# MYOMED™

**SOF-561**
**DOC-084**
**Rev. 1.6**

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# CHAPTER 1

## *Introduction*

MyoMED™ is a customizable state-of-the-art laboratory station for conducting studies on muscle contractility in vitro. The system consists of either four or eight myographs. Each myograph contains a high-resolution force transducer; a high-quality Radnoti™ water-jacketed tissue bath, and an optional electrode assembly for tissue stimulation. The optional stimulator units are individually isolated to allow independent control of stimulation parameters in each myograph.

MyoMED software displays the force recording for each myograph in chart recorder fashion. Modifiable stimulator parameters include pulse rate, pulse width, pulse amplitude, stimulus duration, pulse polarity (+, -, or AC), and stimulus repeat. These controls are all easily modified from the main data acquisition window.

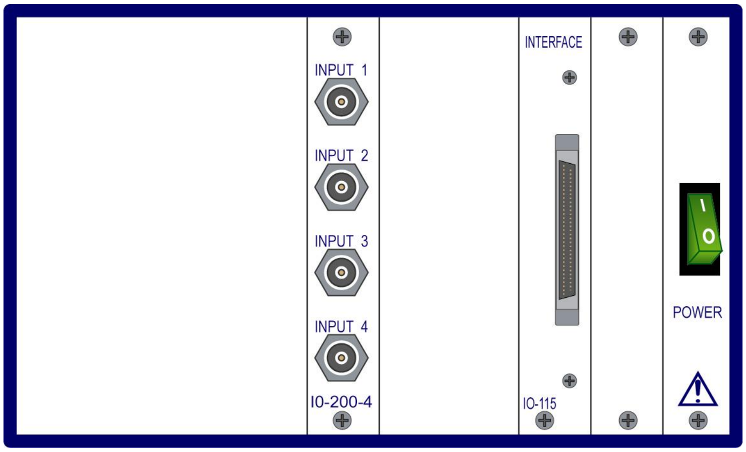
### Computer Requirements

- 3.0GHz Processor
- 512MB RAM
- Windows 2000 SP4 or XP
- Two available PCI slots

### Catamount R&D Hardware Guide

*Figure 1-1 - Computer with DIG-729PCI Card and DIG-744 Card*

*Figure 1-2 – Force Transducer Interface Cabinet (with IO-200-4 and IO-115 Cards)*



## Optional Stimulus Hardware Guide

*Figure 1-3 - Stimulus Interface Cabinet (with SG-510, PHM-152I and PHM-152COM Cards)*

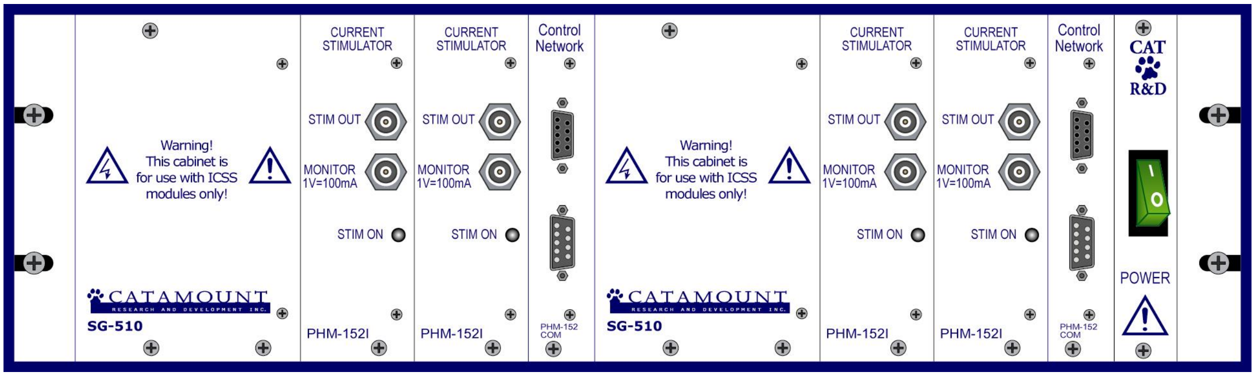
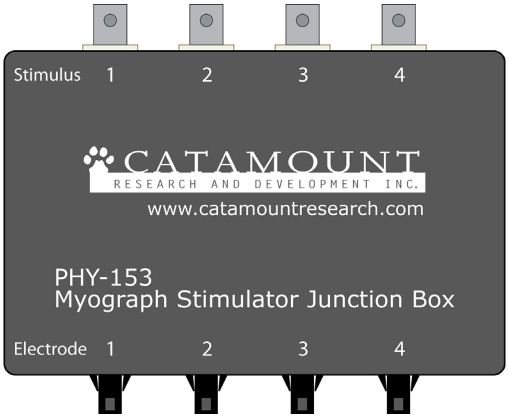


*Figure 1-4 - PHY-153 Stimulus Junction Box*



## Radnoti Hardware Guide

Refer to the Radnoti Manual for quantities and part numbers for all of the hardware shown below.

*Figure 1-5 - Radnoti Hardware Diagram*

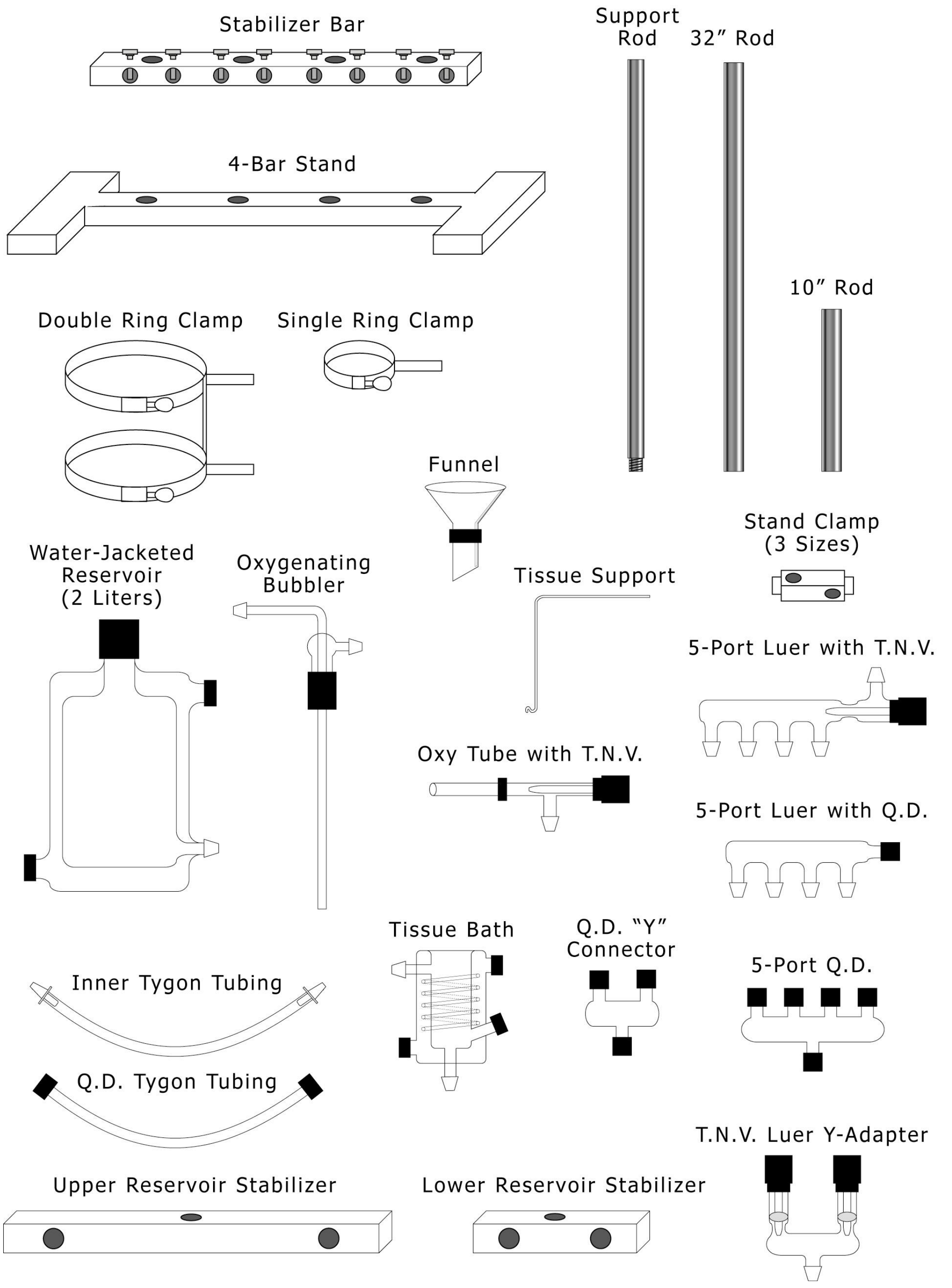
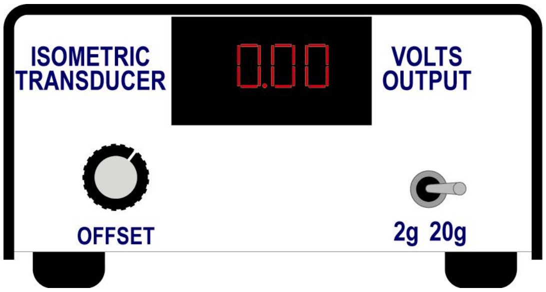


*Figure 1-6 – Radnoti Force Transducer Front Panel*



## Cable Guide

*Figure 1-7 – PHM-155E BNC Cable*

*Figure 1-8 - SG-244 Cable*

*Figure 1-9 – SG-219G DB-9 Cable (Only with Optional Stimulators)*

# CHAPTER 2

## *Hardware Installation*

Some general considerations should be made prior to selecting a location for the completed MyoMED Myograph system. The location should have both easy access to a vacuum line or pump to connect to the drain system of the Myograph and also have access to gas cylinders containing the gas mixture that will be used to aerate the tissue baths.

Unpack all of the Myograph hardware and verify that all of the necessary hardware has been included. Set up the computer and peripherals, referring to the instructions included with the computer.

### Radnoti Equipment Assembly

Refer to the Radnoti Tissue Organ Bath System manual (included with the order) for detailed instructions regarding the assembly of the Radnoti hardware and plumbing, shown in Figure 1-5.

## Connecting Force Transducers

This section describes the connections required for the force transducers.

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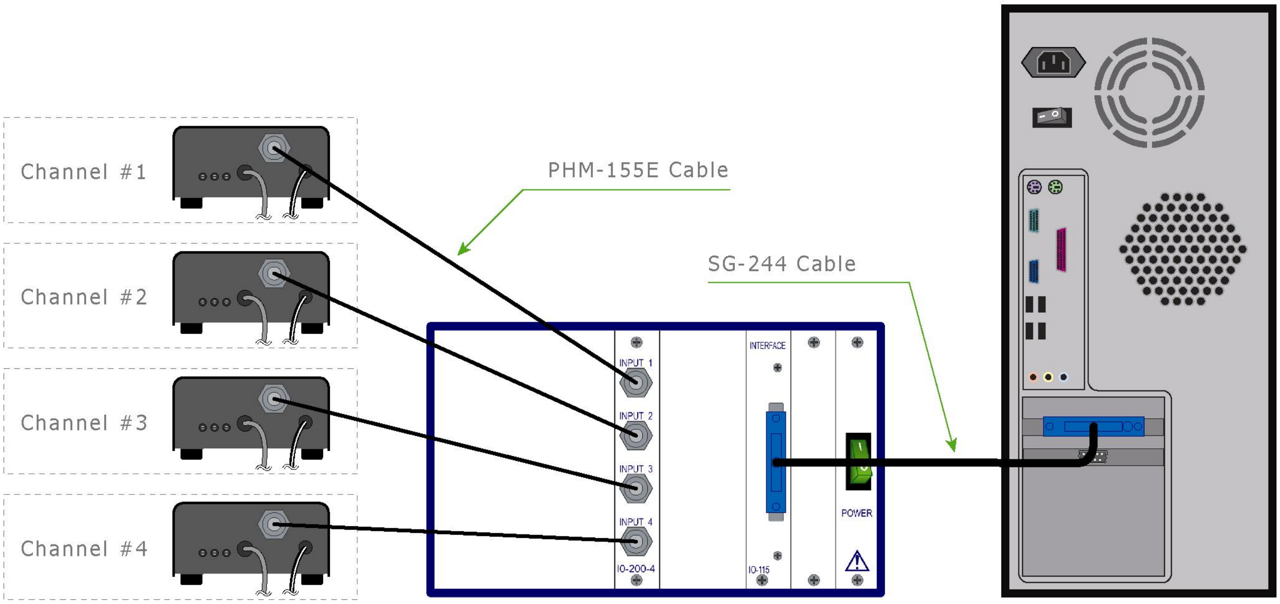
**NOTE:** Be sure that all hardware is disconnected from power prior to completing this section.

---

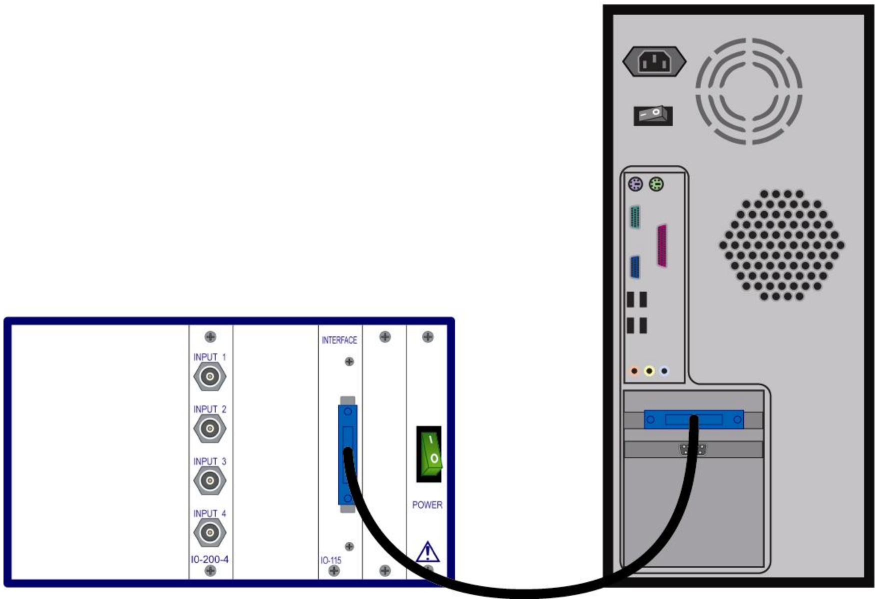
### Quick Reference



## Step-by-Step Instructions

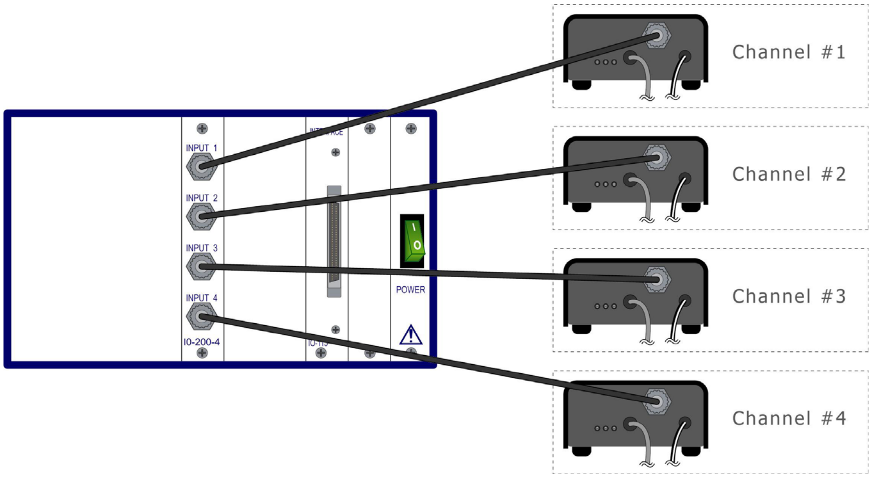
1. Using the SG-244 cable connect the IO-115 Interface Card to the NI-DAQ DIG-744 card as shown in Figure 2-1.

*Figure 2-1 – Connect IO-115 Card to DIG-744 Card Using the SG-244 Cable*



2. Using a PHM-255E BNC cable, connect the BNC Connector on the back of each Radnoti Force Transducer to corresponding **INPUT** connector on the IO-200-4 card, as shown in Figure 2-2.

*Figure 2-2 – Connect Radnoti Transducers to IO-200-4 Using BNC Cables*



3. Connect each Radnoti Force Transducer to a standard wall outlet.
4. Apply power to the computer and the Force Transducer Interface Cabinet.

## Connecting Optional Stimulators

If the myograph system was not purchased with the optional stimulator units, disregard this section.

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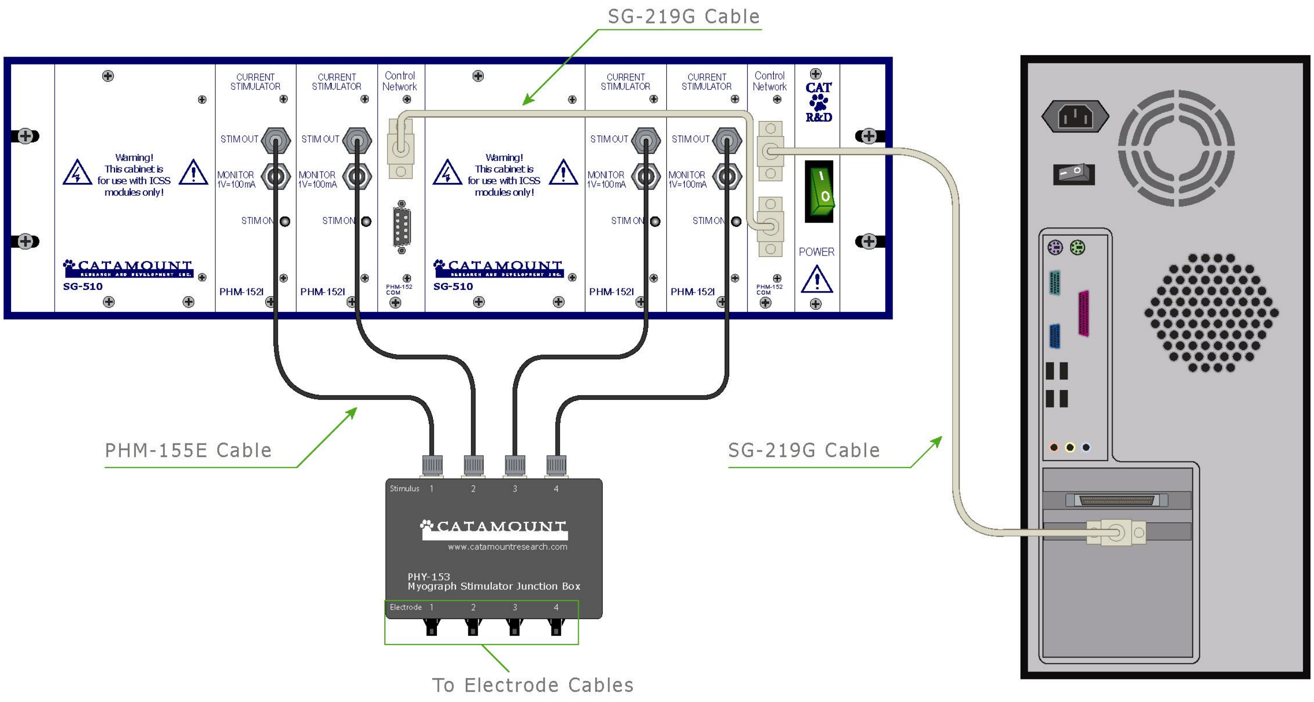
**NOTE:** Be sure that all hardware is disconnected from power prior to completing this section.

