{Binom}(N_{SI_1}(t) + N_{R_2J_1}, \rho, k), \quad (\text{S81})$$

$$C_2(t) = \text{Beta} - \text{Binom}(N_{SI_2}(t) + N_{R_1J_2}, \rho, k), \quad (\text{S82})$$

where ρ represents the reporting probability and k represents the overdispersion parameter of beta-binomial distribution. We assume $\rho = 0.002$ (i.e., 0.2% probability) and $k = 500$. We also consider the total incidence: $C_{\text{total}}(t) = C_1(t) + C_2(t)$.

For both models, we consider a more realistic challenges in intervention effects $\alpha(t)$ to challenge our ability to estimate the intervention effects. Thus, we assume a 40% transmission reduction for 3 months from March 2020, followed by a 10% transmission reduction for 6 months, 20% transmission reduction for 3 months, and

615 a final return to normal levels:

$$\alpha(t) = \begin{cases} 1 & t < 2020.25 \\ 0.6 & 2020.25 \leq t < 2020.5 \\ 0.9 & 2020.5 \leq t < 2021 \\ 0.8 & 2021 \leq t < 2021.25 \\ 1 & 2021.25 \leq t \end{cases}. \quad (\text{S83})$$

616 For all simulations, we truncate the time series from the beginning of 2014 to the
617 end of 2023 and aggregate them into weekly cases.

618 To infer intrinsic resilience from time series, we fit a simple discrete time, deter-
619 ministic SIRS model [4]:

$$\Delta t = 1 \text{ week} \quad (\text{S84})$$

$$\text{FOI}(t) = \beta(t)(I(t - \Delta t) + \omega)/N \quad (\text{S85})$$

$$\Delta S(t) = [1 - \exp(-(\text{FOI}(t) + \mu)\Delta t)] S(t - \Delta t) \quad (\text{S86})$$

$$N_{SI}(t) = \frac{\text{FOI}(t)\Delta S(t)}{\text{FOI}(t) + \mu} \quad (\text{S87})$$

$$\Delta I(t) = [1 - \exp(-(\gamma + \mu)\Delta t)] I(t - \Delta t) \quad (\text{S88})$$

$$N_{IR}(t) = \frac{\gamma \Delta I(t)}{\gamma + \mu} \quad (\text{S89})$$

$$\Delta R(t) = [1 - \exp(-(\nu + \mu)\Delta t)] R(t - \Delta t) \quad (\text{S90})$$

$$N_{RS}(t) = \frac{\nu \Delta R(t)}{\nu + \mu} \quad (\text{S91})$$

$$S(t) = S(t - \Delta t) + \mu S - \Delta S(t) + N_{RS}(t) \quad (\text{S92})$$

$$I(t) = I(t - \Delta t) - \Delta I(t) + N_{SI}(t) \quad (\text{S93})$$

$$R(t) = R(t - \Delta t) - \Delta R(t) + N_{IR}(t) \quad (\text{S94})$$

620 where we include an extra term ω to account for external infections. Although actual
621 simulations do not include any external infections, we found that including this term
622 generally helped with model convergence in previous analyses [4]. The transmission
623 rate is divided into a seasonal term $\beta_{\text{seas}}(t)$ (repeated every year) and intervention
624 term $\alpha(t)$, which are estimated jointly:

$$\beta(t) = \beta_{\text{seas}}(t)\alpha(t), \quad (\text{S95})$$

625 where $\alpha < 1$ corresponds to reduction in transmission due to intervention effects. To
626 constrain the smoothness of $\beta_{\text{seas}}(t)$, we impose cyclic, random-walk priors:

$$\beta_{\text{seas}}(t) \sim \text{Normal}(\beta_{\text{seas}}(t - 1), \sigma) \quad t = 2 \dots 52 \quad (\text{S96})$$

$$\beta_{\text{seas}}(1) \sim \text{Normal}(\beta_{\text{seas}}(52), \sigma) \quad (\text{S97})$$

627 [SWP: I noticed that I forgot to put a prior on σ so need to re-do this but won't
 628 change the results.] We fix $\alpha(t) = 1$ for all $t < 2020$ and estimate α assuming a
 629 normal prior:

$$\alpha \sim \text{Normal}(1, 0.25). \quad (\text{S98})$$

630 We assume weakly informative priors on ω and ν :

$$\omega \sim \text{Normal}(0, 200) \quad (\text{S99})$$

$$\nu \sim \text{Normal}(104, 26) \quad (\text{S100})$$

631 We assume that the true birth/death rates, population sizes, and recovery rates are
 632 known. We note, however, that assuming $\gamma = 1/\text{week}$ actually corresponds to a
 633 mean simulated infectious period of 1.6 weeks, which is much longer than the true
 634 value; this approximation allows us to test whether we can still robustly estimate the
 635 intrinsic resilience given parameter mis-specification. Initial conditions are estimated
 636 with following priors:

$$S(0) = Ns(0) \quad (\text{S101})$$

$$I(0) = Ni(0) \quad (\text{S102})$$

$$s(0) \sim \text{Uniform}(0, 1) \quad (\text{S103})$$

$$i(0) \sim \text{Half-Normal}(0, 0.001) \quad (\text{S104})$$

637 Finally, the Observation model is specified as follows:

$$\text{Cases}(t) \sim \text{Negative-Binomial}(\rho N_{SI}(t), \phi) \quad (\text{S105})$$

$$\rho \sim \text{Half-Normal}(0, 0.02) \quad (\text{S106})$$

$$\phi \sim \text{Half-Normal}(0, 10) \quad (\text{S107})$$

638 where ρ represents the reporting probability and ϕ represents the negative binomial
 639 overdispersion parameter.

640 The model is fitted to four separate time series: (1) incidence time series from
 641 the SIRS model, (2) incidence time series for strain 1 from the two-strain model,
 642 (3) incidence time series for strain 2 from the two-strain model, and (4) combined
 643 incidence time series for strains 1 and 2 from the two-strain model. The model was
 644 fitted using rstan [26, 27]. The resulting posterior distribution was used to calculate
 645 the intrinsic resilience of the seasonally unforced system with the same parameters;
 646 eigenvalues of the discrete-time SIR model were computed by numerically finding
 647 the equilibrium and calculating the Jacobian matrix.

