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² Susceptible host dynamics explain pathogen resilience to
³ perturbations

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¹⁴ **Abstract**

¹⁵ A major priority for epidemiological research in the time of anthropogenic change
¹⁶ is understanding how infectious disease dynamics respond to perturbations. Inter-
¹⁷ ventions to slow the spread of SARS-CoV-2 significantly disrupted the transmission
¹⁸ of other human pathogens. As interventions lifted, whether and when respiratory
¹⁹ pathogens would eventually return to their pre-pandemic dynamics remains to be
²⁰ answered. Here, we present a framework for estimating pathogen resilience based
²¹ on how fast epidemic patterns approach their pre-pandemic, endemic dynamics and
²² analyze time series data from Hong Kong, Canada, Korea, and the US. By quanti-
²³ fying the resilience of common respiratory pathogens, we are able to predict when
²⁴ each pathogen will eventually return to pre-pandemic dynamics. Our predictions
²⁵ closely match the observed deviations (or lack thereof) from its pre-COVID dynam-
²⁶ ics. Discrepancies between predicted and observed dynamics indicate the long-term
²⁷ impacts of pandemic perturbations, suggesting that some pathogens may be con-
²⁸ verging to a different endemic cycle. Finally, we show that the replenishment rate
²⁹ of the susceptible pool is a key determinant of pathogen resilience, which in turn
³⁰ determines the sensitivity of a system to stochastic perturbations. Overall, our anal-
³¹ ysis highlights the persistent nature of common respiratory pathogens compared to
³² vaccine-preventable infections, such as measles.

Introduction

34 Non-pharmaceutical interventions to slow the spread of SARS-CoV-2 disrupted the
 35 transmission of other human respiratory pathogens, adding uncertainties to their future
 36 epidemic dynamics and their public health burden [1]. As interventions lifted,
 37 large heterogeneities in outbreak dynamics were observed across different pathogens
 38 in different countries, with some pathogens exhibiting earlier and faster resurgences
 39 than others [2, 3, 4]. Heterogeneities in the overall reduction in transmission and the
 40 timing of re-emergence likely reflect differences in intervention patterns, pathogen
 41 characteristics, immigration/importation from other countries, and pre-pandemic
 42 pathogen dynamics [5]. Therefore, comparing the differential impact of the pandemic
 43 perturbations across pathogens can provide unique opportunities to learn
 44 about underlying pathogen characteristics, such as their transmissibility or duration
 45 of immunity, from heterogeneities in re-emergence patterns [6].

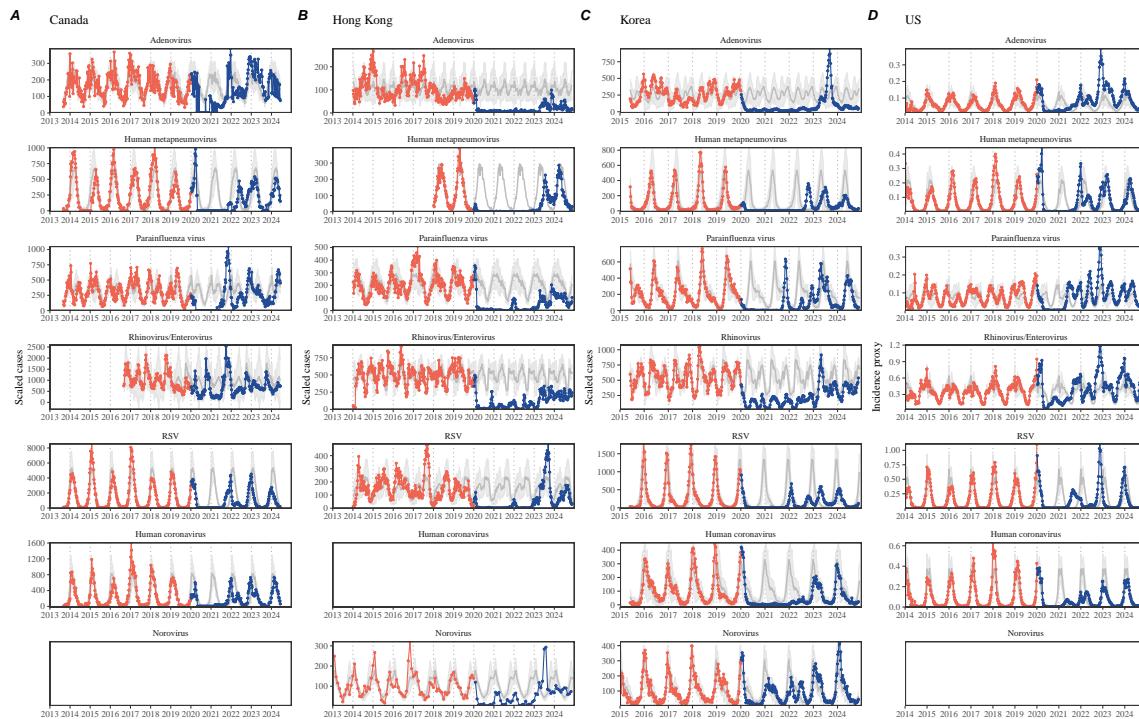


Figure 1: **Observed heterogeneity in responses to pandemic perturbations across respiratory pathogens and norovirus in (A) Canada, (B) Hong Kong, (C) Korea, and (D) US.** Red points and lines represent data before 2020. Blue points and lines represent data since 2020. Gray lines and shaded regions represent 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).

46 Even though more than five years have passed since the emergence of SARS-CoV-
47 2, we still observe persistent changes in pathogen dynamics following the pandemic
48 perturbations. For example, compared to pre-pandemic, seasonal patterns, human
49 metapneumovirus in Korea seems to circulate at lower levels, whereas RSV in Korea
50 seems to exhibit different seasonality (Figure 1). These observations suggest a fun-
51 damental change in pathogen dynamics following the pandemic perturbations, which
52 might be driven by a long-term shift in either human behavior or population-level
53 immunity [7, 8]. For example, the emergence of SARS-CoV-2 could have caused
54 a long-term shift in population-level immunity through its interactions with other
55 pathogens [9], especially with seasonal coronaviruses [7, 10, 11]. The possibility of a
56 long-lasting impact of the pandemic perturbations poses an important question for
57 future infectious disease dynamics: can we predict whether and when other pathogens
58 will eventually return to their pre-pandemic dynamics?

59 So far, most analyses of respiratory pathogens after pandemic perturbations have
60 focused on characterizing the timing of rebound [1, 12, 5]. Instead, we seek to char-
61 acterize how fast (and whether) a pathogen returns to its pre-pandemic dynamics.
62 These two concepts have a subtle but important difference. For example, it took
63 more than 3 years for human metapneumovirus to rebound in Hong Kong, but the
64 observed epidemic patterns in 2024 appear similar to pre-pandemic seasonal means,
65 suggesting a possible return to pre-pandemic dynamics, though confirmation may
66 require multiple seasons (Figure 1). Measuring this rate of return is useful because it
67 allows us to quantify the ecological resilience of a host-pathogen system, which can
68 inform responses to future interventions [13, 14, 15, 16].

69 In this study, we lay out theoretical and statistical approaches to characterizing
70 the resilience of a host-pathogen system based on how fast the system recovers from
71 perturbation. We begin by laying out a few representative scenarios that capture
72 the potential impact of pandemic perturbations on endemic pathogen dynamics and
73 illustrate how resilience can be measured by comparing the pre- and post-pandemic
74 dynamics of susceptible and infected hosts. In practice, information on suscepti-
75 ble hosts is often unavailable, making this theoretical approach infeasible. Instead,
76 we utilize a mathematical technique to reconstruct empirical attractors from the
77 data [17], which allows us to measure the rate at which the host-pathogen system
78 approaches this empirical attractor after a perturbation; we define this rate to be
79 the empirical resilience of the host-pathogen system. We use this method to ana-
80 lyze pathogen surveillance data for respiratory and non-respiratory pathogens from
81 Canada, Hong Kong, Korea, and the US. Finally, we show that susceptible host dy-
82 namics explain variation in pathogen resilience and further demonstrate that more
83 resilient pathogens will be less sensitive to perturbations caused by demographic
84 stochasticity, thereby providing a direct link between pathogen resilience and persis-
85 tence.

86 **Conceptual introduction to pathogen resilience**

87 In classical ecological literature, the resilience of an ecological system is measured by
88 the rate at which the system returns to its reference state following a perturbation
89 [13, 14, 15, 16]. This rate corresponds to the largest real part of the eigenvalues
90 of the linearized system near equilibrium—here, we refer to this value as the *intrinsic*
91 resilience of the system, which represents the expected rate of return from
92 perturbed states. In practice, we rarely know the true model describing population-
93 level dynamics of common respiratory pathogens, limiting our ability to infer the
94 intrinsic resilience of a system. Instead, we can measure the *empirical* resilience
95 of a host-pathogen system by looking at how fast the system returns to the pre-
96 perturbation, endemic dynamics after the perturbation has ended. The COVID-19
97 pandemic provides a particularly useful example of a major perturbation, providing
98 unique opportunities to measure the resilience of a host-pathogen system.

99 **Resilience of a single-strain system.** As an example, we begin with a sim-
100 ple Susceptible-Infected-Recovered-Susceptible (SIRS) model with seasonally forced
101 transmission and demography (i.e., birth and death). The SIRS model is the simplest
102 model that allows for the waning of immunity and is commonly used for modeling
103 the dynamics of respiratory pathogens [18]. First, consider a pandemic perturbation
104 that reduces transmission by 50% for 6 months starting in 2020, which causes epi-
105 demic patterns to deviate from their original stable annual cycle for a short period of
106 time and eventually come back (Figure 2A). To measure the resilience of this system
107 empirically, we first need to be able to measure the distance from its pre-pandemic
108 attractor, which is defined as a set of points in state space or phase plane that the
109 system is pulled towards [19]. There are many ways we can measure the distance from
110 the attractor, but for illustrative purposes, we choose one of the most parsimonious
111 approaches: that is, we look at how the susceptible (S) and infected (I) populations
112 change over time and measure the Euclidean distance on the SI phase plane, using
113 the counterfactual unperturbed phase plane as a reference (Figure 2B; Materials and
114 Methods). In this simple case, the locally estimated scatterplot smoothing (LOESS)
115 fit indicates that the distance from the attractor decreases exponentially (linearly on
116 a log scale) on average (Figure 2C). Furthermore, the overall rate of return approxi-
117 mutes the intrinsic resilience of the seasonally unforced system (Figure 2C).

118 Alternatively, pandemic perturbations can have a lasting impact on the forces
119 driving pathogen dynamics through a long-term reduction in transmission or per-
120 manent change in immunity. As an example, we consider a scenario in which a 10%
121 reduction in transmission persists even after the major pandemic perturbations are
122 lifted (Figure 2D–F). In such cases, we cannot know whether the pathogen will re-
123 turn to its original cycle or a different cycle until many years have passed, and we
124 cannot measure the distance to the new unknown attractor that the system might
125 eventually approach. Nonetheless, we can still measure the distance from the pre-
126 pandemic attractor and ask how the distance changes over time (Figure 2E). The
127 LOESS fit suggests that the distance from the pre-pandemic attractor will initially

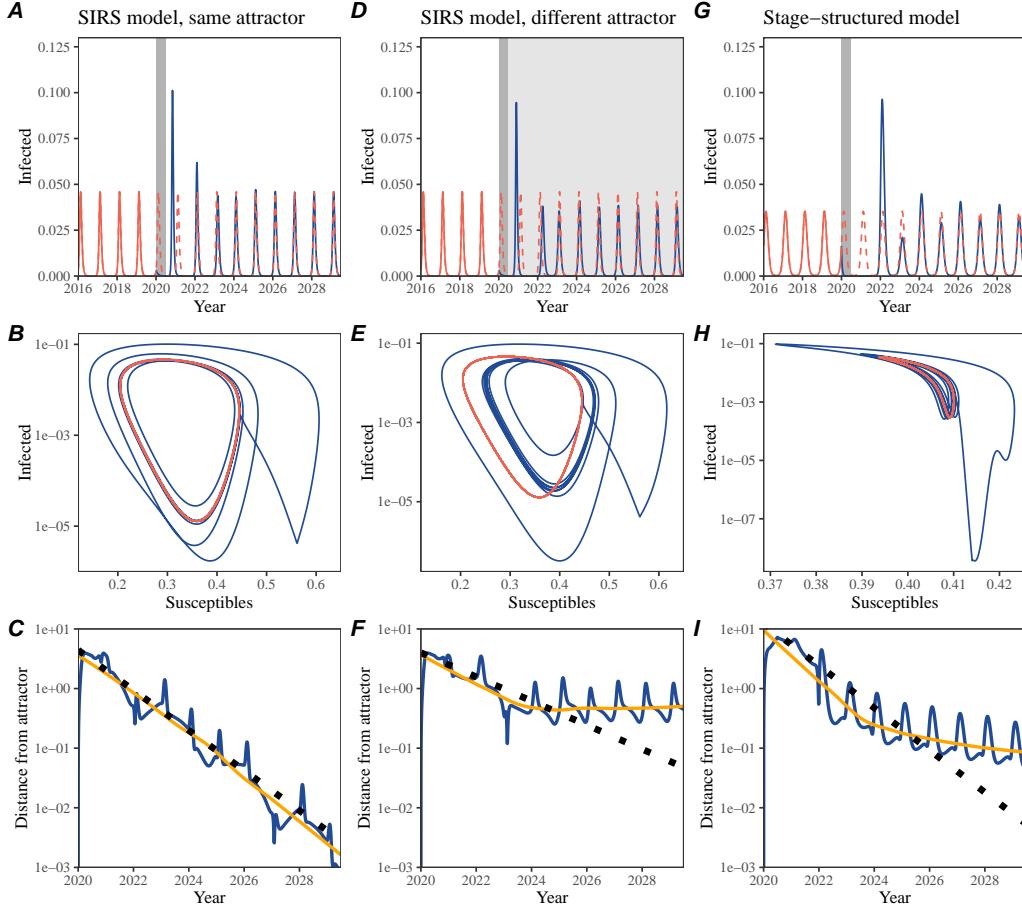


Figure 2: A simple method to measure pathogen resilience following pandemic perturbations across different scenarios. (A, D, G) Simulated epidemic trajectories across various models. Red and blue solid lines represent epidemic dynamics before and after pandemic perturbations are introduced, respectively. Red dashed lines represent counterfactual epidemic dynamics in the absence of perturbations. Gray regions indicate the duration of perturbations with the dark gray region representing a 50% transmission reduction and the light gray region representing a 10% transmission reduction. (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 perturbations are introduced, respectively. (C, F, I) Changes in distance from the attractor over time on a log scale. Blue lines represent the 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.

128 decrease exponentially on average (equivalently, linearly on a log scale) and even-
129 tually plateau (Figure 2F). Here, a permanent 10% reduction in transmission rate
130 slows the system, which causes the distance from the pre-pandemic attractor initially
131 to decrease at a slower rate (Figure 2F) than it would have otherwise (Figure 2C)
132 before plateauing at a fixed distance between the two attractors. This example shows
133 that resilience is not necessarily an intrinsic property of a specific pathogen. Instead,
134 pathogen resilience is a property of a specific attractor that a host-pathogen system
135 approaches, which depends on both pathogen and host characteristics.

136 Finally, transient phenomena can further complicate the picture (Figure 2G–I).
137 For example, a stage-structured model, which accounts for reduction in secondary
138 susceptibility, initially exhibits a stable annual cycle, but perturbations from a 10%
139 reduction in transmission for 6 months cause the epidemic to shift to biennial cycles
140 (Figure 2G). The system eventually approaches the original pre-pandemic attractor
141 (Figure 2H), suggesting that this biennial cycle is a transient phenomenon. The
142 LOESS fit indicates that the distance from the attractor initially decreases expo-
143 nentially at a rate that is consistent with the intrinsic resilience of the seasonally
144 unforced stage-structured system, but the approach to the attractor slows down
145 with the damped oscillations (Figure 2I). This behavior is also referred to as a ghost
146 attractor, which causes long transient dynamics and slow transitions [20]. Strong
147 seasonal forcing in transmission can also lead to transient phenomena for a simple
148 SIRS model, causing a slow return to pre-perturbation dynamics (Supplementary
149 Figure S1).

150 **Resilience of a two-strain system.** This empirical approach allows us to
151 measure the resilience of a two-strain host-pathogen system as well even when we
152 have incomplete observation of the infection dynamics. Simulations from a simple
153 two-strain competition system illustrate that separate analyses of individual strain
154 dynamics (e.g., RSV A vs B) and a joint analysis of total infections (e.g., total
155 RSV infections) yield identical resilience estimates (Supplementary Figure S2, 3).
156 This is expected because eigenvalues determine the dynamics of the entire system
157 around the equilibrium, meaning that both strains should exhibit identical rates of
158 return following a perturbation. However, these conclusions likely depend on the
159 strength of strain interaction as well as the underlying details of the model. For
160 example, ecological interferences between two unrelated pathogens [21] will likely
161 generate weaker coupling than cross immunity between related pathogens; in the
162 former case, we do not necessarily expect two unrelated pathogens to have same
163 resilience despite their ecological interferences. For simplicity, we focus on a simple,
164 two-strain model with cross immunity in this paper. Analogous to a single-strain
165 system, strong seasonal forcing in transmission can cause the two-strain system to
166 slow down through transient phenomena (Supplementary Figure S4).

167 These observations yield three insights. First, we can directly estimate the empi-
168 rical resilience of a host-pathogen system by measuring the rate at which the system
169 approaches an attractor, provided that we have a way to quantify the distance from
170 the attractor—as we discuss later, the attractor of a system can be reconstructed

from data from mathematical theory without making assumptions about the underlying model. The empirical approach to estimating pathogen resilience is particularly convenient because it does not require us to know the true underlying model; estimating the intrinsic resilience from fitting misspecified models can lead to biased estimates (Supplementary Figure S5). Second, resilience estimates allow us to make phenomenological predictions about the dynamics of a host-pathogen system following a perturbation. Assuming that an attractor has not changed and the distance from the attractor will decrease exponentially over time, we can estimate when the system should reach an attractor. Finally, a change in the (exponential) rate of approach provide information about whether the system has reached an alternative attractor, or a ghost attractor, that is different from the original, pre-pandemic attractor. These alternative attractors may reflect permanent changes in transmission patterns as well as changes in immune landscapes. There will be periods of time when it is difficult to tell whether pathogen dynamics are still diverging from the original attractor due to a long-term perturbation, or have entered the basin of attraction of a new attractor. Now that several years have passed since major interventions have been lifted, many respiratory pathogens may have had sufficient time to begin returning to their post-intervention attractors—empirical comparisons between current cases and pre-pandemic cases are consistent with this hypothesis (Figure 1). With recent data, we can start to evaluate whether we see early signs of convergence to the former attractor or a new one.