---

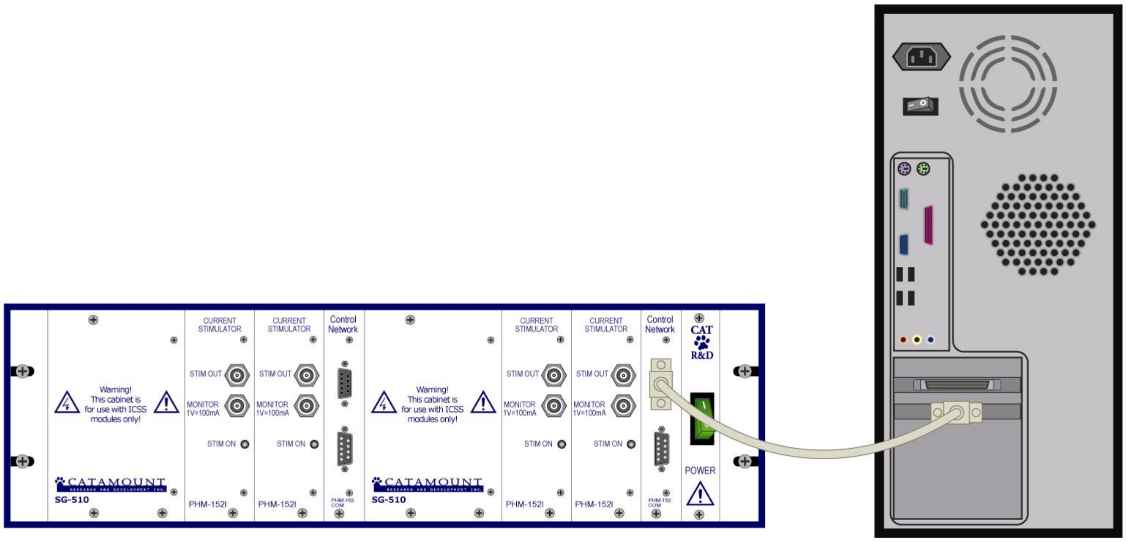
### Quick Reference



### Step-by-Step Instructions

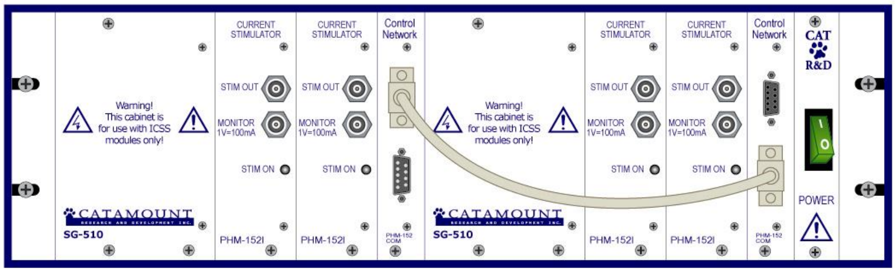
1. Mount the PHY-153 (shown in Figure 1-4) to the Support Rod (shown in Figure 1-5).
2. Using the 10-foot long SG-219G cable, connect the PHM-152 COM Control Network Card to the DIG-729PCI Card, as shown in Figure 2-3.

*Figure 2-3 – Connect the PHM152 COM Card to the DIG-729PCI Card*



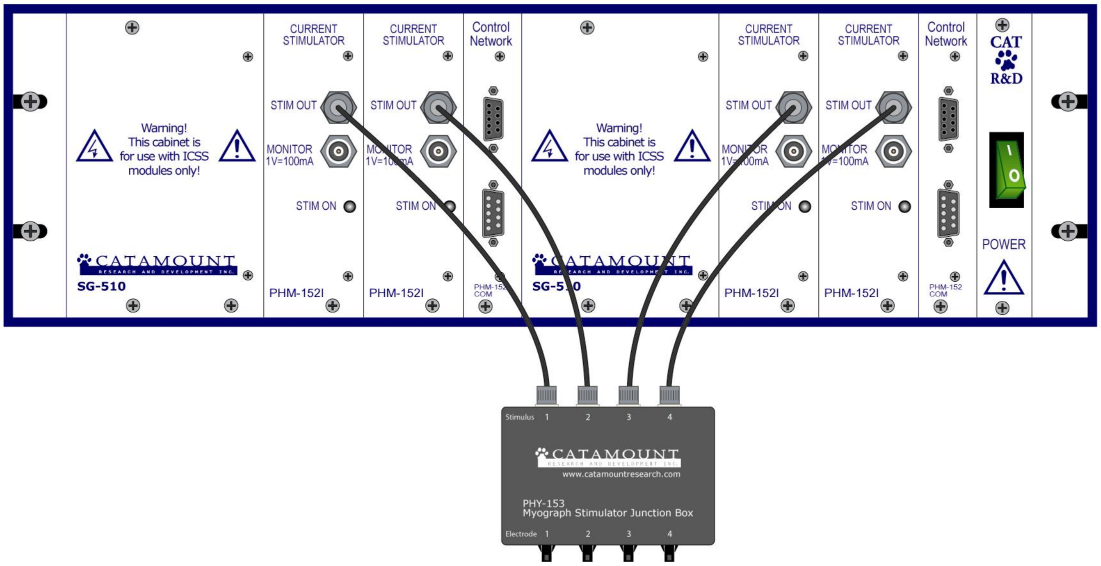
3. Using the 2-foot long SG-219G cable, connect the PHM-152 COM Control Network Cards as shown in Figure 2-4.

*Figure 2-4 – Connect the PHM-152 COM Cards*



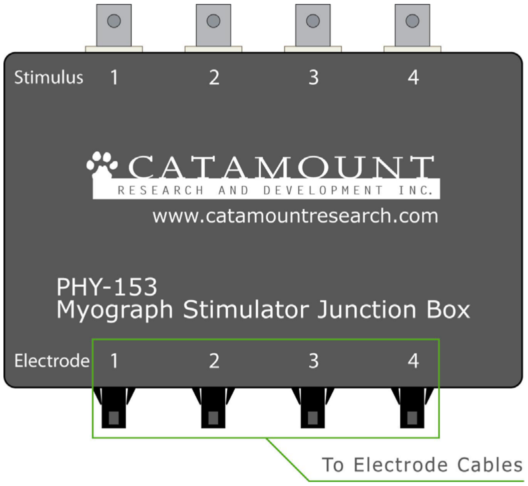
4. Using PHM-155E BNC cables, connect the **STIM OUT** connectors on each of the PHM-152I Current Stimulator Cards to the corresponding **STIM** port on the PHY-153, as shown in Figure 2-5.

*Figure 2-5 – Connect PHM-152I Cards to PHY-153 Using BNC Cables*



5. Connect the electrode cables to the corresponding **Electrode** connectors on the PHY-153, as shown in Figure 2-6.

*Figure 2-6 - Connect Electrode Cables to PHY-153*



6. Apply power to the computer and the Stimulus Interface Cabinet.

# CHAPTER 3

## *MyoMED Software*

MyoMED software is a customized data acquisition program designed specifically for performing contractility measurements in isolated tissues. It is extremely powerful and easy to use.

The MyoMED program acquires data from force transducers for each organ bath in the myograph system. It provides a display of data during an experiment in chart recorder format. The software allows the user to keep track of the timing of an experiment and to enter comments or event marks indicating when drugs are applied, for example. For users who are performing electric field stimulation using our PHM-152 stimulator units, the stimulators can be controlled right from the MyoMED window. Each organ bath receives input from an individually isolated stimulator so that users can study distinct stimulus protocols simultaneously. Data files generated in MyoMED software can be viewed and analyzed using MyoViewer software (Chapter 4).

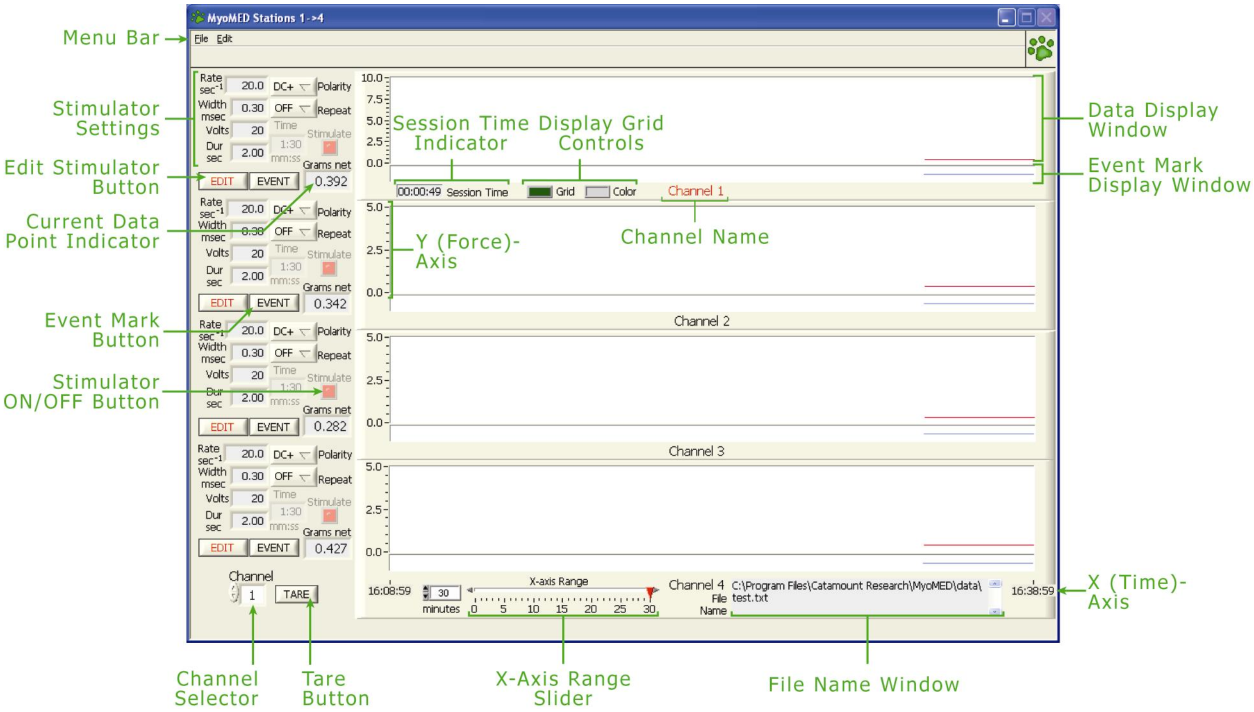
### MyoMED File Format Conventions

MyoMED generates two types of files during data acquisition (Appendix C). Scaled force data from each force transducer are saved in a binary format file with a .RAW extension. All event marks and text associated with an experiment are saved in an ASCII format text file with a .TXT extension. Every experiment performed with MyoMED will consist of a RAW file and a TXT file. When a file name is defined for an experiment, MyoMED will use that file name for the RAW and the TXT files. The RAW and TXT files associated with a given experiment must have the same name. For example, if an experiment is named "force", the RAW file will be "force.raw" and the TXT file will be "force.txt." The names of these files should not be changed after they have been saved, unless both the RAW file and the TXT file are changed to have the same name. MyoViewer data viewing software requires both the RAW and TXT files for a given experiment to have the same name (Chapter 4).

## MyoMED Main Window Layout

Figure 3-1 shows the MyoMED main window and its key features. The functional parts of the MyoMED main window will be described in detail in later sections. This section gives an overview of the items highlighted in Figure 3-1.

*Figure 3-1 - MyoMED Main Window*



There are four **Data Display Windows**, one for each myograph in a four-unit system (Figure 3-1). If an eight-unit myograph system is being used, a second monitor displays a window that contains signals and controls related to organ baths 5 through 8. Data Display Windows show tracings of the signals from the force transducers connected to their corresponding channels. The current value from a force transducer can be read from the **Current Data Point Indicator** located to the left of and towards the bottom of each Data Display Window. The Current Data Point Indicator is a digital meter that is labeled “Grams net.”

There is an **Event Mark Display Window** located below each Data Display Window. This window is narrow and contains a blue line. When an event occurs, a tick mark shows up in the blue line to indicate the event.

The **Channel Name** corresponding to each of the data display and event mark windows is displayed in the center below each Event Mark Display Window.

The space below the Data Display Window for Channel 1 has a **Session Time Indicator** and **Display Grid Controls**. The Session Time Indicator is a timer that starts counting when starting to recording experimental data (Chapter 4). It can be used to keep track of the relative time during an experiment. The **Display Grid Controls** allow the user to enable and disable grid marks in the Data Display Windows and to change their color.

Settings for controlling the X-axis (time axis) are found below the Data Display Window for Channel 4. Changing the X-axis settings affects the time scale for all channels simultaneously. The **X-axis Range Slider** specifies the length of time (up to 30 minutes) that is displayed in the Data Display Windows. The maximum and minimum values for the X (Time)-Axis are also indicated. Again, the values for the X (Time)-axis pertain to all channels. The File Name Window below Channel 4 indicates the full path for the data file that is currently being recorded.

The **Channel Selector** and **TARE Button** located in the bottom left corner of the MyoMED main window are the controls used for adjusting the offset for each channel.

Users who have the optional PHM-152I stimulator units can control the stimulators directly from MyoMED. The **Stimulator Settings** for each channel are displayed to the left of each Data Display Window. To modify the stimulator settings, click the Edit Stimulator Button. The stimulator is turned on and off by clicking the Stimulator ON/OFF Button.

Clicking on the **Event Mark Button**, located to the right of each Edit Stimulator Button, brings up an event mark dialog box and places an event mark in the file.

The **Menu Bar** at the top of the MyoMED window contains the **File** and **Edit Menus**.

## MyoMED Menu Structure

There are two main menus in the Menu Bar of the MyoMED window (Figure 3-1): **File** menu (Figure 3-2) and **Edit** menu (Figure 3-3).

### File Menu

*Figure 3-2 - File Menu*

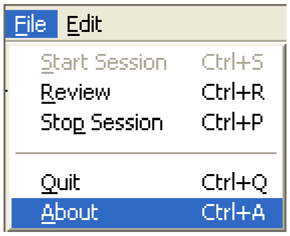
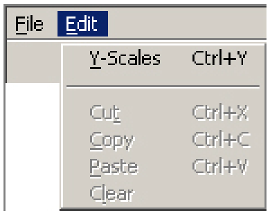


Figure 3-2 shows the File menu as it would appear after an experiment has been started. The appearance of the commands in the File menu will change depending on whether or not an experiment is in progress. Commands that are unavailable, or inactive, will appear grayed out, while commands that are active will appear solid.

- Choose **Start Session** to begin recording data. Start Session is only active before an experiment is started. While data logging is in progress, the Start Session command will be grayed out (inactive).
- **Review** is used during an experiment to inspect the contents of the data file. Review is only active during an experiment. Before an experiment is started, Review is grayed out.
- Choose **Stop Session** to stop recording data when an experiment is finished. Stop Session is only available while an experiment is in progress, and choosing Stop Session will not exit the MyoMED program.
- Choose **Quit** to exit the MyoMED program.
- Choose **About** to open the About dialog box, which contains copyright information and the current software version.

### Edit Menu

*Figure 3-3 - Edit Menu*



- Use **Y-Scales** to modify the range of the Y-axis (force) for each data display window.
- The **Edit** menu also has standard Windows clipboard edit commands: **Cut**, **Copy**, **Paste**, and **Clear**. These commands are only active when the cursor is in a text box.

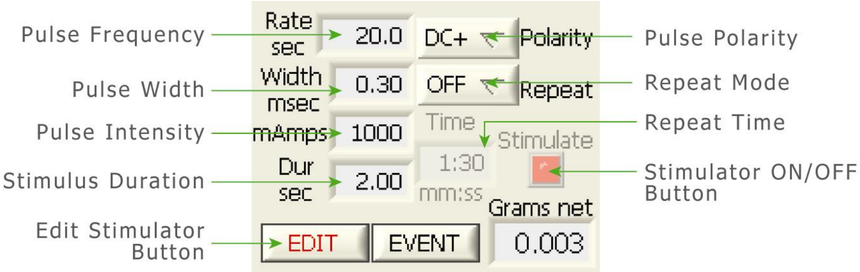
## Controlling Programmable Stimulators (PHM-152) From MyoMED

MyoMED data acquisition software provides an intuitive interface from which to control the PHM-152I series stimulators for performing experiments where electric field stimulation is desired. All stimulator settings and adjustments can be controlled right from the software. No hardware adjustments are needed. The MyoMED main window contains a display of the stimulator settings for each channel in the myograph system (Figure 3-1). If the myograph system was purchased without the PHM-152 stimulator units, the stimulator control functions within MyoMED software will be non-functional. If your system does not have the PHM-152 stimulators and you would like to upgrade, it is a simple matter of purchasing the stimulator units and the computer interface card. No changes to the MyoMED software are necessary.

### Stimulator Settings Display

The Stimulator Settings display is located to the left of each channel in the MyoMED main window (Figure 3-1). Each channel has a corresponding Stimulator Settings display. The Stimulator Settings display indicates the current stimulator settings. Figure 3-4 shows an expanded view a single Stimulator Settings display.

*Figure 3-4 - Stimulator Settings Indicator*



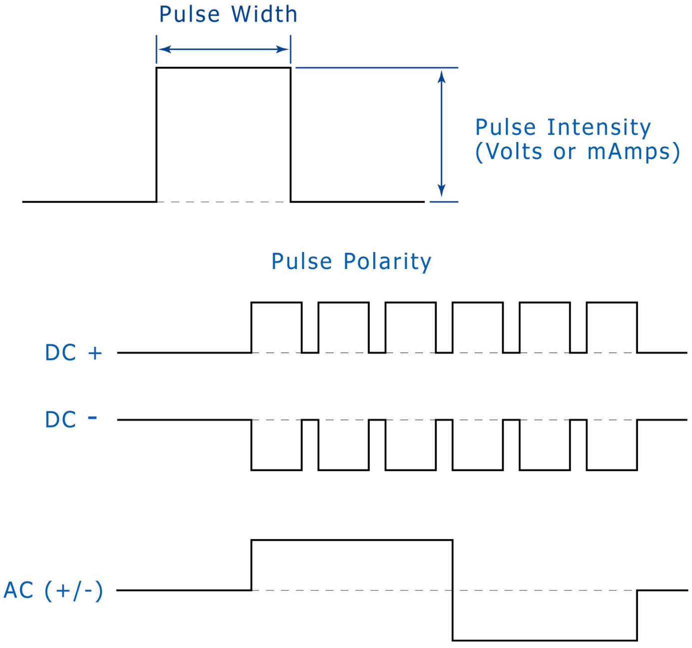
Stimulator settings can be changed at any time simply by clicking the **EDIT** button. Each channel has its own EDIT stimulator button.

## Stimulus Parameters Defined

### Individual Pulse Parameters

- The **Pulse Width** defines the duration of a single stimulus pulse. Units for the pulse width are milliseconds, and typical values are in tenths of a millisecond range. The range of the pulse width is 0.1 to 32 ms, depending on the frequency.
- The **Pulse Intensity** defines the amplitude of a single stimulus pulse. For the PHM-152V constant voltage stimulators, pulse amplitudes are given in volts. For PHM-152I constant current stimulators, pulse amplitudes are given in milliamps. The range of the pulse intensity is 0 to 40 Volts (0 to 400 milliamps).
- **Pulse Polarity** defines the polarity of an individual stimulus pulse. As shown in Figure 3-5, pulses can be positive, negative, or alternating polarity, referred to as DC+, DC-, or AC (+/-) for convenience. When trains of pulses are to be used, setting the pulse polarity to alternate (AC+/-) minimizes electrode polarization. This helps avoid stimulus artifacts due to electrode polarization.

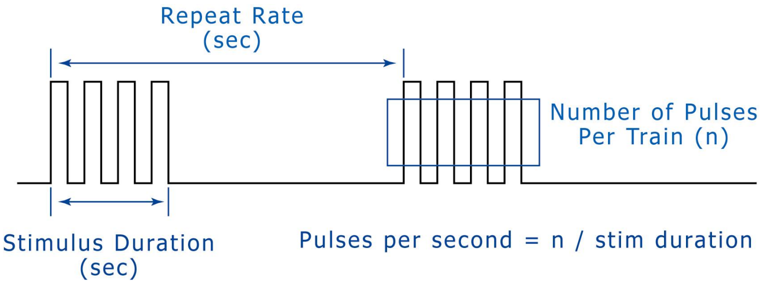
*Figure 3-5 - Individual Pulse Parameters*



## Pulse Train Parameters

- **Pulse Frequency** is the number of stimulus pulses per second. The range of the pulse frequency is 1 to 2000 pulses per second, depending on the pulse width.
- The **Stimulus Duration** is the length of time, in seconds that a train of pulses is applied. The minimum stimulus duration is 0.01 seconds and the maximum is the time it takes to generate 65,500 pulses.
- The **Repeat Mode** determines whether or not a stimulus train will be repeated. The options are ON, OFF and File. Refer to the Repeat Mode section of this manual (below) for more detailed information.
- If it is desired to have a pulse train repeated at set intervals, the **Repeat Time** defines the amount of time (in mm:ss) from the start of one pulse train to the start of the next pulse train.

