

# Time-scale separation in a minimal model for a vector-borne disease

Peter Rashkov

Institute of Mathematics and Informatics  
Bulgarian Academy of Sciences  
p.rashkov@math.bas.bg



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## 1 Introduction

## 2 SISUV model

- Geometric singular perturbation technique

## 3 SIRUV model

- Heuristic analysis
- Geometric singular perturbation technique
- Role of seasonality

# State variables in vector-borne disease modelling

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Var.	Description
Host	
$N$	Host population density
$S$	Susceptible Host population density
$I$	Infected Host population density
$R$	Recovered Host population density

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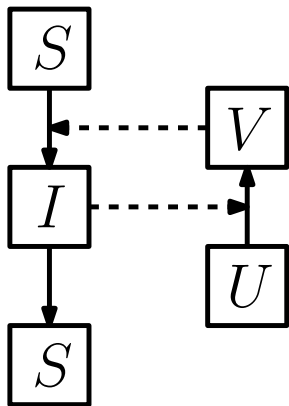
Vector	
$M$	Vector population density
$U$	Susceptible Vector population density
$V$	Infected Vector population density

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# Basic reproduction number

In the epidemiological literature, the basic reproduction number  $R_0$  represents the number of secondary cases one infected case generates on average over the course of its infectious period in an otherwise uninfected population.

host      vector



Four-dimensional system

$$\frac{dS}{dt} = \varepsilon \left( -\frac{\beta}{M}SV + \mu I \right)$$

$$\frac{dI}{dt} = \varepsilon \left( \frac{\beta}{M}SV - \mu I \right)$$

$$\frac{dU}{dt} = -\frac{\vartheta}{N}UI + \nu V$$

$$\frac{dV}{dt} = \frac{\vartheta}{N}UI - \nu V$$

# SISUV model

Assumed constant host and vector population densities

$$N = S(t) + I(t), \quad M = U(t) + V(t), \quad \forall t \geq 0$$

Two-dimensional equivalent system<sup>1</sup>

$$\frac{dV}{dt} = \underbrace{\frac{\vartheta}{N}(M - V)I - \nu V}_{=f(V,I,\varepsilon)}$$

$$\frac{dI}{dt} = \varepsilon \underbrace{\left( \frac{\beta}{M}(N - I)V - \mu I \right)}_{=g(V,I,\varepsilon)}$$

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<sup>1</sup>Rocha, Aguiar, Souza and Stollenwerk, *Int J Computer Math* (2013).

# Equilibria SISUV model

- **trivial, disease-free** equilibrium

$$I^0 = 0, V^0 = 0, S^0 = N, U^0 = M$$

- **interior, endemic** equilibrium

$$I^* = N \frac{\beta\vartheta - \mu\nu}{(\mu + \beta)\vartheta}, V^* = M \frac{\beta\vartheta - \mu\nu}{\beta(\nu + \vartheta)}, S^* = N - I^*, U^* = M - V^*$$

In the SISUV model  $R_0 = \frac{\beta\vartheta}{\mu\nu}$

- $R_0 = 1$  at the transcritical bifurcation point, where the endemic equilibrium coincides with the disease-free equilibrium
- endemic equilibrium is biologically relevant and globally asymptotically stable if  $R_0 > 1$

## SISUV model – Singular perturbation

Singular perturbation theory deals with systems whose solutions evolve on different time scales whose ratio is characterised by a small parameter  $0 < \varepsilon \ll 1$ .

