



University of
Zurich ^{UZH}

Using DEB theory at the population scale to limit the risk of structural sensitivity

Cl ment Aldebert^(1,2), BW Kooi⁽³⁾, D Nerini⁽¹⁾, JC Poggiale⁽¹⁾

⁽¹⁾ Mediterranean Institute of Oceanography, Aix-Marseille University, France

⁽²⁾ Institute of Environmental Sciences, University of Z rich, Switzerland

⁽³⁾ Vrije University, Amsterdam, Netherlands

31st May 2017

DEB symposium in Troms , Norway

Modelling a process (e.g. predation)

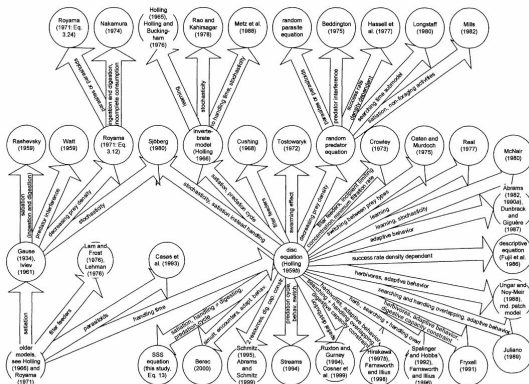
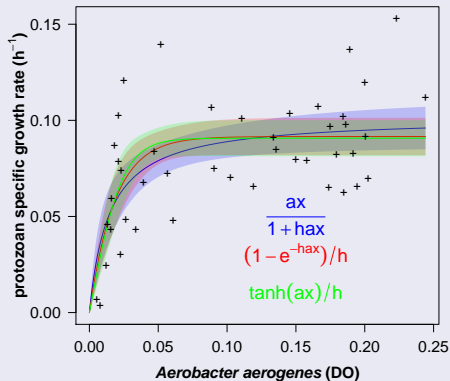


FIG. 1. A “family tree” of functional response models. (Jeschke et al., 2002)

find / attack, handling, digestion / metabolism, spatial heterogeneity, individual variability, collective behaviour, ...

Modelling predation at the population scale

Tetrahymena pyriformis (Ciliate) (Canale et al., 1973)

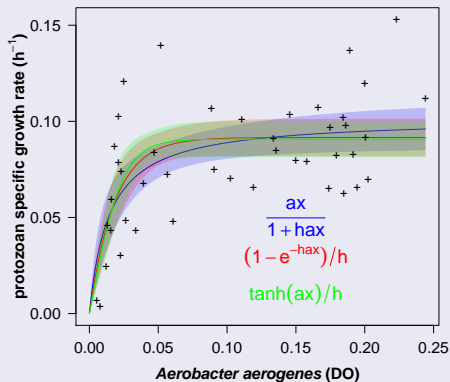


functional response

- prey eaten / predator / time

Modelling predation at the population scale

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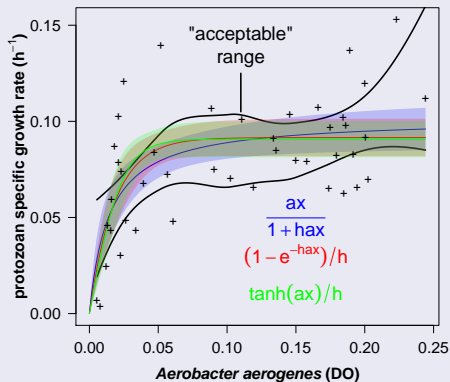


functional response

- prey eaten / predator / time
- 3 functions with the same mathematical properties \Rightarrow same hypotheses on **process shape**
- different hypotheses on **underlying mechanisms**

Modelling predation at the population scale

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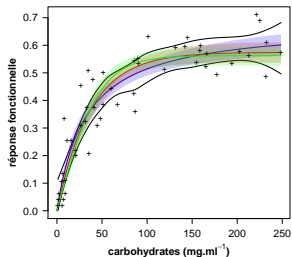


functional response

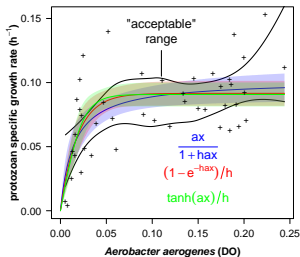
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Modelling predation at the population scale