Inferring pathogen resilience from real data

Based on these observations, we now lay out our approach to estimating pathogen resilience from real data (Figure 3). We first tested this approach against simulations and applied it to real data. Specifically, we analyzed case time series of respiratory pathogens from four countries: Canada, Hong Kong, Korea, and the US.

So far, we have focused on simple examples that assume a constant transmission reduction during the pandemic. However, in practice, the impact of pandemic perturbations on pathogen transmission was likely more complex (Figure 3A), reflecting introduction and relaxation of various intervention strategies. In some cases, strong perturbations likely caused local fadeouts, requiring immigration/importation from another location for epidemic rebound. Such complexities could lead to longer delays between the introduction of pandemic perturbations and pathogen rebound as well as temporal variation in outbreak sizes (Figure 3B); in this example, continued transmission reduction from interventions limits the size of the first outbreak in 2021 following the rebound, allowing for a larger outbreak in 2022 when interventions are further relaxed.

Previously, we relied on the dynamics of susceptible and infected hosts to compute the distance from the attractor (Figure 2), but information on susceptible hosts is rarely available in practice. In addition, uncertainties in case counts due to ob-

211 servation error, strain evolution, and multiannual cycles in the observed epidemic
212 dynamics (e.g., adenovirus circulation patterns in Hong Kong and Korea) add chal-
213 lenges to defining pre-pandemic attractors, which limits our ability to measure the
214 distance from the attractor. To address these challenges, we can reconstruct an em-
215 pirical attractor by utilizing Takens' theorem [17], which states that an attractor of a
216 nonlinear multidimensional system can be mapped onto a delayed embedding (Mate-
217 rials and Methods). For example, we can use delayed logged values of pre-pandemic
218 cases $C(t)$ (Figure 3C) to reconstruct the attractor:

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

219 where the delay τ and embedding dimension M are determined based on autocor-
220 relations and false nearest neighbors, respectively [22, 23]. This allows us to define
221 the pre-pandemic attractor as a points on an M dimensional space. We can then
222 apply the same delay and embedding dimensions to the entire time series to deter-
223 mine the position in multi-dimensional state space (Figure 3D), which allows us to
224 measure the nearest neighbor distance between the current state of the system and
225 the empirical pre-pandemic attractor (Figure 3E). Specifically, the nearest neighbor
226 distance is calculated by computing the distance between the current position on
227 the M dimensional space and all points in the empirical attractor set and taking the
228 minimum value. In theory, we can now quantify how fast this distance decreases by
229 fitting a linear regression on a log scale, where the slope of the linear regression em-
230 pirically measures pathogen resilience with a steeper slope corresponding to a higher
231 resilience estimate (Figure 3E). However, resulting estimates of pathogen resilience
232 can be sensitive to choices about embedding delays and dimensions. For example,
233 using longer delays and higher dimensions tends to smooth out temporal variations
234 in the distance from the attractor (Supplementary Figure S6).

235 Complex changes in the distance from the attractor suggest that estimating
236 pathogen resilience from linear regression will be particularly sensitive to our choice
237 of fitting windows for the regression (Figure 3E). Therefore, before we tried estimat-
238 ing resilience from real data, we explored an automated window selection criterion
239 for linear regression and tested it against randomized, stochastic simulations across
240 a range of realistic pandemic perturbation shapes. In doing so, we also explored
241 optimal choices for embedding dimensions and evaluated our choices of fitting win-
242 dows parameters and embedding dimensions by quantifying correlation coefficients
243 between the estimated resilience and the intrinsic resilience of a seasonally unforced
244 system (Materials and Methods). Overall, we found large variation in estimation
245 performances with correlation coefficient ranging from 0.21 to 0.61 (Supplementary
246 Figure S7). In almost all cases, the automated window selection approach outper-
247 formed a naive approach, which performs regression between the peak distance and
248 current distance (Supplementary Figure S7).

249 Based on the best performing window selection criteria and embedding dimen-
250 sion, we applied this approach to pathogen surveillance data presented in Figure
251 1 (Materials and Methods). For each time series, we applied Takens' theorem in-

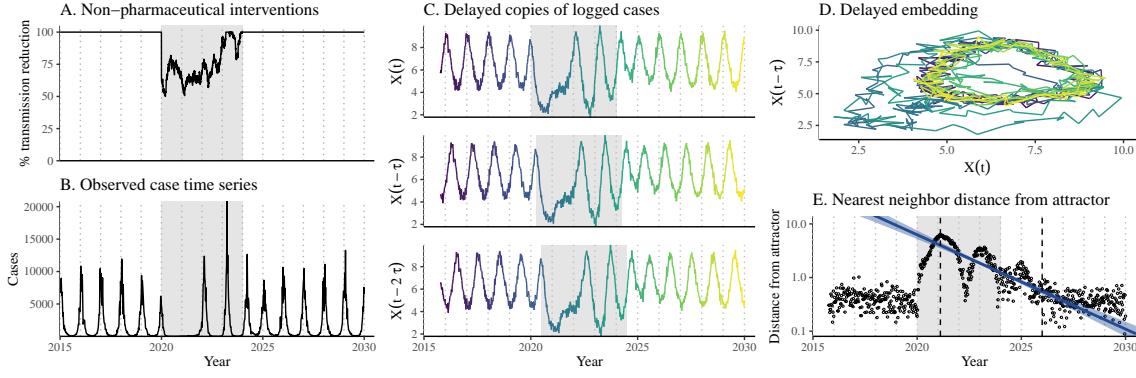


Figure 3: **A schematic diagram explaining the inference of pathogen resilience from synthetic data.** (A) A realistic example of simulated pandemic perturbations, represented by a relative reduction in transmission. (B) The impact of the synthetic pandemic perturbation on epidemic dynamics simulated 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. Blue lines and dashed regions represent the linear regression fit and the associated 95% confidence interval. This distance time series can be used to infer pathogen resilience after choosing an appropriate window for linear regression. For illustration purposes, an arbitrary fitting window was chosen.

dependently to reconstruct the empirical attractor and obtained the corresponding time series of distances from attractors (Supplementary Figure S8). Then, we used the automated window selection criterion to fit a linear regression and estimated 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 (Supplementary Figure S9; Materials and Methods).

For all pathogens we considered, resilience estimates fell between 0.4/year and 1.8/year (Figure 4A). We estimated the mean resilience of common respiratory pathogens to be 0.99/year (95% CI: 0.81/year–1.18/year). For reference, this is ≈ 7.5 times higher than the intrinsic resilience of pre-vaccination measles in England and Wales ($\approx 0.13/\text{year}$). Finally, resilience estimates for norovirus, a gastrointestinal pathogen, were comparable to those of common respiratory pathogens: 1.44/year (95% CI: 1.01/year–1.87/year) for Hong Kong and 1.07/year (95% CI: 0.86/year–1.29/year) for Korea. Based on a simple ANOVA test, we did not find significant differences in resilience estimates across countries ($p = 0.25$) or pathogens ($p = 0.67$).

Using resilience estimates, we predicted when each pathogen would hypothetically return to their pre-pandemic dynamics, assuming no long-term change in the attrac-

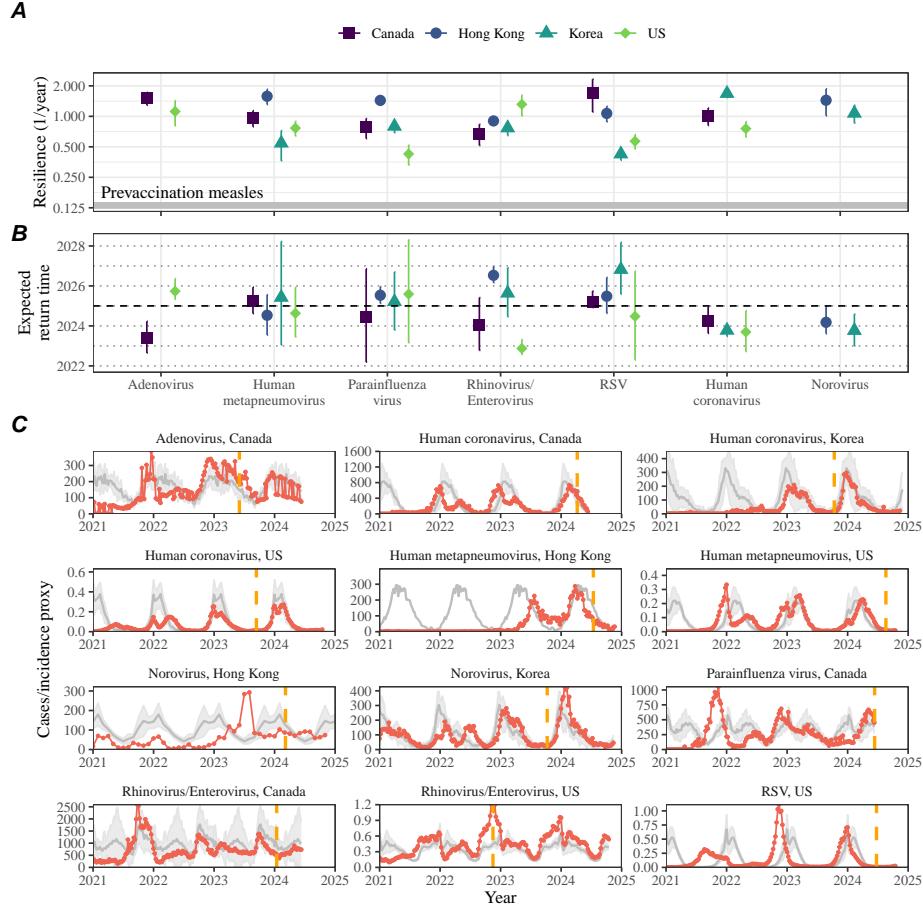


Figure 4: **Summary of resilience estimates and predictions for return time.** (A) Estimated pathogen resilience. The gray horizontal line represents the intrinsic resilience of pre-vaccination measles dynamics. (B) Predicted timing of when each pathogen will return to their pre-pandemic cycles. The dashed line in panel B indicates the end of 2024. 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.

271 tor. Specifically, we extended our linear regression fits to distance-from-attractor
 272 time series and ask when the predicted regression line will cross a threshold value;
 273 since we relied on nearest neighbor distances, pre-pandemic distances are always
 274 greater than zero (Figure 3E), meaning that we can use the mean of pre-pandemic
 275 distances as our threshold.

276 We predicted that a return to pre-pandemic cycles has occurred or would be

imminent for most pathogens (Figure 4B). In particular, we predicted that 12 out of 23 pathogen-country pairs should have already returned before the end of 2024. For almost all pathogens that were predicted to have returned already, the observed epidemic dynamics showed clear convergence towards their pre-pandemic seasonal averages, confirming our predictions (Figure 4C). However, there were a few exceptions, including norovirus in Hong Kong and rhinovirus/enterovirus in the US, where the observed epidemic dynamics in 2024 exhibit clear deviation from their pre-pandemic seasonal averages (Figure 4C; Figure S9). These observations suggest a possibility that some common respiratory pathogens may have converged to different attractors or are still exhibiting non-equilibrium dynamics. In contrast, pathogens that were predicted to have not returned yet also showed clear differences from their pre-pandemic seasonal averages; as many of these pathogens are predicted to return in 2025–2026, we may be able to test these predictions in near future (Supplementary Figure S10). Our reconstructions of distance time series and estimates of pathogen resilience and expected return time were generally robust to choices of embedding dimensions (Supplementary Figure S11–12).

Susceptible host dynamics explain variation in pathogen resilience

So far, we have focused on quantifying pathogen resilience from the observed patterns of pathogen re-emergence following pandemic perturbations. But what factors determine how resilient a host-pathogen system is? To address this question, we used the SIRS model to explore how changes in susceptible host dynamics affect pathogen resilience. To do so, we varied the basic reproduction number \mathcal{R}_0 , which represents the average number of secondary infections caused by a newly infected individual in a fully susceptible population, and the duration of immunity and computed intrinsic resilience for each parameter.

We found that an increase in \mathcal{R}_0 and a decrease in the duration of immunity correspond to an increase in pathogen resilience (Figure 5A). Similarly, an increase in \mathcal{R}_0 and a decrease in the duration of immunity corresponds to a faster per-capita rate of susceptible replenishment, which is defined as the ratio between absolute rate at which new susceptibles enter the population and the equilibrium number of susceptible individuals in the population, S^* (Figure 5B). We note that a higher \mathcal{R}_0 drives a faster per-capita susceptible replenishment rate by decreasing the susceptible proportion at equilibrium, S^* . For a simple SIR model that assumes a life-long immunity, we can show analytically that pathogen resilience is proportional to the per-capita rate of susceptible replenishment (Materials and Methods). Overall, these observations suggest that a faster per-capita susceptible replenishment rate causes the system to be more resilient.

By taking the average values of empirical resilience values for each pathogen, we were able to map each pathogen onto a set of parameters of the SIRS model that are

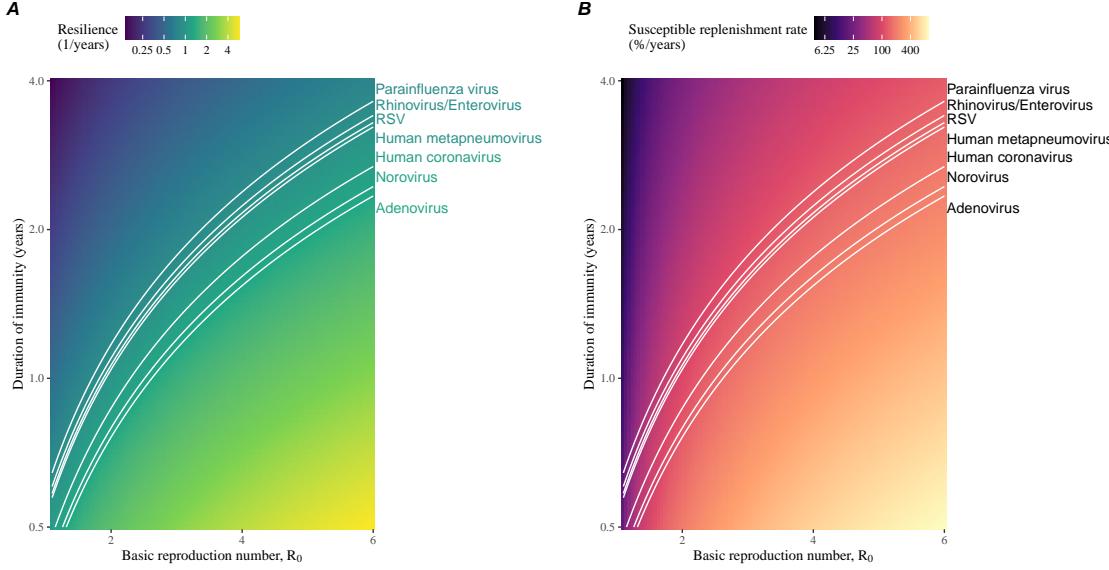


Figure 5: Linking pathogen resilience to epidemiological parameters and susceptible host dynamics. (A) Intrinsic resilience as a function of the basic reproduction number \mathcal{R}_0 and the duration of immunity. (B) Per-capita susceptible replenishment rate as a function of the basic reproduction number \mathcal{R}_0 and the duration of immunity. The standard SIRS model without seasonal forcing is used to compute intrinsic resilience and the per-capita susceptible replenishment rate. Lines correspond to a set of parameters that are consistent with mean resilience estimates for each pathogen, averaged across different countries.

317 consistent with corresponding resilience estimates (Figure 5A). Across all pathogens
 318 we considered, we estimated that the average duration of immunity is likely to be
 319 short (< 4 years) across a plausible range of \mathcal{R}_0 (< 6). We were also able to obtain
 320 a plausible range of susceptible replenishment rates for each pathogen (Figure 5B),
 321 but there was a large uncertainty in the estimates for susceptible replenishment rates
 322 due to a lack of one-to-one correspondence between susceptible replenishment rates
 323 and pathogen resilience.

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

326 Even in the absence of major pandemic perturbations, host-pathogen systems are
 327 expected to experience continued perturbations of varying degrees from changes in
 328 epidemiological conditions, such as human behavior, climate, and viral evolution.
 329 These perturbations can also arise from demographic stochasticity, which is inherent
 330 to any ecological systems. Here, we used a seasonally unforced SIRS model

331 with birth/death to explore how resilience of a host-pathogen system determines
 332 the sensitivity to perturbations caused by demographic stochasticity (Materials and
 333 Methods).