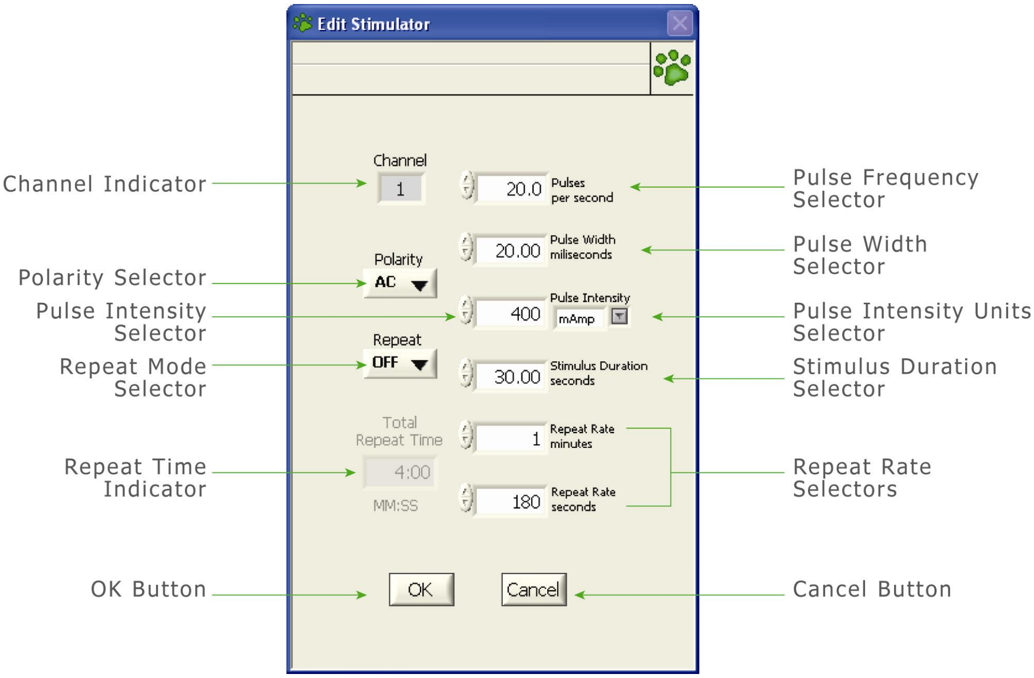
*Figure 3-6 - Pulse Train Parameters*



### Making Changes to the Stimulator Settings

To make changes to stimulator settings, click on the **Edit** stimulator button corresponding to the stimulator for the channel to change (Figure 3-1 and Figure 3-4). The **Edit Stimulator** window will appear (Figure 3-7).

*Figure 3-7 - Edit Stimulator Window*



Edit Stimulator

Channel: 1

Pulses per second: 20.0

Pulse Width miliseconds: 20.00

Polarity: AC

Pulse Intensity: 400 mAmp

Repeat: OFF

Stimulus Duration seconds: 30.00

Total Repeat Time: 4:00 MM:SS

Repeat Rate minutes: 1

Repeat Rate seconds: 180

The Channel Indicator shows which stimulator is currently being edited. Pulse Polarity is chosen from a drop down selector containing the available choices: DC+, DC-, AC+/-. Pulse Frequency, Pulse Width, Pulse Intensity, Stimulus Duration, and Repeat Rate are all set by either manually typing in the desired setting in the corresponding selector box or using the up/down arrows to the left of each box. The Repeat Mode is chosen from a drop down selector containing the available choices: ON, OFF, or File. Settings for Repeat Rate are only active if the Repeat Mode is set to ON.

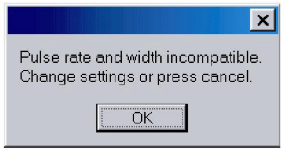
When the changes to the stimulator settings are complete, click the **OK** button. Exit the **Edit Stimulator** window without making any changes by clicking the **Cancel** button.

When the stimulator is set to manual mode, i.e. **Repeat Mode** is set to **OFF**, or when **Repeat Mode** is turned **ON**, stimulator settings can be edited at any point during data acquisition. Set the **Repeat Mode** to **File** if using pre-programmed protocol files (Chapter 5).

To review, when it is desired to change stimulator settings, click on the Edit stimulator button to open the Edit Stimulator window. Make the desired changes to the stimulator parameters and click OK to exit. Once back to the MyoMED main window, the settings that were just made should be displayed in the Stimulator Settings Indicator for the corresponding channel. If operating the stimulator in manual mode (i.e. Repeat is set to

OFF), the Stimulator ON/OFF button will have a bright red color (Table 3-1). To activate the stimulator, click the Stimulator ON/OFF button. The Stimulator ON/OFF button will flash bright green while the stimulus is being delivered. As soon as the stimulus is completed, the Stimulator ON/OFF button will return to a bright red color, indicating the stimulator is OFF. The color of the Stimulator ON/OFF button indicates important information about the status of the stimulator. Table 3-1 shows the various Stimulator ON/OFF button colors and defines their meanings.

*Table 3-1 - Stimulator Light Indicators and their Meanings*

| Stimulator Status Indicator | Description | Meaning |
|---|---|---|
|  | Grayed-Out Red | Communication error between computer and stimulators. Check cables and power. |
|  | Bright Red | Stimulator is **OFF**. Repeat is set to **OFF**. Stimulator is in "Manual Mode." |
|  | Flashing Bright Green | Stimulation is in progress using the current settings. |
|  | Dark Green | Stimulator is set to Repeat **ON** or **File** but is not activated. |
|  | Bright Green | Stimulator is set to Repeat **ON** or **File** and has been activated. Stimulator is in between stimulations. |
| Pulse rate and width incompatible.<br>Change settings or press cancel. | Invalid Settings Error | This error message appears when you have incompatible settings, such as a pulse rate of 100 pulses per second and a pulse width of 15 ms. Double check your settings. |

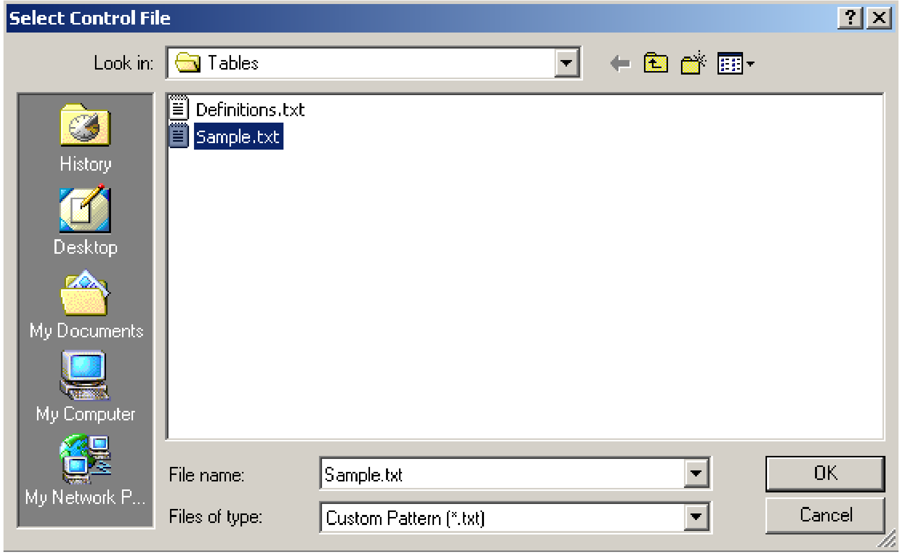
### Using the Repeat Mode

If it is desired to stimulate the preparation using the same parameters at set intervals, set the **Repeat Mode** to **ON**. Enter the desired **Repeat Rate** in the **Edit Stimulator** window. The **Repeat Rate** is the amount of time from the start of one stimulus to the start of the subsequent stimulus, refer to Figure 3-6. For example, if the **Repeat Mode** is **ON** and the **Repeat Rate** is set to 1:30 (1 minute 30 seconds), the selected stimulus parameters will be repeated every minute and a half. Click on the **Stimulator ON/OFF** button to deliver the first stimulus, the button will flash bright green (Table 3-1). When the stimulus is finished, the button will stay bright green, indicating that the stimulator is in standby waiting for the time between repeats to elapse. When the time set as the **Repeat Rate** has elapsed, the stimulator will automatically deliver the stimulus using the same settings. The repeating will continue until the **Stimulator ON/OFF** button is clicked again. The button will change to bright red indicating that the stimulator is OFF. If the stimulator is in Repeat Mode, Edit can be clicked to change certain settings between successive repeats. This is useful if it is desired to increase or decrease certain parameters from stimulus to stimulus.

## Using Repeat Mode with Protocol Files

A more advanced and powerful way to change stimulus settings between successive stimulations is to use the "**File**" feature of **Repeat Mode**. Setting **Repeat Mode** to **File** will load a pre-programmed stimulus protocol into memory and execute stimulations based on parameters set in the file. To use a pre-programmed protocol, click the **Edit** button for the desired stimulator(s). From the Repeat Mode selector, choose File. This will open a window titled "Select Control File" (Figure 3-8). Browse to the directory where the protocol file was stored. It should have a "txt" extension. There is a sample protocol file called **Sample.txt** that is installed in the **...\MyoMED\Tables** directory. Highlight the protocol file and click **OK**. Click **OK** once again from the **Edit Stimulator** window to return to the main MyoMED window. The Stimulator Settings Indicator (Figure 3-1 and Figure 3-4) should show File listed for the Repeat Mode along with the first set of stimulus parameters. The **Stimulator ON/OFF** button should be bright red, indicating the stimulator is **OFF**. During an experiment, when the **Stimulator ON/OFF** button is clicked for a stimulator that has a protocol file loaded, the stimulator will deliver the first stimulus and then go into standby while waiting for the **Repeat Time** to elapse before delivering the next stimulus. After a stimulus is delivered, the **Stimulator Settings Indicator** will be updated automatically to reflect the settings that will be used in the next stimulus. As soon as all the stimulations coded for in the protocol file have been delivered, the stimulator will automatically turn **OFF**, the **Stimulator ON/OFF** button will change to bright red to indicate the stimulator is **OFF**, and the **Stimulator Settings Indicator** will be updated with the parameters for the first stimulation coded for by the file. If the **Stimulator ON/OFF** button is clicked again, the stimulator will execute the stimulations in the protocol file once again.

*Figure 3-8 - Loading a Stimulus Protocol File*



Select Control File

Look in: Tables

Definitions.txt

Sample.txt

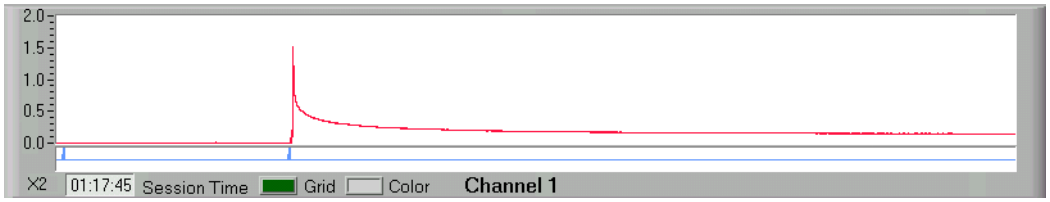
File name: Sample.txt

Files of type: Custom Pattern (*.txt)

## Using Event Marks

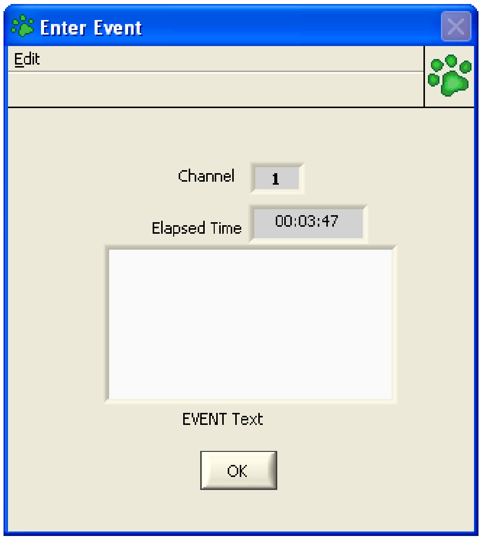
Each channel has a corresponding Event button located to the left of the Data Display Window (Figure 3-1). Pushing the Event button places a tick mark on the blue trace located in the Event Mark Display Window (Figure 3-9) and opens the Enter Event window (Figure 3-10).

*Figure 3-9 - Event Marks*



The **Enter Event** window (Figure 3-10) allows the user to type in a text comment that will appear in the recorded data file at the time of the experiment when the **Event** button is pressed. Enter the comment in the **EVENT Text** box.

*Figure 3-10 - Enter Event Window*



Channel 1

Elapsed Time 00:03:47

EVENT Text

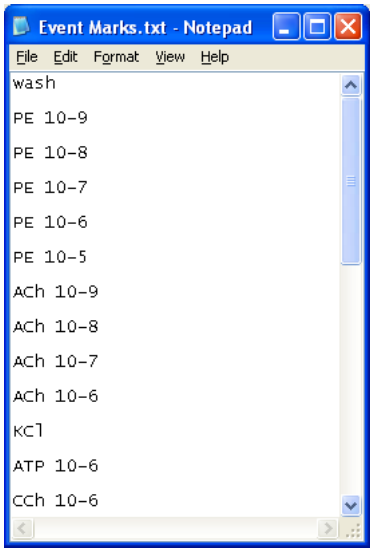
### Setting Up Event Lists in Windows Notepad

It may be found that there will be several events that are identical from experiment to experiment, such as doses of drugs that will be added in a cumulative manner. Rather than entering in the same event over and over, it may be easier to create a text file in Windows Notepad that contains a list of some frequently used events (Figure 3-11).

To construct such an event list, open Windows Notepad, which is located in the **Accessories** folder of the Windows **Start Menu**. Type each individual event on a separate line of the Notepad file (Figure 3-11). When all of the events are listed in

Notepad, save the file with a name such as "EventMarks.txt" that will allow it to be located easily at a later date. Each time that MyoMED is run, have the Notepad file loaded in the background. Entering events in MyoMED is then a simple matter of clicking the **Event** button, copying an event text from the Notepad file, and pasting it into the **Enter Event** window. The **Enter Event** window does have an **Edit** menu with the Windows clipboard edit commands. Shortcut keys (Control+C = Copy, Control+V = Paste) may also be used. Another great solution is to use a mouse that has programmable buttons. Program the buttons for the Windows Copy and Paste commands and use these shortcut buttons to copy and paste events from Notepad to MyoMED.

*Figure 3-11 - Event Mark File in Notepad*



```
wash
PE 10-9
PE 10-8
PE 10-7
PE 10-6
PE 10-5
ACh 10-9
ACh 10-8
ACh 10-7
ACh 10-6
KCl
ATP 10-6
CCh 10-6
```

## Changing the Offset

The offset for each channel is controlled using the **TARE** button located in the bottom left corner of the MyoMED window (Figure 3-1, Figure 3-12). Use the offset control at the beginning of an experiment when hanging the preparation from the force transducer. The **TARE** button zeros the signal from the force transducer that is currently selected in the **Channel** selector (Figure 3-12). When hanging the tissue hook from the force transducer, pressing the **TARE** button will negate the weight of the hook. **TARE** each force transducer just prior to applying any load to the preparation.

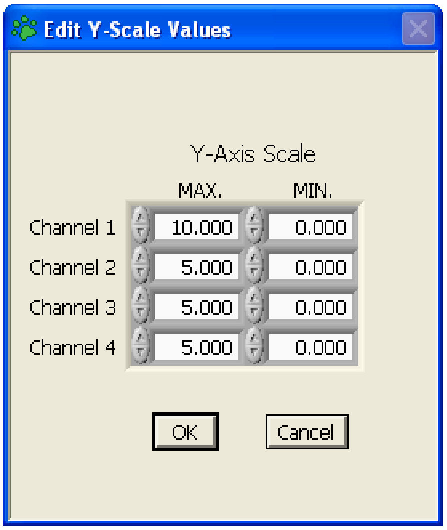
*Figure 3-12 – Channel Selector and TARE Button*

## Changing the Appearance of Data Display Windows

### Setting the X-Axis and Y-Axis Scales

To change the scale for the Y-axes, select **Y-Scales** from the **Edit** menu (Figure 3-3). This opens the **Edit Y-Scale Values** window (Figure 3-13). The **MAX** and **MIN** values for any of the channels in the myograph system can be changed. When the desired changes have been made, click **OK**. Clicking on **Cancel** will keep the Y-axes the same as they were before opening the **Edit Y-Scale Values** window.

*Figure 3-13 - Changing the Y-Axes Scales*

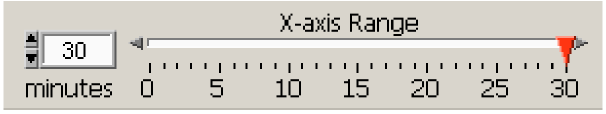


Y-Axis Scale

| | MAX. | MIN. |
|---|---|---|
| Channel 1 | 10.000 | 0.000 |
| Channel 2 | 5.000 | 0.000 |
| Channel 3 | 5.000 | 0.000 |
| Channel 4 | 5.000 | 0.000 |

The X-axes (Time) can be set to show from 1 to 30 minutes of data during data acquisition. Change the X-axis range by using the **X-axis Range Slider** located below the **Data Display Window** for **Channel 4** (Figure 3-1, Figure 3-14).

*Figure 3-14 - X-Axis Range Slider*



X-axis Range

30 minutes

### Enabling Grid Lines

The grid lines in the **Data Display Windows** can be enabled/disabled. To enable grid lines, click the **Grid** button located below the **Data Display Window** for **Channel 1** (Figure 3-1). To change the grid line color, click the **Color** button (next to the **Grid** button) and select the desired color. To turn grid lines off, click on the **Grid** button again.

## Reviewing an Experiment During Data Acquisition

When in the middle of an experiment and recording data, the entire contents of the experiment can be examined up to the present point in time by selecting **Review** from the **File** menu. This opens a separate window running MyoViewer software. Refer to Chapter 4 for operation of MyoViewer software. Keep in mind that reviewing an experiment in progress can be very slow, depending on how large the data file is at that point.

# CHAPTER 4

## *MyoViewer Software*

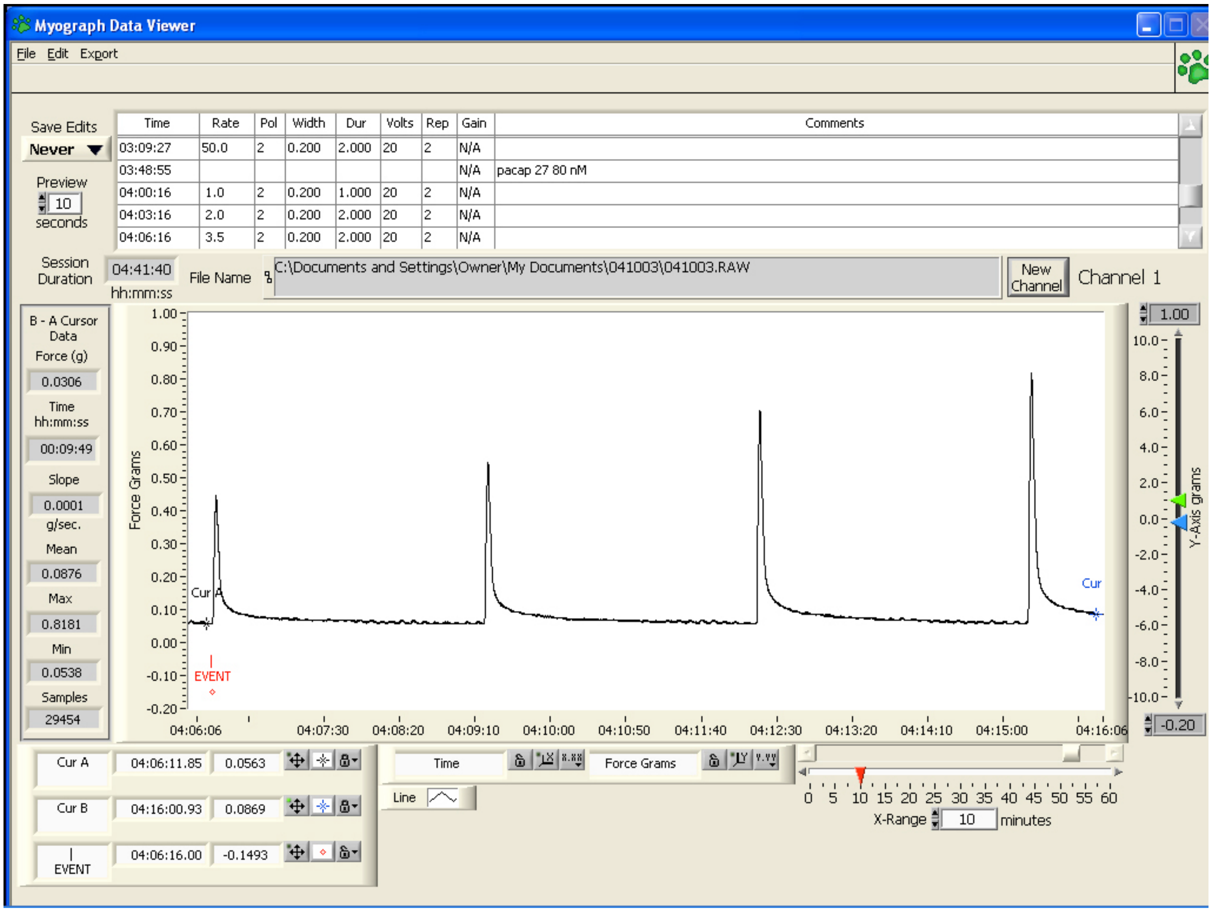
MyoViewer software is a user-friendly program for off-line inspection of RAW files recorded in MyoMED data acquisition software. Basic data analysis routines, such as measuring the average contraction force during a given treatment, can be performed in MyoViewer. For more demanding analysis techniques, the user can export selected regions of data as ASCII text files for importing into a spreadsheet or other analysis program. The export feature of MyoViewer is also very helpful for constructing publication-quality illustrations of the raw data. Please feel free to contact the staff at Catamount Research and Development, Inc. for assistance.

