## Practical 2: Modelling single neuron activity

Get the Matlab files from http://www.biological-networks.org/t/cneurosci/practical2.zip

## Matlab practice

If you do not have previous experience of Matlab go through chapters 2 and 3 (pages 3-56 to 3-70).

## Differential equations

Run the function *app\_numinte*. Using the Matlab editor, change the code to

1) Show labels for the x- and y-axis, provide a title and plot the name of the curve into the figure (either interactively with the figure editor or automatically using the text command).

2) Test other functions for discretization (*ode45*, *ode113*, *ode15s*, *ode23s*, *ode23t*, *ode23tb*). you can get more information about any Matlab function f with *help f* or *doc f*.

3) Which function shows the best performance (being closest to the exact function)?

## Model of neural response to stimuli (sensorymotor cortex)

For localized tactile stimulation by a pin, only a small amount of receptors and therefore only a small region of the somatosensory cortex will be activated. This small activated module can be represented through two neuron populations: an inhibitory population and an excitatory population. The results of the model can then be compared to experimentally measured activity (e.g. in the rat) depending on stimulus duration and amplitude.

In the model, the mean membrane potential of excitatory neurons is given by u and the mean membrane potential for inhibitory neurons by v. The coupling between both populations is equal (exc. -> inh. connection strength is the same as inh. -> exc. ). There is also coupling within each population (exc. -> exc. and inh.->inh.) which can be adjusted.

The differential equations for changing both membrane potentials are:

$$du = -u - w \cdot f(v) + w_{ffx} \cdot s + h$$
  

$$\tau \ dv = -v + w \cdot f(u)$$

$$u = -v + w \cdot f(u)$$

$$w = -v + w \cdot f(u)$$
w (inh.)



(u: mean membrane potential of the excitatory neurons; v: mean membrane potential of the inhibitory neurons; w: coupling strength between populations, coupling strength within populations not shown;  $w_{ffx}$ : coupling strength of the stimulus; s: stimulus; h: additive constant; f(x): activation function;  $\tau$ : time constant)

The activation function, a sigmoid function, is non-linear. This causes non-linear dynamics of the population activities. The additive constant corresponds to the resting potential of the excitatory neurons. The time constant  $\tau$  determines the speed of the potential change of the inhibitory population relative to the excitatory population ( $\tau := \tau_{inhibitory} / \tau_{excitatory}$ ). A delayed activation of the inhibitory populatoin is necessary to get a suppression. The stimulus s corresponds to the amplitude of the stimulus weighted by the coupling strength  $w_{ffx}$ .

Run the script *one\_module*. It will show a plot of the stimulus and the resulting population activities and a second plot with the phase space of the simulation. The phase is the current state of the system given by the value of *u* and *v*. Each state can be represented by a point in (in this case two-dimensional) phase space. Over time, the system will visit different states and this change is shown as a trajectory in the second plot.

1) Why is the mean membrane potential zero and not -80mV?

2) Plot the activation sigmoid activation function which is used in the script.

3) Why is the activity of the excitatory population lower for the second stimulus? What happens if the second stimulus is presented earlier or later?

4) What happens if only one stimulus is presented for a long time (100 ms)?

5) Change the amplitude of the stimulus. Does the peak excitatory population activity depend linearly or non-linearly on the stimulus amplitude?

6) Adjusting the model parameters, is it possible to get a longer fluctuation of the population activity (say beyond 400 ms)?

7) What are iso-clines (check on the internet)? What is the meanding of the dashed iso-cline which does not run through the origin?