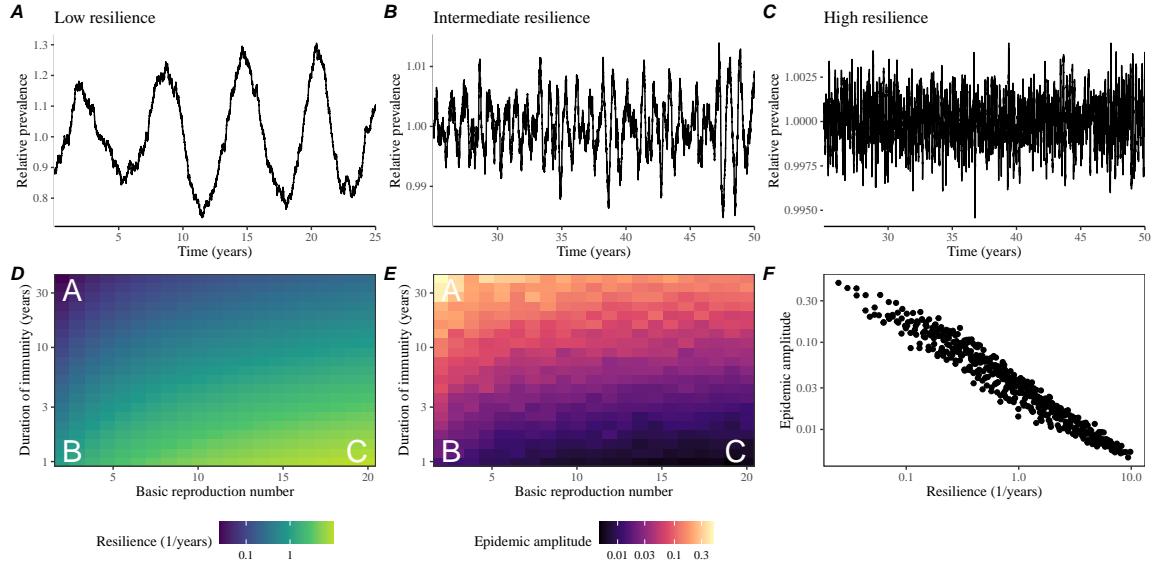


Figure 6: Linking resilience of a host-pathogen system to its sensitivity to stochastic perturbations. (A–C) Epidemic trajectories of a stochastic SIRS model across three different resilience values: low, intermediate, and high. The relative prevalence was calculated by dividing infection prevalence by its mean value. (D) Intrinsic resilience of a system as a function of the basic reproduction number \mathcal{R}_0 and the duration of immunity. (E) Epidemic amplitude as a function of the basic reproduction number \mathcal{R}_0 and the duration of immunity. The epidemic amplitude corresponds to $(\max I - \min I)/(2\bar{I})$, where \bar{I} represents the mean prevalence. Labels A–C in panels D and E correspond to scenarios shown in panels A–C. (F) The relationship between pathogen resilience and epidemic amplitude.

334 We found that resilience of a host-pathogen system determines the amount of de-
 335 viation from the deterministic trajectory caused by demographic stochasticity, with
 336 less resilient systems experiencing larger deviations (Figure 6). Notably, less resilent
 337 systems also exhibited slower epidemic cycles (Figure 6A–C). The periodicity of this
 338 epidemic cycle matched those predicted by the intrinsic periodicity of the system
 339 (Supplementary Figure S13) where the intrinsic resilience of the system is inversely
 340 proportional to its intrinsic periodicity (Supplementary Figure S14). However, we
 341 note that the interplay between seasonal transmission and intrinsic periodicity can
 342 also lead to complex cycles, as illustrated by a recent analysis of *Mycoplasma pneumoniae*
 343 dynamics [24].

344 We also note that the intrinsic resilience is not the sole determinant for how sen-
 345 sitive the system is to stochastic perturbations. For example, the population size

346 and average duration of infection also affect the amount of deviation from the deter-
347 ministic trajectory caused by demographic stochasticity, even though these quantities
348 have little to no impact on the intrinsic resilience (Supplementary Figure S15). These
349 conclusions were robust for the seasonally forced SIRS model (Supplementary Figure
350 S16).

351 Discussion

352 COVID-19 pandemic interventions caused major disruptions to circulation patterns
353 of both respiratory and non-respiratory pathogens, adding challenges to predicting
354 their future dynamics [1, 2, 3, 4]. However, these perturbations offer large-scale natu-
355 ral experiments for understanding how different pathogens respond to perturbations.
356 In this study, we showed that pathogen re-emergence patterns following pandemic
357 perturbations can be characterized through the lens of ecological resilience and pre-
358 sented a new method for estimating pathogen resilience from time series data. We
359 showed that variation in pathogen resilience can be explained by the differences in
360 susceptible host dynamics, where faster replenishment of the susceptible pool corre-
361 sponds to a more resilient host-pathogen system. Finally, we showed that pathogen
362 resilience also determines the sensitivity to stochastic perturbations.

363 We analyzed case time series of common respiratory infections and norovirus
364 infections from Canada, Hong Kong, Korea, and the US to estimate their resilience.
365 Overall, we estimated the resilience of these pathogens to range from 0.4/year to
366 1.8/year, which is 3–14 times more resilient than prevaccination measles. Consistent
367 with other epidemiological evidence [25, 26, 27, 28], these resilience estimates indicate
368 that common respiratory pathogens and norovirus likely exhibit faster susceptible
369 replenishment and are therefore more persistent, indicating potential challenges in
370 controlling these pathogens.

371 Based on our resilience estimates, we made phenomenological predictions about
372 when each pathogen will return to their endemic cycles. For the most part, we
373 accurately predicted which pathogens should have already returned before the end
374 of 2024. However, there were two main exceptions (i.e., norovirus in Hong Kong
375 and rhinovirus/enterovirus in the US), suggesting that these pathogens may be con-
376 verging to new endemic cycles or experiencing long-term transient behavior. These
377 changes may reflect changes in surveillance or actual shift in the dynamics, caused
378 by permanent changes in behavior or population-level immunity. While it may seem
379 unlikely that permanent changes in behavior would only affect a few pathogens and
380 not others, we cannot rule out this possibility given differences in the observed mean
381 age of infections and therefore the differences in age groups that primarily drive
382 transmission [29, 30]. Differences in the mode of transmission between respiratory
383 vs gastrointestinal pathogens may also contribute to the differences in responses to
384 pandemic perturbations.

385 For almost half of the pathogens we considered, we predicted that their return

386 to original epidemic patterns is imminent. We will need a few more years of data
387 to test whether these pathogens will eventually return to their original dynamics or
388 eventually converge to a different attractor. We also cannot rule out the possibility
389 that some pathogens may exhibit long-term transient behaviors following pandemic
390 perturbations. Overall, these observations echo earlier studies that highlighted the
391 long-lasting impact of pandemic perturbations [8, 31, 32, 4, 24].

392 We showed that susceptible host dynamics shape pathogen resilience, where faster
393 replenishment of the susceptible population causes the pathogen to be more resilient.
394 For simplicity, we focused on waning immunity and birth as the main drivers of the
395 susceptible host dynamics but other mechanisms can also contribute to the replenish-
396 ment of the susceptible population. In particular, pathogen evolution, especially the
397 emergence of antigenically novel strains, can cause effective waning of immunity in
398 the population; therefore, we hypothesize that the rate of antigenic evolution is likely
399 a key feature of pathogen resilience. Future studies should explore the relationship
400 between the rate of evolution and resilience for antigenically evolving pathogens.

401 Quantifying pathogen resilience also offers novel approaches to validating population-
402 level epidemiological models. So far, most model validation in infectious disease ecol-
403 ogy is based on the ability of a model to reproduce the observed epidemic dynamics
404 and to predict future dynamics [33, 34, 27, 35, 36]. However, many models can
405 perform similarly under these criteria. For example, two major RSV models have
406 been proposed to explain biennial epidemic patterns: (1) a stage- and age-structured
407 model that allows disease severity to vary with number of past infections and age of
408 infection [27] and (2) a pathogen-interaction model that accounts for cross immunity
409 between RSV and human metapneumovirus [34]. Since both models can accurately
410 reproduce the observed epidemic patterns, standard criteria for model validation
411 do not allow us to distinguish between these two models from population-level data
412 alone. Instead, it would be possible to measure the empirical resilience of each model
413 by simulating various perturbations and comparing the simulations to estimates of
414 empirical resilience from data, using pandemic perturbations as a reference.

415 There are several limitations to our work. First, we did not extensively explore
416 other approaches to reconstructing the attractor. Recent studies showed that more
417 sophisticated approaches, such as using non-uniform embedding, can provide more
418 robust reconstruction for noisy data [23]. In the context of causal inference, choices
419 about embedding can have major impact on the resulting inference [37]. Our re-
420 silience estimates are likely overly confident given a lack of uncertainties in attractor
421 reconstruction as well as the simplicity of our statistical framework. Nonetheless,
422 as illustrated in our sensitivity analyses, inferences about pathogen resilience in our
423 SIRS model appear to be robust to decisions about embedding lags and dimensions—
424 this is because tracking the rate at which the system approaches the attractor is likely
425 a much simpler problem than making inferences about causal directionality. Short
426 pre-pandemic time series also limit our ability to accurately reconstruct the attrac-
427 tor and contribute to the crudeness of our resilience estimates; although this is less
428 likely a problem for respiratory pathogens that are strongly annual, our attractor

429 reconstruction may be inaccurate for those exhibiting multi-annual cycles, such as
430 adenovirus in Hong Kong and Korea. Our framework also do not allow us to distin-
431 guish whether a system has settled to a new attractor or is experiencing long-term
432 transient behavior. Uncertainties in pathogen dynamics due to changes in testing
433 patterns further contribute to the crudeness of our resilience estimates. Despite these
434 limitations, our qualitative prediction that common respiratory pathogens are more
435 resilient than prevaccination measles is also likely to be robust, given how rapidly
436 many respiratory pathogens returned to their original cycles following pandemic per-
437 turbations.

438 Predicting the impact of anthropogenic changes on infectious disease dynamics
439 is a fundamental aim of infectious disease research in a rapidly changing world. Our
440 study illustrates that how a host-pathogen system responds to both small and large
441 perturbations is largely predictable through the lens of ecological resilience. In par-
442 ticular, quantifying the resilience of a host-pathogen system offers a unique insight
443 into questions about endemic pathogens' responses to pandemic perturbations, in-
444 cluding whether some pathogens will exhibit long-lasting impact from the pandemic
445 perturbation or not. More broadly, a detailed understanding of the determinants of
446 pathogen resilience can provide deeper understanding of pathogen persistence.

447 Materials and Methods

448 Data

449 We gathered time series on respiratory infections from Canada, Hong Kong, Korea,
450 and United States (US). As a reference, we also included time series data on norovirus
451 infections when available. In contrast to respiratory pathogens, we hypothesized
452 gastrointestinal viruses, such as norovirus, to be differently affected by pandemic
453 perturbations.

454 Weekly time series of respiratory infection cases in Canada came from a publicly
455 available website by the Respiratory Virus Detection Surveillance System, which
456 collects data from select laboratories across Canada [38]. Weekly time series of
457 respiratory infection cases in Hong Kong came from a publicly available website by
458 the Centre for Health Protection, Department of Health [39, 40]. Weekly time series
459 of acute respiratory infection cases in Korea came from a publicly available website
460 by the Korea Disease Control and Prevention Agency [41]. Finally, weekly time series
461 of respiratory infection cases in the US were obtained from the National Respiratory
462 and Enteric Virus Surveillance System. Time series on number of tests were also
463 available in Canada, Hong Kong, and the US, but not in Korea.

464 Data processing

465 For all time series, we rounded every year to 52 weeks by taking the average number
466 of cases and tests between the 52nd and 53rd week. We also rescaled all time series to

467 account for changes in testing patterns, which were then used for the actual analysis.

468 For Canada, an increase in testing was observed from 2013 to 2024 (Supplementary
469 Figure S17). To account for this increase, we calculated a 2 year moving average
470 for the number of tests for each pathogen, which we used as a proxy for testing effort.
471 Then, we divided the smoothed testing patterns by the smoothed value at the final
472 week such that the testing effort has a maximum of 1. We then divided weekly cases
473 by the testing effort to obtain a scaled case time series. A similar approach was used
474 earlier for an analysis of RSV time series in the US to account for changes in testing
475 patterns [27].

476 For Hong Kong, we applied the same scaling procedure to the time series as we
477 did for Canada. In this case, we only adjusted for testing efforts up to the end of 2019
478 because there was a major reduction in testing for common respiratory pathogens
479 between 2020 and 2023 (Supplementary Figure S18).

480 For Korea, while we did not have information on testing, the reported number
481 of respiratory infections consistently increased from 2013 to the end of 2019, which
482 we interpreted as changes in testing patterns (Supplementary Figure S19). Since
483 we did not have testing numbers, we used the weekly sum of all acute respiratory
484 viral infection cases as a proxy for testing, which were further smoothed with moving
485 average and scaled to have a maximum of 1. For Korea, we also only adjusted for
486 testing efforts up to the end of 2019.

487 In the US, there has been a large increase in testing for some respiratory pathogens,
488 especially RSV, which could not be corrected by simple scaling (Supplementary Figure
489 S20). Instead, we derived an incidence proxy by multiplying the test positivity
490 with influenza-like illness positivity, which was taken from <https://gis.cdc.gov/grasp/fluvie>. This method of estimating an incidence proxy has been recently applied in the analysis of seasonal coronaviruses [7] and *Mycoplasma pneumoniae* infections [4]. Detailed assumptions and justifications are provided in [42].

495 Data summary

496 To make qualitative comparisons between pre- and post-perturbation dynamics of
497 respiratory pathogen circulation patterns, we calculated the mean seasonal patterns
498 using time series of either rescaled cases or incidence proxy estimates before 2020. We
499 did so by taking the mean value in each week across all years before 2020. Confidence
500 intervals around the means were calculated using a simple t test.

501 Estimating pathogen resilience

502 In order to measure pathogen resilience from surveillance data, we first reconstructed
503 the empirical pre-pandemic attractor of the system using Takens' embedding theorem
504 [17]. Specifically, for a given pathogen, we took the pre-pandemic (before 2020) case
505 time series $C(t)$ and reconstructed the attractor using delayed embedding with a

506 uniform delay of τ and dimension M :

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

507 Here, the delay τ was determined by calculating the autocorrelation of the logged
 508 pre-pandemic time series and asking when the autocorrelation crosses 0 for the first
 509 time [23]; a typical delay for an annual outbreak is around 13 weeks.

510 Then, for a given delay τ , we determined the embedding dimension M using the
 511 false nearest neighbors approach [22, 23]. To do so, we started with an embedding
 512 dimension e and constructed a set of points $A_{\tau,e} = \{X_{\tau,e}(t) | t < 2020\}$. Then, for
 513 each point $X_{\tau,e}(t)$, we determined the nearest neighbor from the set $A_{\tau,e}$, which we
 514 denote $X_{\tau,e}(t_{nn})$ for $t \neq t_{nn}$. Then, if the distance between these two points in the
 515 $e+1$ dimension, $D_{\tau,e+1}(t) = \|X_{\tau,e+1}(t_{nn}) - X_{\tau,e+1}(t)\|_2$, is larger than their distance in
 516 the e dimension, $D_{\tau,e}(t) = \|X_{\tau,e}(t_{nn}) - X_{\tau,e}(t)\|_2$, these two points are deemed to be
 517 false nearest neighbors; specifically, we used a threshold R for the ratio between two
 518 distances $D_{\tau,e+1}(t)/D_{\tau,e}(t)$ to determine false nearest neighbors. The first embed-
 519 ding dimension e that does not have any false nearest neighbors corresponds to the
 520 embedding dimension M for a given pathogen-country pair. For the main analysis,
 521 we used $R = 10$, which was chosen from a sensitivity analysis against simulated data
 522 (Supplementary Text). Once we determined the embedding lag τ and dimension M ,
 523 we apply the embedding to the entire time series and calculate the nearest neigh-
 524 bor distance against the attractor $A_{\tau,M}$ to obtain a time series of distance from the
 525 attractor $D_{\tau,M}(t)$.

526 From a time series of distances from the attractor, we estimated pathogen re-
 527 silience by fitting a linear regression to an appropriate window. To automatically
 528 select fitting windows, we began by smoothing the distance time series using locally
 529 estimated scatterplot smoothing (LOESS) to obtain $\hat{D}_{\tau,M}(t)$, where the smoothing
 530 is performed on a log scale and exponentiated afterwards. This smoothing allowed
 531 us to find appropriate threshold values for selecting fitting windows that are insensi-
 532 tive to errors in our estimates of distance from the attractor. Then, we determined
 533 threshold values (T_{start} and T_{end}) for the smoothed distances and choose the fitting
 534 window based on when $\hat{D}_{\tau,M}(t)$ crosses these threshold values for the first time.
 535 These thresholds were determined by first calculating the maximum distance,

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

536 and the mean pre-pandemic distance,

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

537 as a reference, and then dividing their ratios into K equal bins,

$$T_{\text{start}} = \hat{D}_{\text{mean}} \times \left(\frac{\max \hat{D}}{\hat{D}_{\text{mean}}} \right)^{(K-a)/K}, \quad (5)$$

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

538 where a represents the truncation threshold. This allows us to discard the initial
 539 period during which the distance increases (from the introduction of intervention
 540 measures) and the final period during which the distance plateaus (as the system
 541 reaches an attractor). The fitting window is determined based on when the smoothed
 542 distance $\hat{D}_{\tau,M}(t)$ crosses these threshold values for the first time; then, we fit a
 543 linear regression to logged (unsmoothed) distances $\log D_{\tau,M}(t)$ using that window.
 544 Alongside the threshold R for the false nearest neighbors approach, we tested optimal
 545 choices for K and a values using simulations (Supplementary Text). We used $K = 19$
 546 and $a = 2$ throughout the paper based on the simulation results.

547 Mathematical modeling

548 Throughout the paper, we use a series of mathematical models to illustrate the
 549 concept of pathogen resilience and to understand the determinants of pathogen re-
 550 silience. In general, the intrinsic resilience of a given system is given by the largest
 551 real part of the eigenvalues of the linearized system at endemic equilibrium. Here, we
 552 focus on the SIRS model with demography (birth and death) and present the details
 553 of other models in Supplementary Text. The SIRS (Susceptible-Infected-Recovered-
 554 Susceptible) model is the simplest model that allows for waning of immunity, where
 555 recovered (immune) individuals are assumed to become fully susceptible after an
 556 average of $1/\delta$ time period. The dynamics of the SIRS model is described by the
 557 following set of differential equations:

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

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

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

558 where μ represents the birth and death rates, $\beta(t)$ represents the time-varying trans-
 559 mission rate, and γ represents the recovery rate. The basic reproduction number
 560 $\mathcal{R}_0(t) = \beta(t)/(\gamma + \mu)$ is defined as the average number of secondary infections that
 561 a single infected individual would cause in a fully susceptible population at time t
 562 and measures the intrinsic transmissibility of a pathogen.

