

Contents

- [News](#) – Updates & meetings
- [Spike2](#) – Detecting EPSP's
- [Spike2 Script](#) – Blood pressure measurements
- [Signal](#) – Dynamic clamping
- [Signal Script](#) – Measurement of intracellular action potentials
- [Did you know...?](#) – Apply Active Cursors settings to any data file
- [Recent questions](#) – Background images for target tracking

News

UK Training Days 2011

Our UK training days will take place on Thursday 19th and Friday 20th May in Cambridge. These training days are for existing and prospective users of Spike2 and Signal and are suitable for beginners and advanced users.

If you or any of your colleagues would like to attend, please follow the links to view the [training day program](#) and complete the [booking form](#).

Future meetings and events

Biophysical Society Annual Meeting 2011

Baltimore Convention Center,
Baltimore, MD, USA
March 5th – 9th 2011

Experimental Biology 2011

Walter E. Washington Convention Center,
Washington, DC, USA
April 9th – 13th 2011

British Neuroscience Association 2011

Harrogate International Conference Centre
Harrogate, UK
April 17th – 20th 2011

Young Life Scientists Symposium: Autonomic Control in Health and Disease

University of Birmingham
Birmingham, UK
May 26th 2011

UCL Neuroscience Symposium 2011

University College London
London, UK
July 1st 2011

Physiology 2011

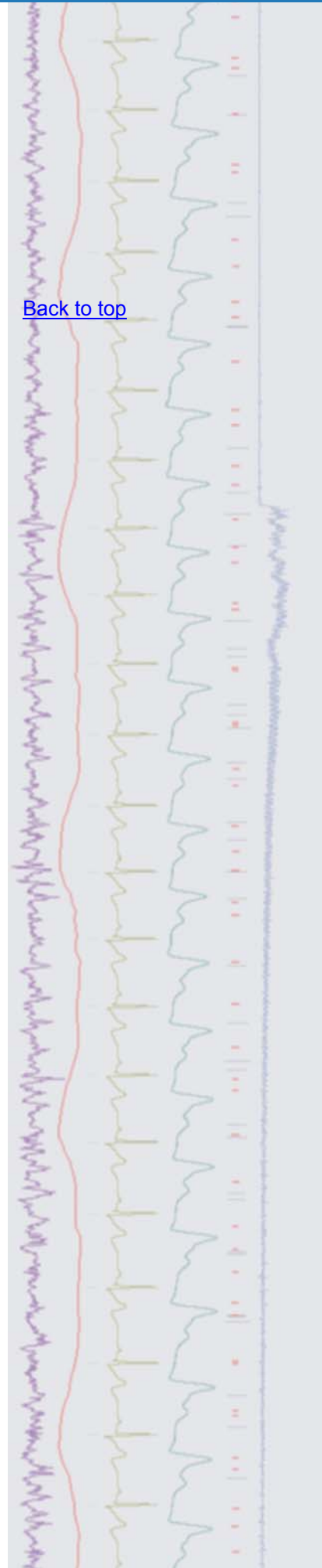
University of Oxford,
Oxford, UK
July 11th – 14th 2011

Latest versions of Spike2 and Signal

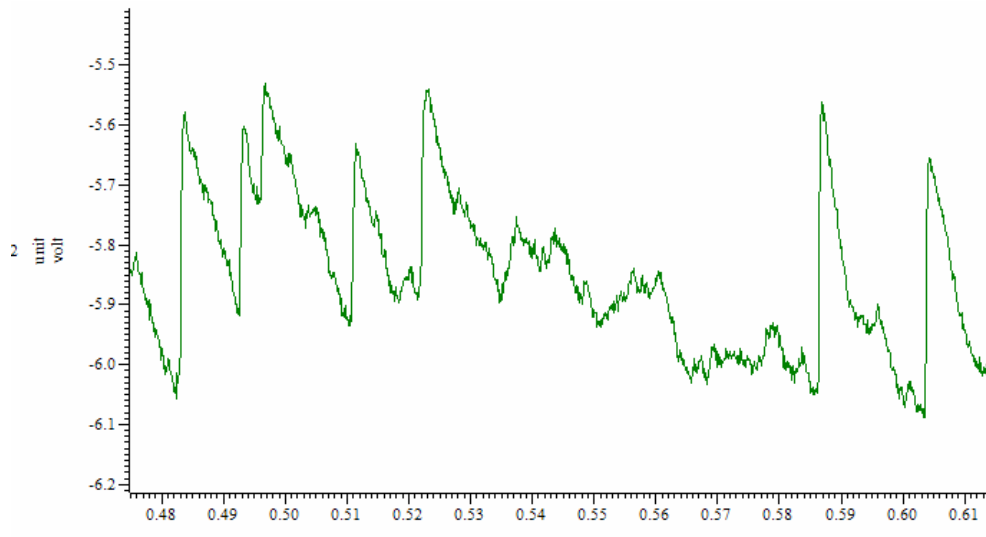
Updates for Spike2 and Signal are available from the [CED downloads](#) page, or by clicking on the links in the table below. Demonstration versions of the latest software are also available.

