Computer Sessions' Manual

We will use AUTO-07P [2]. In each session start by making a new directory using the command **mkdir dirname**, then enter in that directory using **cd dir name**:

1. **mkdir dirname**
2. **cd dirname**

Get the two Computer sessions files Practicum 1 (`ecotox.zip`) and Practicum 2 (`rm3.zip`) from the web-site `http://www.bio.vu.nl/thb/course/mri/mri.html`:

1. copy the two files *.zip to the Desktop.
2. unzip the just copied files `unzip -a *.zip` into the directory **dirname** just made.

Observe that in `ecotox.zip` two subdirectories are present in the directory `ecotox`. We will use only the directory `pirttox` in the first computer session on Tuesday Apr 13.

In the directories you will find the files to run all calculations when running AUTO-07P using Unix Commands as described in Chapter 5 of the AUTO-07P manual. These Unix commands run both directly in the shell and at the AUTO Python prompt. By extracting the two *.zip files into the created new directory which is the current user directory you got a **Makefile**, an equations-file xxx.f and all the corresponding constants-files c.xxx in this (see Section 3) current user directory. Be sure that in the Makefile the Fortran compiler **gfortran** is called.

You can run the complete analysis directly in the Unix shell. The AUTO aliases must have been activated; see Section 1.1 of the AUTO-07P manual. Then:

- **make run**

Another option is to use AUTO Python for instance under Windows. Double click atro.py to start a `cmd window` called auto.py with prompt AUTO. You use the `pfortran` compiler with '`-fopenmp -O`'. Note that if there is a 'name'.o object file in the directory created with anotther compiler and when you run for the first time in this directory auto, you have to delete it.

At the AUTO Python prompt use the Basic commands in Section 5.1 of the AUTO-07P manual. For instance in the first computer session on Tuesday Apr 13 you can start in the directory `pirttox` with:

1. **@R pirt 1**: run AUTO-07P with equations-file pirt.f, constants-file c.pirt.1
2. **@sv pirt**: save the output-files fort.7, fort.8, fort.9, as b.pirt, s.pirt, d.pirt, respectively. Existing files by these names will be deleted.

   and so on.

When you want to plot the results from multiple runs use

> **@ap pirt**: append the output-files fort.7, fort.8, fort.9, to existing data- files b.pirt, s.pirt, d.pirt, resp.

1 Exercise: Computer session Tuesday Apr 13

The nutrient–prey model reads

$$\frac{dN}{dt} = (N_r - N)D - I_{NR}\frac{N}{k_{NR}+N}\,R\,, \tag{1a}$$

$$\frac{dR}{dt} = \big(\mu_{NR}\frac{N}{k_{NR}+N} - (D + m_R(c_R))\big)\,R\,, \tag{1b}$$

$$\frac{dc_T}{dt} = (c_r - c_T)D\,, \tag{1c}$$

where

$$m_R(c_R) = m_{R0}\big(1 + \frac{(c_R - c_{RM0})_+}{c_{RM}}\big)\,, \tag{1d}$$

$$c_T = c_W + c_R R = c_W\,(1 + \mathrm{BCF}_{WR} R)\,. \tag{1e}$$

where the subscript plus operator is defined as $x_+ = \max(0, x)$.

The parameter values are given in Table 1:

Table 1: Parameter set for the population model in a chemostat: m mass of toxicant, t time, v is dimension of the volume of the reactor and V biovolume or biomass of organism.

Nutrient–Prey			
μ_{NR}	Max. growth rate	t^{-1}	0.5 h^{-1}
I_{NR}	Max. ingestion rate	t^{-1}	1.25 h^{-1}
k_{NR}	Saturation constant	$\mathrm{V\,v}^{-1}$	8.0 mg dm^{-3}
m_{R0}	Maintenance rate coefficient	t^{-1}	0.025 h^{-1}
c_{RM0}	NoEffect Concentration (NEC)	$\mathrm{m\,V}^{-1}$	0.1 μg mg^{-1}
c_{RM}	Tolerance concentration	$\mathrm{m\,V}^{-1}$	0.5 μg mg^{-1}
BCF_{WR}	BioConcentration Factor	$\mathrm{v\ V}^{-1}$	1.0 dm^3 mg^{-1}

- Rewrite the system of ODEs with N, R, c_T as state variables (1) into a system with state variables N, R, c_W. The reason is that one is interested in the concentration in the water which can be measured. In practice the data can be used to estimate parameters in a curve fit procedure. For the equilibrium values calculating c_W from C_T and R is easy but for extreme values with periodic solutions this is not possible since the extrema for c_T and R occur generally at different times.