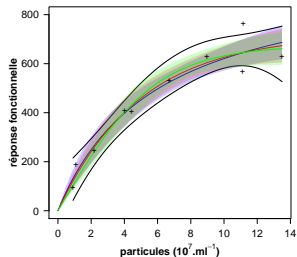
Aerobacter aerogenes (bactérie) (Canale *et al.*, 1973)



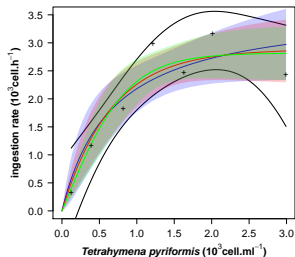
Tetrahymena pyriformis (Ciliatè) (Canale *et al.*, 1973)



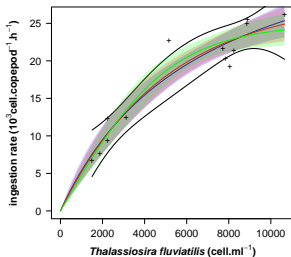
Glaucoma scintillans (cilié) (Fenchel, 1980)



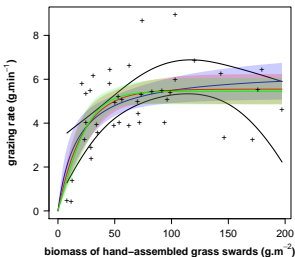
Daphnia magna (McMahon & Rigler, 1965)



Calanus pacificus (Copepod) (Frost, 1972)

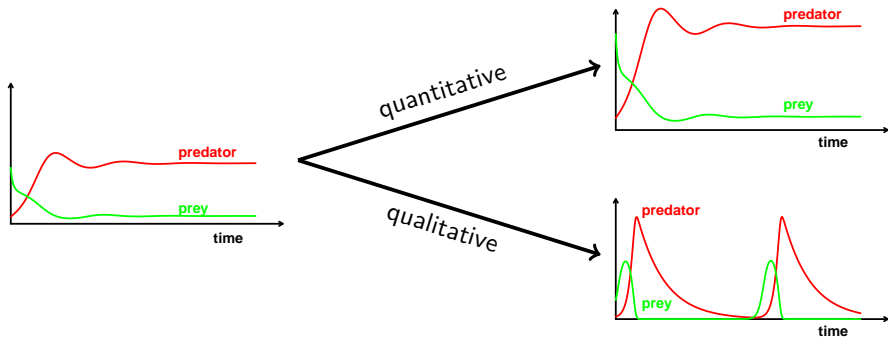


Gazella thomsoni (Wilmshurst *et al.*, 1999)



Different model... different predictions

- change in numerical values (equilibrium, period of oscillations)
- change on existence and stability of invariant sets (bifurcation) (Kuznetsov, 2004)



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structural sensitivity

- functions with the same mathematical properties, that fit data and have theoretical support \Rightarrow different predictions

Different model... different predictions

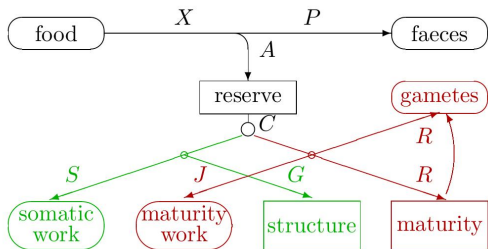
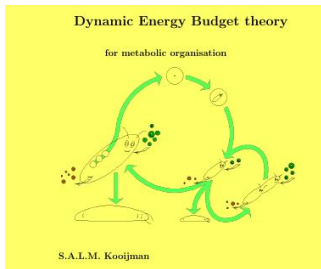
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structural sensitivity