563 When we introduced the idea of pathogen resilience (Figure 2), we imposed sinu-
 564 soidal changes to the transmission rate to account for seasonal transmission,

$$\beta(t) = b_1(1 + \theta \cos(2\pi(t - \phi)))\alpha(t), \quad (10)$$

565 where b_1 represents the baseline transmission rate, θ represents the seasonal ampli-
 566 tude, and ϕ represents the seasonal offset term. Here, we also introduced an extra

567 multiplicative term $\alpha(t)$ to account for the impact of pandemic perturbations, where
 568 $\alpha(t) < 1$ indicates transmission reduction. Figure 2A and 2B were generated assuming
 569 $b_1 = 3 \times (365/7 + 1/50)/\text{years}$, $\theta = 0.2$, $\phi = 0$, $\mu = 1/50/\text{years}$, $\gamma = 365/7/\text{years}$,
 570 and $\delta = 1/2/\text{years}$. Specifically, $b_1 = 3 \times (365/7 + 1/50)/\text{years}$ implies $\mathcal{R}_0 = 3$, where
 571 $(365/7 + 1/50)/\text{years}$ represent the rate of recovery. In Figure 2A, we imposed a 50%
 572 transmission reduction for 6 months from 2020:

$$\alpha(t) = \begin{cases} 0.5 & 2020 \leq t < 2020.5 \\ 1 & \text{otherwise} \end{cases} \quad (11)$$

573 In Figure 2B, we imposed a 50% transmission reduction for 6 months from 2020 and
 574 a permanent 10% reduction onward:

$$\alpha(t) = \begin{cases} 1 & t < 2020 \\ 0.5 & 2020 \leq t < 2020.5 \\ 0.9 & 2020.5 \leq t \end{cases} \quad (12)$$

575 In both scenarios, we simulated the SIRS model from the same initial conditions
 576 ($S(0) = 1/\mathcal{R}_0$, $I(0) = 1 \times 10^{-6}$, and $R(0) = 1 - S(0) - I(0)$) from 1900 until 2030.
 577 Throughout the paper, all deterministic models were solved using the `lsoda` solver
 578 from the `deSolve` package [43] in R [44].

579 To measure the empirical resilience of the SIRS model (Figure 2C and 2F), we
 580 computed the normalized distance between post-intervention susceptible and logged
 581 infected proportions and their corresponding unperturbed values at the same time:

$$\sqrt{\left(\frac{S(t) - S_{\text{unperturbed}}(t)}{\sigma_S}\right)^2 + \left(\frac{\log I(t) - \log I_{\text{unperturbed}}(t)}{\sigma_{\log I}}\right)^2}, \quad (13)$$

582 where σ_S and $\sigma_{\log I}$ represent the standard deviation in the unperturbed susceptible
 583 and logged infected proportions. The unperturbed values were obtained by simulating
 584 the same SIRS model without pandemic perturbations ($\alpha = 1$). We normalized
 585 the differences in susceptible and logged infected proportions to allow both quantities
 586 to equally contribute to the changes in distance from the attractor. We used logged
 587 prevalence, instead of absolute prevalence, in order to capture epidemic dynamics
 588 in deep troughs during the intervention period. In Supplementary Materials, we
 589 also compared how the degree of seasonal transmission affects empirical resilience
 590 by varying θ from 0 to 0.4; when we assumed no seasonality ($\theta = 0$), we did not
 591 normalize the distance because the standard deviation of pre-intervention dynamics
 592 are zero.

593 We used the SIRS model to understand how underlying epidemiological parameters
 594 affect pathogen resilience and determine the relationship to underlying sus-
 595 ceptible host dynamics. For the simple SIRS model without seasonal transmission
 596 ($\theta = 0$), the intrinsic resilience equals

$$-\frac{\text{Re}(\lambda)}{2} = \frac{\delta + \beta I^* + \mu}{2}. \quad (14)$$

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

$$I^* = \frac{(\delta + \mu)(\beta - (\gamma + \mu))}{\beta(\delta + \gamma + \mu)}. \quad (15)$$

598 The susceptible replenishment rate is given by

$$S_{\text{replenish}} = \frac{\mu + \delta R}{S^*}, \quad (16)$$

599 where $S^* = 1/\mathcal{R}_0$ represents the equilibrium proportion of susceptible individuals.
600 We varied the basic reproduction number \mathcal{R}_0 between 1.1 to 6 and the average
601 duration of immunity $1/\delta$ between 2 to 4 years, and computed these two quantities.
602 In doing so, we fixed all other parameters: $\mu = 1/80/\text{years}$ and $\gamma = 365/7/\text{years}$.
603 When infection provides a life-long immunity ($\delta = 0$), the intrinsic resilience is
604 inversely proportional to the susceptible replenishment rate:

$$-\frac{\text{Re}(\lambda)}{2} = \frac{\mu}{2S^*} = \frac{S_{\text{replenish}}}{2}. \quad (17)$$

605 Finally, we used a seasonally unforced stochastic SIRS model without demog-
606 raphy to understand how pathogen resilience affects sensitivity of the system to
607 demographic stochasticity (see Supplementary Text for the details of the stochas-
608 tic SIRS model). By varying the basic reproduction number \mathcal{R}_0 between 2 to 20
609 and the average duration of immunity $1/\delta$ between 1 to 40 years, we ran the SIRS
610 model for 100 years and computed the epidemic amplitude, which we defined as
611 $(\max I - \min I)/(2\bar{I})$. Each simulation began from the equilibrium, and we trun-
612 cated the initial 25 years before computing the epidemic amplitude. In doing so,
613 we assumed $\gamma = 365/7/\text{years}$ and fixed the population size to 1 billion to prevent
614 any fadeouts. We also considered a seasonally forced stochastic SIRS model without
615 demography, assuming an amplitude of seasonal forcing of 0.04; in this case, we com-
616 puted the relative epidemic amplitude by comparing the deterministic and stochastic
617 trajectories (Supplementary Materials).

618 Data availability

619 All data and code are stored in a publicly available GitHub repository (<https://github.com/cobeylab/return-time>).

621 Funding

622 S.W.P. is a Peter and Carmen Lucia Buck Foundation Awardee of the Life Sciences
623 Research Foundation. S.C. was supported by Federal funds from the National Insti-
624 tute of Allergy and Infectious Diseases, National Institutes of Health, Department of
625 Health and Human Services under CEIRR contract 75N93021C00015. The content is
626 solely the responsibility of the authors and does not necessarily represent the official
627 views of the NIAID or the National Institutes of Health.

628 **Supplementary Text**

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

630 In Figure 2G–I, we used a more realistic, stage-structured model to illustrate how
 631 transient phenomena can cause the system to slow down. Specifically, we used the
 632 stage-structured RSV model proposed by [27], which assumes that subsequent rein-
 633 fections cause an individual to become less susceptible and transmissible than previ-
 634 ous infections. In contrast to a standard SIRS model, this model does not include a
 635 recovered compartment, which allow for temporary protection against new infections,
 636 and assumes that recovered individuals are immediately susceptible to new infections.
 637 The model dynamics can be described as follows:

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

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

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

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

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

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

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

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

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

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

$$\beta(t) = b_1(1 + \theta \cos(2\pi(t - \phi)))\alpha(t) \quad (S10)$$

$$\lambda(t) = \beta(I_1 + \rho_1 I_2 + \rho_2(I_3 + I_4)), \quad (S11)$$

645 where b_1 represents the baseline transmission rate; θ represents the seasonal ampli-
 646 tude; ϕ represents the seasonal offset term; $\alpha(t)$ represents the intervention effect;

and ρ_i represents the impact of immunity on transmission reduction. We used the following parameters to simulate the impact of interventions on epidemic dynamics [27]: $b_1 = 9 \times (365/10 + 1/80)/\text{years}$, $\theta = 0.2$, $\phi = -0.1$, $\omega = 365/112/\text{years}$, $\gamma_1 = 365/10/\text{years}$, $\gamma_2 = 365/7/\text{years}$, $\gamma_3 = 365/5/\text{years}$, $\sigma_1 = 0.76$, $\sigma_2 = 0.6$, $\sigma_3 = 0.4$, $\rho_1 = 0.75$, $\rho_2 = 0.51$, and $\mu = 1/80/\text{years}$. We assumed a 50% transmission reduction for 6 months from 2020:

$$\alpha(t) = \begin{cases} 0.5 & 2020 \leq t < 2020.5 \\ 1 & \text{otherwise} \end{cases} \quad (\text{S12})$$

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

$$\bar{S} = S_0 + \sigma_1 S_1 + \sigma_2 S_2 + \sigma_3 S_3, \quad (\text{S13})$$

and total prevalence,

$$I_{\text{total}} = I_1 + I_2 + I_3 + I_4. \quad (\text{S14})$$

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

Resilience of a multistain system.

We used a simple two-strain model to show that a multistain host-pathogen system that is coupled through cross immunity can be described by a single resilience value. The model dynamics can be described as follows [34]:

$$\frac{dS}{dt} = \mu - \mu S - (\lambda_1 + \lambda_2)S + \delta_1 R_1 + \delta_2 R_2 \quad (\text{S15})$$

$$\frac{dI_1}{dt} = \lambda_1 S - (\gamma_1 + \mu)I_1 \quad (\text{S16})$$

$$\frac{dI_2}{dt} = \lambda_2 S - (\gamma_2 + \mu)I_2 \quad (\text{S17})$$

$$\frac{dR_1}{dt} = \gamma_1 I_1 - \lambda_2 \epsilon_{21} R_1 - \delta_1 R_1 + \delta_2 R - \mu R_1 \quad (\text{S18})$$

$$\frac{dR_2}{dt} = \gamma_2 I_2 - \lambda_1 \epsilon_{12} R_2 - \delta_2 R_2 + \delta_1 R - \mu R_2 \quad (\text{S19})$$

$$\frac{dJ_1}{dt} = \lambda_1 \epsilon_{12} R_2 - (\gamma_1 + \mu) J_1 \quad (\text{S20})$$

$$\frac{dJ_2}{dt} = \lambda_2 \epsilon_{21} R_1 - (\gamma_2 + \mu) J_2 \quad (\text{S21})$$

$$\frac{dR}{dt} = \gamma_1 J_1 + \gamma_2 J_2 - \delta_1 R - \delta_2 R - \mu R \quad (\text{S22})$$

664 where S represents the proportion of individuals who are fully susceptible to infections
 665 by both strains; I_1 represents the proportion of individuals who are infected with strain 1 without prior immunity; I_2 represents the proportion of individuals who are infected with strain 2 without prior immunity; R_1 represents the proportion of individuals who are fully immune against strain 1 and partially susceptible to reinfection by strain 2; R_2 represents the proportion of individuals who are fully immune against strain 2 and partially susceptible to reinfection by strain 1; J_1 represents the proportion of individuals who are infected with strain 1 with prior immunity against strain 2; J_2 represents the proportion of individuals who are infected with strain 2 with prior immunity against strain 1; R represents the proportion of individuals who are immune to infections from both strains; μ represents the birth/death rate; λ_1 and λ_2 represent the force of infection from strains 1 and 2, respectively; δ_1 and δ_2 represent the waning immunity rate; γ_1 and γ_2 represent the recovery rate; ϵ_{21} and ϵ_{12} represent the susceptibility to reinfection with strains 2 and 1, respectively, given prior immunity from infection with strains 1 and 2, respectively. The force of infection is modeled as follows:
 679

$$\beta_1 = b_1(1 + \theta_1 \sin(2\pi(t - \phi_1)))\alpha(t) \quad (\text{S23})$$

$$\beta_2 = b_2(1 + \theta_2 \sin(2\pi(t - \phi_2)))\alpha(t) \quad (\text{S24})$$

$$\lambda_1 = \beta_1(I_1 + J_1) \quad (\text{S25})$$

$$\lambda_2 = \beta_2(I_2 + J_2) \quad (\text{S26})$$

680 In Supplementary Figures S2–S4, we assumed the following parameters: $b_1 = 2 \times$
 681 $52/\text{years}$, $b_2 = 4 \times 52/\text{years}$, $\phi_1 = \phi_2 = 0$, $\epsilon_{12} = 0.9$, $\epsilon_{21} = 0.5$, $\gamma_1 = \gamma_2 = 52/\text{years}$,
 682 $\delta_1 = \delta_2 = 1/\text{years}$, and $\mu = 1/70/\text{years}$. For all simulations, we assumed a 50%
 683 transmission reduction for 6 months from 2020:

$$\alpha(t) = \begin{cases} 0.5 & 2020 \leq t < 2020.5 \\ 1 & \text{otherwise} \end{cases} \quad (\text{S27})$$

684 The seasonal amplitude θ is varied from 0 to 0.4. All simulations were run from 1900
 685 to 2030 with following initial conditions: $S(0) = 1 - 2 \times 10^{-6}$, $I_1(0) = 1 \times 10^{-6}$,
 686 $I_2(0) = 1 \times 10^{-6}$, $R_1(0) = 0$, $R_2(0) = 0$, $J_1(0) = 0$, $J_2(0) = 0$, and $R(0) = 0$.

687 We considered three scenarios for measuring pathogen resilience: (1) we only have
 688 information about strain 1, (2) we only have information about strain 2, and (3) we
 689 are unable to distinguish between strains. In the first two scenarios (see panels A–C
 690 for strain 1 and panels D–F for strain 2), we considered the dynamics of average
 691 susceptibility for each strain and total prevalence:

$$\bar{S}_1 = S + \epsilon_{12}R_2 \quad (\text{S28})$$

$$\hat{I}_1 = I_1 + J_1 \quad (\text{S29})$$

$$\bar{S}_2 = S + \epsilon_{21}R_1 \quad (\text{S30})$$

$$\hat{I}_2 = I_2 + J_2 \quad (\text{S31})$$

692 In the third scenario (panels G–I), we considered the dynamics of total susceptible
693 and infected populations:

$$\hat{S} = S + R_2 + R_1 \quad (\text{S32})$$

$$\hat{I} = I_1 + J_1 + I_2 + J_2 \quad (\text{S33})$$

694 These quantities were used to compute the normalized distance from the attractor,
695 as described in the main text.

696 Estimating intrinsic resilience using a mechanistic model

697 We tested whether we can reliably estimate the intrinsic resilience of a system by fit-
698 ting a mechanistic model. Specifically, we simulated case time series from stochastic
699 SIRS and two-strain models and fitted a simple, deterministic SIRS model using a
700 Bayesian framework [4, 24, 45].

701 We simulated the models in discrete time with a daily time step ($\Delta t = 1$),
702 incorporating demographic stochasticity:

$$\beta(t) = \mathcal{R}_0 \left(1 + \theta \cos \left(\frac{2\pi t}{364} \right) \right) \alpha(t)(1 - \exp(-\gamma)) \quad (\text{S34})$$

$$\text{FOI}(t) = \beta(t)I(t - \Delta t)/N \quad (\text{S35})$$

$$B(t) \sim \text{Poisson}(\mu N) \quad (\text{S36})$$

$$\Delta S(t) \sim \text{Binom}(S(t - \Delta t), 1 - \exp(-(\text{FOI}(t) + \mu)\Delta t)) \quad (\text{S37})$$

$$N_{SI}(t) \sim \text{Binom}\left(\Delta S(t), \frac{\text{FOI}(t)}{\text{FOI}(t) + \mu}\right) \quad (\text{S38})$$

$$\Delta I(t) \sim \text{Binom}(I(t - \Delta t), 1 - \exp(-(\gamma + \mu)\Delta t)) \quad (\text{S39})$$

$$N_{IR}(t) \sim \text{Binom}\left(\Delta I(t), \frac{\gamma}{\gamma + \mu}\right) \quad (\text{S40})$$

$$\Delta R(t) \sim \text{Binom}(R(t - \Delta t), 1 - \exp(-(\delta + \mu)\Delta t)) \quad (\text{S41})$$

$$N_{RS}(t) \sim \text{Binom}\left(\Delta R(t), \frac{\delta}{\delta + \mu}\right) \quad (\text{S42})$$

$$S(t) = S(t - \Delta t) + N_{RS}(t) + B(t) - \Delta S(t) \quad (\text{S43})$$

$$I(t) = I(t - \Delta t) + N_{SI}(t) - \Delta I(t) \quad (\text{S44})$$

$$R(t) = R(t - \Delta t) + N_{IR}(t) - \Delta R(t) \quad (\text{S45})$$

703 where FOI represents the force of infection; N_{ij} represents the number of individuals
704 moving from compartment i to j on a given day; and $B(t)$ represents the number
705 of new births. All other parameters definitions can be found in the description of
706 the deterministic version of the model. We simulated the model on a daily scale—
707 assuming 364 days in a year so that it can be evenly grouped into 52 weeks—with
708 the following parameters: $\mathcal{R}_0 = 3$, $\theta = 0.1$, $\gamma = 1/7/\text{days}$, $\delta = 1/(364 \times 2)/\text{days}$,

⁷⁰⁹ $\mu = 1/(364 \times 50)/\text{days}$, and $N = 1 \times 10^8$. The model was simulated from 1900 to
⁷¹⁰ 2030 assuming $S(0) = N/3$, $I(0) = 100$, and $R(0) = N - S(0) - I(0)$. The observed
⁷¹¹ incidence from the model was then simulated as follows:

$$C(t) = \text{Beta-Binom}(N_{SI}(t), \rho, k), \quad (\text{S46})$$

⁷¹² where ρ represents the reporting probability and k represents the overdispersion
⁷¹³ parameter of beta-binomial distribution. Here, we used the beta-binomial distribu-
⁷¹⁴ tion to account for overdispersion in reporting. We assumed $\rho = 0.002$ (i.e., 0.2%
⁷¹⁵ probability) and $k = 1000$.

