NON-LINEAR DYNAMICAL SYSTEMS

Tutorials

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NON-LINEAR DYNAMICAL SYSTEMS
Tutorials

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Chapter 1

Introduction to MAPLE

1.1 Numerical Calculations

To start Maple type `xmaple`. Note, that any completed Maple command should have `;` at the end.

At any moment, you can use the `restart` command to clear Maple’s internal memory and reset everything. Tour.

```maple
> restart;
```

Computations with Integers

Commands.

A MAPLE command is a statement of a calculation followed by a semicolon (the result is displayed on the screen) or a colon (the result is stored but not displayed). Following are some commands followed by the displayed results. Enter the commands on your worksheet and verify the given results. When you get to "Save the file," select "Save" under the "File" menu or type CTRL-S.

```maple
> 4 + 5;
9

> 6^2;
36

> 3*4 + 7;
19
```
operating on the last result.

Use a quotation mark (%) to refer to the result of the last calculation, and a double quotation mark (%%) to refer to the next-to-last result. For example,

\[
3 * (4 + 7);
\]

\[
33
\]

\[
5 * 2;
\]

\[
10
\]

\[
7 + \%
\]

\[
17
\]

\[
\% \times \%\%
\]

\[
170
\]

At its most basic level, you can use Maple as a very powerful calculator.

To calculate \((32) \times (12^{13})\), you would enter the following:

\[
32 \times 12^{13};
\]

Maple recognizes many special operators, including factorial, greatest common divisor, least common multiple, and computation over the integers modulo \(m\). The following line is an example of the factorial operator in use.

\[
200!;
\]

You can easily include the previous expansion of 200! in any subsequent calculation without having to type it. The ditto operator, represented by a percent sign (%), refers to the last expression computed by Maple. (For more information on the ditto operator, see the help page for ditto.) The command `ifactor` factors the previous result into its prime factors.

\[
\text{ifactor(\%)};
\]

The next command calculates the product again, which is precisely the value of 200!.

\[
\text{expand(\%)};
\]

**Floating-point Arithmetic**

A principal strength of Maple is its ability to do exact arithmetic. Fractions and radicals during computation are not converted to their decimal equivalent, thereby avoiding round-off errors. When you do need to use decimal equivalents, Maple has a command that approximates the
value of the expression in a floating-point form.

Consider the expression \(\frac{2^{30}\sqrt{3}}{3^{20}}\), which is entered on the Maple command line as follows:

\[
> \ (2^{30}/3^{20})\*\text{sqrt}(3);
\]

Use the \texttt{evalf} command to generate an approximation in the form of a floating-point value.

\[
> \ \text{evalf}(\%);
\]

Alternatively, you can begin a computation with floating-point values, in which case Maple will automatically use floating-point arithmetic to compute the result. For example, we enter the previous expression using the floating-point value 3.0 in the square root:

\[
> \ (2^{30}/3^{20})\*\text{sqrt}(3.0);
\]

**Specifying the number of digits (significant figures) in your results.**

When you do floating point arithmetic, MAPLE defaults to 10 significant figures:

\[
> \ \text{evalf}(5/2);
\]

2.500000000

You can change the default by setting a variable ”Digits” equal to the desired number of significant figures.

\[
> \ \text{Digits} := 4; \ (\text{Make sure you capitalize the word Digits}.)
\]

Digits := 4

\[
> \ \text{evalf}(5/2);
\]

2.500

**Finite and Infinite Sums and Products**

You can calculate both finite and infinite sums.

Consider the finite sum \(\sum_{i=1}^{10} \frac{1+i}{1+i^4}\). You calculate its value as follows:

\[
> \ \text{sum}( \ (1+i)/(1+i^4), \ i=1..10 ) ;
\]

Consider the infinite sum \(\sum_{k=1}^{\infty} \frac{1}{k^2}\). To calculate its value, enter:

\[
> \ \text{sum}( \ 1/k^2, \ k=1..\text{infinity} );
\]

Maple also calculates both finite and infinite products.
To evaluate the finite product \( \prod_{i=0}^{10} \frac{i^2+3i-11}{i+3} \), you would enter the following Maple command:

\[
> \text{product}( ((i^2+3*i-11)/(i+3)), i=0..10 );
\]

You can do arithmetic with floating-point numbers to any desired precision. In fact, Maple handles numbers up to \textit{hundreds of thousands of digits} of precision on most operating systems. The following command calculates a 50-digit floating-point approximation of the fraction in the previous calculation.

\[
> \text{evalf}[50](%);
\]

### 1.2 Algebraic Computations

\textit{Maple} is a very powerful algebraic calculator that can manipulate and find solutions to many problems symbolically. Being able to use variables instead of specifying numbers at the beginning of a problem allows you to ask ”What if...?” types of questions.

#### Working with Expressions

Maple provides different ways of manipulating and displaying expressions to make them easier to verify, or more effective to use. This flexibility allows you to do such things as expand binomials, factor results, simplify trigonometric expressions, assign results to variable names, and convert expressions to different forms.

#### Expanding and Factoring Expressions

Maple can expand binomials such as \((x+y)^4\). The following Maple commands create the expression, and then expand it.

\[
> \text{expr} := (x+y)^15;
> \text{expand}(\text{expr});
\]

After viewing the results, you can use the \texttt{factor} command to factor the last result and check the computation.

\[
> \text{factor}(\%);
\]

#### Simplifying Expressions

Maple can apply identities to simplify many lengthy mathematical expressions, such as trigonometric expressions.
Consider \( \cos(x)^5 + \sin(x)^4 + 2\cos(x)^2 - 2\sin(x)^2 - \cos(2x) \).

\[ > \text{simplify( } \cos(x)^5 + \sin(x)^4 + 2\cos(x)^2 - 2\sin(x)^2 - \cos(2x) \text{ )}; \]

Another way to simplify expressions is to use the \text{normal} command, which puts fractions on a common denominator and removes common factors in the numerator and denominator.

The fraction \( \frac{x^3-y^3}{x^2+x-y-y^2} \) is much simpler after Maple removes the common factors.

\[ > \text{normal( } (x^3-y^3)/(x^2+x-y-y^2) \text{ )}; \]

**Assigning Results to Names**

You can assign the results of a computation to a Maple name (sometimes loosely referred to as a variable). Assigning to names is essential for managing large numbers of expressions and results, especially if you want to reuse them later in a session.

For example, create the expression \((41x^2+x+1)^2(2x-1)\), and store it as \textit{expr1}.

\[ > \text{expr1 := (41*x^2+x+1)^2*(2*x-1)}; \]

Use the \text{expand} command on \textit{expr1} and store the result as a variable, \textit{expr2}.

\[ > \text{expr2 := expand(expr1)}; \]

Evaluate \textit{expr2} at \(x=1\).

\[ > \text{eval(expr2 , x=1 )}; \]

In the next example, \textit{answer} is assigned as the normalized quotient of the expansion of two expressions, \textit{top} and \textit{bottom}.

\[ > \text{top := expr2}; \]
\[ > \text{bottom := expand((3*x+5)*(2*x-1))}; \]
\[ > \text{answer := normal( top/bottom )}; \]

**Converting Expressions to Different Forms**

The \text{convert} command allows you to convert many types of expressions into specific forms. For a complete list of conversions available in Maple, see the Help page for the \text{convert} command.

The following example converts a symbolic expression, \( \frac{ax^2+b}{x(-3x^2-x+4)} \), into its partial fraction decomposition.

\[ > \text{my_expr := (a*x^2+b)/(x*(-3*x^2-x+4))}; \]
\[ > \text{convert( my_expr, parfrac, x )}; \]
Function Notation

Maple provides several ways to define functions. One way is to use arrow notation (which closely resembles standard mathematical notation for a mapping). You can also use the `unapply` command, which turns an expression into a function.

Define the function \( x \rightarrow x^2 + \frac{1}{2} \).

\[
> f := x \rightarrow x^2 + 1/2;
\]

Evaluate the function at numeric and symbolic values.

\[
> f(2);
> f(a+b);
\]

Use the `unapply` command to turn an expression into a function.

\[
> g := \text{unapply}(x^2 + 1/2, x);
\]

Solving Equations and Systems of Equations

You can use Maple to solve and verify solutions to equations and systems of equations.

Solving an Equation

Use Maple to solve the following equation:

\[
x^3 - \frac{a x^2}{2} + \frac{13x^2}{3} = \frac{13ax}{6} + \frac{10x}{3} - \frac{5a}{3}.
\]

\[
> \text{eqn} := x^3 - 1/2*a*x^2 + 13/3*x^2 = 13/6*a*x + 10/3*x - 5/3*a;
> \text{solve( eqn, \{x\} )};
\]

To verify one of the solutions, evaluate the equation at that particular value of \( x \).

\[
> \text{eval( eqn, x=1/2*a )};
\]

Solving a System of Equations

Defining equations

Equations are expressions, so we can use the colon-equal (:=) to define equations involving one or more variables. (This will be the first step in getting MAPLE to solve the equations.)

Suppose equations relating two variables are

\[
2x_1 - 5x_2 = 12
\]

10
12x1 + 4x2 = 17

To enter and store these equations for subsequent processing, enter the commands

> eq1 := 2*x1 - 5*x2 = 12:
> eq2 := 12*x1 + 4*x2 = 17:

(Don’t forget the multiplication symbols.) We used colons instead of semicolons in these commands, so MAPLE does not reproduce the equation definitions.

Solving sets of linear algebraic equations.

Suppose you wish to solve the pair of equations defined above for the variables x1 and x2. Use the solve (exact arithmetic) or fsolve (floating point arithmetic) command as follows: (Type these commands carefully; if you make the slightest mistake, like omitting a comma or typing the wrong kind of brace, MAPLE will give you nothing but heartache.)

> sol := solve({eq1, eq2}, {x1,x2});
sol={ x2=-\frac{55}{34}, x1 = \frac{133}{68} }
> sol := fsolve({eq1, eq2}, {x1,x2});
sol := x2 = -1.618, x1 = 1.956

(There does not seem to be any way to predict which variable MAPLE will print first.)

The argument of the solve or fsolve command consists of two sets of curly braces enclosed in parentheses. (If you only have one equation in one unknown, you don’t need the braces.) The first set of braces contains the equations to be solved or the symbols for them, separated by commas; the second set contains the set of unknown variables to be solved for.

Extracting components of a solution.

The solution set sol generated with the fsolve command in the previous step contains two components: the equation x1 = 1.9559, and the equation x2 = -1.6176. You can extract either of these equations or only their right-hand sides as follows (the example shows the procedure for the first element).

> sol[2];
x1 = 1.956
> rhs(sol[2]);
1.956
You could also use the \texttt{lhs} function to extract the left-hand side of the equation.

Consider the following set of four equations and five unknowns:
\begin{verbatim}
> eqn1 := a+2*b+3*c+4*d+5*e=41;
> eqn2 := 5*a+5*b+4*c+3*d+2*e=20;
> eqn3 := 3*b+4*c-8*d+2*e=125;
> eqn4 := a+b+c+d+e=9;
\end{verbatim}

Now solve the system for the variables $a$, $b$, $c$, and $d$. Maple will return its solutions in terms of the fifth variable, $e$. Since there are four equations and five unknowns, we will have a parametric set of solutions. On the other hand, if we solved for $a$, $b$, $c$, $d$, and $e$, Maple would choose one of the variables (at random) as a free parameter.

\begin{verbatim}
> solve( {eqn1, eqn2, eqn3, eqn4}, {a, b, c, d} );
\end{verbatim}

To verify that this solution satisfies \texttt{eqn1} and \texttt{eqn2}, evaluate both of them at this solution.

\begin{verbatim}
> eval( {eqn1, eqn2} , % );
\end{verbatim}

\section*{1.3 Graphics}

Maple supports both two-dimensional and three-dimensional graphics. You can graph explicit, implicit, and parametric functions, as well as data sets. By default, graphs and animations appear as \textit{inline graphics} in your worksheet.

Related functions in Maple are grouped into packages and can be accessed by using the notation \texttt{package[function](arguments)}. The \texttt{with} command allows you to access the functions in a library package by their short names. If you enter the command followed by a semicolon (instead of a colon), a list of the functions available in the package is displayed.

\begin{verbatim}
> with(plots);
> with(plottools);
\end{verbatim}

\textbf{Two-dimensional Graphs}

Maple’s two-dimensional plotting tools allow you to graph multiple functions, produce conformal plots of complex-valued functions, and generate log, loglog, parametric, phase, polar, and contour plots. You can graph inequalities, implicitly given functions, solutions to differential equations, and root loci. You also have full control over the fonts used for titles, labels, and other text in your plots.
Example of 2-D Plotting

The following example generates the plot of $y = \tan(x)$.

```maple
plot( tan(x), x=-2*Pi..2*Pi, y=-4..4, discont=true,
     title="y = tan(x)" );
```

Notice how Maple handles functions with discontinuities.

The implicitplot Command

The command `implicitplot` (from the `plots` package) graphs an implicit equation of two variables without resorting to an explicit solution of any variable.

The following command simultaneously graphs the unit circle $x^2 + y^2 = 1$ and the exponential function $y = e^x$:

```maple
implicitplot( { x^2+y^2=1, y=exp(x) }, x=-Pi..Pi, y=-Pi..Pi,
              scaling=CONSTRAINED);
```

The plottools Package

The `plottools` package contains many commands for generating and manipulating graphical objects, for example, you can specify an ellipse with axes 2 and 1 centered at (0,0):

```maple
elli := ellipse( [0, 0], 2, 1, color=green ):
> display( elli, scaling=CONSTRAINED, view=[-2..2,-2..2], title="An Ellipse" );
```

Three-dimensional Graphs

Maple can plot surfaces and curves in three dimensions. This includes explicitly and parametrically given surfaces, as well as solutions to differential equations. You can modify the display of your graphics by changing aspects such as fonts, lighting, and coloring.

The following example plots a function of two variables, namely the function defined by $z = xe^{(-x^2-y^2)}$.

```maple
plot3d( x*exp(-x^2-y^2), x=-2..2, y=-2..2, axes=BOXED,
        lightmodel=light1,
        title="A Surface Plot" );
```
To rotate the plot, click the plot to select it. Position the mouse pointer in the plot, but not directly on the curve or surface. Drag the mouse pointer to reorient the plot. Release the mouse button when the plot is oriented correctly.

Maple can construct nested polyhedra.

```maple
> p := display( seq( cutout(v, 4/5), v=stellate(dodecahedron(), 3) ),
  style=PATCH):
> q := display( cutout(icosahedron([0, 0, 0], 2.2), 7/8) ):
> display( p, q, scaling=CONSTRAINED, title="Nested Polyhedra" );
```

**Animation of Graphs**

The plots package supports two- and three-dimensional animations. You can use this feature to illustrate real-world processes in which information changes over time.

```maple
> animate3d( cos(t*x)*sin(t*y), x=-Pi..Pi, y=-Pi..Pi, t=1..2 );
```

*To begin the animation: From the Animation menu, choose Play. To stop the animation at any time: From the Animation menu, choose Stop.*

**Limits**

Maple can compute the limits of functions approaching finite and infinite values. It can take the limits in both positive and negative directions, and compute limits involving absolute values. Maple also recognizes undefined limits.

**Finite and Infinite Values**

Maple can compute limits of functions approaching finite and infinite values, as shown in the following example.

```maple
> expr := (2*x+3)/(7*x+5):
> limit( expr, x=infinity );
```

**Absolute Values**

Maple can compute limits involving absolute values. Consider \( \lim_{x \to 4} \frac{|x-4|}{x-4} \).

```maple
> limit( abs(x-4)/(x-4), x=4, right );
```
1.4 Online Help

You can get help on Maple commands and concepts in various ways. These are the main methods:

- Context-sensitive help: Place your cursor on a word that you want more information about. From the Help menu, choose Help on word (where word is the word the cursor is on), or hold down the Ctrl key and press F1.

- Help browser: The help browser appears at the top of most help windows. (For example, from the Help menu, choose Introduction, and look at the top of the window.) In the first column of the browser, click on the general subject that interests you. If the topic name you choose has subtopics, the list of subtopics appears in the second column. Subtopics that can be subdivided still further display a list of sub-subtopics in the next column, and so on, up to five columns. When you have found the specific topic of your choice, click on the topic name. The help page for that topic appears in the display area of the help window, below the help browser.

- Topic search: From the Help menu, choose Topic Search. In the dialog box, type in the first few letters of the topic that you are interested in. Maple displays the matching topics in such a way that you are likely to find the help page you need near the top.

- Topic name: If you know the name of the help topic that you want to read, you can access the help page directly from the worksheet by typing ?name. For example, type ?plot at the command prompt to open the help page on the plot command.

- Full text search: From the Help menu, choose Full Text Search. In the dialog box, type in the word or words that you want to search for. Maple displays the matching topics in such a way that you are likely to find the help page you need near the top.

- History: To revisit any help page that you have seen in your current Maple session, from the Help menu, choose History. From the list, select the topic to revisit.

1.5 Exercises

1. Factorise the polynomial $2x^4 + 7x^3 - 11x^2 - 22x + 24$
2. Plot the graph of the function $\frac{1}{2x+1}$ for $-5 < x < 5$.

3. Plot the graph of the function $\frac{10(x^2-7)}{x^2-16}$. Choose a suitable range and domain to display your results, explaining your choice.

4. Find the values of $x$ for which $f(x) = 0$, and draw the graph of:

$$f(x) = x \left( \frac{2x}{x+0.2} - 0.1 \right) - x(x+0.2)$$

Draw the phase portrait of the system:

$$\frac{dx}{dt} = f(x)$$
Opgave 2.1
Bereken de 22e decimaal van $\ln(7)$, $e^7$, $2^{71}$, $\pi$.

Opgave 3.1
Bepaal de nulpunten van $\sin(2x + 1) \cos(3x - 5) + \sin(3x - 5) \cos(2x + 1)$.

Opgave 3.4
Raadpleeg ?convert om
\[
\frac{\tan(x)}{1 + 2 \tan^3(x)}
\]
uit te drukken in $\sin(x)$ en $\cos(x)$.

Opgave 3.5
Transformeer de expressie $x + y + 3z$ naar $a + y + 3b$.

Opgave 3.6
Soms kunnen we aan simplify een voorwaarde opgeven, waardoor we uitdrukkingen waarin een bepaalde expressie vaak voorkomt eenvoudiger kunnen schrijven. Zo levert
\[
\text{simplify}(x \cdot y \cdot z + x \cdot y \cdot 2, x \cdot y = 0)
\]
het resultaat $x \cdot z + y \cdot 2$.
Vereenvoudig nu zelf
\[
(\sin(x \cdot y \cdot z) \cdot y \cdot z + x \cdot y \cdot z^2) \cdot x
\]
tot een uitdrukking waarin slechts één sinus, twee vermenigvuldigingen en één optelling voorkomt.

Opgave 5.1
Voor elke $p \in [0, 4]$ is gegeven de functie $f_p : x \rightarrow 2 \sin^2 x - p \sin x$, met domein $[0, \pi]$. Ten opzichte van een assenstelsel $Oxy$ is $K_p$ de grafiek van $f_p$. Teken in één figuur de grafieken $K_0, K_1, K_2, K_3, K_4$. Neem voor $x$ het interval $[0, \pi]$ en voor $y$ het interval $[-2, 2]$. Maak een afdruk van dit plaatje.

Opgave 5.4
Maak een plot van de kromme $K$ gedefinieerd door de vergelijking $x^3 + y^2 = a$, voor $a = 2$, $a = 1$, $a = 0$ en $a = -1$.

Opgave 5.5
Maak, voor verschillende waarden van $\phi$, een plaatje van de kromme $K$ gegeven door de parametervoorstelling $x = \cos(\phi)t^2 + t^3$, $y = \sin(\phi)t^2 + t^3$. Wat kun je zeggen over de richting van de "punt van de grafiek"? Formuleer hierover een vermoeden en bewijs het.

Opgave 5.6
Probeer een parametervoorstelling te vinden voor onderstaande kromme.
Opgave 6.1
Maak een schets van de ruimtekrumme \( t \rightarrow (\sin(t), \cos(t) \sin(t), \cos^2(t)) \).

Opgave 6.3
Maak een plaatje van de grafiek van de functie \((x, y) \rightarrow x^2 y \sin(xy)\) voor \((x, y) \in [0, 2\pi] \times [0, 1]\). Neem het gezichtspunt achtereenvolgens
a. op de y-as
b. op de x-as
c. op de z-as
d. op de lijn door de oorsprong en met richtingsvector \((1, 1, 1)\).
Chapter 2

Derivatives

2.1 Ordinary derivatives

Maple can symbolically display and compute derivatives and integrals.

For example, define the function \( x \rightarrow x \sin(ax) + bx^2 \).

\[
> f := x -> x*\sin(a*x) + b*x^2;
\]

Construct an expression for the derivative, \( \frac{\partial}{\partial x} (x \sin(ax) + bx^2) \), and call the computed value \( f_{\text{prime}} \).

\[
> f_{\text{prime}} := \text{diff}( f(x), x);
\]

If you compute \( f_{\text{prime}} \)’s antiderivative, you get the original function. Verify this assumption by using the following commands:

\[
> \int(f_{\text{prime}}, x);
> \text{simplify}(%);
\]

We can do differentiation without introduction of a function as:

\[
> F := x*\sin(a*x) + b*x^2;
\]

the derivative can be found as:

\[
> \text{DF := diff}( F, x);
\]

1. Find derivatives of the following functions. Compute the derivatives using pencil and paper, then check your result using MAPLE.

(a) \( x^4 \)
(b) \( 5x - 20x^3 \)
(c) \( \sin 2x \)
(d) $3x^{2/3} - 2x^{5/2} + x^{-3}$  
(e) $\cos x$  
(f) $e^{\sqrt{x}}$  
(g) $4 \ln x$

2. Find derivatives of the following functions using the product and the ratio rule. Compute the derivatives using pencil and paper, then check your result using MAPLE. Remember:

$$(uv)' = u'v + v'u$$

$$(\frac{u}{v})' = \frac{u'v - v'u}{v^2}$$

(a) $x^7e^x$ 
(b) $e^x \cos x$ 
(c) $\frac{x^2}{\ln x}$ 
(d) $\frac{x^3}{e^x}$

3. Find derivatives of the following functions using the chain rule. Compute the derivatives using pencil and paper, then check your result using MAPLE. Remember:

$$(f(g(u)))' = f'(g(u)) \ast g'(u)$$

(a) $4 \sin x^2$ 
(b) $(3 + 2x^2)^4$ 
(c) $\sqrt{xe^x + x}$ 
(d) $\frac{1}{3(\cos x)^3}$

4. Find the 6th derivative of $x^2e^x$ using MAPLE.

2.2 Partial derivatives

Find the following partial derivatives using pencil and paper, then check your result using MAPLE.

1. $\frac{\partial z}{\partial x}$ for $z(x,y) = x^2 + y^2 - 4$ 
2. $\frac{\partial z}{\partial x}$ for $z(x,y) = \sqrt{1-x^2-y^2}$ 
3. $\frac{\partial z}{\partial x}$ and $\frac{\partial z}{\partial y}$ for $z(x,y) = \sqrt{y\sin x}$
NOTE: To find partial derivatives using MAPLE use the same procedure `diff` and specify the variable with respect to which you want to find the partial derivative.

For example, if we define the function \( f = (1 + x^2 + y)^2 \) using:

\[
> f := (1 + x^2 + y)^2;
\]

then in order to find \( \frac{\partial f}{\partial x} \) we use:

\[
> \text{diff}(f, x);
\]

### 2.3 Differential Equations

Defining an ordinary differential equation, for example

\[ x' = 3x \]

\[
> \text{de} := \text{diff}(x(t), t) = 3*x(t);
\]

Note: When defining a differential equation, include the independent variable; for example, enter `diff(x(t),t)`, not `diff(x,t)`.

Solving the ordinary differential equation for \( x(t) \)

\[
> X := \text{rhs( dsolve(de, x(t)) )};
\]

The solution is called \( X \)

Solving the ordinary differential equation subject to initial conditions. For example, solve the initial value problem

\[ x' = 3x \]

\[ x(0) = 5 \]

\[
> X := \text{rhs( dsolve(\{de, x(0)=10\},x(t)) )};
\]

the solution is called \( X \)

\[
> \text{plot}(X, t=0..1); \text{plots the solution } X \text{ from } t = 0 \text{ to } 1
\]
Logistic equation

In this part we explore Maple’s ability to solve the logistic equation

\[
dy/dt = y (1 - y)
\]

and to check the solution. Then we will adapt the solution procedure to an initial value problem with this same differential equation. In the next part, we will relate these algebraic calculations to the geometry of direction fields.

1. Give the differential equation a name by entering

   \[
   \text{DE1 := diff(y(t), t) = y(t)*(1 - y(t));}
   \]

   Then ask Maple to solve the equation for \( y \) by entering

   \[
   \text{dsolve(DE1, y(t));}
   \]

   Note that Maple uses \( _C1 \) to represent an arbitrary constant.

2. Differentiate your solution expression with respect to \( t \) to get an explicit expression for \( dy/dt \). Then use your solution expression to find an explicit formula in \( t \) for \( y(1 - y) \). Is this formula the same as the one for \( dy/dt \)? You may want to simplify the output before you try to answer this.

3. Now we add the initial condition \( y(0) = 0.1 \) to determine a single solution of the differential equation. To tell Maple to solve the initial value problem, put the two parts of the problem – the differential equation and the initial condition – in a list:

   \[
   \text{dsolve ( { DE1, y(0) = 1/10 }, y(t) );}
   \]

4. Plot graph of this solution.

5. Do the same for other initial values, compare your results with the predictions from the phase portrait.
Chapter 3

Taylor series

3.1 Examples

Example 1

Find the Taylor expansion of $\cos x$ at $x = 0$ up to $O(x^4)$. Using this expansion find $\cos 0.1$ and compare it with the exact value.

Solution: The Taylor formula for approximation of the function of one variable up to the 4th order around the point $x_0 = 0$ is:

$$ f(x) \approx f(0) + f'(0) \cdot x + \frac{f''(0)}{2!} x^2 + \frac{f'''(0)}{3!} x^3 + \frac{f^{(4)}(0)}{4!} x^4 + \cdots $$

In case of the function $\cos x$ we get:

1. $f(0) = \cos 0 = 1$
2. $f'(x) = (\cos x)' = -\sin x$, hence $f'(0) = \sin 0 = 0$
3. $f''(x) = -\cos x$, hence $f''(0) = -\cos 0 = -1$
4. $f'''(x) = \sin x$, hence $f'''(0) = \sin 0 = 0$
5. $f^{(4)}(x) = \cos x$, hence $f^{(4)}(0) = \cos 0 = 1$

therefore the approximation is:

$$ \cos x \approx 1 + 0 \cdot x + \frac{-1}{2!} x^2 + \frac{0}{3!} x^3 + \frac{1}{4!} x^4 + \cdots $$

$$ = 1 - \frac{x^2}{2} + \frac{x^4}{24} $$
Now, using this formula and MAPLE we find:

\[
\cos 0.1 \approx 1 - \frac{0.01}{2} + \frac{0.0001}{24} = 0.9950041667
\]

the exact value is:

\[
\cos 0.1 = 0.9950041653
\]

**The same example using MAPLE**

There are two ways to do it:

**WAY I:**

```maple
> f:=cos(x);
f := \cos(x)
> g:=diff(f,x);
g := -\sin(x)
> h:=subs(x=0,g);
h := -\sin(0)
> coef1:=evalf(h);
coef1 := 0.
```

Now we compress all these operations into one line:

```maple
> coef1:=evalf(subs(x=0,diff(f,x)));
coef1 := -0.
> coef2:=evalf(subs(x=0,diff(f,x,x)));
coef2 := -1.
> coef3:=evalf(subs(x=0,diff(f,x,x,x)));
coef3 := 0.
> coef4:=evalf(subs(x=0,diff(f,x,x,x,x)));
coef4 := 1.
> ccos:=1+coef2*x^2/2!+coef4*x^4/4!;
ccos := 1 - .5000000000 x^2 + .0416666667 x^4
> evalf(subs(x=0.1,ccos));
.9950041667
> evalf(cos(0.1));
.9950041653
```
WAY II: Now let us do the same making use of the special command `taylor(expr, eq/nm, n)`. The first argument here is the expression of which you want to compute a Taylor expansion, the second argument is the point around which you want to compute the expansion and the third argument is the order of the Taylor expansion you want. But... pay attention! If you type here 4, then you get a Taylor expansion up to the third order and all fourth and higher order terms are summarized in the following term: \( O(x^4) \). This means that if you want to see what the fourth order term looks like, you have to type 5 here. Type `?taylor;` for a detailed description of this command.

```maple
> ccos:=taylor(cos(x),x=0,5);
cos := 1 - \frac{1}{2} x^2 + \frac{1}{24} x^4 + O(x^5)
> convert(%^,polynom);
1 - \frac{1}{2} x^2 + \frac{1}{24} x^4
> plot({cos(x),convert(taylor(cos(x),x=0,4),polynom)},x=-3..3);
```

The graph is shown in Fig. 3.1.

![Graph of cos(x) and its 4th order Taylor approximation](image)

Figure 3.1: The function \( \cos x \) and its 4th order Taylor approximation.