## MyoViewer Layout

### MyoViewer Main Window

This section provides an overview of the MyoViewer main window (Figure 4-1). All of the functions are discussed in more detail in subsequent sections.

*Figure 4-1 - MyoViewer Main Window*



Save Edits: Never

Preview 10 seconds

| Time | Rate | Pol | Width | Dur | Volts | Rep | Gain | Comments |
|---|---|---|---|---|---|---|---|---|
| 03:09:27 | 50.0 | 2 | 0.200 | 2.000 | 20 | 2 | N/A | |
| 03:48:55 | | | | | | | N/A | pacap 27 80 nM |
| 04:00:16 | 1.0 | 2 | 0.200 | 1.000 | 20 | 2 | N/A | |
| 04:03:16 | 2.0 | 2 | 0.200 | 2.000 | 20 | 2 | N/A | |
| 04:06:16 | 3.5 | 2 | 0.200 | 2.000 | 20 | 2 | N/A | |

Session Duration 04:41:40 hh:mm:ss

File Name C:\Documents and Settings\Owner\My Documents\041003\041003.RAW

B - A Cursor Data
Force (g) 0.0306
Time hh:mm:ss 00:09:49
Slope 0.0001 g/sec.
Mean 0.0876
Max 0.8181
Min 0.0538
Samples 29454

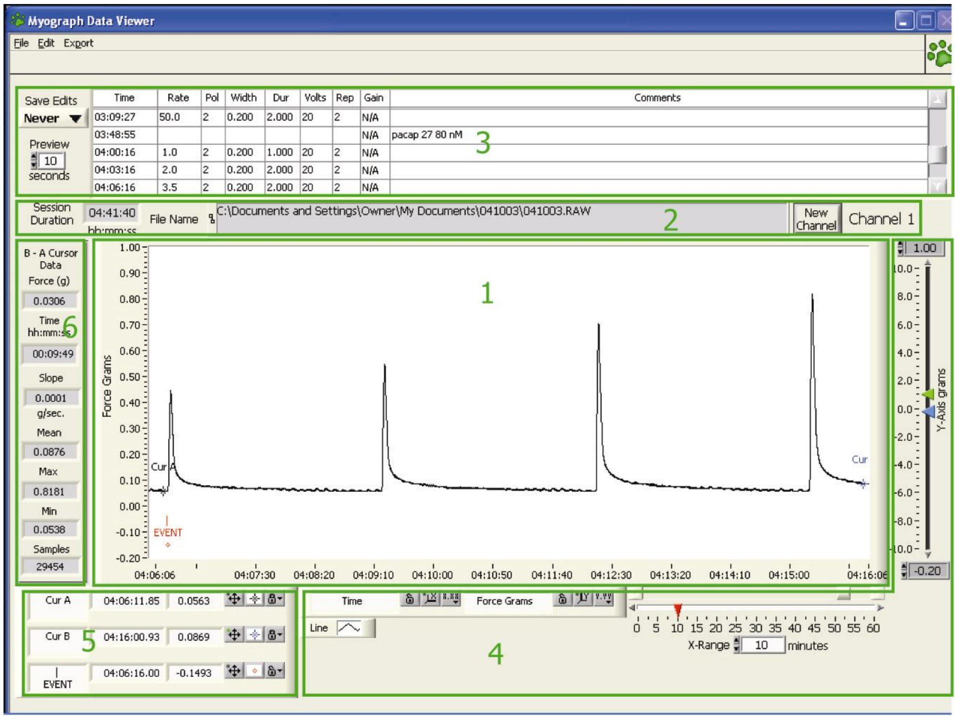
| | | |
|---|---|---|
| Cur A | 04:06:11.85 | 0.0563 |
| Cur B | 04:16:00.93 | 0.0869 |
| EVENT | 04:06:16.00 | -0.1493 |

X-Range 10 minutes

The MyoViewer Window is made up of six distinct sections (Refer to Figure 4-2):

- Section 1 is the most important section of the MyoViewer Window, the Data Display Window. This display shows a trace corresponding to the force signal recorded during an experiment.
- Section 2 contains information about the current file, including the file path, channel displayed, and total experiment time.
- Section 3 lists all of the event marks that were entered during an experiment in a spreadsheet format. For each event, the event mark section contains the time of the event, the parameters of the electric field stimulator (if used), the amplifier gain at that point of the experiment, and any comments entered as text into the Event Mark box.
- Section 4 is the Graph Control Section. This section contains all controls for changing the properties of the data display window. This includes adjusting the X- and Y-axes, changing the color of the data trace line, and enabling/disabling grid mark display.
- Section 5 is the Cursor Control section, which contains settings for the navigation cursors. There are three cursors used to navigate a file: Cursor A, Cursor B, and Event Cursor. Cursor colors can be modified in the Cursor Control section.
- Section 6 is the Data Analysis Section. This section contains basic statistics for the data between cursors A and B. These include average force between the cursors, maximum and minimum values between cursors, difference in force between cursors A and B, etc.

*Figure 4-2 - Six Sections of the MyoViewer Window*



Save Edits: Never

Preview: 10 seconds

| Time | Rate | Pol | Width | Dur | Volts | Rep | Gain | Comments |
|---|---|---|---|---|---|---|---|---|
| 03:09:27 | 50.0 | 2 | 0.200 | 2.000 | 20 | 2 | N/A | |
| 03:48:55 | | | | | | | N/A | pacap 27 80 nM |
| 04:00:16 | 1.0 | 2 | 0.200 | 1.000 | 20 | 2 | N/A | |
| 04:03:16 | 2.0 | 2 | 0.200 | 2.000 | 20 | 2 | N/A | |
| 04:06:16 | 3.5 | 2 | 0.200 | 2.000 | 20 | 2 | N/A | |

Session Duration: 04:41:40 hh:mm:ss

File Name: C:\Documents and Settings\Owner\My Documents\041003\041003.RAW

Channel 1

B - A Cursor Data
Force (g): 0.0306
Time hh:mm:ss: 00:09:49
Slope: 0.0001 g/sec.
Mean: 0.0876
Max: 0.8181
Min: 0.0538
Samples: 29454

| | | |
|---|---|---|
| Cur A | 04:06:11.85 | 0.0563 |
| Cur B | 04:16:00.93 | 0.0869 |
| EVENT | 04:06:16.00 | -0.1493 |

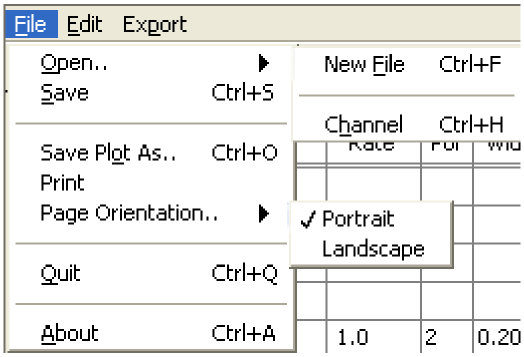
Time
Force Grams
Line
1.00
-0.20
X-Range: 10 minutes

## MyoViewer Menu Structure

In addition to the major sections of the MyoViewer main window, there are three menus that contain additional settings/functions. The three menus are the **File** menu (Figure 4-3), **Edit** menu (Figure 4-4), and **Export** menu (Figure 4-5).

### File Menu

*Figure 4-3 - File Menu*



The **File** menu (Figure 4-3) is divided into 4 sections. The first section contains the **Open** and **Save** options.

- Use the **Open** command to open either a **New File** or a new **Channel** in the currently loaded file.
- Use the **Save** command to save any changes made to the event mark comments. **Save** does not alter raw data or information in the original event mark file. A new file is created with the modified event comments.

The next section contains options for printing hard copies of the data displayed in the MyoViewer data display window. MyoViewer will print only to the default Windows printer. If it is desired to print to a printer other than the default Windows printer, the default Windows printer must be changed prior to starting MyoViewer software.

- The **Save Plot As** option is used to save the printout to disk. This command generates three files, two of which have the *.png extension, and a third file with an .htm extension. The HTML (.htm) file is the actual file that contains the desired printout. This file uses the png files to construct the images it contains. If the png files are deleted or moved, the HTML file will not work properly.
- The **Print** option sends a printout of the data currently displayed in the data display window, along with event mark information associated with the data, to the default Windows printer.
- The **Page Orientation** option allows the user to print in either **Portrait** or **Landscape** orientation.

The next section of the **File** menu has the **Quit** command.

- Select **Quit** from the File menu to exit the MyoViewer program.

The last section of the **File** menu has the **About** command.

- Use **About** to view information regarding the version of MyoViewer being run.

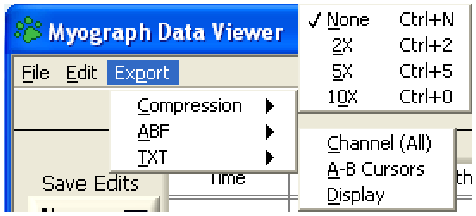
## Edit Menu

*Figure 4-4 - Edit Menu*

The **Edit** menu (Figure 4-4) contains basic Windows edit tools: **Cut**, **Copy**, and **Paste**. These functions are used only when making changes to the event mark comments. Refer to section 3 of Figure 4-2.

## Export Menu

*Figure 4-5 - Export Menu*



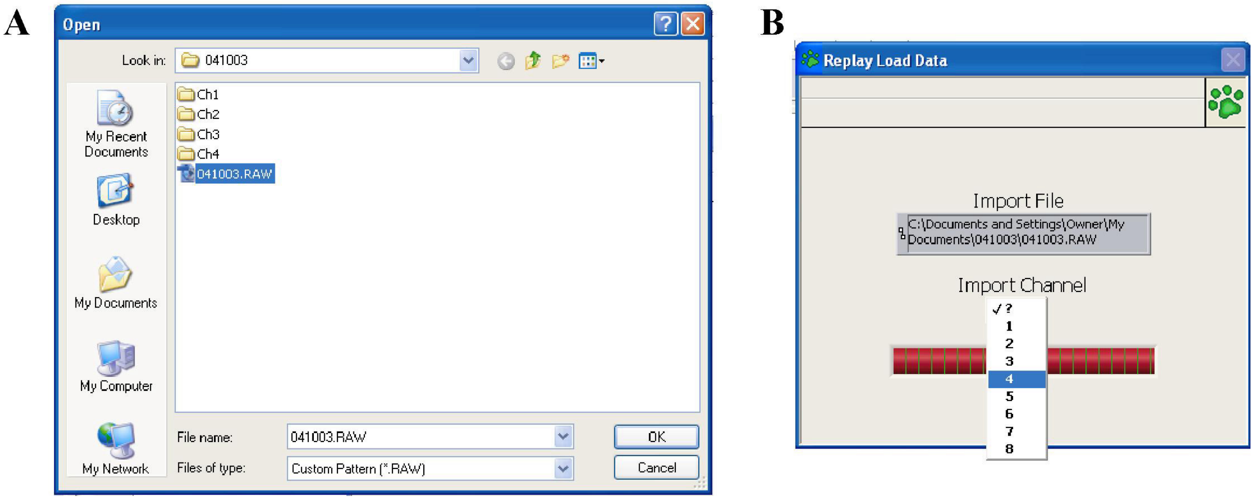
The **Export** menu (Figure 4-5) has options for exporting selected regions of data from the data display window. The exported file can then be imported into a graphing or spreadsheet program for further analysis or construction of figures.

- Use the **Compression** setting to determine the compression of the data file. **None** will export all data points within the range specified. Selecting **2X**, **5X**, or **10X** will compress the file by saving every other data point, every fifth data point, or every tenth data point, respectively.
- Select **ABF** to export the data into an axon binary file (*.ABF). The ABF submenu allows the user to select the range of data to be exported. Selecting **Channel (All)** will export data from the entire channel that is currently loaded, **A-B Cursors** will export only the data between cursors A and B and **Display** will export the data that is currently displayed in the data display window.
- Select **TXT** to export the data into a text file (*.TXT). The TXT submenu allows the user to select the range of data to be exported. Selecting **Channel (All)** will export data from the entire channel that is currently loaded, **A-B Cursors** will export only the data between cursors A and B and **Display** will export the data that is currently displayed in the data display window.

## Opening a File

When MyoViewer is first started, the **Open** file dialog box is displayed (Figure 4-6A). Select the RAW file to load. After selecting the RAW file, the **Import Channel** dialog box appears (Figure 4-6B). Select the desired channel to load. The number of channels listed will depend on the version of MyoMED being used. Loading a file can take several minutes, depending on the size of the file and the speed of the computer. While the file is loading, the progress indicator will change from red to green. If a file is currently open and an additional file needs to be opened, go to the **File** menu and choose **Open⇨New File** (Figure 4-3).

*Figure 4-6 - Opening a File in MyoViewer*



Look in: 041003

File name: 041003.RAW

Files of type: Custom Pattern (*.RAW)

Import File: C:\Documents and Settings\Owner\My Documents\041003\041003.RAW

Once a file is loaded, the MyoViewer window will look similar to Figure 4-1. The path of the currently loaded file is displayed in the File information section (part 2 on Figure 4-2). The channel number that is currently loaded is displayed next to the file path. The **Session Duration** is displayed on the left side of the screen, above the data display window. This information indicates the total time (hours:minutes:seconds) of the experiment that is currently loaded.

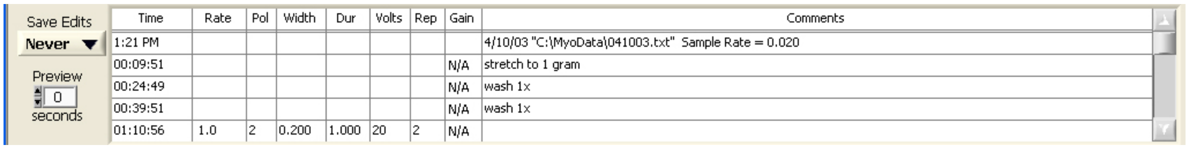
### Selecting a Different Channel

If it is desired to change to a different channel in the currently loaded file, simply press the **New Channel** button next to the file path above the data display window, or choose **File⇨Open⇨New Channel**. In either case, the **Import Channel** dialog box will be displayed (Figure 4-6B).

## Event Marks Associated With a RAW Data File

When experimental data is acquired using MyoMED, two files are saved: a **RAW** file that contains the force transducer signals in binary format, and a **TXT** file that contains information and comments about events that occurred during the experiment (Appendix C). When a file is loaded into MyoViewer, the event marks are displayed as a spreadsheet in the Event Mark section of the MyoViewer window (part 3 of Figure 4-2; Figure 4-7).

*Figure 4-7 - Event Mark Section in MyoViewer*



Save Edits: Never

Preview: 0 seconds

| Time | Rate | Pol | Width | Dur | Volts | Rep | Gain | Comments |
|---|---|---|---|---|---|---|---|---|
| 1:21 PM | | | | | | | | 4/10/03 "C:\MyoData\041003.txt" Sample Rate = 0.020 |
| 00:09:51 | | | | | | | N/A | stretch to 1 gram |
| 00:24:49 | | | | | | | N/A | wash 1x |
| 00:39:51 | | | | | | | N/A | wash 1x |
| 01:10:56 | 1.0 | 2 | 0.200 | 1.000 | 20 | 2 | N/A | |

- The **Time** column shows the time in the experiment that the event occurred.
- The **Rate**, **Pol**, **Width**, **Dur**, **Volts**, and **Rep** columns all contain information about the stimulator settings.
- The **Gain** column indicates the amplifier gain setting at the point in the experiment that a given event occurred.
- The **Comments** column lists any text entered into the Event dialog box during an experiment. The first row of the event mark section shows the absolute time the experiment was started (determined by the clock setting on the computer). The comments section of the first row indicates the date the file was created, the path of the file name, and the data sample rate in seconds per sample. All subsequent rows list the events that occurred during an experiment. The time information for experiment events is the relative time, with time zero being the beginning of an experiment.

### Jumping to a Specific Event in an Experiment

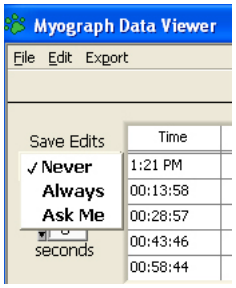
Use the scroll bar on the right side of the event mark spreadsheet to scroll up and down through the list of events. Jump to a specific event in an experiment by clicking the mouse pointer on any of the columns, other than the comments column, for the desired event in the event mark spreadsheet. By default, the event jumped to will be at the left-most edge of the data display window. If it is desired to have a segment of data displayed before (to the left of) the event of interest, change the **Preview** setting, located next to the event mark spreadsheet. The default value of 0 seconds results in the event of interest being placed on the left-most edge of the data display window. If 1 min of data should be displayed before the event of interest, enter 60 seconds into the **Preview** setting, and click on the event of interest in the event mark spreadsheet. The event of interest will now be preceded by 60 seconds of data in the data display window. The **Event** cursor in the data display window indicates the event of interest that was selected by clicking in the event mark spreadsheet. Each time a new event is clicked on, the data display window will jump to that point of the experiment, and the Event mark cursor will indicate the selected event.

### Modifying Event Mark Comments

While working with files in MyoViewer, it is possible to modify the comments for any event that occurred during an experiment. This option is particularly useful if there is an error in the event comment or if it is desired to append information to an event, such as cursor data measurements. Note that only the **Comments** section can be modified. The other parameters of the events cannot be changed.

To change the text in the **Comments** section of the event mark, simply place the cursor in the **Comments** section to be modified. Text can be entered/manipulated in the **Comments** section just like any other Windows application. Use the **Edit** menu (Figure 4-4) to **Cut**, **Copy**, or **Paste** information in the **Comments** section.

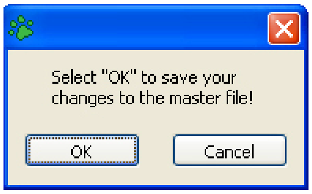
*Figure 4-8 - Save Edits Controller*



| Time |
|---|
| 1:21 PM |
| 00:13:58 |
| 00:28:57 |
| 00:43:46 |
| 00:58:44 |

Once the desired changes have been made, there are a number of ways to save the changes to disk. To save the altered comments to the original TXT file that was created with the RAW file during data acquisition, use the **Save Edits** control located to the left of the event mark spreadsheet (Figure 4-7 and Figure 4-8). By default, this control is set to **Never**, which means that any changes made to the comments will not alter the original TXT events file. Changing this controller to **Always** will result in the comment changes being saved over the original TXT file comments automatically when quitting MyoViewer, loading another file, or loading a new channel. Setting this controller to **Ask Me** will cause MyoViewer to prompt the user to select whether or not to save the changes to the original TXT file as soon as MyoViewer is quit, another file is loaded, or a new channel is loaded (Figure 4-9). Choosing **OK** in response to the prompt will write the changes over the original TXT file. Choosing **Cancel** will discard the changes.

*Figure 4-9 -* Ask Me *Save Edits Prompt*



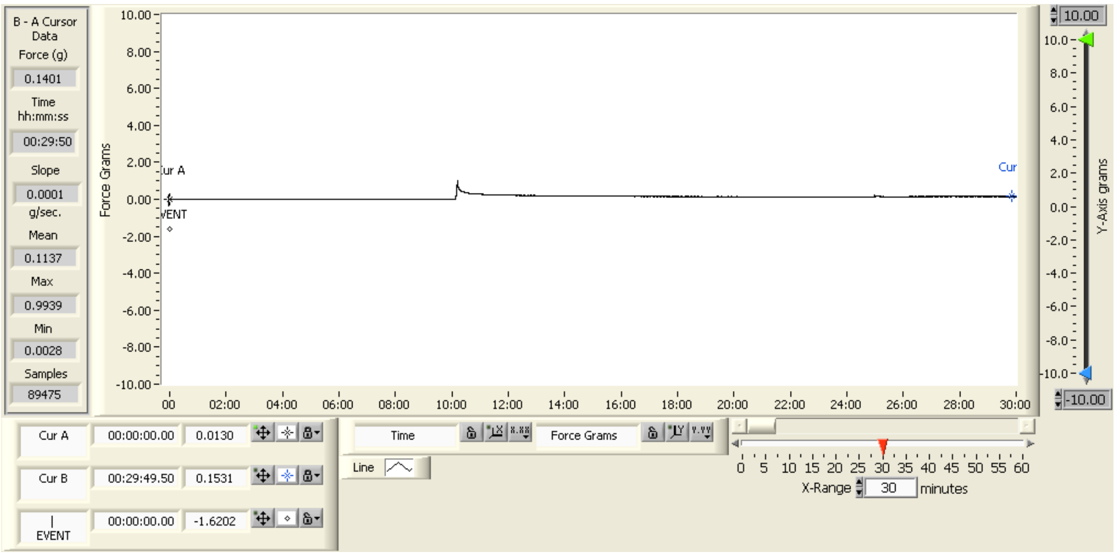
Select "OK" to save your changes to the master file!