⁷¹⁶ We used an analogous approach for the two-strain model:

$$\beta_1(t) = b_1 \left(1 + \theta_1 \cos \left(\frac{2\pi(t - \phi_1)}{364} \right) \right) \alpha(t) \quad (\text{S47})$$

$$\beta_2(t) = b_2 \left(1 + \theta_2 \cos \left(\frac{2\pi(t - \phi_2)}{364} \right) \right) \alpha(t) \quad (\text{S48})$$

$$\text{FOI}_1(t) = \beta_1(t)(I_1(t - \Delta t) + J_1(t - \Delta t))/N \quad (\text{S49})$$

$$\text{FOI}_2(t) = \beta_2(t)(I_2(t - \Delta t) + J_2(t - \Delta t))/N \quad (\text{S50})$$

$$B(t) \sim \text{Poisson}(\mu N) \quad (\text{S51})$$

$$\Delta S(t) \sim \text{Binom}(S(t - \Delta t), 1 - \exp(-(\text{FOI}_1(t) + \text{FOI}_2(t) + \mu)\Delta t)) \quad (\text{S52})$$

$$N_{SI_1}(t) \sim \text{Binom}\left(\Delta S(t), \frac{\text{FOI}_1(t)}{\text{FOI}_1(t) + \text{FOI}_2(t) + \mu}\right) \quad (\text{S53})$$

$$N_{SI_2}(t) \sim \text{Binom}\left(\Delta S(t), \frac{\text{FOI}_2(t)}{\text{FOI}_1(t) + \text{FOI}_2(t) + \mu}\right) \quad (\text{S54})$$

$$\Delta I_1(t) \sim \text{Binom}(I_1(t - \Delta t), 1 - \exp(-(\gamma_1 + \mu)\Delta t)) \quad (\text{S55})$$

$$N_{I_1 R_1}(t) \sim \text{Binom}\left(\Delta I_1(t), \frac{\gamma_1}{\gamma_1 + \mu}\right) \quad (\text{S56})$$

$$\Delta I_2(t) \sim \text{Binom}(I_2(t - \Delta t), 1 - \exp(-(\gamma_2 + \mu)\Delta t)) \quad (\text{S57})$$

$$N_{I_2 R_2}(t) \sim \text{Binom}\left(\Delta I_2(t), \frac{\gamma_2}{\gamma_2 + \mu}\right) \quad (\text{S58})$$

$$\Delta R_1(t) \sim \text{Binom}(R_1(t - \Delta t), 1 - \exp(-(\epsilon_{21}\text{FOI}_2(t) + \rho_1 + \mu)\Delta t)) \quad (\text{S59})$$

$$N_{R_1 S}(t) \sim \text{Binom}\left(\Delta R_1(t), \frac{\rho_1}{\epsilon_{21}\text{FOI}_2(t) + \rho_1 + \mu}\right) \quad (\text{S60})$$

$$N_{R_1 J_2}(t) \sim \text{Binom}\left(\Delta R_1(t), \frac{\epsilon_{21}\text{FOI}_2(t)}{\epsilon_{21}\text{FOI}_2(t) + \rho_1 + \mu}\right) \quad (\text{S61})$$

$$\Delta R_2(t) \sim \text{Binom}(R_2(t - \Delta t), 1 - \exp(-(\epsilon_{12}\text{FOI}_1(t) + \rho_2 + \mu)\Delta t)) \quad (\text{S62})$$

$$N_{R_2 S}(t) \sim \text{Binom}\left(\Delta R_2(t), \frac{\rho_2}{\epsilon_{12}\text{FOI}_1(t) + \rho_2 + \mu}\right) \quad (\text{S63})$$

$$N_{R_2 J_1}(t) \sim \text{Binom}\left(\Delta R_2(t), \frac{\epsilon_{12}\text{FOI}_1(t)}{\epsilon_{12}\text{FOI}_1(t) + \rho_2 + \mu}\right) \quad (\text{S64})$$

$$\Delta J_1(t) \sim \text{Binom}(J_1(t - \Delta t), 1 - \exp(-(\gamma_1 + \mu)\Delta t)) \quad (\text{S65})$$

$$N_{J_1R}(t) \sim \text{Binom}\left(\Delta J_1(t), \frac{\gamma_1}{\gamma_1 + \mu}\right) \quad (\text{S66})$$

$$\Delta J_2(t) \sim \text{Binom}(J_2(t - \Delta t), 1 - \exp(-(\gamma_2 + \mu)\Delta t)) \quad (\text{S67})$$

$$N_{J_2R}(t) \sim \text{Binom}\left(\Delta J_2(t), \frac{\gamma_2}{\gamma_2 + \mu}\right) \quad (\text{S68})$$

$$\Delta R(t) \sim \text{Binom}(R(t - \Delta t), 1 - \exp(-(\rho_1 + \rho_2 + \mu)\Delta t)) \quad (\text{S69})$$

$$N_{RR_1}(t) \sim \text{Binom}\left(\Delta R(t), \frac{\rho_1}{\rho_1 + \rho_2 + \mu}\right) \quad (\text{S70})$$

$$N_{RR_2}(t) \sim \text{Binom}\left(\Delta R(t), \frac{\rho_2}{\rho_1 + \rho_2 + \mu}\right) \quad (\text{S71})$$

$$S(t) = S(t - \Delta t) - \Delta S(t) + B(t) + N_{R_1S}(t) + N_{R_2S}(t) \quad (\text{S72})$$

$$I_1(t) = I_1(t - \Delta t) - \Delta I_1(t) + N_{SI_1}(t) \quad (\text{S73})$$

$$I_2(t) = I_2(t - \Delta t) - \Delta I_2(t) + N_{SI_2}(t) \quad (\text{S74})$$

$$R_1(t) = R_1(t - \Delta t) - \Delta R_1(t) + N_{I_1R_1}(t) + N_{RR_1}(t) \quad (\text{S75})$$

$$R_2(t) = R_2(t - \Delta t) - \Delta R_2(t) + N_{I_2R_2}(t) + N_{RR_2}(t) \quad (\text{S76})$$

$$J_1(t) = J_1(t - \Delta t) - \Delta J_1(t) + N_{R_2J_1}(t) \quad (\text{S77})$$

$$J_2(t) = J_2(t - \Delta t) - \Delta J_2(t) + N_{R_1J_2}(t) \quad (\text{S78})$$

$$R(t) = R(t - \Delta t) - \Delta R(t) + N_{J_1R}(t) + N_{J_2R}(t) \quad (\text{S79})$$

717 We simulated the model on a daily scale with previously estimated parameters for the
 718 RSV-HMPV interaction [34]: $b_1 = 1.7/\text{weeks}$, $b_2 = 1.95/\text{weeks}$, $\theta_1 = 0.4$, $\theta_2 = 0.3$,
 719 $\phi_1 = 0.005 \times 7/364$, $\phi_2 = 4.99 \times 7/364$, $\epsilon_{12} = 0.92$, $\epsilon_{21} = 0.45$, $\gamma_1 = 1/10/\text{days}$,
 720 $\gamma_2 = 1/10/\text{days}$, $\rho_1 = 1/364/\text{days}$, $\rho_2 = 1/364/\text{days}$, $\mu = 1/(70 \times 364)/\text{days}$, and
 721 $N = 1 \times 10^8$. The model was simulated from 1900 to 2030 assuming $S(0) = N - 200$,
 722 $I_1(0) = 100$, $I_2(0) = 100$, $R_1(0) = 0$, $R_2(0) = 0$, $J_1(0) = 0$, $J_2(0) = 0$, and $R(0) = 0$.
 723 The observed incidence for each strain is then simulated as follows:

$$C_1(t) = \text{Beta-Binom}(N_{SI_1}(t) + N_{R_2J_1}, \rho, k), \quad (\text{S80})$$

$$C_2(t) = \text{Beta-Binom}(N_{SI_2}(t) + N_{R_1J_2}, \rho, k), \quad (\text{S81})$$

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

727 For both models, we considered a more realistically shaped pandemic pertur-
 728 bation $\alpha(t)$ to challenge our ability to estimate the intervention effects. Thus, we
 729 assumed a 40% transmission reduction for 3 months from March 2020, followed by a
 730 10% transmission reduction for 6 months, 20% transmission reduction for 3 months,

⁷³¹ and a final return to normal levels:

$$\alpha(t) = \begin{cases} 1 & t < 2020.25 \\ 0.6 & 2020.25 \leq t < 2020.5 \\ 0.9 & 2020.5 \leq t < 2021 \\ 0.8 & 2021 \leq t < 2021.25 \\ 1 & 2021.25 \leq t \end{cases}. \quad (\text{S82})$$

⁷³² For all simulations, we truncated the time series from the beginning of 2014 to the
⁷³³ end of 2023 and aggregated them into weekly cases.

⁷³⁴ To infer intrinsic resilience from time series, we fitted a simple discrete time,
⁷³⁵ deterministic SIRS model in a Bayesian framework [4]:

$$\Delta t = 1 \text{ week} \quad (\text{S83})$$

$$\text{FOI}(t) = \beta(t)(I(t - \Delta t) + \omega)/N \quad (\text{S84})$$

$$\Delta S(t) = [1 - \exp(-(\text{FOI}(t) + \mu)\Delta t)] S(t - \Delta t) \quad (\text{S85})$$

$$N_{SI}(t) = \frac{\text{FOI}(t)\Delta S(t)}{\text{FOI}(t) + \mu} \quad (\text{S86})$$

$$\Delta I(t) = [1 - \exp(-(\gamma + \mu)\Delta t)] I(t - \Delta t) \quad (\text{S87})$$

$$N_{IR}(t) = \frac{\gamma \Delta I(t)}{\gamma + \mu} \quad (\text{S88})$$

$$\Delta R(t) = [1 - \exp(-(\nu + \mu)\Delta t)] R(t - \Delta t) \quad (\text{S89})$$

$$N_{RS}(t) = \frac{\nu \Delta R(t)}{\nu + \mu} \quad (\text{S90})$$

$$S(t) = S(t - \Delta t) + \mu S - \Delta S(t) + N_{RS}(t) \quad (\text{S91})$$

$$I(t) = I(t - \Delta t) - \Delta I(t) + N_{SI}(t) \quad (\text{S92})$$

$$R(t) = R(t - \Delta t) - \Delta R(t) + N_{IR}(t) \quad (\text{S93})$$

⁷³⁶ where we include an extra term ω to account for importation. Although actual
⁷³⁷ simulations did not include any importation, we had found that including this term
⁷³⁸ generally helped with model convergence in previous analyses [4]. The transmission
⁷³⁹ rate was divided into a seasonal term $\beta_{\text{seas}}(t)$ (repeated every year) and intervention
⁷⁴⁰ term $\alpha(t)$, which were estimated jointly:

$$\beta(t) = \beta_{\text{seas}}(t)\alpha(t), \quad (\text{S94})$$

⁷⁴¹ where $\alpha < 1$ corresponds to reduction in transmission due to intervention effects. To
⁷⁴² constrain the smoothness of $\beta_{\text{seas}}(t)$, we imposed cyclic, random-walk priors:

$$\beta_{\text{seas}}(t) \sim \text{Normal}(\beta_{\text{seas}}(t - 1), \sigma) \quad t = 2 \dots 52 \quad (\text{S95})$$

$$\beta_{\text{seas}}(1) \sim \text{Normal}(\beta_{\text{seas}}(52), \sigma) \quad (\text{S96})$$

$$\sigma \sim \text{Half-Normal}(0, 1) \quad (\text{S97})$$

⁷⁴³ We fixed $\alpha(t) = 1$ for all $t < 2020$ and estimate α assuming a normal prior:

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

⁷⁴⁴ We assumed weakly informative priors on ω and ν :

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

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

⁷⁴⁵ We assumed that the true birth/death rates, population sizes, and recovery rates
⁷⁴⁶ are known. We note, however, that assuming $\gamma = 1/\text{week}$ actually corresponds to
⁷⁴⁷ a mean simulated infectious period of 1.6 weeks due to a time discretization, which
⁷⁴⁸ is much longer than the true value; this approximation allows us to test whether we
⁷⁴⁹ can still robustly estimate the intrinsic resilience given parameter mis-specification.
⁷⁵⁰ Initial conditions were estimated with following priors:

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

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

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

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

⁷⁵¹ Finally, the observation model was specified as follows:

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

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

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

⁷⁵² where ρ represents the reporting probability and ϕ represents the negative binomial
⁷⁵³ overdispersion parameter.

⁷⁵⁴ The model was fitted to four separate time series: (1) incidence time series from
⁷⁵⁵ the SIRS model, (2) incidence time series for strain 1 from the two-strain model,
⁷⁵⁶ (3) incidence time series for strain 2 from the two-strain model, and (4) combined
⁷⁵⁷ incidence time series for strains 1 and 2 from the two-strain model. The model
⁷⁵⁸ was fitted using rstan [46, 47] with 4 chains, each consisting of 2000 iterations.
⁷⁵⁹ The resulting posterior distribution was used to calculate the intrinsic resilience of
⁷⁶⁰ the seasonally unforced SIRS model with the same parameters; eigenvalues of the
⁷⁶¹ discrete-time SIR model were computed by numerically finding the equilibrium and
⁷⁶² calculating the Jacobian matrix.

⁷⁶³ **Validations for window-selection criteria**

⁷⁶⁴ We used stochastic SIRS simulations to identify optimal parameters for the window-
⁷⁶⁵ selection criteria that we used for the linear regression for estimating empirical re-
⁷⁶⁶ silience. For each simulation, we began by generating a random perturbation $\alpha(t)$

767 from a random set of parameters. First, we drew the duration of perturbation τ_{npi}
 768 from a uniform distribution between 1 and 2 years. Then, we drew independent
 769 normal variables z_i of length $\lfloor 364\tau_{\text{npi}} \rfloor$ with a standard deviation of 0.02 and took a
 770 reverse cumulative sum to obtain a realistic shape for the perturbation:

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

771 In contrast to simple perturbations that assume a constant reduction in transmission,
 772 this approach allows us to model transmission reduction that varies over time
 773 smoothly. We repeated this random generation process until less than 10% of x_n
 774 exceeds 1—this was done to ensure the perturbation term $\alpha(t)$ stays below 1 (and
 775 therefore reduce transmission) for the most part. Then, we set any values that are
 776 above 1 or below 0 to 1 and 0, respectively. Then, we randomly drew the minimum
 777 transmission during perturbation α_{\min} from a uniform distribution between 0.5 and
 778 0.7 and scale x_n to have a minimum of α_{\min} :

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

779 This allowed us to simulate a realistically shaped perturbation:

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

780 Given this perturbation function, we draw \mathcal{R}_0 from a uniform distribution between
 781 1.5 and 4 and the mean duration of immunity $1/\delta$ from a uniform distribution be-
 782 tween 1 and 4. Then, we simulate the stochastic SIRS model from $S(0) = 10^8/\mathcal{R}_0$
 783 and $I(0) = 100$ from 1990 to 2025 and truncate the time series to 2014–2025; if the
 784 epidemic becomes extinct before the end of simulation, we discard that simulation
 785 and start over from the perturbation generation step.

786 For each epidemic simulation, we computed the empirical resilience by varying
 787 the threshold R for the nearest neighbor approach from 4 to 14 with increments of
 788 2, the number of divisions K for the window selection between 8 and 25, and the
 789 truncation threshold a for the window selection between 1 to 3; this was done for all
 790 possible combinations of R , K , and a . We also compared this with the naive approach
 791 that uses the entire distance-from-attractor time series, starting from the maximum
 792 distance to the end of the time series. We repeated this procedure 500 times and
 793 quantified the correlation between empirical and intrinsic resilience estimates across
 794 two approaches.

795 **Supplementary Figures**

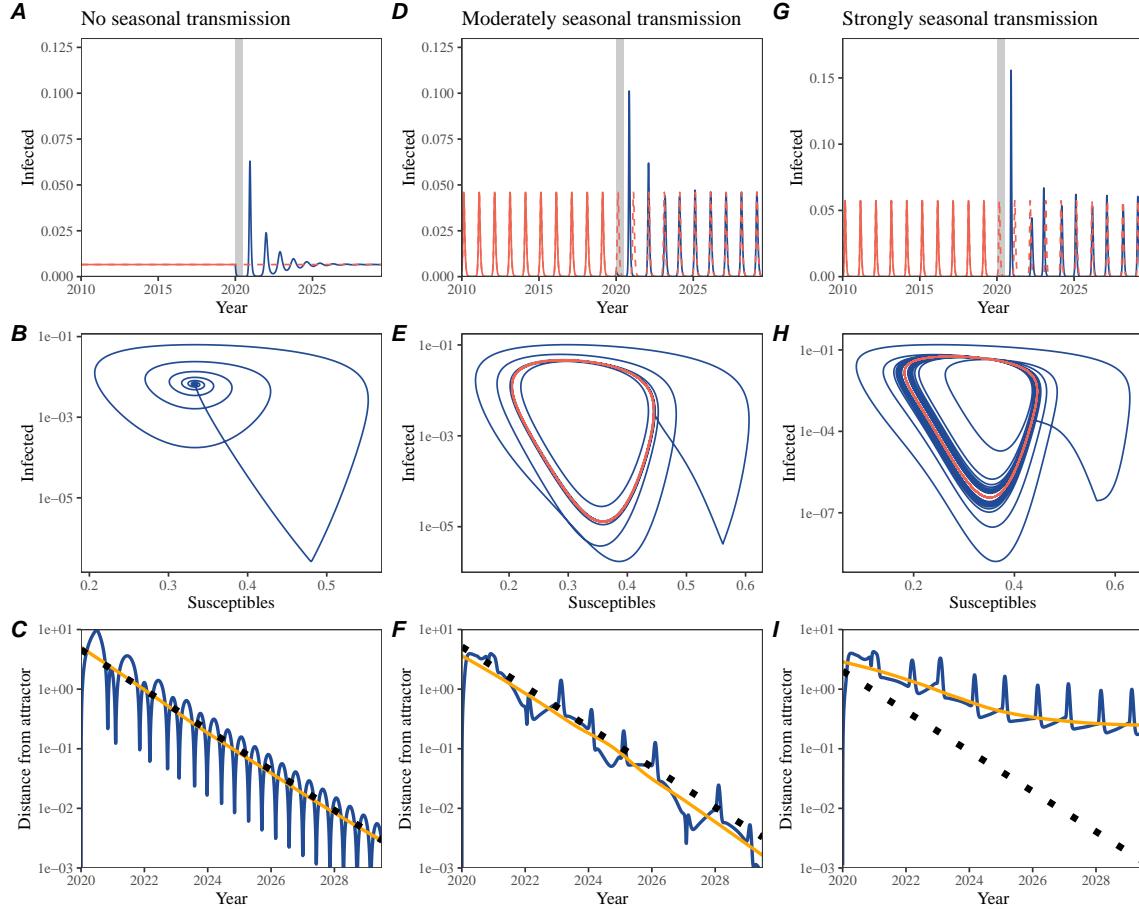


Figure S1: Impact of seasonal transmission on pathogen resilience. (A, D, G) Simulated epidemic trajectories using the SIRS model without seasonal forcing (A), with seasonal forcing of amplitude of 0.2 (D), and with seasonal forcing of amplitude of 0.4 (G). Red and blue solid lines represent epidemic 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 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.