**Example 2**

Find the Taylor expansion of \( e^{(x+y^2)} \) at \( x = 0, y = 0 \) up to the second order.
**Solution:** The Taylor formula for an approximation of a function of two variables up to the 2nd order around the point \(x = 0, y = 0\) is:

\[
f(x, y) \approx f(0, 0) + \frac{\partial f}{\partial x} x + \frac{\partial f}{\partial y} y + \frac{\partial^2 f}{\partial x^2} \frac{x^2}{2} + \frac{\partial^2 f}{\partial x \partial y} xy + \frac{\partial^2 f}{\partial y^2} \frac{y^2}{2} + \cdots
\]

In the case of function \(e^{(x+y^2)}\) we get:

1. \(f(0, 0) = e^0 = 1\)
2. \(\frac{\partial f}{\partial x} = e^{(x+y^2)}\), hence \(\frac{\partial f}{\partial x}(0, 0) = e^0 = 1\)
3. \(\frac{\partial f}{\partial y} = 2ye^{(x+y^2)}\), hence \(\frac{\partial f}{\partial y}(0, 0) = 2 \times 0 \times e^0 = 0\)
4. \(\frac{\partial^2 f}{\partial x^2} = e^{(x+y^2)}\), hence \(\frac{\partial^2 f}{\partial x^2}(0, 0) = e^0 = 1\)
5. \(\frac{\partial^2 f}{\partial x \partial y} = 2ye^{(x+y^2)}\), hence \(\frac{\partial^2 f}{\partial x \partial y}(0, 0) = 2 \times 0 \times e^0 = 0\)
6. \(\frac{\partial^2 f}{\partial y^2} = \frac{\partial^2 ye^{(x+y^2)}}{y} = (4y^2 + 2)e^{(x+y^2)}\), hence \(\frac{\partial^2 f}{\partial y^2}(0, 0) = 2 \times e^0 = 2\)

Hence:

\[
e^{(x+y^2)} \approx 1 + 1 \times x + 0 \times y + 1 \times \frac{x^2}{2} + 0 \times xy + 2 \times \frac{y^2}{2} = 1 + x + \frac{x^2}{2} + y^2
\]

**The same example using MAPLE**

The plan is exactly the same as in the one dimensional case:

```maple
> f:=exp(x+y^2);
f := e^{(x+y^2)}
> coef0:=evalf(subs(x=0.,y=0.,f));
  coef0 := 1.
> coefx:=evalf(subs(x=0.,y=0.,diff(f,x)));
  coefx := 1.
> coefy:=evalf(subs(x=0.,y=0.,diff(f,y)));
  coefy := 0.
> coefxy:=evalf(subs(x=0.,y=0.,diff(f,x,y)));
  coefxy := 0.
> coefxx:=evalf(subs(x=0.,y=0.,diff(f,x,x)));
  coefxx := 1.
> coefyy:=evalf(subs(x=0.,y=0.,diff(f,y,y)));
```

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Here we can also use a shorter way of finding a Taylor series using the command mtaylor.
Type ?mtaylor for details. The command mtaylor has the same arguments as its one dimensional equivalent taylor.

```
> readlib(mtaylor):
> mtaylor(exp(x+y^2),[x,y],3);
 1 + x + y^2 + \frac{1}{2} x^2
> plot3d({exp(x+y^2),mtaylor(exp(x+y^2),[x,y],3)},{x=-1..1,y=-1..1});
```

The graph is shown in Fig. 3.2.

Figure 3.2: The function \(\exp(x+y^2)\) and its second order Taylor approximation

### 3.2 Exercises

1. Find the Taylor expansion of \(\sin x\) at \(x=0\) up to the 5th order using pencil and paper and using MAPLE. Draw the graph of \(\sin x\) and its approximation.

2. Find the Taylor expansion of \(f(x,y) = (x + 1)e^{x+y}\) at \(x=0, y=0\) up to the 2nd order using pencil and paper and using MAPLE. Draw the graph of \(f(x,y) = (x + 1)e^{x+y}\) and its approximation.
Chapter 4

Change of variables

4.1 Examples

Example 1. Shift

Consider the following differential equation:

\[
\frac{dx}{dt} = x^2 - 4
\]

1. Find equilibria.

2. Move the equilibrium point to 0 (i.e., introduce a new variable \(v\) such that \(v = 0\) is an equilibrium point).

Solution:

1. Equilibria:

    \[
    x^2 - 4 = 0 \quad x_1 = 2 \quad x_2 = -2
    \]

2. Shift:

    (a) \(x_1 = 2\). Introduce \(v = x - 2\), hence \(x = v + 2\).

    \[
    \frac{dx}{dt} = \frac{dv}{dt} \quad x^2 - 4 = (v + 2)^2 - 4 = v^2 + 4v
    \]

    Therefore the new ODE is:

    \[
    \frac{dv}{dt} = v^2 + 4v
    \]
(b) $x_1 = -2$. Introduce $v = x + 2$, hence $x = v - 2$.

\[
\frac{dx}{dt} = \frac{dv}{dt} \quad x^2 - 4 = (v - 2)^2 - 4 = v^2 - 4v
\]

Therefore the new ODE is:

\[
\frac{dv}{dt} = v^2 - 4v
\]

**Example 2. Logistic equation**

Consider the following equation describing the logistic growth of a population:

\[
\frac{dN}{dt} = rN\left(1 - \frac{N}{K}\right) \quad (4.1)
\]

Before analysing the model it is essential to reduce the number of parameters. We can achieve this by using two transformations: rescaling the amplitude and rescaling of time. The main idea behind these transformations is: rescaling the amplitude can map the carrying capacity $K$ to the value 1, and rescaling of time can adjust the rate constant $r$ to the value 1.

Let us do it formally:

Rescaling the amplitude is the introduction of a new variable: $y = AN$, rescaling of time is the introduction of a new time variable: $T = Bt$. The idea is to perform all the transformations while keeping $A$ and $B$ as unknown constants and to fix their values later, in order to simplify the equation.

The direct and the inverse transformations are:

\[
y = AN \quad N = y/A \\
T = Bt \quad t = T/B
\]

First, we make the rescaling of amplitude:

\[
\frac{dy/A}{dt} = \frac{ry}{A(1 - y/(AK))} \\
\frac{dy}{dt} = ry(1 - y/(AK))
\]

Now the new time:

\[
\frac{dy}{dt} = \frac{dy}{dT} \frac{dT}{dt} = \frac{dy}{dT} * B
\]

Therefore equation (4.1) becomes:

\[
\frac{dy}{dT} = \frac{r}{B}y(1 - y/(AK))
\]

Hence, if we choose

\[
A = \frac{1}{K} \quad B = r
\]

equation (4.1) becomes:

\[
\frac{dy}{dT} = y(1 - y)
\]
4.2 Exercises

1. Consider the following differential equations:

   (a) \[ \frac{dx}{dt} = 2x - x^2 + 3 \]

   (b) \[ \frac{dx}{dt} = e^{3x^2} - 3 - 1 \]

   i. Find equilibria

   ii. Move the equilibrium points to 0 (i.e., introduce a new variable \( v \) such that \( v = 0 \) is an equilibrium point).

2. Use rescaling of amplitude and rescaling of time to transform the equation

   \[ \frac{dx}{dt} = Cx - Bx^3 \]

   into the form:

   \[ \frac{dy}{dT} = y - y^3 \]
Chapter 5

Normal form for the fold bifurcation

Study the ODE

\[ \frac{dx}{dt} = 2e^{-2t-2c+4} - 6 + 4x \]

Find the normal form for this ODE in the same way as we did for the fold bifurcation. Use pencil and paper. Check your computations using MAPLE wherever it is possible.

**PLAN:**

1. Find the non-hyperbolic equilibrium.
2. Shift it to (0, 0).
3. Expand the right hand side up to the second order, using Taylor series.
4. Remove linear terms.
5. Introduce a new parameter and rescale the amplitude.
6. Write the normal form and write how the variable and the parameter in the normal form are related to the variable and the parameter in the original ODE.
Chapter 6

Fold, transcritical and pitchfork bifurcations in a 1D system using Content

6.1 Fold

One of the programs we are going to use, besides Maple, which you have already encountered, is Content, which is designed to study bifurcations.

The first system we are going to study with Content is the following:

\[ \frac{dx_1}{dt} = p_1 - x_1^2 \]

To start Content, go to the directory called content and type content.

What you now see is the main window of the Content program.

As you will soon see, Content works with a lot of different windows that are appearing and disappearing while you work. As the monitors you are working on are not so big these windows will soon start overlapping each other. With the Alt-Tab combination you can easily switch between windows.

First we are going to define the type of dynamical system we are going to work on. Press Select, Class and select ODE’s as we are going to work with an ordinary differential equation. If all is OK you see that behind Class it now says ODE.

As we are going to work with a specific ODE that still needs to be specified, press Select, System. In the window that now appears press Actions, New. Now again a new window appears. In this window we define the name of our system, after that press OK. In this case we will call our system “fold” as it is meant to illustrate the fold bifurcation. We see a window appearing titled fold, in this window we can define our new system. Behind coordinates we fill in the variables of our system, of course in our one dimensional system we only have one
variable, namely x. Behind parameters we fill in the parameters on which our system depends, in our case p1. Behind time we fill in the name with which we wish to designate the time variable, for ODE’s it is common to use t. Now we select ‘first three derivatives numerically’. After that we type the equation(s) that describe the system. Note that \( \frac{dx}{dt} \) should be typed as x’ and that each equation should be ended by ;. Note also that Content does not know \(^\wedge\) as a power-operator, so instead of \(x^2\) you should type x*x for \(x^2\). Now all is ready, so we can press OK. Content starts compiling the program, in the main window you can see whether content is ready or still busy.

Now that we have specified the system, we can study it. Press Type, Initial Point, Point and Type, Curve, Orbit. We see two new windows appearing, one called Starter, the other called Integrator. In the Integrator window change the value behind Interval in 200. In the main window press Options, Archive Filter and set Path filter from 1 to 2000. Press OK. To see what happens press in the main window Window, Open, 2DGraphics. This gives us a graphical window for display in two dimensions. It is better never to change the size of this window, as this can cause Content to crash. More than 1 2DGraphics windows can be opened at the same time, which sometimes can be very practical. In this new window press Attributes, Current. This gives us yet another window. In this window we can choose what is to be put along the x-axis (abcissa) and y-axis (ordinate). From the list of names first choose the category (time, parameter, coordinate) and then the specific item (t, p1, x1) you want to put along the axis. Put t along the x-axis and x1 along the y-axis. Press OK. Now, in the graphical window choose the range of the axis. After having changed the ranges, always press Enter. Choose t (x-axis) from 0 to 50 and x1 (y-axis) from -2 to 2. In the Starter window choose initial values for your variables and parameters. Choose x1=0.1 and p1=0.5. Now we have chosen the initial point of our orbit and we can see in the graphical window what happens to it in time, so press in the graphical window Compute, Forward.

If all is OK, you will see an orbit that approaches an equilibrium at which x1=0.707. Now that we have found this equilibrium, we can follow this equilibrium as a function of the parameter p1 and see what kind of bifurcations occur. This means that we now no longer are studying “simple” points on an orbit, but equilibria on a line of equilibria. In the main window press Select, Initial Point and in the window that appears select O: last point (O means orbit, so you are selecting the last point of the orbit, which is an equilibrium as the starting point of our further computations) and press OK. After we have done this, you can see that the initial values in the Starter window have changed to the values of the selected equilibrium point. Now press in the main window Type, Initial Point, Equilibrium and Type, Curve, Equilibrium. this gives us a new Starter window and the Integrator window is replaced by a Continuer window. In the Starter window select p1, to make clear to content you are going to continue a line of equilibria along the parameter p1. In the main window press Options, Pause Mode, select enable pause buttons and press OK. This gives you a small window with pause buttons which will soon come in handy. Another option which is practical to change, is Options, Archive Filter, Max number. Increase this to 20, in order to keep more runs in the memory. In the main window also press Window, Open, Numeric. A new, numeric window appears. In this window press Window, Layout. This gives us again a new window. In this window select eigenvalues with your mouse, press select all and OK. Now in the numeric window the eigenvalue(s) of your system are displayed. These you can use to determine the stability of our system at a certain equilibrium point. In the graphical window press Attributes, Current. This time choose p1 along the x-axis and x1 along the y-axis. Change the range of the axes, such that
−3 < x < 3; −2 < y < 2. Press OK. We now are going to compute our line of equilibria. Pay attention to the value of the eigenvalue (Re₀, which equals \( df/dx \)). In the graphical window press Compute, Forward. If the line leaves the plot, press the abort button. Also press Compute, Backward. If all is OK, content stops at a point it designates as LP. LP stands for limit point, which is the word content uses for the point where a fold bifurcation occurs. Press the resume and abort button, to complete the line. If things went too fast to see what happened to the value of Re₀, then press in the graphics window Window, Clear, and in the main window press Options, Pause Mode and select ‘at each point’. Now content computes stepwise. (To go back to the default setting in which content only stops at special (bifurcation) points press Options, Pause Mode and select ‘at special points’). You can see that Re₀ is approximately equal to 0 in the LP designated point. Draw the bifurcation diagram with pencil and paper. Include the stability of the equilibria in your diagram. For stable equilibria use a bold line, for unstable equilibria use a dashed line. Finally, if problems occur, it often helps to change the parameter maxstepsize.

Now let’s check our results by computing some orbits. In the main window press Type, Initial Point, Point and Type, Curve, Orbit. In the starter window first put the initial value for \( t=0, x_1=-1 \) and \( p_1=0.5 \). Compute the orbit belonging to this initial point. Now do the same for \( t=0, x_1=0.6 \) and \( p_1=0.5 \) and for \( t=0, x_1=1.5 \) and \( p_1=0.5 \). If all is OK these orbits confirm the bifurcation diagram you have just drawn.

### 6.2 Pitchfork bifurcation

Now let’s study a new system:

\[
\frac{dx_1}{dt} = p_1 * x_1 - x_1^3
\]

In main window:
Select, Class: ODE
Select, System
In new window:
Actions, New
type “pitch” as name for new system, OK
In new window:
coordinates: x1
parameters: p1
time: t
select ‘first three derivatives derive numerically’
type equation
OK
compilation of system
In main window:
Type, Initial Point, Point
Type, Curve, Orbit
Window, Open, 2DGraphic
In graphical window:
**Attributes, Curren**

In new window:

- abcissa: t
- ordinate: x

In graphical window:

- ranges:
  - x-axis: 0..50
  - y-axis: -2..2

In **Starter** window:

- initial values:
  - x1=0.1
  - pa=0.5

In **Integrator** window:

- interval: 200

In main window:

**Options, Archive Filter**

- Path filter from 1 to 2000

In graphical window:

**Compute, Forward**

We again attain an equilibrium.

In main window:

**Select, Initial Point**

- select O:Last Point

**Type, Initial Point, Equilibrium**

**Type, Curve, Equilibrium**

**Options, Pause Mode**

- enable pause buttons

**Window, Open Numeric**

In new window:

**Window, Layout**

- select eigenvalues, select all, OK

In **Starter** window:

- activate p1

- Change the coordinates to \((p1, x)\) through **Attributes, Curves**

In graphical window:

**Compute, Forward (abort)**

**Compute, Backward**

Content stops at a point which it designates as **BP**. **BP** stands for branching point, by which is meant that the line of equilibria at this bifurcation point branches into several equilibria lines. This is both the case for the transcritical and for the pitchfork bifurcation.

**resume, abort**

Now we have the line of trivial (equal to zero) equilibria. If we doubleclick the BP designated point with our mouse, content automatically switches to the other line of equilibria.

**Compute, Forward (abort)**

**Compute, Backward (abort)**
To find out about the stability of the different pieces of the different lines, we can recompute the equilibria lines and watch the sign of Re$_0$, but we can also compute some orbits as we did in the case of the fold bifurcation example.

In the main window:

**Type, Initial Point, Point**

**Type, Curve, Orbit**

In the **Starter** window:

\[
t=0 \\
x_1=-1 \\
p_1=-1
\]

(In the graphics window: **Compute, Forward**)

\[
t=0 \\
x_1=1 \\
p_1=-1
\]

(In the graphics window: **Compute, Forward**)

\[
t=0 \\
x_1=-0.5 \\
p_1=1
\]

(In the graphics window: **Compute, Forward**)

\[
t=0 \\
x_1=0.5 \\
p_1=1
\]

(In the graphics window: **Compute, Forward**)

Draw the bifurcation diagram with pencil and paper, indicate the stability.
6.3 Transcritical bifurcation

Follow the same procedure as for the pitchfork bifurcation in the following case:

\[ x_1' = p_1 x_1 - x_1^2 \]

This is the normal form for the transcritical bifurcation.

Remember that once you have a line of equilibria with a point designated \textbf{BP} on it, you can doubleclick this point and content then automatically switches to the continuation of the other line of equilibria.

Draw the bifurcation diagram with pencil and paper, indicate the stability.
Chapter 7

Exercises on 1D bifurcations

Exercise 1

Consider the following equation:

\[
\frac{dx}{dt} = a - \frac{x^2}{1+x^2}
\]

1. Show that this equation has a fold bifurcation at \( x = 0 \) and \( a = 0 \).

2. Study the bifurcation numerically using MAPLE. For this, use:
   \[
   > f := a -> a - x^2/(1+x^2);
   > plot([f(-0.2),f(0.),f(0.2)],x=-1..1);
   \]

3. Sketch the bifurcation diagram with \( a \) on the x-axis and \( x \) on the y-axis. Indicate the stability of the equilibria.

4. Check your bifurcation diagram (both position and stability) using Content.
Exercise 2

Study the following equations.

**PLAN:**

1. Try to understand the situation using MAPLE.

2. Compute the bifurcation diagrams using Content, and draw them with pencil and paper (indicate also the stability of the equilibria).

3. Draw for each region the phase portraits and basins of attraction.

1. \( \frac{dx}{dt} = a + x - x^3 \)

2. \( \frac{dx}{dt} = 1 + ax - x^3 \)

3. \( \frac{dx}{dt} = a^2 + x^2 - 1 \)

4. \( \frac{dx}{dt} = 2a^3 + 3a^2x - x^3 \)

*Some remarks regarding eq. 4:*

From the Maple results you can already tell that there is one line of stable equilibria crossing another line of non-hyperbolic (these equilibria have a stable and a non-stable direction) equilibria. This means that the bifurcation here is not a classical transcritical bifurcation.

Content has some problems with this bifurcation. Once you have reached a single stable equilibrium and you continue this equilibrium Content does not stop at the bifurcation point, it does not recognize it. So instead of giving us a BP-kind of point at which we can click to get the other line of equilibria we have to search for the other line by hand.

We can do this by pressing in the main window **Type, Initial Point, Point** and **Type, Curve, Orbit**. Now we type in the **Starter** window reasonable initial values. By that we mean values for which it can be expected that you approach the other line of equilibria. As the equilibria on this line have one stable and one unstable direction, we have to look at the other line of (in this case stable) equilibria to see whether we can expect to approach the line of non-hyperbolic equilibria from a position above or from a position beneath it.

After having found an equilibrium on this line we can continue it. We encounter a series of BP-points, one of them is the bifurcation point Content could not recognize while continuing the first line of equilibria.

Upon selecting one of these other BP designated points we get even more of these BP-points on the same line. These are computational artefacts. We must not forget that the computations of Content are not based on the exact solutions of the differential equations but on numerical approximations. As the second line consists of non-hyperbolic equilibria,
equilibria which are structurally unstable a small computational deviation easily leads to the apparent occurrence of a bifurcation.

5. \[ \frac{dx}{dt} = (a + x - x^3)(a^2 + x^2 - 1) \]

Note that this last differential equation is pretty complicated, it is the product of the first and the third differential equation. You don’t need to study it by hand, study it in Content right away.
Chapter 8

GRIND Introduction

Introduction

This tutorial introduces you to GRIND and its mostly used commands. GRIND is a command line driven system for analysing models in terms of differential or difference equations. GRIND consists of two parts. The first part is a preprocessor reading your model. The second part is the command line driven system in which you set (or vary) parameters and initial conditions, and in which you perform the numerical analysis of your choice. GRIND commands have long names but can be abbreviated to the first two (or more) characters of the name of the command.

Model definition

Use any text editor (emacs, xedit, vi) to define your model by writing a plain ASCII file of the following format:

\[ fc = b \cdot n \cdot (k - n); \]
\[ n' = fc - d; \]

If you look at this model carefully you can see that the equation for \( fc \) gives us the logistic growth equation. The extra term \(-d\) is the harvesting of the population with a constant amount. In this model \( n \) is a variable, \( b, k, d \) are the parameters and \( fc \) is an algebraic expression. Algebraic expressions have to be defined before the differential equations. The GRIND preprocessor will also understand you if you use functions like \( \sin() \), \( \cos() \), \( \log() \), \( \exp() \), \( \text{sign()} \), \( \text{sqrt}() \), \( \text{abs()} \), \( \text{mod}(x,y) \), \( \text{max}(x,y) \) and \( \text{min}(x,y) \).

Model analysis

When GRIND is installed properly you start GRIND by typing \texttt{grind model} where we assume that the file that you made above is called \texttt{model}. GRIND will check if your model has
been pre-processed before, and will start up its command line driven interface. Just wait until
GRIND prompts you by something like
G R I N D (2003) model analysis:
after this you just start typing commands like
b=1.
k=1.
d=0.
n=0.1
par
which initializes all parameters, the initial condition, and gives an overview of all parameter
values. Parameter values can be stored for later usage by a command like
par par
and can be read by GRIND by a command like
read par
In fact you can read files with all sorts of GRIND commands. By the way, you can quit from
GRIND by the bye command.

**Numerical integration**

Now that the parameters and the initial conditions are defined one can run the model by a
numerical integrator
finish 20 20
run
will “run” your model for 20 time steps printing some output in 20 intervals (i.e., at every time
step). The variables that are printed can be modified with the output command.

We can plot the output of this numerical integration by
axis v 0 2
timeplot
which tells GRIND that the vertical axis of the time plot should be scaled between zero and two,
after which the data of the previous run is plotted. So, first do a run, and then call timeplot!

Another way to analyse 1D models in GRIND, is to introduce time as a variable, using the
following trick:
fc=b*n*(k-n);
t'=1.1;
n ' = fc- d;
Now we can make parameters time-dependent.

The axis command is used for defining a two-dimensional (or three-dimensional) phase space.
axis x t 0. 20.
axis y n 1e-3 2.
The two axis commands define the phase space. The horizontal “x” axis gives t, and goes from
t=0.0 to t=20. The population size n goes along the vertical “y” axis, and runs from n=0.001
to n=2. The following commands will draw a two-dimensional frame on your screen.
2d
You can use the run command now and you can display different trajectories.

To clean the window use:
erase
2d

**Set file**

In many cases it is useful to keep information about the axes, parameter values and integration in a parameter file. You can create it in advance. For example for the last model you can create a file set and type into it:

```
b=1.
k=1.
d=0.
n=0.1
t=0.
finish 20 20
option trunc
option event
axis v 0 2
axis x t 0. 20.
axis y n 1e-3 2.
```

Here we have the new option trunc which truncates the program if the value of a variable becomes too large, and the new option event with allows you to abort computations by pressing Esc. This option becomes very important once we start working on stable manifolds and unstable limitcycles for which it is necessary to compute in the backward direction (option back on). This is a very tricky thing to do. It often causes GRIND to get stuck in it's own computations, pressing Esc in the graphical window then is a way to stop these computations.

After starting up GRIND, you can just read the set file:
read set
and then type:
2d
run
to get a trajectory. You can change the initial conditions, parameter values or axes by typing:
```
n=1.5
d=0.1
ax y n -1. 2.
```

Study the system using GRIND. Find out what the maximum harvesting rate (maximum value for d) is.
Help

GRIND has a rudimentary help facility, which you activate by typing `help command` (where `command` is the name of the command you need some information about). For detailed information you will have to consult the GRIND manual.
Chapter 9

Biological problems on 1D bifurcations

Exercise 1

A gene product with concentration $g$ catalyses its own production and decays linearly according to the following kinetics equation:

$$\frac{dg}{dt} = k_1 \frac{g^2}{1 + g^2} - k_2 g, \quad g \geq 0,$$

where $k_1$ and $k_2$ are positive constants.

1. We can see that the variable $g$ has already been scaled (by some change of variables), since the original term $g^2/(k_3^2 + g^2)$ is now $g^2/(1 + g^2)$. Reduce the number of parameters further by rescaling time.

2. Study the behaviour of the system:
   - Find equilibria.
   - Find how the number and stability of the equilibria depend on the parameter.
   - Describe all distinct possibilities and find parameter regions for them.

3. In this system there is a region in which a biochemical switch can take place. In this region there is one equilibrium with a low concentration (zero), and one with a high concentration of the gene product.
   - How can we switch from the low to the high equilibrium without changing the parameter?
   - Find the exact switching conditions and the final value of the product concentration.

4. Assume that our system is in a state with a high concentration of the gene product.
   - Discuss a possibility of switching the system to the low equilibrium by changing the parameter.
   - Find the exact conditions for this switch.
   - How can we get this switch with $k_1$ and/or $k_2$ in the original model?
Exercise 2

A model for the fast inward current of an excitable cell (Na$^+$ influx into a neuron) can be written as the following differential equation:

$$\frac{dx}{dt} = kx(a - x)(x - 1)$$

Here $x$ denotes the normalised membrane potential of the excitable cell and $k > 0$, $0 < a < 1$ are parameters of the model.

1. Reduce the number of parameters as much as possible.
2. Study the model: find equilibria and their stability, draw the phase-portrait and indicate the basins of attraction.
3. What is the biological interpretation of the equilibria?

As we know from biology, one way to excite a neuron is to apply an external current $I(t)$. In that case, the model becomes:

$$\frac{dx}{dt} = kx(a - x)(x - 1) + I(t)$$

A researcher studies a cell whose membrane potential can be described by the latter equation. He applies the following external stimulus:

4. What will be the membrane potential of the cell after the stimulus is over? Consider all possibilities.

It is possible to study the equation using GRIND.
To get a stepwise function for the current we need to introduce an extra equation for time $t$: $t' = 1$. After this we will be able to use time as a variable.

$I(t)$ is a stepwise function, as can be seen in the figure. In GRIND, such a function can be described by using the function $\text{sign}(a, b)$:

$$\text{sign}(a, b) = \begin{cases} 
  a & \text{if } b \geq 0 \\
  -a & \text{if } b < 0 
\end{cases}$$

To make a stepwise function which is zero when $t \leq 5$ or $t > 5 + \tau$, and $I_0$, when $5 < t \leq \tau$, we can use the following: $I = I_0 * (\text{sign}(0.5, t-5.) + \text{sign}(0.5, 5. + \tau - t))$.

5. Write a GRIND-file for this model, with $I(t)$, $t' = 1$ and $dx/dt$. (Ignore messages such as “No Jacobian: switched to Runge Kutta integration” during GRIND compilation).
6. Study the system. Fix parameter \( a = 0.3 \). Try the following combinations of \( \tau \) and \( I_0 \):

\[
\begin{align*}
\tau &= 1, I_0 = 1 \\
\tau &= 0.5, I_0 = 1 \\
\tau &= 0.2, I_0 = 1 \\
\tau &= 1, I_0 = 0.5 \\
\tau &= 1, I_0 = 0.2
\end{align*}
\]

Discuss the influence of the latter two parameters on the excitation.

One can study the threshold for excitation analytically, if we assume that the duration of the stimulus is very long. In this case, \( I(t) \) can be considered constant.

7. Find the minimal value of \( I \) for which the cell goes to the excited state for all values of \( a \). Use pencil, paper and MAPLE.

8. Draw the graph of the threshold as a function of \( a \), using MAPLE.

9. Fix the parameter \( a \). Study the bifurcations in the equation under changing the parameter \( I_0 \) using Content. Which bifurcation gives the excitation of the cell?

**EXTRA Exercise 3**

Consider two strategies of harvesting of a population:

"constant yield"

\[
\frac{dN}{dt} = a * N \left(1 - \frac{N}{K}\right) - \gamma
\]

and harvesting proportional to the population size:

\[
\frac{dN}{dt} = a * N \left(1 - \frac{N}{K}\right) - \gamma N
\]

1. Describe all distinct possibilities and draw phase portraits for them. Which bifurcations are possible here. At which parameter values?

2. Find the maximal yield in each case.

3. Which strategy is better?
Chapter 10

Linear Algebra

10.1 Determinant

To find the determinant of a 2x2 matrix we use the following formula:

\[
\begin{vmatrix} a & b \\ c & d \end{vmatrix} = ad - cb
\]

(10.1)

To find the determinant of a 3x3 or of a higher order matrix we use the following recursive formula.

\[
\begin{vmatrix} a_{11} & a_{12} & a_{13} \\ a_{21} & a_{22} & a_{23} \\ a_{31} & a_{32} & a_{33} \end{vmatrix} = \\
(-1)^{1+1}a_{11} \begin{vmatrix} a_{22} & a_{23} \\ a_{32} & a_{33} \end{vmatrix} + (-1)^{1+2}a_{12} \begin{vmatrix} a_{21} & a_{23} \\ a_{31} & a_{33} \end{vmatrix} + (-1)^{1+3}a_{13} \begin{vmatrix} a_{21} & a_{22} \\ a_{31} & a_{32} \end{vmatrix}
\]

(10.2)

Note, that instead of the first row we can use any row or column of our matrix.