- functions with the same mathematical properties, that fit data and have theoretical support \Rightarrow different predictions
- previous studies : **functional response** in predator-prey model, pathogen infection, colimited uptake of nutrients (Myerscough et al., 1996, Wood & Thomas, 1999, Gross et al., 2004, Fussmann & Blasius, 2005, Anderson et al., 2010, Poggiale et al., 2010, Cordoleani et al., 2011)

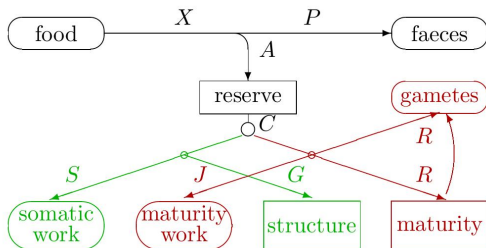
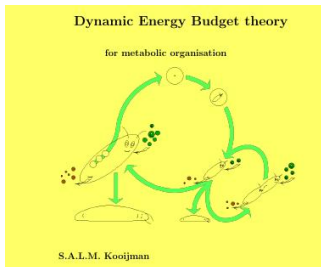
simple assumptions on individual metabolism

An interesting framework : DEB theory



Dynamic Energy Budget theory

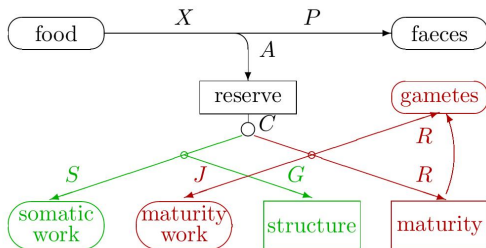
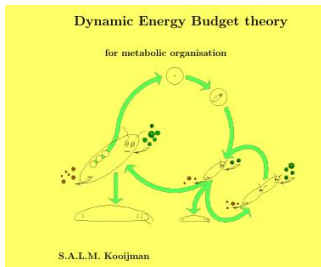
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Dynamic Energy Budget theory

- focus on **individual** and **energy**, mechanistic hypotheses on metabolism
- energy allocation scheme is common to most species

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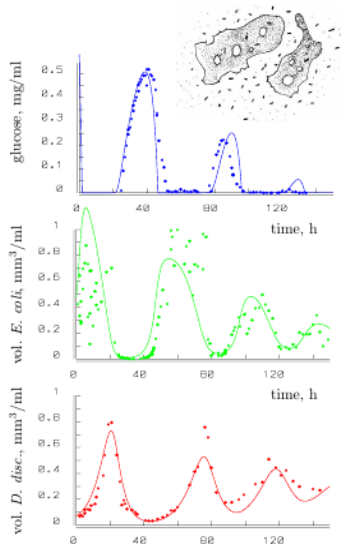


Dynamic Energy Budget theory

- focus on **individual** and **energy**, mechanistic hypotheses on metabolism
- energy allocation scheme is common to most species
- framework to build \pm detailed models **consistent** between each others

A useful example : dividing unicellular organisms

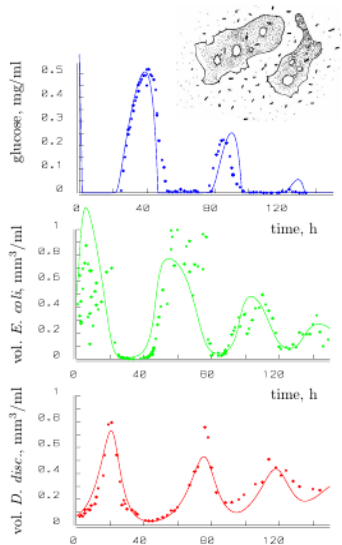
- individual \Rightarrow population
- reproduction easier to model



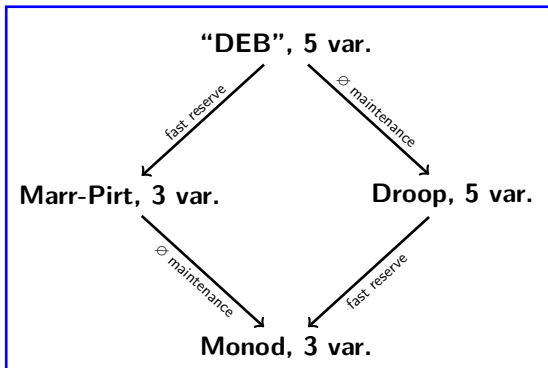
“DEB”, 5 var.

