RESEARCH

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Application Note 253   Getting Started in BIOPAC Basic Scripting

BIOPAC Basic Scripting is a scripting language development option for executing, authoring, and debugging BIOPAC Basic scripts. It allows for viewing of runtime variables, creating new script files and editing existing script files, triggering of individual script functions for testing and single step functionalities.

This application note begins to explain the tools available for writing scripts for Acq*Knowledge* version 4.1.

Scripting functionality is available through an optional license available with Acq*Knowledge* 4.1.1 or above. The Scripting license must be authorized to access Script functionality.Scripting is available for Windows Vista and Mac OS X 10.5 or above and also requires Qt SDK 4.5.0 or higher for rich dialog development

The Scripting license enables the Script menu, adds the Calculation channel Preset "Run Macro", links the **BIOPAC Basic Reference** under Help, and adds Preferences for Scripting.

1. Launch a version of Acq*Knowledge* 4.1.1 or above with an authorized Scripting license.

2. Information about the BIOPAC Scripting language – general information about the structure of the language as well as specific information about statements that can be executed – is available in the "BIOPAC Basic Reference" manual. This document is available via the "Help" menu of Acq*Knowledge*. Open this document to help convert actions that would normally be manually performed within Acq*Knowledge* to statements that will be executed automatically when the script is run.
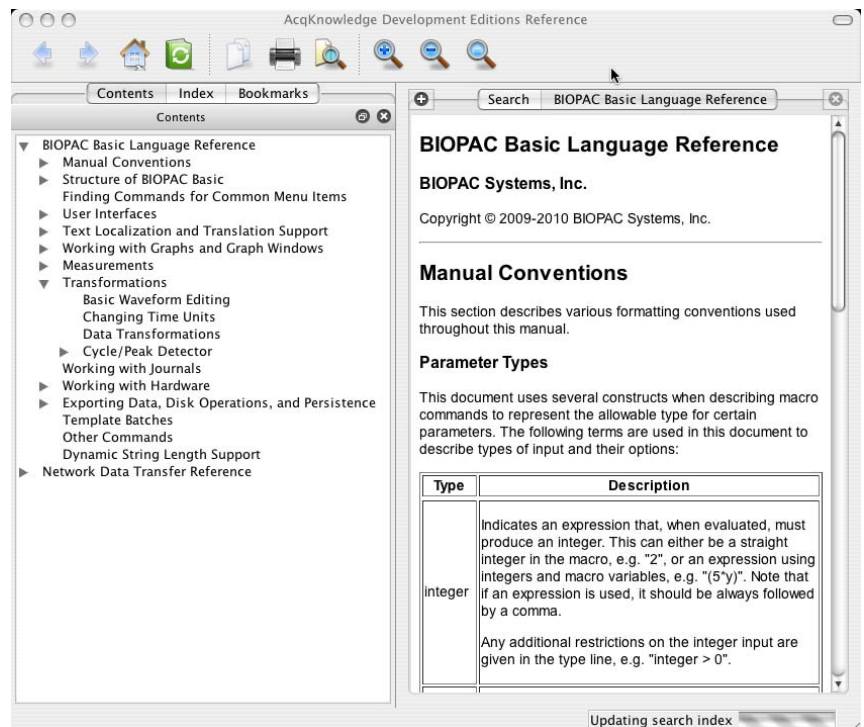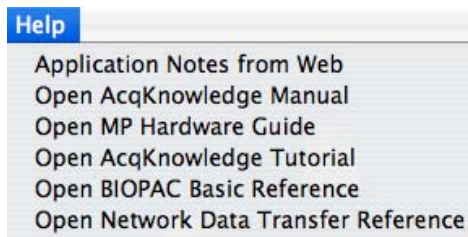
Review the manual to get an overall sense of the language. An effective way to use the manual is to browse through the Contents or Index tabs to find out how to generate statements to perform particular tasks.

