

# A Novel Approach to Analyzing Seasonal Patterns in Epidemics Using a Higher-Dimensional State Space

Lenka Příbylová (email: [pribylova@math.muni.cz](mailto:pribylova@math.muni.cz)), Veronika Eclerová, Deeptajyoti Sen

Department of Mathematics and Statistics, Faculty of Science, Masaryk University, Brno, Czech Republic

## RESULTS

### BACKGROUND and METHODS

Compared to the analysis of endemic equilibrium, analyzing the dependence of the endemic cycle on the epidemiological parameters is a complex and relatively unexplored problem. Even the question of cycle continuation with respect to parameters presents a significant challenge. The concept of 'cycle continuation' refers to how cyclic dynamics change as the parameter changes. Understanding how this continuation works — whether the cycle remains stable or persists — provides valuable insights into the emergence and disappearance of endemic seasonal epidemics, as well as the possibility of biennial or multi-year cyclic outbreaks. Our approach offers a new tool for addressing these challenging questions and sheds light on the complex dynamics of infectious diseases over time.

The approach is based on bifurcation theory, a rigorously derived methodology designed to study nonlinear dynamical systems with parameters and the qualitative changes in their dynamics. Most importantly, this method allows us to move within parameter ranges or intervals where we can confidently predict certain qualitative dynamics. This includes equilibria, which may relate to disease eradication or endemic stability, and cycle attractors, signifying endemic cycles. Furthermore, the theory allows us to understand their synchronization or desynchronization with seasonal variations and other external factors.

### Epidemic cycles and seasonality

Endemic cycles can arise due to various factors, such as seasonal vaccination or waning immunity, where individuals lose their immunity after a certain period and become susceptible again, limited capacity of the health care system, or externally driven factors, where transmission rates vary with seasons due to environmental changes or due to some behavioral changes. Such cyclic behaviors can result in regular outbreaks or oscillations in disease prevalence, even in the absence of new external infections. [1]

We present a novel method for analyzing seasonality in compartmental epidemiological models. Our method involves embedding a dynamical system, such as the SEIRS type model, into a higher-dimensional state space with a seasonal attracting cycle. To achieve this, we use a parameterized normal form of the Hopf bifurcation to introduce an artificial variable that impacts the parameters with variable amplitude seasonal fluctuations. Despite the additional complexity, our approach affords the ability to analyze the system using standard detection and continuation methods and programs, such as MatCont. [2]

### Embedding method (technical)

Seasonality is usually implemented as harmonically driven SEIRS model. Let us briefly explain the embedding method that enables using standard cycle continuation methods. Suppose, the system can be expressed in the following form:

$$\dot{\mathbf{x}} = \mathbf{f}(\mathbf{x}, A \sin \omega t, \boldsymbol{\alpha}), \quad (1)$$

where  $\mathbf{f} : \mathbb{R}^{m+p+1} \rightarrow \mathbb{R}^m$  is a function smooth enough, and  $\boldsymbol{\alpha} \in \mathbb{R}^p$  are given parameters,  $A \sin \omega t$  signifies a harmonic external force. When amplitude  $A$  and frequency  $\omega$  are adjusted appropriately, the external oscillation causes the oscillator to synchronize. The system (1) can be embedded into an autonomous system:

$$\begin{aligned} \dot{\mathbf{x}} &= \mathbf{f}(\mathbf{x}, u_2, \boldsymbol{\alpha}), \\ \dot{u}_1 &= \varepsilon u_1 - \omega u_2 - u_1(u_1^2 + u_2^2), \\ \dot{u}_2 &= \omega u_1 + \varepsilon u_2 - u_2(u_1^2 + u_2^2), \end{aligned} \quad (2)$$

The newly incorporated 2-dimensional driving system for  $\mathbf{u} = (u_1, u_2)^T$  is a normal form of a supercritical Hopf bifurcation. For negative  $\varepsilon$ , it possesses a stable equilibrium at the origin, whereas, for positive  $\varepsilon$ , a stable limit cycle  $S = \{(u_1, u_2) : u_1^2 + u_2^2 = \varepsilon\}$  exists. Thus, for  $\varepsilon = A^2$ , the dynamics of the system (2) on the invariant manifold  $\mathbb{R}^m \times S$  are identical (topologically equivalent) to the system (1) dynamics. The asymptotic stability of cycle  $S$  assures good numerical properties for the continuation of bifurcation manifolds of the system. While in the driving system the artificial parameter  $\varepsilon$  introduces a stable limit cycle at zero, in the system (2), the manifold  $\varepsilon = 0$  gives birth to a torus as the original system already has natural oscillations.