Spike2 downloads	Released	Signal downloads	Released
Spike2 version 7.06	02/11	Signal version 5.01	02/11
Spike2 version 6.15	10/10	Signal version 4.08	10/10
Spike2 demo		Signal demo	

[Back to top](#)



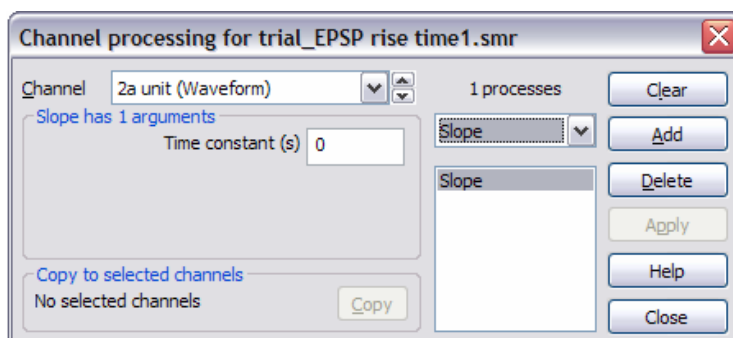
- Q. I am recording EPSP data and would like to be able to detect these in the file so that I can automatically get the time of each EPSP and perhaps take measurements. The only problem is that the baseline of the data shows a slow voltage oscillation which makes them hard to find reliably.
- A. Spike2 has a number of built-in functions that can be used to find and identify features of interest in a data channel. Active cursors can be set-up to find peaks, troughs and threshold crossings (as well as many other features) and automatically take measurements from each instance. In addition there are a number of channel processing options that can be used to condition the data so that relevant features can be detected with greater reliability.



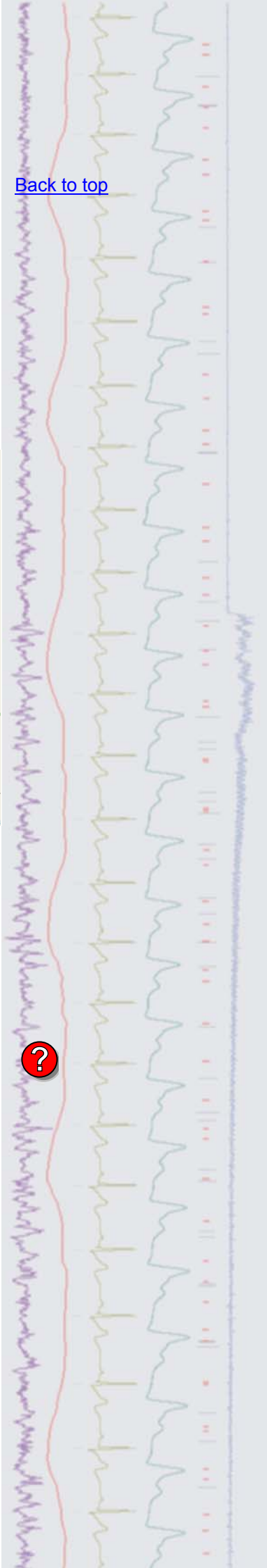
Raw EPSP data

In this example the EPSP's can be difficult to detect because of the oscillation of the baseline membrane voltage. We can however make use of the channel process commands in Spike2 to condition this trace and make the EPSP's more prominent and thus, easier to detect. Channel processes are dynamic and do not affect the data stored on disk, but use the raw data to display a calculated version of the trace on-screen. To view a copy of the processed data alongside the raw trace, use Duplicate Channel from the Analysis menu.