3. Select Script > Script Editor.
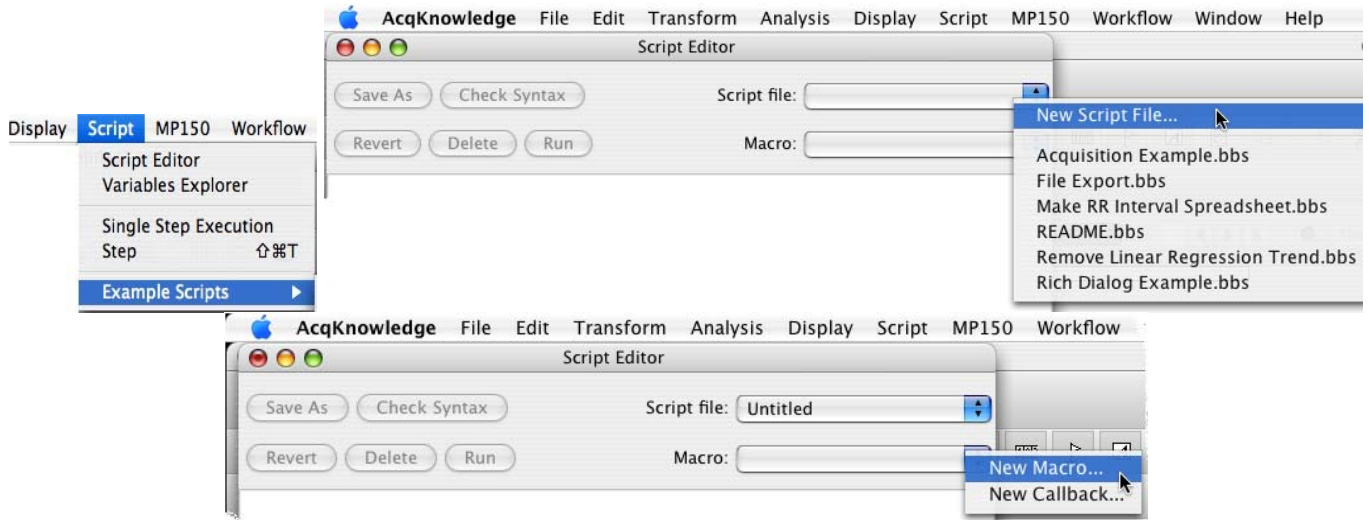
4. Click the Script file pull-down menu and select New Script file. This will create a script file to edit; existing script files can also be opened to edit.

5. Click the Macro pull-down menu and select New Macro. Scripts files are partitioned into Macros.

    a. When prompted, enter a name and click OK. It is a good idea to give the Macro a name describing its function. The Macro created in this example can be used to modify one of the methods for deriving a phasic skin conductance level (SCL) from a tonic SCL. When prompted, provide the name "GeneratePhasicSCL" for this example.

6. Set Script Editor Preferences to modify the appearance of the editor.

    ▪ Windows OS: Click Display > Preferences
   ▪ Mac OS: Click AcqKnowledge > Preferences
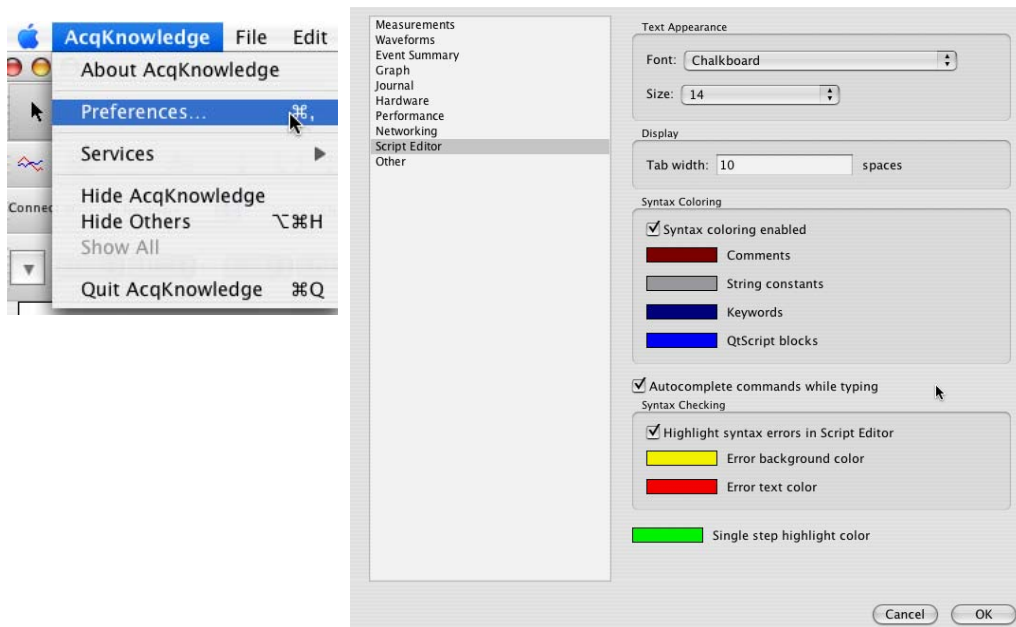
    a. A major feature of the editor is the color coding of different types of text. By default, statements will appear orange on a yellow background when the editor does not recognize them as valid instructions. "Script Editor" preferences can be set to modify this behavior as well as the colors of other types of text.