- Analyse the nutrient–prey model using AUTO or another computer package. Use the parameter values in Table 1. Generate a one-parameter bifurcation diagram with the toxicity concentration c_r as free parameter for the nutrient–prey system (1) with toxicity stress in the chemostat. The dilution rate equals $D = 0.02$. The session looks as follows:

1. **@R pirt 1**: run AUTO-07P with equations-file pirt.f, constants-file c.pirt.1
2. **@sv pirt**: save the output-files fort.7, fort.8, fort.9, as b.pirt, s.pirt, d.pirt, respectively. Existing files by these names will be deleted.

3. **@R pirt 3**: run AUTO-07P with equations-file pirt.f, constants-file c.pirt.3 and restart data-file s.pirt

   You have now all the results to plot the one-parameter bifurcation diagram. Check that the periodic solution are calculated in the second run starting at the Hopf bifurcation. Observe that the period becomes very high at the last calculated point. Can you explain what happens? The one-parameter c_r-diagram should like Fig. 1

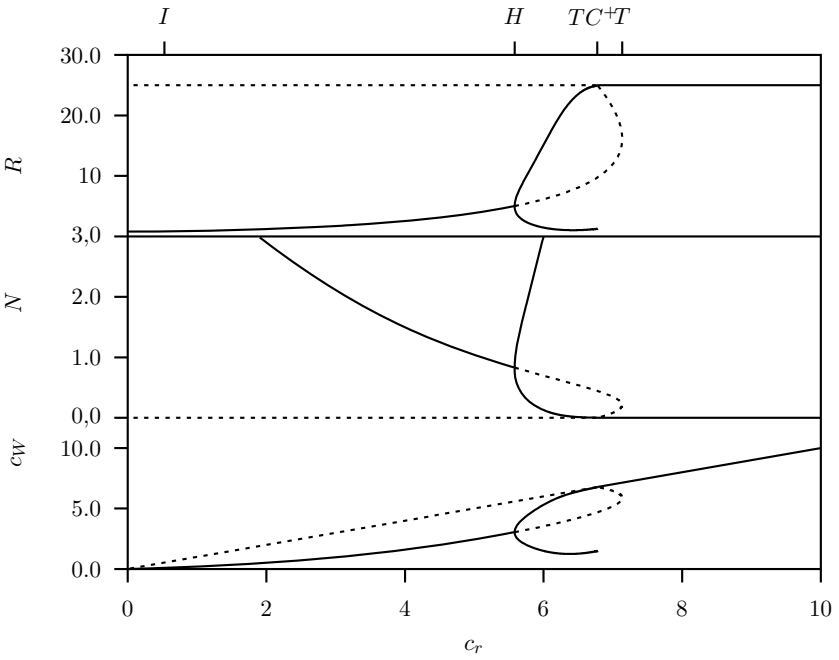

Figure 1: A one-parameter bifurcation diagram with toxicant concentration in the inflow c_r as free parameter for system (1) where $N_r = 25$ and $D = 0.02$. Solid lines are stable equilibria E_0, E_1 and dashed curved lines ones E_2. Point T is a tangent bifurcation, TC a transcritical bifurcation and H a Hopf bifurcation.