Note that the coefficients of the row or column we have picked are multiplied by -1 to the power (\texttt{rownumber+columnnumber}) and then are multiplied by the determinant of the matrix that is left if you \textbf{omit the row and column in which the coefficient is in}, finally you sum this for all coefficients in the particular row or column you picked. So for the calculation of the determinant of a \(n^n\) matrix you have to compute the determinants of \(n (n-1)^{(n-1)}\) matrices etc. (The procedure is recursive.)
Example 1

\[
\begin{vmatrix}
1 & 3 & 0 \\
2 & 6 & 4 \\
-1 & 0 & 2
\end{vmatrix} = 
\]

\[
(-1)^{(1+1)} * 1 * \begin{vmatrix}
6 & 4 \\
0 & 2
\end{vmatrix} + (-1)^{(1+2)} * 3 * \begin{vmatrix}
2 & 4 \\
-1 & 2
\end{vmatrix} + (-1)^{(1+3)} * 0 * \begin{vmatrix}
2 & 6 \\
-1 & 0
\end{vmatrix} 
\]

\[
= \begin{vmatrix}
6 & 4 \\
0 & 2
\end{vmatrix} - 3 * \begin{vmatrix}
2 & 4 \\
-1 & 2
\end{vmatrix} + 0
\]

\[
= (12 - 0) - 3(4 + 4) = -12 
\]

We can do the same using any other column or row. For example the 3rd column gives:

\[
\begin{vmatrix}
1 & 3 & 0 \\
2 & 6 & 4 \\
-1 & 0 & 2
\end{vmatrix} = 
\]

\[
(-1)^{(1+3)} * 0 * \begin{vmatrix}
2 & 6 \\
-1 & 0
\end{vmatrix} + (-1)^{(2+3)} * 4 * \begin{vmatrix}
1 & 3 \\
-1 & 0
\end{vmatrix} + (-1)^{(3+3)} * 2 * \begin{vmatrix}
1 & 3 \\
2 & 6
\end{vmatrix} 
\]

\[
= 0 - 12 + 0 = -12 
\]

Exercises

Evaluate the following determinants:

1. \[
\begin{vmatrix}
3 & -1 \\
2 & 4
\end{vmatrix}
\]

2. \[
\begin{vmatrix}
3 & 5 & -2 \\
0 & 6 & 1 \\
-2 & 0 & -4
\end{vmatrix}
\]

10.2 Eigen vectors, eigen values

If \( A \) is a square matrix, the eigen value problem is to find solutions of the following system of algebraic equations:

\[
A\vec{V} = \lambda \vec{V} 
\]

In the two dimensional case this problem can be written as:

\[
\lambda \begin{pmatrix} v_x \\ v_y \end{pmatrix} = \begin{pmatrix} a & b \\ c & d \end{pmatrix} \begin{pmatrix} v_x \\ v_y \end{pmatrix} 
\]

By using the unity matrix \( I \) (1’s one the diagonal of the matrix 0’s elsewhere) the problem can be rewritten as:

\[
A\vec{V} = \lambda I \vec{V} 
\]
As $\lambda I$ gives us a matrix we can now bring everything to the left-hand-side:

$$(A - \lambda I)\vec{V} = 0$$

This simply is a system of linear equations. The vector $\vec{V}$ forms the solution of this system. By definition, an eigenvector is nonzero. From linear algebra theory it then follows that the system only has a non-trivial (nonzero) solution if the determinant of the matrix $(A - \lambda I)$ equals zero.

To solve it we need:

1. Find the eigen values from the characteristic equation:

$$\text{Det}(A - \lambda I) = 0, \quad \text{or in } 2D \quad \text{Det}\left(\begin{array}{cc} a - \lambda & b \\ c & d - \lambda \end{array}\right) = 0$$

2. Find the eigen vectors of $A$. For that we need to solve the following system of equations:

$$\left(\begin{array}{cc} a - \lambda & b \\ c & d - \lambda \end{array}\right)\left(\begin{array}{c} v_x \\ v_y \end{array}\right) = 0 \quad (10.5)$$

or a similar system in three dimensional case.

In the two dimensional case we can find the eigen vectors using the express method:

$$\left(\begin{array}{c} v_{1x} \\ v_{1y} \end{array}\right) = \left(\begin{array}{c} -b \\ a - \lambda_1 \end{array}\right) \quad \left(\begin{array}{c} v_{2x} \\ v_{2y} \end{array}\right) = \left(\begin{array}{c} -b \\ a - \lambda_2 \end{array}\right) \quad (10.6)$$

where $a, b$ are the corresponding elements of the matrix $A$. This express method can only be used if $b$ and $a-\lambda$ are not zero at the same time, in that case you have to use the normal procedure.

**Example 2**

Let us find the eigen vectors and the eigen values of the following matrix:

$$\lambda \left(\begin{array}{c} v_x \\ v_y \end{array}\right) = \left(\begin{array}{cc} 8 & -4 \\ 2 & 2 \end{array}\right) \left(\begin{array}{c} v_x \\ v_y \end{array}\right) \quad (10.7)$$

The eigen values are given by:

$$\text{Det}\left(\begin{array}{cc} 8 - \lambda & -4 \\ 2 & 2 - \lambda \end{array}\right) = (8 - \lambda)(2 - \lambda) + 8 = \lambda^2 - 10\lambda + 24 = 0$$

Hence $\lambda_1 = 4, \lambda_2 = 6$

The eigen vectors from the express formula are:

$$\lambda_1 = 4; \quad \left(\begin{array}{c} v_{1x} \\ v_{1y} \end{array}\right) = \left(\begin{array}{c} 4 \\ 8 - (4) \end{array}\right) = \left(\begin{array}{c} 4 \\ 4 \end{array}\right) \quad \lambda_2 = 6; \quad \left(\begin{array}{c} v_{2x} \\ v_{2y} \end{array}\right) = \left(\begin{array}{c} 4 \\ 2 \end{array}\right). \quad (10.8)$$

Note, that in the 3D case we cannot use the express method and should solve the 3D system similar to (10.7) directly.
10.3 Matrix multiplication

Let’s say we do the following multiplication:

\[ A \ast B = C \]

Where \( A, B \) and \( C \) are matrices. To get the product matrix \( C \) we multiply the rows of \( A \) by the columns of \( B \). So the get \( C_{ij} \) which is the element of \( C \) in the \( i \)-th row and \( j \)-th column, we multiply the \( i \)-th row of \( A \) with the \( j \)-th column of \( B \). Note that this is only possible if the number of columns of \( A \) equals the number of rows of \( B \).

For example:

\[
\begin{pmatrix}
0 & 1 \\
2 & 3
\end{pmatrix}
\ast
\begin{pmatrix}
4 & 5 \\
6 & 7
\end{pmatrix}
\]

\[
a_{11} = 0 \ast 4 + 1 \ast 6 = 6 \\
a_{12} = 0 \ast 5 + 1 \ast 7 = 7 \\
a_{21} = 2 \ast 4 + 3 \ast 6 = 26 \\
a_{22} = 2 \ast 5 + 3 \ast 7 = 31
\]

Therefore:

\[
\begin{pmatrix}
0 & 1 \\
2 & 3
\end{pmatrix}
\ast
\begin{pmatrix}
4 & 5 \\6 & 7
\end{pmatrix}
=
\begin{pmatrix}
6 & 7 \\
26 & 31
\end{pmatrix}
\]

Exercises

Find \( A \ast B \) if

1. \( A = \begin{pmatrix} 3 & 1 \\ 1 & 4 \end{pmatrix} \quad B = \begin{pmatrix} 8 & 1 \\ -2 & 3 \end{pmatrix} \)

2. \( A = \begin{pmatrix} 1 & 0 & 2 \\ 4 & 1 & 3 \\ 5 & 1 & 1 \end{pmatrix} \quad B = \begin{pmatrix} 0 & 4 & 5 \\ 1 & 3 & 0 \\ 5 & 6 & 1 \end{pmatrix} \)

10.4 Inverse matrix

The matrix \( A^{-1} \) is the inverse matrix to the matrix \( A \) if \( A \ast A^{-1} = I \), where \( I \) is a unit matrix. Note that in the previous section about matrix multiplication it says that for the multiplication to be possible the number of columns of the first matrix has to equal the number of rows of the second matrix. From this it is easy to see that it is only possible to find an inverse matrix if the matrix is square (number of rows equals number of columns).

PLAN:
1. For each \( a_{ij} \) find the cofactor \( A_{ij} \). The cofactor is the determinant of the matrix obtained from \( A \) by removing the \( i-th \) row and \( j-th \) column with the weight \((-1)^{(i+j)}\).

2. Write a cofactor matrix \( A_{ij} \)

3. Find \( detA \)

4. Transpose the cofactor matrix \( A_{ij} \) and divide each element in it by \( detA \).

**Example 3**

Let us find the inverse matrix of: \[ A = \begin{pmatrix} 2 & 1 \\ 5 & 3 \end{pmatrix} \]

1. Cofactors:
   \[ A_{11} = 3 \times (-1)^{(1+1)} = 3 \]
   \[ A_{12} = 5 \times (-1)^{(1+2)} = -5 \]
   \[ A_{21} = 1 \times (-1)^{(2+1)} = -1 \]
   \[ A_{22} = 2 \times (-1)^{(2+2)} = 2 \]

2. The cofactor matrix is: \[ A_{ij} = \begin{pmatrix} 3 & -5 \\ -1 & 2 \end{pmatrix} \]

3. \( detA = 6 - 5 = 1 \)

4. Transpose the cofactor matrix \( A_{ij} \) and divide each element in it by \( detA = 1 \) gives: \[ A^{-1} = \begin{pmatrix} 3 & -1 \\ -5 & 2 \end{pmatrix} \]

5. Check.
   \[ A \times A^{-1} = \begin{pmatrix} 2 & 1 \\ 5 & 3 \end{pmatrix} \times \begin{pmatrix} 3 & -1 \\ -5 & 2 \end{pmatrix} = \begin{pmatrix} 6 - 5 & -2 + 2 \\ 15 - 15 & -5 + 6 \end{pmatrix} = \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix} \]

Note, that for the 2x2 matrix, the inverse can be found using a simple formula:

\[ A = \begin{pmatrix} a & b \\ c & d \end{pmatrix} \quad A^{-1} = \frac{1}{detA} \begin{pmatrix} d & -b \\ -c & a \end{pmatrix} \quad \text{(10.9)} \]

**Exercise**

\[ A = \begin{pmatrix} 3 & -2 \\ -5 & 4 \end{pmatrix} \]. Find the inverse matrix \( A^{-1} \) using the above plan and using the formula (10.9). Verify the answer by \( A \times A^{-1} \).
10.5 Canonical form

If \( \lambda_1 \neq \lambda_2 \) are the eigen values of the matrix \( A \) and \( v_1 \) corresponds to \( \lambda_1 \) and \( v_2 \) corresponds to \( \lambda_2 \), then the matrix whose columns are the vectors \( v_1 \) and \( v_2 \) transforms the matrix \( A \) into the canonical form \( D \) by the transformation:

\[
D = T^{-1}AT = \begin{pmatrix} \lambda_1 & 0 \\ 0 & \lambda_2 \end{pmatrix} \tag{10.10}
\]

Example 4

Let us transform the matrix \( A = \begin{pmatrix} 8 & -4 \\ 2 & 2 \end{pmatrix} \) from (10.7) to its canonical form. As we computed in (10.8):

\[
\lambda_1 = 4; \quad \begin{pmatrix} v_{1x} \\ v_{1y} \end{pmatrix} = \begin{pmatrix} 4 \\ 4 \end{pmatrix} \quad \lambda_2 = 6; \quad \begin{pmatrix} v_{2x} \\ v_{2y} \end{pmatrix} = \begin{pmatrix} 4 \\ 2 \end{pmatrix}.
\]

hence:

\[
T = \begin{pmatrix} 4 & 4 \\ 4 & 2 \end{pmatrix}
\]

from (10.9)

\[
T^{-1} = \frac{1}{-8} \begin{pmatrix} 2 & -4 \\ -4 & 4 \end{pmatrix}
\]

therefore:

\[
A*T = \begin{pmatrix} 8 & -4 \\ 2 & 2 \end{pmatrix} * \begin{pmatrix} 4 & 4 \\ 4 & 2 \end{pmatrix} = \begin{pmatrix} 16 & 24 \\ 16 & 12 \end{pmatrix}
\]

\[
T^{-1}A*T = \frac{1}{-8} \begin{pmatrix} 2 & -4 \\ -4 & 4 \end{pmatrix} * \begin{pmatrix} 16 & 24 \\ 16 & 12 \end{pmatrix} = \frac{1}{-8} \begin{pmatrix} 32 - 64 & 48 - 48 \\ -64 + 64 & -96 + 48 \end{pmatrix} = \begin{pmatrix} 4 & 0 \\ 0 & 6 \end{pmatrix}
\]

Exercise

For the matrix \( A = \begin{pmatrix} 2 & 1 \\ 2 & 3 \end{pmatrix} \) find \( T \) and its canonical form. Verify by direct multiplication.

10.6 Linear systems

\[
\begin{align*}
\frac{dx}{dt} &= ax + by \\
\frac{dy}{dt} &= cx + dy
\end{align*}
\]

General solution:

\[
\begin{pmatrix} x \\ y \end{pmatrix} = C_1 \begin{pmatrix} v_{1x} \\ v_{1y} \end{pmatrix} e^{\lambda_1 t} + C_2 \begin{pmatrix} v_{2x} \\ v_{2y} \end{pmatrix} e^{\lambda_2 t}
\]

53
where $\lambda_1, \lambda_2$ are the eigen values of the matrix
\[
A = \begin{pmatrix} a & b \\ c & d \end{pmatrix},
\]
and
\[
\begin{pmatrix} v_{1x} \\ v_{1y} \end{pmatrix}, \begin{pmatrix} v_{2x} \\ v_{2y} \end{pmatrix}
\]
are the corresponding eigen vectors.

In the canonical coordinate system given by transformation $T$ the differential equations will be:
\[
\frac{dy_1}{dt} = \lambda_1 y_1 \\
\frac{dy_2}{dt} = \lambda_2 y_2
\]

**Exercise**

Consider the following system of ODE:
\[
\dot{x} = Ax \\
A = \begin{pmatrix} 1 & -2 \\ 5 & 8 \end{pmatrix}
\]

1. Find the general solution.
2. Find the transformation matrix $T$ and transform the system into its canonical form.

### 10.7 Linear algebra using MAPLE

**Determinant**

```maple
> with(linalg):
Warning, the protected names norm and trace have been redefined and unprotected
```

Let us define a 3x3 matrix:

```maple
> A:=array([[1,2,3],[4,5,6],[3,1,2]]);
A :=
\[
\begin{pmatrix}
1 & 2 & 3 \\
4 & 5 & 6 \\
3 & 1 & 2
\end{pmatrix}
\]
```
To find determinant, use the command det(A):

```maple
> A:=array([[a,b],[c,d]]);
A :=
[ a  b ]
[ c  d ]

> det(A);

ad - bc
```

```maple
> A:=array([[1,4],[-3,2]]);
A :=
[ 1  4 ]
[ -3  2 ]

> det(A);
14
```

Let's do Example 1 which we did analytically:

```maple
> A:=array([[1,3,0],[2,6,4],[-1,0,2]]);
A :=
[ 1  3  0 ]
[ 2  6  4 ]
[ -1  0  2 ]

> det(A);

-12
```

Eigen values and eigen vectors

There are several procedures which help in finding the eigen values and eigen vectors:

To find the characteristic polynomial use the command charpoly(A,\lambda) which will compute the characteristic polynomial for matrix \( A \) and \( \lambda \). Then we can find the eigen values from the solution of the characteristic equation.

Here follows Example 2 which we did analytically:

```maple
> A:=array([[8,-4],[2,2]]);
A :=
[ 8  -4 ]
[ 2   2 ]

> cpoly:=charpoly(A,x);

cpoly := x^2 - 10x + 24

> solve(cpoly,x);
6, 4
```
There is also a command `eigenvals(A)` which finds the eigen values of matrix A without intermediate steps:

\[
\text{eigenvals}(A);
\]

\[
6, 4
\]

As well as a command `eigenvects(A)` which finds the eigen vectors of matrix A:

\[
\text{eigenvects}(A);
\]

\[
[4, 1, \{[1, 1]\}], [6, 1, \{[2, 1]\}]
\]

Here we have the following information: 4 is the first eigen value, 1 is its multiplicity, and \([1,1]\) is the corresponding eigen vector; the same for the second eigen value, 6.

**Matrix operations**

The command `evalm(operation)` makes an ‘operation’ with our matrices. If we have matrices A and B then \(A+B\) is just \(A+B\); and \(A*B\) is \(A&*B\).

\[
\text{A}:=\text{array}([[1,4],[0,2]]);
\]

\[
A := \begin{bmatrix} 1 & 4 \\ 0 & 2 \end{bmatrix}
\]

\[
\text{B}:=\text{array}([[1,2],[3,1]]);
\]

\[
B := \begin{bmatrix} 1 & 2 \\ 3 & 1 \end{bmatrix}
\]

\[
\text{evalm}(A&*B);
\]

\[
\begin{bmatrix} 13 & 6 \\ 6 & 2 \end{bmatrix}
\]

To find the inverse matrix we can use two commands: \(\text{inverse}(A)\) or \(\text{evalm}(1/A)\).

**This is Example 3 which we did analytically:**

\[
\text{A}:=\text{array}([[2,1],[5,3]]);
\]

\[
A := \begin{bmatrix} 2 & 1 \\ 5 & 3 \end{bmatrix}
\]

\[
\text{inverse}(A);
\]
or:

\[
\begin{bmatrix}
3 & -1 \\
-5 & 2
\end{bmatrix}
\]

To check the result we can use:

\[
B := \text{inverse}(A);
\]

\[
B :=
\begin{bmatrix}
3 & -1 \\
-5 & 2
\end{bmatrix}
\]

\[
\text{evalm}(A \times B);
\]

\[
\begin{bmatrix}
1 & 0 \\
0 & 1
\end{bmatrix}
\]

Canonical form

To find the canonical form, we use the command \text{jordan}(A) or \text{jordan}(A,P). A is a square matrix and P is optional, used to return the transition matrix.

This is Example 4 which we did analytically:

\[
A := \text{array}([[8,-4],[2,2]]);
\]

\[
A :=
\begin{bmatrix}
8 & -4 \\
2 & 2
\end{bmatrix}
\]

\[
\text{jordan}(A);
\]

\[
\begin{bmatrix}
4 & 0 \\
0 & 6
\end{bmatrix}
\]

If we need a transformation matrix T:

\[
\text{jordan}(A,P);
\]

\[
\begin{bmatrix}
4 & 0 \\
0 & 6
\end{bmatrix}
\]
Maple returns the transition matrix $T$ itself

$$ T := \begin{bmatrix} -1 & 2 \\ -1 & 1 \end{bmatrix} $$

Systems of linear differential equations

The procedure is similar to the one used to find the solution of a 1D ODE, just take care of the ‘{’ symbol which we use to describe a set of expressions.

```maple
> ode := {diff(x1(t),t)=3*x1(t)+x2(t), diff(x2(t),t)=3*x1(t)+5*x2(t)};
    ode := \{ \frac{\partial}{\partial t} x1(t) = 3 x1(t) + x2(t), \frac{\partial}{\partial t} x2(t) = 3 x1(t) + 5 x2(t) \}
> dsolve(ode,{x1(t),x2(t)});
    \{ x1(t) = C1 e^{(6t)} + C2 e^{(2t)}, x2(t) = 3 C1 e^{(6t)} - C2 e^{(2t)} \}
```

To find the canonical form and the transformation matrix we use:

```maple
> A:=array([[3,1],[3,5]]);
    A := \begin{bmatrix} 3 & 1 \\ 3 & 5 \end{bmatrix}
> jordan(A,P);
    \begin{bmatrix} 2 & 0 \\ 0 & 6 \end{bmatrix}
> T:=evalm(P);
    T := \begin{bmatrix} 3 & 1 \\ \frac{3}{4} & \frac{1}{4} \\ \frac{3}{4} & \frac{3}{4} \end{bmatrix}
```

EXTRA Exercises

1. Using MAPLE and pencil and paper find: \[ \text{Det} A = \begin{vmatrix} 13 & 24 & 12 \\ 0 & 6 & 0 \\ 12 & 81 & 5 \end{vmatrix} \]
2. Using MAPLE and pencil and paper find the eigen vectors and eigen values of:

\[
\begin{pmatrix}
5 & 10 \\
4 & -1
\end{pmatrix}
\]

3. Using MAPLE and pencil and paper find \(A^{-1}\) of

\[
\begin{pmatrix}
2 & 0 & -1 \\
5 & 1 & 0 \\
0 & 1 & 3
\end{pmatrix}
\]

Verify by \(A * A^{-1}\).

4. Using MAPLE find the canonical form of the following matrix

\[
\begin{pmatrix}
1 & 0 & 0 \\
8 & 1 & 1 \\
12 & -2 & 4
\end{pmatrix}
\]

Find the transformation matrix and check that \(T^{-1}AT = D\).

5. Using MAPLE find the eigen vectors and eigen values of the following matrix:

\[
\begin{pmatrix}
3 & 1 & 0 \\
6 & -2 & 0 \\
0 & 0 & 2
\end{pmatrix}
\]

and construct the general solution of \(\dot{x} = Ax\). Check the result using ‘dsolve’ of MAPLE.
Chapter 11

Complex numbers

\[ i = \sqrt{-1} \]  \hspace{1cm} (11.1)

Here \( i \) is the basic complex number which is similar to \( \sqrt{1} \) for real numbers.

Example. Solve the equation \( \lambda^2 + 2\lambda + 10 = 0 \).

Solution.

\[ \lambda_{1,2} = \frac{-2 \pm \sqrt{4 - 4 \times 10}}{2} = \frac{-2 \pm \sqrt{-36}}{2} = \frac{-2 \pm 6i}{2}, \]

or \( \lambda_1 = -1 + 3i \) \( \lambda_2 = -1 - 3i \)

\[ z = \alpha + i\beta \]  \hspace{1cm} (11.2)

where \( \alpha \) is called the **real part** of the complex number \( z \), and \( \beta \) is called the **imaginary part** of \( z \). The notation for the real part is \( Re(z) \) and for the imaginary part is \( Im(z) \). In our example \( Re(\lambda_1) = -1; Im(\lambda_1) = 3 \).

We can work with complex numbers in the same way as with usual real numbers and expressions. The only thing which we need to remember, is that \( i^2 = -1 \).

To add two complex numbers we need to add their real and imaginary parts. For example

\[ z_1 = 3 + 10i, z_2 = -5 + 4i, \quad z_1 + z_2 = (3 + 10i) + (-5 + 4i) = 3 + 10i + -5 + 4i = -2 + 14i. \]

Similarly, multiplication by a real number results in multiplication of the real and imaginary part by this number

\[ z_1 = 3 + 10i; \quad 10z_1 = 10 \times (3 + 10i) = 30 + 100i. \]

Multiplication of two complex numbers is just multiplication of two expressions \( z_1 = 3 + 10i, z_2 = -5 + 4i; \quad z_1 \times z_2 = (3 + 10i) \times (-5 + 4i) = 3 \times (-5) + 3 \times 4i + 10i \times (-5) + 10i \times 4i = -15 + 12i - 50i + 40i^2 = -15 - 38i - 40 (as \ i^2 = -1) = -55 - 38i. \)
Similarly
\[(z_1)^2 = (3 + 10i)^2 = 3^2 + 2 \cdot 3 \cdot 10i + (10i)^2 = 9 + 60i + 100i^2 = 9 + 60i - 100 = -91 + 60i.\]

Now we can check that \(\lambda_1 = -1 + 3i\) is a solution of the equation in our example. In fact:
\[
\lambda_2 + 2\lambda + 10 = (1 - 1 + 3i)^2 + 2 \cdot (1 - 1 + 3i) + 10 = (-1)^2 + 2 \cdot (-1) \cdot 3i + (3i)^2 - 2 + 6i + 10 = 1 - 6i - 9 - 2 + 6i + 10 = (1 - 9 - 2 + 10) - 6i + 6i = 0 - 0i = 0, \text{ i.e., all is OK and } \lambda_1 = -1 + 3i \text{ is the root of this equation.}
\]

The number \(z_2 = a - ib\) is called the complex conjugate to the number \(z_1 = a + ib\) and is denoted as \(\bar{z}_1 = z_2 = a - ib\). Complex conjugate numbers have the same real parts, but their imaginary parts have opposite signs.

Roots of a quadratic equation with real coefficients are complex conjugate to each other.
\[
\lambda_1 = \frac{-B + i\sqrt{-D}}{2}, \quad \lambda_2 = \frac{-B - i\sqrt{-D}}{2} \tag{11.3}
\]
hence, if \(D < 0:\)
\[
\lambda_2 = \bar{\lambda}_1; \quad Re\lambda_1 = Re\lambda_2 = \frac{-B}{2}, \quad Im\lambda_1 = -Im\lambda_2 = \frac{\sqrt{-D}}{2} \tag{11.4}
\]

Finally consider two more basic operations. If \(z = a + ib\), then, \(|z| = \sqrt{a^2 + b^2}\) is called the absolute value, or modulus of \(z\). Note, that \(|z|^2 = z\bar{z}\), as \((a + ib) \cdot (a - ib) = a^2 - (ib)^2 = a^2 + b^2\).

We use this trick to introduce division of two complex numbers
\[
\frac{z_1}{z_2} = \frac{z_1\bar{z}_2}{z_2\bar{z}_2}
\]
So, to divide two complex numbers we multiply the numerator and the denominator of the fraction by a number which is the complex conjugate to the denominator, and we get the answer in the usual form.

Example
\[
\frac{1 + 3i}{1 - 4i} = \frac{1 + 3i}{1 - 4i} \cdot \frac{1 + 4i}{1 + 4i} = \frac{(1 + 3i)(1 + 4i)}{1^2 + 4^2} = \frac{1 + 3i + 4i + 12i^2}{17} = \frac{-11 + 7i}{17} = \frac{-11}{17} + \frac{7}{17}i \diamond
\]

The Euler formula gives a representation of \(e^{i\phi}\) in terms of trigonometric functions.
\[
e^{i\phi} = \cos \phi + i\sin \phi \tag{11.5}
\]

The polar form of complex numbers. Because complex numbers can be represented as a point on the Oxy plane, we can use the polar coordinate system for their description. First remember
the relation between polar coordinates and Cartesian coordinates:
From Cartesian to polar coordinates:

\[ r = \sqrt{x^2 + y^2} \]

\[ \phi = \arctan \frac{y}{x} \]

From polar to Cartesian coordinates:

\[ x = r \cos \phi \]

\[ y = r \sin \phi \]

If we remember that \( r = |z| \) and the Euler formula you can understand that complex numbers can be written as follows:

\[ z = x + iy = |z|(\cos \phi + i \sin \phi) = |z|e^{i\phi} \]

**Example 1**

\[ z = 1 + i. \] Therefore \( |z| = \sqrt{1^2 + 1^2} = \sqrt{2}. \) \( \phi = \pi/4, \) therefore \( z = \sqrt{2}e^{i\pi/4}. \)

**exercises**

1. Find the polar form of \( z = 3 + 3\sqrt{3}i. \)
2. Find \( \frac{2-i}{3-i}. \)

**11.1 General solution of a system with complex eigen values**

\[ e^{(\alpha+i\beta)t} = e^{\alpha t}e^{i\beta t} = e^{\alpha t} (\cos \beta t + i \sin \beta t) \]

\[ \begin{pmatrix} x \\ y \end{pmatrix} = A_1 \begin{pmatrix} v_{1x} \\ v_{1y} \end{pmatrix} e^{\alpha t} (\cos \beta t + i \sin \beta t) \]

\[ + A_2 \begin{pmatrix} v_{2x} \\ v_{2y} \end{pmatrix} e^{\alpha t} (\cos \beta t - i \sin \beta t), \]

where \( A_1,A_2 \) are arbitrary complex constants and \( \begin{pmatrix} v_{1x} \\ v_{1y} \end{pmatrix} \) and \( \begin{pmatrix} v_{2x} \\ v_{2y} \end{pmatrix} \) are complex eigen vectors.

\[ Y_1 = \begin{pmatrix} v_{1x} \\ v_{1y} \end{pmatrix} e^{\alpha t} (\cos \beta t + i \sin \beta t) \]
If we extract real and imaginary parts of this term we get:

\[ Y_1 = y_1 + i y_2. \]

where

\[ y_1 = e^{\alpha t} (v_r \cos \beta t - v_i \sin \beta t) \]
\[ y_2 = e^{\alpha t} (v_r \sin \beta t + v_i \cos \beta t) \]
\[ \begin{pmatrix} v_{1x} \\ v_{1y} \end{pmatrix} = v_r + i v_i \]

Both \( y_1 \) and \( y_2 \) are the real solutions of our system.

The general solution is given by the formula:

\[ \begin{pmatrix} x \\ y \end{pmatrix} = C_1 y_1 + C_2 y_2 \]

where \( C_1 \) and \( C_2 \) are arbitrary constants.

**Example 2**

Find the general solution and the canonical form of the following system of ODEs:

\[ \begin{pmatrix} \dot{x} \\ \dot{y} \end{pmatrix} = \begin{pmatrix} 1 & -5 \\ 2 & 7 \end{pmatrix} \begin{pmatrix} x \\ y \end{pmatrix} \]

**solution**

Eigen values:

\[ \text{Det} \begin{pmatrix} 1 - \lambda & -5 \\ 2 & 7 - \lambda \end{pmatrix} = \lambda^2 - 8\lambda + 17 = 0 \]

Hence \( \lambda_{12} = 4 \pm i \)

One eigen vector from the express formula is

\[ \lambda_1 = 4 + i; \begin{pmatrix} v_{1x} \\ v_{1y} \end{pmatrix} = \begin{pmatrix} 5 \\ 1 - (4 + i) \end{pmatrix} = \begin{pmatrix} 5 \\ -3 - i \end{pmatrix} = \begin{pmatrix} 5 \\ -3 \end{pmatrix} + i \begin{pmatrix} 0 \\ -1 \end{pmatrix} \] \hspace{1cm} (11.6)

Therefore the general solution is:

\[ \begin{pmatrix} x \\ y \end{pmatrix} = e^{\alpha t} \{ C_1 [ \begin{pmatrix} 5 \\ -3 \end{pmatrix} \cos t - \begin{pmatrix} 0 \\ -1 \end{pmatrix} \sin t ] + C_2 [ \begin{pmatrix} 0 \\ -1 \end{pmatrix} \cos t + \begin{pmatrix} 5 \\ -3 \end{pmatrix} \sin t ] \}

The canonical transformation is given by the matrix \( T = \begin{pmatrix} 5 & 0 \\ -3 & -1 \end{pmatrix} \)

\[ T^{-1} = \begin{pmatrix} 1/5 & 0 \\ -3/5 & -1 \end{pmatrix} \]
\[
AT = \begin{pmatrix} 20 & 5 \\ -11 & -7 \end{pmatrix}
\]

\[
T^{-1}AT = \begin{pmatrix} 4 & 1 \\ -1 & 4 \end{pmatrix}
\]

**Exercise**

Find the general solution and the canonical form of the following system of ODEs:

\[
\begin{pmatrix} \dot{x} \\ \dot{y} \end{pmatrix} = \begin{pmatrix} -1 & 1 \\ -5 & 3 \end{pmatrix} \begin{pmatrix} x \\ y \end{pmatrix}
\]

### 11.2 Complex numbers using MAPLE

**NOTE:** \(i\) is ‘I’ in MAPLE.

```maple
> I*I;
-1

> (x+I*y)*(x-I*y);
(x+I*y)(x-I*y)

> expand(%);
x^2 + y^2
```

**Example 1 on polar form of complex numbers:**

```maple
> z:=1+I;
z := 1 + I

> abs(z);
\sqrt{2}

> arctan(1./1.);
.7853981634
```

To find the absolute value of a complex number use:

To find angle of \(z\) we take the ratio of Im and Re:
And to get angle in degrees:

```maple
> convert(%,degrees);
141.3716694 \frac{degrees}{\pi}
```

```maple
> evalf(%);
44.99999998 degrees
```

Simple arithmetic operations:

```maple
> 1/(1+I);
\frac{1}{2} - \frac{1}{2} I
```

```maple
> (1+I)^2/(3+2*I);
\frac{4}{13} + \frac{6}{13} I
```

To get the eigen values and eigen vectors in the case of complex numbers we use the command `Eigenvals(A,vecs)`, which will compute the eigen values of A and give a matrix ‘vecs’ with the eigen vectors. In the complex case the program will give the real and imaginary parts of the eigen vector.