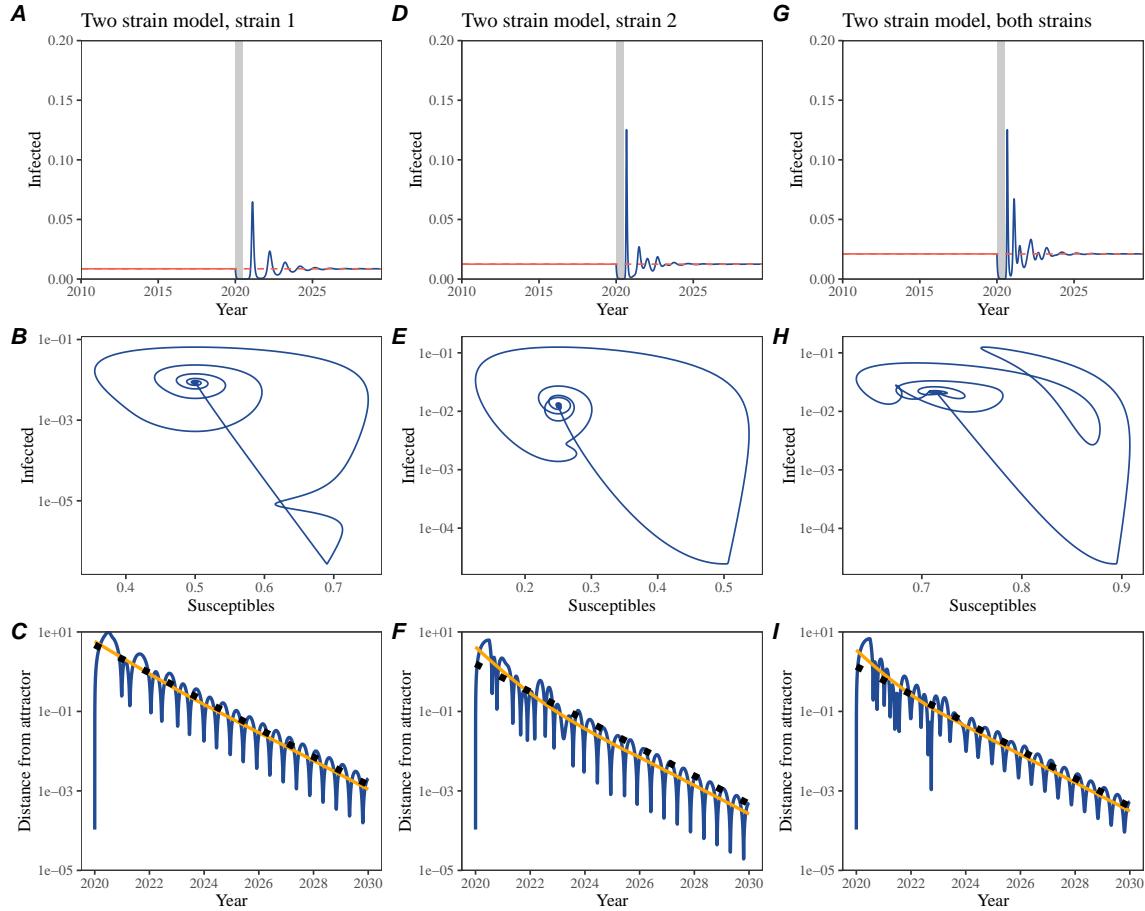


Figure S2: A simple method to measure pathogen resilience following pandemic perturbations for a two-strain competition system without seasonal forcing. (A, D, G) Simulated epidemic trajectories using a two-strain system without seasonal forcing. In this model, two strains compete through cross immunity. 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. Blue solid lines represent epidemic trajectories on an SI phase plane before and after interventions. (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.

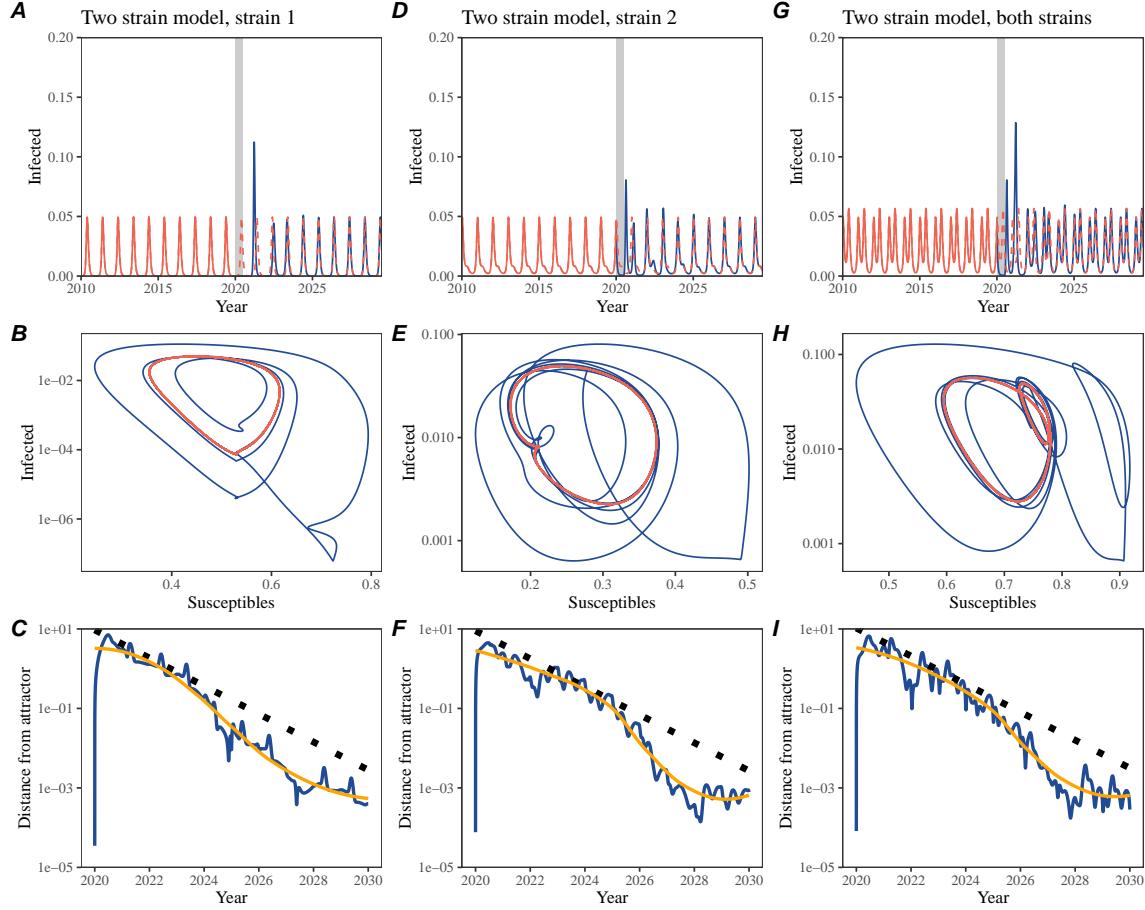


Figure S3: A simple method to measure pathogen resilience following pandemic perturbations for a two-strain competition system with seasonal forcing. (A, D, G) Simulated epidemic trajectories using a two-strain system with seasonal forcing (amplitude of 0.2). In this model, two strains compete through cross immunity. 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.

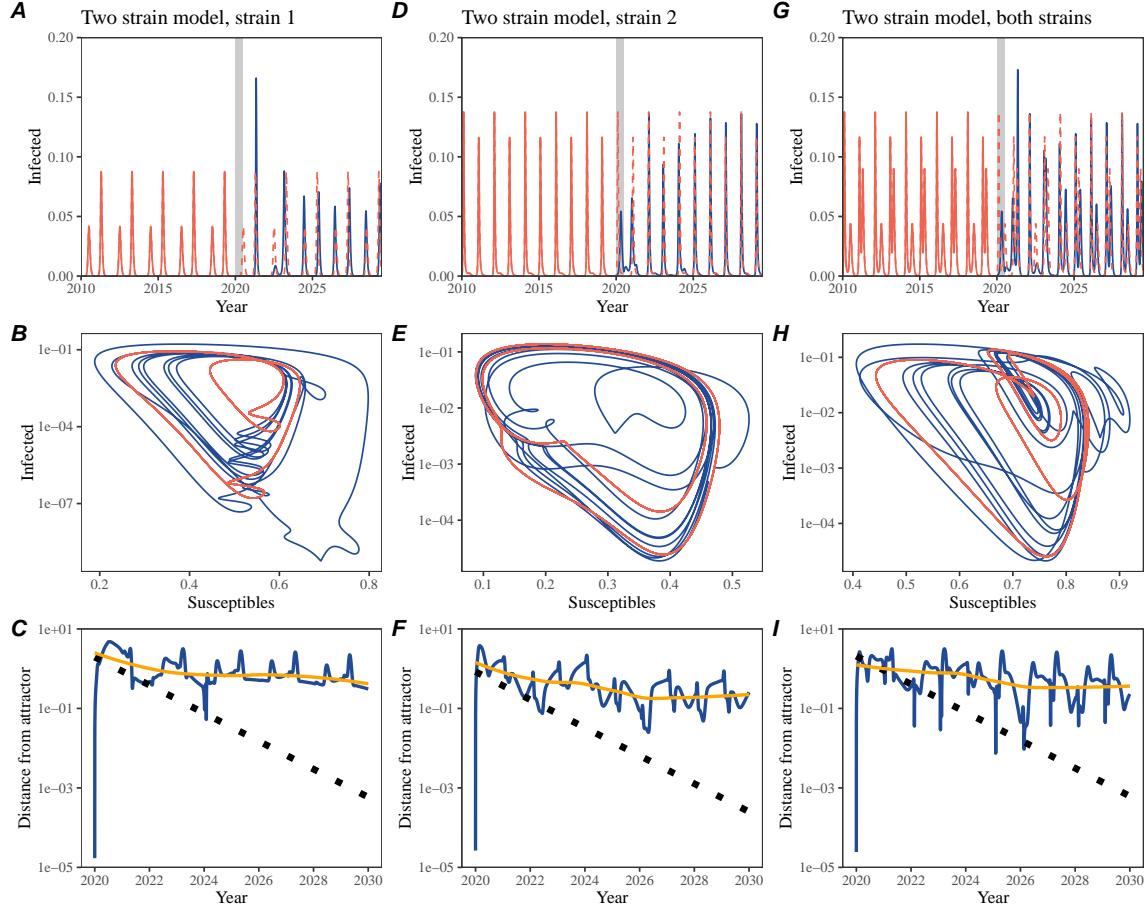


Figure S4: A simple method to measure pathogen resilience following pandemic perturbations for a multi-strain competition system with strong seasonal forcing. (A, D, G) Simulated epidemic trajectories using a two-strain system with seasonal forcing (amplitude of 0.2). In this model, two strains compete through cross immunity. 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.

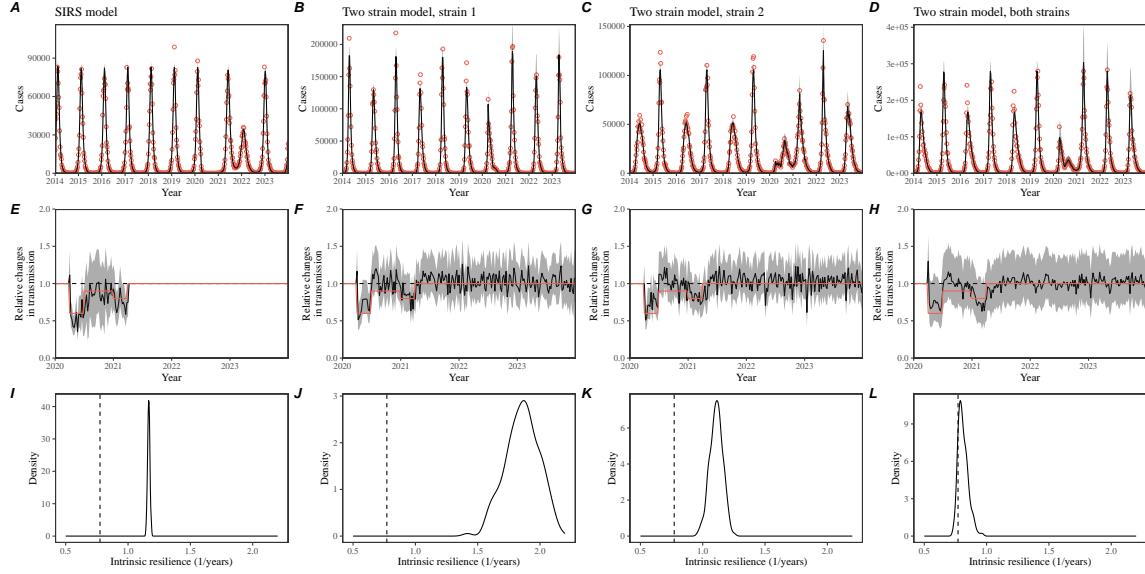


Figure S5: Mechanistic model fits to simulated data and inferred intrinsic resilience. We simulated discrete time, stochastic epidemic trajectories using a seasonally forced SIRS model (A,E,I) and a seasonally forced two-strain model (B–D, F–H, and J–L) and tested whether we can estimate the intrinsic resilience of the seasonally unforced versions of the model by fitting a mechanistic model (Supplementary Text). We fitted the same discrete time, one strain, deterministic SIRS model in each scenario. (A–D) Simulated case time series from corresponding models shown in the title (red) and SIRS model fits (black). (E–H) Assumed changes in transmission due to pandemic perturbations (red) and estimated time-varying relative transmission rates for the perturbation impact from the SIRS model fits (black). Solid lines and shaded regions represent fitted posterior median and 95% credible intervals. (I–L) Comparisons between the true and estimated intrinsic resilience of the seasonally unforced system. Vertical lines represent the true intrinsic resilience of the seasonally unforced system. Density plots represent the posterior distribution of the inferred intrinsic resilience of the seasonally unforced SIRS model using fitted parameters.

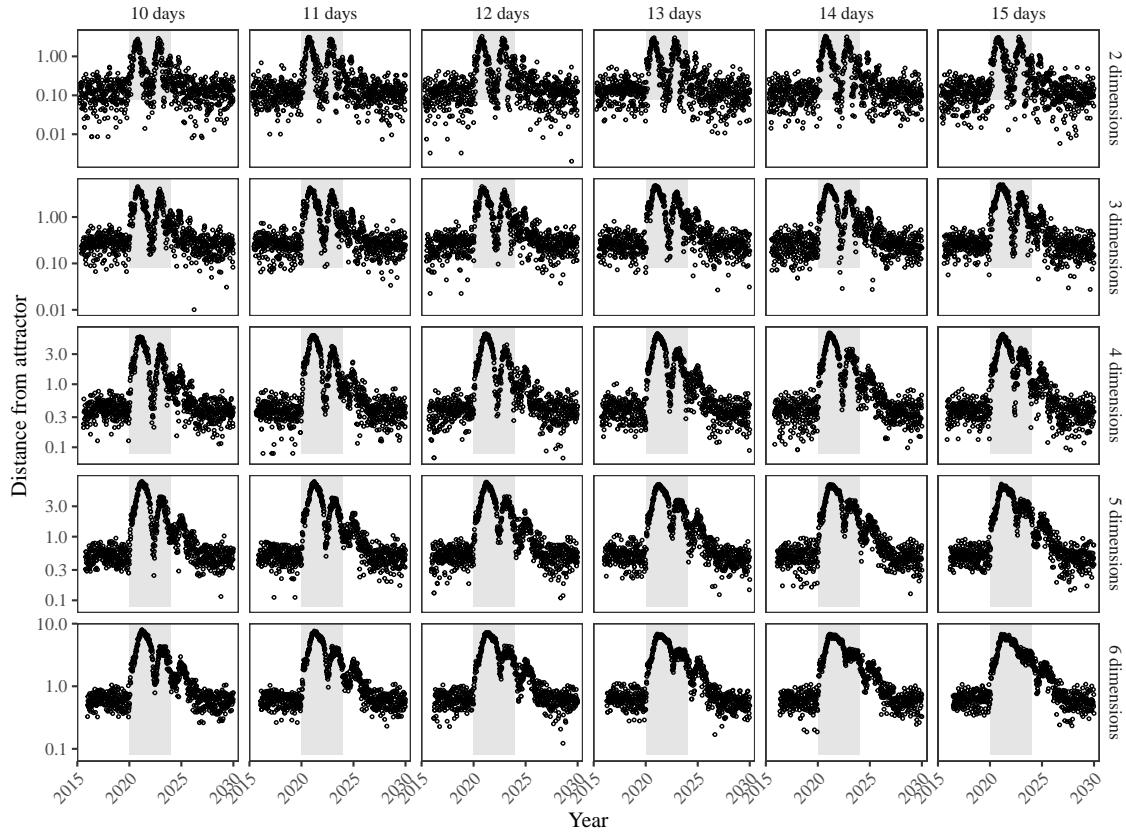


Figure S6: Sensitivity of the distance from the attractor to choice of embedding lags and dimensions. Sensitivity analysis for the distance-from-attractor time series shown in Figure 3E in the main text by varying the embedding lag between 10–15 days and embedding dimensions between 2–6 dimensions. The gray region represents the assumed period of pandemic perturbation.