- Generate a two-parameter bifurcation diagram with nutrient inflow and toxicity concentration c_r as free parameters for the nutrient–prey system (1). The dilution rate equals again $D = 0.02$. Continue after the previous run with:

  4. **@R pirt 51**
  5. **@R pirt 52**
  6. **@R pirt 53**
  7. **@R pirt 54**
  8. **@R pirt 61**
  9. **@R pirt 62**

  Identify all codim-two points. The two-parameter (N_r, c_r)-diagram should like Fig. 2:

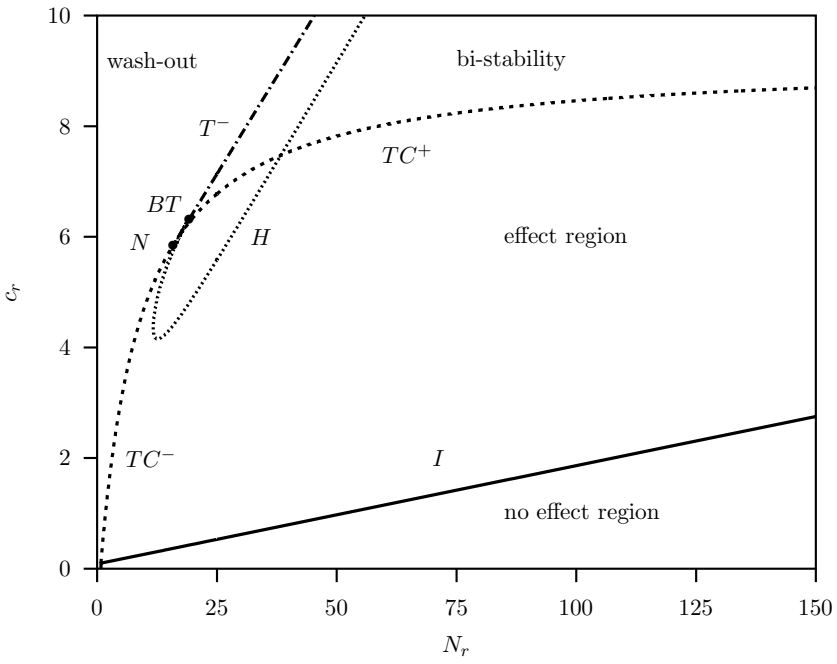

Figure 2: A two-parameter bifurcation diagram with nutrient inflow N_r and dilution rate c_r as free parameters for the population with toxicity stress in the chemostat system (1) where $D = 0.02$. The codim-one curves are the transcritical bifurcation curves $TC^{\pm}$, the tangent bifurcations T. At point N the tangent curve T originates and the transcritical bifurcation changes for supercritical TC^- in subcritical TC^+. There is also a Hopf bifurcation curve H originating from a Bogdanov-Takens point BT at the tangent curve T. Between the two curves T and TC^- bi-stability is possible.

- Calculate the discontinuity curve (curve I in Fig. 2) in the (N_r, c_r)-diagram where $c_W = c_{RM0}$. At this point the elements of the Jacobian matrix evaluated at the equilibrium point can be discontinuous functions of the state variables. This makes this right-hand side of the set of ODEs piecewise smooth functions of the state variables. Describe the region in the diagram with no toxic effects.

2 Exercise: Computer session Thursday Apr 15

The three-level food chain the Rosenzweig–MacArthur model is given by

$$\begin{cases} \dot{x}_1 &= x_1(1-x_1) - f_1(x_1,x_2), \\ \dot{x}_2 &= f_1(x_1,x_2) - f_2(x_2,x_3) - d_1 x_2, \\ \dot{x}_3 &= f_2(x_2,x_3) - d_2 x_3, \end{cases} \tag{2}$$

with Holling Type-II functional responses

$$f_i(u,v) = \frac{a_i u v}{1 + b_i u}\ , \quad i = 1,2. \tag{3}$$

The death rates d_1 and d_2 are used as bifurcation parameters, with the other parameters set at $a_1 = 5$, $a_2 = 0.1$, $b_1 = 3$, and $b_2 = 2$.

- Analyse the bi-trophic Rosenzweig–MacArthur model. Derive for this two-dimensional system expressions for the equilibria. Derive the critical values for the carrying capacity K at the transcritical and Hopf bifurcation. Show that at the Hopf bifurcation the two nullclines intersect at the top of the parabola.