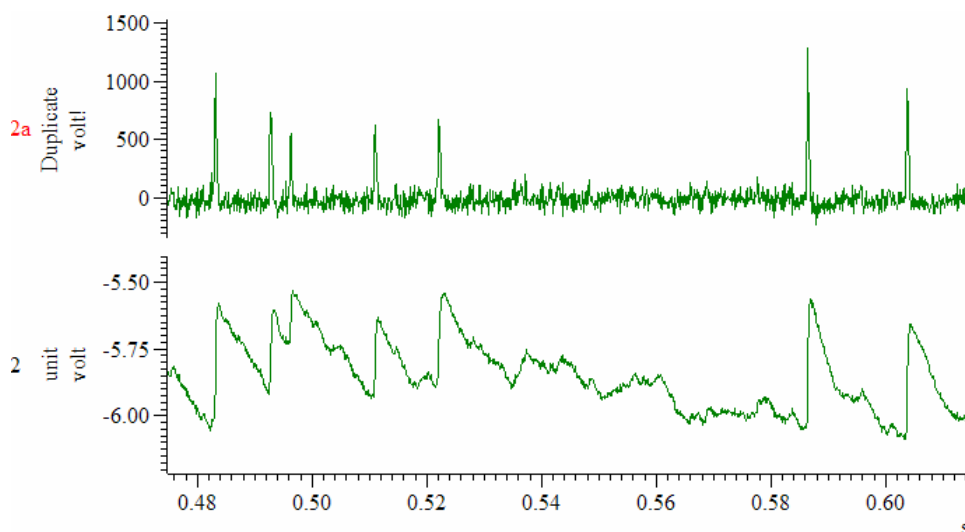
Channel processes are applied from the Channel Process dialog, which is available from the Analysis menu. The process to apply and the channel to process (our duplicate channel) are selected from the appropriate drop-down lists in the dialog. Select Slope from the drop-down process list and click the Add button. The Slope process is then added to the list below the drop-down field, which shows all of the processes that are being applied to the channel. Slope uses one argument, a time period in seconds which should be set to 0 for this example.



Channel process dialog



This modified copy of the channel shows detectable peaks marking the position of the maximum slope for each EPSP in the raw trace. You could then use Cursor 0 in active mode to find the time of these peaks and set-up additional active cursors to take measurements from the raw EPSP data based on this reference point.



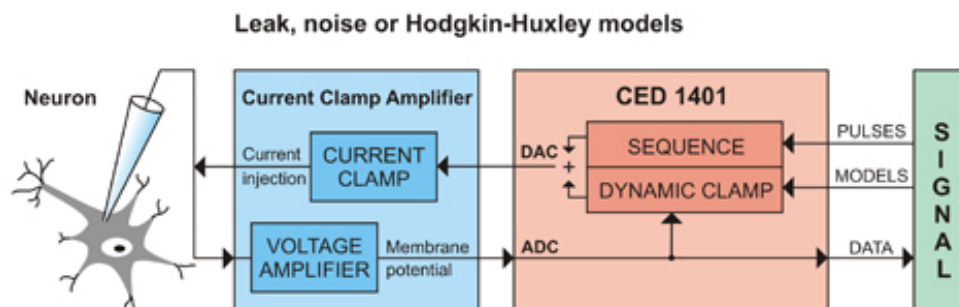
Raw (channel 2) and Processed (channel 2a) EPSP data

Scripts: Spike2 

- Q. I am recording blood pressure and would like to take a variety of measurements from these traces automatically during analysis.
- A. The script, `hrbp.s2s`, allows you to take a series of off-line measurements from a blood pressure trace. It creates additional channels containing measurements of heart rate, diastolic and systolic BP, pulse BP, and mean blood pressure. This script requires Spike2 version 6 or higher. A suitable example data file, `Blood Pressure Waveform.smr`, can be found in the data folder of your Spike2 directory.