It uses invariant manifolds in phase space in order to understand the global structure of the phase space or to construct orbits with desired properties.

$$\frac{dl}{dt} = \varepsilon g(V, l, \varepsilon) \quad \text{slow variable}$$

$$\frac{dV}{dt} = f(V, l, \varepsilon) \quad \text{fast variable}$$



## SISUV model – fast system

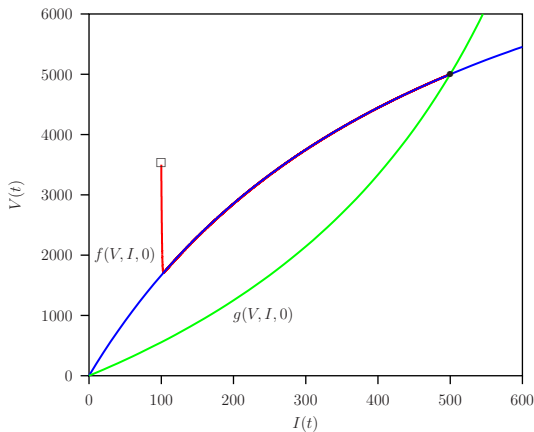
With  $\varepsilon = 0$  we have the fast system

$$\frac{dI}{dt} = 0$$

$$\frac{dV}{dt} = f(V, I(0), 0) = \frac{\vartheta}{N}(M - V)I(0) - \nu V$$

The infected host population  $I$  remains constant over  $t$ , so that the trajectory is a **vertical line** in the  $(I, V)$  phase space plot

# Phase-space plot SISUV model



The **solid red line** is the trajectory starting at the point  $\square$ . Two curves represent the two nullclines  $f(V, I, 0) = 0$  and  $g(V, I, 0) = 0$

## SISUV model – slow system

With a change of time-scale  $\tau = \varepsilon t$  the resulting system with  $\varepsilon \ll 1$  is called the *slow or reduced system*:

$$\begin{aligned}\varepsilon \frac{dl}{d\tau} &= \varepsilon g(V, I, \varepsilon) = \varepsilon \left( \frac{\beta}{M}(N - I)V - \mu I \right) \\ \varepsilon \frac{dV}{d\tau} &= f(V, I, \varepsilon) = \frac{\vartheta}{N}(M - V)I - \nu V\end{aligned}$$

Substitution of  $\varepsilon = 0$  gives a **differential-algebraic system** describing the evolution of the slow variable  $I(\tau)$  constrained to the set  $f = 0$ .

$$\begin{aligned}0 = f(V, I, 0) &\Leftrightarrow V = \frac{\vartheta IM}{\vartheta I + N\nu} \\ \frac{dl}{d\tau} &= g(V, I, 0) = \frac{\beta}{M}(N - I)V - \mu I\end{aligned}$$

# Time-scale separation

These heuristic results suggest the following approach for dealing with the two different time scales:

- 1 set  $\varepsilon = 0$  in the slow system, which gives the set of fast equilibria  $f = 0$ .

The *critical manifold* is the  $f$ -nullcline.

- 2 with a good Ansatz the relation  $f(V, I, 0) = 0$  can be rewritten as  $I = q(V)$  and we can substitute  $V = q^{-1}(I)$ .
- 3 the result is the 1-dimensional **reduced system** with  $\varepsilon = 0$ :

$$\frac{dI}{d\tau} = g(q^{-1}(I), I, 0) = \frac{\beta}{M}(N - I)q^{-1}(I) - \mu I$$

## Geometric singular perturbation technique

In order to get a better approximation for  $0 < \varepsilon \ll 1$ , we follow the **geometric singular perturbation technique**.

For  $\varepsilon = 0$  the  $f$ -nullcline

$$\{(V, I) | f(V, I, 0) = 0, V \geq 0, I \geq 0\}$$

consists of the **critical manifold**

$$\mathcal{M} = \left\{ (V, I) \mid I = \frac{\nu V N}{\vartheta(M - V)}, 0 \leq V \leq M, 0 \leq I \leq N \right\}$$

$\mathcal{M}$  forms a set of equilibria of the fast system

## Application of Fenichel's theorem

Fenichel's theorem states that there exists  $\varepsilon_0$  such that for  $0 < \varepsilon < \varepsilon_0$ , there exist locally invariant manifolds  $\mathcal{M}_\varepsilon$ ,  $\mathcal{O}(\varepsilon)$ -close and diffeomorphic to  $\mathcal{M}$ . Using their **invariance**, the perturbed manifold  $\mathcal{M}_\varepsilon$  can be approximated by an **asymptotic expansion** in  $\varepsilon$ .