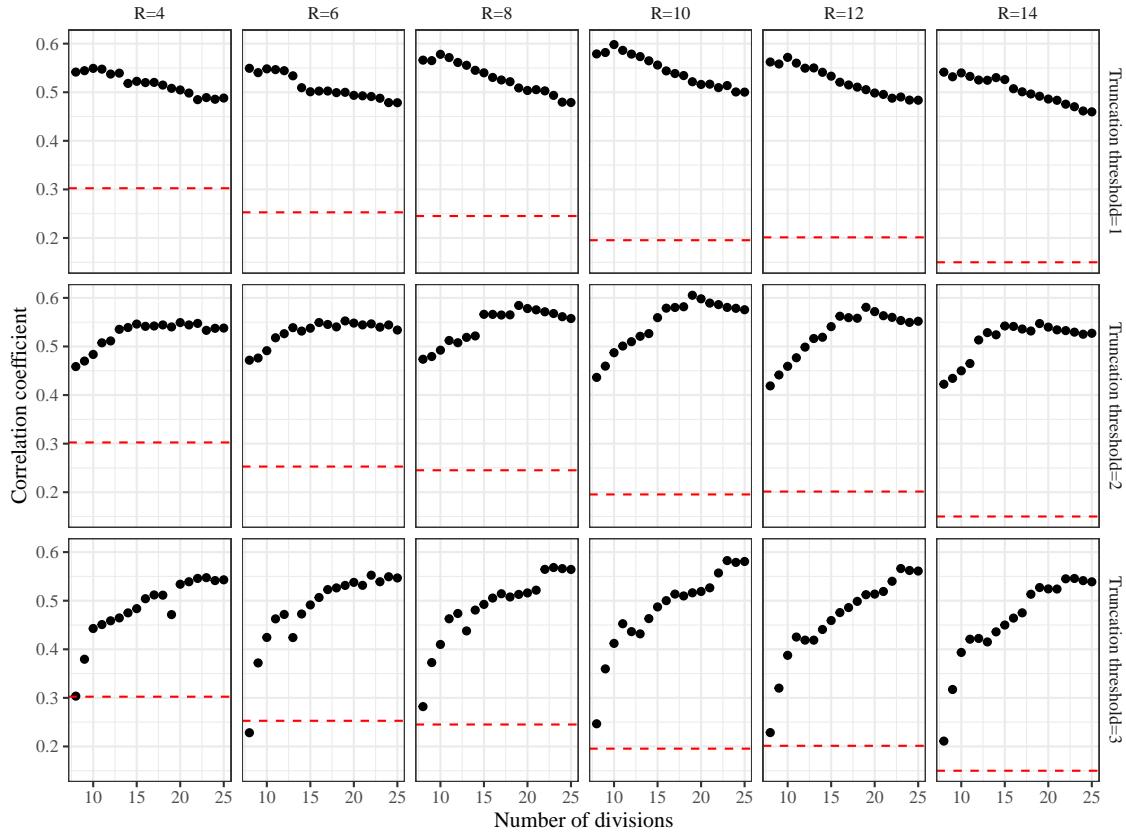


Figure S7: Impact of fitting window selection on the estimation of empirical resilience. We simulated 500 epidemics of a stochastic SIRS model with randomly drawn parameters and randomly generated pandemic perturbations (Supplementary Text). For each simulation, we varied the false nearest neighbor threshold R for reconstructing the empirical attractor as well as the parameters for regression window selection (i.e., the truncation threshold a and the number of divisions K). Each point represents the resulting correlation coefficient between empirical and intrinsic resilience estimates for a given scenario. Dashed lines represent the correlation coefficient between empirical and intrinsic resilience estimates for the naive approach that fits a linear regression on a log scale, starting from the maximum distance until the end of the time series.

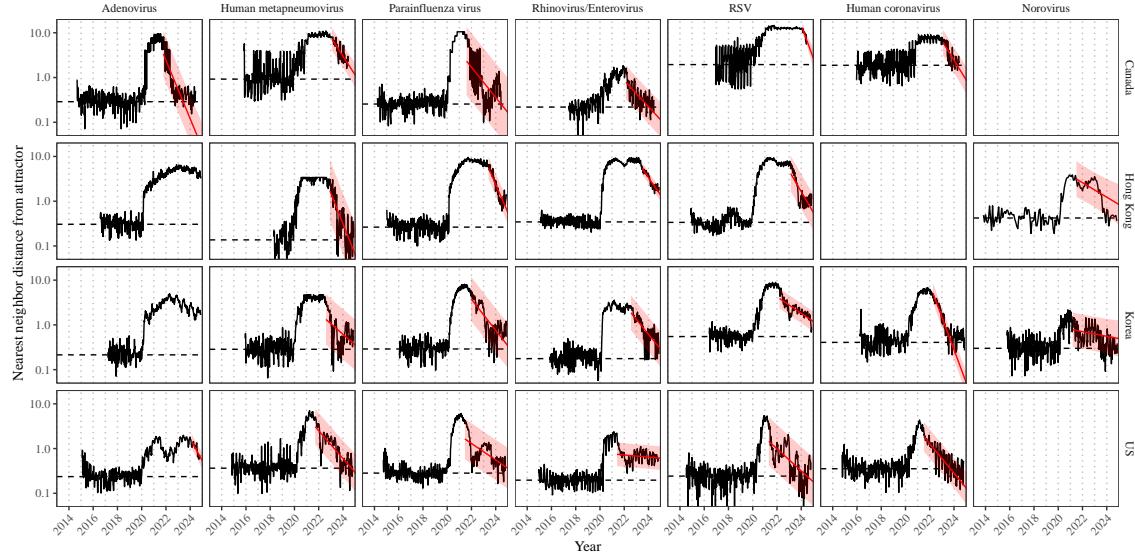


Figure S8: Estimated time series of distance from the attractor for each pathogen and corresponding linear regression fits using automated window selection criterion across Canada, Hong Kong, Korea, and the US. Black lines represent the estimated distance from the attractor. Red lines and shaded regions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

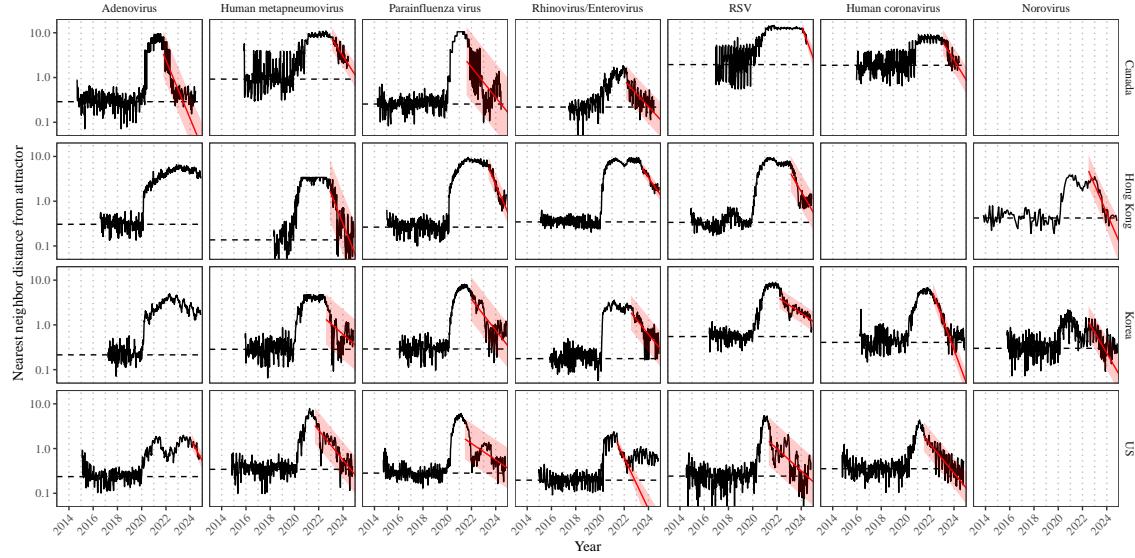


Figure S9: Estimated time series of distance from the attractor for each pathogen and corresponding linear regression fits across Canada, Hong Kong, Korea, and the US, including ad-hoc regression window selection. We used ad-hoc regression windows for norovirus in Hong Kong and Korea and rhinovirus/enterovirus 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.

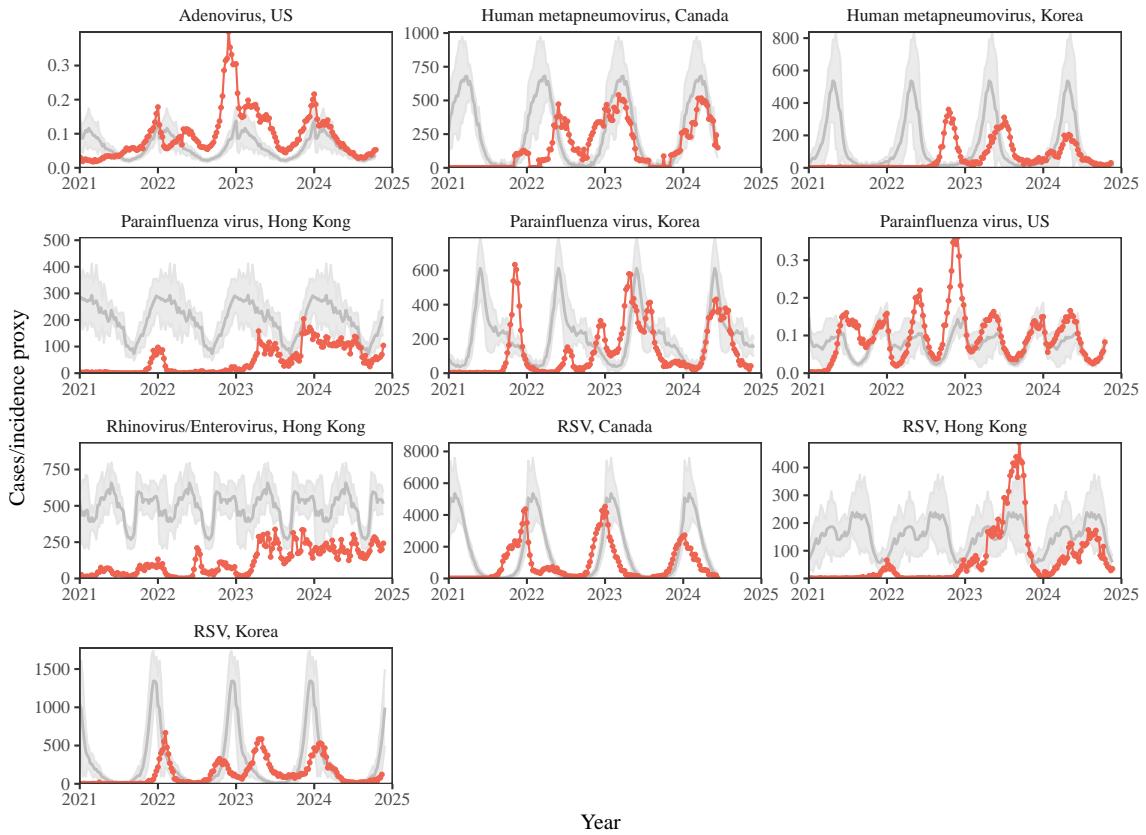


Figure S10: Observed dynamics for pathogen that are predicted to return after the end of 2024. Red points and lines represent data before 2020. Gray lines and shaded regions represent the mean seasonal patterns and corresponding 95% confidence intervals around the mean, previously shown in Figure 1.

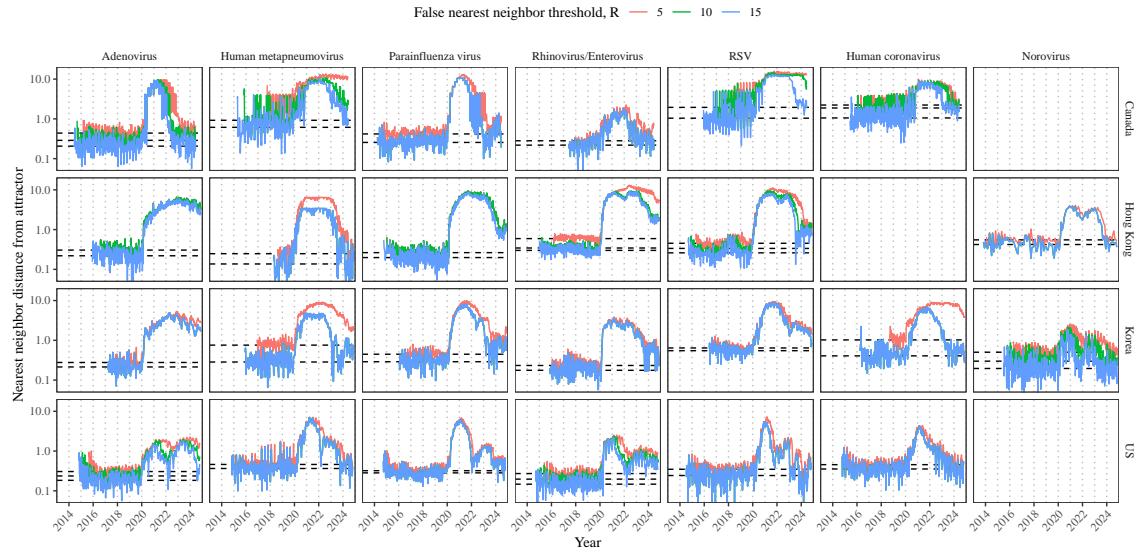


Figure S11: Estimated time series of distance from the attractor for each pathogen across different choices about false nearest neighbor threshold values. Using higher threshold values for the false nearest neighbor approach gives lower embedding dimensions. Colored lines represent the estimated distance from the attractor for different threshold values.

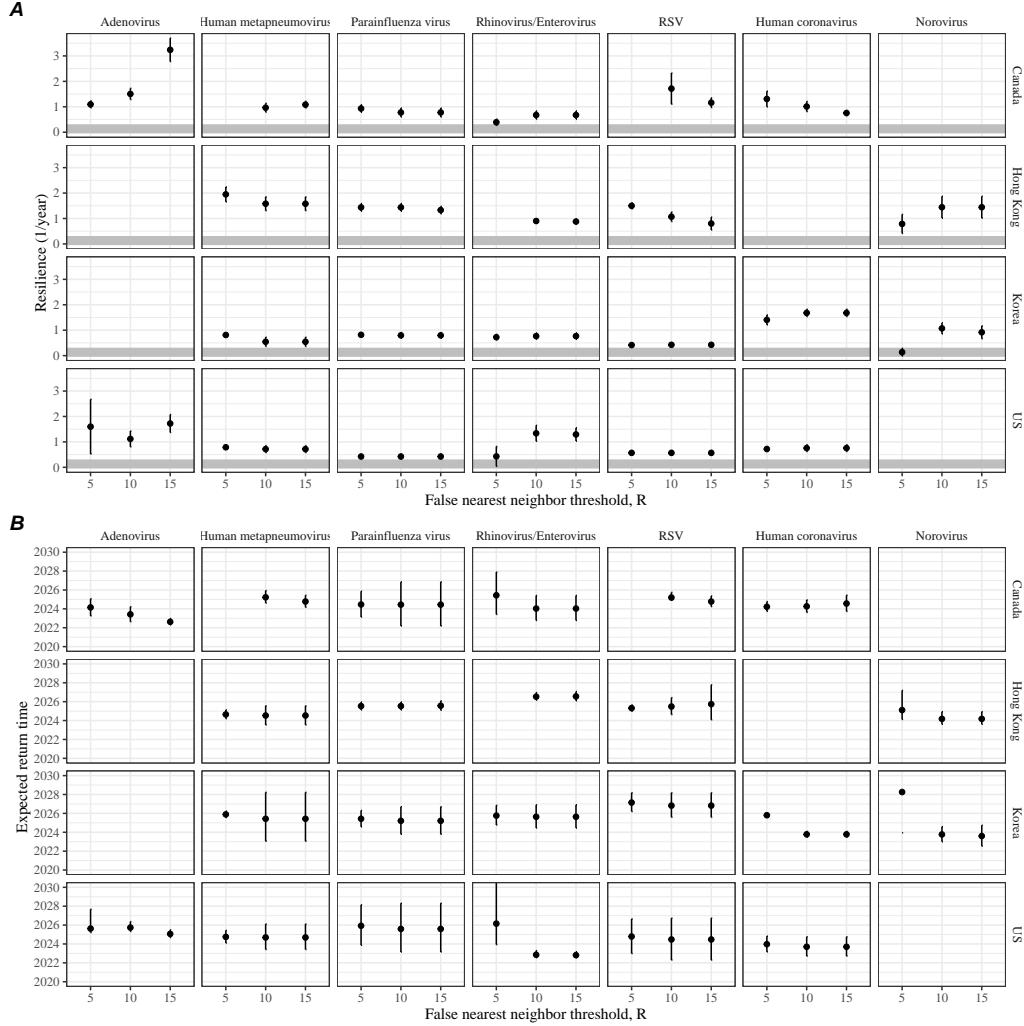


Figure S12: Summary of resilience estimates and predictions for return time across different choices about false nearest neighbor threshold values. The automated window selection method was used for all scenarios to estimate pathogen resilience, except for norovirus in Hong Kong and Korea and rhinovirus/enterovirus in the US. We used the same ad-hoc regression windows for norovirus in Hong Kong and Korea and rhinovirus/enterovirus in the US as we did in the main analysis. (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. Error bars represent 95% confidence intervals.

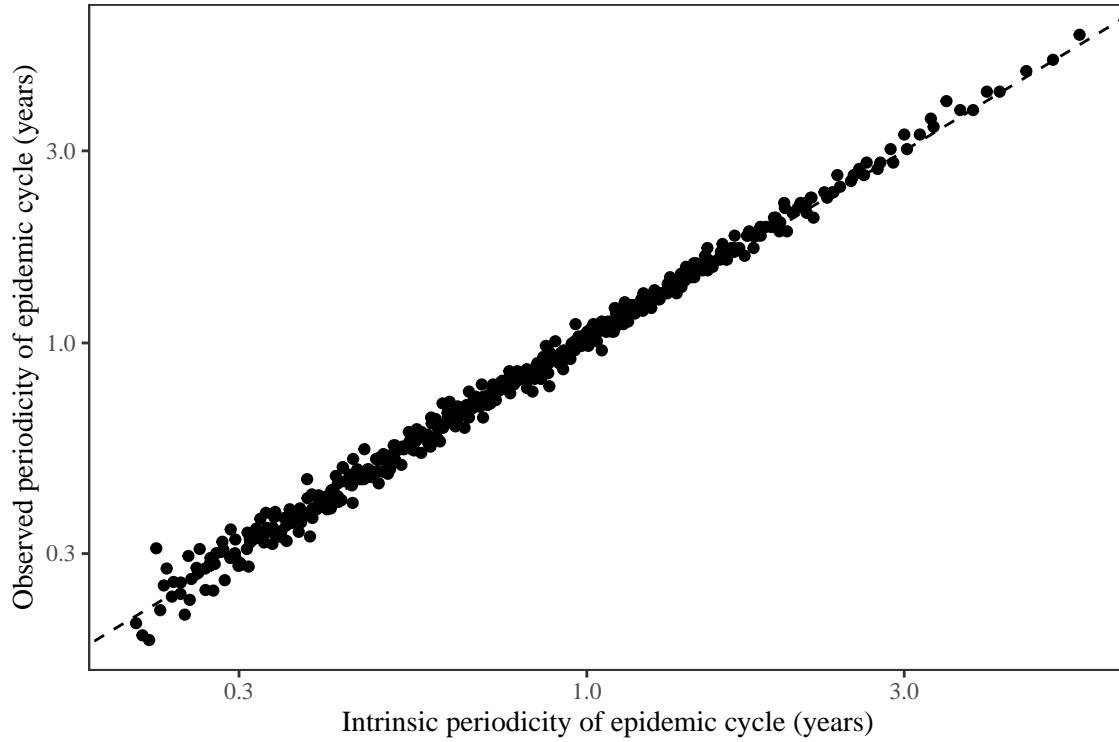


Figure S13: **Comparison between the observed and intrinsic periodicity of the epidemic cycle of the seasonally unforced SIRS model.** The observed periodicity of the epidemic corresponds to the periodicity at which maximum spectral density occurs. The intrinsic periodicity of the epidemic corresponds to $2\pi/\text{Im}(\lambda)$, where $\text{Im}(\lambda)$ is the imaginary part of the eigenvalue.