648 Validations for window-selection criteria

649 We use stochastic SIRS simulations to validate the window-selection criteria that we
 650 use for the linear regression for estimating empirical resilience. For each simulation,
 651 we begin by generating a random intervention $\alpha(t)$ from a random set of parameters.

652 First, we draw the duration of intervention τ_{npi} from a uniform distribution between
 653 0.5 and 3.5 years. Then, we draw independent normal variables z_i of length $\lfloor 364\tau_{\text{npi}} \rfloor$
 654 with a standard deviation of 0.02 and take a reverse cumulative sum to obtain a
 655 realistic shape for the intervention:

$$x_n = 1 + \sum_{i=n}^{\lfloor 364\tau_{\text{npi}} \rfloor} z_i, \quad n = 1, \dots, \lfloor 364\tau_{\text{npi}} \rfloor. \quad (\text{S108})$$

656 We repeat this random generation process until less than 10% of x_n exceeds 1. Then,
 657 we set any values that are above 1 or below 0 as 1 and 0, respectively. Then, we
 658 randomly draw the minimum transmission during intervention α_{\min} from a uniform
 659 distribution between 0.5 and 0.7 and scale x_n to have a minimum of α_{\min} :

$$x_{\text{scale},n} = \alpha_{\min} + (1 - \alpha_{\min}) \times \frac{x_n - \min x_n}{1 - \min x_n}. \quad (\text{S109})$$

660 This allows us to simulate a realistically shaped intervention:

$$\alpha(t) = \begin{cases} 1 & t < 2020 \\ x_{\text{scale},364(t-2020)} & 2020 \leq t < 2020 + \tau_{\text{npi}} \\ 1 & \tau_{\text{npi}} \leq t \end{cases}. \quad (\text{S110})$$

661 Given this intervention function, we draw \mathcal{R}_0 from a uniform distribution between 1.5
 662 and 3 and the mean duration of immunity $1/\delta$ from a uniform distribution between
 663 0.5 and 2. Then, we simulate the stochastic SIRS model from $S(0) = 10^8/\mathcal{R}_0$ and
 664 $I(0) = 100$ from 1990 to 2025 and truncate the time series to 2014–2025; if the
 665 epidemic becomes extinct before the end of simulation, we discard that simulation
 666 and start over from the intervention generation step. We then apply the window
 667 selection criteria described in the main text to compute the empirical resilience and
 668 compare it against the intrinsic resilience of the seasonally unforced system. We also
 669 compare this with the naive approach that uses the entire distance-from-attractor
 670 time series, starting from the maximum distance. We repeat this procedure 500
 671 times and quantify the correlation between empirical and intrinsic resilience estimates
 672 across two approaches.

