
Dynamic Models in Biology

Computer Lab: **Bifurcation analysis**

In this lab, you will use numerical simulation of two different models to investigate bifurcations.

1. Saddle-node bifurcation

Model

You'll investigate the prototypical saddle-node bifurcation model:

$$\begin{aligned}\dot{x} &= \mu - x^2 \\ \dot{y} &= -y\end{aligned}$$

Pre-bifurcation

Generate the phase portrait for $\mu = 0.5$ by superimposing a **quiver** plot, the nullclines, and trajectories. (Obtain the trajectories by implementing the model in Matlab using the `ode45` solver and running integrations starting from different initial conditions).

How does your phase portrait compare to that in the textbook (Fig. 8.1.1)? Can you explain differences? **reponse1** **stable & unstable vs. collapse**

Bifurcation

Generate the phase portrait for $\mu = 0.0$ using the same approach as for $\mu = 0.5$. Does this phase portrait look the one at bifurcation point in the text book? **reponse2** **Yes**

Post-bifurcation

Generate the phase portrait for $\mu = -0.5$ and compare it to that in the text book.

Inspect the times series data (i.e., $x(t)$ and $y(t)$). Can you see signs of the ghost of the bifurcation? How does this manifest?

2. Homoclinic bifurcation

Model

In this second part, you'll investigate a model in which the dynamics undergoes a homoclinic bifurcation:

$$\begin{aligned}\dot{x} &= \mu x + y - x^2 \\ \dot{y} &= -x + \mu y + 2x^2\end{aligned}$$

Bifurcation point

Find the value of μ at which the system undergoes the homoclinic bifurcation. (Hint: compute phase portraits for different values of μ).

Show the phase portraits just before and after the bifurcation.