VII Biological Oscillators

VII. 1. Limit cycles

The nullclines are:

During class we consider the following two coupled differential equations:

$$\dot{x} = -x + ay + x^2 y$$
 $\dot{y} = b - ay - x^2 y$
[VII.1]

From the phase plane analysis it was clear that for certain values of a and b this system exhibits periodic oscillations as a function of time. Let us analyze [VII.1] in more detail.

$$y = \frac{x}{a + x^2}$$

$$y = \frac{b}{a + x^2}$$
[VII.2]

There is only one fixed point (x^*,y^*) :

$$x^* = b$$
 $y^* = \frac{b}{a + b^2}$
[VII.3]

The matrix A is (using [VI.4] and [VI.5]):

$$A = \begin{bmatrix} -1 + 2x^*y^* & a + (x^*)^2 \\ -2x^*y^* & -(a + (x^*)^2) \end{bmatrix}$$
 [VII.4]

The determinant and trace are:

$$\Delta = a + b^{2} > 0$$

$$\tau = -\frac{b^{4} + (2a - 1)b^{2} + (a + a^{2})}{a + b^{2}}$$
[VII.5]

The fixed point is stable when τ < 0. The region in a-b-parameter space where the system is oscillating (stable limit cycle) and is not oscillating (stable fixed point) is illustrated in Fig. 14.

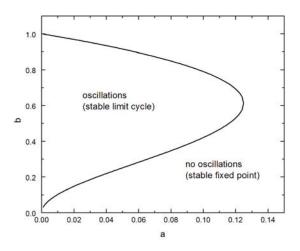


Figure 14. *a-b*-parameter space indicating for which values of a and b the system exhibits stable oscillations and a stable fixed point.

MATLAB code 3: Limit cycle

```
% filename: limitcycle.m
close;
clear;
a=0.1;
b=0.5;
options=[];
[t y]=ode23('cyclefunc',[0 50],[0.6 1.4],options,a,b);
plot(y(:,1),y(:,2));
```

VII.2 Synthetic genetic oscillators

The first synthetic genetic oscillator was constructed by Elowitz *et al.* in the bacterium *Escherichia coli*. Details of these experiments can be found in:

Reference:

 M. B. Elowitz and S. Leibler. A synthetic oscillatory network of transcriptional regulators. *Nature* 403, 335-338 (2000).

In class we derived the conditions under which the network exhibits oscillations. The chemical reactions describing the concentration of mRNA m and protein concentration p are (see Box):

$$\frac{dm_i}{dt} = -m_i + \frac{\alpha}{(1+p_j^n)} + \alpha_o$$

$$\frac{dp_i}{dt} = -\beta(p_i - m_i)$$
[VII.6]

where the index i=[lacl,tetR,cl] and the index j=[cl,lacl,tetR]. Below will we use numerical indices to represent the repressors. Let us assume that we can ignore the intermediate step of mRNA synthesis. This leads to the following three equations:

$$\frac{dp_1}{dt} = -p_1 + \frac{\alpha}{1 + p_3^n} + \alpha_o$$

$$\frac{dp_2}{dt} = -p_2 + \frac{\alpha}{1 + p_1^n} + \alpha_o$$

$$\frac{dp_3}{dt} = -p_3 + \frac{\alpha}{1 + p_2^n} + \alpha_o$$
[VII.7]

In the analysis below we will assume that all three genes have the same basal synthesis rate α_0 , maximum synthesis rate α , and Hill coefficient n. Note that time is measured with respect to protein decay rate. As all three genes have the same properties, the steady-state values of the mRNA and protein concentrations will be:

$$p \equiv p_1 = p_2 = p_3$$
 [VII.8]

therefore in steady-state,

$$p = \frac{\alpha}{1 + p^n} + \alpha_o$$
 [VII.9]

For the stability analysis we have to determine the matrix A (Jacobian) as described before (see chapter VI):

$$A = \begin{bmatrix} -1 & 0 & X \\ X & -1 & 0 \\ 0 & X & -1 \end{bmatrix}$$
 [VII.10]

where

$$X \equiv -\frac{\alpha n p^{n-1}}{\left(1 + p^n\right)^2}$$
 [VII.11]

For the steady state to be stable, the real part of the eigenvalues of matrix A have to be negative. As mentioned in chapter VI the eigenvalues can be found by solving:

$$\det \begin{bmatrix}
-1-\lambda & 0 & X \\
X & -1-\lambda & 0 \\
0 & X & -1-\lambda
\end{bmatrix} = 0$$
[VII.12]

Leading to

$$-(1+\lambda)^3 + X^3 = 0$$
 [VII.13]

This equation has three solutions, one real and two complex:

$$\begin{split} \lambda_1 &= X - 1 \\ \lambda_2 &= -1 - \frac{1}{2}X + i\frac{\sqrt{3}}{2}X \\ \lambda_3 &= -1 - \frac{1}{2}X - i\frac{\sqrt{3}}{2}X \end{split}$$
 [VII.14]

For a stable fixed point the real part of all eigenvalues should be negative. Therefore the system is stable for:

$$-2 < X < 1$$
 [VII.15]

X is negative by definition (see [VII.11]) so the final stability condition is:

$$\frac{\alpha n p^{n-1}}{\left(1+p^n\right)^2} < 2$$
 [VII.16]