It can (at least locally) be described as a graph

$$\{(V, I) \mid I = q(V, \varepsilon), V \geq 0, I \geq 0\}$$

due to normal hyperbolicity and inverse function theorem.

This manifold is invariant when the **invariance equation** holds

$$\frac{dI}{d\tau} = \frac{dI}{dV} \frac{dV}{d\tau} = \frac{\partial q(V, \varepsilon)}{\partial V} \frac{dV}{d\tau}$$

## Asymptotic expansion of $\mathcal{M}_\varepsilon$ for the SISUV model

Introduce an **asymptotic expansion** in  $0 < \varepsilon \ll 1$

$$I(V) = q(V, \varepsilon) = q_0(V) + \varepsilon q_1(V) + \varepsilon^2 q_2(V) + \dots$$

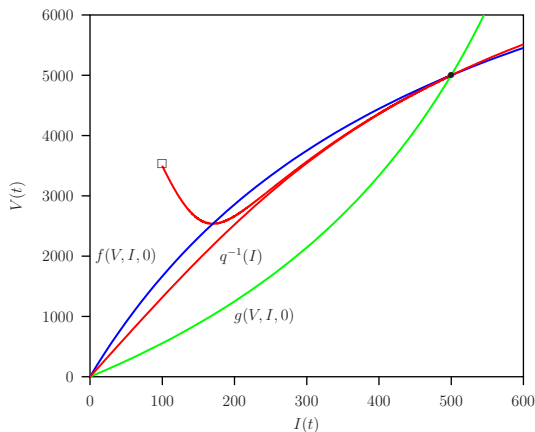
Formally differentiating by  $V$  and substituting into the invariance equation, gathering equal order terms of  $\varepsilon$  and assuming  $V > 0$  results in

$$I(V, \varepsilon) = q(V, \varepsilon) = q_0(V) + \varepsilon q_1(V) + \mathcal{O}(\varepsilon^2)$$

with

$$q_0(V) = \frac{\nu NV}{\vartheta(M - V)}$$
$$q_1(V) = \left( \frac{\beta}{\nu M} (M - V - \frac{\nu}{\vartheta} V) - \frac{\mu}{\vartheta} \right) \frac{NV}{M}.$$

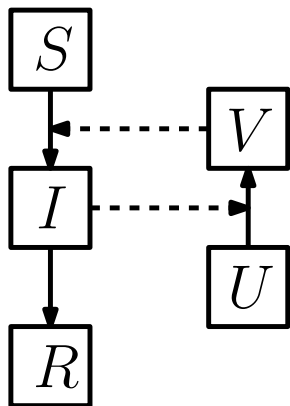
# Invariant manifold SISUV model



One **line** is the trajectory starting at the point  $\square$ . The other is the **curve**  $V(I) = q^{-1}(I, \varepsilon)$ . Two nullclines  $f(V, I, 0) = 0$  and  $g(V, I, 0) = 0$ .



host      vector



$$\frac{dS}{dt} = \varepsilon \left( -\frac{\beta}{M}SV + \mu(N - S) \right)$$

$$\frac{dI}{dt} = \varepsilon \left( \frac{\beta}{M}SV - (\gamma + \mu)I \right)$$

$$\frac{dR}{dt} = \varepsilon (\gamma I - \mu R)$$

$$\frac{dU}{dt} = -\frac{\vartheta}{N}UI + \nu(M - U)$$

$$\frac{dV}{dt} = \frac{\vartheta}{N}UI - \nu V$$

# SIRUV model

Assuming constant host and vector population densities

$$N = S(t) + I(t) + R(t), \quad M = U(t) + V(t), \quad \forall t \geq 0$$

yields an equivalent **3-dimensional** system<sup>2</sup>

$$\begin{aligned} \frac{dS}{dt} &= \varepsilon g_1(S, I, V) = \varepsilon \left( -\frac{\beta}{M} SV + \mu(N - S) \right), \\ \frac{dI}{dt} &= \varepsilon g_2(S, I, V) = \varepsilon \left( \frac{\beta}{M} SV - (\gamma + \mu)I \right), \\ \frac{dV}{dt} &= f(S, I, V) = \frac{\vartheta}{N} (M - V)I - \nu V. \end{aligned}$$

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<sup>2</sup>Rashkov, Venturino, Aguiar, Stollenwerk, and Kooi, *Math Biosci Eng* 16 (2019), 4314-4338.