Example 2 which we did analytically:

```maple
> A:=array([[1,-5],[2,7]]);
A :=
\begin{bmatrix}
1 & -5 \\
2 & 7
\end{bmatrix}
```

```maple
> evalf(Eigenvals(A,vecs));
\begin{bmatrix}
4.000000000 + 1.000000000 I, 4.000000000 - 1.000000000 I
\end{bmatrix}
```

```maple
> evalm(vecs);
\begin{bmatrix}
-0.5000000000 & -1.500000000 \\
0. & 1.
\end{bmatrix}
```

Exercise: Why is this eigen vector different from the analytical eigen vector: (5,−3)+
(0,−1)I?

We can find eigen vectors in another way, using the function eigenvects in the following way:
With(linalg):

Warning, the protected names norm and trace have been redefined and unprotected

> a:=eigenvects(A);

\[ a := [4+I, 1, \begin{bmatrix} 1, & \frac{-3}{5} - \frac{1}{5}I \end{bmatrix}], [4-I, 1, \begin{bmatrix} 1, & \frac{-3}{5} + \frac{1}{5}I \end{bmatrix}] \]

To find the canonical form we use the matrix vecs, and its inverse:

> vecs_1:=evalm(1/vecs);

\[ \text{vecs}_1 := \begin{bmatrix} -2.000000000 & -3.000000000 \\
0. & 1.000000000 \end{bmatrix} \]

> canonic:=evalm(vecs_1&*A&*vecs);

\[ \text{canonic} := \begin{bmatrix} 4.000000000 & 1.000000000 \\
-1.000000000 & 4.000000000 \end{bmatrix} \]

To solve the system of differential equations in Example 2, use the dsolve command:

> ds:={diff(x(t),t)=x(t)-5*y(t),
    diff(y(t),t)=2*x(t)+7*y(t)};

\[ ds := \begin{cases} \frac{\partial}{\partial t} x(t) = x(t) - 5 y(t), \\
\frac{\partial}{\partial t} y(t) = 2 x(t) + 7 y(t) \end{cases} \]

> dsolve(ds,{x(t),y(t)});

\[ \begin{align*}
&\{x(t) = e^{(4t)} (\_C1 \sin(t) + \_C2 \cos(t)), \\
y(t) = -\frac{1}{5} e^{(4t)} (3 \_C1 \sin(t) + \_C1 \cos(t) + 3 \_C2 \cos(t) - \_C2 \sin(t))\}\end{align*} \]
Chapter 12

Linearization of a system of ODEs, Jacobian

12.1 Trace and determinant

**Definition 1** The trace of the matrix \( \begin{pmatrix} a & b \\ c & d \end{pmatrix} \) is:

\[ \text{tr} A = a + d. \]

The determinant of the matrix A is:

\[ \text{det} A = ad - cb. \]

The solid line which forms the border between real valued and complex eigenvalues is given by:

\[ \text{det} A = \left( \frac{\text{tr} A}{2} \right)^2 \]

12.2 Jacobian

Consider a general system of two differential equations:

\[
\begin{align*}
\frac{dx}{dt} &= f(x,y) \\
\frac{dy}{dt} &= g(x,y)
\end{align*}
\]  \hspace{1cm} (12.1)

The Jacobian of this system is

\[
J = \begin{pmatrix}
\frac{\partial f}{\partial x} & \frac{\partial f}{\partial y} \\
\frac{\partial g}{\partial x} & \frac{\partial g}{\partial y}
\end{pmatrix}
\]  \hspace{1cm} (12.2)
Close to the equilibrium system (12.1) is equivalent to the linear system:

\[
\begin{pmatrix}
\frac{du}{dt} \\
\frac{dv}{dt}
\end{pmatrix} = J \begin{pmatrix} u \\ v \end{pmatrix}
\]  

(12.3)

where J is the Jacobian computed at this equilibrium point, and u and v form a change of variables that shifts the equilibrium to the origin.

**Example 1**

Find the linearization of the following system around the equilibrium point \(x = 0, y = 0\) and determine the type of this equilibrium:

\[
\begin{cases}
\frac{dx}{dt} = -4x + 5 \tan y \\
\frac{dy}{dt} = -6 \sin x + 4y^3
\end{cases}
\]  

(12.4)

**solution:**

\[
\begin{align*}
\frac{\partial f}{\partial x} &= -4 \quad \frac{\partial f}{\partial x}(0,0) = -4 \\
\frac{\partial f}{\partial y} &= \frac{5}{(\cos y)^2} \quad \frac{\partial f}{\partial y}(0,0) = 5 \\
\frac{\partial g}{\partial x} &= -6 \cos x \quad \frac{\partial g}{\partial x}(0,0) = -6 \\
\frac{\partial g}{\partial y} &= 12y^2 \quad \frac{\partial g}{\partial y}(0,0) = 0
\end{align*}
\]
Hence:

\[ J = \begin{pmatrix} -4 & 5 \\ -6 & 0 \end{pmatrix} \]

To find the equilibrium type we compute:

\[ trA = -4 \quad detA = 30; \quad (trA)^2 < 4detA \]

Hence, the equilibrium is a stable spiral.

**Jacobian using MAPLE**

**Example 1:**

\[
\begin{aligned}
\text{with(linalg):} \\
\text{Warning, the protected names norm and trace have been redefined and unprotected} \\
\text{A:=vector([-4*x+5*tan(y),-6*sin(x)+4*y^3]);} \\
A := \begin{bmatrix} -4x + 5\tan(y) \\ -6\sin(x) + 4y^3 \end{bmatrix} \\
\text{J:=jacobian(A,[x,y]);} \\
J := \begin{bmatrix} -4 & 5 + 5\tan(y)^2 \\ -6\cos(x) & 12y^2 \end{bmatrix}
\end{aligned}
\]

**Question:** Why is \( \frac{\partial f}{\partial y} \) in MAPLE different from our analytical study of Example 1?

To substitute \( x=0 \) and \( y=0 \) into the Jacobian, use:

\[
\begin{aligned}
\text{A:=evalf(subs(} \{x=0,y=0\},\text{evalm(J)));} \\
A := \begin{bmatrix} -4 & 5 \\ -6 & 0 \end{bmatrix}
\end{aligned}
\]

Now we can the find eigen values and we can determine the type of equilibrium point:

\[
\begin{aligned}
\text{eigenvals(A);} \\
-2 + 5.099019514I, -2 - 5.099019514I
\end{aligned}
\]

i.e., it is a stable spiral.

To see the picture of this spiral use the following steps:
\[\text{de} := \frac{\partial}{\partial t} x(t) = -4x(t) + 5y(t), \quad \frac{\partial}{\partial t} y(t) = -6x(t)\]

\[\text{aa} := \text{dsolve}\{\text{de}, x(0)=0.1, y(0)=0.1\}\{x(t), y(t)\}\]

\[\text{ax} := \text{rhs}(\text{aa}[1]);\]

\[\text{ay} := \text{rhs}(\text{aa}[2]);\]

\[\text{plot}([\text{ax}, \text{ay}, t=0..20]);\]

The graph is shown in Fig. 12.1.

Figure 12.1: A particular solution of a given system close to the equilibrium point.

Exercises

1. Check that 0, 0 is an equilibrium point of the following system. Find the linearization around \(x = 0, y = 0\) analytically and using MAPLE and determine the type of this equilibrium.

\[\begin{align*}
\frac{dx}{dt} &= x + 4y + e^x - 1 \\
\frac{dy}{dt} &= -y - ye^x
\end{align*}\]

2. Show that the system

\[\begin{align*}
\frac{dx}{dt} &= e^{x+y} - y \\
\frac{dy}{dt} &= -x + xy
\end{align*}\]

has only one equilibrium. Find this equilibrium. Find the linearization around it and determine the type of this equilibrium.
EXTRA Exercises

1. Check that the given equilibrium is an equilibrium point of the system. Find the linearization around it analytically and using MAPLE and determine the type of this equilibrium.

   (a) \[
   \begin{align*}
   \frac{dx}{dt} &= x + \frac{xy^3}{(1+x^2)^2} \\
   \frac{dy}{dt} &= 2x - 3y \\
   \end{align*}
   \] (0,0)

   (b) \[
   \begin{align*}
   \frac{dx}{dt} &= x^2 + \sin y - 1 \\
   \frac{dy}{dt} &= \frac{e^{x+1} - e^{-x+1}}{2} \\
   \end{align*}
   \] (1,0)

2. Find all equilibrium points of the following systems analytically and using MAPLE and determine the type of these equilibria.

   (a) \[
   \begin{align*}
   \frac{dx}{dt} &= y^2 - 3x + 2 \\
   \frac{dy}{dt} &= x^2 - y^2 \\
   \end{align*}
   \]

   (b) \[
   \begin{align*}
   \frac{dx}{dt} &= y \\
   \frac{dy}{dt} &= -x - x^3 \\
   \end{align*}
   \]

   (c) \[
   \begin{align*}
   \frac{dx}{dt} &= \sin (x+y) \\
   \frac{dy}{dt} &= y \\
   \end{align*}
   \]

   (d) \[
   \begin{align*}
   \frac{dx}{dt} &= x - y - e^x \\
   \frac{dy}{dt} &= x - y - 1 \\
   \end{align*}
   \]

   (e) \[
   \begin{align*}
   \frac{dx}{dt} &= -y + x + xy \\
   \frac{dy}{dt} &= x - y - y^2 \\
   \end{align*}
   \]
Chapter 13

Linear systems in 2D using GRIND

Create a new file \textit{rhs} with the text:

\[
x' = a_{11}x + a_{12}y; \\
y' = a_{21}x + a_{22}y;
\]

For initial values, graphics and some other things we need an auxiliary file. Let us name it \textit{set}.

Type into this file:

\[
a_{11} = -1. \\
a_{12} = 2. \\
a_{21} = -2. \\
a_{22} = 0.3 \\
axis \, x \, x \, -10 \, 10 \\
axis \, y \, y \, -10 \, 10 \\
axis \, v \, 0 \, 150 \\
finish \, 50 \, 300 \\
option \, initial \\
option \, trunc \\
option \, event \\
terminal \, x11 \\
x = 1. \\
y = 9.
\]

Here we set up the values for our parameters, the ranges of our axes, and choose the x-axis for the \textit{x} variable and the y-axis for the \textit{y} variable.

The line \textit{finish} shows that the time interval of integration will be until time 50, and we will have a lot of points on our trajectory (300), i.e., the picture will be smooth. We also set up the initial values of \textit{x} and \textit{y}. The option \textit{trunc} truncates the program if the values of variables become too large, and the option \textit{initial} marks the initial point of integration. The option \textit{event} enables you to stop integrations by pressing \texttt{Esc} (if things are going wrong while backcomputing). \textit{terminal x11} defines the terminal type.
Now type `grind rhs` for preprocessing. And when it is over type `read set` to get the initial data.

Then type `2d` to get our phase plane.

The command `nu x y` will give the nullclines of the system, the command `vec` will display the direction field on our phase plane, and `run` will give us the first trajectory. We see that it is a stable spiral.

To get a bunch of trajectories, type `grid 3`, and you will get trajectories starting from 3x3 equally spaced points.

Using GRIND we can also study the eigen system at the equilibrium point. For this, we first need to show to GRIND the point which we want to study. In our case, the point is stable, and we can approach it just along the trajectory (using the `run` command).

**NOTE:** in general you should use the command `newton`, which searches an equilibrium using Newton-Rhapson’s method.

After we arrived to the equilibrium, type `eigen jac` and we will get the message:

```
 Stable point
 Population State Derivative
 x:  1.054964E-07  4.086289E-07
 y:  2.570626E-07 -1.338739E-07
 Jacobian matrix:
 -1.00000  2.00000
 -2.00000  0.30000
 Lambda: i / Vector:
 1:  -0.35000 + i 1.89143
 2:  -0.35000 + i -1.89143
```

In the first line GRIND tells us that the equilibrium is stable, the next line shows the coordinates of the equilibrium and the derivatives at this point. We know that all derivatives ($dx/dt$ and $dy/dt$) must be zero at the equilibrium. Let us check it here. If we note that $E-07$ is an extremely small number, we see that our equilibrium is at the point $x = 0, y = 0$; and that $dx/dt = 0$ and $dy/dt = 0$; so that’s O.K.

The next lines give the Jacobian matrix. In our example it coincides with the RHS of our system (since we study a linear system).

The next lines show the eigen values (which are complex with negative real part, i.e., again the equilibrium is stable). In this case we do not have eigen vectors, as they are complex.

**NOTE:** if the eigen values are real, GRIND will give us the eigen vectors under the header `i / Vector`.

Let us change our system. Let us make $a_{21} = 2$.~
So our system will be:

\[
\begin{align*}
\frac{dx}{dt} &= (-1) \times x + 2 \times y \\
\frac{dy}{dt} &= 2 \times x + 0.3 \times y
\end{align*}
\]

1. Compute \( tr(A) \) and \( det(A) \) and decide which kind of equilibrium point we have here.

2. Study it in a similar way, using the \texttt{run} and \texttt{grid} commands.

**NOTE:** If the graphics are too messy, change the parameter finish. For example, type \texttt{finish 5 300}. Our trajectories will be computed until time \( t = 5 \), i.e., they will become shorter. (The previous value of finish was \texttt{finish 50 300}, so our trajectories become 10 times shorter).

3. We need to find the eigenvalues and eigenvectors now (the eigenvalues and eigenvectors of a system are together called the eigensystem of that system). But how can we find it if the equilibrium is nonstable? Please, recall our note about the \texttt{newton} command, and use it.

4. Next, find the eigen values and eigen vectors using \texttt{eig jac}. **NOTE:** in this case, we get the eigen vectors as well.

Lines which you should get on the screen are:

\begin{verbatim}
newton
Converged into:
Population State Derivative
x:  0.000000E+00  0.000000E+00
y:  0.000000E+00  0.000000E+00
eig jac
Unstable point:
Population State Derivative
x:  0.000000E+00  0.000000E+00
y:  0.000000E+00  0.000000E+00
Jacobian matrix:
-1.00000  2.00000
2.00000  0.30000
Lambda: i / Vector:
1:  1.75297 -0.59 -0.81
2:  -2.45297 -0.81  0.59
\end{verbatim}

For this equilibrium point (saddle) we can find the stable and nonstable manifolds using the GRIND command \texttt{perturb}.

To find the first manifold, type \texttt{perturb 1} and then \texttt{run}; to find the second manifold, type \texttt{perturb 2} and \texttt{run}. However, the manifolds will be extended in one direction only. To get the other branches, you should change the initial data for the command \texttt{perturb}. By default, the
integration starts in positive direction at distance 0.0001 from the equilibrium. To get the other branch type `perturb 1 -0.0001`. The integration will now be in opposite direction and you will get the second branch of the 1st manifold. Do the same for the second manifold.

Sketch by hand the qualitative phase portrait of this system, indicating nonstable and stable manifolds.

**NOTE:** Please be careful when you use command `perturb`. It automatically switches the direction of integration from forward to backwards. Before you start a new integration make sure that the option backwards is not active. To switch it off use `op backwards off`. If the option backwards is on, all stable points will look as nonstable and vise versa.

**NOTE:** Sometimes, GRIND crashes due to different reasons. If you want to restart it without changes in the `rhs` file, just type `rhs` and it will start working without recompilation.
Chapter 14

Phase portrait of 2D systems using GRIND and analytical estimates

Consider the following system for noncompeting species:

\[
\begin{align*}
\frac{dx}{dt} &= a_1 x (1 - x) \\
\frac{dy}{dt} &= a_2 y (1 - y)
\end{align*}
\]

with \( a_1 = 2 \) and \( a_2 = 1 \). Let us draw its complete phase portrait. It should include all equilibria and separatrices between different regions. In this case \( x \) and \( y \) represent species, i.e., they are non negative and we need to draw the phase portrait for \( x \geq 0; y \geq 0 \) only. Our steps are the following:

1. **Analytical estimate.** Let us find as many equilibria as we can analytically. The equation for the equilibria is:

\[
0 = a_1 x (1 - x), \quad 0 = a_2 y (1 - y)
\]

from here we see that we have 4 equilibria: \((0, 0), (0, 1), (1, 0), (1, 1)\).

2. **Nullclines using GRIND.** We put this system into GRIND and draw the nullclines. From the points of intersection we see that we have 4 equilibria here. We were lucky to find all of them analytically.

3. **Study of each equilibrium using GRIND.** We need to study the different equilibria. By using the command **cursor** we can select a point on the phase portrait with our mouse-button. If we now use the command **newton** grind will converge to the equilibrium that is close to the previously selected point. (Of course it is more easy to converge to a stable point than to an unstable point, so to be sure to actually reach a specific equilibrium, select a point in the close neighborhood of that equilibrium). Once we have reached the equilibrium use the command **eigen jac** to find out about the jacobian and eigenvalues of the equilibrium. We find that \((0, 0)\) is an nonstable node; \((1, 1)\) is a stable node, and \((0, 1)\) and \((1, 0)\) are saddle points.
It is important: to find the stable and unstable manifolds of saddlepoints as they form separatrices which form borders between different domains of attraction. How to find these manifolds. First use the command cursor to select a point, then use the command newton to reach the equilibrium, and then use the command eigen to find out about the stability of the equilibrium. Now you can use the command perturb (this command assumes that before you use it you have reached equilibrium and used the command eigen). This command computes the manifolds of the equilibrium (this means it is nonsense to use it for spirals and center points). To compute both manifolds in both directions from the equilibrium point you have to use perturb 1 0.0001 (this is what grind does by default if you type perturb), perturb 1 -0.0001, perturb 2 0.0001 and perturb 2 -0.0001. As one of the manifolds of the saddle node is unstable, it goes away from the equilibrium point and hence can simply be computed by integrating in the forward direction, but the other, stable manifold, goes towards the equilibrium and hence has to be computed in backward direction. Computations in the backward direction are always tricky to do so pay attention you have the option event selected. Also remember that once you are computing in the backward direction it stays that way unless you switch it off by using option back off.

4. Representation of the phase portrait. You can first try the grid command. Then draw schematically the phase portrait by pencil and paper; show all equilibria, their local phase portraits, trajectories of the stable and nonstable manifolds and a few interesting trajectories which show the flow from one equilibrium to another

Exercises

Study the following systems using the same approach as above:
NOTE: For each of these exercises it turns out to be important to type nu 5 before you start working with nullclines. This command puts the algorithm that computes the nullclines to a higher level of precision, which turned out to be necessary for the computation of the nullclines in these exercises.

1. Lotka-Voltera predator prey system:
   \[
   \frac{dx}{dt} = ax - xy, \quad \frac{dy}{dt} = xy - by
   \]
   with \(a = 2, b = 1\).

2. Competing species:
   \[
   \frac{dx}{dt} = a_1 x(1 - x) - c_1 xy, \quad \frac{dy}{dt} = a_2 y(1 - y) - c_2 xy
   \]
   with \(a_1 = a_2 = 1, c_1 = 2, c_2 = 1.5 \) and \(a_1 = a_2 = 1, c_1 = 0.5, c_2 = 0.7\).

3. Holling type-II predator prey model:
   \[
   \frac{dx}{dt} = ax(1 - x) - yf(x), \quad \frac{dy}{dt} = yf(x) - by, f(x) = \frac{x}{k+x}
   \]
   with \(a = 1, b = 0.6, k = 0.2 \) and \(a = 1, b = 0.75, k = 0.2\).
4. **EXTRA** Symbiotic system:

\[
\frac{dx}{dt} = \frac{a_1 xy}{k_1 + y} - x^2 - d_1 x, \quad \frac{dy}{dt} = \frac{a_2 xy}{k_2 + y} - y^2 - d_2 y
\]

with \( a_1 = a_2 = 2, d_1 = d_2 = 0.5, k_1 = 0.1, k_2 = 0.5 \).
Hopf bifurcation revisited

1. During the lectures we have derived the normal form for the Hopf bifurcation. We told you that all but one of the 2nd and 3rd order terms can be removed, but not all of those removals have been shown.

Therefore, show how the following term:

\[ \frac{dz}{dt} = \lambda z + F z \bar{z}^2 \]

can be removed by means of the following transformation:

\[ z = w + f w \bar{w}^2 \]

Show that in order to remove this cubic term the right choice for \( f \) is:

\[ f = \frac{F}{2\lambda} \]

(a) Find \( w, \bar{w}, z, \bar{z}, \dot{z}, \dot{\bar{z}} \).

(b) Find the dynamics of the new variable \( w \).

(c) Replace \( \dot{z}, \dot{\bar{z}} \) by their full expressions.

(d) Denote terms of 4th or higher order as \( O(|z|^4) \).

(e) Replace \( z, \bar{z} \) using the direct transformations.

(f) Denote terms of 4th or higher order as \( O(|w|^4) \).

(g) Find the right choice to remove the cubic term.

2. Calculate by hand the stability of the origin for the following system:

\[
\begin{align*}
\frac{dx}{dt} &= y - x^3 + xy^2 \\
\frac{dy}{dt} &= -x - xy^2
\end{align*}
\]

Afterwards you don’t have to type in a file with the stability index in order to check the result. This file is already available on your computer.
Chapter 15

Hopf bifurcation

We know that the normal form for the supercritical Hopf bifurcation is:

\[
\begin{align*}
\frac{dx}{dt} &= -y + x[\mu - (x^2 + y^2)] \\
\frac{dy}{dt} &= x + y[\mu - (x^2 + y^2)]
\end{align*}
\]

In this case we have a stable limit cycle at \( \mu > 0 \).

**Hopf bifurcation using GRIND**

1. Obtain phase portraits of the above system before and after the Hopf bifurcation using GRIND. Is the equilibrium stable at the point of bifurcation?

2. Write a normal form for the subcritical Hopf bifurcation. Study it in a similar way.

   **NOTE:** In the case of the subcritical Hopf bifurcation we expect an unstable limit cycle. How can we find this limit cycle as we do not approach it but go away from it. Put **option back on** temporarily, so everything you normally go away from you now approach.

**Hopf bifurcation using Content**

Let us now study the normal form for the Hopf bifurcation using Content.

Start Content
In main window:
Select, Class: ODE
Select, System
In new window:
type: hopf
OK
In window titled hopf:
variables: x,y
parameters: u (\( \mu \))
time: t
select first 3 derivatives numerically
type equations
OK
System is being compiled now.

When ready:
In main window:
Type, Initial Point, Point
Type, Curve, Orbit
Window, 2DGraphic
In graphical window:
Attributes, Current
In new window:
abcissa: t
ordinate: x
In graphical window:
range:
x-axis: 0..50
y-axis: -2..2
(enter)
In Integrator window:
interval: 200
In main window:
Options, Archive Filter
In new window:
put Path filter from 1 to 200
In main window:
Options, Pause Mode
In new window:
select enable pause buttons
In starter window:
Initial values:
x=0.1
y=0.1
u=-1 (we expect a stable equilibrium for \( \mu < 1 \) so for this value it should be easy to find an equilibrium)
In graphical window:
Compute, Forward
You can see that the orbit approaches an equilibrium.

abort
Let us continue this equilibrium
In main window:
Select, Initial Point
In new window:
choose: O: Last Point
OK
In main window:
Type, Initial Point, Equilibrium
Type, Curve, Equilibrium
Window, Numeric
In numeric window:
Window, Layout
In new window:
select eigenvalues with mouse
select all
OK
As we now have a system of two variables, we now have two
eigenvalues. They together determine the stability of the equilibrium.
In graphical window:
Attributes, Current
In new window:
abcissa: u
ordinate: x
In graphical window:
range:
x-axis: -2..2
y-axis: -2..2
Compute, Forward/Backward
Watch the eigenvalues!
If all is OK you have encountered a point labelled H.
H of course means point of Hopf bifurcation.
Select this point by doubleclicking it with your mouse.
Automatically the following changes occur in the main window:
behind point type it says: Hopf
behind curve type it says: Hopf(standard)
The point type is OK as we are in a point of Hopf bifurcation.
The curve type is not OK. If Content encounters a point of Hopf
bifurcation it standard wants to continue a line of Hopf bifurcation
points. In the current model this is not possible, as for having not a
single Hopf bifurcation point but a line of Hopf bifurcation points an
extra parameter and hence an extra dimension is needed.
What we want to do is to continue the limitcycle that appears once you
Hopf bifurcation has occured, so:
In main window:
Type, Curve, Limitcycle
In graphical window:
Compute, Forward
First you encounter a series of points designated BP. These are
artefacts of the computation algorithm so just ignore them and keep
pressing resume until Content starts computing the limitcycles you
want to continue.
(To explain what you are seeing if all is OK:
Content draws a few points on each limitcycle corresponding to a
specific value of u, and connects the corresponding points of the
different limitcycles.)
abort to stop computations.

To see how the system behaves when it is on a limitcycle:
In main window:
Select, Initial Point
In new window:
choose: LC: Last Point
So now we have chosen the last point of the last computed limitcycle as the starting point of our computations.
In main window:
Type, Initial Point, Point
Type, Curve, Orbit
In the graphical window:
Attributes, Current
In the new window:
abcissa: t
ordinate: x
OK
In the graphical window:
r
range:
x-axis: 0..50
y-axis: -2..2
Compute, Forward

Draw the bifurcation diagram and the timeseries if you are on the limitcycle.
15.1 Brusselator

In 1968 Prigogene and Lefever introduced a famous model for oscillatory phenomena which is based on the following reaction mechanism:

\[ A \rightarrow^{k_1} X, B + X \rightarrow^{k_2} Y + D, \quad 2X + Y \rightarrow^{k_3} 3X, \quad X \rightarrow^{k_4} E \]

where the \( k \)'s are the rate constants, and the reactant concentrations of A and B are kept constant.

1. Write down the governing differential equation system for the concentrations of X and Y and transform the equations into the form:

\[
\frac{dx}{dt} = a - (b + 1)x + x^2y \quad (15.1)
\]

\[
\frac{dy}{dt} = bx - x^2y \quad (15.2)
\]

2. How are the parameters \( a, b \) and the variables \( x, y \) related to the reaction constants and concentrations of species in the original reaction?

3. Find analytically the parameter values for which a Hopf bifurcation occurs.

4. Study the system at \( a = 1 \) using Content. (NOTE:: if we fix \( a = 1 \), we can just substitute 1 for \( a \) in the system, so we are left with only one parameter: b) Find the value of \( b \) when a Hopf bifurcation occurs. Compare it to the value obtained in the analytical study. Draw the phase portrait before and after the bifurcation. (You can use GRIND). Which kind of Hopf bifurcation (sub- or supercritical) do we have here?

5. Study the system at \( a = 1 \) using Content. Find and continue the limit cycle along the parameter \( b \) (that is, select the point designated by H, etc).

6. Let us study some limitcycles in the \( x, y \) plane and the corresponding timeseries in a \( x, t \) plot for different values of \( b \).

   In main window:
   Type, Initial Point, Point
   Type, Curve, Point

   In graphical window:
   Attributes, Current

   In new window:
   abcissa: t
   ordinate: x

   In graphical window:
   x-axis: 0..50
   y-axis: -5..5

   In Starter window:
   t=0
   x=0.1
   y=0.1
b=2.5

In graphical window:

**Compute, Forward**

After a while you get periodic behavior, so you know you are on the limit cycle.

**abort**

You can save the curve you got as follows:

In main window:

**Select, Curve**

In new window:

**Actions, Rename**

type new name

**OK**

In the main window:

**Select, Initial Point**

In new window:

choose: O:Last Point

As you have selected the last point of the orbit, and the orbit was then already exhibiting periodic behavior, you have selected a point on the limit cycle.

In graphical window:

**Attributes, Current**

In new window:

abcissa: x
ordinate: y

In graphical window:

range:
x-axis:-5..5
y-axis:-5..5

**Compute, Forward**

If limit cycle has reached closure: **abort**

Save this curve too.

If you repeat this procedure, but then put b to different values, you get a set of time-series which you can load and plot in one graph, and you can do the same for the set of limit cycles you have.

What happens to the period and amplitude of the limit cycle when you increase b?
15.2 Stability index

The central part of the analytical study of the Hopf bifurcation is finding the bifurcation type (supercritical or subcritical). As we know, this type is determined by the stability of the equilibrium at the bifurcation point. One way of determining the stability is by computing the stability index $I$. 