Signal

- Q. I would like to know more about Signal's new capabilities for Dynamic Clamping.
- A. Dynamic clamp is a specialised technique in which current is delivered to a cell to represent the actions of virtual ion channels, allowing ion channels or synapses to be simulated or the actions of existing channels to be nullified; in effect adding or subtracting conductance to or from the cell membrane. These virtual ion channels or synapses are modeled using equations. A model can define something as simple as an ohmic leak conductance or as complex as a population of Hodgkin-Huxley ion channels, or a synapse. These models take sampled waveform channels as inputs and apply a set of equations that determine the current to be injected by the amplifier, which is controlled by a DAC output from the 1401.



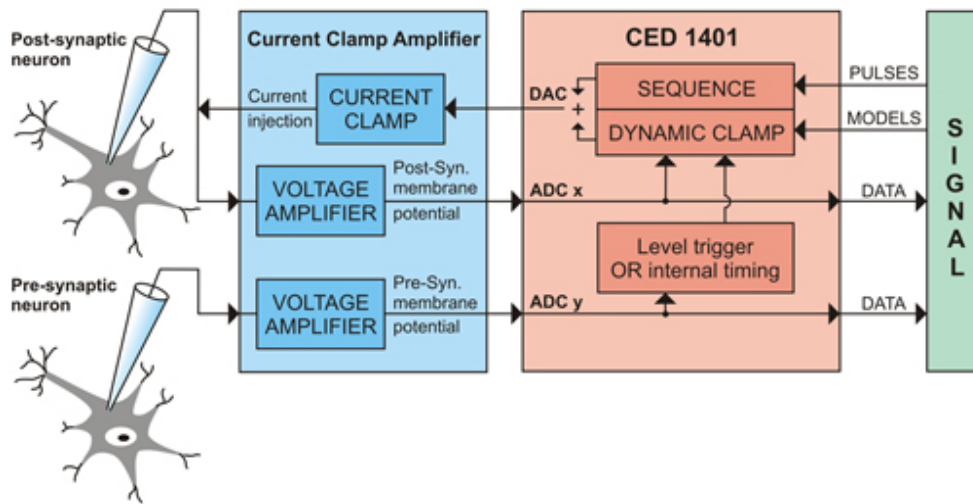
[Back to top](#)

Right-click the script icon and save to disk.

If you have any problems opening the embedded scripts in this newsletter please let us know.

[Back to top](#)

Synapse models (except electrical)



Signal control of dynamic clamping

The main areas of research that dynamic clamping is used for are:

- Isolating the ionic conductance of a particular ion type in order to study specific effects on the cell
- Connecting two cells in a brain slice with a virtual synapse in order to study a cell's response to synaptic input, or generate hybrid networks. The pre-synaptic cell can also be replaced with an artificially generated action potential

To be useful for research, this process has to be done quickly, relative to the speed of the biological process being simulated, therefore the mechanisms used to evaluate the equations need to be fast. Signal version 5 includes a high performance, easily configurable, dynamic clamping system which is fully integrated into the sampling configuration. It makes use of the Power1401 mk II design to evaluate the model equations at the same rate as the ADC inputs are sampled, ensuring that the timing is fast and unaffected by the non real-time aspects of the Windows operating system.