7. The example script generated below circumvents a problem with an analysis of skin conductance data. If a 0.05 Hz high pass filter is used to generate phasic SCL from tonic SCL data, the first 30 seconds or so of the resulting phasic SCL are unusable. The problem is that the filter has to "settle". A simple way to overcome this problem is to offset the tonic SCL data so that the first point is zero. To do that, find the value of the first data point and then subtract that value from the entire wave.

   The remainder of this note details steps to learn how to generate a script that will accomplish this task and then automatically generate a phasic SCL unaffected by any filter settling.

8. The first step in this process is the determination of the value of the first data point. To perform that task manually, either use the "Selection Palette" or select the I-beam tool and then use the mouse and/or cursor keys to move the cursor to the first data point. Find its value by setting one of the Measurement boxes to "Value."

9. The first step in BIOPAC Basic script requires a selected area.

   a. Browse through the Contents tab of the Reference and double-click "Selecting Data in the Graph" in the left pane to display that section of the manual in the right pane. Scroll down in the reading pane to the "Set Hcursor" description.
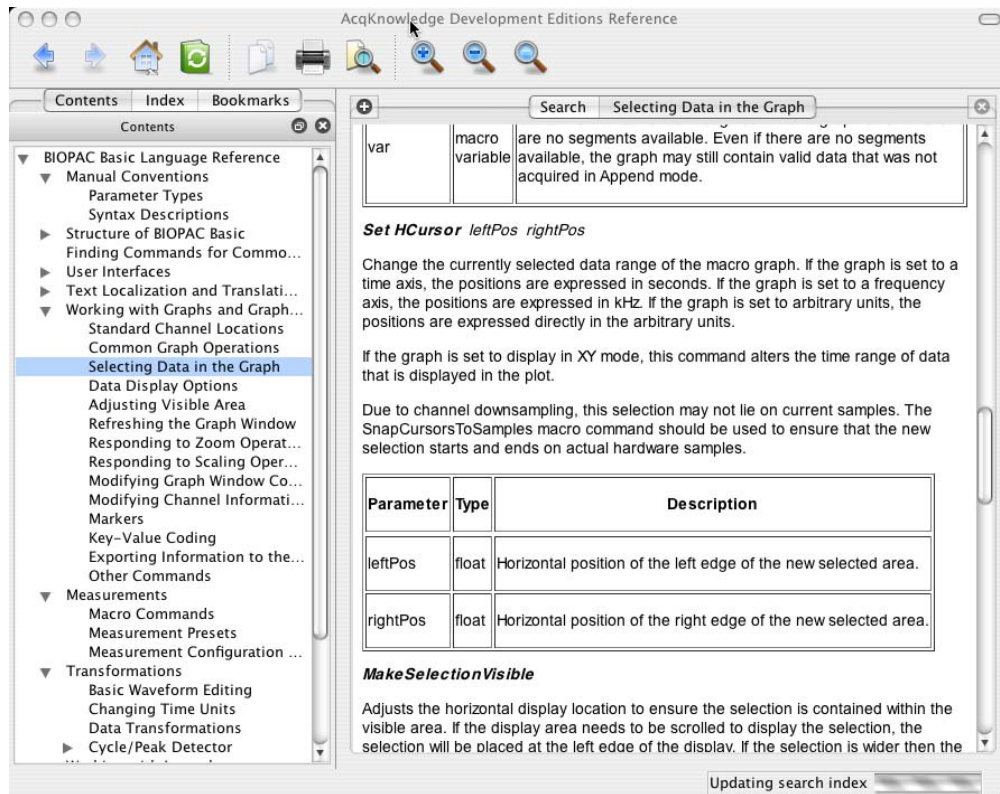
   The example script created here will assume that the user has already selected the tonic SCL data channel, so the first task for the script is to move the cursor to the first data point. At that point, the time (the x axis value) is zero. Set both the left and right edge of the selected area to zero.