For the system
\[
\begin{align*}
\frac{dx}{dt} &= \omega y + Y^1 \\
\frac{dy}{dt} &= -\omega x + Y^2
\end{align*}
\]
the stability index is:
\[
I = \omega (Y_{111}^1 + Y_{122}^1 + Y_{112}^2 + Y_{122}^1) \\
+ (Y_{111}^1 Y_{112}^2 - Y_{112}^1 Y_{112}^1 + Y_{111}^2 Y_{112}^2) \\
+ (Y_{122}^1 Y_{112}^1 - Y_{122}^2 Y_{112}^1 - Y_{112}^1 Y_{122}^2)
\]
where
\[
Y_{12}^1 = \frac{\partial^2 Y^1}{\partial x \partial y} (0,0) \quad Y_{112}^2 = \frac{\partial^3 Y^2}{\partial x^3 \partial y} (0,0); \quad \text{etc.}
\]

For the system
\[
\begin{align*}
\frac{dx}{dt} &= -\omega y + Y^1 \\
\frac{dy}{dt} &= \omega x + Y^2
\end{align*}
\]
the stability index is:
\[
I = \omega (Y_{111}^1 + Y_{122}^1 + Y_{112}^2 + Y_{122}^1) \\
+ (-Y_{111}^1 y^2 + Y_{111}^1 Y_{112}^1 - Y_{111}^2 Y_{112}^2) \\
- Y_{122}^2 Y_{112}^1 - Y_{122}^1 Y_{112}^1 + Y_{122}^1 Y_{112}^2)
\]

If the index $I$ is negative, then the origin is stable.

Exercises

1. Put the general expression for the stability index into MAPLE and save it on disk. If the name of the expression is $ind$, to save it type: save ind, filename. To read the saved expression type: read filename.

2. To check your expression compute the stability index for:
\[
\begin{align*}
\frac{dx}{dt} &= ay + (1 - a^2) ax^2 + 2a^2 xy - a^4 x^3 + a^3 x^2 y \\
\frac{dy}{dt} &= -ax
\end{align*}
\]
The correct answer is:
\[
I = -2a^5 - 4a^3
\]

3. Find the stability of the origin for the following systems:
(a) \[
\begin{align*}
\frac{dx}{dt} &= y - x^3 + xy^2 \\
\frac{dy}{dt} &= -x - xy^2
\end{align*}
\]

(b) \[
\begin{align*}
\frac{dx}{dt} &= y + x^2 \sin(x) \\
\frac{dy}{dt} &= -x + xy + 2x^3
\end{align*}
\]

(c) \[
\begin{align*}
\frac{dx}{dt} &= y - x^2 + 2xy + y^2 \\
\frac{dy}{dt} &= -x + xy + y^2
\end{align*}
\]

4. Check the answers using GRIND.

EXTRA Questions

1. Put system (15.2) into the canonical form and determine the type of Hopf bifurcation using the stability index.

2. Study analytically and numerically (using Content, GRIND and MAPLE) the Hopf bifurcation for the following systems:

   (a) \[
   \begin{align*}
   \frac{dx}{dt} &= ax + (11 + 2a)y - 2(x - y)^3 \\
   \frac{dy}{dt} &= -2x + (a + 6)y - (x - y)^3
   \end{align*}
   \]

   (b) \[
   \begin{align*}
   \frac{dx}{dt} &= -1 - x - y + a - ax \\
   \frac{dy}{dt} &= 7 + x + 12y + 6y^2 + y^3
   \end{align*}
   \]

   (c) \[
   \begin{align*}
   \frac{dx}{dt} &= y \\
   \frac{dy}{dt} &= y^3 + y - ay - x
   \end{align*}
   \]
We can use the following two-variable system to model the cell division cycle:

\[
\begin{align*}
\frac{du}{dt} &= f(u) - v \\
\frac{dv}{dt} &= k(u - b)
\end{align*}
\]

where \( f(u) \) is a nonlinear function with the following graph, for example:

![Graph of f(u)](image)

We consider oscillations of the variables in this model as rapid division cycles and behaviour associated with a stable equilibrium as a metaphase arrest.

Study this model:

1. Find the regions where oscillation occur in this system. Relate it to specific points on the graph of \( f(u) \).

2. Try to find “analytically” the type of Hopf bifurcation using the stability index. In order to be able to do this, make explicit assumptions about the shape of the function \( f(u) \).

3. Draw a bifurcation diagram for parameter \( b \).

4. Give an example of \( f(u) \) which exhibits a supercritical bifurcation and an example of a function which exhibits a subcritical bifurcation. (The function can be different from the function sketched above). Draw the expected phase portraits for each case, and confirm your findings using GRIND. Draw the bifurcation diagrams for both cases.
Chapter 16

Center manifold

16.1 Plan for center manifold computation

**Step 1** Put the system into the canonical form. You should transform linear as well as nonlinear terms.

**Step 2** Find the equation for the center manifold and add it to the system in the following way:

\[
\begin{align*}
\frac{dx}{dt} &= f(x, y) \\
\frac{dy}{dt} &= \lambda_2 y + g(x, y) \\
 y &= h^c(x)
\end{align*}
\]

or

\[
\begin{align*}
\frac{dx}{dt} &= \lambda_1 x + f(x, y) \\
\frac{dy}{dt} &= g(x, y) \\
 x &= h^c(y)
\end{align*}
\]

(16.1)

**Step 3** Solve the system using Taylor expansions, and find the Taylor expansion for \( y = h^c(x) \) or \( x = h^c(y) \).

**Step 4** Find the flow on the center manifold as:

\[
\frac{dx}{dt} = f(x, h^c(x)) \quad \text{or} \quad \frac{dy}{dt} = g(h^c(y), y)
\]

Example

Study the following system around the point \((0, 0)\):

\[
\begin{align*}
\frac{dx}{dt} &= -x + y^2 \\
\frac{dy}{dt} &= xy^2 - y^5
\end{align*}
\]

(16.2)

Solution

1. **The canonical form.** The Jacobian of the system around the point \((0, 0)\) is:

\[
J = \begin{pmatrix} -1 & 0 \\ 0 & 0 \end{pmatrix}
\]

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Note that our system is already in the canonical form and that $\lambda_1 = -1$ and $\lambda_2 = 0$:

\[
\begin{aligned}
&\frac{dx}{dt} = \lambda_1 x + f(x,y) \\
&\frac{dy}{dt} = g(x,y)
\end{aligned}
\]

2. **The equation for the center manifold.** Let us find the third order approximation for the center manifold: $x = h^c(y) = ay^2 + by^3$. The equations for finding the center manifold will be:

\[
\begin{aligned}
&\frac{dx}{dt} = -x + y^2 \\
&\frac{dy}{dt} = xy^2 - y^5 \\
&x = h^c(y) = ay^2 + by^3
\end{aligned}
\]

3. **Finding the solution by using Taylor series.**

(a) Substitute for $x$ its value on the center manifold, i.e., $x = ay^2 + by^3$:

\[
\begin{aligned}
&\frac{d}{dt} (ay^2 + by^3) = -ay^2 - by^3 + y^2 \\
&\frac{dy}{dt} = (ay^2 + by^3) y^2 - y^5
\end{aligned}
\]

(b) Substitute $\frac{dy}{dt}$ from the second equation to the first equation, and get an algebraic equation:

\[
(2ay + 3by^2) \frac{dy}{dt} = (2ay + 3by^2)(ay^2 + y^5(b - 1)) = y^2(1 - a) - by^3
\]

(c) Collect terms with the same power of $y$:

\[
(2ay + 3by^2)(ay^2 + y^5(b - 1)) = y^2(1 - a) - by^3
\]

or

\[
y^73b(b - 1) + y^6(3ba + 2a(b - 1)) + 2a^2y^5 = y^2(1 - a) - by^3
\]

(d) Choose the unknown coefficients in such a way, that the coefficients at the lower powers are zeroes:

\[
\begin{aligned}
y^2(1 - a) & = 1 \\
by^3 & = 0
\end{aligned}
\]

(e) The center manifold is:

\[
x = ay^2 + by^3 = y^2
\]

4. **The flow on the center manifold** is given by:

\[
\begin{aligned}
\frac{dy}{dt} &= g(h^c(y),y) \\
\frac{dy}{dt} &= xy^2 - y^5 = y^4 - y^5 \approx y^4
\end{aligned}
\]

The flow is presented in Fig. 16.1, and the 2D phase portrait is shown in Fig. 16.2.

Figure 16.1: Flow on the center manifold $\frac{dy}{dt} = y^4$ of system (16.2).
Exercise

Find the flow of system (16.2) by using GRIND, for 
\(-0.3 < x < 0.3\) and 
\(-0.3 < y < 0.3\).

16.2 Center manifold using MAPLE

\[
\begin{align*}
\text{de1} := & \frac{\partial}{\partial t} x(t) = -x(t) + y(t)^2; \\
\text{de2} := & \frac{\partial}{\partial t} y(t) = y(t)^2 x(t) - y(t)^5;
\end{align*}
\]

Since we know that the center manifold for this system is \(x = f(y)\), we can specify the center manifold as:

\[
\text{cm} := x(t) = ay(t)^2 + by(t)^3;
\]

Then we load a library called “student”, to use the command ‘powsubs’:

\[
> \text{newde1} := \text{powsubs(cm,de1)};
\]
\[
\text{newde1} := 2 ay(t) \left( \frac{\partial}{\partial t} y(t) \right) + 3 b y(t)^2 \left( \frac{\partial}{\partial t} y(t) \right) = - ay(t)^2 - by(t)^3 + y(t)^2
\]

> newde2 := powsubs(cm, de2);
\[
\text{newde2} := \frac{\partial}{\partial t} y(t) = y(t)^2 ( ay(t)^2 + by(t)^3 ) - y(t)^5
\]

Now we need to substitute \( dy/dt \) from newde2 in newde1 (as we did in the analytical solution):

> newnewde1 := powsubs(newde2, newde1);
\[
\text{newnewde1} := 2 ay(t) (y(t)^2 ( ay(t)^2 + by(t)^3 ) - y(t)^5) + 3 b y(t)^2 ( y(t)^2 ( ay(t)^2 + by(t)^3 ) - y(t)^5 ) - ay(t)^2 - by(t)^3 + y(t)^2
\]

and we need to collect terms with equal degrees in \( y \):

> collect(newnewde1, y(t));
\[
3 b ( b - 1 ) y(t)^7 + ( 2 a ( b - 1 ) + 3 b a ) y(t)^6 + 2 a^2 y(t)^5 = - b y(t)^3 + (-a + 1) y(t)^2
\]

From the above equation we see that \( a = 1 \) and \( b = 0 \). Let us fix these values:

> a := 1;
\[
a := 1
\]

> b := 0;
\[
b := 0
\]

As MAPLE automatically substitutes these values in all expressions, we can find the center manifold by just typing cm:

> cm;
\[
x(t) = y(t)^2
\]

and the projection to the center manifold, by just typing newde2 (i.e., the equation after the substitution of the center manifold):

> newde2;
\[
\frac{\partial}{\partial t} y(t) = y(t)^4 - y(t)^5
\]
16.3 Exercises

1. Study the following system using pencil/paper and check the answer using MAPLE. Draw the phase portrait and check it using GRIND.

\[
\frac{dx}{dt} = xy, \quad \frac{dy}{dt} = -y + ax^2
\]

2. Study the following system using MAPLE.

\[
\begin{aligned}
\frac{dx}{dt} &= -y + xz \\
\frac{dy}{dt} &= x + yz \\
\frac{dz}{dt} &= -z - x^2 - y^2 + z^2
\end{aligned}
\]

HINTS:

(a) The normal form for \( \lambda = \alpha \pm i \beta \) is 
\[
\begin{pmatrix}
\alpha & -\beta \\
\beta & \alpha
\end{pmatrix}
\quad \text{or} \quad 
\begin{pmatrix}
\alpha & \beta \\
-\beta & \alpha
\end{pmatrix}
\]

(b) If \( W^c \) is \( z = f(x,y) \), then \( z \simeq ax^2 + bxy + cy^2 + \ldots \) (as a Taylor series of a function of 2 variables).

(c) To study the stability, you’ll have to compute the stability index, as we know from the tutorial on Hopf bifurcation.

(d) You can check the stability by using GRIND.

An example of a MAPLE session to solve exercise 2:

```maple
> de1:=diff(x(t),t)=-y(t)+x(t)*z(t);
> de2:=diff(y(t),t)=x(t)+y(t)*z(t);
> de3:=diff(z(t),t)=-z(t)-x(t)^2-y(t)^2+z(t)^2;

> cm:=z(t)=a*x(t)^2+b*x(t)*y(t)+c*y(t)^2;

> with(student):
> newde1:=powsubs(cm,de1);
> newde2:=powsubs(cm,de2);
> newde3:=powsubs(cm,de3);
```

\[
\begin{aligned}
\text{newde1} &= \frac{\partial}{\partial t} x(t) = -y(t) + x(t) (ax(t)^2 + bx(t)y(t) + cy(t)^2) \\
\text{newde2} &= \frac{\partial}{\partial t} y(t) = x(t) + y(t) (ax(t)^2 + bx(t)y(t) + cy(t)^2) \\
\text{newde3} &= 2ax(t) \frac{\partial}{\partial t} x(t) + b \left( \frac{\partial}{\partial t} x(t) \right) y(t) + bx(t) \left( \frac{\partial}{\partial t} y(t) \right) + 2cy(t) \left( \frac{\partial}{\partial t} y(t) \right) = -ax(t)^2 - bx(t)y(t) - cy(t)^2 - x(t)^2 - y(t)^2 + (ax(t)^2 + bx(t)y(t) + cy(t)^2)^2
\end{aligned}
\]
> nnewde3 := powsubs (newde1, newde3);

nnewde3 := 2ax(t) (−y(t) + x(t) %1) + b (−y(t) + x(t) %1) y(t) + bx(t) (∂x y(t))
+ 2cy(t) (∂y y(t)) = −ax(t)^2 − bx(t) y(t) − cy(t)^2 − x(t)^2 − y(t)^2 + %1^2
%1 := ax(t)^2 + bx(t) y(t) + cy(t)^2
  > nnewde3 := powsubs (nnewde2, nnewde3);

nnewde3 := 2ax(t) (−y(t) + x(t) %1) + b (−y(t) + x(t) %1) y(t) + bx(t) (x(t) + y(t) %1)
+ 2cy(t) (x(t) + y(t) %1) = −ax(t)^2 − bx(t) y(t) − cy(t)^2 − x(t)^2 − y(t)^2 + %1^2
%1 := ax(t)^2 + bx(t) y(t) + cy(t)^2
  > nnewde3 := expand (nnewde3);

nnewde3 := −2ax(t) y(t) + 2a^2 x(t)^4 + 4ax(t)^3 by(t) + 4ax(t)^2 cy(t)^2 − by(t)^2
+ 2b^2 y(t)^2 x(t)^2 + 4by(t)^3 x(t) c + bx(t)^2 + 2cy(t) x(t) + 2c^2 y(t)^4 = −ax(t)^2
− bx(t) y(t) − cy(t)^2 − x(t)^2 − y(t)^2 + ax(t)^2 + 2ax(t)^3 by(t) + 2ax(t)^2 cy(t)^2
+ b^2 y(t)^2 x(t)^2 + 2by(t)^3 x(t) c + c^2 y(t)^4 = 0
  > nnewde3 := lhs (nnewde3) − rhs (nnewde3) = 0;

nnewde3 := −2ax(t) y(t) + ax^2 x(t)^4 + 2ax(t)^3 by(t) + 2ax(t)^2 cy(t)^2 − by(t)^2
+ b^2 y(t)^2 x(t)^2 + 2by(t)^3 x(t) c + bx(t)^2 + 2cy(t) x(t) + c^2 y(t)^4 + ax(t)^2
+ bx(t) y(t) + cy(t)^2 + x(t)^2 + y(t)^2 = 0
  > nnewde3 := collect (nnewde3, [x(t), y(t)], distributed);

nnewde3 := 2ax(t)^3 by(t) + 2by(t)^3 x(t) c + (b^2 + 2ac) y(t)^2 x(t)^2
+ (−2a + 2c + b) y(t) x(t) + c^2 y(t)^4 + (−b + 1 + c) y(t)^2 + (a + b + 1) x(t)^2
+ a^2 x(t)^4 = 0
  > cl := {b+1+a=0,1+c−b=0,2*c−2*a+b=0};

cl := {−2a + 2c + b = 0, a + b + 1 = 0, −b + 1 + c = 0}
  > solve (cl, {a, b, c});

{b = 0, c = −1, a = −1}
  > a := −1;

  a := −1
  > b := 0;

  b := 0
  > c := −1;

  c := −1
  > cm;

z(t) = −x(t)^2 − y(t)^2
  > newde1;

∂x x(t) = −y(t) + x(t) (−x(t)^2 − y(t)^2)
  > newde2;

∂y y(t) = x(t) + y(t) (−x(t)^2 − y(t)^2)
EXTRAExercise

3. Study the following system using pencil and paper, MAPLE and GRIND. Find only the flow on the center manifold, not the center manifold itself.

\[
\frac{dx}{dt} = (x^2 + y^2 - 2)x, \quad \frac{dy}{dt} = -y^3 + x
\]
Chapter 17

1D maps using GRIND

17.1 Analysing a map in GRIND

To get a map in GRIND we use the following trick. We can integrate ODEs by using the Euler method. In the Euler method the derivative of a function is approximated using the following formula:

\[
\frac{dx}{dt} \approx \frac{x(t+h) - x(t)}{h}
\]

Therefore, if we integrate a differential equation \( \frac{dx}{dt} = f(x) \) by using the Euler method, we get:

\[
\frac{x(t+h) - x(t)}{h} = f(x(t))
\]

or:

\[
x(t+h) = x(t) + hf(x(t))
\]

and if \( h = 1 \):

\[
x(t+1) = x(t) + f(x(t)) \quad (17.1)
\]

Therefore, if we solve the differential equation

\[
\frac{dx}{dt} = f(x) - x
\]

while using the Euler method with the step \( h = 1 \), formula (17.1) becomes:

\[
x(t+1) = x(t) + (f(x) - x) = f(x(t))
\]

So we got a map:

\[
x_{t+1} = f(x_t)
\]
Conclusion

In order to study in GRIND the dynamics of the map \( x_{t+1} = f(x_t) \), we need to study the differential equation \( dx/dt = f(x) - x \), and to use the Euler integrator with a fixed time step of \( h = 1 \).

17.2 An example of map analysis in GRIND

Now we will do an example session in which we analyse the following map:

\[
x_{t+1} = b + \frac{a x_t}{1 + x_t^2},
\]

which has been studied by Bier and Bountis ([1984], Phys. Lett. A, 104, 239–244.).

To study this map in GRIND make the following file:

\[
\text{x' } = b + a \times x/(1.0 + x^2) - x;
\]

Note that the equation has to be entered as a differential equation. Thus the right-hand-side describes the increase of \( x \). Since the term \( b + a \times x/(1.0 + x^2) \) in fact describes the new value of \( x \), we subtract \( x \) from this term to get an equation in terms of increases and decreases. If we study this differential equation by Euler integration with a time step of one, the differential equation is identical to the original difference equation.

Suppose that you have called your file map, then start GRIND by typing 'grind map' to your operating system. Then this is what you get:

\[
\text{GRIND MAP}
\]

As soon as you get the string ‘GRIND model analysis’ GRIND is ready to read commands typed by you. In this tutorial we show the commands to be typed by you in capital letters. This is just to distinguish the things you type from the things GRIND replies.

Thus, first enter the following five lines:

\[
\text{OP MAP}
\]

The first line sets the OPTION MAP. The second line sets the FINISH. FIN 10 10 means that
you want to integrate for 10 steps having 10 samples of output. The last three lines define the x-axis of the phase space, the y-axis of the phase space, and the vertical axis of time plots.

Having set the GRIND environment, you can enter your parameter values and the initial condition for \( x \). Then use the RUN command to start the numerical integration. For example:

\[
a=11.5; \ b=0
\]

\[
x=1
\]

RUN

<table>
<thead>
<tr>
<th>Time</th>
<th>x</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.0000E+00</td>
<td>1.000</td>
</tr>
<tr>
<td>1.000</td>
<td>5.750</td>
</tr>
<tr>
<td>2.000</td>
<td>1.941</td>
</tr>
<tr>
<td>3.000</td>
<td>4.682</td>
</tr>
<tr>
<td>4.000</td>
<td>2.349</td>
</tr>
<tr>
<td>5.000</td>
<td>4.144</td>
</tr>
<tr>
<td>6.000</td>
<td>2.622</td>
</tr>
<tr>
<td>7.000</td>
<td>3.829</td>
</tr>
<tr>
<td>8.000</td>
<td>2.812</td>
</tr>
<tr>
<td>9.000</td>
<td>3.631</td>
</tr>
<tr>
<td>10.00</td>
<td>2.944</td>
</tr>
</tbody>
</table>

End of Euler

The system seems to be approaching an equilibrium.

The output of RUNs can be plotted with the TIMEPLOT command:

```
ti Opening X11 graphics
```

On your screen appears a zigzag line which is decreasing its amplitude.

Now let's take the last value attained by \( x \) as the new initial condition. Then use a Newton-Raphson iteration to attain the equilibrium from this initial condition:

```
keep
newton
Converged into:

<table>
<thead>
<tr>
<th>Population</th>
<th>State</th>
<th>Derivative</th>
</tr>
</thead>
<tbody>
<tr>
<td>x</td>
<td>3.24037</td>
<td>2.408296E-12</td>
</tr>
</tbody>
</table>
```

Let's continue this equilibrium attained by NEWTON in a bifurcation diagram. First ERASE your screen, and ask for a 2D plot. Then invoke the CONTINUE command. This starts at the point attained by the last NEWTON, and continues it in two directions.

```
er
2d
co
Done!
```

Done: 3 bifurcation(s) in b around -0.8017 -4.322 -4.825

On your screen appears a folded line. Along the line there are three points where the colour...
changes. This represents a change in stability of the fixed point. At the end CONTINUE reports the location of these three bifurcations.

Thus, between $-4.4 < b < -0.81$ there is no stable fixed point. Let's have a look at the dynamical behaviour in this region. A nice feature is to immediately make a bifurcation diagram. The BIFURCATE command has several options. The first is the axis which holds the parameter along which you want to bifurcate. The diagram starts at the current value of that parameter. The diagram ends at the parameter value provided by the second argument (i.e., $-5$ in the example below). To reduce the effects of transients when you make small steps along the parameter you may tell GRIND to wait before it starts plotting points. This is the third parameter (here 100 time steps). The fourth parameter is the number of samples of the parameter that you want to see. The last parameter is the number of points to be plotted for each parameter value. Thus,

```
bif x -5 100 100 10
```

Done!

gives you a nice bifurcation diagram with roughly $100 \times 10$ points. **HINT**: if the bifurcation diagram stops at some value of $b$ before $b = -5$, change $x$ to $x = 1$ and start BIFURCATE again.

Note that the meaning of BIFURCATE is different for differential equations, i.e., when OPTION MAP is not ON. When OPTION MAP is OFF BIFURCATE continues Poincaré sections.

### 17.3 Drawing the graph of a map using GRIND

The next trick is not so obvious. Our aim is to get a picture of the successive iterations on a graph, with the reflections on the $y = x$ line. It turns out that the following trick works here. To get the graph of the map $x_{t+1} = f(x_t)$, we need to study in GRIND the following system of differential equations:

\[
\begin{align*}
\frac{dx}{dt} &= y - x \\
\frac{dy}{dt} &= f(x) - y \\
\end{align*}
\]

(17.2)

while using the Euler integrator with fixed time step $h = 1$, and the initial conditions $x_0 = y_0$.

Why does this work? The first step is obvious. System (17.2) with Euler step $h = 1$ is equivalent to the following 2D map:

\[
\begin{align*}
x_{t+1} &= y_t \\
y_{t+1} &= f(x_t) \\
\end{align*}
\]

(17.3)

Second, if we start from the initial conditions at the diagonal $x_0 = y_0 = a$, we will get the following successive iterations of our map:

\[
\begin{align*}
x_0 &= a; \quad x_1 = a; \quad x_2 = f(a); \quad x_3 = f(a); \\
y_0 &= a; \quad y_1 = f(a); \quad y_2 = f(a); \quad y_3 = f(f(a)); \\
\end{align*}
\]
If we represent the successive coordinates of our iterations on a graph, we obtain the desired graph of the map (see Fig. 17.1).

![Diagram](image)

Figure 17.1: Scheme of the successive iterations of map (17.3).

Note that the nullclines of system (17.2) are:

\[
\begin{align*}
\frac{dx}{dt} &= 0 \quad \rightarrow \quad y = x \\
\frac{dy}{dt} &= 0 \quad \rightarrow \quad y = f(x)
\end{align*}
\]

Therefore we automatically get a graph of our map as well as the line \(y = x\) by using the \texttt{nu x y} command.

**NOTE:** The method works only for initial conditions on the line \(x = y\). If \(x \neq y\) the map diverges and does not correspond to our map anymore.

**Conclusion**

To study the dynamics of the map \(x_{t+1} = f(x_t)\) on the graph of the map we need to:

1. Put the following system into GRIND:

\[
\begin{align*}
\frac{dx}{dt} &= y - x \\
\frac{dy}{dt} &= f(x) - y
\end{align*}
\]

2. Setup initial conditions on the line \(x_0 = y_0\).

3. Use the Euler integrator with fixed time step \(h = 1\).

4. Type \texttt{nu x y} to display the graphs.

**NOTES:**

1. The map can become nonstable during the integration if the integration interval is too long. To avoid this, decrease the value of the first parameter in the \texttt{finish} option.

2. \texttt{op map} automatically sets up the Euler integration with step \(h = 1\).
Chapter 18

Bifurcations of 1D maps

18.1 GRIND

Analyse the following bifurcations by using GRIND:

1. The fold bifurcation.
   (a) Create a file fold:
       \[ x' = y - x; \]
       \[ y' = a + x + x^2 - y; \]
   and data file rfold:
       \[ \text{te x11} \]
       \[ \text{op trunc} \]
       \[ \text{op map} \]
       \[ a = -0.2 \]
       \[ \text{axis x x -1. 1.} \]
       \[ \text{axis y y -1. 1.} \]
       \[ \text{finish 20 20} \]
       \[ \text{option initial} \]
       \[ x = 0.3 \]
       \[ y = 0.3 \]
   (b) Type:
       \[ \text{grind fold} \]
       \[ \text{read rfold} \]
       \[ 2d \]
       \[ \text{nu x y} \]
       and run the program.
   (c) Try several other initial points,
       \[ \begin{align*}
       x &= -0.9 \\
       x &= 0.6
       \end{align*} \]
y=-0.9 \hspace{1cm} y=0.6

(NOTE: x must be equal to y.)

Which points are stable/nonstable?

(d) Change the parameter a=0.05, type e2n (to refresh the screen), and run the program again.

e) Set up:
\[ x=-0.9 \hspace{0.5cm} y=-0.9 \]

and run again.

(f) Finally, draw the bifurcation diagram.

2. Do the same for the pitchfork bifurcation:
\[ x_{t+1} = a \cdot x_t + x_t - x_t^3, \]

3. for the transcritical bifurcation:
\[ x_{t+1} = a \cdot x_t + x_t - x_t^2, \]

4. and for the flip bifurcation:
\[ x_{t+1} = -(1+a) \cdot x_t + x_t^3. \]

5. Show that in the double iterated map the flip bifurcation becomes a pitchfork bifurcation.
This can be achieved by modelling the double iterated map and studying its bifurcation changing parameter a.

HINT: If you want to display the orbit on an attractor, i.e., after some number of iterations, use “finish” with an even number of steps, and then “keep”, “erase” and “run”.

Example:
\[ \text{finish 50 50} \]
\[ \text{run} \]
\[ \text{keep} \]
\[ \text{e2n} \]
\[ \text{run} \]

18.2 Exercises

1. Consider the map:
\[ x_{n+1} = 7.86x_n - 23.31x_n^2 + 28.75x_n^3 - 13.3x_n^4 \]

(a) Find fixed points using MAPLE.
(b) Find the phase portrait using GRIND.

**HINT:** Try a lot of different values for \( x = y \) and watch to which attractor the system goes. (use the command `keep` if after running it is still not clear where the system is going and run again) Contrast the behavior you see to the behavior of ODE systems.

2. Consider the following system(s). Find the location of the equilibria using MAPLE, and compute the bifurcations diagrams using Content.

(a) \( x_{n+1} = 5x_n - x_n^2 - b \) As this is the first time we are going to use Content to study a map, you again will be provided with a sort of recipe of things to do. Pay attention to the differences in the procedure of studying ODE’s and maps.

In main window:
**Select, Class:** Iterated maps

**Select, System**

In new window:
**Actions, New**

In new window:
type name, OK

In new window:
coordinates: x
parameters: b

time:n

For ODE’s we usually use t to designate the continuous time, for maps we will use n to designate the discrete time (n designates the number of the timestep).

Select the first three derivatives symbolically.

Now we have to type the equation that describes our system. Remember that in Grind to describe the map \( x_{n+1} = f(x_n) \) we typed \( x' = f(x) - x \). This is **not** the way it has to be done in Content. In Content we describe our map as \( x' = f(x) \), so we do not work with differences, but instead let \( x' \) designate x at the next time step.

**OK**

The system is now being compiled.

When ready:

In main window:
**Type, Initial Point, Point**

**Type, Curve, Orbit**

This gives us a **Starter** window like for the ODE’s and a **Iterator** window (instead of the **Integrator** window we get for ODE’s).

**Window, Open, 2DGraphic**

In graphical window:
**Attributes, Current**

In new window:
abcissa: n
ordinate: x

**OK**
In graphical window:
range:
x-axis: 0..50
y-axis: -3..3
(enter)
In Iterator window:
Number of Iterations: 100
In Starter window:
Initial Point:
x=0.1
b=0.5
In graphical window:
Compute, Forward
This gives you the message: overflow exception
It turns out to be very hard to find an equilibrium here.
From the Maple results we know that if b=4 we have one equilibrium at x=2. If we put these values in the Starter window and press Compute, Forward, we stay at the same spot, so we are indeed in an equilibrium.