(Dent et al., 1976; Kooi & Kooijman, 1994; Kooijman, 2010)

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∈ DEB theory

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Different chemostat models : “DEB”

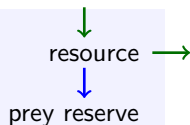
$$\left\{ \begin{array}{l} \frac{dX_0}{dt} = h(X_r - X_0) \end{array} \right.$$

↓
resource →

“DEB”, 5 var.

Different chemostat models : "DEB"

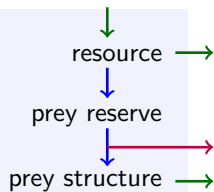
$$\left\{ \begin{array}{l} \frac{dX_0}{dt} = \dot{h}(X_r - X_0) - f_1(X_0)j_{XAm}^1 X_1 \\ \frac{de_1}{dt} = k_E^1 (f_1(X_0) - e_1) \end{array} \right.$$



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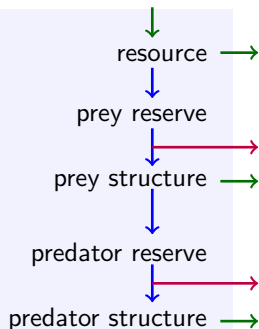
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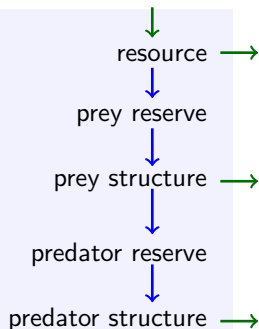
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"DEB", 5 var.

Different chemostat models : Droop

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$$k_M^i = 0$$

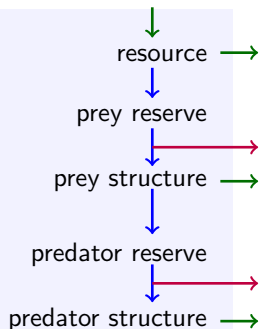
"DEB", 5 var.



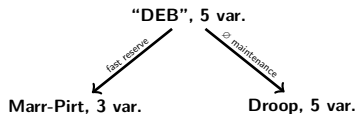
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Different chemostat models : Marr-Pirt

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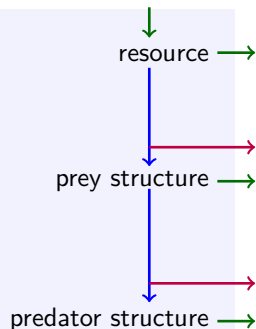


$$k_E^i, g_i \rightarrow +\infty, \frac{k_E^i}{g_i} = \dot{\mu}_i$$

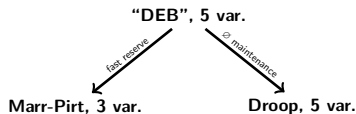


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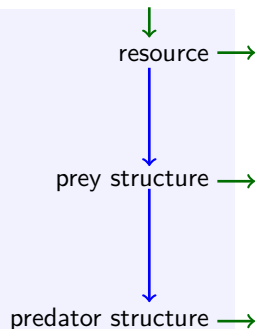


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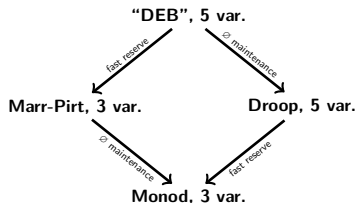
Different chemostat models : Monod

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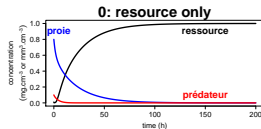
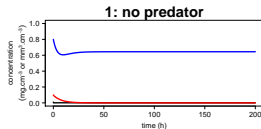