   ▪ As text is typed, the editor highlights orange with a yellow background (unless the Preferences were changed).
   ▪ The editor attempts to anticipate by offering choices that will complete words that have been partially typed. Scrolling down the list and clicking on the selection will complete the word. In this case, once "Set " has been entered, the editor provides choices for what can be set. Scroll down and select "HCursor" without typing it:
   ▪ Note that "Set" is no longer in orange because although the entire statement is not executable (as indicated by the yellow background), the word "Set" is recognized as the start of a valid statement.
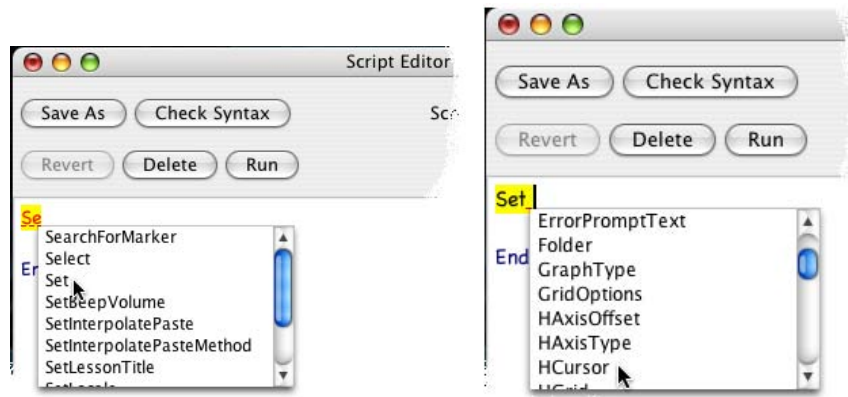
    b.   As indicated in the BIOPAC Basic Reference, "Set Hcursor" takes two arguments, the left and right edges of the area to be selected. Statements that require multiple arguments must have those arguments separated by commas. With this information, the first line of BIOPAC Basic script can be completed.