Now we are going to continue this equilibrium.
In main window:
Select, Initial Point
In new window:
select: O:Last Point
Automatically we get a new Starter window, the Iterator window is replaced by a Continuer window. In the main window, behind curve type it says fixed point. Behind point type it still says point, do not change this into fixed point!
In graphical window:
Attributes, Current
In new window:
abcissa: b
ordinate: x
In graphical window:
range:
x-axis: -8..8
y-axis: -8..8
In main window:
Options, Pause Buttons
In new window:
select enable pause buttons
In main window:
Options, Archive Filter
In new window:
put Maximum Number of untitled curves to 20.
(Do this step always before drawing a bifurcation diagram, otherwise using redraw diagram will only the last, or last few curves instead of all of them.)
In main window:
**Window, Open, Numeric**

In numeric window:
**Window, Layout**

In new window:
select multipliers, select all, OK

In the case of ODE’s we speak of **eigenvalues**, and they are represented by their real and imaginary part, in the case of maps we speak of **multipliers** and they are not only represented by their real and imaginary parts but also by their **modulus** and **argument**. Remember:

modulus: $|z|$

argument $\theta$

polar representation of $z$:

$$z = |z| \cdot e^{i\theta}$$

Remember that in the one dimensional case the value of the derivative tells you whether equilibrium is non-hyperbolic, stable or unstable. This derivative corresponds to the real part of the single multiplier you have in the one dimensional case.

In **Starter** window:
activate b to make clear to Content this is the parameter along which we wish to continue the equilibrium.

In graphical window:
**Compute, Forward/Backward resume/abort**

Because of the shape of the equilibrium line and the equations for the equilibria you could have guessed that a fold bifurcation has taken place. Content however fails to recognize the bifurcation point as a LP (limit point). To find out about stability, watch the multiplier. If computations are to fast, press **Clear**, then in the main window, via **Options, Pause Mode** select at each point, so computations go on point by point. Then recompute the line.

Content however does stop computing at a point it designates by **PD**. PD stands for period doubling, so this is the point where the flip or period doubling bifurcation occurs. Doubleclick the PD point.

We get a new **Starter** and **Continuer** window.

We see a new flip bifurcation occurring, designated by two PD points,
which can be studied in a similar way.

**EXTRA**

(a) \( x_{n+1} = x_n^2 + (a - 2)x_n - 2a^2 + 3a \)

(b) \( x_{n+1} = x_n^3 - x_n^2 + (1 - b)x_n + b \)

### 18.3 EXTRA Exercises

Consider the following systems.

Find the location of equilibria using MAPLE and compute the bifurcation diagrams using Con-tent.

1. \( x_{n+1} = x_n + (\lambda + 2)^2 + x_n^2 - 1 \)
2. \( x_{n+1} = x_n + (\lambda x_n - x_n^3) \ast ((\lambda + 2)^2 + x_n^2 - 1) \)
3. \( x_{n+1} = x_n + 0.1 + 2\lambda^2 + 3\lambda^2 x_n - x_n^3 \)
Chapter 19

Flip bifurcation normalisation using MAPLE

Here we show how it is possible to obtain the normal form of the flip bifurcation by using MAPLE.

Our map is:

\[
> x[t+1] := (-1 - \mu) x[t] + A x[t]^2 + B x[t]^3;
\]

\[x_{t+1} := (-1 - \mu) x_t + A x_t^2 + B x_t^3\]

The direct transformation is:

\[
> x = y + \delta y^2;
\]

\[x = y + \delta y^2\]

The inverse transformation is:

\[
> Y = X - \delta X^2 + 2 \delta^2 X^3;
\]

\[Y = X - \delta X^2 + 2 \delta^2 X^3\]

First find \(Y[t+1]\) using the inverse transformation:

\[
> Y[t+1] := X[t+1] - \delta X[t+1]^2 + 2 \delta^2 X[t+1]^3;
\]

\[Y_{t+1} := X_{t+1} - \delta X_{t+1}^2 + 2 \delta^2 X_{t+1}^3\]
Now find $X[t+1]$ from our original map:

\[ X_{t+1} := (-1 - \mu) x_t + A x_t^2 + B x_t^3 \]

Next, let us drop all terms with power above $x^3$ and group them:

\[ Y_{t+1} := \text{rem}(Y[t+1], x[t]^4, x[t]) \]

Now express $x[t]$ in terms of $Y[t]$, by using the direct change of variables:

\[ x_t := Y_t + \delta Y_t^2 \]

The new map becomes:

\[ Y_{t+1} := (B - 6 \delta^2 \mu + 2 \delta \mu A - 6 \delta^2 \mu^2 - 2 \delta^2 - 2 \delta^2 \mu^3 + 2 \delta A) x_t^3 \]

We also drop all terms that are higher than the 3rd power:

\[ Y_{t+1} := \text{rem}(Y[t+1], Y[t]^4, Y[t]) \]

Let us find the coefficient at $Y^2$:
coef2 := coeff(Y[t+1], Y[t]^2);

\[ coef2 := A - 2\delta - \delta\mu^2 - 3\delta\mu \]

and the value of \(\delta\):

\[ \delta := \frac{A}{2 + \mu^2 + 3\mu} \]

The normalisation is done; now compute the new coefficient \(B\) at \(\mu = 0\):

\[ \mu := 0 \]

\[ \delta := \frac{1}{2}A \]

\[ (A^2 + B)Y_t^3 - Y_t \]
Chapter 20

Bifurcations of the logistic map using GRIND and MAPLE

Study the map:

\[ x_{t+1} = ax_t(1-x_t) \]

**GRIND**

Answer the following questions. **NOTE**: If you fail to write your own GRIND programs, examples are given on the next page.

1. Write a program for GRIND for the logistic map (without reflection). Compute and display timeplots for the following values of the parameter \( a \): 1.8; 2.8; 3.; 3.2; 3.52; 3.55; 3.567; and 3.891. Which attractors do we have in each case? (Do not study it, just guess.)

2. Write a GRIND program for the logistic map (with reflection y=x). Do not delete the program without reflection, as we will use it again later.

3. Study the map at the same parameter values: \( a=1.8; 2.8; 3.; 3.2; 3.52; 3.55; 3.567; \) and 3.891. Where possible, find attractors for the listed parameter values. Redraw them schematically from the screen.

4. Study the system at \( a = 3.839 \). What is the attractor here?

5. Write a program for the double iterated logistic map.

6. Study the appearance of a period 2 orbit around \( a = 3 \).

7. Write a program for the 4 times iterated logistic map.

8. Study the appearance of a period 4 orbit around \( a = 3.5 \ldots \)
9. Go back to the GRIND program for the logistic map without reflection. Find a bifurcation diagram using the command **bifurcate**.

**Example files**

(With reflection)

**lomap:**

\[
\begin{align*}
x' &= y - x; \\
y' &= a * x * (1 - x) - y;
\end{align*}
\]

**rlomap:**

\[
\begin{align*}
t & x11 \\
op & map \\
a & = 1.5 \\
axis & x x 0. 1.5 \\
axis & y y 0. 1.5 \\
finish & 10 10 \\
option & initial \\
x & = 0.5 \\
y & = 0.5
\end{align*}
\]

**lomap2:**

\[
\begin{align*}
zz &= a * x * (1 - x); \\
x' &= y - x; \\
y' &= a * zz * (1 - zz) - y;
\end{align*}
\]

**lomap4:**

\[
\begin{align*}
zz &= a * x * (1 - x); \\
yy &= a * zz * (1 - zz); \\
ww &= a * yy * (1 - yy); \\
x' &= y - x; \\
y' &= a * ww * (1 - ww) - y;
\end{align*}
\]

**MAPLE**

We know that the fixed point of the doubling operator is:

\[
\phi \approx 1. - 1.52763x^2 + 0.104814x^4 + \cdots \quad \delta = 2.50290
\]

1. By using MAPLE, find: \( \phi_2 = T\phi \equiv -\delta\phi(-\frac{x}{\delta}) \)

2. Compare the coefficient at \( x^2 \) and \( x^4 \) in \( \phi \) and \( \phi_2 \).

3. To see the difference between \( \phi \) and \( \phi_2 \), plot both in the same graph on the interval \(-1.5 < x < 1.5\).
Chapter 21

General problems on 1D bifurcations for maps

Exercise 1

Consider the following model for a population that is harvested with a “constant yield”:

\[ N_{t+1} = a \cdot N_t \left( 1 - \frac{N_t}{K} \right) - \gamma \]

1. Find the maximal possible yield \( \gamma_{\text{max}} \). Which bifurcation occurs if \( \gamma = \gamma_{\text{max}} \)? Draw the bifurcation diagram.

2. Is the system stable if the yield is close to its maximal value?

3. Can the harvesting make the dynamics of population more stable? Confirm your answer by computing a bifurcation diagram using GRIND.

Exercise 2

We could define that if the population size drops to a value \( N_t < 1 \), the species becomes extinct. Find the conditions for a possible extinction of the population in the following model:

\[ N_{t+1} = N_t \exp \left( a \left( 1 - \frac{N_t}{K} \right) \right) \]

Which population is more stable, one with a low value, or one with a higher value of the reproduction parameter \( a \)?
Exercise 3

Consider the following model for a population with a so called “Allee effect”, i.e., when the population becomes very small it is difficult to find a partner to mate with:

\[ N_{t+1} = a \frac{N_t^2}{b^2 + N_t^2} \]

1. Explain why this model indeed describes an “Allee effect”.
2. What is the meaning of the parameters \( a \) and \( b \)?
3. Find equilibria and determine their stability.
4. At which parameter values can the population be driven to extinction?

Exercise 4

It has been suggested that a means of controlling insect numbers is to introduce and maintain a number of sterile insects in the population. The following model describes that a fraction of the mating partners is sterile:

\[ N_{t+1} = b \frac{N_t}{c + N_t S/N_{t+S}} \]

where \( S \) is the number of sterile insects.

1. Explain why this model describes the growth of a population with sterile insects.
2. Show that this model can be rewritten as:

\[ N_{t+1} = \frac{aN_t^2}{\frac{a-1}{M}N_t^2 + N_t + S}; \quad a > 1 \]

where \( a \) is the maximum offspring per insect, and \( M \) the carrying capacity of the insect population when no sterile insects are around.
3. Find the equilibria of this model and their stability.
4. Find the critical value \( S_c \) of the sterile population, such that if \( S > S_c \) the insect population is eradicated. Which bifurcation occurs at \( S = S_c \)?
Chapter 22

One parameter analysis of the Soberon model

In 1981 Soberon et al. proposed a model of interaction between a plant population $p$ and its animal pollinator population $a$ ([1981], *J. theor. Biol.*, 91, 363–378.). If we fix several parameters of Soberon’s model we can obtain the following system:

$$\begin{align*}
\frac{da}{dt} &= a \left( k - a + \frac{p}{1+p} \right) \quad a \geq 0 \\
\frac{dp}{dt} &= -\frac{p}{2} + \frac{ap}{1+p} \quad p \geq 0, k \geq 0
\end{align*}$$

(22.1)

Study this system analytically as well as by using MAPLE, Content and GRIND, and give a biological interpretation of the results obtained.

We ask you to write a short report upon this tutorial, which contains the answers to all questions, your final bifurcation diagram, and phase portraits of all regions of different behaviour.

1. Study the system analytically and using MAPLE:

   (a) Find equilibria. How many non-trivial equilibria can we have in this system?

   (b) At which value of $k$ does the number of non-trivial equilibria bifurcate from 0 to 2?

   (c) Compute the Jacobian of the system, and find its value at the bifurcation point.

   (d) Compute the eigen values; which bifurcation do we have here?

2. Study the system using Content: After you have entered the system in Content, press in the main window: Archive Filter, in the new window put maximum number of untitled curves to 20. This serves the following purpose: You will get a series of different equilibrium lines. If you want to redraw these lines by the Redraw Diagram command (under Window in the graphical window) it will redraw only the last one or two curves you have drawn if the maximum number of untitled curves is not put to a higher value.
(a) Numerically find a non-trivial equilibrium at \( k = 1 \). As our system has two variables it is necessary, if you have found an equilibrium for which the variable you are now plotting is not zero, to check whether for the specific equilibrium the other variable is also not zero.

(b) Now put \( k \) along the abscissa, \( a \) along the ordinate and continue this equilibrium forwards and backwards along parameter \( k \), to find bifurcations. In the main window press **Options, Pause mode**, in the new window select at each point. This means computations will proceed in a step by step manner. In this way it is possible to see what happens to the eigenvalues of our system and hence what kind of equilibria and bifurcations take place.

(c) Draw this line schematically on paper, and show the stability of the equilibrium by using either a solid or a dashed line.

(d) Continue the second line of equilibria. For that, select the point designated BP by doubleclicking it.

(e) Find another bifurcation on this second line (at small \( k \)). What is the type of this bifurcation? Which equilibria cross here?

(f) Find the stability as well as type of the equilibria along this line. Add it to your paper graph.

(g) Find the third line of equilibria, and continue it. Find the stability, and add it to your bifurcation diagram.

(h) Now put \( k \) along the abscissa and \( p \) along the ordinate and use the **Redraw Diagram** command to plot the same lines of equilibria for the second variable. Why do we have only two lines here? **HINT:** Look at the equilibria you found for the system.

3. Study the system using GRIND:

   (a) Use GRIND to draw phase portraits for each of the parameter regions for which we found different behaviour. These phase portraits must show nullclines, the vector field, all equilibria, nonstable and stable manifolds for saddle points, and the fate of the manifolds.

   (b) Show attractors, find their basins of attraction, and explain the behaviour of the system in the different parameter regions.

   (c) Use GRIND to draw the nullclines of the system just before and after the bifurcation point at \( k = 0.41 \). Why is this bifurcation called tangent?

4. Interpretation of the results:

   (a) Explain the biological meaning of each term in system (22.1).

   (b) The authors use the parameter \( k \) as a measure of the degree of specialisation of a pollinator upon the plant. Explain why.

   (c) Explain the changes in a plant-pollinator system under the change of the degree of specialisation \( k \). Which zone is “dangerous” for the system, and which zone is “fatal”? 

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Chapter 23

Neimark-Sacker bifurcation

23.1 Neimark-Sacker bifurcation in the delayed logistic map

Consider the delayed logistic map:

\[ y_{n+1} \rightarrow \lambda y_n(1 - y_{n-1}) \]  

(23.1)

1. Write this 2nd order map as a planar map of the 1st order.

2. Find the fixed points of this map.

3. Input this map into GRIND. (Just as a usual 2D map without any reflections!)

4. Reproduce Fig. 23.1.

**HINT:** Use, in GRIND, option points to plot only the dots, not the connecting lines.

5. Reproduce the left of Fig. 23.2.

6. Rescale your window and reproduce the right of Fig. 23.2.

7. Increase parameter \( \lambda \) to values larger than 2, and find a region of phase locking. What is the period of this orbit?

**HINTS:**

(a) Do not display the first points of the orbit; use the trick with `keep`, `erase`, `run`.

(b) Use the `bifurcate` command to study the map.

(c) Don’t use values of \( \lambda > 2.27 \), since \( y \) will go to \(-\infty\) and therefore GRIND will crash.
Figure 23.1: Supercritical Neimark-Sacker bifurcation in the delayed logistic map (23.1) for $\lambda = 1.990, 2.000, 2.003,$ and 2.010.

Figure 23.2: Far away from the bifurcation value, at $\lambda = 2.265$, the invariant “circle” of the delayed logistic map (23.1) folds onto itself and becomes non-smooth. For emphasis, a piece of the invariant curve near its tip is enlarged.
23.2 Neimark-Sacker bifurcation in a discrete predator prey model

Consider the following planar map, which depends on the two parameters \( a \) and \( b \):

\[
\begin{align*}
x_1' &= a \cdot x_1 \cdot (1 - x_1) - x_1 \cdot x_2 \\
x_2' &= (1/b) \cdot x_1 \cdot x_2
\end{align*}
\]

with \( a > 0 \) and \( b > 0 \).

This map describes a discrete model of interactions between two species: a prey, \( x_1 \), and a predator, \( x_2 \). In the absence of the predator, the prey population is governed by the logistic equation. Furthermore, it is assumed that each predator consumes a number of prey proportional to the abundance of the prey. For the growth rate of the predator it is assumed that the number of offspring produced by each predator is proportional to the number of preys it kills. For further information on this model see (Maynard Smith, J. [1968], Mathematical Ideas in Biology., CUP, NY.)

1. Find the non-trivial equilibrium.
2. For which values of \( a \) and \( b \) can we expect a Neimark-Sacker bifurcation for the non-trivial equilibrium?
3. Study the system using Content, and find the line of Neimark-Sacker bifurcation on the plane of the two parameters \( a \) and \( b \). Compare it to the analytical prediction.

**HINT:** Proceed as normal: find equilibrium, continue it and find bifurcation points. Once you have found the Neimark-Sacker bifurcation point, select it by doubleclicking it. In the main window, behind point it now says Neimark-Sacker and behind curve it says Neimark-Sacker (standard). This means that Content default want to continue the Neimark-Sacker bifurcation in a two parameter plane.

4. Study the system using GRIND at \( b=0.31 \), and vary \( a \) from 2.0 to 3.7. Observe the birth, evolution, and breakdown of an attracting invariant closed curve.

**HINT:** Use the option points.

23.3 Nicholson-Bailey model

One of the most famous discrete time models for host-parasitoid interaction can be written as follows:

\[
\begin{align*}
N_{t+1} &= r \cdot N_t \cdot e^{-a \cdot P_t} \quad b, a > 0 \\
P_{t+1} &= b \cdot N_t \cdot (1 - e^{-a \cdot P_t}) \quad r > 1
\end{align*}
\]
1. Maximally reduce the number of parameters.

2. Find the non-trivial equilibrium and study its stability (use MAPLE or pencil/paper). Describe the dynamics of the system.

3. **ODE vs. maps.** Write a continuous time model on the basis of the Nicholson-Bailey map, and study its dynamics. Compare the dynamics of the ODE and the map.

Write a map which has the following property: under the change of a parameter the map changes from the original map representation of the Nicholson-Bailey model into a map with dynamics indistinguishable from the ODE representation of the Nicholson-Bailey model.

4. Which bifurcation occurs under the change of this parameter?

5. Explain how the dynamics of the Nicholson-Bailey map emerges from the dynamics of the ODE.

**EXTRA** One of modifications of the Nicholson-Bailey model is introduction of a density dependent growth of the host:

\[
\begin{align*}
N_{t+1} &= N_t \cdot \lambda(N_t) e^{-a P_t} \\
P_{t+1} &= b \cdot N_t \cdot (1 - e^{-a P_t})
\end{align*}
\]

where \( \lambda(N_t) = \exp r (1 - N_t / K) \)

6. Maximally reduce the number of parameters.

7. Find, using Content, the region of parameters where the equilibrium is stable. Due to which bifurcation does the equilibrium loose its stability?
Chapter 24

Maps on a circle

24.1 Maps on a circle using Content

Use Content to study the shift map and the standard circular map.

Exercises

1. Study the shift map:

\[ x' = x + \alpha \pmod{1} \]

Display this map on a circle with radius 1 and show its behaviour at \( \alpha = 0.5, 0.25, 0.333, \) etc., and at “irrational” \( \alpha \), i.e., values of \( \alpha \) which are not a simple fraction.

How to do this in Content?

In main window:
Select, Class, Iterated maps
Select, System
In new window:
Action, New
shiftmap, OK
In new window:
coordinates: z
parameters: a
time: n
Do not change compute derivatives to symbolically, let it stay at numerically.

Type for the equation that describes your system:

\[ z' = a + z - \text{floor}(a+z); \]

The last part: floor(a+z) is a way to do (mod 1) in Content.

OK

As we want to display this map on a circle with radius one, we need
some extra variables.
In main window:
Select, Userfunctions
In new window:
label: p
name: x
Add
Behind Value type instead of the ? $\cos(2\cdot \pi \cdot z)$, which means $\cos(2\Pi z)$
Again:
label: q
name: y
Add
Behind Value type instead of the ? $\sin(2\cdot \pi \cdot z)$, which means $\sin(2\Pi z)$
OK
In main window:
Type, Initial Point, Point
Type, Curve, Orbit
Open, 2dGraphics
In graphical window:
put x and y along the axis.
take both ranges from -1 to 1.
Attributes, Current
In new window:
In the section Set Attributes, select Paths
In the section Join, select no
Now content no longer displays lines, only points.
(To get lines again: select Paths, select solid.)
OK
In Starter window:
In section User defined functions:
put both x and y from ignore to monitor.
In section Initial point, put n and z to zero and choose a value for a.

2. Study the standard circular map:

$$x' = x + \omega + \frac{\varepsilon}{2\pi} \sin(2\pi x) \pmod{1}$$

Our plan is to find “wedges” of phase locking in the $\omega, \varepsilon$ plane for rotation numbers 0, 1/2 and 1/3. As you should know from the chapter on maps on a circle the boundaries of these “wedges” are formed by lines of fold bifurcations. Check whether you understand why it is a fold bifurcation that occurs.
(HINT: the standard circular map equals the shift map if $\varepsilon$ equals zero, if $\varepsilon$ does not equal zero an extra sinus function is added to the simple shift map.)
This means that our job will be to find equilibria, continue these equilibria to find fold bifurcations and then to continue these fold bifurcations to find the boundaries of the wedges.
A rotation number \( p/q \) means that in one timestep you travel \( p/q \) part of the unit circle. Supposing that \( p \) and \( q \) do not have a common factor, it means that our map has a periodicity of \( q \).

After \( q \) timesteps you are back where you started and you have a period \( q \) orbit consisting of \( q \) points. If you have a period \( q \) orbit consisting of \( q \) points, these \( q \) points will be equilibria on the \( q \) times iterated map.

As we have a map on a circle, the presence of a stable point means there must also be an unstable point and the presence of a stable period \( q \) orbit means there is also an unstable period \( q \) orbit, which points are in between the points of the stable period \( q \) orbit.

**HINTS:** If you want to establish the boundaries for the “wedge” corresponding to rotation number \( p/q \) keep the following in mind:

(a) Only look at values for \( \omega \) and \( \varepsilon \) between zero and one.
(b) If \( \varepsilon \) equals zero you get the ordinary shift map. In the shift map to get rotation number \( p/q \), you simply put \( \omega \) to \( p/q \). So here you have to take \( \omega \) close to \( p/q \).
(c) As the “wedges” are broader for larger values of \( \varepsilon \) and the wedges start to cross for values of \( \varepsilon \) bigger than one, always start searching at values for \( \varepsilon \) smaller than but close to one.
(d) If the rotation number \( p/q \) is not an integer but is a rational number, you do not have a stable and unstable equilibrium but instead have a stable and unstable period \( q \) orbit. These points can be found as equilibria of the \( q \) times iterated map. To get the \( q \) times iterated map, put in the **Starter** window **Superposition** to \( q \).
(e) The number of fold bifurcations you see occurring is always a multiple of two, as two equilibria (one stable, one unstable) disappear via one and appear via the other fold bifurcation (via which fold appearance and disappearance occur depends on in which directions your parameters change). If you continue both fold bifurcations from such a pair, you will get both sides of a “wedge”.
(f) As you have to select two fold bifurcations from one line of equilibria to continue them and as you want to draw all wedges in one diagram it is a good idea to save your lines of equilibria and the sides of your wedges.

How to do this in Content: Once you have drawn a line, in the main window press **Select, Curve**. In new window press **Actions, Rename**, then give your curve a new name, press **OK** and press **Cancel**. Note that the curves have a “+” and a “-” part which are respectively computed by the **Compute, Forward** and **Compute, Backward** commands. To save you complete curve, you have to do the above for both parts of the curve.

(g) Once you have selected a fold bifurcation point, it automatically says Limit Point behind point type and curve type. In the **Starter** window in the section **Monitor singularities** is says yes behind Cusp. It turns out that in this particular case, Content has trouble with monitoring the test functions that are needed to see whether a Cusp bifurcation (a type of bifurcation we will encounter later on in the course) will occur. To avoid trouble change this yes in a no.

(h) To draw all “wedges” in one diagram, select them by **Select, Curve** one by one, and then use **Window, Redraw Curve** in the **main** window, instead of in the graphical window. (This is to make sure that the popup menu’s do not destroy part of your diagram.)
24.2 EXTRA Study of the standard circular map using MAPLE

Study the standard circular map using MAPLE.
To setup this map you could use the following functions of MAPLE:

Function \texttt{trunc} – truncate a number to the next nearest integer towards 0.
Function \texttt{round} – round a number to the nearest integer.
Function \texttt{frac} – fractional part of a number.
Function \texttt{floor} – greatest integer less than or equal to a number.
Function \texttt{ceil} – smallest integer greater than or equal to a number.

It is also convenient to use procedures to set up computations.

A simple example of a procedure is:

\begin{verbatim}
#proc(x) defines the beginning of a procedure to be carried out on
#end defines the end of a procedure
fr:=proc(x) x*x end;
fr(2);
\end{verbatim}

It can also be convenient to use the loop operator:

\begin{verbatim}
cubesum:=proc(n)
    local s,i;
    s:=0;
    for i from 1 to n do
        s:=s+i*i;
    od;
    s
end;
\end{verbatim}

cubesum := proc(n) local s, i; s := 0; for i from 0 to n do s := s + i^2 end do; s end proc
>
cubesum(10);
>
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You can also use the if operator. In case of questions use help: ?if or ?for, etc.

**Exercise**

1. Write a procedure for finding the rotation number of the standard circular map as a function of the parameter $\omega$. If you don’t manage to write one, use the example below.

2. Plot the graph using the commands:

   ```
   > plot('rotnr(w)',w=0..1,numpoints=100,style=point);
   > plot('rotnr(w)',w=0.405..0.415,numpoints=100,style=point);
   > plot('rotnr(w)',w=-0.7..0.7,numpoints=100,style=point);
   ```

   where rotnr(w) is a procedure for finding the rotation number, and $w$ gives the value of $\omega$. Compare the graphs.

3. Plot the first of these graphs for several values of $\epsilon$. What changes if you lower the value of $\epsilon$?

We want to compute the rotation number of the standard circular map as a function of the parameter omega, for a given value of the parameter epsilon. For simplicity we use $w$ to designate omega and $e$ to designate epsilon. The first (sub)procedure is to compute $x \pmod{1}$:

```
> fr:=proc(x) x-floor(x) end;
fr := proc(x) x-floor(x) end proc
```

As we need the value of Pi we use a variable pi which is approximately equal to $\pi$:

```
> pi:=evalf[40](Pi);
pi := 3.141592653589793238462643383279502884197
```

Now we write a procedure which computes the rotation number:

```
> rotnr:=proc(w)
> #local variables
```
local result,i,y,sum,x,z;
#initialisation of variables
x:=0;
sum:=0;
#now we are going to iterate the variable x of our standard circular map:
for i from 1 to nrofiterations do
  #first we compute the shift and store this value in z:
  z:=w+0.5*e*(sin(2*pi*x))/pi;
  #now we compute the new value of x, but store it in y
  y:=fr(x+z);
  if i>(nrofiterations/2) then
    sum:=sum+z;
  fi;
  #now we give the new value of x, stored in y, to x
  x:=y;
#end of 'for' loop
od;
#computation of average shift
result:=2*sum/nrofiterations;
#returnvalue of procedure
result
end;

Our goal was to compute the rotationnumber of this map. The rotation number gives you the part of the unitcircle you travel during one iteration. You can approximate the rotationnumber by computing the average shift along the unitcircle of a lot of iterations. To get a better approximation we start taking the average of the shift we get when iterating after we are halfway the number of iterations we are going to do. This is because if you do not start iterating at one of the points belonging to a certain periodicity orbit you have to converge towards one of these points. In the phase that the system still is converging the shifts will be much unlike the rotationnumber you are finally going to approach and hence will disturbe the average a lot. After half of the iterations the system is assumed to have approached one of these points belonging to a periodic orbit.
rotnr := proc(w)
local result, i, y, sum, x, z;
x := 0;
sum := 0;
for i to nrofiterations do
    z := w + .5 * e * sin(2 * π * x) / π;
y := fr(x + z);
    if 1/2 * nrofiterations < i then sum := sum + z end if;
x := y
end do;
result := 2 * sum / nrofiterations;
result
end proc

nrofiterations := 1000;
e := 0.9
rotnr(0.5);

This procedure is somewhat long, but it works.
24.3 EXTRA Analytical study of maps on a circle

Study the standard map:

\[ x_{t+1} = x_t + \omega + \frac{\varepsilon}{2\pi} \sin(2\pi x_t) \]

Approximate the shape of the wedge which starts at \( \omega = 0.5 \). To find this approximation we assume that \( \varepsilon \ll 1 \); as well as that \( \omega = 0.5 + a \), with \( a = O(\varepsilon^2) \).

1. We know that at \( \omega = 0.5 \) a wedge starts with a phase-locked rotation number 0.5, i.e., this is the wedge which contains the period-2 cycles. In order to find fixed points we therefore have to look at the double iterated map:

\[ x_{t+2} = x_t + 2\omega + \frac{\varepsilon}{2\pi} \sin(2\pi x_t) + \frac{\varepsilon}{2\pi} \sin(2\pi x_t + 2\pi \omega + \varepsilon \sin(2\pi x_t)) \]

Using the assumptions \( \varepsilon \ll 1 \), and \( \omega = 0.5 + a \) with \( a = O(\varepsilon^2) \), this can be simplified into:

\[ x_{t+2} = 2a - \frac{\varepsilon^2}{4\pi} \sin(4\pi x_t) \]

Derive this simplified form using the above assumptions as well as the following rules:

\[
\begin{align*}
\sin(\alpha + \beta) &= \sin(\alpha)\cos(\beta) + \cos(\alpha)\sin(\beta) \\
\sin(\alpha + \pi) &= -\sin(\alpha) \\
\cos(\alpha + \pi) &= -\cos(\alpha) \\
\sin(-\alpha) &= -\sin(\alpha) \\
\cos(-\alpha) &= \cos(\alpha) \\
\sin(2\alpha) &= 2\sin(\alpha)\cos(\alpha)
\end{align*}
\]

Also use the fact that when \( \alpha \) is small, \( \sin(\alpha) \) and \( \cos(\alpha) \) can be replaced by a Maclaurin series. Cut off the series at \( O(\alpha^2) \).