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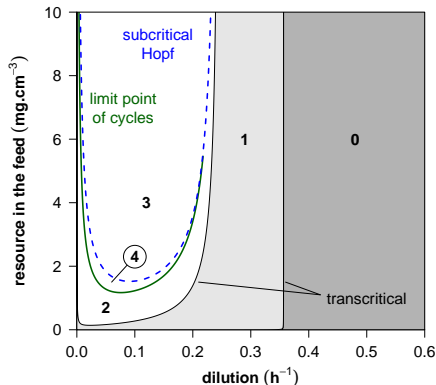
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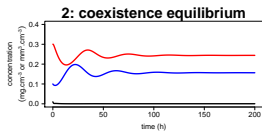
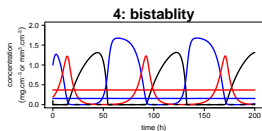
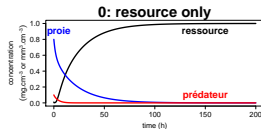
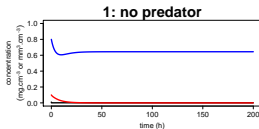
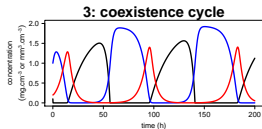
Dynamics predicted by model "DEB"



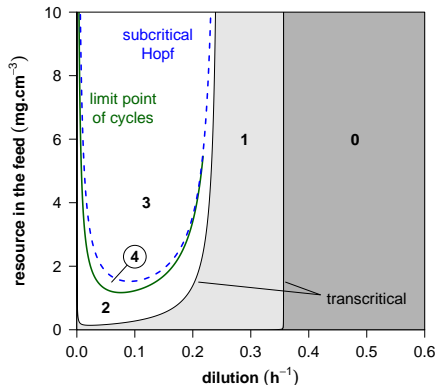
Holling



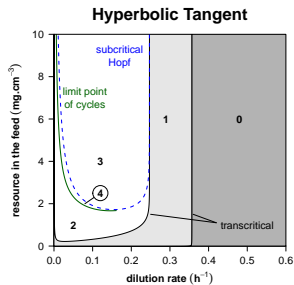
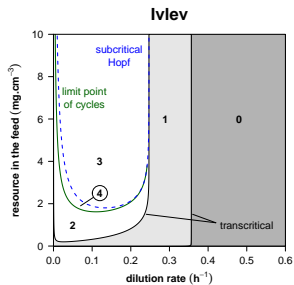
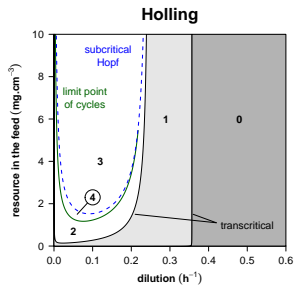
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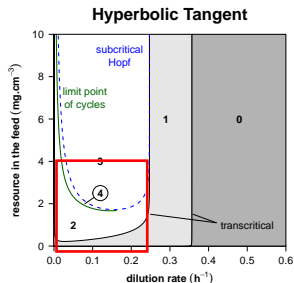
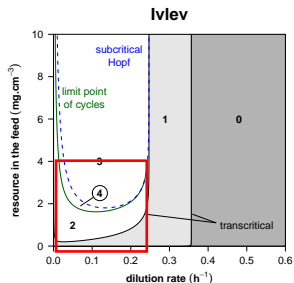
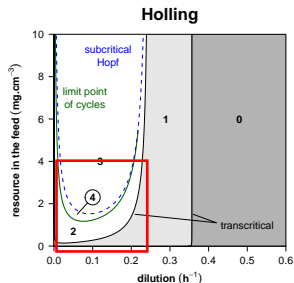
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Structural sensitivity in model "DEB"