# Equilibria SIRUV model

- trivial, disease-free equilibrium  $S^0 = N, I^0 = 0, V^0 = 0$
- **endemic equilibrium** whenever  $R_0 = \frac{\vartheta\beta}{\nu(\mu+\gamma)} > 1$ :

$$S^* = N \frac{\nu(\gamma + \mu) + \mu\vartheta}{\vartheta(\beta + \mu)}, \quad I^* = \mu N \frac{\beta\vartheta - \nu(\gamma + \mu)}{\vartheta(\beta + \mu)(\gamma + \mu)}$$
$$V^* = \mu M \frac{\beta\vartheta - \nu(\gamma + \mu)}{\beta(\nu(\gamma + \mu) + \mu\vartheta)},$$

## Theorem

*When  $R_0 > 1$ , the endemic equilibrium is locally asymptotically stable. It is a spiral as long as  $\mu$  is sufficiently small.*

## Heuristic analysis SIRUV model

It is convenient to analyse the behaviour of the fast variable  $V$  in the  $(V, I)$ -system with the **slow variable  $\bar{S}$  as a parameter**

$$\frac{dI}{dt} = \frac{\beta}{M} \bar{S} V - (\mu + \gamma) I, \quad \frac{dV}{dt} = \frac{\vartheta}{N} (M - V) I - \nu V$$

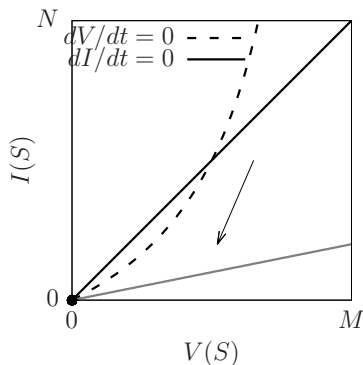
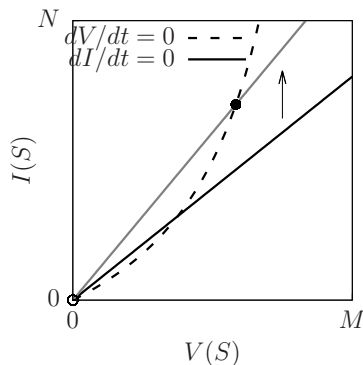
### Theorem

Let  $S_c = \frac{\nu(\mu + \gamma)}{\vartheta\beta} N$ . For  $\bar{S} \leq S_c$ , trivial equilibrium  $(0, 0)$  is the single global asymptotically stable equilibrium. For  $\bar{S} \geq S_c$ , the interior equilibrium

$$I^*(\bar{S}) = \frac{\beta\bar{S}}{(\mu + \gamma)} \left( 1 - \frac{\nu(\mu + \gamma)N}{\vartheta\beta\bar{S}} \right), \quad V^*(\bar{S}) = M \left( 1 - \frac{\nu(\mu + \gamma)N}{\vartheta\beta\bar{S}} \right)$$

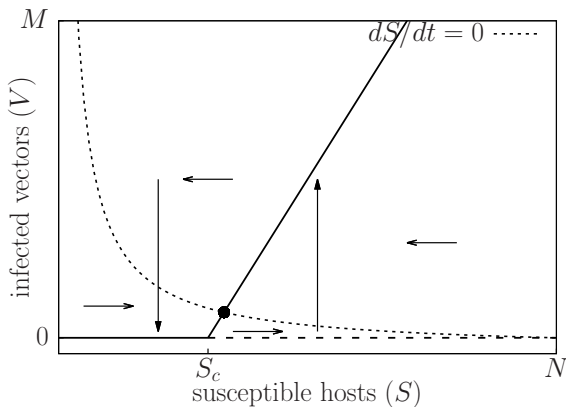
is globally asymptotically stable.