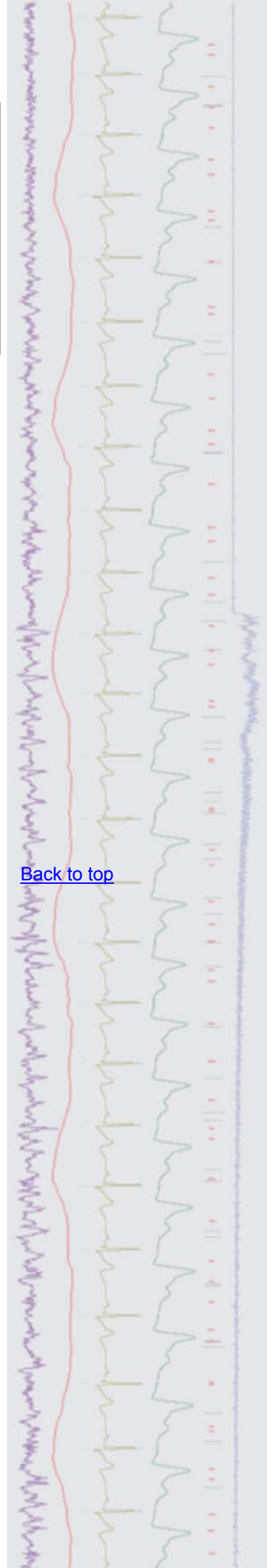
A simple GHK Leak example

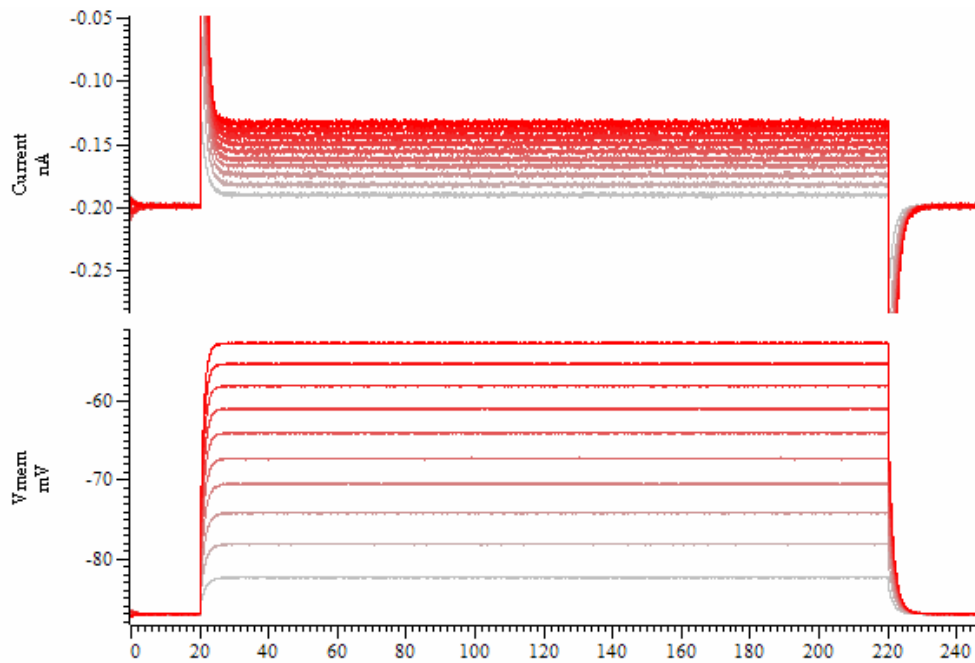
A Goldman-Hodgkin-Katz leak is a model which generates a simulation of permanently-open ion channels where ionic movement through the channels is driven by a difference in the ionic concentration across the membrane.

Leak model dialog

The input channel is used to record the membrane potential and should be connected to the scaled output port of your current clamp amplifier. The Control DAC should be connected to both the external command input of the amplifier and an ADC channel of your choice to visualise the current being injected into the cell. The input channel should be calibrated in mV and the Control DAC and current channel calibrated in nA or pA. To show the leak in action we also need a varying current input, which is achieved by adding a varying current stimulation pulse (200 ms, amplitude 0.1 nA increasing to 1nA in steps of 0.1 nA) to the Control DAC output in the pulse configuration dialog.

[Back to top](#)





GHK leak example

The simulated ion diffusion generated by this model has the effect of driving down the baseline membrane potential towards a resting potential generated by to the ionic conduction difference, partly canceling out the effect of the input pulse

A more complex Hodgkin-Huxley example

A Hodgkin-Huxley model simulates ion channels whose behaviour is voltage dependent with complex dynamics. This example aims to simulate action potentials by starting with the example GHK model used above and adding suitable voltage-dependent sodium channels.

