Analysis of a predator-prey model with two different time scales

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Outline

- Introduction

- Rosenzweig-MacArthur predator–prey RM model
  - □ Fast-slow analysis, Relaxation oscillations
  - □ Asymptotic expansion
  - □ Canard location
  - □ Geometric singular perturbation theory (GSPT)
  - □ Blow-up technique, Existence of Canards

- Mass Balance nutrient–prey–predator MB model
  - □ Fast-slow analysis, Bifurcation theory

- Conclusions

MB nutrient–prey-predator model

$$\frac{dx_0}{dt} = (x_r - x_0)\varepsilon d - a_0 x_0 x_1$$
$$\frac{dx_1}{dt} = a_0 x_0 x_1 - \varepsilon d x_1 - \varepsilon \frac{a_1 x_1 x_2}{1 + b_1 x_1}$$
$$\frac{dx_2}{dt} = \varepsilon \frac{a_1 x_1 x_2}{1 + b_1 x_1} - \varepsilon d x_2$$

parameter	Interpretation
t	Fast time variable
x_0	Nutrient density
x_i	Population biomass density
x_r	Nutrient concentration in reservoir
d	Dilution rate
a_0	Searching rate
a_1	Searching rate
b_1	Searching rate $\times$ handling time

It is possible to decouple the system by introduction of the total biomass

$$H(t) = x_0(t) + x_1(t) + x_2(t) - x_r \quad t \geq 0$$
$$\frac{dH}{dt} = -\varepsilon dH$$

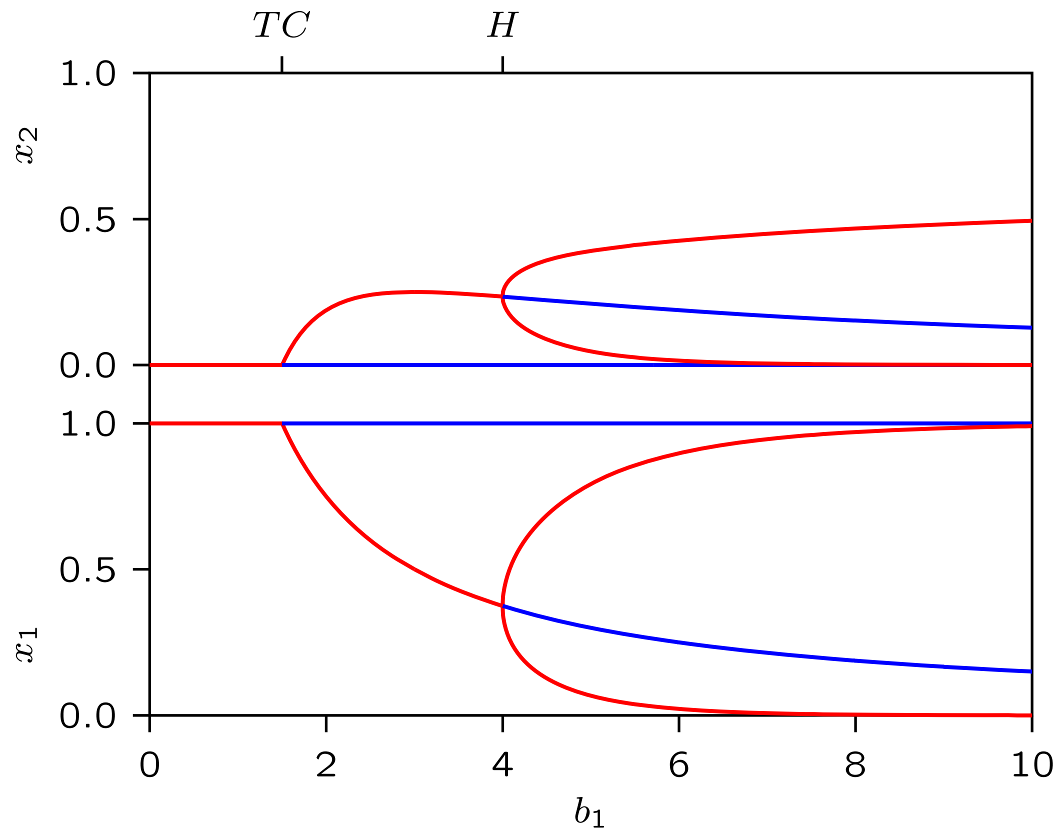
In order to be able to compare the two models RM, and MB we make the following assumptions: $H(0) = 0$ and this gives:

$$\frac{dx_1}{dt} = x_1\left(1 - x_1 - x_2 - \varepsilon\frac{a_1 x_2}{1 + b_1 x_1}\right)$$
$$\frac{dx_2}{dt} = \varepsilon x_2\left(\frac{a_1 x_1}{1 + b_1 x_1} - 1\right)$$

Extra x_2 shows that prey has less nutrients available that are indirectly consumed by the predator and ε to avoid extra assumption on efficiency

RM-model

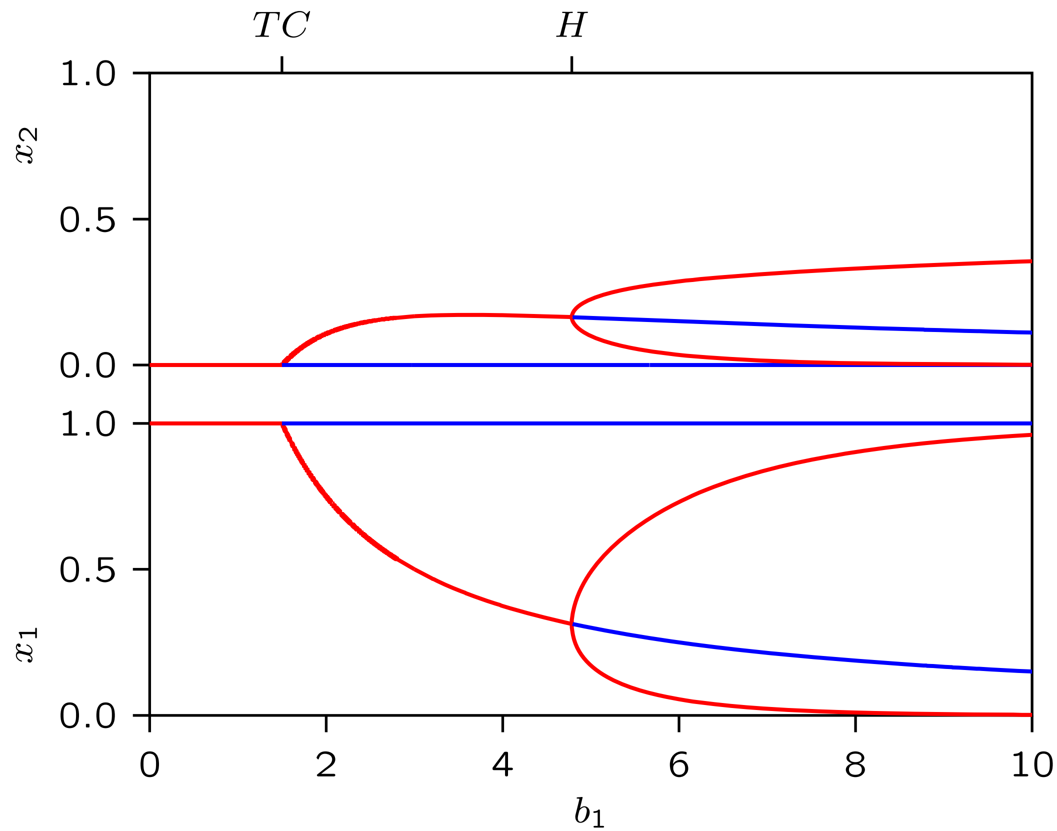
One-parameter diagram x_i vs b_1: $a_1 = 5/3\, b_1$, $\varepsilon = 1$