## Dependence of nullclines on $\bar{S}$



Left panel: with  $\bar{S} > S_c$ , the trajectory converges to the interior equilibrium  
Right panel: when  $\bar{S} < S_c$ , the trajectory approaches the origin

## Fast and slow flow in the $SV$ -plane



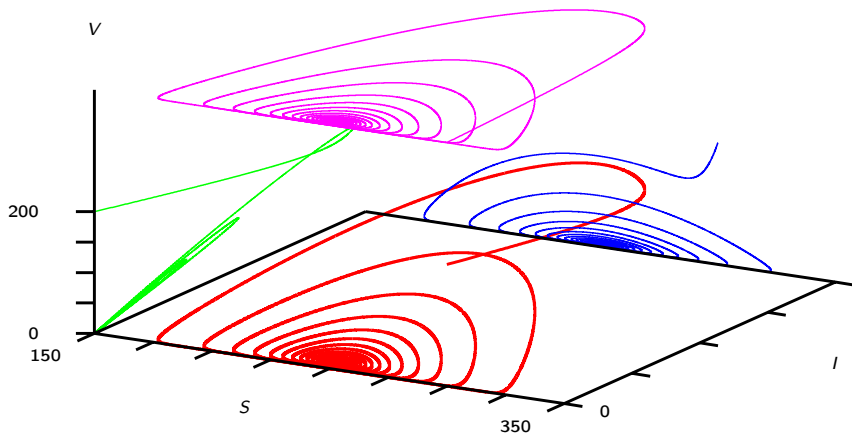
The locus of *fast* equilibria  $V^*$  is shown as solid line.

long arrows: direction of fast  $V$ -flow

short arrows: direction of slow  $S$ -flow

The interior equilibrium  $(S^*, V^*)$  is shown as ●

Figure: Phase-space result for the SIRUV model.



## SIRUV model – slow system

With a change of time-scale  $\tau = \varepsilon t$  the resulting system with  $\varepsilon \ll 1$  is called the *slow or reduced system*:

$$\begin{aligned}\varepsilon \frac{dS}{d\tau} &= \varepsilon g_1(S, I, V, \varepsilon) = \varepsilon \left( -\frac{\beta}{M} SV + \mu(N - S) \right) \\ \varepsilon \frac{dI}{d\tau} &= \varepsilon g_2(S, I, V, \varepsilon) = \varepsilon \left( \frac{\beta}{M} SV - (\gamma + \mu)I \right) \\ \varepsilon \frac{dV}{d\tau} &= f(V, I, \varepsilon) = \frac{\vartheta}{N}(M - V)I - \nu V\end{aligned}$$

Substitution of  $\varepsilon = 0$  gives an **differential-algebraic system** describing the evolution of the slow variables  $S(\tau), I(\tau)$  constrained to the set  $f = 0$

$$\begin{aligned}0 = f(S, I, V, 0) &\Leftrightarrow V = \frac{\vartheta IM}{\vartheta I + N\nu} \\ \frac{dS}{d\tau} &= g_1(S, I, V, 0), \quad \frac{dI}{d\tau} = g_2(S, I, V, 0)\end{aligned}$$



## Singular perturbation of SIRUV model

Using the time-scale argument with  $\varepsilon = 0$ , we obtain the two-dimensional  $f$ -nullspace, consisting of the **critical manifold**

$$\mathcal{M} = \left\{ 0 \leq S \leq N, I = \frac{\nu NV}{\vartheta(M - V)}, 0 \leq I \leq N \mid 0 \leq V \leq M \right\},$$

The system with **hyperbolic expression**

$$V(S, I) = \frac{\vartheta MI}{\nu N + \vartheta I}$$

is the **reduced system**.

Note  $V(S, I)$  is the same as  $V(I)$  in the SISUV model

**Fenichel's theorem** states that there exists  $\varepsilon_0$  such that for  $0 < \varepsilon < \varepsilon_0$ , there are locally invariant manifolds  $\mathcal{M}_\varepsilon$ . Using its **invariance**, the perturbed manifold  $\mathcal{M}_\varepsilon$  can be approximated by an **asymptotic expansion** in  $\varepsilon$ .