The other option for saving modified event comments is to use the **Save** command in the **File** menu (Figure 4-3). Using **File⇨Save** will open a **Save As** dialog box prompting the user to enter a file name (or use the default name provided) that has a **CH*x*** extension, where ***x*** is the channel number of the desired file. Choosing this method will not affect the original TXT file containing event mark information saved during data acquisition. Unlike the original TXT event mark file, which contains events for all channels in the myograph system, the **CH*x*** file contains only the modified events for the channel it was created for. For example, if viewing channel 3 of a data file, and errors are noticed in the event comments, the comments may be changed and **File⇨Save** selected. The resulting file would be in ASCII format, and would have "**CH3**" as its extension.

## Using the Data Display Window

The data display window (Section 1 on Figure 4-2; Figure 4-10), in conjunction with its related sections, is where the bulk of the focus will be while using MyoViewer.

*Figure 4-10 - Data Display Window with Graph and Cursor Control Sections*



B - A Cursor Data
Force (g): 0.1401
Time hh:mm:ss: 00:29:50
Slope: 0.0001 g/sec.
Mean: 0.1137
Max: 0.9939
Min: 0.0028
Samples: 89475

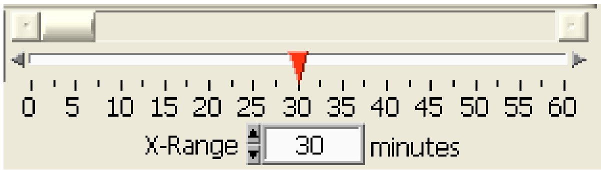
| | | |
|---|---|---|
| Cur A | 00:00:00.00 | 0.0130 |
| Cur B | 00:29:49.50 | 0.1531 |
| EVENT | 00:00:00.00 | -1.6202 |

X-Range 30 minutes

When a file is loaded into MyoViewer, the data recorded during an experiment will be displayed in the data display window, and will look similar to Figure 4-10. The Y-axis range is –10 grams to +10 grams, and the X-axis range is 0 to 30 minutes by default. These ranges can be changed quite easily using the graph controls.

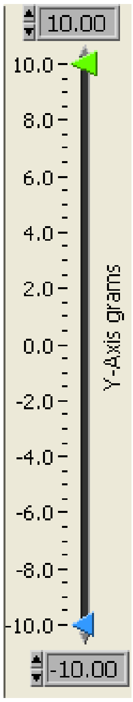
## Changing the X-Axis and Y-Axis Settings

*Figure 4-11 - X-Axis Controls*



Changing the length of time displayed in the data display window is done using the X-Range slider and scroll bar located in the bottom right corner of the screen (Figure 4-11). The length of time displayed in the data display window is indicated by the position of the red arrow on the X-range slider. Figure 4-11 shows a setting of 30 minutes. A value can be entered in the X-Range box. Unlike MyoMED data acquisition software, which is limited to displaying 30 minutes in the display windows, MyoViewer can display any length of time greater than or equal to 1 minute. To increase the maximum time displayed highlight the maximum value under the X-range slider, type in a new value, and press enter. The X-range slider will be updated to reflect the change. Move the red pointer to any position on the slider to set the amount of time displayed in the data display window. To navigate through the file while maintaining the length of time displayed constant, move the scroll bar located above the X-range slider.

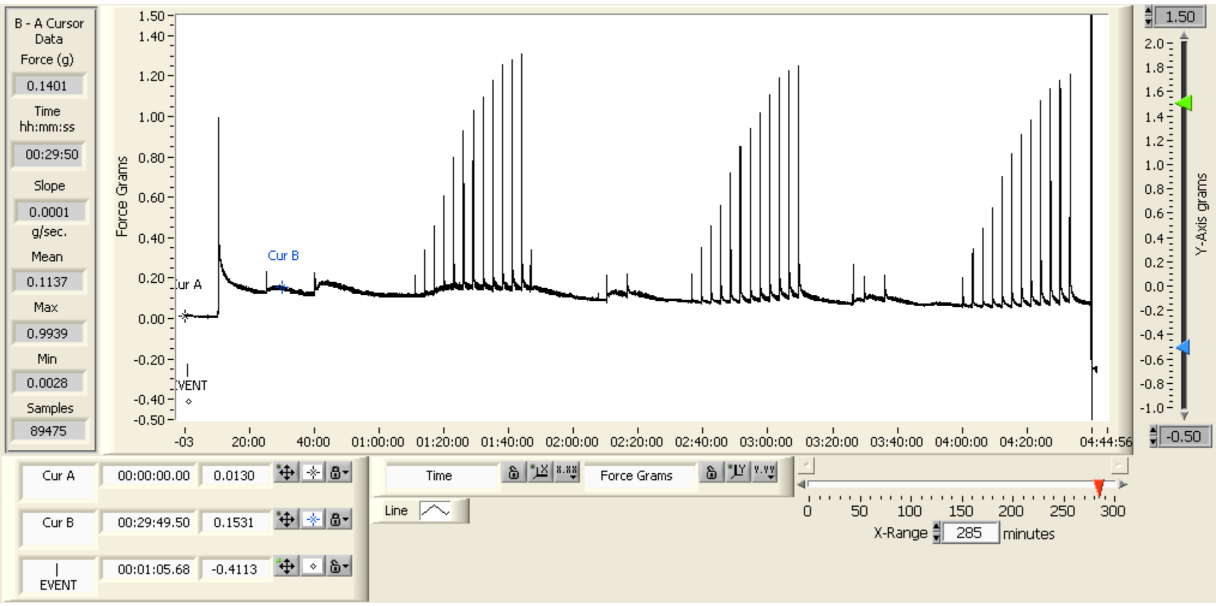
*Figure 4-12 - Y-Axis Controls*



The Y-axis can be adjusted using the Y-Axis slider control located to the right of the data display window (Figure 4-12). Moving the top green pointer changes the maximum force on the Y-axis. Moving the lower blue pointer adjusts the minimum force displayed on the Y-axis. These values may also be entered manually into the text boxes above and below the Y-axis slider. Furthermore, if it is desirable to work within a more limited range of forces, the range of the Y-axis slider may be changed from the default of –10.0 grams to +10.0 grams to any range of interest. To change the range on the Y-axis slider, highlight the maximum or minimum value, type in a new value, and press enter. The slider will be updated to reflect the change. For example, if the forces measured in a particular experiment range from 1 to 3 grams, the minimum value on the slider could be changed to 0.0 grams and the maximum value to 4.0 grams, and this would give more precise control over the Y-axis while using the pointers on the slider.

Figure 4-13 shows an example where the X- and Y-axes have been adjusted to show the contents of an entire experiment. Contrast the X- and Y-axis range sliders in Figure 4-10 and Figure 4-13.

*Figure 4-13 - Adjusted X- and Y-Axes*



B - A Cursor Data

Force (g) 0.1401

Time hh:mm:ss 00:29:50

Slope 0.0001 g/sec.

Mean 0.1137

Max 0.9939

Min 0.0028

Samples 89475

Cur A 00:00:00.00 0.0130

Cur B 00:29:49.50 0.1531

EVENT 00:01:05.68 -0.4113

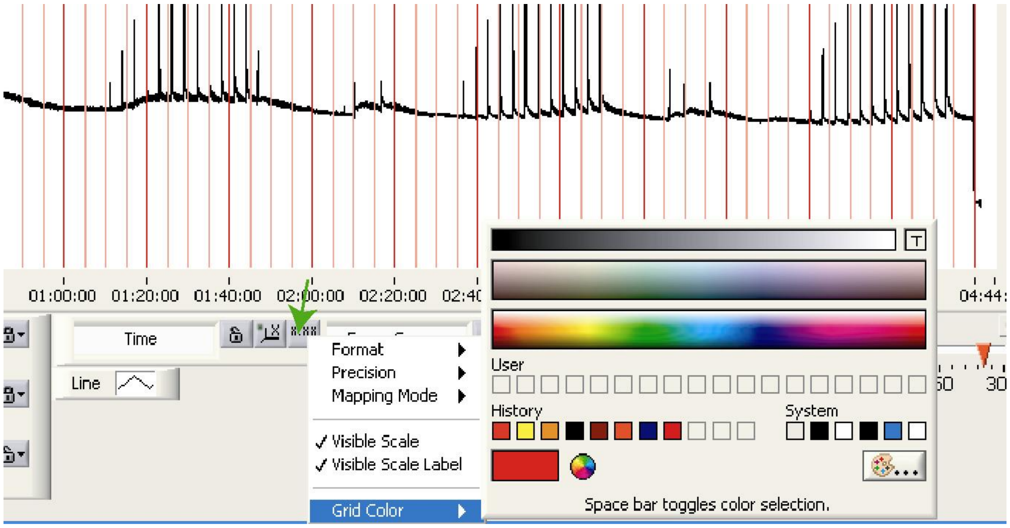
Y-Axis grams: 1.50 / -0.50

X-Range 285 minutes

### Displaying Grid Marks and Modifying Line Colors

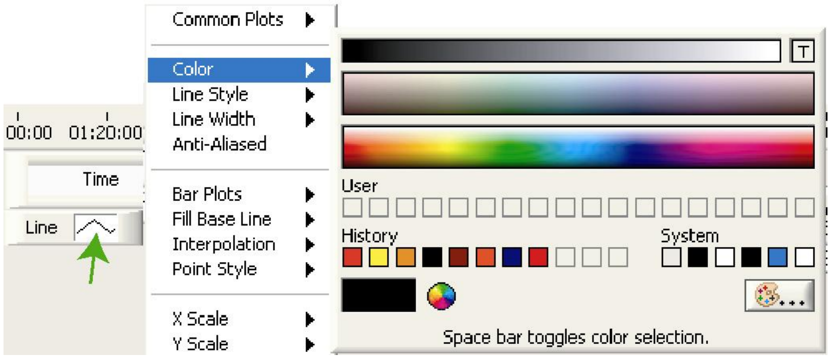
The data display window can be configured to display grid marks for both the X- and Y-axes. To enable the X-axis grid marks, click on the **X.XX** button located below the data display window (Figure 4-14, green arrow). Highlight **Grid Color** from the pop-up menu. Place the mouse pointer over the desired grid line color, and the grid lines will be displayed (Figure 4-14). To enable the Y-axis grid marks, repeat this process after clicking the **Y.YY** button below the data display window.

*Figure 4-14 - Turning on Grid Marks*



To alter the line color of the force trace, click on the **Line** button (Figure 4-15, green arrow). Select **Color** from the pop-up menu, and place the cursor over the desired line color. The trace in the data display window will be updated accordingly.

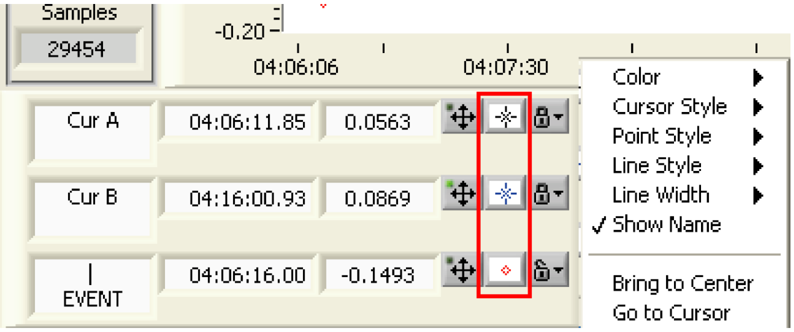
*Figure 4-15 - Changing the Line Color*



## Cursor Properties

There are three cursors in the data display window: Cursor A, Cursor B, and Event Cursor. Cursors A and B are used to make measurements and define regions of data to export as ASCII files. The Event Cursor indicates the position of the most-recently selected event from the Event Mark list. Cursor properties can be changed in the Cursor Control section of MyoViewer (Section 5 on Figure 4-2; Figure 4-16).

*Figure 4-16 - Cursor Control Section*



Samples: 29454

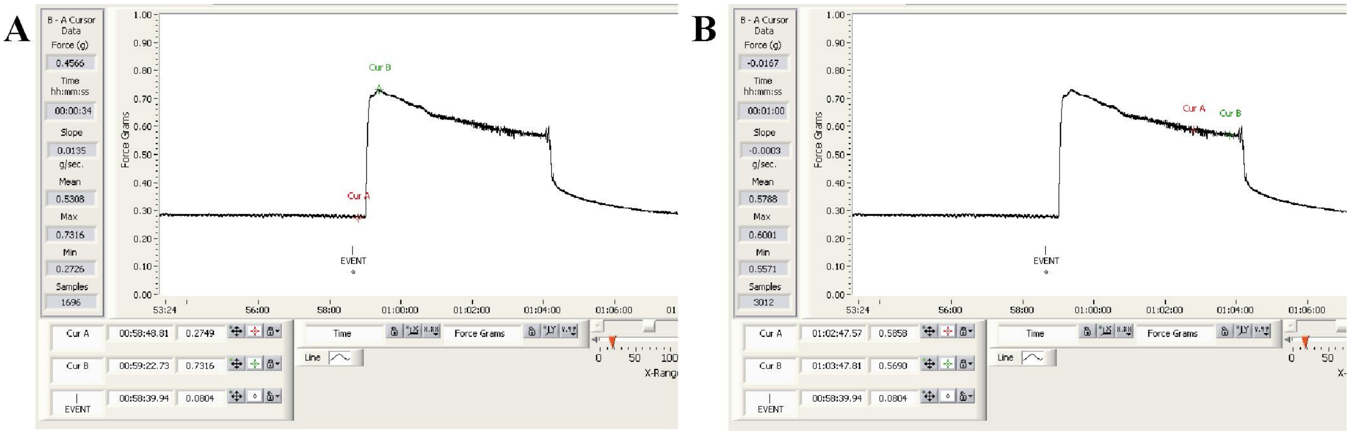
| | | |
|---|---|---|
| Cur A | 04:06:11.85 | 0.0563 |
| Cur B | 04:16:00.93 | 0.0869 |
| EVENT | 04:06:16.00 | -0.1493 |

The X and Y positions of each cursor are displayed next to the cursor names. To change the cursor properties, click on the Cursor button corresponding to the cursor to be changed (Figure 4-16, red box). This brings up the cursor properties menu. Cursor color, style, and thickness can all be changed from this menu. Another useful feature is the **Bring to Center** command. Use this command to relocate a cursor to the center of the screen while navigating throughout a file.

## Making Measurements With the Cursors

Cursors A and B can be positioned to make some basic measurements from data files, such as contraction amplitudes. For example, to measure the peak of a contraction, place Cursor A at the baseline and Cursor B at the peak (Figure 4-17A). The absolute X- and Y-positions for Cursors A and B can be seen in the Cursor Properties section. The Cursor Data section to the left of the data display window shows the relative measurements between Cursor A and B. Keep in mind that the relative data are taken as the Y-position of Cursor A subtracted from the Y-position of Cursor B (B-A). When measuring contraction amplitudes, always place Cursor A at the desired baseline position and place Cursor B at the peak position. The **Force (g)** summarized in the **Cursor Data** section in the example from Figure 4-17A shows a reading of **0.4566**. This value is the amplitude of the contraction.

*Figure 4-17 - Using the Cursors to Make Basic Measurements*



A

B - A Cursor Data
Force (g) 0.4566
Time hh:mm:ss 00:00:34
Slope 0.0135 g/sec.
Mean 0.5308
Max 0.7316
Min 0.2726
Samples 1696
Cur A 00:58:48.81 0.2749
Cur B 00:59:22.73 0.7316
EVENT 00:58:39.94 0.0804

B

B - A Cursor Data
Force (g) -0.0167
Time hh:mm:ss 00:01:00
Slope -0.0003 g/sec.
Mean 0.5788
Max 0.6001
Min 0.5571
Samples 3012
Cur A 01:02:47.57 0.5858
Cur B 01:03:47.81 0.5690
EVENT 00:58:39.94 0.0804

Another way to use the cursors is to measure the average force between Cursor A and Cursor B (Figure 4-17B). For example, to measure the steady-state force during a contraction, place Cursor A and Cursor B at the desired spacing. In Figure 4-17B, Cursors A and B were placed at the steady state of a contraction. The cursors were placed one minute apart. The spacing between the cursors can be determined by observing the value in the **Time hh:mm:ss** window in the Cursor Data section. In this example, the average (**Mean**) force during the one-minute interval between Cursors A and B is **0.5788 g**. The maximum (**Max**) force during that interval is **0.6001 g**, and the minimum (**Min**) force is **0.5571 g**.

## Exporting Data as an ASCII (*.txt) File

For some purposes, more advanced analysis must be performed on the data, or a figure based on the raw data recordings in an experiment will be created for publication. In these cases, it is desirable to export selected regions of data to be manipulated in another application, such as a spreadsheet or graphics program. There are several options available for exporting data from MyoViewer. The compression settings can be especially useful when exporting large sections of data, such as an entire channel, to use in constructing a representative figure. For data analysis purposes, it is generally not advisable to use compression, as the resulting data could be affected.

## Event Mark Cursor

The vertical position of the Event Cursor is especially important when it comes to printing a hardcopy of the data shown in the data display window.

By default, Cursors A and B can be moved along a trace by using the mouse to drag them to desired locations. In contrast, the Event Cursor can be freely moved anywhere in the data display window using the mouse to drag it around. When the user clicks on an event of interest in the event mark list above the data display window, the data display window will jump to that location in the file, and the Event Cursor will indicate the position of the event. Depending on the Y-axis scale settings, the Event Cursor may be in an undesirable location. For example, the Event cursor may not show up at all, it may be located way at the bottom of the data display window, or it may be superimposed on the data trace. If the Event cursor doesn't show up at all, recall it to the center of the data display window. Once the Event cursor is visible, orient it in the desired vertical position. The Y-axis scaling can be adjusted to eliminate extraneous space below the trace. Once the desired vertical position of the Event Cursor is set, it will appear in this vertical position whenever subsequent events in the event mark list are clicked on.

### Printing a Hardcopy of Experimental Recordings

It is often desirable to have a hardcopy of the experimental results available for archiving and quick inspection of the results. A copy of the contents of the data display window can be printed using the **Print** command in the **File Menu**. The **File Menu** section summarizes the options for printing from MyoViewer. Appendix D shows a sample of the printout obtained from MyoViewer using the **Print** command. Notice that the raw data recording appears at the top of the page, along with a summary of all the events below the trace. There are numbered event marks that indicate the position of the events. The event list below the trace is numbered to correspond to the event marks. The position of the event marks (Y-axis position) in the printout will be defined by the Y-axis position of the Event Cursor in the data display window. Before printing, be sure that the Event Cursor is in the desired vertical location, and that the X- and Y-axes are scaled in the desired manner.

# CHAPTER 5

## *Running an Experiment*

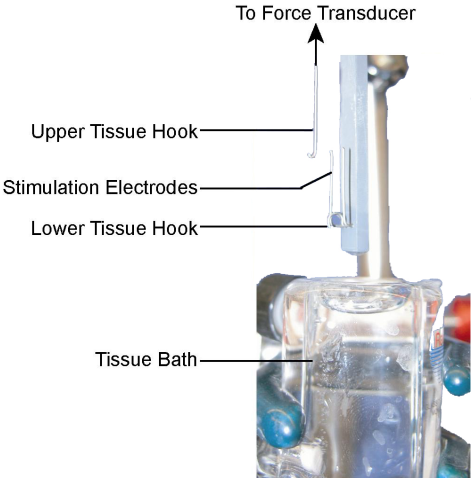
This chapter provides a brief overview of the basic process involved when performing experiments with MyoMED. It is assumed that users have read through prior sections to understand the features of MyoMED software. The information in this chapter serves as a quick reference highlighting important steps that are common to all experiments with MyoMED. Individual users will develop their own systems depending upon the nature of the experiments they will be performing.

To calibrate the force transducers, refer to Appendix A. Catamount Research and Development, Inc. recommends calibrating force transducers during initial setup of the myograph system, and then periodically depending on how frequently the system is used. Once a month calibrations should be sufficient in most cases.