- Analyse with AUTO the Rosenzweig–MacArthur tri-trophic food chain model. Calculate the local bifurcation curves. First calculate the one-parameter diagram with d_2 as free parameter.

  1. **sol1=r(e='rm3', c='rm3.11')**: run AUTO-07P with equations-file rm3.f, constants-file c.rm3.11
  2. **sv('rm3')**: save the output-files fort.7, fort.8, fort.9, as b.rm3, s.rm3, d.rm3, respectively.

  plot **plot('rm3')**: plot figure (PAR(2) vs U(3))

  3. **sol2=r(e='rm3', c='rm3.31', s='rm3')**: run AUTO-07P with equations-file rm3.f, constants-file c.rm3.31 and restart data-file s.rm3 (at label 2)
  4. **ap('rm3')**: append the output-files fort.7, fort.8, fort.9, as b.rm3, s.rm3, d.rm3, respectively.
  5. **p2('rm3')**: plot the one-parameter. diagram with d_2 as varying parameter and choose MAX U(3) for the y-axis and correct with `Options` [minx maxx miny maxy]=[0.008 0.018 0 15]. Compare the results with Fig. 3.
  6. **sol3=r(e='rm3', c='rm3.12')**: run AUTO-07P with equations-file rm3.f, constants-file c.rm3.12
  7. **sv('rm3')**: save the output-files fort.7, fort.8, fort.9, as b.rm3, s.rm3, d.rm3, respectively. Existing files by these names will be deleted.
  8. **sol4=r(e='rm3', c='rm3.32', s='rm3')**: run AUTO-07P with equations-file rm3.f, constants-file c.rm3.32 and restart data-file s.rm3 (at label 2)
  9. **ap('rm3')**: append the output-files fort.7, fort.8, fort.9, as b.rm3, s.rm3, d.rm3, respectively.
  10. **p2('rm3')**: plot the one-parameter. diagram with d_2 as varying parameter and choose MAX U(3) for the y-axis and correct with `Options` [minx maxx miny maxy]=[0.008 0.018 0 15]. Compare the results with Fig. 3.