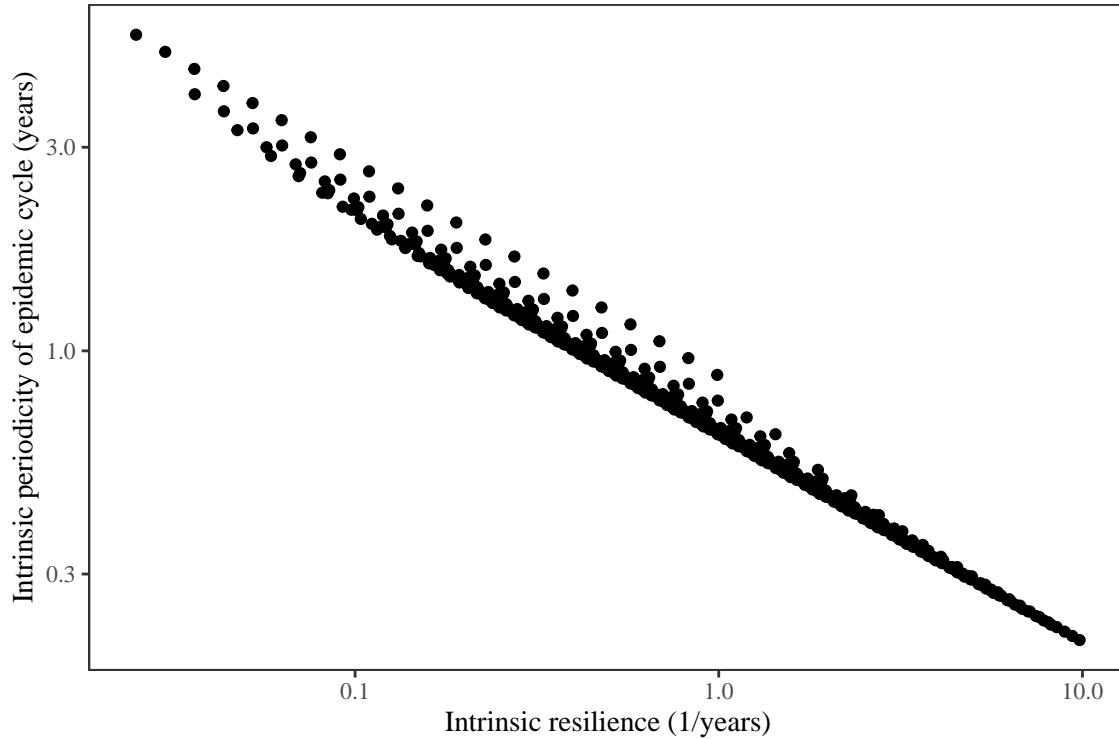


Figure S14: **Comparison between the intrinsic resilience and periodicity of the epidemic cycle of the seasonally unforced SIRS model.** The intrinsic resilience of the epidemic corresponds to the negative of the real value of the eigenvalue $-\text{Re}(\lambda)$. The intrinsic periodicity of the epidemic corresponds to $2\pi/\text{Im}(\lambda)$, where $\text{Im}(\lambda)$ is the imaginary part of the eigenvalue.

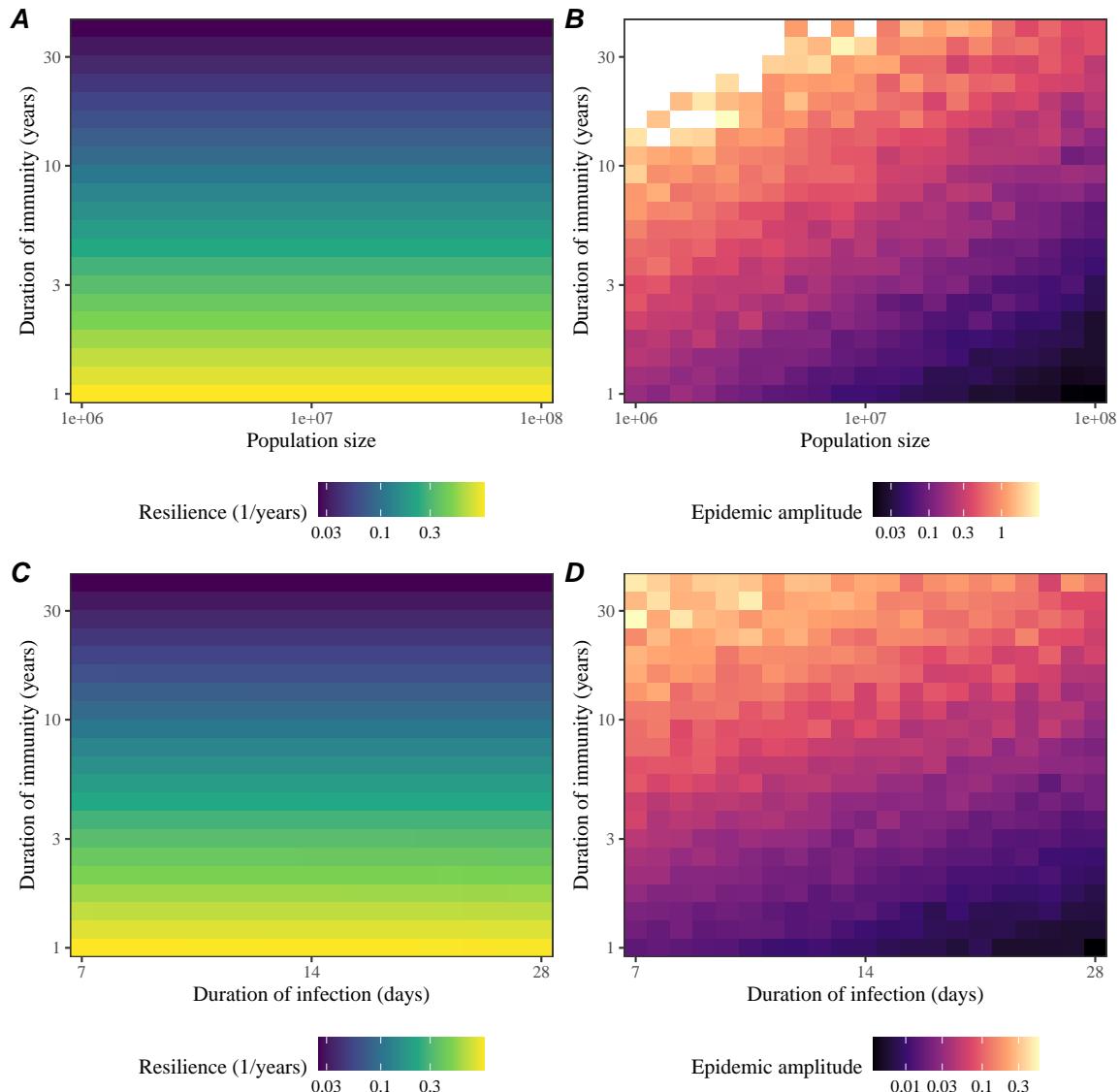


Figure S15: **Impact of population size and the average duration of infection of a host-pathogen system on its sensitivity to stochastic perturbations.** (A) Intrinsic resilience of a system as a function of population size and the average duration of immunity. (B) Epidemic amplitude as a function of population size and the average duration of immunity. (C) Intrinsic resilience of a system as a function of the average duration of infection and immunity. (D) Epidemic amplitude as a function of the average duration of infection and immunity. The epidemic amplitude corresponds to $(\max I - \min I)/(2\bar{I})$, where \bar{I} represents the mean prevalence.

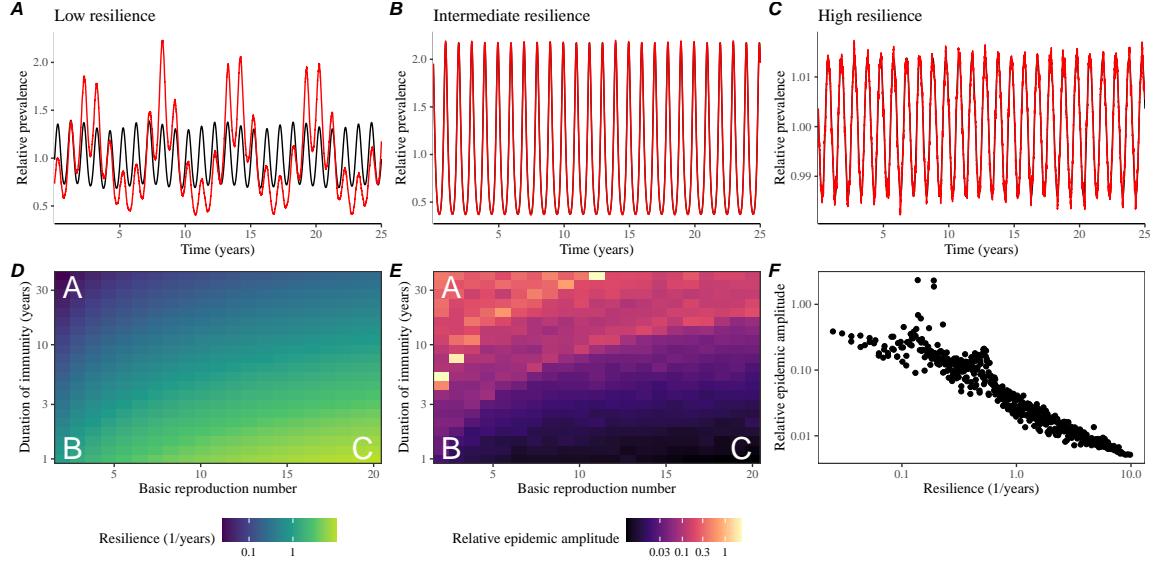


Figure S16: Linking resilience of a host-pathogen system to its sensitivity to stochastic perturbations for the seasonally forced SIRS model. (A–C) Epidemic trajectories of a stochastic SIRS model with demographic stochasticity across three different resilience values: low, intermediate, and high. The relative prevalence was calculated by dividing infection prevalence by its mean value. Black lines represent deterministic epidemic trajectories. Red lines represent stochastic epidemic trajectories. (D) The intrinsic resilience of the seasonally unforced system as a function of the basic reproduction number \mathcal{R}_0 and the duration of immunity. (E) The relative epidemic amplitude, a measure of sensitivity to stochastic perturbations, as a function of the basic reproduction number \mathcal{R}_0 and the duration of immunity. To calculate the relative epidemic amplitude, we first take the relative difference in infection prevalence between stochastic and deterministic trajectories: $\epsilon = (I_{\text{stoch}} - I_{\text{det}})/I_{\text{det}}$. Then, we calculate the difference between maximum and minimum of the relative difference and divide by half: $(\max \epsilon - \min \epsilon)/2$. Labels A–C in panels D and E correspond to scenarios shown in panels A–C. (F) The relationship between pathogen resilience and relative epidemic amplitude.

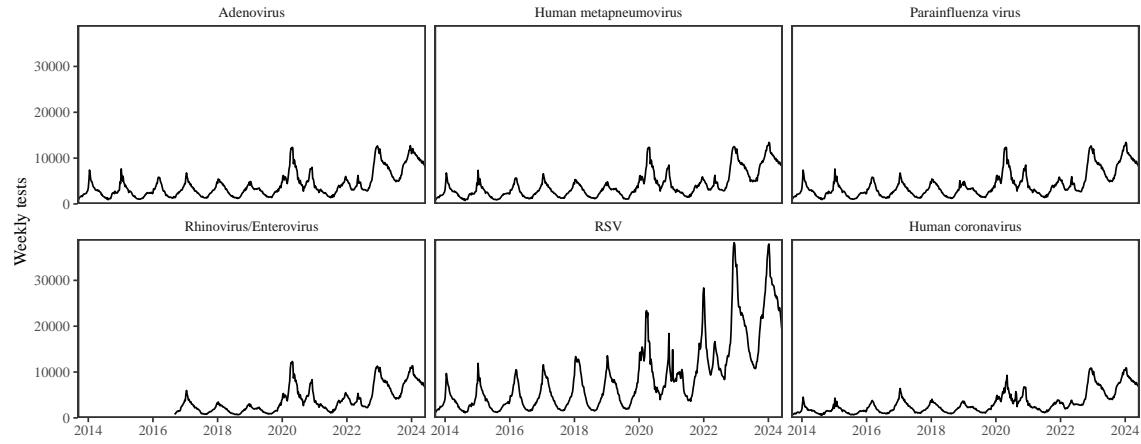


Figure S17: Testing patterns for respiratory pathogens in Canada.

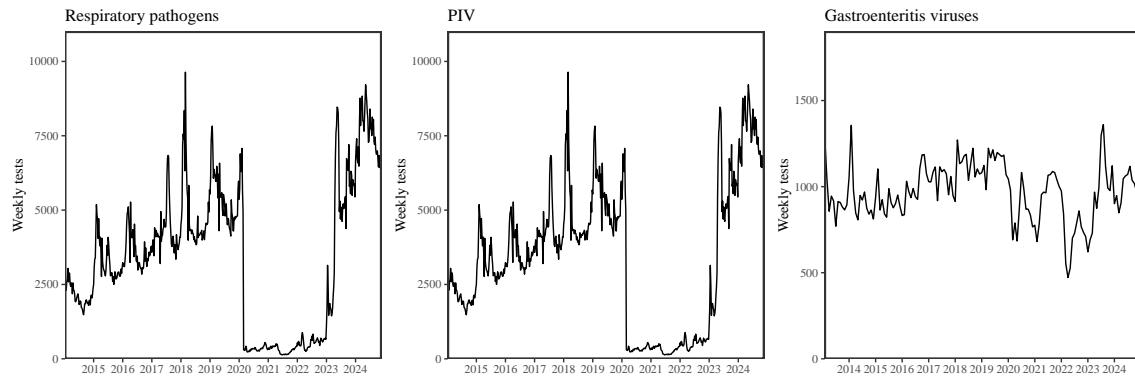


Figure S18: Testing patterns for respiratory pathogens, PIV, and gastroenteritis viruses in Hong Kong.

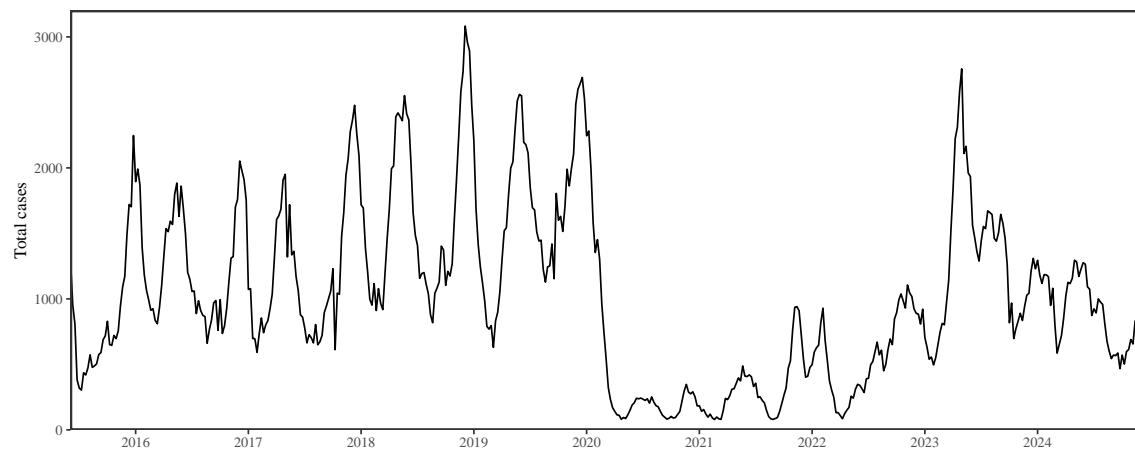


Figure S19: Total number of reported respiratory infection cases in Korea.

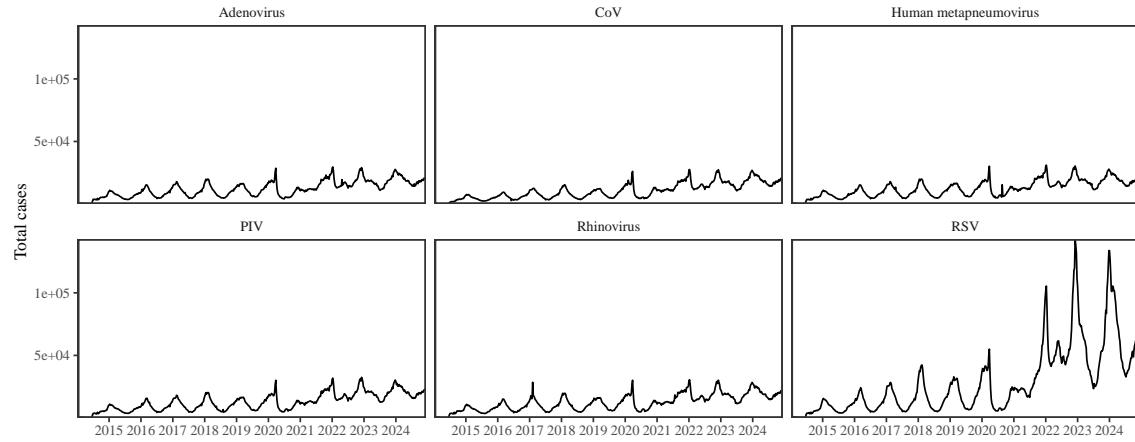


Figure S20: Testing patterns for respiratory pathogens in the US reported through the NREVSS.

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