It can be described as a graph

$$\{(S, I, V) | V = p(S, I, \varepsilon), V \geq 0, I \geq 0\}$$

This manifold is invariant when

$$\frac{dV}{d\tau} = \frac{\partial V}{\partial S} \frac{dS}{d\tau} + \frac{\partial V}{\partial I} \frac{dI}{d\tau}$$

which yields with  $V = p(S, I, \varepsilon)$  the **invariance equation**

$$\frac{dp(S, I)}{d\tau} = \frac{\partial p(S, I)}{\partial S} \frac{dS}{d\tau} + \frac{\partial p(S, I)}{\partial I} \frac{dI}{d\tau}$$

## Asymptotic expansion of $\mathcal{M}_\varepsilon$ for the SIRUV model

Introduce an **asymptotic expansion** in  $0 < \varepsilon \ll 1$

$$V(S, I) = p(S, I, \varepsilon) = p_0(S, I) + \varepsilon p_1(S, I) + \varepsilon^2 p_2(S, I) + \dots$$

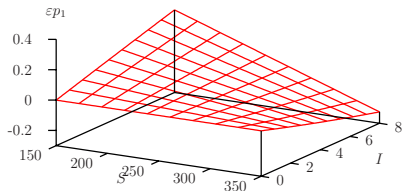
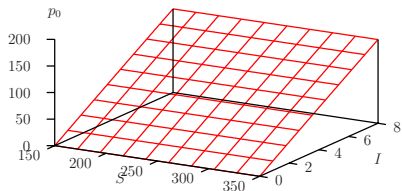
Differentiating formally by  $S, I$ , substituting into the invariance equation, gathering the zero order terms of  $\varepsilon$  and assuming  $V > 0$  gives

$$V(S, I) = p(S, I, \varepsilon) = p_0(S, I) + \varepsilon p_1(S, I) + \mathcal{O}(\varepsilon^2),$$

with

$$p_0(S, I) = \frac{\vartheta MI}{\vartheta I + \nu N},$$
$$p_1(S, I) = -\frac{M\nu\vartheta N^2}{(\vartheta I + \nu N)^3} \left( \frac{\beta\vartheta SI}{\vartheta I + \nu N} - (\gamma + \mu)I \right).$$

Figure: Plots of the coefficients of first two terms in the asymptotic expansion for  $V = p(S, I, \varepsilon)$  with  $\varepsilon = 1/365$



The size of the first-order term in the right panel shows that the contribution of the  $p_1$  term is marginal

# Observations

The usage of such a power series approximation is, however, counterproductive if we don't know its radius of convergence

Numerical experiments show that

- either spurious equilibria can occur when the trajectory starts not sufficiently close to the equilibrium
- or the trajectory escapes to infinity

Results are not shown here

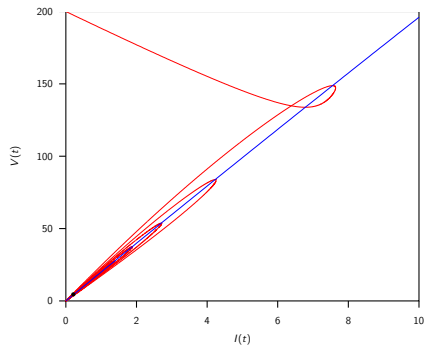
Refer also to the examples in Hek (2010)<sup>3</sup>

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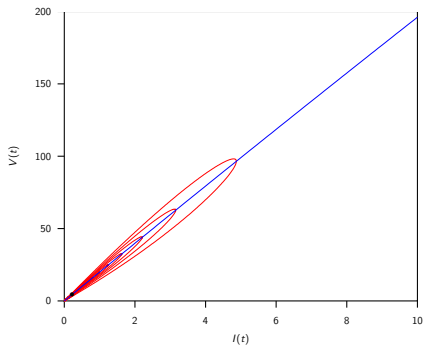
<sup>3</sup>G. Hek, Geometric singular perturbation theory in biological practice, *J Math Biol*, **60** (2010), 347–386.