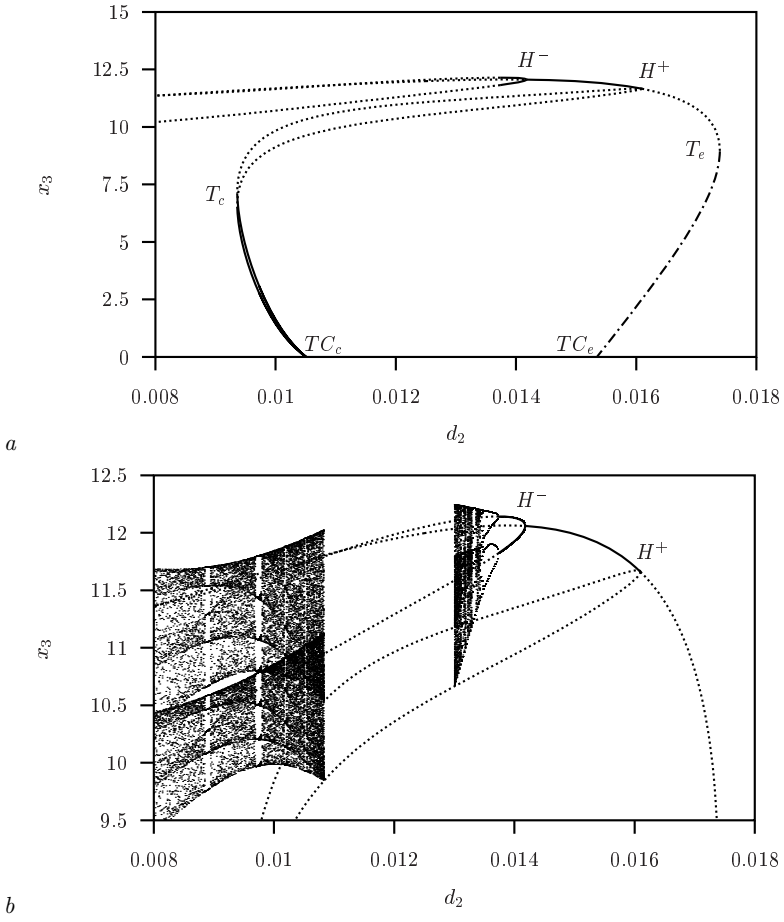

Figure 3: From top to bottom *a*: One-parameter bifurcation diagram of the 3D RM model, Eqn. (2), with d_2 as free parameter ($d_1 = 0.25$). Depicted are the equilibrium densities and the extreme values of x_3. Solid indicates stable, dotted indicated saddle or unstable. *b*: Detail of Figure *a*, now with the regions indicated where chaos occurs. The labels are explained in the main text.

- Secondly, calculate the two-parameter diagram with d_2 and d_1 as free parameters.

  10. **r(e='rm3', c='rm3.101', s='rm3')**: run AUTO-07P with constants-file c.rm3.101 and solution-file s.rm3 (restart at label 37)
  11. **ap('rm3')**: append the output-files fort.7, fort.8, fort.9, as b.rm3, s.rm3, d.rm3, respectively.
  12. **sol5=r(e='rm3', c='rm3.102', s='rm3')**: run AUTO-07P with constants-file c.rm3.102 and restart data-file s.rm3 (at label 39)
  13. **ap('rm3')**: append the output-files fort.7, fort.8, fort.9, as b.rm3, s.rm3, d.rm3, respectively.
  14. **r(e='rm3', c='rm3.103')**: run AUTO-07P with constants-file c.rm3.103 (restart at label 22)
  15. **ap('rm3')**: append the output-files fort.7, fort.8, fort.9, as b.rm3, s.rm3, d.rm3, respectively.

16. **sol6=r(e='rm3', c='rm3.104', s='rm3')**: run AUTO-07P with constants-file c.rm3.104 and restart data-file s.rm3 (restart at label 67)
17. **ap('rm3')**: append the output-files fort.7, fort.8, fort.9, as b.rm3, s.rm3, d.rm3, respectively.
18. **r(e='rm3', c='rm3.105', s='rm3')**: run AUTO-07P with constants-file c.rm3.105 and restart data-file s.rm3 (restart at label 67)
19. **ap('rm3')**: append the output-files fort.7, fort.8, fort.9, as b.rm3, s.rm3, d.rm3, respectively.
20. **sol7=r(e='rm3', c='rm3.51')**: run AUTO-07P with constants-file c.rm3.51 (restart at label 3)
21. **ap('rm3')**: append the output-files fort.7, fort.8, fort.9, as b.rm3, s.rm3, d.rm3, respectively.
22. **sol8=r(e='rm3', c='rm3.52', s='rm3')**: run AUTO-07P with constants-file c.rm3.52 and restart data-file s.rm3 (restart at label 3)
23. **ap('rm3')**: append the output-files fort.7, fort.8, fort.9, as b.rm3, s.rm3, d.rm3, respectively.
24. **sol9=r(e='rm3', c='rm3.53', s='rm3')**: run AUTO-07P with constants-file c.rm3.53 and restart data-file s.rm3 (restart at label 7)
25. **ap('rm3')**: append the output-files fort.7, fort.8, fort.9, as b.rm3, s.rm3, d.rm3, respectively.
26. **sol10=r(e='rm3', c='rm3.54', s='rm3')**: run AUTO-07P with constants-file c.rm3.54 and restart data-file s.rm3 (restart at label 7)
27. **ap('rm3')**: append the output-files fort.7, fort.8, fort.9, as b.rm3, s.rm3, d.rm3, respectively.
28. **sol11=r(e='rm3', c='rm3.61')**: run AUTO-07P with constants-file c.rm3.61 (restart at label 2)
29. **ap('rm3')**: append the output-files fort.7, fort.8, fort.9, as b.rm3, s.rm3, d.rm3, respectively.
30. **sol12=r(e='rm3', c='rm3.62', s='rm3')**: run AUTO-07P with constants-file c.rm3.62 and restart data-file s.rm3 (restart at label 2)
31. **ap('rm3')**: append the output-files fort.7, fort.8, fort.9, as b.rm3, s.rm3, d.rm3, respectively.
32. **p2('rm3')**: plot the one-parameter diagram with d_2 as varying parameter, Compare the results with Fig. 4.