Supplementary Figures

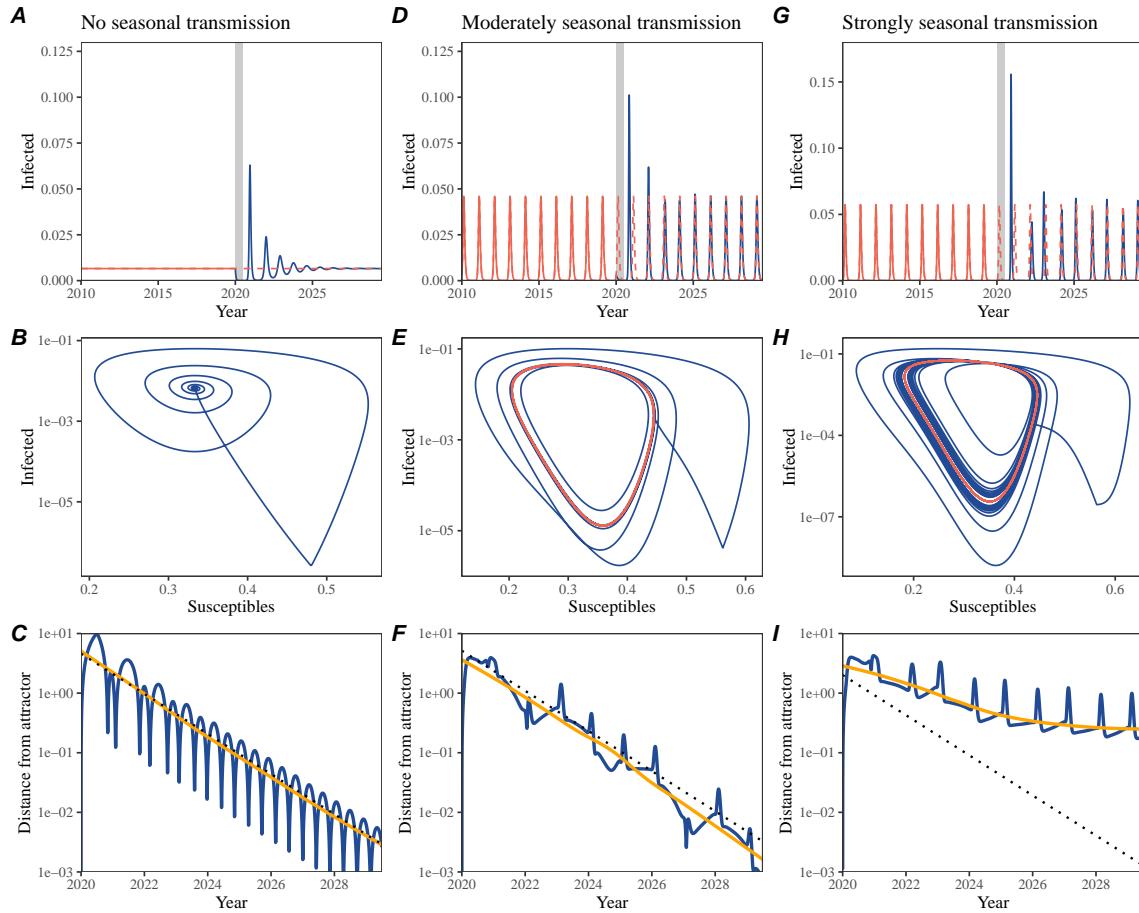


Figure S1: Impact of seasonal transmission on pathogen resilience. (A, D, G) Simulated epidemic trajectories using the SIRS model without seasonal forcing (A), with seasonal forcing of amplitude of 0.2 (D), and with seasonal forcing of amplitude of 0.4 (G). Red and blue solid lines represent epidemic dynamics before and after interventions are introduced, respectively. Red dashed lines represent counterfactual epidemic dynamics in the absence of interventions. Gray regions indicate the duration of interventions. (B, E, H) Phase plane representation of the corresponding model. Red and blue solid lines represent epidemic trajectories on an SI phase plane before and after interventions are introduced, respectively. (C, F, I) Changes in logged distance from the attractor over time. Blue lines represent the logged distance from the attractor. Orange lines represent the locally estimated scatterplot smoothing (LOESS) fits to the logged distance from the attractor. Dotted lines are superimposed as a comparison to have the same slope as the intrinsic resilience of the seasonally unforced system.

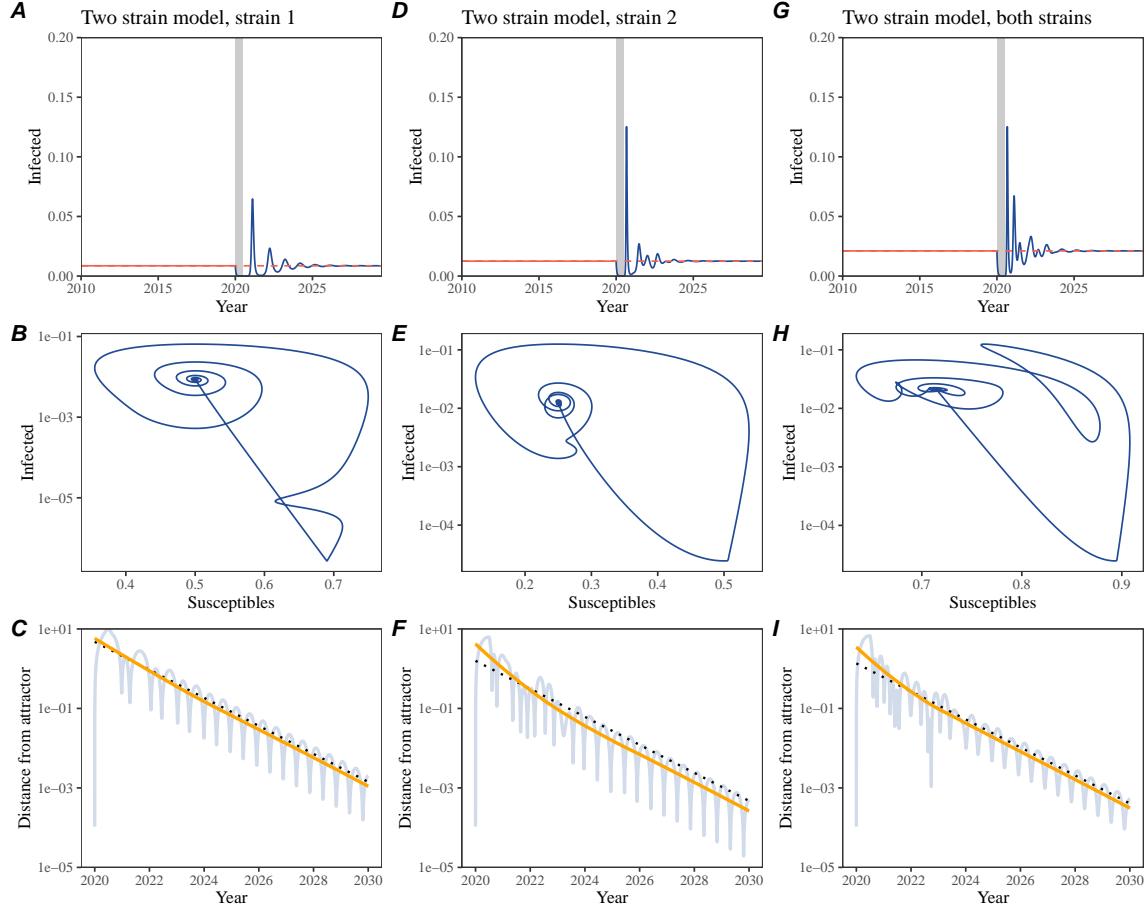


Figure S2: Conceptual framework for measuring pathogen resilience following NPIs for a two-strain system without seasonal forcing. (A, D, G) Simulated epidemic trajectories using a multi-strain system without seasonal forcing. Red and blue solid lines represent epidemic dynamics before and after interventions are introduced, respectively. Red dashed lines represent counterfactual epidemic dynamics in the absence of interventions. Gray regions indicate the duration of interventions. (B, E, H) Phase plane representation of the corresponding model. Blue solid lines represent epidemic trajectories on an SI phase plane before and after interventions are introduced, respectively. (C, F, I) Changes in logged distance from the attractor over time. Blue lines represent the logged distance from the attractor. Orange lines represent the locally estimated scatterplot smoothing (LOESS) fits to the logged distance from the attractor. Dotted lines are superimposed as a comparison to have the same slope as the intrinsic resilience of the seasonally unforced system.