2. Find fixed points of the simplified map.

3. For which values of \( \omega \) and \( \varepsilon \) do fixed points exist?

4. Find the bifurcation line and draw the shape of the wedge.

5. What is the width of the wedge at \( \varepsilon = 0.5, \varepsilon = 0.9, \varepsilon = 0.01? \)

6. Compare those values with numerically obtained ones.
Chapter 25

General study of several ecological models

Exercise 1

Consider an ecological model for two competing species:

\[
\frac{dx}{dt} = a_1 x - b_1 xy - c_1 x^2 \quad x, a_1, b_1, c_1 \geq 0
\]
\[
\frac{dy}{dt} = a_2 y - b_2 xy - c_2 y^2 \quad y, a_2, b_2, c_2 \geq 0
\]

1. Give a biological interpretation for each parameter.

2. Change variables to reduce the number of parameters.

3. Find and study all qualitatively distinct possibilities. Draw a phase portrait for each possibility.

4. Analytically determine the parameter range for each possibility.

5. Which bifurcations are possible in this system? At which parameter values?

6. Give a biological interpretation for each type of behaviour.

Exercise 2

Answer the same questions for the following predator-prey model with competition:

\[
\frac{dx}{dt} = a_1 x - b_1 xy - c_1 x^2 \quad x, a_1, b_1, c_1 \geq 0
\]
\[
\frac{dy}{dt} = -a_2 y + b_2 xy - c_2 y^2 \quad y, a_2, b_2, c_2 \geq 0
\] (25.1)
EXTRA Exercise 3

Study model (25.1) at $c_1 = c_2 = 0$:

1. Draw the phase portrait.
2. Analytically estimate the period of the oscillations.
3. Find the period of the oscillations numerically.
4. Compare the analytical and numerical results.
Chapter 26

One parameter analysis of predator prey systems

Exercise 1

Consider a system:

\[
\begin{align*}
\frac{dx}{dt} &= x \left( 1 - \frac{x}{K} \right) - \frac{2xy}{1+x} \\
\frac{dy}{dt} &= -y + \frac{2xy}{1+x}
\end{align*}
\] (26.1)

1. Analytically find all equilibria of this system.

2. Using Content, continue the non-trivial equilibrium along parameter \( K \), and find bifurcations.

3. Using Content, find a limit cycle and continue it along parameter \( K \).

4. Draw the bifurcation diagram; how many regions of different behaviour do we have here?

5. Use GRIND to answer the following questions:
   
   (a) Draw phase portraits in each region.
   (b) Show attractors, and find their basins of attraction.
   (c) Explain the behaviour of the system in the different regions.

6. What is the fate of the limit cycle in this system?

7. Give a biological interpretation of the results obtained. Demonstrate the paradox of enrichment.
Exercise 2

1. Answer the same questions for a system with a Holling type-III response:

\[
\begin{align*}
\frac{dx}{dt} &= x \left(1 - \frac{x}{K}\right) - \frac{2x^2y}{1+x^2} \\
\frac{dy}{dt} &= -y + \frac{2x^2y}{1+x^2}
\end{align*}
\] (26.2)

2. Compare the behaviour of systems (26.1) and (26.2). Which system is biologically more stable?

Exercise 3

Consider the models (26.1) and (26.2) which depend on 2 parameters, \(K\) and \(a\):

\[
\begin{align*}
\frac{dx}{dt} &= x \left(1 - \frac{x}{K}\right) - \frac{axy}{1+x} \\
\frac{dy}{dt} &= -y + \frac{axy}{1+x}
\end{align*}
\] (26.3)

\[
\begin{align*}
\frac{dx}{dt} &= x \left(1 - \frac{x}{K^2}\right) - \frac{ax^2y}{1+x^2} \\
\frac{dy}{dt} &= -y + \frac{ax^2y}{1+x^2}
\end{align*}
\] (26.4)

1. What is the biological meaning of parameter \(a\)?

2. Fix parameter \(K = 10\), and study the systems (26.3) and (26.4) by changing parameter \(a\).
   Draw bifurcation diagrams and phase portraits, and explain the biological behaviour of the systems.

3. Try to explain why the difference between the two systems in terms of nullclines. Which system is biologically more stable?

Exercise 4

1. Perform a simple two parametric study of the systems (26.3) and (26.4), by continuation of the line of Hopf bifurcation on the plane of the two parameters \(a\) and \(K\). Show the region in which we have oscillations. Explain the results of the previous one parametric studies with this two parametric plane (which path did you travel across these planes in the different exercises).

2. In Exercise 1 and 2 we got different bifurcation diagrams. The parameter value of \(a\) was equal to 2. Can we make the diagrams of the systems (26.1) and (26.2) similar by replacing ‘2’ by another value? Which value of \(a\) should we use? Confirm your answer by bifurcation analysis using Content.
**EXTRA Exercise 5**

Use MAPLE to get the line of Hopf bifurcation for system (26.4). To obtain this curve, calculate the parameter combinations for which the trace of the Jacobian is 0. Plot this curve, and compare it to the curve obtained using LOCBIF. Below we have given an example of such a MAPLE session.

```maple
> f := x*(1-x/k) - a*x*y/(1+x);

> g := -y + a*x*y/(1+x);

> solve({f=0, g=0}, {x, y});

{x = 0, y = 0}, {x = k, y = 0}, {x = 1/(-1+a), y = -k+a*k-1/k*(1-2*a+a^2)}

> x1 := %[3];

x1 := \{x = 1/(-1+a), y = -k+a*k-1/k*(1-2*a+a^2)\}

> xe := rhs(x1[1]);

xe := 1/(-1+a)

> ye := rhs(x1[2]);

ye := -k+a*k-1/k*(1-2*a+a^2)

> with(linalg):

Warning, the protected names norm and trace have been redefined and unprotected

> A := vector([f, g]);

A := \[x*(1-x/k) - a*x*y/(1+x), -y + a*x*y/(1+x)\]

> J := jacobian(A, [x, y]);

J := \[
\begin{bmatrix}
1 - \frac{2x}{k} - \frac{a y}{1+x} + \frac{a x y}{(1+x)^2} & -\frac{ax}{1+x} \\
-\frac{a y}{1+x} - \frac{a x y}{(1+x)^2} & -1 + \frac{ax}{1+x}
\end{bmatrix}
\]

> A := evalf(subs({x=xe, y=ye}, evalm(J)));
```
\[ A := \begin{bmatrix} 1. - \frac{2}{(-1. + a)k} & - \frac{1. a(-1. k + a k - 1.)}{k(1. - 2. a + a^2)(1. + \frac{1}{-1. + a})} \\ & + \frac{a(-1. k + a k - 1.)}{(-1. + a)k(1. - 2. a + a^2)(1. + \frac{1}{-1. + a})^2} - \frac{1. a}{(-1. + a)(1. + \frac{1}{-1. + a})} \\ & -1. + \frac{a}{(-1. + a)(1. + \frac{1}{-1. + a})} \end{bmatrix} \]

> fff := trace(A);

\[
fff := -2 - \frac{1}{(-1. + a)k} - \frac{1. a(-1. k + a k - 1.)}{k(1. - 2. a + a^2)(1. + \frac{1}{-1. + a})} \\
+ \frac{a(-1. k + a k - 1.)}{(-1. + a)k(1. - 2. a + a^2)(1. + \frac{1}{-1. + a})^2} + \frac{a}{(-1. + a)(1. + \frac{1}{-1. + a})} 
\]

> simplify(fff);

\[
\frac{a k - 1. a - 1. k - 1.}{a(-1. + a)k}
\]

> solve(%, a);

\[
\frac{1. + k}{k - 1.}
\]

> plot(%, k=1.1..10);
Chapter 27

One parameter analysis of ecological models

27.1 One parameter analysis of a predator-prey model with predator competition

Consider the following predator-prey model with predator competition:

\[
\begin{align*}
\frac{dx}{dt} &= x - \frac{xy}{1 + 0.45 * x} - 0.02 * x^2 \quad x \geq 0 \\
\frac{dy}{dt} &= -y + \frac{xy}{1 + 0.45 * x} - 0.1 \alpha * y^2 \quad y \geq 0 \quad \alpha > 0
\end{align*}
\]  

(27.1)

1. Study the dynamics of this system using Content and GRIND. Draw the bifurcation diagram on the \((\alpha, y)\) plane and phase portraits in each region of different behaviour. Show attractors and find basins of attraction.

2. In some parameter regions system (27.1) has multiple attractors. Demonstrate this using GRIND. Display timeplots of trajectories approaching these different attractors.

3. Study the limit cycle in this system:

   (a) Find the limit cycle and continue it along parameter \(\alpha\) using Content.

   (b) What is the fate of this limit cycle?

4. Explain in biological terms the changes in the behaviour of the system when the predator competition increases.
27.2 One parameter analysis of an ecological model with harvesting

Doedel in ([1984], J. Math. Biol., 20, 1–14.) proposed a model for plankton, fish and shark interaction. Here we study the part of the model, which represents the fish-shark interaction:

\[
\begin{align*}
\frac{dx}{dt} &= p2 \ast x \ast (1 - x) - p5 \ast x \ast y - p1 \ast (1 - e^{-p3 \ast x}) & x \geq 0 \\
\frac{dy}{dt} &= -y + p4 \ast x \ast y & y \geq 0
\end{align*}
\]

Here \( x \) is the fish population, \( y \) the shark population, and \( p1 \) the fishing quorum per unit of time.

Exercise

1. What is the biological meaning of the parameters \( p2, p3, p4 \) and \( p5 \)?

Fix the parameters at: \( p2 = 3, p3 = 5, p4 = 3 \) and \( p5 = 5 \)

2. Find the bifurcation diagram and draw phase portraits of this model under change of parameter \( p1 \). If all is OK, one of the bifurcations you found is a Hopf-bifurcation. For continuation of the limitcycle this Hopf-bifurcation produces, proceed as normal, that is select the Hopf point and change curve type to limitcycle.

To get some more information about what happens to the limitcycle we are going to monitor it’s period. To achieve this, in the numeric window select Layout, in the new window select Period, press select all and OK. Now go about continuing the limitcycle.

After a while you see the following things happening: the parameter along which you are continuing the limitcycle changes hardly, the period of the limitcycle gets very big (a period of 20 is supposed to be very big, is approximating a period infinity), and content gives messages as Period doubling(?) and Limit cycle point(?) indicating that it is not quite sure about what is happening.

The period of a limitcycle going to infinity indicates that a homoclinic or heteroclinic bifurcation of a limitcycle is occurring. To approximate the parameter value at which the bifurcation occurs we can do the following: In the main window, press Select, User functions. In the new window, behind label type p, behing name type h (homo- or heteroclinic), press Add and then behind value type Period-20.0. Now press OK. In the Starter window, in the section User defined functions, put h to detect. Now content will monitor when the function h=Period-20.0 equals 0 and put a p (the label) there. This is the point where the period of the limitcycle equals 20.0, which approximates the point where the period goes to infinity. Now start the continuation of the limitcycle again and see for which value of the parameter this happens.

To see whether a homo- or heteroclinic bifurcation occurs we need to look at the phase-portraits.
(a) How many regions of different behaviour do we have here?
(b) Draw phase portraits for each of these regions.
(c) Show attractors and find their basins of attraction.

3. Give a biological interpretation of each type of phase portrait, i.e., what is the behaviour of the fish and shark populations.

4. Try to explain in biological terms why an increase of the fishing quota causes the observed changes in behaviour.

5. At which value of $p_1$ can both populations become extinct?

6. At which parameter value will both populations become extinct?

7. **EXTRA** Analytically find the value of $p_1$ for which both populations can become extinct.
The general plan of studying differential equations with two parameters is the following:

**PLAN:**

1. Compute an orbit and find an equilibrium.
2. Continue this equilibrium along one of the parameters, and find a bifurcation point.
3. Continue this point of bifurcation along two parameters and find bifurcation lines.
4. Find regions of different behaviour on the plane of two parameters.
5. Show phase portraits of each region.
6. Show which bifurcations occur at the boundaries of the regions.

**Exercise 1**

Study the following ODE which is the normal form for the cusp bifurcation:

\[
\frac{dx}{dt} = \alpha + \beta x - x^3
\]

1. Follow step 1–6 from the above plan.
2. Archive the cusp line.
3. Fig. 28.1 shows several bifurcation diagrams. Predict in which parameter region they will occur. Which parameter should we use to get them? Confirm your ideas by computing the predicted diagrams using Content.
4. “Paradox”. Compute an orbit at $\alpha = 0.5, \beta = 0.5$ starting from the initial point $x = 1.2$. You will approach the equilibrium $x = 1$. Insert this point. Browse the “cusp” line on the $\alpha, \beta$ plane. Activate $\beta$ and continue the equilibrium line along $\beta$. You will see that the equilibrium line will cross the cusp line and will go further. But there will be no indication of the fold bifurcation here. Why?

Exercise 2

Study the following system using Content. Draw phase portraits of the different behaviours using GRIND.

\[
\begin{align*}
\frac{dx}{dt} &= y + 0.3a - 0.5 + bx - 0.4x^2 \\
\frac{dy}{dt} &= -y + x^3
\end{align*}
\]

Exercise 3

Consider the following predator-prey model with predator competition:

\[
\begin{align*}
\frac{dx}{dt} &= x(1 - x/K) - \frac{2xy}{1+x} \quad x \geq 0 \quad \delta > 0 \\
\frac{dy}{dt} &= -y + \frac{2xy}{1+x} - 0.1 \cdot \delta \cdot y^2 \quad y \geq 0 \quad K > 0 \tag{28.1}
\end{align*}
\]

1. Find a point of cusp bifurcation.

2. Check using GRIND what is going on with the nullclines close to the cusp point. Show how many equilibria we have in each region.

**NOTE:** This system is quite complicated. Do not perform a complete study of all bifurcations!
EXTRA Exercise 4

Consider a predator-prey system which is similar to the system (28.1), but uses another set of parameters:

\[
\begin{align*}
\frac{dx}{dt} &= x(1 - x/50.) - \frac{xy}{1 + \alpha x} \quad x \geq 0 \quad \delta > 0 \\
\frac{dy}{dt} &= -y + \frac{xy}{1 + \alpha x} - 0.1 \times \delta \times y^2 \quad y \geq 0 \quad \alpha > 0
\end{align*}
\]

(28.2)

HINT: Do not put derivatives to symbolically in Content but leave them at numerically.

1. Find point/points of cusp bifurcation.
2. Check using GRIND what is going on with the nullclines close to the cusp point. Show how many equilibria we have in each region.
3. Try to explain the difference between the systems (28.1) and (28.2).
Chapter 29

The Lorenz attractor

Here we study the Lorenz system (Lorenz, [1963]. J. Atmos. Sci., 20, 130–141.). This system has a well-known chaotic attractor. Because the system is three-dimensional, we rely heavily on GRIND’s three-dimensional graphical features.

**Input system to GRIND**

The Lorenz system consist of three differential equations

\[
\frac{dX}{dt} = -\sigma(X - Y) \quad , \quad \frac{dY}{dt} = rX - Y - XZ \quad , \quad \frac{dZ}{dt} = XY - bZ ,
\]

in which \( Z > 0 \) and any particular choice of \( X,Y \) is a mirror image of \( -X, -Y \). The variables \( X,Y,Z \) correspond to the rotation, and the temperature of convective eddies in a fluid. Lorenz studied the system for \( \sigma = 10 \) and \( b = 8/3 \). He varied \( r \), a dimensionless Rayleigh number. For \( r = 28 \) the system was apparently chaotic. To analyse this system with GRIND, make a file called lorenz which specifies the Lorenz equations as follows:

\[
x ~=~ -s*(x-y);
y ~=~ r*x - y - x*z;
z ~=~ x*y - (8./3.)*z;
\]

Note that we have replaced the parameter \( b \) by a constant, and the parameter \( \sigma \) by \( s \). Further make a file called run1or2 which pre-defines (1) the values of \( r \) and \( s \), (2) four macros called zero, a1, a2, and a3 (3) defines the vertical axis of time plots, (4) sets the FINISH to be 10 and asks for 500 points per integration, and (5) executes the ZERO and the A1 macros:

```
TE X11
r=10
s=10
ax v -30 30
macro zero x=0;y=0;z=0
macro a1 ax x x -30 30; ax y z 0 50; ax z y -30 30
macro a2 ax x r 0 30;ax y x -30 30;ax z z 0 50
```
macro a3 ax x y -30 30; ax y z 0 50
finish 10 500
a1
zero

**Nullclines**

Compile the program:

```plaintext
grind lorenz
```

As soon as you see ‘GRIND model analysis’ appear on your screen you may start typing commands. GRIND has no further prompts. The first thing to do is to read the file runlorz with all your definitions. Use the READ command. GRIND will signal that it is ready with “Enter input”:

```plaintext
READ RUNLORZ
Enter input
```

Check whether your parameters have indeed been set by the PARAMETERS command:

```plaintext
PA
r = 10.00
s = 10.00
```

Let's go into graphics mode by setting up a three-dimensional phase space.

```plaintext
3D
```

![3D nullclines](image)

**Figure 29.1: 3D nullclines**

Now draw the three nullclines by typing

```plaintext
NU X; NU Y; NU Z
```

These look pretty complicated. The x-nullcline is a straight plane, but the y and z nullclines are curved. Let's try to get a better view by shading the nullclines:
Well, the default shading of the $z$-nullcline (i.e., shading along the Z-axis) didn’t work very well. Since the $z$-nullcline is roughly vertical we better shade along the Y-axis:

$$\text{SH Y Z}$$

That does look better, but the whole picture is rather messy.

Although the picture is messy, we are still able to see how the nullclines depend on the parameter values. First erase the screen and redraw all three nullclines:

$$\text{ER}$$
$$\text{3D}$$
$$\text{NU X Y Z}$$

Figure 29.2: 3D nullclines

This is the nullcline situation for $r = 10, s = 10$. Now change $r$ a few times and redraw the three nullclines:

$$\text{R=28}$$
$$\text{E3N}$$
$$\text{R=1}$$
$$\text{E3N}$$

Thus only the $y$-nullcline depends on $r$. $r$ doesn’t change the shape of the nullcline, it only changes the location of the nullcline.

**Equilibria**

For $r > 1$ the Lorenz equations are known to have three equilibria. The first is always $x = y = z = 0$. Find two other equilibria at $r = 10$. For that use the the analytical formula for equilibria, put the initial values of $x, y$ and $z$ close to the equilibrium and use the `new` command. Determine the type of each equilibrium using `eig`. How many nonstable and stable manifolds do they have;
are they stable? Save the values of the variables at the non-trivial equilibria into a file. You can do it using the WHERE command which can have a filename as an argument. For example we found the following equilibrium at \( r = 6 \):

\[
\begin{align*}
X &= 1 \\
Y &= 1 \\
R &= 7 \\
Z &= 6 \\
\end{align*}
\]

Converged into:

Population State Derivative
---
x : 4.00000 0.000000E+00 \\
y : 4.00000 0.000000E+00 \\
z : 6.00000 5.093544E-06 \\

EIG

Stable point:

Population State Derivative
---
x : 4.00000 0.000000E+00 \\
y : 4.00000 0.000000E+00 \\
z : 6.00000 5.093544E-06 \\

Lambda: i / Vector:

1: -0.78060 + i 5.08183 \\
2: -0.78060 + i -5.08183 \\
3: -12.10547 -0.93 0.20 0.31 \\

We create the file pos, for this positive equilibrium.

\texttt{WH POS}

This creates a file named \texttt{pos} in your directory. Later we will read this file into GRIND again. You may inspect its contents with the DISPLAY command:

\texttt{DI POS}

\texttt{x = 4.000} \\
\texttt{y = 4.000} \\
\texttt{z = 6.000}

**Bifurcations of equilibria**

Having the three equilibria established we may study them as a function of the parameters. Let's plot the three equilibria as a function of \( r \). The CONTINUE command allows you to follow an equilibrium along one axis of the phase space. Thus associate the X-axis with the parameter \( r \), and let \( x \) be on the Y-axis. In the runlorz we have already defined the MACRO A2 to do this for us. Thus,

\texttt{A2} \\
\texttt{2D}

gives us a two-dimensional plot. Now we want to continue a steady state. The procedure is
to give an initial point close to the equilibrium. Then attain the equilibrium by the NEWTON keyword. Subsequently invoke the CONTINUE command. Thus to continue from the 0-state:

ZERO
NEW
CO
Done!
Done: 1 bifurcations in r around 1.000

A horizontal line at \( x = 0 \) appears. The line changes colour around \( r = 1.0 \). In this region GRIND detected a change in stability which is reported as a bifurcation. Do the same continuation of the other two equilibria by reading them from the files pos and neg:

READ POS

Get Fig. 29.3.

Which bifurcations we can see here?

Note, that when you have problems with the command CO, try another value of the parameter real, which is the step size of the continuation algorithm:

\[ \text{CO} \times \text{real} \]

\( x \) here is the axis along which we have continuation (which is \( x \) in our case).

Global bifurcations: homoclinic connection

Thus far we have seen that, for \( r > 1 \), the system has a nonstable equilibrium at \( x = y = z = 0 \) and a pair of equilibria with complex eigen values that are only stable when \( r < 24.7 \). For \( r > 24.7 \) the three equilibria are all nonstable. Thus we cannot have any stationary behaviour. Apart from the three local bifurcations that we have seen so far (i.e., \( r = 1 \) and \( r = 24.76 \), it
is known that the system has global bifurcations involving the stable and nonstable manifolds of the 0-state. First study the 2D picture of the double homoclinic connection. Display the 2D projection of the phase space on the $y, z$ plane. For that we have macro a3.

Perturb the nonstable manifold of the zero equilibrium in both directions, and see how the pattern is changing if we increase the parameter $r$. An example of two trajectories at $r = 10$ is shown in Fig. 29.4.

![Figure 29.4: Perturbation of the nonstable manifold at $r=10$.](image)

Find approximately the value of $r$ when we get a homoclinic connection. Increase the parameter further. Observe how the trajectory will jump from one to the other half-plane.

Now a 3D view: The exact value of parameter when we get a double homoclinic connection is $r = 13.926$. After this global bifurcation we get two nonstable limit cycles which later disappear via a Hopf bifurcation.

Let's have a 3D look at it.

First, set $r = 13.926$, go back to the 0-state, and attain the equilibrium by the NEWTON command. Then you get the eigen values and the eigen vectors by invoking the EIGEN command. Finally, use PERTURB 1 0.01 to make a perturbation of 0.01 along the eigen vector associated with the first eigen value:

- R=13.926
- a1
- 3d
- ZERO
- NEW
- EIG
- PER 1 0.01
This selects a new initial state. Thus, we may use RUN to plot the nonstable manifold of the 0-state. First, change the FINISH, and then call RUN:

```plaintext
FIN 3 500
RUN
```

We can do the same in the other direction of the eigen vector:

```plaintext
PER 1 -0.01
RUN
```

Now we have two trajectories leaving the 0-state along its nonstable manifold. Both come back to it via the stable manifold. Such a connection is called a homoclinic connection.

**Global bifurcations: heteroclinic connection**

Display again a 2d view using the `a3` macro. Perturb the nonstable manifold at values of \( r > 20 \). Try to find a value of \( r \) when we have a heteroclinic connection from this manifold to a nonstable limit cycle. Increase the parameter \( r \) further. Observe the appearance of chaotic behaviour (jumps between the equilibria). At which parameter values do they occur?

Finally, get a 3D view of this connection using macro `a1` at \( r = 24.06 \):

At \( r = 24.06 \) the 0-state is involved in a heteroclinic connection. Set \( r = 24.06 \), erase the screen, redraw the phase space, and run using the NEP command which stands for NEWTON;EIGEN;PERTURB, and the E3R command (for ERASE;3D;RUN).

```plaintext
R=24.06
a1
3d
zero
NEP
```
What we see (Fig. 29.5(b)) is a trajectory leaving the 0-state along its nonstable manifold and attaining a limit cycle. Thus, we have a heteroclinic connection between the one-dimensional nonstable manifold of the 0-state and the stable manifold of the limit cycle. Note that this limit cycle is nonstable. It is born at the supercritical Hopf bifurcation at $r = 24.76$. Beyond this heteroclinic connection, i.e., for $r > 24.76$, the typical behaviour of the system is apparently chaotic.

**Figure 29.6: Numerical integration and time plots**

### Numerical integration

Let's first start somewhere for $r = 28$:

```
ER;3D
R=28
X=1;Y=1;Z=1
RUN
```

This looks like the beginning of the famous chaotic Lorenz attractor. Use the KEEP command to continue from the last point of the trajectory, and let it run a little longer by the FINISH command:

```
KEEP
FIN 20 2000
RUN
```

Here we have a beautiful trajectory spiralling around the nonstable nodes hopping from left to right at unpredictable points. To look at this behaviour in time we use the TIMEPLOT command. The vertical axis of the timeplot has already been defined by reading the runlorz file. Thus, you only have to erase the screen and type

```
ER
```
to get a nice plot of $x, y$ and $z$ in time. In the GRIND manual you will find that the data required for making a timeplot can be saved on an external file. Thus, you may export these data to other plot packages. Additionally, you may load such a data file back into GRIND again (see the LOAD and PLOT commands).

To see the dependence on the initial conditions try to compute two close trajectories. To see the difference use the command `wh` which gives you the last point of the trajectory.

\[ z \quad x \]

\[ 50.0 \quad 30.0 \]

\[ 25.0 \quad 0.0 \]

\[ 0.0 \quad -30.0 \]

\[ -30.0 \quad 30.0 \]

Figure 29.7: Poincaré sections and continuations

**Poincaré sections**

The chaotic regime may be studied by making Poincaré sections. One has to define a Poincaré plane by a constant value of one of the variables. The points where trajectories cross this plane form the Poincaré section. We here choose $z$ as the variable defining the Poincaré plane. For $r = 28, z = 27$ seems to be a good value (remember that $z = r - 1$). Thus, first erase the screen, redraw a two-dimensional phase space, and set the FINISH to 10 steps with 100 intervals again. Then set the Poincaré section at $z = 27$ and ask for 10 points.

ER
2D
FIN 10 100
POINC Z 27
POINC 10

On your screen you see two groups of points around the two attractors.

Now, by changing $r$, we make a continuation of Poincaré sections to get an estimate of the bifurcation diagram. Let's again associate the parameter $r$ with the X-axis, and the variable $x$ with the Y-axis. Then you call BIFURCATE X 30 10 50 10 to change $r$ along the X-axis until $r = 30$, wait 10 time steps before recording any Poincaré crosses, make 50 samples of $r$, and record 10 points. Choose $r = 25$ as a starting value.
What you get is a rather boring bifurcation diagram. It will look a lot better when you increase the number of samples and the number of points to be recorded. However, then it takes even more time.
Chapter 30

Two parametric study of differential equations: Bogdanov-Takens

Perform a complete two-parametric study of the following predator-prey model:

\[
\frac{dx}{dt} = x - \frac{xy}{1 + \alpha x} \quad x \geq 0 \quad \delta > 0
\]

\[
\frac{dy}{dt} = -2y + \frac{xy}{1 + \alpha x} - 0.1 \delta y^2 \quad y \geq 0 \quad \alpha > 0
\]

The study should include the finding of all bifurcation lines, the finding of all co-dimensional 2 bifurcations, the (at least approximately) studying of bifurcations of limit cycles, and the finding and studying of all regions of different behaviour.

**HINT:** Again, in Content do not use derivatives symbolically, but keep them at numerically.

We ask you to write a short report upon this tutorial, which contains the following elements:

1. The two-dimensional bifurcation diagram, which shows type and position of all the bifurcation lines (including the global bifurcation lines), and of the co-dimensional 2 bifurcations, and which indicates all regions of different behaviour.

2. The phase portraits in each region of different behaviour, which show nullclines, the vector field, all equilibria, nonstable and stable manifolds for saddle points, and the fate of the manifolds.

3. A biological description of the population dynamics in each region.

If all is OK, one of the codimension-2 bifurcations you find is the Bogdanov-Takens bifurcation. As you know in this point meet the lines of local bifurcations namely fold and Hopf, but also the line of a global bifurcation, namely the homoclinic bifurcation.

As we saw in a previous chapter a homoclinic or heteroclinic bifurcation point can be approximated by finding a point where the period of the limitcycle has grown very big. But how can
we find a line of such points? It seems natural to find a point where we have a limitcycle with a large period, to take this point as an initial point in our two parameter plane and to continue this point, and hence to continue a limitcycle with a certain (large) period.

This turns out to be quite difficult for Content. Because we still want to have some idea about where the homoclinic bifurcation line lies in our two parameter plane we follow the following plan:

1. Draw the fold, Hopf and neutral saddle lines.
2. Save the fold and neutral saddle lines but not the Hopf line.
3. Clear your two parameter plane and redraw only the fold and neutral saddle lines.
4. Figure out in which region of the two parameter plane, especially in which position relative to the Hopf line the homoclinic bifurcation line should be.
5. Select as initial point the Bogdanov-Takens point and make sure curve type says Hopf.
6. Start recomputing your Hopf line but do it pointwise.
   **HINT:** Make sure you are on the Hopf line and not on the neutral saddle line by checking eigenvalues.
7. After having computed part of the Hopf line abort computations and select as initial point the last Hopf point you just computed.
8. Now put curve type to limitcycle, monitor the period of the limitcycle in the numeric window and activate the parameter along which you have to move to reach the region where you expect your homoclinic bifurcation line.
9. Stop computing if the period reaches the value of 20 or if you do not seem to be able to get any further. Do not pay attention to messages as Limit Point Cycle, Neimark-Sacker and Period Doubling.
10. Again select the Bogdanov-Takens point and again start recomputing the Hopf line pointwise, stop in a point further along the Hopf line than before and repeat the above procedure.
11. By doing this a few times you will get a few points that lie approximately on the line of homoclinic bifurcation.
Chapter 31

Synthetic biology

One of the first classical systems obtained in synthetic biology was construction of a toggle switch in E-coli (Gardner et al., Nature, v.403, p.339, 2000). The authors constructed a bistable gene-regulatory network which shows bi-stability. The toggle was constructed from a simple model of the promoter repressor network which is shown in fig. 31.1.