- Run the `c2c` demo from section 15.12 on page 159 of the Auto manual. Continue the homoclinic cycle-to-cycle connection.

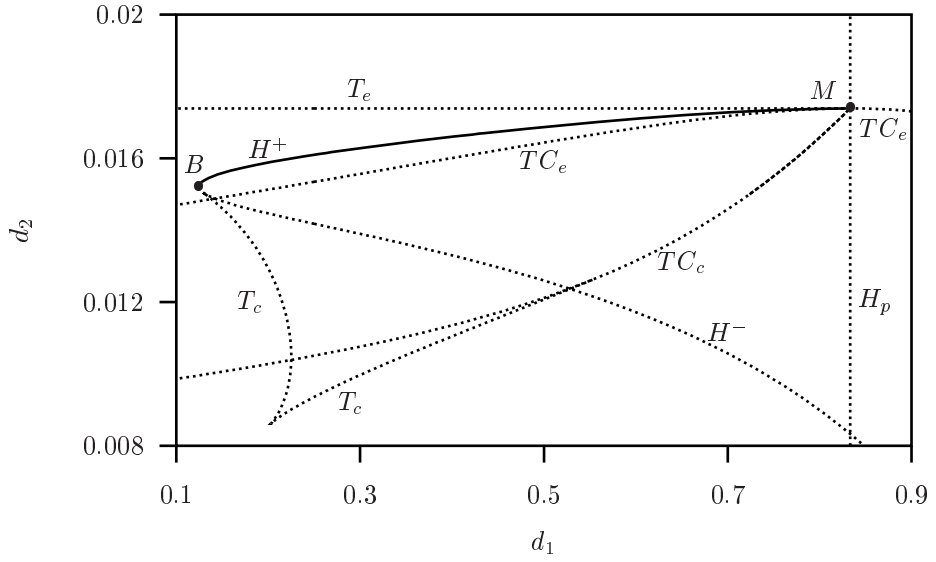

Figure 4: Two-parameter bifurcation diagram of the 3D RM model, Eqn. (2), with d_1 and d_2 as free parameters.

3 Home assignment

The Forest-Pest model described in [1] reads

$$\frac{dx}{dt} = \rho y - (y-1)^2 x - sx - xz \;, \tag{4a}$$

$$\frac{dy}{dt} = x - hy \;, \tag{4b}$$

$$\frac{dz}{dt} = -\epsilon z + Bxz \;, \tag{4c}$$

The parameter values are given in Table 2:

Table 2: Parameter values after [1, Table 1] and the used dimensionless values with the calculation of the bifurcation diagrams.

Parameter	Units	Values	dimensionless Values
a	$\mathrm{ha}^2(103\ \mathrm{trees})^{-2}\mathrm{yr}^{-1}$	0.00606	—
b	$10^3\ \mathrm{trees\ ha}^{-1}$	0.247	—
c	yr^{-1}	0.01	—
ρ	yr^{-1}	0.134	variable
f	yr^{-1}	0.017	—
h	yr^{-1}	0.04	variable
A	yr^{-1}	0.004	—
ϵ	yr^{-1}	1.5	2
B	yr^{-1}	0.8	1
s	yr^{-1}	—	1

- Analyse this model where ρ and h are compound parameters which serve as bifurcation parameters. Use the dimensionless parameter values given in Table 2. Use AUTO or another computer package to continue the local bifurcations.
- Use the Homcont facilities of AUTO to continue the heteroclinic point–to–point connection.

References

[1] M. Ya. Antonovsky, R. A. Fleming, Yu. A. Kuznetsov, and W. C. Clark. Forest–pest interaction dynamics: The simplest mathematical models. *Theoretical Population Biology*, 37:343–367, 1990.

[2] E. J. Doedel and B. Oldeman. Auto 07p: Continuation and bifurcation software for ordinary differential equations. Technical report, Concordia University, Montreal, Canada, 2009.