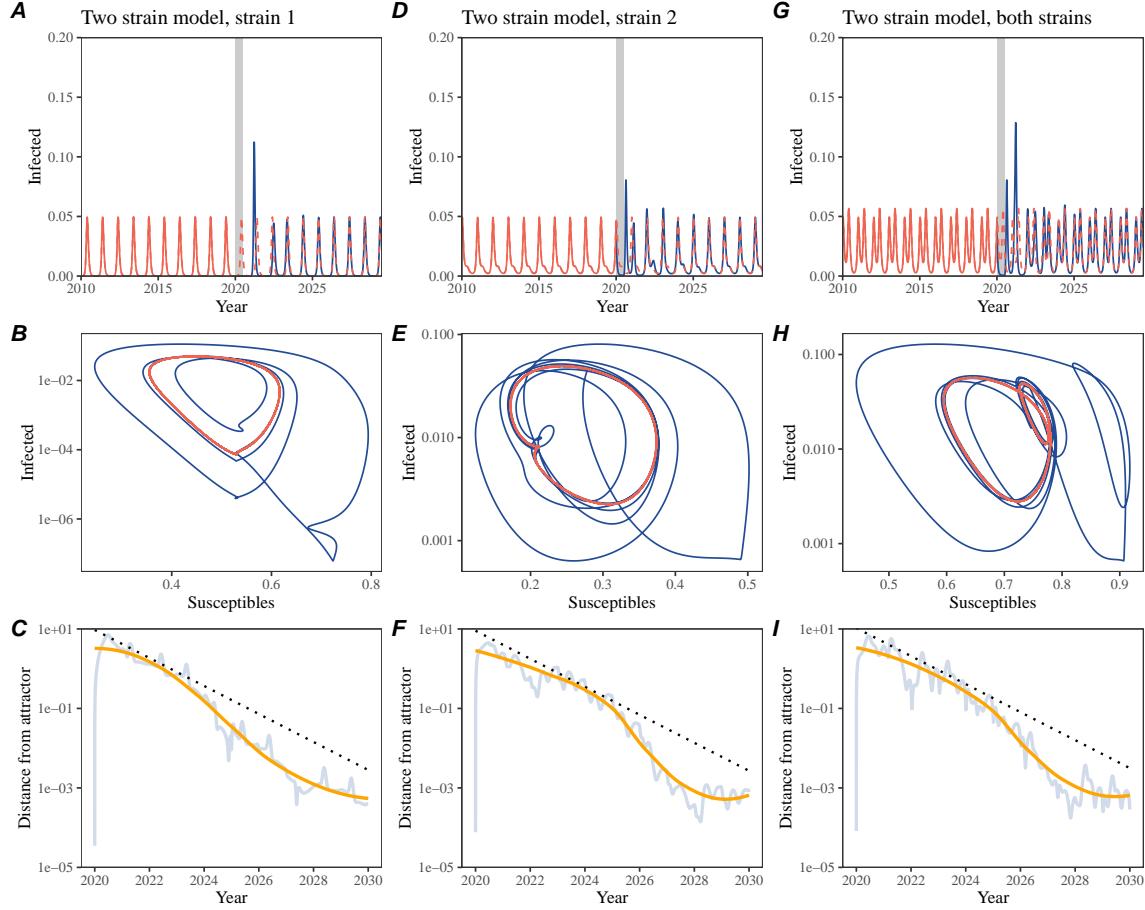


Figure S3: Conceptual framework for measuring pathogen resilience following NPIs for a multi-strain system with seasonal forcing. (A, D, G) Simulated epidemic trajectories using a multi-strain system with seasonal forcing (amplitude of 0.2). Red and blue solid lines represent epidemic dynamics before and after interventions are introduced, respectively. Red dashed lines represent counterfactual epidemic dynamics in the absence of interventions. Gray regions indicate the duration of interventions. (B, E, H) Phase plane representation of the corresponding model. Red and blue solid lines represent epidemic trajectories on an SI phase plane before and after interventions are introduced, respectively. (C, F, I) Changes in logged distance from the attractor over time. Blue lines represent the logged distance from the attractor. Orange lines represent the locally estimated scatterplot smoothing (LOESS) fits to the logged distance from the attractor. Dotted lines are superimposed as a comparison to have the same slope as the intrinsic resilience of the seasonally unforced system.