Transcritical TC, Hopf H bifurcations

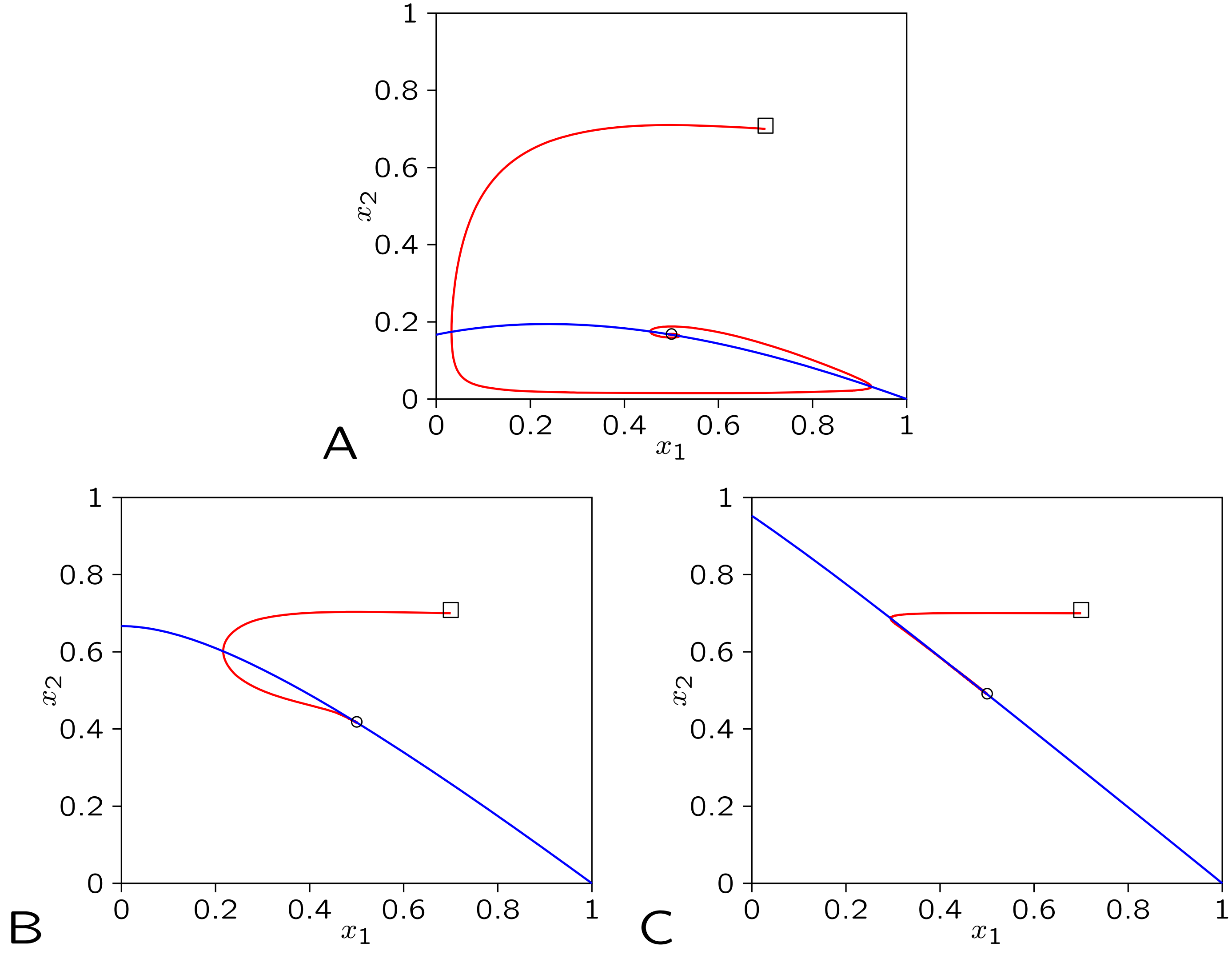
MB-model

One-parameter diagram x_i vs b_1: $a_1 = 5/3\, b_1$, $\varepsilon = 1$

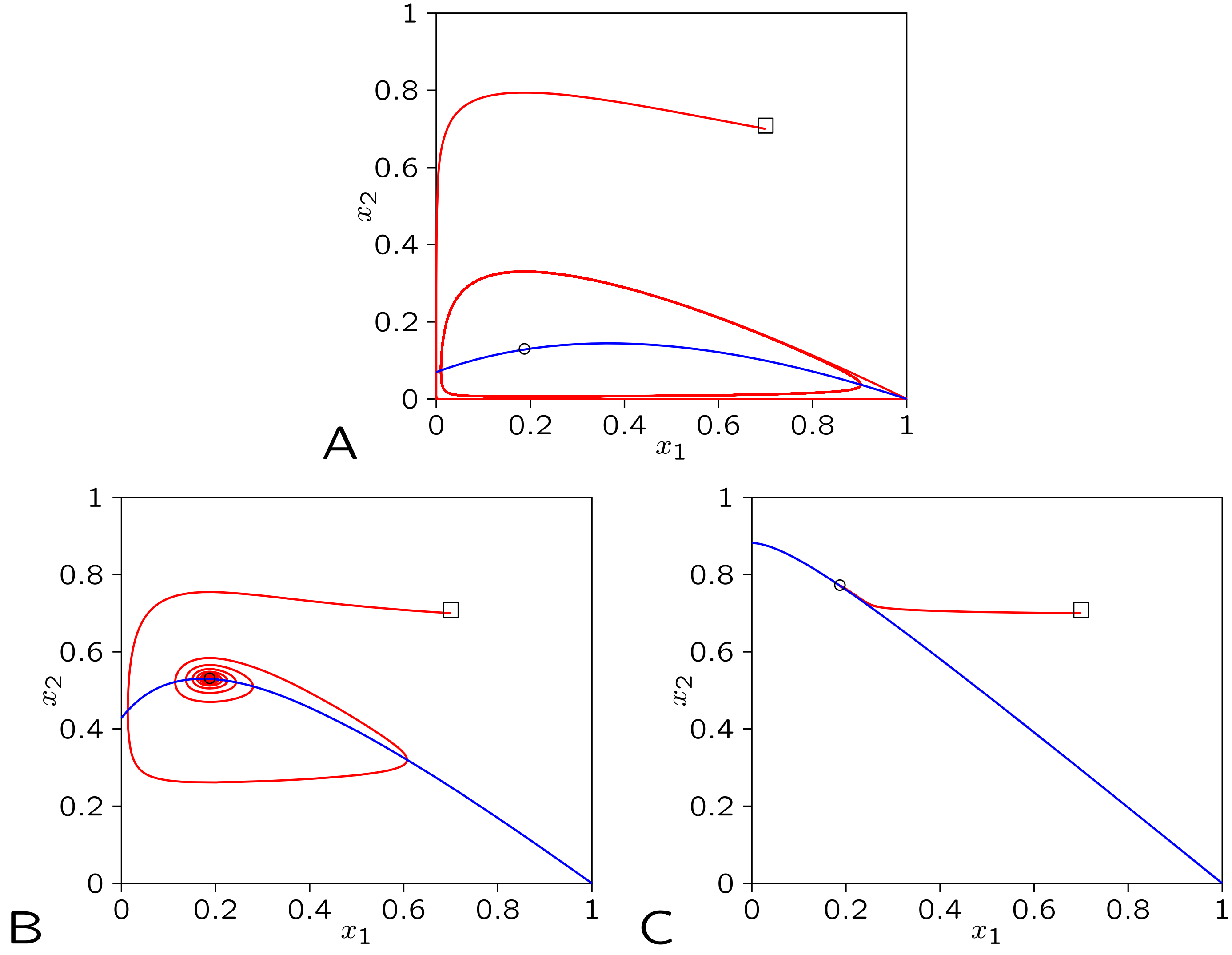


Transcritical TC, Hopf H bifurcations

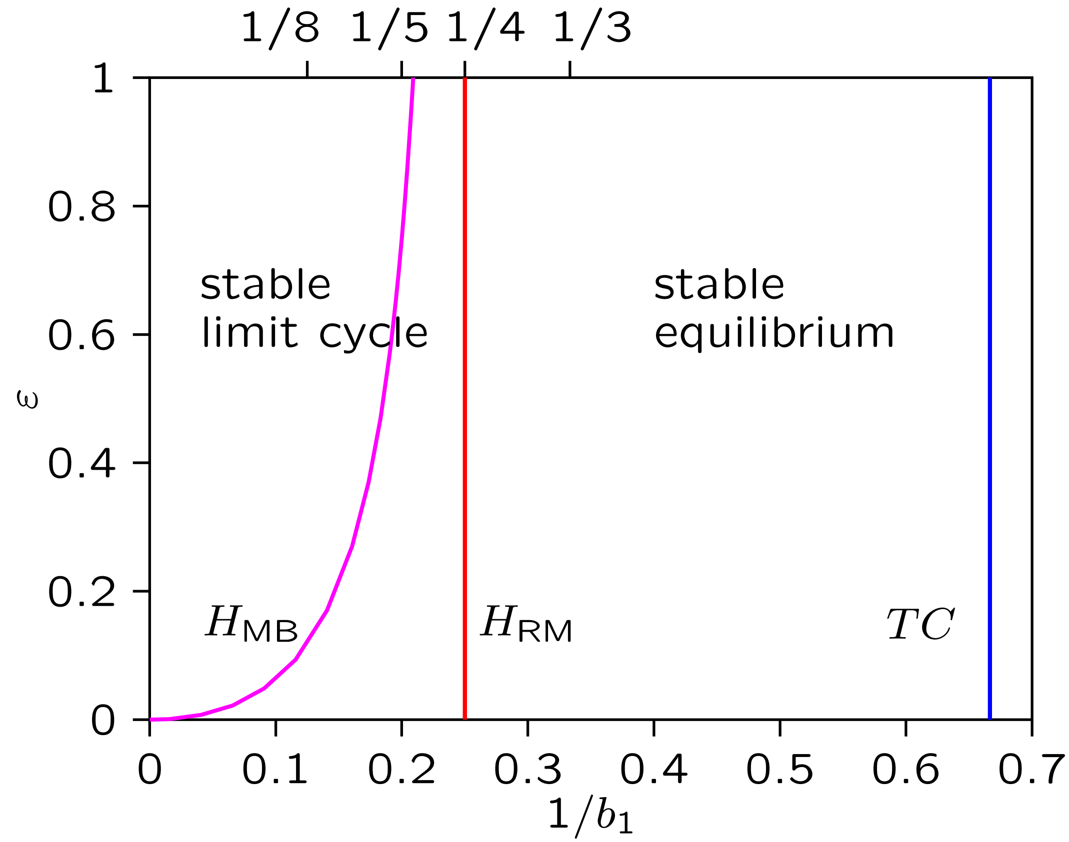
$b_1 = 3$ and A:$\varepsilon = 1$, B: $\varepsilon = 0.1$, C: $\varepsilon = 0.01$



$b_1 = 8$ and A:$\varepsilon = 1$, B: $\varepsilon = 0.1$, C: $\varepsilon = 0.01$



Two-parameter bifurcation diagram ε vs b_1



Hopf H_{MB}; H_{RM}; Transcritical TC both models

Hopf bifurcation differ substantially for $\varepsilon \downarrow 0$

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Conclusions

- RM $\Rightarrow$ MB: Introduction of fixed efficiency and of dynamics of nutrients in the model leads to realistic solution and less complex dynamics when $\varepsilon \to 0$

- Integrated approach is important: Modelling, bifurcation analysis and perturbation theory

- Proper modelling gives perturbation parameter ε a biological interpretation not just a mathematical perturbation parameter

- In RM model a canard occurs just above the Hopf bifurcation and not in the MB model

Literature

B.W. Kooi and J-C. Poggiale, Modelling, singular perturbation and bifurcation analyses of bitrophic food chains, *Mathematical Bioscience*, 301:93-110 2018.

J-C. Poggiale, C. Aldebert, B. Girardot and B.W. Kooi, Analysis of a predator-prey model with specific time scales : a geometrical approach proving the occurrence of canard solutions *Journal of Mathematical Biology*, 2019.