### Acknowledgements

This work was supported from the European Horizon MSCA grant 101063853, and from the Mathematical and Statistical modelling project MUNI/A/1132/2022.

The authors declare that they have no conflicts of interest.

We demonstrate the advantages of this approach and its potential applications in both theoretical biology and practical problems related to respiratory epidemics, including the Covid-19 pandemic. We demonstrate how to address important epidemiological questions using our approach. These questions can include determining the feasibility of eradicating an endemic disease, assessing the possibility of a transition from massive COVID-19 outbreaks in a naive population to a seasonally synchronized respiratory disease, and exploring other important issues related to the control and prevention of infectious diseases.

As an model example we use a SEIRS-type model with transmissibility rates  $\beta_{1,2}$ , partial immunization with waning rate  $w$ , standard parameters  $\sigma, \gamma$  ( $1/\sigma$  average incubation duration,  $1/\gamma$  average infectious period), and  $q, \xi$  denoting the rate of getting partial immunity due to vaccination or infection. But any other model can be taken.

### SEIRS-type model

$$\begin{aligned} \dot{S} &= -\beta_1(1+f(t))(SI)^p + wM - qS, && \text{susceptibles} \\ \dot{M} &= -\beta_2(1+f(t))(MI)^p + qS - wM + \xi(1-S-M-E-I), && \text{partially immunized} \\ \dot{E} &= \beta_1(1+f(t))(SI)^p + \beta_2(1+f(t))(MI)^p - \sigma E, && \text{exposed} \\ \dot{I} &= \sigma E - \gamma I, && \text{infectious} \end{aligned}$$

with rate of nonlinearity  $p$ , seasonal variation  $f(t)$  and parameters  $\beta_{1,2}, w, q, \gamma, \xi$ , and  $\sigma$ .

### Tending to a seasonal attractor

Seasonality cannot be measured during beginning states, since the dynamical system has to settle down to a 1-year cycle attractor. The seasonal effect is observed after this transient period. Massive COVID-19 outbreaks are not in contradiction with seasonally synchronized respiratory disease cycles after a few years.