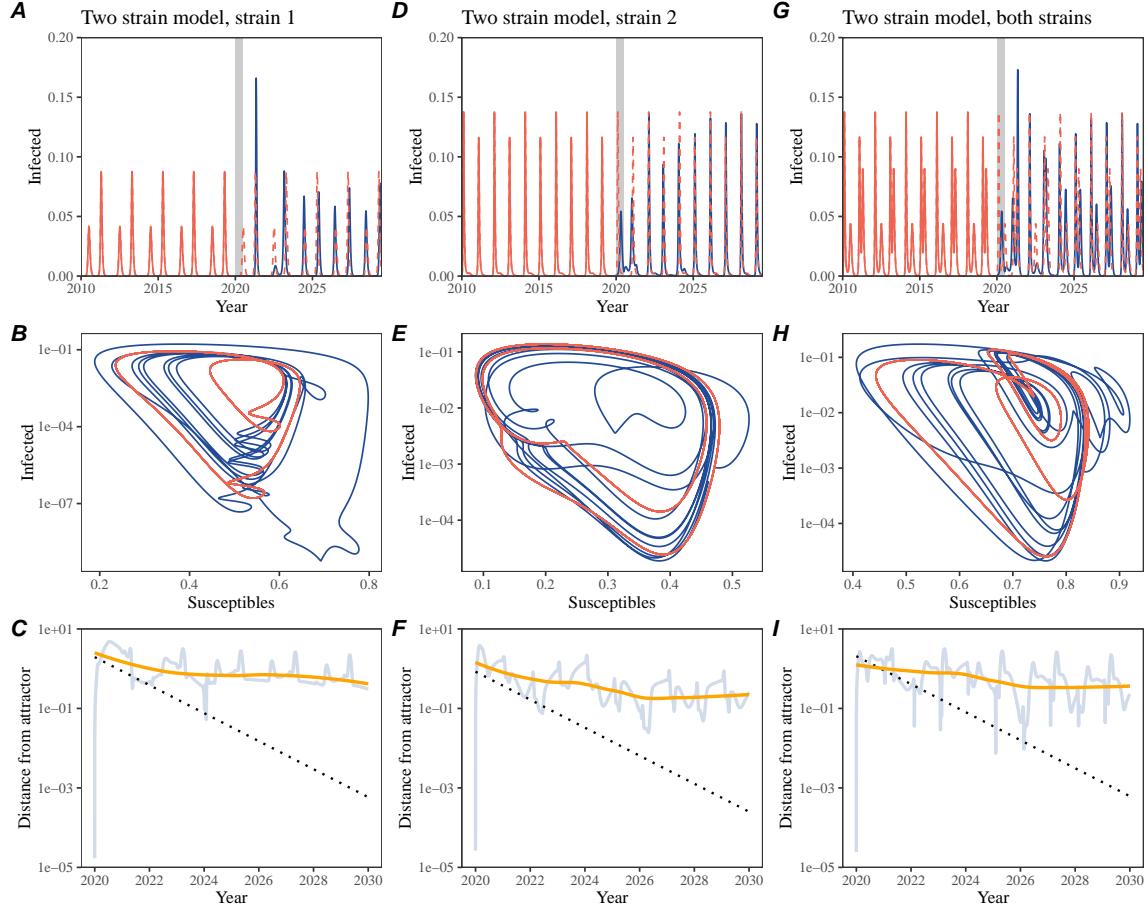


Figure S4: Conceptual framework for measuring pathogen resilience following NPIs for a multi-strain system with strong seasonal forcing. (A, D, G) Simulated epidemic trajectories using a multi-strain system with seasonal forcing (amplitude of 0.4). Red and blue solid lines represent epidemic dynamics before and after interventions are introduced, respectively. Red dashed lines represent counterfactual epidemic dynamics in the absence of interventions. Gray regions indicate the duration of interventions. (B, E, H) Phase plane representation of the corresponding model. Red and blue solid lines represent epidemic trajectories on an SI phase plane before and after interventions are introduced, respectively. (C, F, I) Changes in logged distance from the attractor over time. Blue lines represent the logged distance from the attractor. Orange lines represent the locally estimated scatterplot smoothing (LOESS) fits to the logged distance from the attractor. Dotted lines are superimposed as a comparison to have the same slope as the intrinsic resilience of the seasonally unforced system.

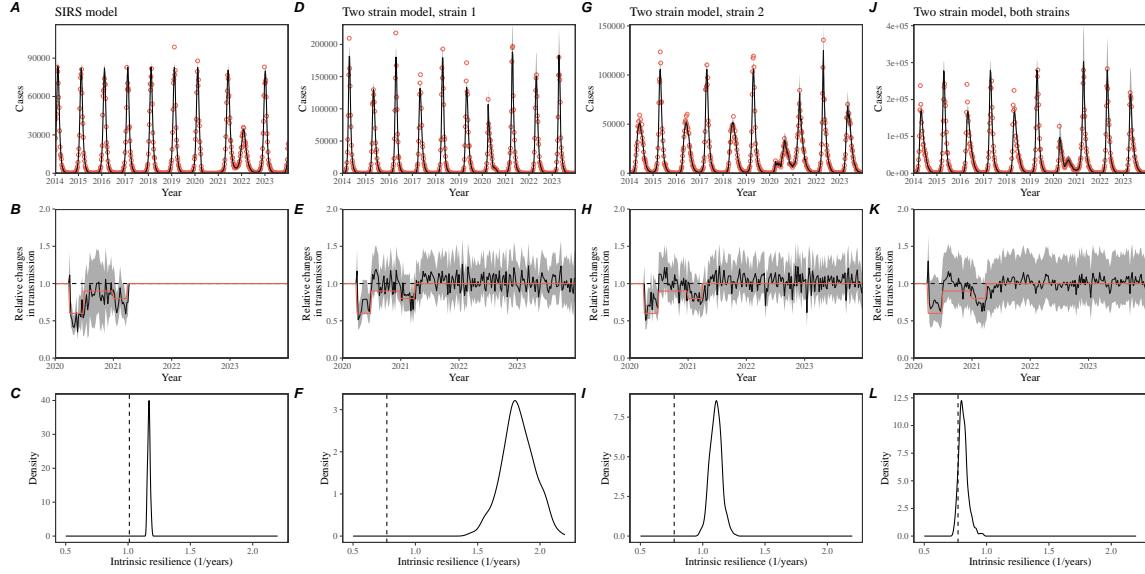


Figure S5: Mechanistic model fits to simulated data and inferred intrinsic resilience. (A, D, G, J) Simulated case time series from corresponding models (red) and SIRS model fits (black). (B, E, H, K) Assumed changes in transmission due to pandemic NPIs (red) and estimated changes from the SIRS model (black). Solid lines and shaded regions represent fitted posterior median and 95% credible intervals. (C, F, I, L) True intrinsic resilience of the seasonally unforced system (vertical lines) and the posterior distribution of the inferred intrinsic resilience from the SIRS model (density plots).