# Trajectory in $(I, V)$ space

SIRUV model



Reduced SIRUV model



The point  $\bullet$  is endemic stable spiral equilibrium

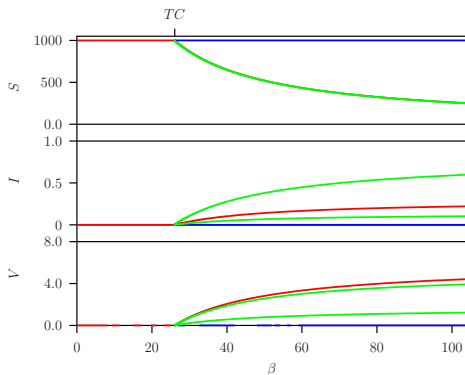
## Role of seasonality

Introduce seasonality in the SIRUV system by assuming that the density of the vector population  $M$  changes in a perfect sinusoidal way, motivated by dengue fever epidemiology data

$$M(t) = M_0 (1 + \rho \cos(2\pi t))$$

with a reference value  $M_0$  and amplitude  $\rho$

Numerical bifurcation analysis for reference parameter set gives the role of vector on the epidemics by calculation of the threshold value of  $\beta$  where the disease becomes **endemic**

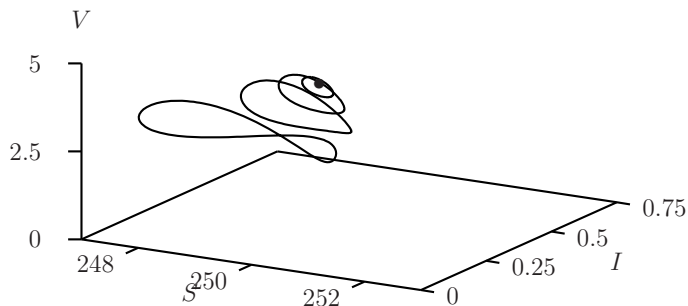


**curve:** non-seasonal equilibria

**curve:** seasonal maximum and minimum, TC transcritical bifurcation



# Limit cycles



**Figure:** The amplitude of cycles is proportional to the value of  $\rho$ . The period of oscillation equals that of the forcing term.

# Thank you for your attention!

P. Rashkov, E. Venturino, M. Aguiar, N. Stollenwerk, B.W. Kooi, On the role of vector modeling in a minimalistic epidemic model, *Math Biosci Eng* 16 (2019), 4314-4338

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# Parameters

Parameter	Description	SIRUV	SISUV
Host			
$N$	Host population density	1000	1000
$\beta$	Infection rate	730/7	0.2
$\mu$	Susceptible birth rate	1/65	0.1
$\gamma$	Recovery rate	365/7	n/a
Vector			
$M$	Vector population density	10000	10000
$\vartheta$	Infection rate	73	73
$\nu$	Susceptible birth rate	36.5	36.5
$\rho$	Magnitude sinusoidal fluctuation vector	0.9	n/a

## Theorem

*Suppose  $\mathcal{M}$  is compact and normally hyperbolic, that is, the eigenvalues  $\lambda$  of the Jacobian  $\frac{\partial f}{\partial V}(V, I)|_{\mathcal{M}}$  are uniformly bounded away from the imaginary axis.*

*Then there exists  $\varepsilon_0 > 0$  such that the critical manifold persists as a locally invariant slow manifold  $\mathcal{M}_\varepsilon$  of the full problem that is  $\mathcal{O}(\varepsilon)$  close to  $\mathcal{M}$  for  $0 < \varepsilon < \varepsilon_0$ . The restriction of the flow to  $\mathcal{M}_\varepsilon$  is a small perturbation of the flow of the limiting problem.<sup>a</sup>*

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<sup>a</sup>G. Hek, Geometric singular perturbation theory in biological practice, *J Math Biol*, **60** (2010), 347–386.