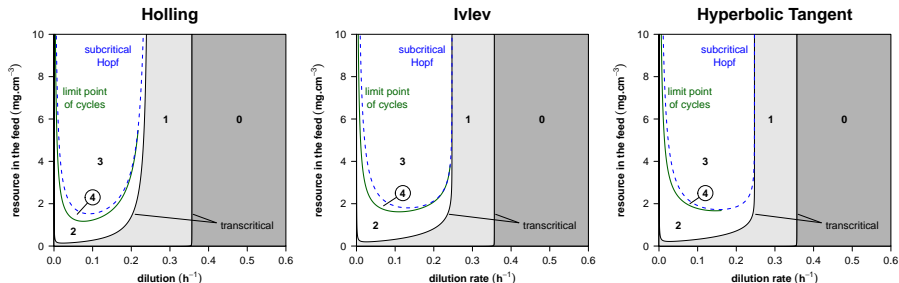
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there is sensitivity... yes but

- same qualitative bifurcations (position \approx)
- differences \subset subspace of parameter values

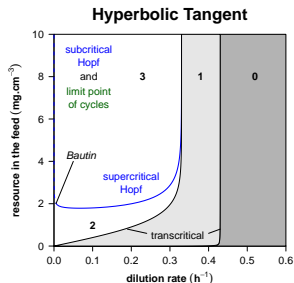
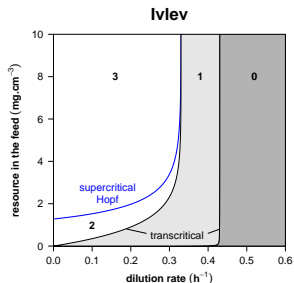
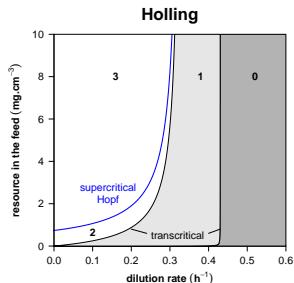
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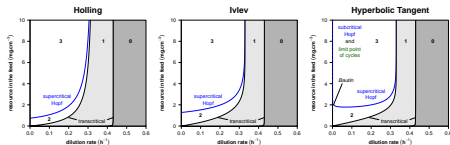
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- same qualitative bifurcations (position \approx)
- differences \subset subspace of parameter values
- **sensitivity** \ll **previous models** (no “new” dynamics)
- same conclusion for Droop & Marr-Pirt models (middle complexity)

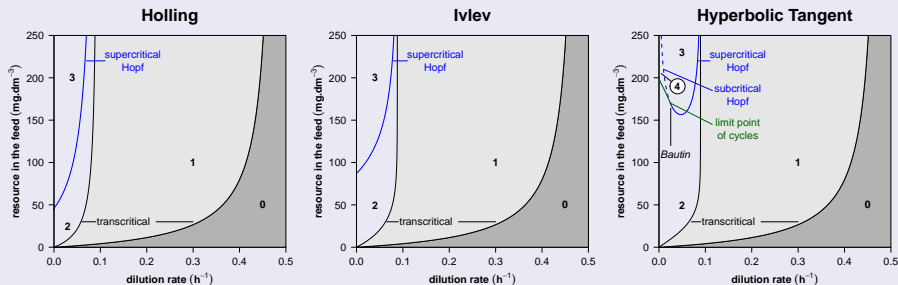
What about Monod model? (simplest)



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other micro-organisms (data from Canale et al., 1973)



A summary of structural sensitivity in predator-prey models

model	maintenance or mortality	explicit reserve	explicit resource
Rosenzweig-MacArthur <i>(Fussmann & Blasius, 2005)</i>	x		
Bazykin <i>(Aldebert et al., 2016)</i>	x		
Monod			x
Marr-Pirt	x		x
Droop		x	x
“DEB”	x	x	x

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Monod			x
Marr-Pirt	x		x
Droop		x	x
"DEB"	x	x	x

⇓ sensitivity (qualitatively similar bifurcations)

explicit resource + (maintenance OR explicit reserve)

a solution to structural sensitivity?

- general across a wide range of parameter values / species? (ongoing work)
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Thank you for your attention !