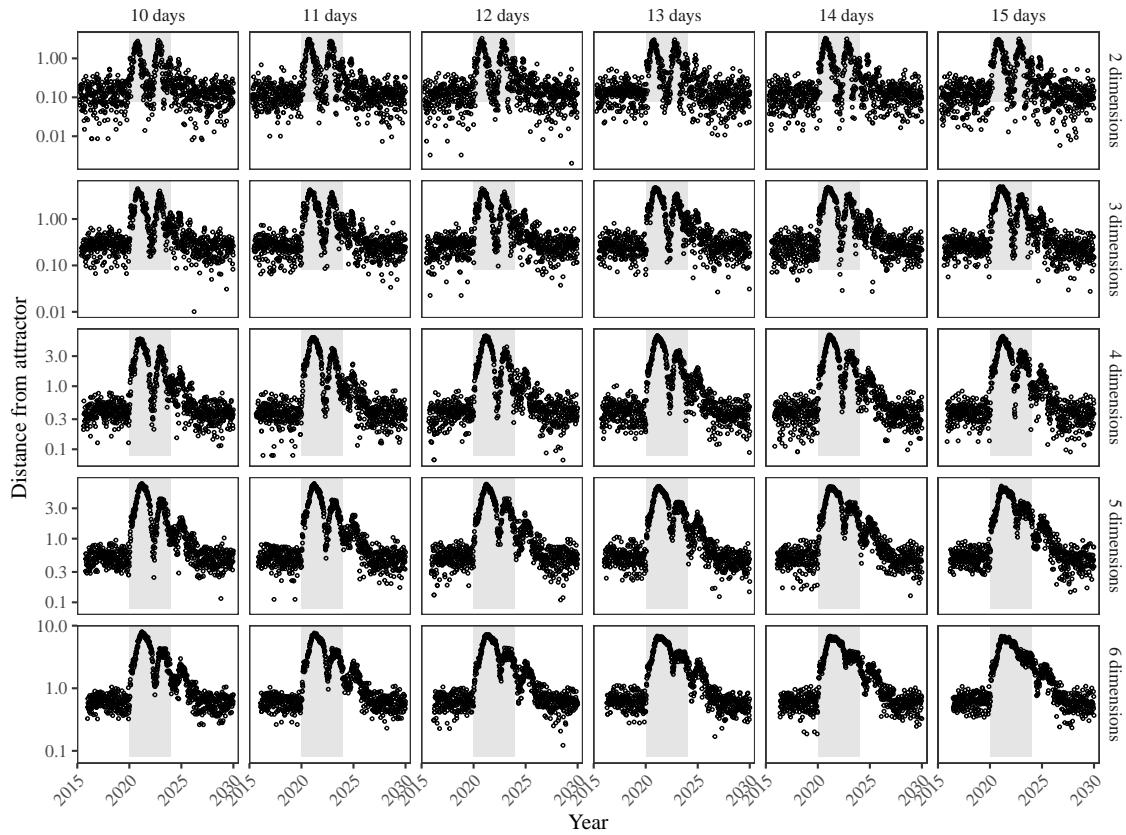


Figure S6: Sensitivity of the distance from the attractor to choices about embedding lags and dimensions. Sensitivity analysis for the distance-from-attractor time series shown in Figure 3E in the main text by varying the embedding lag between 10–15 days and embedding dimensions between 2–6 dimensions.

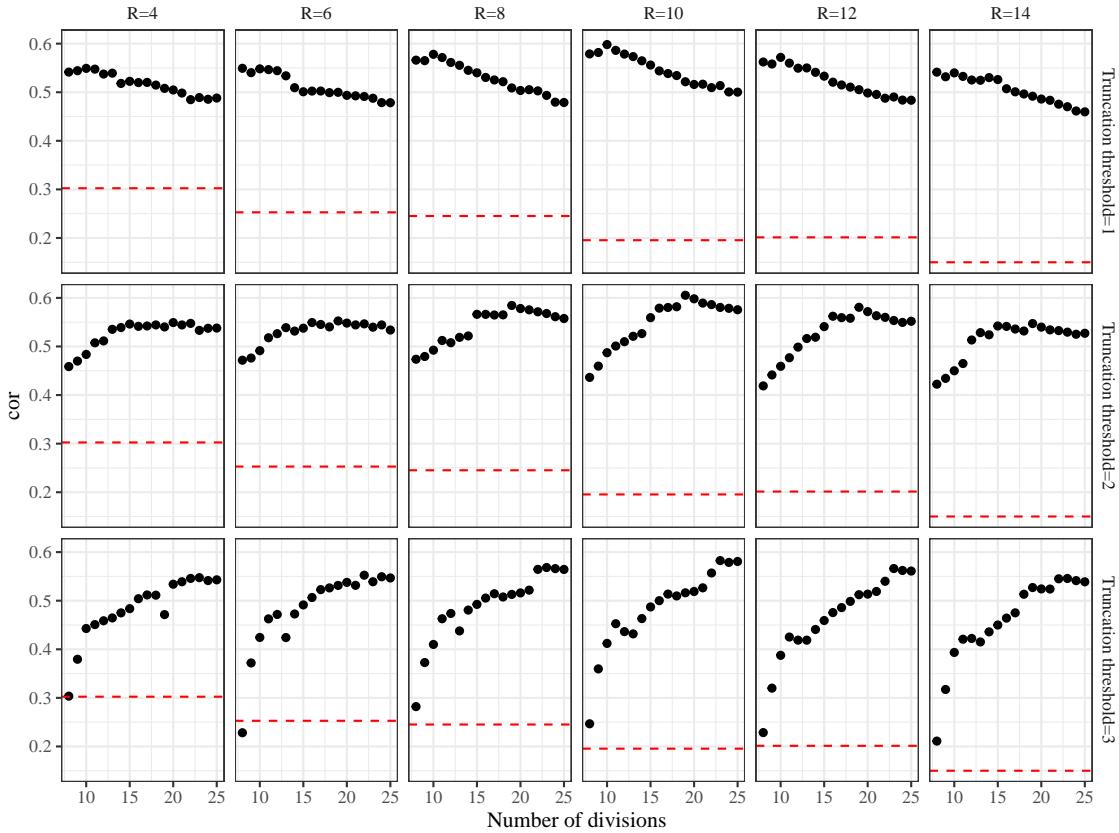


Figure S7: Impact of fitting window selection on the estimation of empirical resilience. We simulated 500 epidemics of a stochastic SIRS model with randomly drawn parameters and randomly generated intervention impacts. For each simulation, we reconstructed the empirical attractor based on the approach outlined in Figure 3 and estimate the distance from the attractor. The naive approach fits a linear regression on a log scale, starting from the maximum distance until the end of the time series. The window-based approach tries to select an appropriate window by smoothing the distance estimates and finding the time period when the smoothed time series crosses pre-determined threshold, relative to the maximum distance; then, a linear regression is fitted by using the raw distance within this time period.