10. The next step is to subtract the value at that point from the entire waveform. Write the transformed values to a different channel to maintain the original waveform. To do this manually, choose Transform > Waveform Math and set the Destination to New. A good way to find relevant script commands is to search the index for words in the menu items. By selecting the Index tab and typing, in this case, "Math" in the "Look for:" box, the appropriate script command will be displayed.
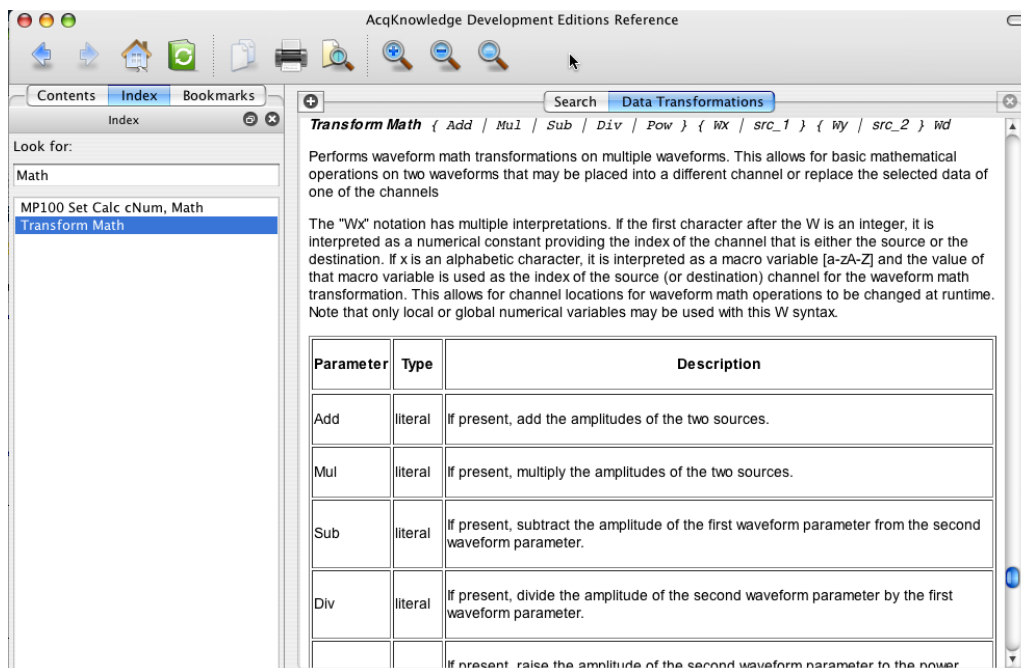
11. Create a destination channel. The description doesn't indicate a way to set the destination to "New"; this feature is not

available for this command. One way to do this manually would be to choose Edit > Duplicate Waveform. A search of the Index for "Duplicate" indicates that this function is scripted as "Edit Duplicate" with an optional output argument. The output, if requested, is the channel number of the new channel created by this command.

12. By assigning the channel to a variable, it can be specified as one of the sources as well as the destination when "Transform Math" is executed. "Transform Math" takes up to four input arguments.

   a. The first argument specifies the operation. To perform a subtraction, that argument should be "Sub".

   b. The second argument specifies what will be subtracted. "Value" is equivalent to a "Value" measurement – it is the y-value of the selected channel at the cursor location. As noted above, this script assumes the original tonic SCL channel is selected before the script is run. The "W" notation specifies that the next letter (or number) is to be interpreted as a channel number. In the example code below, the duplicated channel number was assigned to the variable "a".

   c. The next two arguments (both of which are "Wa") thus specify that channel as the source from which Value will be subtracted and also the channel that will hold the results of the transformation.

```
Script Editor

[ Save As ]  [ Check Syntax ]        Script file: [ CustomPhasicFromTonic.t ⬍ ]

[ Revert ] [ Delete ] [ Run ]        Macro: [ GeneratePhasicSCL        ⬍ ]

Set HCursor 0, 0
Edit Duplicate a

Transform Math Sub Value, Wa, Wa

Select Wave a
Edit SelectAll

Transform IIRFilter HighPass, 0.05, 0.707

Set Channel a, Label, "Phasic SCL"

Autoscale

End
```

13. After the program executes the previous statements, the original tonic SCL channel is still selected. Select the channel, "a", that was just created and transformed. To make sure the next transformation is applied to the entire data set, the selected area must also be changed. Searching the Index for "Select" produces a list that includes "Select Wave" and "Edit SelectAll"; these are the statements that must be included to select all data in the new channel.

14. The phasic SCL will be created with an IIR Filter. A search for "Filter" brings up a list including "Transform IIRFilter." The *AcqKnowledge* manual specifies that the filter normally used to derive a phasic SCL signal has a cutoff frequency of 0.05 Hz and a Q value of 0.707. With this information and the description of Transform IIRFilter in the BIOPAC Basic reference, the next statement can be written.

15. Two typical cosmetic fixes, changing the label and vertical autoscaling, will make the data more readily interpretable. The statements required to produce these fixes complete the sample script.