### Procedure Checklist

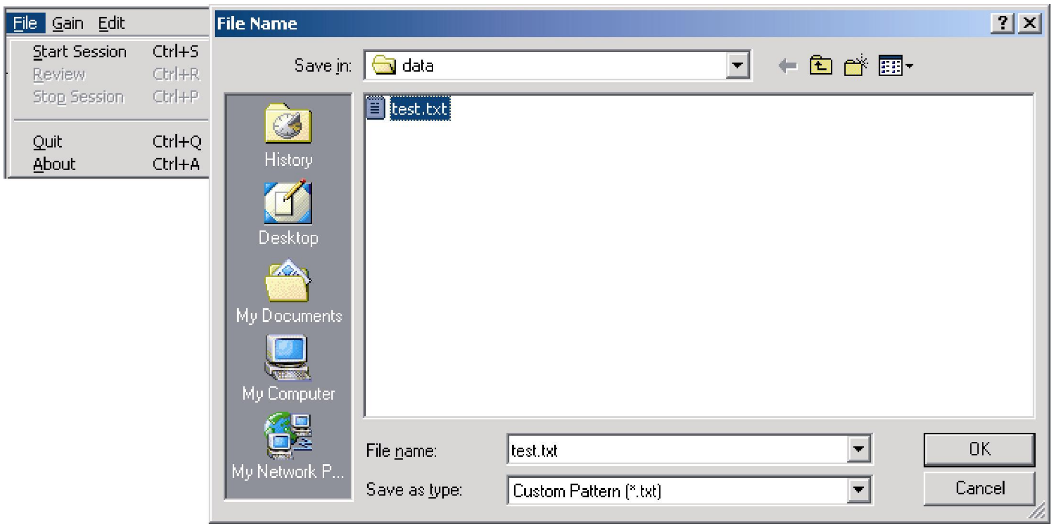
1. Turn on the computer and all electronic devices and leave them on while preparing for an experiment (making solutions, dissecting, specimen preparation, etc). This should be an adequate amount of time for the system to warm up, which will minimize force transducer drift during an experiment.
2. Once the MyoMED software is loaded, set the stimulator settings (if used).
3. Open the Windows Notepad file containing event mark text.
4. Turn the heated water circulating pump(s) on to allow the water jacket to warm up to the appropriate temperature.
5. Fill the water-jacketed saline reservoir with the saline solution to be used for experimentation. Turn on the gas cylinder to equilibrate the saline with the appropriate gas mixture.
6. If there is a vacuum pump connected to the tissue bath drain system, turn it on.
7. Complete any dissections or manipulations that are necessary to prepare the muscle tissue specimen for study in the myograph.
8. Fill the tissue baths with saline from the 2 L saline reservoir. Adjust the flow of saline to each reservoir from the 2 L reservoir using the corresponding stopcock. Adjust the level of saline in each tissue bath by opening the stopcock connected to the vacuum system to remove excess saline. Adjust the flow of gas into the tissue bath using the needle valve on the tissue bath oxygenator.
9. To mount a tissue sample in a tissue bath, make sure that the tissue bath is lowered out of the way of the tissue support rod (Figure 5-1). Begin by hanging a tissue attachment hook to the force transducer (see Figure 5-1). Depending on the type of specimen, the tissue attachment hook may vary. For example, the hook styles for vascular ring segments and smooth muscle strips are different. Use the hook that is appropriate for the type of sample being used.

*Figure 5-1 - Tissue Bath Position for Hanging Tissue Samples*



10. When the upper tissue hook is hanging from the force transducer, TARE the weight of the hook so that it does not add an offset to the force measurement. (The use of a different upper tissue hook requires adjusting the load amplifier knob to "0" and running the full calibration procedure as outlined in Appendix A). In the MyoMED window, choose the channel being used with the Channel Selector in the bottom left corner (see Figure 3-12). Press the TARE button. The "**Grams net**" (Figure 3-1) field of the **Current Data Point Indicator** for the selected channel should go to 0.000 grams.
11. Hang the tissue from the top hook first.
12. Attach the tissue to the bottom hook. Ensure that the specimen is slack while doing this. Do not apply unnecessary stretch to the specimen, as it may damage the muscle. If there are stimulating electrodes on the rigid tissue support rod, be sure that the specimen is situated between the two electrodes (Figure 5-1).
13. When the tissue is connected to the upper and lower hooks, submerge the tissue support rod in the saline-filled tissue bath by raising the tissue bath. Make sure the tissue is completely slack (no tension on the specimen). Check this by moving the upper and lower tissue support hooks closer together by turning the micrometer head. As the upper and lower hooks are moved closer, there should be no change in the force reading (as viewed in the **Current Data Point Indicator**, Figure 3-1). When it is certain that the specimen is slack, press TARE once again to cancel any offset that is present.
14. Change the Channel Selector (Figure 3-12) to the next tissue bath and repeat the tissue attachment procedure.
15. When all of the samples are mounted in tissue baths, the system is ready to begin recording data.
16. To begin recording data, Choose **Start Session** from the **File** menu. This opens the **File Name** window (Figure 5-2). Type in a file name for the experiment. The name that is chosen will be used for both the **TXT** file containing event comments and the **RAW** file containing raw data. Click **OK**.

*Figure 5-2 - Starting an Experiment in MyoMED*



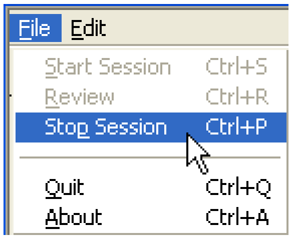
Save in: data

File name: test.txt

Save as type: Custom Pattern (*.txt)

17. At this point, data is being recorded from each channel. Traces will appear in the **Data Display Windows** that correspond to the force measured by each force transducer.
18. The user may now apply stretch to the samples by turning the micrometer heads. Estimate the amount of stretch by looking at the **Current Data Point Indicator** while the tissue is being stretched.
19. Conduct the experiment.
20. When the experiment is completed, stop recording data by selecting **Stop Session** from the File menu (Figure 5-3). Quit MyoMED by choosing Quit from the File menu.

*Figure 5-3 - Stopping an Experiment*



21. If another experiment will be completed, it is a good idea to exit MyoMED software and reload MyoMED before starting the next experimental session.
22. It is a good practice to clean tissue baths with a dilute solution of hydrochloric acid (HCl, 0.1 N) after use. This removes salt deposits and keeps glassware clean. Rinse with three washes of distilled water after doing an acid wash.

# CHAPTER 6

## *Designing Protocols for Programmable Stimulators*

User-defined protocols may be created that will perform a series of stimulations in a specified pattern. This feature is particularly useful when the user wishes to stimulate the preparation in a repeating fashion, while incrementally changing certain stimulus parameters with each successive stimulation. Measuring the peak contraction in response to stimulations of increasing pulse frequencies, while maintaining all other stimulus parameters constant, is an example of such an application.

## Stimulus Protocol Tutorial

### General Information about Protocol Files

This section is a brief tutorial that describes how to construct protocol files for controlling the programmable stimulators. Refer to Chapter 3 for general information about the MyoMED programmable stimulators, including definitions of terms and other conventions.

A protocol file is a tab-delimited ASCII text file (*.txt) that contains the desired stimulus parameters. Protocol files can be made in any text editor, and should be saved as tab-delimited ASCII files with a "txt" extension. This tutorial will use Microsoft® Excel to construct a protocol file.

Each stimulus in a protocol is coded by a single column in the protocol file. After all stimuli have been coded, a final column of zeros must be included to indicate the end of the file. Thus, a protocol file consists of *n*+1 total columns of data, where *n* is the total number of stimulations to be conducted. For example, if a protocol file that will perform 10 stimulations is created, there will be 11 total columns (10 stimulations plus final column of zeros). Each column will have 8 rows of data that contain the desired settings for an individual stimulus. Table 6-1 shows the definitions for each row in the protocol file. A file named "Definitions.txt" that contains the information in Table 6-1 is created in the **…\MyoMED\Tables** directory when the software is installed.

*Table 6-1 - Protocol File Definitions*

| | | |
|---|---|---|
| Row 1 | Pulses/sec X 10 | Example: 15 = 1.5 pulses/sec. |
| Row 2 | Polarity | 0=DC+, 1=DC-, 2=AC (+/-) |
| Row 3 | Pulse Width (msec) | See Figure 3-5 |
| Row 4 | Stimulus Duration (sec) | See Figure 3-6 |
| Row 5 | Intensity (Volts) | 0 to 40 (or 0 to 400 milliamps) |
| Row 6 | Repeat Mode | Must be 2 to continue using File |
| Row 7 | Repeats | # of stimulus repeats before moving to next column |
| Row 8 | Repeat Rate (sec) | Delay before next stimulation for Repeat or next column |

- Row 1 contains the value for pulse rate in Hz, or pulses per second, multiplied by 10. It is important to remember the 10-times multiplication factor. If a pulse rate of 1 pulse per second is desired, the value entered into row 1 should be 10. For a pulse rate of 2.5 pulses per second, the value entered into row 1 should be 25. For 15 pulses per second, enter 150 into row 1. Keep in mind that the total number of pulses during a given stimulus will be the result of the pulse rate multiplied by the stimulus duration. If it is desired to have a stimulus that consists of a single pulse, one way to achieve this would be to enter "10" into row 1 for 1 pulse per second, and enter "1" into row 4 for 1 sec stimulus duration (1 pulse per sec X 1 sec = 1 pulse).
- Row 2 contains the setting for pulse polarity. A value of "0" will give positive pulses. A value of "1" will give negative pulses. A value of "2" will give alternating positive and negative pulses.
- Row 3 contains the value for the pulse width in msec. This value must be valid for the specified frequency. MyoMED features error checking that ensures compatibility between the specified frequency and pulse width.
- Row 4 contains the value for stimulus duration in sec. Note that the total number of pulses delivered during a given stimulus is the result of the pulse rate (pulses per sec) multiplied by the stimulus duration (sec).
- Row 5 of the protocol file contains the value for the stimulus intensity, or the amplitude of a stimulus pulse, in volts or milliamps. The PHM-152V Constant Voltage Programmable Stimulators are capable of pulse amplitudes ranging from 0 to 40 Volts. PHM-152I Constant Current Stimulators can produce pulses from 0 to 400 milliamps.
- Row 6 is the Repeat Mode setting, and must be set to 2 when using a protocol file. The value in row 6 should always be "2." Other values are invalid for proper stimulator control.

- Row 7 contains the value for the number of stimulations using the current set of parameters to perform before moving on to the next set of parameters. In other words, row 7 tells the stimulator how many times to use the settings in the current column before moving to the next column. In most cases, the value in row 7 will be "1" and the settings in a given column will be used once before moving to the next column.
- Row 8 contains the value for repeat rate in sec. This value determines the delay between successive stimulations. It is the length of time from the start of one stimulus to the start of the next stimulus. Keep in mind that the repeat rate must be entered in seconds.

### Using Microsoft® Excel to Construct Protocol Files

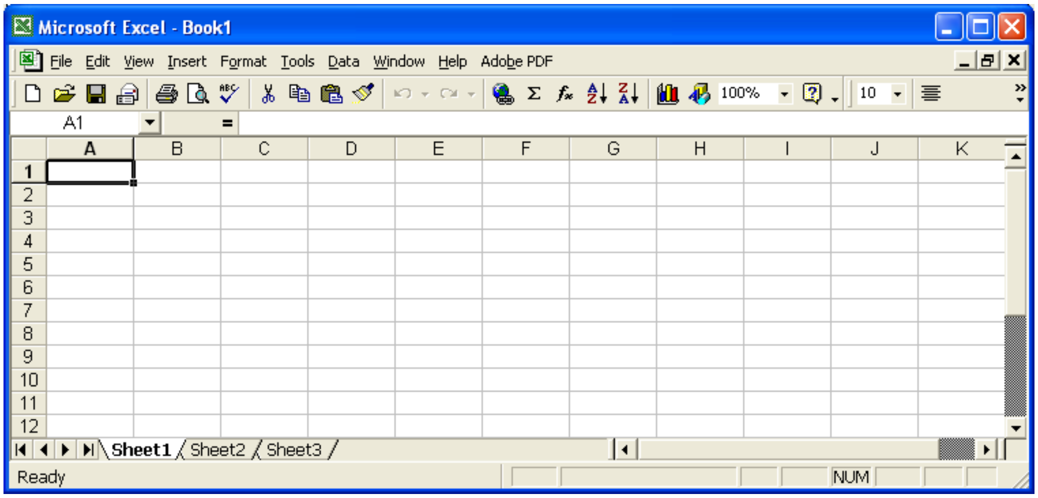
Take a few moments to plan the experimental protocol. In most cases, users will want to do a series of stimulations with one parameter varying incrementally while all other parameters are held constant. First, decide which stimulus parameter to vary. Then, decide what the fixed values of the other parameters will be. Finally, decide how many successive stimulations to perform.

In this example, a protocol file will be created that will change the pulse frequency while holding the pulse polarity, pulse width, stimulus duration, stimulus intensity, and repeat rate constant. This file will contain 12 individual stimulations, with 3 minutes (180 sec) between each stimulus. Thus, the protocol file will consist of 13 columns, 12 columns for the stimulations and a final column of zeros to signal the end of the protocol.

Pulse frequencies of 1, 2, 3.5, 5, 7.5, 10, 12.5, 15, 20, 30, 40, and 50 pulses/sec will be used. Pulse polarity will be AC (+/-), pulse width will be 0.2 msec, stimulus duration will be 2 sec, stimulus intensity will be 20 Volts, and the repeat rate will be 180 sec. Refer to Chapter 3 if more information is needed regarding any of these stimulus parameters.

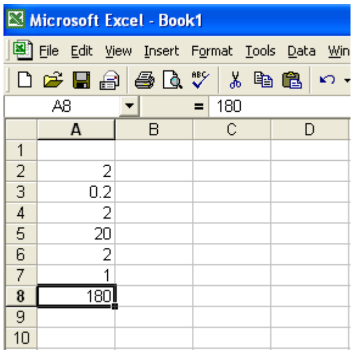
Once the stimulus settings for the protocol file have been selected, begin by opening a new worksheet in Excel (Figure 6-1).

*Figure 6-1 - New Microsoft Excel Worksheet*



In column A, enter the fixed stimulus settings in their respective rows. Refer to Table 5-1 to see which rows the individual parameters should be entered into. In this example, leave row 1 blank since this row will contain the stimulus frequency, which will change from stimulus to stimulus. Enter "2" in row 2 to indicate AC (+/-) polarity. Enter "0.2" in row 3 for 0.2 msec pulse duration. Enter "2" in row 4 for a stimulus duration of 2 sec. Enter "20" in row 5 for a pulse intensity of 20 Volts. Enter "2" in row 6 to enable the MyoMED software to use the protocol file. Enter "1" in row 7. This indicates that the programmable stimulator will use settings from this column once, and then use the next column for the next stimulus. Enter "180" in row 8 to indicate a delay of 180 sec until the next stimulus is initiated. Figure 6-2 illustrates how the Excel spreadsheet should appear at this point.

*Figure 6-2 - First Column of Sample Protocol File*

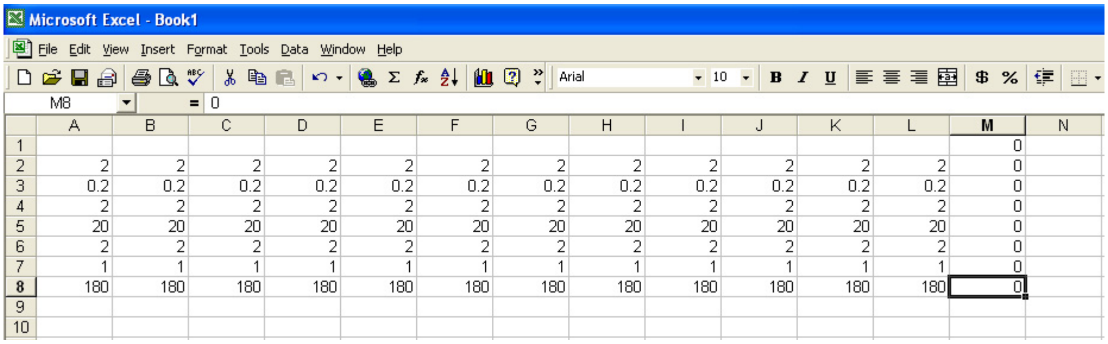


A8 = 180

|  | A | B | C | D |
|---|---|---|---|---|
| 1 |  |  |  |  |
| 2 | 2 |  |  |  |
| 3 | 0.2 |  |  |  |
| 4 | 2 |  |  |  |
| 5 | 20 |  |  |  |
| 6 | 2 |  |  |  |
| 7 | 1 |  |  |  |
| 8 | 180 |  |  |  |
| 9 |  |  |  |  |
| 10 |  |  |  |  |

Now highlight rows 2 through 8 in column A and copy them to the clipboard. Since we want 11 more columns to code the 12 total stimulations, paste the values from column A rows 2 through 8 into rows 2 through 8 of columns B through L. Enter "0" in rows 1 through 8 of column M to indicate the end of the protocol file. Figure 6-3 shows how the Excel spreadsheet should appear at this point.

*Figure 6-3 - Constant Settings Entered in Protocol File*

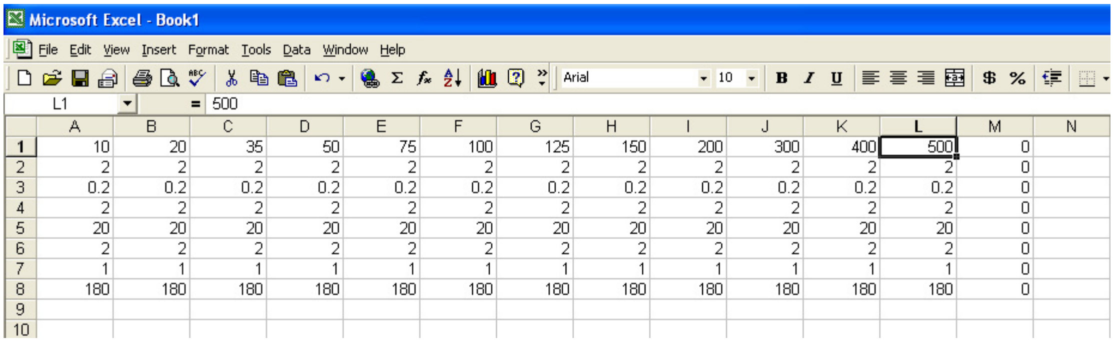


M8 = 0

|  | A | B | C | D | E | F | G | H | I | J | K | L | M | N |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 |  |  |  |  |  |  |  |  |  |  |  |  | 0 |  |
| 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 0 |  |
| 3 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0 |  |
| 4 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 0 |  |
| 5 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 0 |  |
| 6 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 0 |  |
| 7 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 |  |
| 8 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 0 |  |
| 9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 10 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

Now, enter the value for stimulus frequencies in row 1 of columns A through L. Recall that the value entered into row 1 will be the desired stimulus frequency multiplied by 10. In this example, we want stimulus frequencies of 1, 2, 3.5, 5, 7.5, 10, 12.5, 15, 20, 30, 40, and 50 pulses per second. Enter 10 in cell A1 (row 1 column A). Enter 20 in cell B1. Enter 35 in cell C1. Enter 50 in cell D1. Enter 75 in cell E1. Enter 100 in cell F1. Enter 125 in cell G1. Enter 150 in cell H1. Enter 200 in cell I1. Enter 300 in cell J1. Enter 400 in cell K1. Enter 500 in cell L1. Again, column M should contain all zeros. Figure 6-4 shows how the Excel spreadsheet should appear at this point.

*Figure 6-4 - Completed Protocol File*

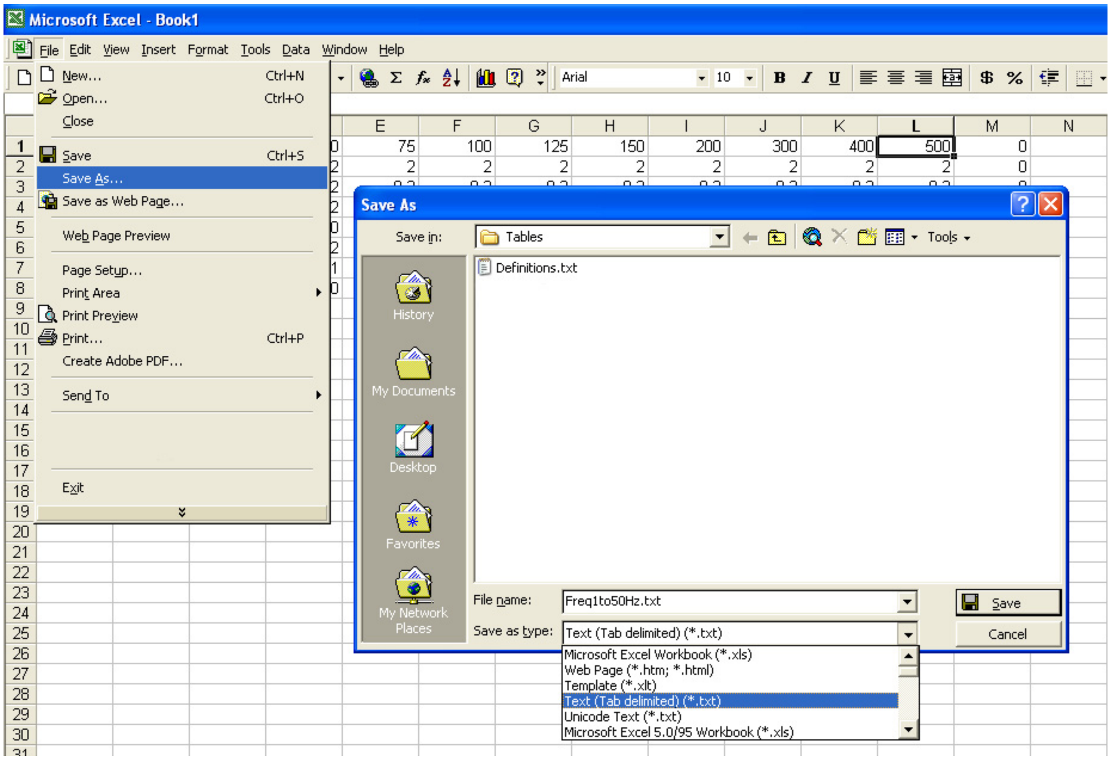


L1 = 500

| | A | B | C | D | E | F | G | H | I | J | K | L | M | N |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 10 | 20 | 35 | 50 | 75 | 100 | 125 | 150 | 200 | 300 | 400 | 500 | 0 | |
| 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 0 | |
| 3 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0.2 | 0 | |
| 4 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 0 | |
| 5 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 20 | 0 | |
| 6 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 0 | |
| 7 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | |
| 8 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 180 | 0 | |
| 9 | | | | | | | | | | | | | | |
| 10 | | | | | | | | | | | | | | |

Now the protocol file must be saved as an ASCII text tab-delimited file. In Excel, go to **File | Save As**. This will bring up the Save As dialog (Figure 6-5). In the "Save in:" field, select a directory to store the protocol file. A "Tables" directory is created in the MyoMED program directory when the software is installed and it is a convenient directory in which to store protocol files. This directory is used for this example. From the "Save as type:" drop-down list, select "Text (Tab delimited) (*.txt)" for the file type. In the "File name:" box enter a name that will allow easy recognition the protocol file at a later date. In this example, the name "Freq1to50Hz.txt" is used. Once the file is named, click **Save** in the Save As dialog.