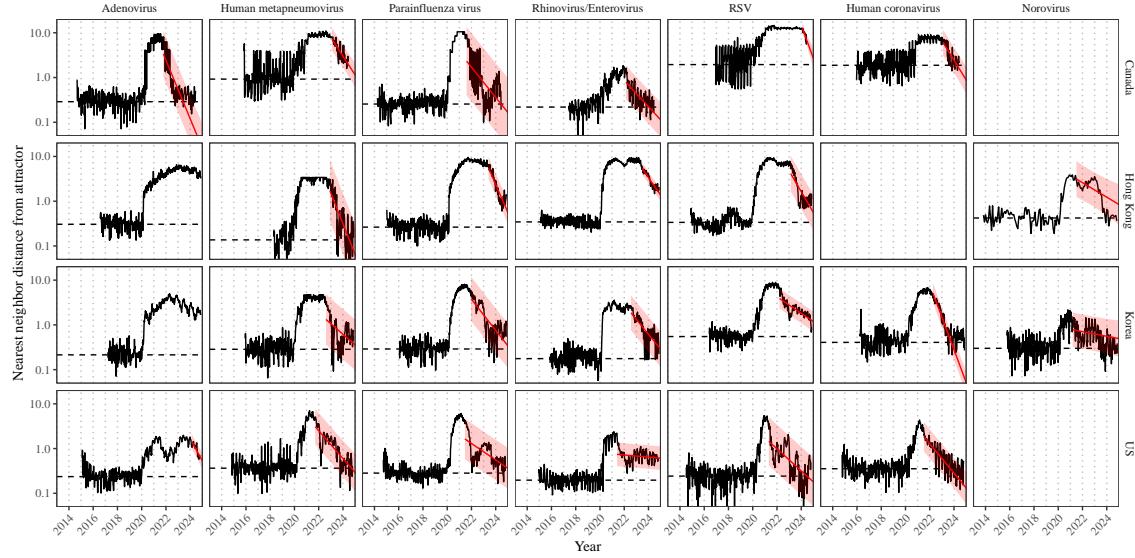


Figure S8: Estimated time series of distance from the attractor for each pathogen and corresponding linear regression fits using automated window selection criterion across Canada, Hong Kong, Korea, and the US. Black lines represent the estimated distance from the attractor. Red lines and shaded regions represent the linear regression fits and corresponding 95% confidence intervals. Dashed lines represent the average of the pre-pandemic nearest neighbor distances.

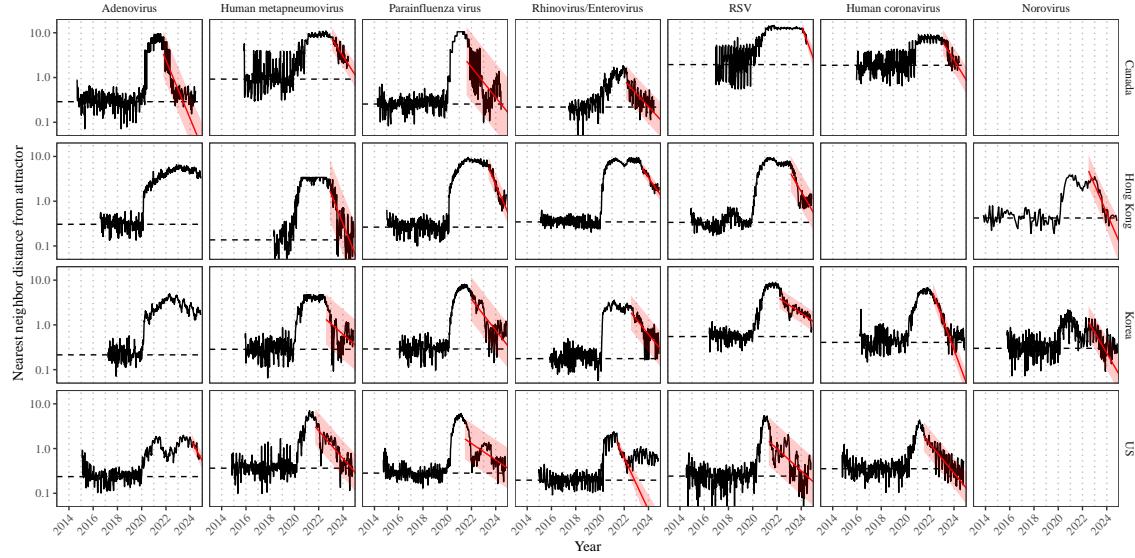


Figure S9: Estimated time series of distance from the attractor for each pathogen and corresponding linear regression fits across Canada, Hong Kong, Korea, and the US, including ad-hoc regression window selection. We used ad-hoc regression windows for norovirus in Hong Kong and Korea and Rhinovirus/Enterovirus in the US. Black lines represent the estimated distance from the attractor. Red lines and shaded regions represent the linear regression fits and corresponding 95% confidence intervals. Dashed lines represent the average of the pre-pandemic nearest neighbor distances.

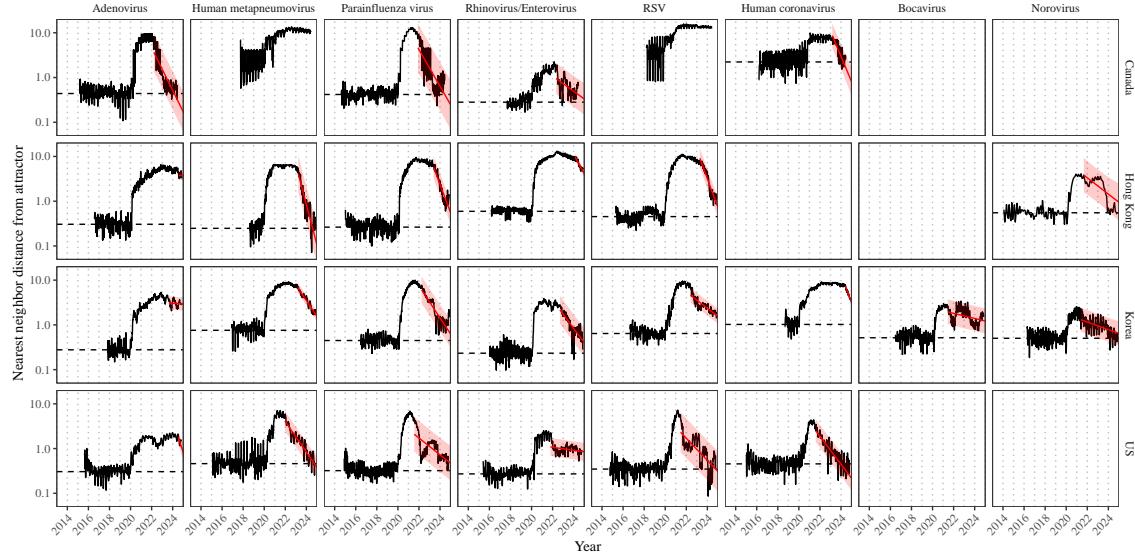


Figure S10: Estimated time series of distances from the attractor for each pathogen across Canada, Hong Kong, Korea, and the US using higher embedding dimensions. Black lines represent the estimated distance from the attractor. Red lines and shaded regions represent the linear regression fits and corresponding 95% confidence intervals. Dashed lines represent the average of the pre-pandemic nearest neighbor distances. A lower threshold is used for determining embedding dimensions with the false nearest neighbors approach, thereby yielding a higher embedding dimension.