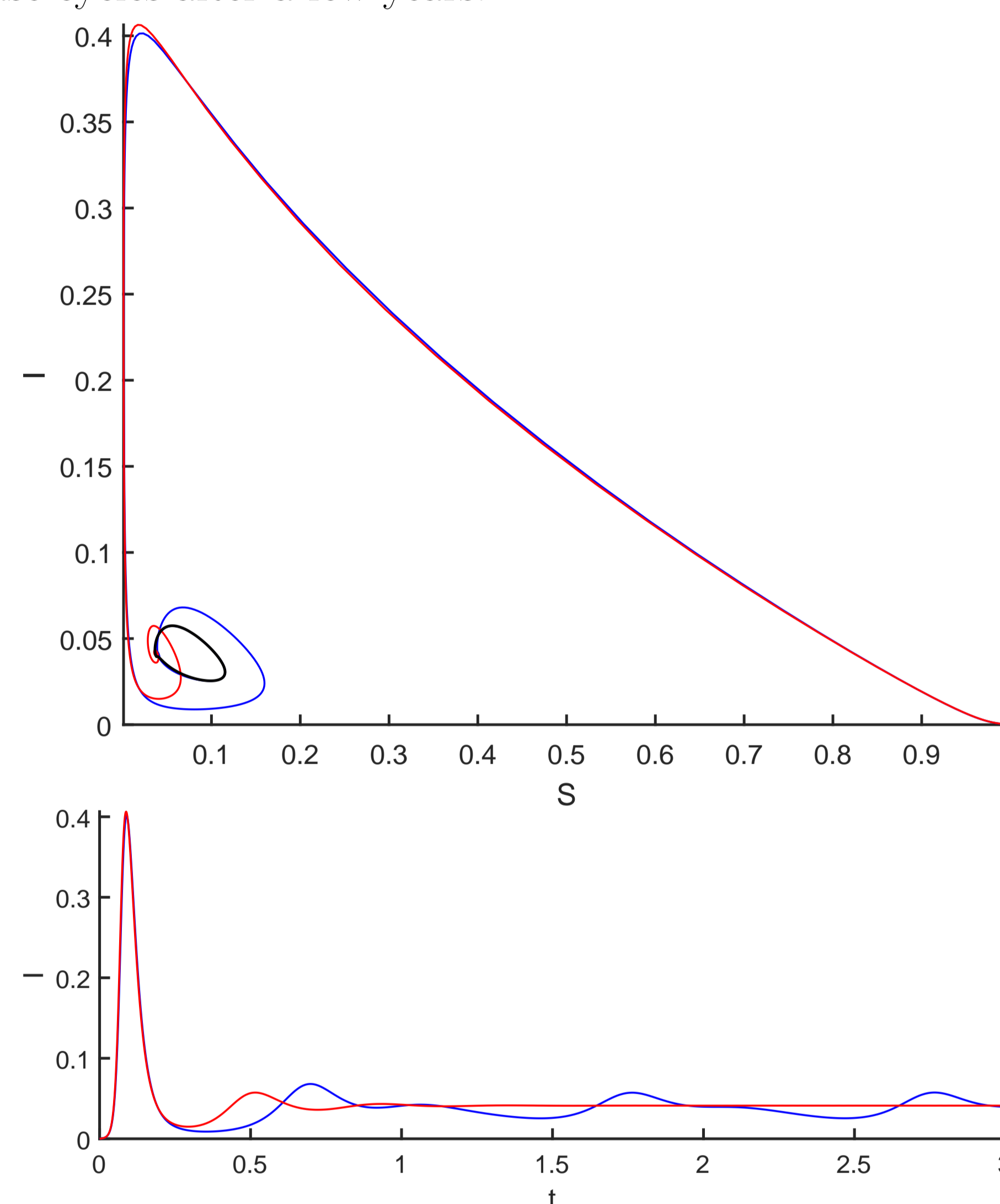


Figure 1: In case of a new disease/variant, seasonal cycles can be observed after 2 or 3 years, but not immediately within the first 2 outbreaks. Here, we simulated 0% (red) and 30% (blue) seasonal transmissibility variation with partial immunization and immunity waning. Parameters used:  $\beta_1 = 400, \beta_2 = 133, \varepsilon = 0$  (red trajectory tending to endemic equilibrium), or  $\beta_1 = 300, \beta_2 = 100, \varepsilon = 0.09$  (blue trajectory, black endemic cycle),  $q = 1, w = 4, \xi = 2, \sigma = 70, \gamma = 36, p = 1$  simulate COVID-19. Moreover, you can see that the immunity waning and other parameters may influence the prevalence fluctuation period in case of no or small seasonal transmissibility variation.

### Effect of nonlinear incidence rate

In the real-world, nonlinear incidence rates in SEIRS-type models arises due to a variety of factors (saturation effects in crowded settings, behavioral changes, limitations in health-care resources, the existence of multiple pathogen strains with different transmission rates; and environmental factors like weather and humidity, etc.). Measuring of this parameter  $p$  is an issue that can be overcome by setting it as an unknown parameter.

### Embedding

$$\begin{aligned} \dot{S} &= -\beta_1(1+x)(SI)^p + wM - qS, \\ \dot{M} &= -\beta_2(1+x)(MI)^p + qS - wM + \xi(1-S-M-E-I), \\ \dot{E} &= \beta_1(1+x)(SI)^p + \beta_2(1+x)(MI)^p - \sigma E, \\ \dot{I} &= \sigma E - \gamma I, \\ \dot{x} &= \varepsilon x - 2\pi y - x(x^2 + y^2), \\ \dot{y} &= 2\pi x + y\varepsilon - y(x^2 + y^2). \end{aligned}$$

Embedding and continuation of cycles with respect to  $p$  reveals a hysteresis phenomenon. Existence of two branches of cycles leads to abrupt jump to massive outbreaks and desynchronization due to period doubling route to chaos.