*Figure 6-5 - Saving the Protocol File*

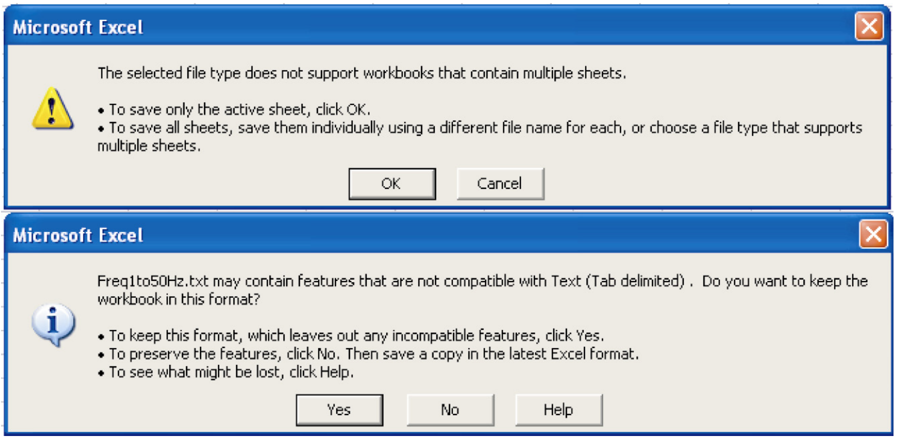


File name: Freq1to50Hz.txt

Save as type: Text (Tab delimited) (*.txt)

At this point, a warning message will appear indicating that "the selected file type does not support workbooks that contain multiple sheets" (Figure 6-6). Click **OK**. A second message appears stating "*your_file_name*.txt may contain features that are not compatible with Text (Tab delimited)…" (Figure 6-6). Click **OK**. The protocol file is now ready to be used in MyoMED.

*Figure 6-6 - Warning Messages When Saving a Protocol File*



The selected file type does not support workbooks that contain multiple sheets.

- To save only the active sheet, click OK.
- To save all sheets, save them individually using a different file name for each, or choose a file type that supports multiple sheets.

Freq1to50Hz.txt may contain features that are not compatible with Text (Tab delimited) . Do you want to keep the workbook in this format?

- To keep this format, which leaves out any incompatible features, click Yes.
- To preserve the features, click No. Then save a copy in the latest Excel format.
- To see what might be lost, click Help.

# APPENDIX A

## *Force Transducer Calibration*

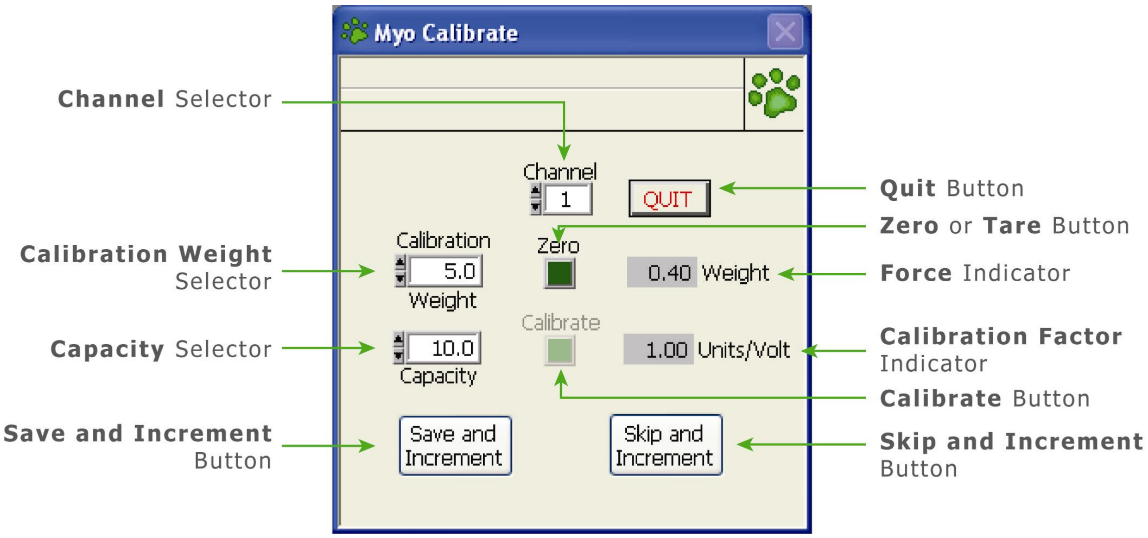
MyoMED myograph systems include a useful software utility for calibrating force transducers called MyoCalibrate. A shortcut to this program is created on the desktop at the time of software installation.

Catamount Research and Development, Inc. recommends that users perform the calibration procedure for all force transducers in a new system before beginning experiments. MyoMED myograph systems also include a set of calibration weights of masses 1 gram, 2 grams, and 5 grams.

### MyoCalibrate Software Overview

The MyoCalibrate interface is shown in Figure A-1.

*Figure A-1 - MyoCalibrate Utility*



Myo Calibrate

Channel: 1

Calibration Weight: 5.0

Capacity: 10.0

0.40 Weight

1.00 Units/Volt

**Channel** Selector

**Calibration Weight** Selector

**Capacity** Selector

**Save and Increment** Button

**Quit** Button

**Zero** or **Tare** Button

**Force** Indicator

**Calibration Factor** Indicator

**Calibrate** Button

**Skip and Increment** Button

The **Channel** selector indicates the channel affected by the calibration procedure. Use the up and down arrows to change channels.

The **Zero** (**Tare**) button compensates for offset.

The **Calibrate** button updates the **Calibration Factor**.

The **Save and Increment** button records the **Calibration Factor** for the currently selected channel to a configuration file and automatically advances to the next channel. Previously saved **Calibration Factors** are overwritten in this process.

The **Skip and Increment** button ignores the **Calibration Factor** for the currently selected channel and automatically advances to the next channel. Previously saved **Calibration Factors** are not changed in this process.

The **Calibration Factor** indicator shows the sensitivity of the force transducer in units per volt. It is updated when the **Calibrate** button is pressed. The **Calibration Factor** is used by MyoMED software during data acquisition so that recorded data are in units of grams.

The **Force** indicator displays the reading from the force transducer using the current **Calibration Factor**.

The **Quit** button exits the MyoCalibrate program.

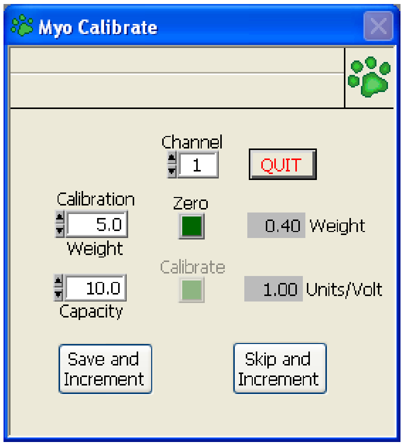
## Calibration Procedure

Run the MyoCalibrate program by clicking on the desktop shortcut. Start by calibrating the force transducer connected to Channel 1. Channel 1 should be listed in the **Channel** selector box (Figure A-3).

Begin by choosing the appropriate calibration weight, and then select the calibration weight value in the **Calibration weight** box in the MyoCalibrate window (Figure A-3).

*Figure A-2 - Calibration Kit (1,2 and 5 grams)*

*Figure A-3 - Selecting Calibration Weight Value*



Channel 1

Calibration Weight 5.0

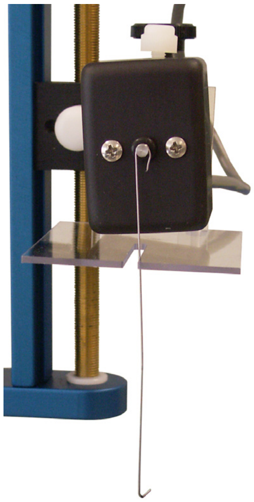
Capacity 10.0

0.40 Weight

1.00 Units/Volt

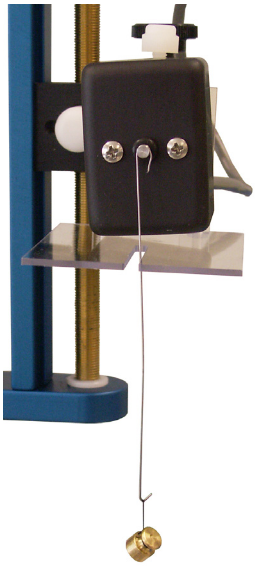
Attach the tissue hook to the force transducer as shown Figure A-4. Once the weight hanger is attached to the force transducer adjust the Offset knob on the Radnoti Isometric Transducer (Figure 1-6) until the "Volts Output" display on the Transducer reads "0", then click the **Zero** button in the MyoCalibrate window. The **Weight** indicator should read close to 0 grams.

*Figure A-4 - Attaching the Tissue Hook*



Next, hang the weight on the tissue hook (Figure A-5). Wait a few moments for the reading on the **Force** indicator to stabilize. Press the **Calibrate** button. Notice the **Calibration Factor** indicator has been updated. Press **Save and Increment** to record the new **Calibration Factor** to the configuration file, remove the calibration weight and leave the tissue hook, then proceed with calibrating the next channel.

*Figure A-5 - Calibration Using the 5-Gram Weight*



Once all channels have been calibrated, press the **Quit** button to exit MyoCalibrate. The system is now ready to record data using the MyoMED software.

# APPENDIX B

## *MyoMED Calibration Exercise*

### Purpose

This exercise is a simple procedure that presents the user with a series of steps that progress through the basic stages of calibration and validation of the myograph instrument. The user will become familiar with basic operation of the myograph hardware and software, including analyzing raw data.

### Procedure

#### Calibration

1. Calibrate the system following the instructions in Appendix A.

#### Validation

There are three stages to the validation portion of the exercise: 1) Acquiring data, 2) Analyzing data, and 3) Calculations.

#### Acquiring data

1. Run MyoMED software by clicking on the desktop shortcut.
2. Begin recording an experimental session by choosing **Start Session** from the **File** menu. This opens the **File Name** window. Type in a file name, such as **CalibrationTest**, for the experiment. Click **OK**. The system is now acquiring data.
3. Make sure the channel selector is set to Channel 1.
4. Be sure that the tissue hook used during the calibration procedure is attached to the force transducer.
5. Tare the weight of the hook.
6. On the Calibration Worksheet included in this section, record the force observed in the force display window (labeled "Grams Net") next to the force trace. This value should be close to "0".
7. Attach the 1-gram weight from the calibration kit to the tissue hook and allow about 30 seconds for stabilization, then record the force observed on the Calibration Worksheet.
8. Remove the 1-gram weight from the tissue hook.
9. Attach a 2-gram weight to the tissue hook and allow about 30 seconds for stabilization, then record the force observed on the Calibration Worksheet.
10. Remove the 2-gram weight from the tissue hook.
11. Attach a 5-gram weight to the weight hook and allow about 30 seconds for stabilization, then record the force observed on the Calibration Worksheet.
12. Remove the 5-gram weight from the force transducer.

13. Change the Channel Selector to the next channel.
14. Repeat steps 4-13 for the remaining channels.
15. Stop recording data in MyoMED by selecting **Stop Session** from the **File Menu**, and then close MyoMED by selecting **Quit** from the **File Menu**.

**Analyzing data**

1. Open MyoViewer data analysis software by clicking on the desktop shortcut.
2. Open the data file that was just created (e.g. **CalibrationTest**). Start by loading Channel 1 of the data file.
3. Configure the MyoViewer data display window to show the portion of the data file where the calibration weights were being applied. There should be a staircase pattern with 3 steps (one for each calibration weight).
4. Place the data analysis Cursors A and B at a distance of 10 sec apart in the region of the trace after the weight of the weight hanger hook was tared, but before the 1-gram weight was applied.
5. Recorded the Mean Grams measured between Cursors A and B in the space **10 sec Avg Force (grams)** on the Calibration Worksheet included in this section.
6. Move Cursors A and B to the part of the trace that was stable after adding the 1 gram weight. Again, place the cursors 10 sec apart.
7. Record the Mean Grams between the analysis cursors in the space **10 sec Avg Force (grams)** on the Calibration Worksheet.
8. Move cursors to the part of the trace that was stable after adding the 2-gram weight. Again, place the cursors 10 sec apart.
9. Record the Mean Grams between the analysis cursors in the space **10 sec Avg Force (grams)** on the Calibration Worksheet.
10. Move the cursors to the part of the trace that was stable after adding the 5-gram weight. Again, place the cursors 10 sec apart.
11. Record the Mean Grams between the analysis cursors in the space **10 sec Avg Force (grams)** on the Calibration Worksheet.
12. Repeat Steps 3 - 11 for the remaining channels.
13. Once all of the calibration data has been recorded for each channel, quit MyoViewer software.

### Calculations

There are two calculations associated with determining the effectiveness of the calibration and validation procedure.

1. Determine the difference between the actual weight applied (grams) and the measured force (grams) for each weight level using the following formula:

   ***Force measured (10 sec Avg Force (grams)) – Weight Applied (grams) = Difference (grams)***

   Record the Difference (grams) in the spaces provided on the Calibration Worksheet.

2. Determine the percent error in the measured force from the actual weight applied using the following formula:

   ***[Difference (grams) / Weight Applied (grams)] * 100 = Error (%)***

   Record the Error % in the space provided on the Calibration Worksheet.

**NOTE:** There is no Error % for the baseline condition where no weight is applied (0 grams). The mathematical operation is undefined (contains a divide by 0).

**NOTE:** The Error % varies slightly from channel to channel. However in most cases, the error will be less than 1 %, and is rarely greater than 3 %. Errors much greater than this indicate a problem in the calibration. Attempt to recalibrate the affected channels. Take special care to ensure the tissue hook is attached to the force transducer consistently each time. This can take some practice. With practice, the errors should drop to an acceptable percent. If this is not the case, there may be a problem with the force transducer.

# Calibration Worksheet

**Channel 1**

| Weight Applied (grams) | 10 sec Avg Force (grams) | Difference (grams) | Error % |
|---|---|---|---|
| 0 | | | |
| 1 | | | |
| 2 | | | |
| 5 | | | |

**Channel 2**

| Weight Applied (grams) | 10 sec Avg Force (grams) | Difference (grams) | Error % |
|---|---|---|---|
| 0 | | | |
| 1 | | | |
| 2 | | | |
| 5 | | | |

**Channel 3**

| Weight Applied (grams) | 10 sec Avg Force (grams) | Difference (grams) | Error % |
|---|---|---|---|
| 0 | | | |
| 1 | | | |
| 2 | | | |
| 5 | | | |

**Channel 4**

| Weight Applied (grams) | 10 sec Avg Force (grams) | Difference (grams) | Error % |
|---|---|---|---|
| 0 | | | |
| 1 | | | |
| 2 | | | |
| 5 | | | |

**Channel 5**

| Weight Applied (grams) | 10 sec Avg Force (grams) | Difference (grams) | Error % |
|---|---|---|---|
| 0 | | | |
| 1 | | | |
| 2 | | | |
| 5 | | | |

**Channel 6**

| Weight Applied (grams) | 10 sec Avg Force (grams) | Difference (grams) | Error % |
|---|---|---|---|
| 0 | | | |
| 1 | | | |
| 2 | | | |
| 5 | | | |

**Channel 7**

| Weight Applied (grams) | 10 sec Avg Force (grams) | Difference (grams) | Error % |
|---|---|---|---|
| 0 | | | |
| 1 | | | |
| 2 | | | |
| 5 | | | |

**Channel 8**

| Weight Applied (grams) | 10 sec Avg Force (grams) | Difference (grams) | Error % |
|---|---|---|---|
| 0 | | | |
| 1 | | | |
| 2 | | | |
| 5 | | | |

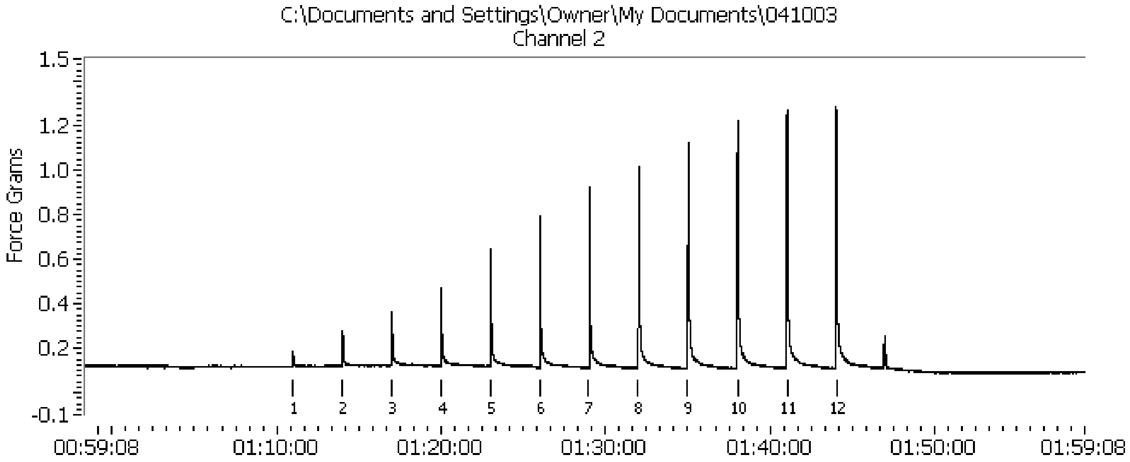
# APPENDIX C

## *File Types*

RAW (experiment)
TXT (event marks)
CH*x* (modified event comments, X = channel number)
TXT (exported data)
TXT (protocol file)
HTM (printout)
PNG (printout)

# APPENDIX D

## *Sample MyoViewer Printout*



```
    TIME        RATE      POL   WIDTH     DUR       VOLTS     REP    GAIN COMMENTS
 1 01:10:59      1.0       2    0.200    1.000       20        2       N/A
 2 01:13:59      2.0       2    0.200    2.000       20        2       N/A
 3 01:16:59      3.5       2    0.200    2.000       20        2       N/A
 4 01:19:59      5.0       2    0.200    2.000       20        2       N/A
 5 01:22:59      7.5       2    0.200    2.000       20        2       N/A
 6 01:25:59     10.0        2    0.200    2.000       20        2      N/A
 7 01:28:59     12.5        2    0.200    2.000       20        2      N/A
 8 01:31:59     15.0        2    0.200    2.000       20        2      N/A
 9 01:34:59     20.0        2    0.200    2.000       20        2      N/A
10 01:37:59     30.0         2    0.200    2.000       20        2     N/A
11 01:40:59     40.0         2    0.200    2.000       20        2     N/A
12 01:43:59     50.0         2    0.200    2.000       20        2     N/A
```

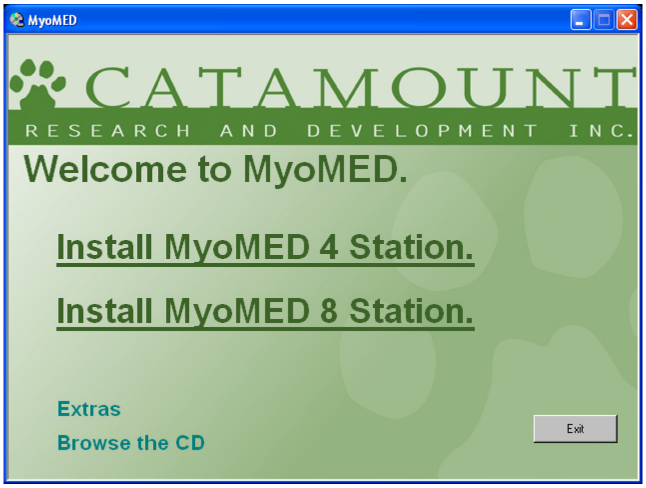
# APPENDIX E

## *Software Installation*

If a computer was purchased from Catamount Research and Development, Inc. as part of the myograph system, all software and drivers are pre-installed and it is not necessary to perform any software installation. Software installation is only necessary if the computer being used with the system was not purchased from Catamount Research and Development, or data acquisition computers will be changed at a later date.