Hodgkin-Huxley (Alpha - Beta)

Model Name:

Input Channel (mV): G_{max} : nS

Control DAC (nA): E_r : mV

Activation

Include

p :

$F_{\alpha}(x)$: ▾

k_{α} : ms^{-1}

V_{α} : mV

S_{α} : mV

$F_{\beta}(x)$: ▾

k_{β} : ms^{-1}

V_{β} : mV

S_{β} : mV

Inactivation

Include

q :

$F_{\alpha}(x)$: ▾

k_{α} : ms^{-1}

V_{α} : mV

S_{α} : mV

$F_{\beta}(x)$: ▾

k_{β} : ms^{-1}

V_{β} : mV

S_{β} : mV

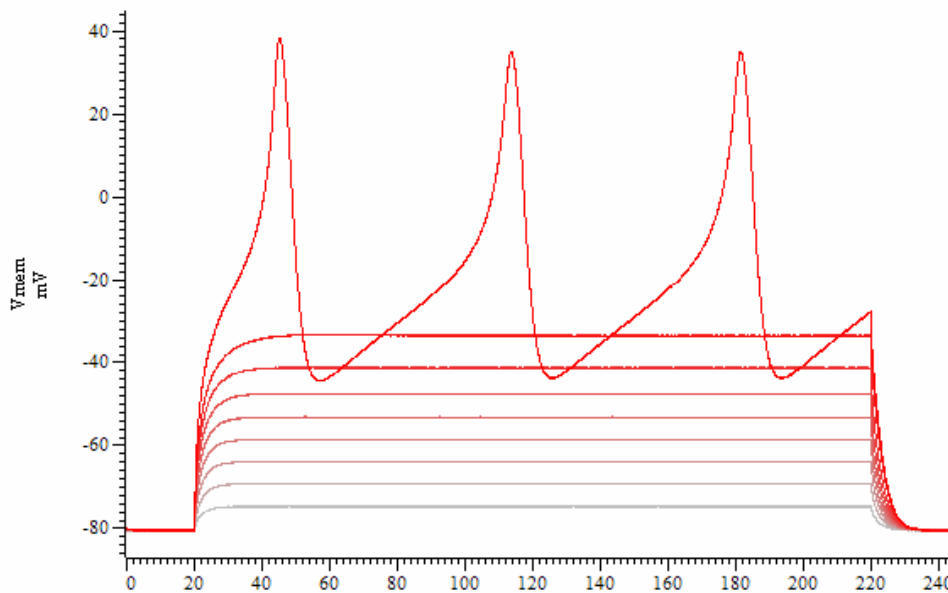
Disable model

Hodgkin-Huxley (Alpha-Beta) Model dialog

When this sampling configuration is run with both models enabled it generates simulated action potentials in response to the increasing current injection, as displayed below.



[Back to top](#)



Simulated action potentials generated using dynamic clamping

The attached sampling configuration, `DynClampTest.sgc`, contains both of the models described above and should be ready to run with Signal version 5, a Power1401 mk II and a suitable patch clamp amplifier, in current clamp mode, that has an external command sensitivity of 2 nA/V and output gain settings which give a scaled membrane potential sensitivity of 10 mV/mV. This should be connected to a model cell that has an internal 500 MOhm internal resistance for these testing purposes.

Scripts: Signal 

Q. I'm recording intracellular action potentials and want to analyse multiple parameters. Are there any scripts available that would allow me to automate this?

A. The script, `IntraSpikeAnalysis.sgs`, will automatically run through a data file finding and taking measurements from each action potential. The user sets a level threshold using a horizontal cursor and the script then detects each potential that crosses this level and takes the following measurements;

- Time
- Amplitude
- Rise time from 10% to 90%
- Half width
- AHP (After Hyper Polarisation) peak amplitude

This script requires Signal version 4 or higher. A suitable example data file, `Actions.cfs`, can be found in the data folder of your Signal directory.

Did you know...?

Spike2 Active Cursor settings are stored in the accompanying resource file (.s2r) of the data file. You can apply these cursor parameters to any data file by using the `Global resources` function in the `File` menu.

Recent questions

Q. It would be very useful to be able to show images for use in eye tracking experiments, either in an XY window or the data file channels.

A. You can now set background bitmap images in data files, result views and XY channels from Spike2 version 7.06 for use in tracking experiments. Images can be controlled interactively using the `View` menu `Channel Image` command or with the `ChanImage()` script command.

[Back to top](#)

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[Back to top](#)

[Back to top](#)

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[Back to top](#)