Figure 31.1: Tutorial witch design. Repressor 1 inhibits transcription from Promoter 1 and is induced by Inducer 1. Repressor 2 inhibits transcription from Promoter 2 and is induced by Inducer 2.

Consider the following series of reactions which reproduce these processes.

Binding of receptors to promoters:

\[ [P1] + [R1γ] \xrightleftharpoons[K1]{\gamma} [P1R1γ], \quad [P2] + [R2β] \xrightleftharpoons[K2]{\beta} [P2R2β], \] (31.1)

multimerization

\[ γ[R1] \xrightarrow[K3]{\gamma} [R1γ], \quad β[R2] \xrightarrow[K4]{\beta} [R2β] \] (31.2)

synthesis of repressors

\[ [P2] + [E] \xrightarrow[k5]{\gamma} [P2] + [E] + n[R1], \quad [P1] + [E] \xrightarrow[k6]{\beta} [P1] + [E] + n[R2] \] (31.3)

conservation of total promoter sites

\[ [P^T] = [P1^T] = [P1] + [P1R1γ] = [P2^T] = [P2] + [P2R2β] \] (31.4)
Here we assume that reactions (31.1-31.2) are in quasi-steady state and constants $K_1, K_2, K_3, K_4$ are the equilibrium constants. For example: $K_1 = \frac{[P_1R_1^\gamma]}{[P_1][R_1^\gamma]}$, etc.

1. Write expression for the velocity of production of $[R1]$ from equation (31.3), express $[P2]$ in terms of $[R2\beta]$ from equation (31.4) and quasi-steady state equation (31.1), express $[R2\beta]$ in terms of concentration of $[R2]$ from quasi-steady-state equation (31.2).

2. Write expression for velocity of production of $[R2]$, express it in terms of concentration of $[R1]$.

3. Add degradation of $[R1]$ and $[R2]$ with constant rate of $\delta$.

4. Prove that description of these processes is given by the following system (31.5):

$$\begin{align*}
\frac{d[R1]}{dt} &= \frac{k_{2n}[E][P^T]}{1+K_2K_4[R2]^\beta} - \delta[R1] \\
\frac{d[R2]}{dt} &= \frac{k_6[P^T]}{1+K_1K_3[R1]^\gamma} - \delta[R2]
\end{align*}$$

(31.5)

5. Make transformation of system (31.5) into form (31.6)

$$\begin{align*}
\frac{du}{dt} &= \frac{\alpha_1}{1+\beta} - u \\
\frac{dv}{dt} &= \frac{\alpha_2}{1+\alpha} - v
\end{align*}$$

(31.6)

6. Consider system (31.6) for $\alpha_1 = 10, \beta = \gamma = 2$. Draw nullclines of (31.6) for various $\alpha_2$. Describe changes in terms of null-clines changes and changes in number of equilibria. Which bifurcations we expect here. In approximately which parameter range.

7. Input system (31.6) to content at $\alpha_1 = 10, \beta = \gamma = 2$ and study bifurcations along parameter $\alpha_2$.

8. Continue study along two parameters ($\alpha_1, \alpha_2$) and find bifurcation lines and co-dim 2 bifurcation point(s).

9. Find regions of different behavior on the plane of two parameters.

10. Show phase portraits of each region and bifurcations occur at the boundaries of the regions.

11. Do we have a bi-stability at $\alpha_1 = 1, \alpha_1 = 5, \alpha_1 = 10$, for which values of $\alpha_2$?

12. Input system to grind. Show that application of pulses of $R1$ or/and $R2$ in region without bi-stability does not result in changes of final concentrations of chemicals. However, if this is done in region of bi-stability we can get a switch from one regime to another.

13. Compare results of your study (qualitatively) with Fig.2 and Fig.4 of paper Gardner et al.. by applying pulses of Inductor 2 ($R1$).
Construction of a genetic toggle switch in *Escherichia coli*

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It has been proposed that gene-regulatory circuits with virtually any desired property can be constructed from networks of simple regulatory elements. These properties, which include multistability and oscillations, have been found in specialized gene circuits such as the bacteriophage λ switch and the Cyanobacteria circadian oscillator. However, these behaviors have not been demonstrated in networks of non-specialized regulatory components. Here we present the construction of a genetic toggle switch—a synthetic, bistable gene-regulatory network—in *Escherichia coli* and provide a simple theory that predicts the conditions necessary for bistability. The toggle is constructed from any two repressible promoters arranged in a mutually inhibitory network. It is flanked between stable states using transient chemical or thermal induction and exhibits a nearly ideal switching threshold. As a practical device, the toggle switch forms a synthetic, addressable cellular memory unit and has implications for biotechnology, biocomputing and gene therapy.

The design and construction of synthetic gene-regulatory networks would be greatly facilitated by a theory with predictive capability. Previous work using a reconfigured enzyme system showed that nonlinear mathematics can predict qualitative behaviors of biochemical reaction networks, including multistability and hysteresis. However, a practical theory of gene-regulatory networks has lagged behind that of enzyme regulatory networks. A variety of physical and mathematical approaches, including logical (discrete)1–10, piecewise linear11, nonlinear12–18, statistical–mechanical19,20 and stochastic17,19 formulations of the underlying biochemical dynamics, have been used in the past. Owing to the difficulty of testing their predictions, these theories have not, in general, been verified experimentally. Here we have integrated theory and experiment by constructing and testing a synthetic, bistable gene circuit based on the predictions of a simple mathematical model.

The toggle switch is composed of two repressors and two constitutive promoters (Fig. 1). Each promoter is inhibited by the repressor that is transcribed by the opposing promoter. We selected this design for the toggle switch because it requires the fewest genes and cis-regulatory elements to achieve robust bistable behaviour. By robust, we mean that the toggle exhibits bistability over a wide range of parameter values and that the two states are tolerant of the fluctuations inherent in gene expression (the toggle switch will not flip randomly between states). Although bistability is theoretically possible with a single, autocatalytic promoter, it would be less robust and more difficult to tune experimentally. In addition, the chosen toggle design does not require any specialized promoters, such as the P3/P3M Promoter of bacteriophage λ. Bistability is possible with any set of promoters and repressors as long as they fulfill the minimum set of conditions described in Box 1 and Fig. 2.

The bistability of the toggle arises from the mutually inhibitory arrangement of the repressor genes. In the absence of inducers, two stable states are possible: one in which promoter 1 transcribes repressor 2, and one in which promoter 2 transcribes repressor 1. Switching is accomplished by transiently introducing an inducer of the currently active repressor. The inducer permits the opposing repressor to be maximally transcribed until it stably represses the originally active promoter.

All toggle switches are implemented on *E. coli* plasmids confering ampicillin resistance and containing the pBR322 CoEl1 replication origin. The toggle switch genes are arranged as a type IV plasmid, as shown in Fig. 3. Although all genes and promoters are

---

**Box 1**

**The toggle model**

The behaviour of the toggle switch and the conditions for bistability can be understood using the following dimensionless model for the network:

\[
\frac{du}{dt} = \frac{\alpha_1 u - u^2}{1 + u^2} - v \quad (1a)
\]

\[
\frac{dv}{dt} = \frac{\alpha_2 v}{1 + v^2} - \beta \quad (1b)
\]

where \( u \) is the concentration of repressor 1, \( v \) is the concentration of repressor 2, \( \alpha_1 \) is the effective rate of synthesis of repressor 1, \( \alpha_2 \) is the effective rate of synthesis of repressor 2, \( \beta \) is the cooperativity of repression of promoter 2 and \( \gamma \) is the cooperativity of repression of promoter 1. The above model is derived from a biochemical rate equation formulation of gene expression12–22. The final form of the toggle equations preserves the two most fundamental aspects of the network: cooperative repression of constitutively transcribed promoters (the first term in each equation), and degradation/dilution of the repressors (the second term in each equation).

The parameters \( \alpha_1 \) and \( \alpha_2 \) are lumped parameters that describe the net effect of RNA polymerase binding, open-complex formation, transcript elongation, transcript termination, repressor binding, ribosome binding and polypeptide elongation. The cooperativity described by \( \beta \) and \( \gamma \) can arise from the multimerization of the repressor proteins and the cooperative binding of repressor multimers to multiple operator sites in the promoter. An additional modification to equation (1) is needed to describe induction of the repressors (Fig. 5).

The geometric structure of equation (1), illustrated in Fig. 2a and b, reveals the origin of the bistability: the nullclines (\( du/dt = 0 \) and \( dv/dt = 0 \) in Fig. 2) intersect at three points, producing one unstable and two stable steady states. From Fig. 2a and b, three key features of the system become apparent. First, the nullclines intersect three times because of their sigmoidal shape, which arises for \( \beta, \gamma > 1 \). Thus, the bistability of the system depends on the cooperative repression of transcription. Second, the rates of synthesis of the two repressors must be balanced. If the rates are not balanced, the nullclines will intersect only once, producing a single stable steady state. This situation arises in plasmid pKE103. Third, the structure of the toggle network creates two basins of attraction. Thus, a toggle with an initial condition anywhere above the separatrix will ultimately settle to state 1, whereas a toggle starting below the separatrix will settle to state 2.

The conditions for a bistable toggle network are illustrated in Fig. 2c and d. As the rates of repressor synthesis are increased, the size of the bistable region increases. Furthermore, the slopes of the bifurcation lines, for large \( \alpha_1 \) and \( \alpha_2 \), are determined by \( \beta \) and \( \gamma \). Thus, to obtain bistability, at least one of the inhibitors must repress expression with cooperativity greater than one. Moreover, higher order cooperativity will increase the robustness of the system, allowing weaker promoters to achieve bistability and producing a broader bistable region.

---

**Figure 1**

Toggle switch design. Repressor 1 inhibits transcription from Promoter 1 and is induced by Inducer 1. Repressor 2 inhibits transcription from Promoter 2 and is induced by Inducer 2.
contained on a single plasmid, they could, in principle, be divided into two separate plasmids without altering the functionality of the toggle. Two classes of toggle switch plasmids were constructed—the pTAK class and the pKE class. Both classes use the lac repressor (lacI) in conjunction with the Prc2 promoter for one promoter—repressor pair. For the second promoter—repressor pair (P1, R1 in Fig. 3), pTAK plasmids use the Pits1con promoter in conjunction with a temperature-sensitive λ repressor (clts), whereas pKE plasmids use the P1tetO-1 promoter in conjunction with the Tet repressor (tetR). pTAK plasmids are switched between states by a pulse of isoprityl-β-d-thiogalactopyranoside (IPTG) or a thermal pulse. pKE plasmids are switched between states by a pulse of IPTG or a pulse of anhydrotreicline (aTc).

The promoters used in the toggle are P1tetO-1 (ref. 20) (TetR repressed), Prc2-2 (lacI repressed) and Pits1con (CI repressed). The ranked order of the transcriptional efficiencies of the promoters is Pits1con > Prc2-2 > P1tetO-1. In all variants of the toggle switch, the sequence of the three promoters is unchanged. The rates of synthesis of the represors (α1 and α2 in the model) or the reporter genes are modified by exchanging the downstream ribosome binding sites (RBS). The promoter and RBS sequences and their relative strengths are described in the Supplementary Information.

In all toggle plasmids, the gfpmut3 gene21 is arranged as the second cistron downstream of the Prc2-2 promoter. Thus, transcription from Prc2-2, and hence, repression of P1, results in the expression of green fluorescent protein (GFPmut3). For clarity, this state is termed the ‘high’ state. The opposing state, in which P1 is transcribed and Prc2-2 is repressed, is termed the ‘low’ state. Unless otherwise indicated, gfpmut3 is the reporter used in all plasmids.

To investigate the conditions required for bistability, six variants of the toggle switch (four pTAK plasmids and two pKE plasmids) were constructed by inserting RBS sequences of differing strengths into the RBS1 site. All four pTAK plasmids exhibited bistability, whereas only one pKE plasmid (pKE107) exhibited bistability. The demonstration of bistability is illustrated in Fig. 4. In this experiment, the toggle and control plasmids were grown in E. coli strain JM2300 for 23.5 h. At 6, 11 and 18 h, samples were washed and diluted into fresh medium with or without inducers, as appropriate. Cells were initially grown for 6 hours with 2 mM IPTG, inducing GFPmut3 expression in all toggles and the IPTG-inducible pTAK102 control plasmid. Cells were grown for an additional 5 h with no IPTG. The five bistable toggle plasmids, which had been switched to the high state, continued to express GFPmut3 in the absence of inducer, whereas the pTAK102 control plasmid and the nonostable pKE105 toggle plasmid returned to the low state. Cells were then grown at 42°C (pTAK plasmids only) or grown in the presence of 500 μg ml⁻¹ aTc (pKE plasmids only). After 7 h of growth, GFPmut3 expression in all toggles was shut off, whereas GFPmut3 expression in the thermally-inducible pTAK106 control and the aTc-inducible pKE108 control was activated. Cells were returned to standard temperature (see Methods) with no inducers. After an additional 5.5 h, the five bistable toggle plasmids remained in the low state, whereas the pTAK106 and pKE108 controls returned, as expected, to their non-induced condition.

Figure 4c shows the long-term stability of the two states of the pTAK117 toggle plasmid. In this experiment, a single culture of pTAK117 cells (initially in the low state) was divided into two cultures. The first group was grown in medium with no inducers, while the second group was grown in medium with 2 mM IPTG. After 6 h, cells were washed and diluted into fresh medium with no inducer. Both groups of cells were grown for an additional 22 h, being sampled and diluted into fresh medium every 6–8.5 h. The two groups of pTAK117 cells remained in their initial high or low states for the entire 22 h.

Although all of the toggle plasmids contain the same configuration of elements, one plasmid, pKE105, does not exhibit bistability. This result is probably due to the reduced efficiency of the Tet repressor relative to the λ repressor. To maintain bistability, the reduced efficiency requires a corresponding decrease in the strength of the P1tetO-1 promoter relative to the Pits1con promoter (see Box 1). The P1tetO-1 promoter in the pKE105 plasmid is not sufficiently reduced in strength to achieve bistability. However, the strength reduction provided by the P1tetO-1 promoter in the pKE107 plasmid is sufficient.

A qualitative prediction of the toggle model is that a genetic toggle will have nearly ideal switching thresholds. Induction by IPTG, aTc or heat alters the dynamic balance between the competing promoters such that the toggle is pushed into a region of monostability. The transition from bistability to monostability occurs in a sharp, discontinuous fashion owing to the existence of a bifurcation. This bifurcation occurs when one of the stable steady states is annihilated by the unstable steady state.

The ideal threshold, or bifurcation, in the pTAK117 toggle switch is illustrated both theoretically and experimentally in Fig. 5. In this experiment, pTAK117 (initially in the low state) and pTAK102 (as a control) were grown in 13 different concentrations of IPTG for 17 h.

**Figure 2** Geometric structure of the toggle equations. a, A bistable toggle network with balanced promoter strengths. b, A monostable toggle network with imbalanced promoter strengths. c, The bistable region. The lines mark the transition (bifurcation) between bistability and monostability. The slopes of the bifurcation lines are determined by the exponents β and γ for large α1 and α2. d, Reducing the cooperativity of repression (β and γ) reduces the size of the bistable region. Bifurcation lines are illustrated for three different values of β and γ. The bistable region lies inside of each pair of curves.

**Figure 3** The toggle switch plasmid. Promoters are marked by solid rectangles with arrowheads. Genes are denoted with solid rectangles. Ribosome binding sites and terminators (T1, T2) are denoted by outlined boxes. Different P1 promoters, RBS1 ribosome binding sites, and/or R1 repressors, are used for the various toggle switches. Plasmid types I–III, used in the construction and testing of the toggle components, are described in the Supplementary Information.
to steady state, being diluted twice (at 6 and 12.5 h) into fresh medium with the same IPTG concentration. Induction of the pTAK102 control has the familiar sigmoidal shape. In contrast, the pTAK117 toggle follows the induction curve of pTAK102 up to an IPTG concentration of 40 μM, at which point it crosses the bifurcation and exhibits a quasi-discontinuous jump to the high expression state. Owing to the natural fluctuations in gene expression, the bifurcation is not a perfect discontinuity as predicted by the deterministic toggle equations. The stochastic nature of gene expression causes variability in the location of the switching threshold and thus blurs the bifurcation point. Near the bifurcation, this blurriness is realized as a bimodal distribution of cells (Fig. 5c).

The switching time of the pTAK117 plasmid from the low to the high state and from the high to the low state is shown in Fig. 6. In this experiment, pTAK117 cells in the low state were diluted in fresh medium and induced with 2 mM IPTG. Separate cultures were grown for 35 min to 6 h before being washed and diluted in fresh medium with no inducer. Growth was continued until 10.25 h after the start of the experiment and cells were assayed in the flow cytometer. Conversely, pTAK117 cells in the high state were diluted in fresh medium with no inducer. Separate cultures were grown at 41 ± 1°C for 35 min to 6 h before being diluted in fresh medium with no inducer. Growth was continued at standard temperature until 10.25 h after the start of the experiment and cells were assayed in the flow cytometer.

As shown by the appearance of a bimodal distribution at 4 h (Fig. 6), the pTAK117 plasmid begins switching to the high state after 3–4 h of IPTG induction. By 5 h the switching is nearly complete, and by 6 h it is complete. On the other hand, switching from the high state to the low state is completed in 35 min or less. The primary determinant of switching time is the rate of elimination of the repressor proteins. Switching from low to high requires the gradual dilution, by cell growth, of the IPTG-bound Lac repressor. On the other hand, switching from high to low is effected by immediate thermal destabilization of the temperature-sensitive λ repressor. Thus, switching to the low state is substantially faster than switching to the high state. Furthermore, the configuration of the pTAK117 plasmid—the rate of Lac repressor synthesis is more than an order of magnitude higher than the rate of λ repressor synthesis—suggests that the low state is more stable than the high state.

Our approach to the construction of a genetic toggle switch represents a significant departure from traditional genetic engineering in that we rely primarily on the manipulation of network components.
architecture, rather than the engineering of proteins and other regulatory elements, to obtain desired behaviours. In addition, the reasonable agreement between the toggle theory and experiment indicates that the theoretical design of complex and practical gene networks is a realistic and achievable goal. Moreover, the genetic toggle switch exemplifies a forward engineering approach to the study of gene regulation in which synthetic gene circuits serve as highly simplified, highly controlled models of natural gene networks. As a practical device, the toggle switch, which requires only transient rather than sustained induction, may find applications in gene therapy and biotechnology. Finally, as a cellular memory unit, the toggle forms the basis for ‘genetic applets’—self-contained, programmable, synthetic gene circuits for the control of cell function.

Methods

Numerics

All theoretical curves were calculated numerically from equation (1) (Box 1) using Matlab (Mathworks), XPP-AUTO, software for simulation and analysis of differential equations (C. B. Ermentrout, University of Pittsburgh, available at http://www.pitt.edu/~phase/); or AUTO, a bifurcation package included in the XPP-AUTO software (E. Doedel, McGill University).

Plasmid construction

Plasmids were constructed using basic molecular cloning techniques as described in standard cloning manuals. Restriction enzymes were from New England Biolabs and Promega; PfuTurbo polymerase was from Stratagene; all other enzymes were from New England Biolabs; all synthetic oligonucleotides were from Operon Technologies. All genes, promoters and transcription terminators were obtained by PCR amplification using PfuTurbo proofreading polymerase and synthetic primers with overhanging ends containing the appropriate restriction sites. Ribosome binding sites were included in the overhanging ends of the primers. Site mutations were performed using either Stratagene QuickChange or ExSite.

Genes, promoters and transcription terminators were obtained as follows: Prcr2 from pTrc99a (AP Biotech); P2 from pXC46 (ATCC); P35et0-1 by total synthesis according to the published sequence; lacI from pTrc99a; dts from pGw7 (ATCC); tetR from psDnA4 TR (Invitrogen); gfpus from pGFPuv (Clontech); gfpus3 from pBluA11 (gift of J. B. Andersen, Technical University of Denmark); and rrrT2T2 terminators from pTrc99a. All plasmids contained the ampicillin resistance region and CoE1 origin and replication from the pTrc99a plasmid. All cloning was performed by TSS transformation into E. coli strain JM2300 (CGSC), IC138 (CGSC) or TAP108 (ATCC).

DNA sequencing was performed using a Perkin-Elmer ABI Prism 377 sequencer.

Strains, growth conditions and chemicals

The host cell for all promoter assays and toggle switch experiments was E. coli strain JM2300 (λ−, lacI22galR153 ScrI, rha-1) (CGSC strain 5002). JM2300, which contains few mutations, is a fast growing strain that can tolerate enormous overexpression of plasmid-bound genes. Because JM2300 contains no λ repressor and carries a nonfunctional Lac repressor (lacI22), it is an ideal host for the toggle switch.

All cells were grown in LB medium (Difco) with 100 μg/ml ampicillin plus inducers as indicated in the text. All Type I and pKIE series plasmids were grown at 37 ± 1 °C, unless otherwise indicated. All pTAK series plasmids were grown at 32 ± 1 °C except during thermal induction. Thermal induction was carried out at 42 ± 1 °C, unless otherwise indicated. For all expression tests, cells were maintained in logarithmic growth phase by periodic 500–1,000-fold dilution into fresh medium. Ampicillin and IPTG were from Sigma. Anhydrotetracycline was from ACROS Organics. All other chemicals were from Fisher.

Assay of gene expression

All expression data were collected using a Becton–Dickinson FACSCalibur flow cytometer with a 488-nm argon excitation laser and a 515–545-nm emission filter. Before assay, cells were pelleted and resuspended in 0.22 μm filtered PBS (58 mM NaH2PO4, 17 mM Na2HPO4, 68 mM NaCl, pH = 7.4). Cells were assayed at low flow rate and fluorescence was calibrated using InSpeck green fluorescent beads (Molecular Probes). All measurements of gene expression were obtained from three independent cultures maintained simultaneously under identical conditions. For each culture, 40,000 events were collected. All flow data were converted to ASCII format using MFI (E. Martz, University of Massachusetts, Amherst, available at http://marlin.bio.umass.edu/mfi/bcfaasflowc. htmlmfi) and analysed with Matlab.

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Supplementary information is available at Nature’s World-Wide Web site (http://www.nature.com) or as paper copy from the London editorial office of Nature.

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Chapter 32

Algae and zooplankton

Read the article from De Volkskrant. Based on this article we made a model of algae ($A$), defending themselves against predation by zooplankton ($Z$):

$$\frac{dA}{dt} = rA \left(1 - \frac{A}{k}\right) - \frac{b_1ZA}{c_1 + A} \ast \frac{c_2^2}{c_2^2 + Z^2}$$

$$\frac{dZ}{dt} = \frac{b_2ZA}{c_1 + A} \ast \frac{c_2^2}{c_2^2 + Z^2} - dZ$$

We ask you to write a report upon this tutorial, which contains the answers to all questions, your final two-dimensional bifurcation diagram, and phase portraits of all regions of different behaviour.

**HINT:** Again, in Content do not use derivatives symbolically, but keep them at numerically.

1. Explain the biological meaning of all the terms in the model.

2. Remove the parameters $r$ and $c_1$ by rescaling of the model.

Now we want to make a bifurcation diagram by varying $k$ and $c_2$. Take $b_1 = 1$, $b_2 = 1$, $d = 0.2$, and both $k$ and $c_2$ between 0 and 5.

3. Why are we interested in $k$ and $c_2$?

4. Using Content, find bifurcations and continue bifurcations along both parameters. Draw the bifurcation diagram.

5. Which two co-dimensional-2 bifurcations do you find?
De eencellige alg Scenedesmus spicatus. FOTO’S D. HESSEN

Algen schudden ophpringerige watervlo af

In een milieu met veel algenetende watervlooien ondergaan sommige algen een gedaanteverandering. Ze zetten stekels op of worden oneetbare bollen. De algenbestrijding heeft er een probleem bij.

Een tweecellige Scenedesmus spicatus. FOTO’S D. HESSEN

Achtcellig stadium van de alg. De eencellige alg Scenedesmus spicatus. FOTO’S D. HESSEN

Imagen
6. Describe the behaviour of the model that you expect around these co-dimensional-2 bi-
furcations. In one of these bifurcations also a line of global bifurcations is born. What kind of bifurcation is this, and between which lines of bifurcations is it located?

You can continue this bifurcation using Content. Find a limit cycle and continue this limit cycle along one parameter until the period becomes very large. Then fix the period and continue the limit cycle along both $k$ and $c_2$.

7. Why can we, using the above method, follow the bifurcation line?

8. Follow the bifurcation line. Save this line, and draw all lines in your final bifurcation diagram.

9. How many regions with different model behaviour do we have? Use GRIND to draw phase-portraits, equilibria and their stability, separatrices, and global attractors for each case.

10. What can happen if we increase $k$ by enrichment? And if we afterwards decrease $k$ again? What are the biological consequences of this?

11. The authors suspect that this interaction stabilises the system. Give your own opinion.

**EXTRA**

The authors suspect that there must be some disadvantage for the algae to clump together. Otherwise they would be always like that.

12. Why is it better to change $k$, instead of $r$, when the algae become clumped?

As new $k$ we take:

$$k_1 = k - \varepsilon \left(1 - \frac{c_2^2}{c_2^2 + Z^2}\right)$$

(32.1)

13. Explain this term.

14. Does your bifurcation diagram change if we introduce this term? You can check this by following, in Content, the co-dimensional-2 bifurcations along $\varepsilon$.

15. Is some influence of clumping on the carrying capacity important for the model behaviour?
Chapter 33

One parametric analysis of a model of HIV infection

A model for the interaction between HIV and the immune system is:

\[ \frac{dT}{dt} = s + T \left( \frac{pV}{k + V} - 1 - jV \right) \quad T \geq 0 \]

\[ \frac{dV}{dt} = V \left( r - cT \right) \quad V \geq 0 \]

Here, \( T \) is a population of \( T \) lymphocytes, \( V \) is the HIV population; \( s \) represents the supply of \( T \) cells from the thymus, \( r \) is the maximum replication rate of the virus, \( cV \) accounts for the immune response, and \( jVT \) represents the infection of \( T \) cells by the virus.

1. Make a change of variables and transform the system into the following form:

\[ \frac{dT}{dt} = \sigma + T \left( \frac{pV}{1 + V} - 1 - vV \right) \]

\[ \frac{dV}{dt} = rV(1 - T) \]

2. Study this model for \( r = 1; p = 2; \sigma = 0.01 \), and different values of \( v \), using GRIND and content.

**HINT:** Use in GRIND logarithmic axes for both variables. For example, for the \( t \) axis you could use:

```
axis x t -3. 4. log
```

which will create a logarithmic axis from \( 10^{-3} \) to \( 10^{4} \).

3. Draw the bifurcation diagram on the \((v, V)\) plane.

4. (a) How many regions of different behaviour do we have here?

(b) Draw phase portraits in each of these regions.

(c) Show attractors and find their basins of attraction.
5. AIDS development in this model is defined as an infinite growth of $V$ after some external infection. The rest state the system is assumed to be the lower equilibrium point $V = 0$. What is the virulence threshold for AIDS in this model? i.e., starting from which value of $v$ will AIDS develop?

6. (more detailed study) Find an analytical formula for the critical value of $v$, provided $\sigma \to 0$. Compare the values given by this formula to the numerical values found using content.

7. Compute, using GRIND, the behaviour of the system below the virulence threshold, at $v = 0.03$. Can AIDS develop at this parameter value? Study the changes of the phase portrait under the change of parameter $v$. Explain the different behaviours of the system. Which global transformation of the phase portrait accounts for the change in behaviour you found? Try to find the new virulence threshold of AIDS.
Chapter 34

Two parametric study of maps

34.1 Hassel-Lawton-May model

Consider the following map, which is a model of population growth:

\[ x_{t+1} = \frac{rx_t}{(1+x_t)^b} \]

1. Change variables and parameters:

   \[ y = \ln x \quad R = \ln r \quad b = \ln \beta \]

2. Study this new map using LBFP.

3. Find and display on the \((R,b)\) plane the lines of flip bifurcations for fixed points, period 2 orbits, and period 4 orbits.

4. In which parameter region do we expect chaos?

5. Confirm this by computation of a bifurcation diagram using GRIND.

NOTES:

1. To study the double iterated map in LBFP, you need to change \texttt{Itmap=1} into \texttt{Itmap=2}, etc.

2. To input \(\ln x\), use \(\log x\).
34.2 Delayed logistic map with influx

Study the following map:

\[ x_{t+1} = rx_t(1-x_{t-1}) + e \quad r > 0 \quad -1.15 < e < 1.15, \]

which is the delayed logistic map with influx.

1. The right hand side of this map has single delayed terms (with \( x_t \)) and double delayed terms (with \( x_{t-1} \)). Transform this map into a two-dimensional map which has only single delayed terms (with \( x_t \) and \( y_t \)).

2. Study this system at \( e = 0 \). Find a Neimark-Sacker bifurcation. Check if it is generic (i.e., if \( \lambda^k \neq 1 \), for \( k = 1, 2, 3, 4 \)).

3. Increase \( r \) above the bifurcational value. Find the first region of phase locking, i.e., find a periodic orbit, and archive it. What is the period of the orbit? Continue this orbit along parameter \( r \). At which values of \( r \) does the phase locking disappear? Through which bifurcation? Archive the resulting curve of continuation of this periodic orbit.

4. Study the system with the two parameters \( r \) and \( e \). Find the line of Neimark-Sacker bifurcation on the \((r,e)\) plane, and archive it.

5. Browse the archived curve of continuation of the periodic orbit. This curve was a continuation along the parameter \( r \). Study the system with two parameters. Find the region of phase locking on the \((r,e)\) plane, and archive it.

6. Browse the archived lines of the Neimark-Sacker bifurcation, and of the phase locking region. Explain the picture.