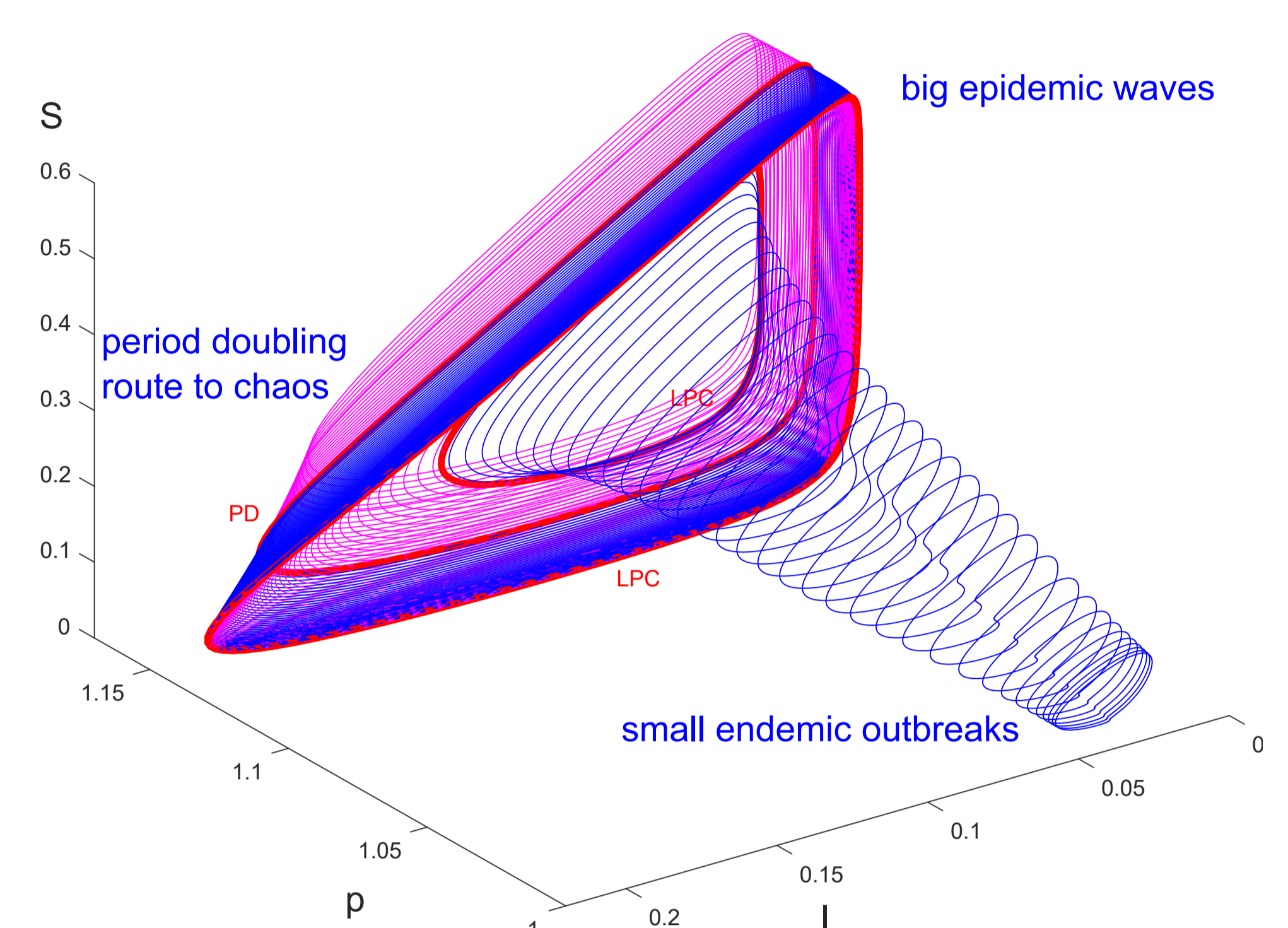


Figure 2: Seasonal cycle continuation with respect to the rate of non-linearity  $p$  reveals hysteresis due to possibility to continue also unstable cycles in the 6D embedding system. Stable seasonal cycles are depicted in blue. Parameters used:  $\beta_1 = 300, \beta_2 = 100, \varepsilon = 0.09, q = 1, w = 4, \xi = 2, \sigma = 70, \gamma = 36$  simulate COVID-19 with 30% seasonal transmissibility variation and partial immunization with waning.

### Jumps from an endemic cycle – possibility of eradication

Non-intuitive jumps to massive outbreaks described above are not the only possible abrupt changes that may emerge. Here, we present a possible non-intuitive eradication due to slightly higher non-linearity in the incidence rate.