16. Select a graph window and then click the "Run" button in the Script Editor window.

   ▪ If, unlike this example, the file contains more than one channel, make sure that the channel containing tonic SCL data is selected.
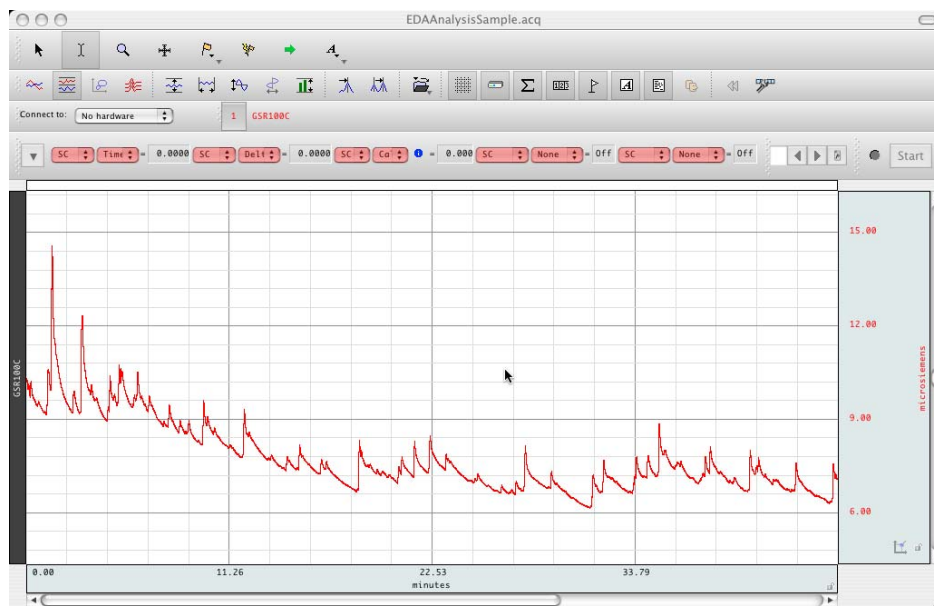
sample EDA data file
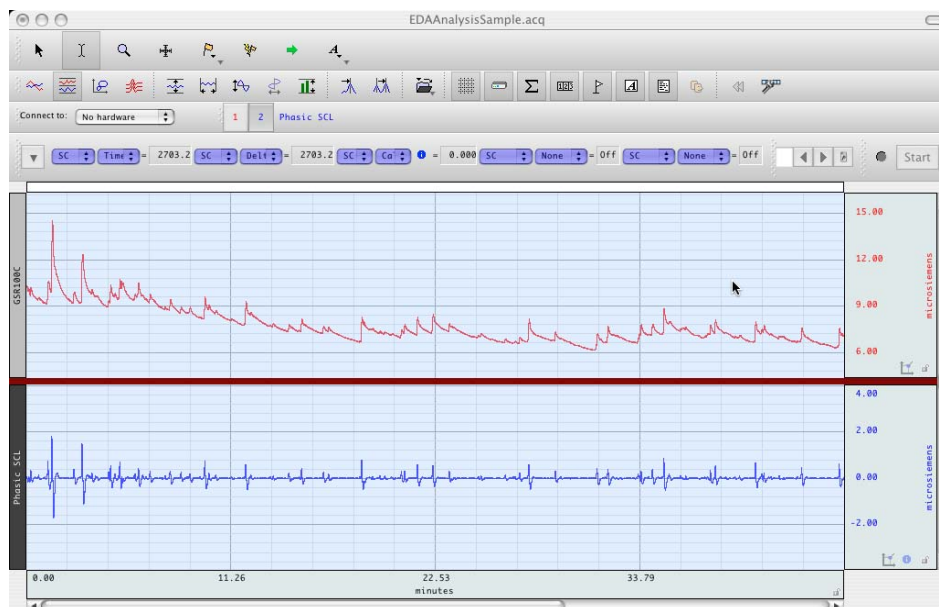
result of running the script.

17. Save the script so that it can be run again on other data files.

    a.   Select the Script Editor window so that file operations will be applied to the script instead of the graph.

    b.   To save a new script, click the "Save As" button or choose File > Save.

18. To access the script again in other *AcqKnowledge* sessions

    a.   Choose File > Open.

    b.   Set the file type to BIOPAC Basic Script (*.bbs).

    c.   Navigate to the file.

    d.   Click "Run" to execute the script on the current graph window.