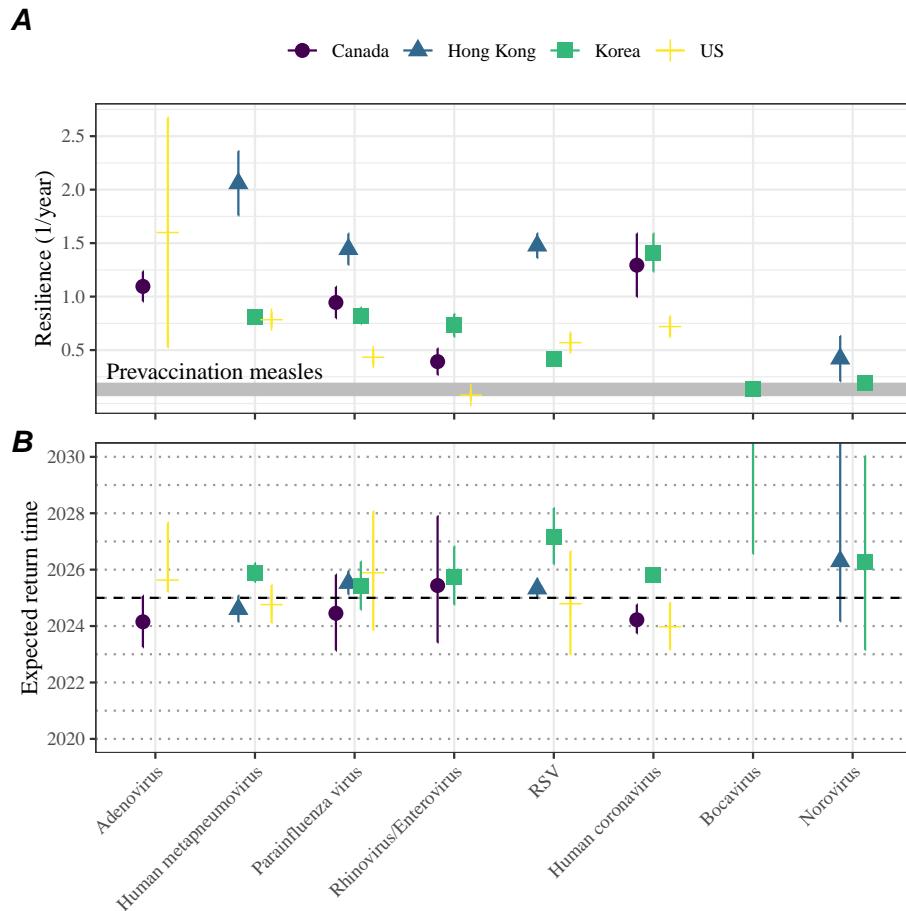


Figure S11: Summary of resilience estimates using higher embedding dimensions. (A) Estimated pathogen resilience. The gray horizontal line represents the intrinsic resilience of pre-vaccination measles dynamics. (B) Predicted timing of when each pathogen will return to their pre-pandemic cycles. The dashed line in panel B indicates the end of 2024 (current observation time). Error bars represent 95% confidence intervals. A lower threshold is used for determining embedding dimensions with the false nearest neighbors approach, thereby yielding a higher embedding dimension.

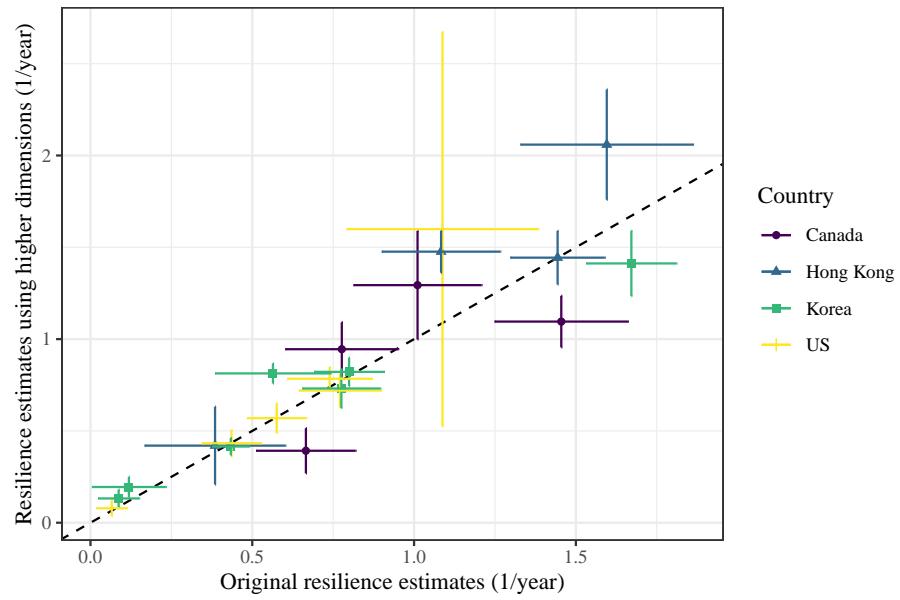


Figure S12: **Comparison of resilience estimates.** Each point represents a resilience estimate for a specific pathogen at a specific country. The x values represent the original resilience estimates presented in Figure 4. The y values represent the original resilience estimates presented in Supplementary Figure S11.

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