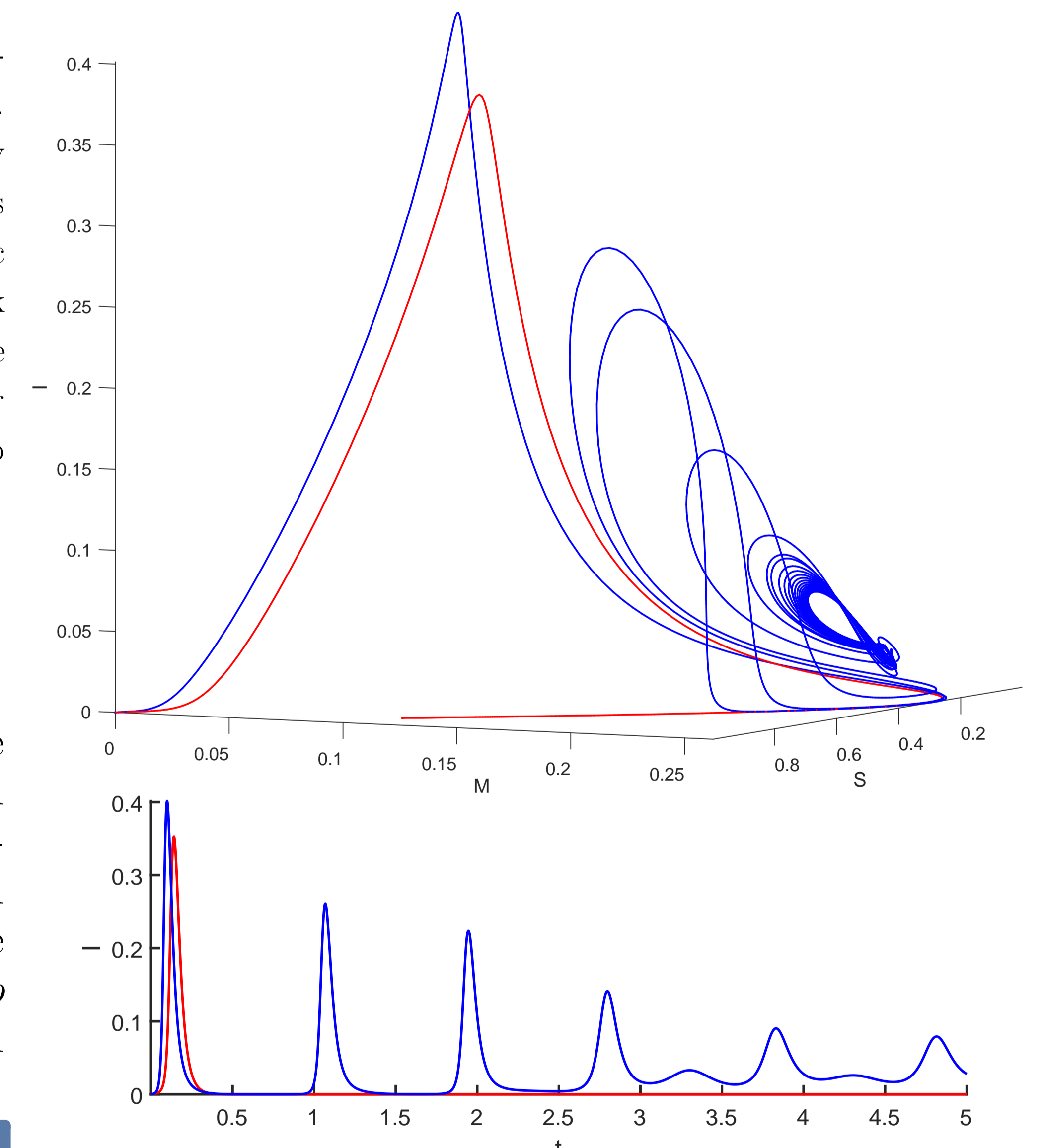


Figure 3: Sometimes non-intuitive dynamics may be explained and visualized in 3D space. Here you can see the attractor endemic cycle with shape that explains two outbreaks in one year and crossing separatrix surface in parameter-state space that enables eradication due to faster transmissions. Parameters used:  $\beta_1 = 300, \beta_2 = 100, \varepsilon = 0.04, q = 0.5, w = 4, \xi = 2, \sigma = 70, \gamma = 36$  simulate COVID-19 with  $p = 1.1$  (blue endemic biannual cycle) and  $p = 1.2$  (red eradication).

### References

- [1] Dushoff, Jonathan, et al. "Dynamical resonance can account for seasonality of influenza epidemics." PNAS (2004)
- [2] Dhooge, Annick, Willy Govaerts, and Yu A. Kuznetsov. "MATCONT: a MATLAB package for numerical bifurcation analysis of ODEs." ACM (2003)