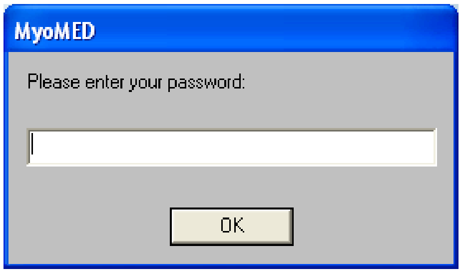
Insert the MyoMED software CD into the CD-ROM drive. The screen shown in Figure E-1 will appear. Select the type of MyoMED system being installed and the screen shown in Figure E-2 will appear.

*Figure E-1 – MyoMED Main Screen*



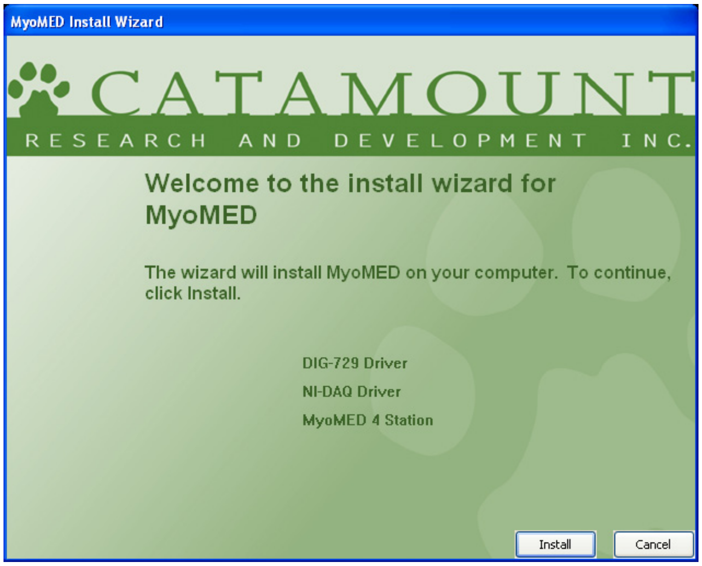
Enter the MyoMED password that was issued when the software was registered and click **OK**. The screen shown in Figure E-3 will appear.

*Figure E-2 – Enter MyoMED Password*



Click **Install** to begin driver and software installation. A successful installation will be indicated with a green check mark, and an unsuccessful installation will be indicated with a red X. If any portion of the installation is unsuccessful, please contact Catamount Research and Development Customer Support.

*Figure E-3 – Begin MyoMED Installation*



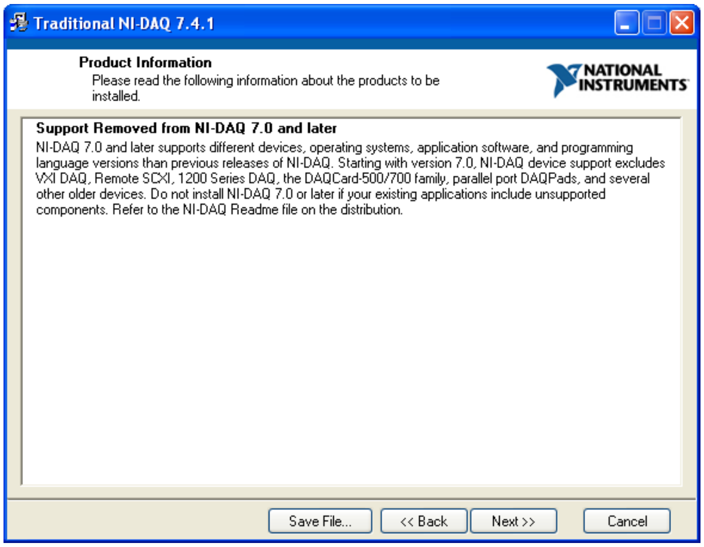
Welcome to the install wizard for MyoMED

The wizard will install MyoMED on your computer. To continue, click Install.

DIG-729 Driver
NI-DAQ Driver
MyoMED 4 Station

Once the DIG-729 driver has been successfully installed, the NI-DAQ driver installation will begin with the screen shown in Figure E-4. Click **Next** to proceed with installation and the screen shown in Figure E-5 will appear.

*Figure E-4 – Beginning NI-DAQ Driver Installation*

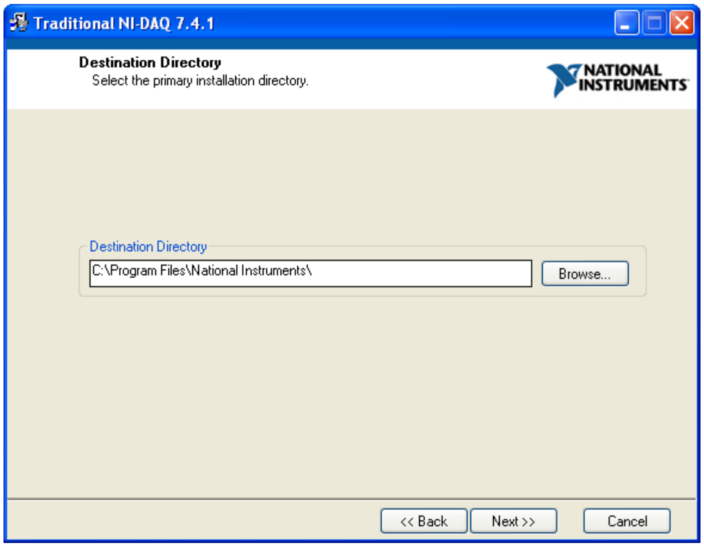


**Product Information**
Please read the following information about the products to be installed.

**Support Removed from NI-DAQ 7.0 and later**
NI-DAQ 7.0 and later supports different devices, operating systems, application software, and programming language versions than previous releases of NI-DAQ. Starting with version 7.0, NI-DAQ device support excludes VXI DAQ, Remote SCXI, 1200 Series DAQ, the DAQCard-500/700 family, parallel port DAQPads, and several other older devices. Do not install NI-DAQ 7.0 or later if your existing applications include unsupported components. Refer to the NI-DAQ Readme file on the distribution.

The default destination directory is shown. If this directory is acceptable, click **Next** to continue and the screen shown in Figure E-6 will appear. If it is not, click **Browse…** and browse to the desired directory.

*Figure E-5 – Select Destination Directory*



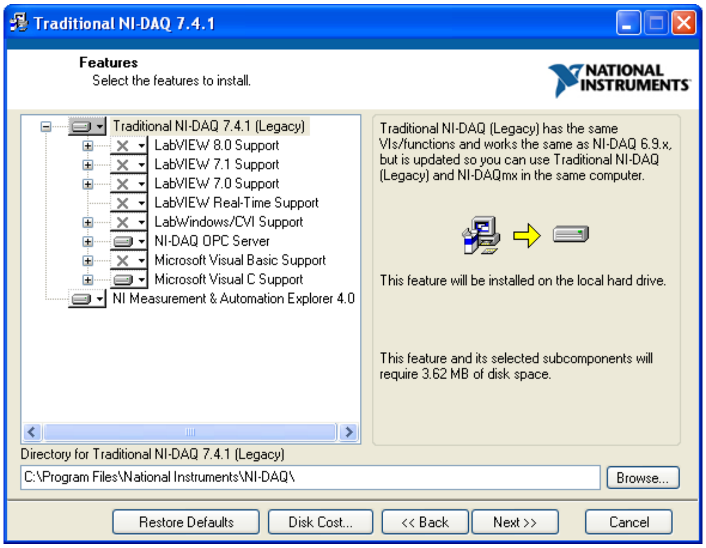
Traditional NI-DAQ 7.4.1

**Destination Directory**
Select the primary installation directory.

Destination Directory
C:\Program Files\National Instruments\

Select the features to install and click **Next** to continue. The screen shown in Figure E-7 will appear.

*Figure E-6 – Select Features*



Traditional NI-DAQ 7.4.1

**Features**
Select the features to install.

- Traditional NI-DAQ 7.4.1 (Legacy)
  - ☒ LabVIEW 8.0 Support
  - ☒ LabVIEW 7.1 Support
  - ☒ LabVIEW 7.0 Support
  - ☒ LabVIEW Real-Time Support
  - ☒ LabWindows/CVI Support
  - NI-DAQ OPC Server
  - ☒ Microsoft Visual Basic Support
  - Microsoft Visual C Support
- NI Measurement & Automation Explorer 4.0

Traditional NI-DAQ (Legacy) has the same VIs/functions and works the same as NI-DAQ 6.9.x, but is updated so you can use Traditional NI-DAQ (Legacy) and NI-DAQmx in the same computer.

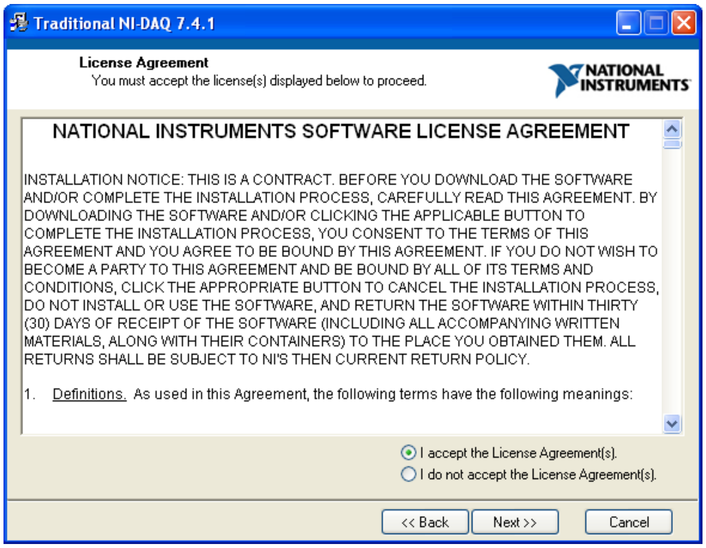
This feature will be installed on the local hard drive.

This feature and its selected subcomponents will require 3.62 MB of disk space.

Directory for Traditional NI-DAQ 7.4.1 (Legacy)
C:\Program Files\National Instruments\NI-DAQ\

Review the National Instruments Software License Agreement, then select **I accept the License Agreement(s)**. Click **Next** to continue and the screen shown in Figure E-8 will appear.

*Figure E-7 – License Agreement*



**License Agreement**
You must accept the license(s) displayed below to proceed.

NATIONAL INSTRUMENTS SOFTWARE LICENSE AGREEMENT

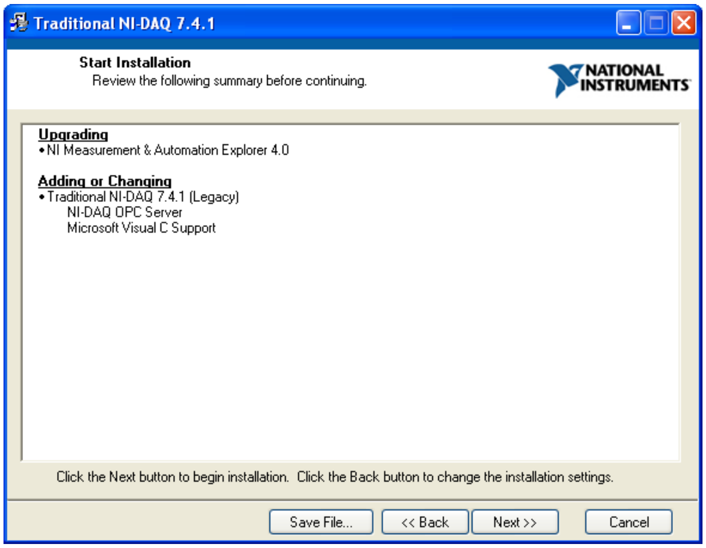
INSTALLATION NOTICE: THIS IS A CONTRACT. BEFORE YOU DOWNLOAD THE SOFTWARE AND/OR COMPLETE THE INSTALLATION PROCESS, CAREFULLY READ THIS AGREEMENT. BY DOWNLOADING THE SOFTWARE AND/OR CLICKING THE APPLICABLE BUTTON TO COMPLETE THE INSTALLATION PROCESS, YOU CONSENT TO THE TERMS OF THIS AGREEMENT AND YOU AGREE TO BE BOUND BY THIS AGREEMENT. IF YOU DO NOT WISH TO BECOME A PARTY TO THIS AGREEMENT AND BE BOUND BY ALL OF ITS TERMS AND CONDITIONS, CLICK THE APPROPRIATE BUTTON TO CANCEL THE INSTALLATION PROCESS, DO NOT INSTALL OR USE THE SOFTWARE, AND RETURN THE SOFTWARE WITHIN THIRTY (30) DAYS OF RECEIPT OF THE SOFTWARE (INCLUDING ALL ACCOMPANYING WRITTEN MATERIALS, ALONG WITH THEIR CONTAINERS) TO THE PLACE YOU OBTAINED THEM. ALL RETURNS SHALL BE SUBJECT TO NI'S THEN CURRENT RETURN POLICY.

1. Definitions. As used in this Agreement, the following terms have the following meanings:

● I accept the License Agreement(s).
○ I do not accept the License Agreement(s).

Review the installation information summary and click **Next** to complete installation. The screen shown in Figure E-9 will appear.

*Figure E-8 – Start NI-DAQ Installation*



**Start Installation**
Review the following summary before continuing.

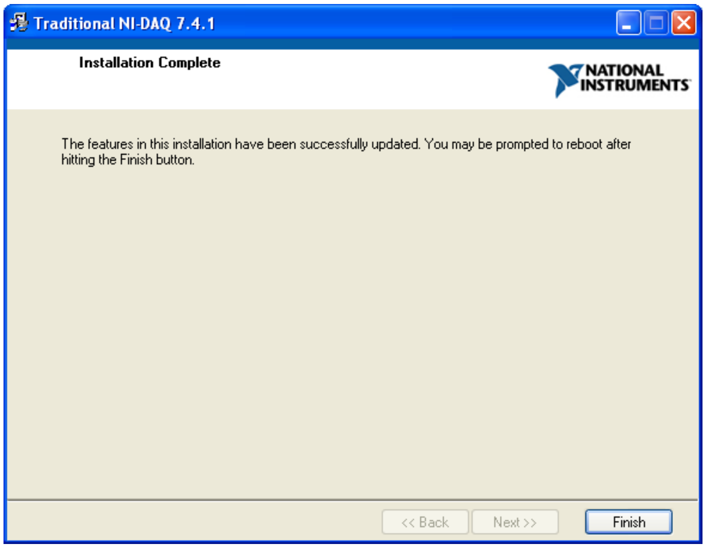
**Upgrading**
- NI Measurement & Automation Explorer 4.0

**Adding or Changing**
- Traditional NI-DAQ 7.4.1 (Legacy)
  NI-DAQ OPC Server
  Microsoft Visual C Support

Click the Next button to begin installation. Click the Back button to change the installation settings.

The NI-DAQ driver installation is now complete. Click **Finish** to close this window and the screen shown in Figure E-10 will appear.

*Figure E-9 – NI-DAQ Driver Installation Complete*



The features in this installation have been successfully updated. You may be prompted to reboot after hitting the Finish button.

Close all programs and click **Next** to proceed with MyoMED software installation. The screen shown in Figure E-11 will appear.

*Figure E-10 – MyoMED Installation Wizard*

Welcome to the MyoMED Installation Wizard

It is strongly recommended that you exit all Windows programs before running this setup program.

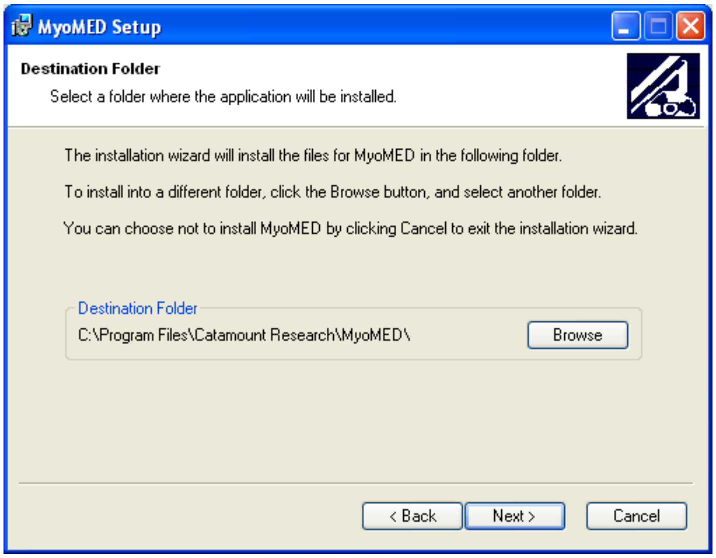
Click Cancel to quit the setup program, then close any programs you have running. Click Next to continue the installation.

WARNING: This program is protected by copyright law and international treaties.

Unauthorized reproduction or distribution of this program, or any portion of it, may result in severe civil and criminal penalties, and will be prosecuted to the maximum extent possible under law.

The default destination folder for the MyoMED software is shown. If this folder is acceptable, click **Next** to continue and the screen shown in Figure E-12 will appear. If this folder is not acceptable, click **Browse** and browse to the desired folder.

*Figure E-11 – MyoMED Destination Folder*



MyoMED Setup

**Destination Folder**

Select a folder where the application will be installed.

The installation wizard will install the files for MyoMED in the following folder.

To install into a different folder, click the Browse button, and select another folder.

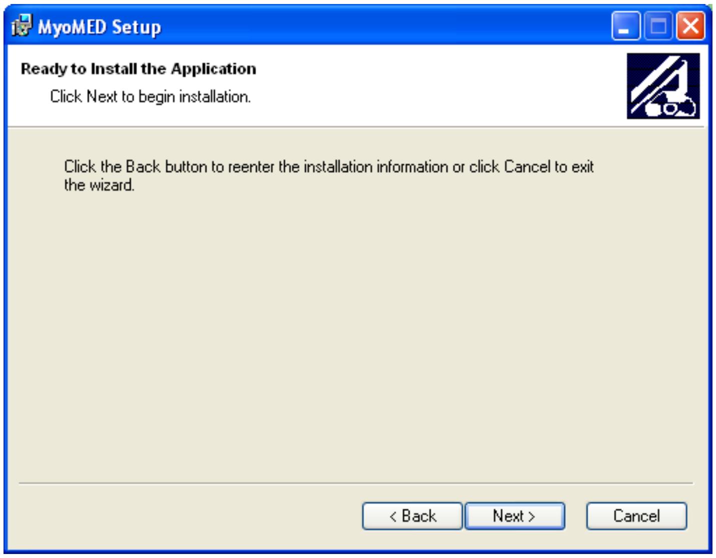
You can choose not to install MyoMED by clicking Cancel to exit the installation wizard.

Destination Folder

C:\Program Files\Catamount Research\MyoMED\

Click **Next** to complete the MyoMED software installation and the screen shown in Figure E-13 will appear.

*Figure E-12 – Ready to Install the Application*



MyoMED Setup

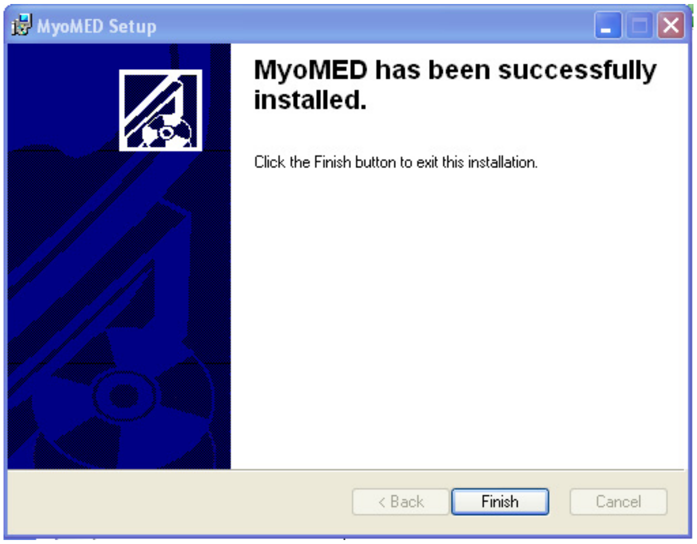
**Ready to Install the Application**

Click Next to begin installation.

Click the Back button to reenter the installation information or click Cancel to exit the wizard.

The MyoMED software installation is now complete; click **Finish** to close this window and the screen shown in Figure E-14 will appear.

*Figure E-13 – MyoMED Installation Complete*

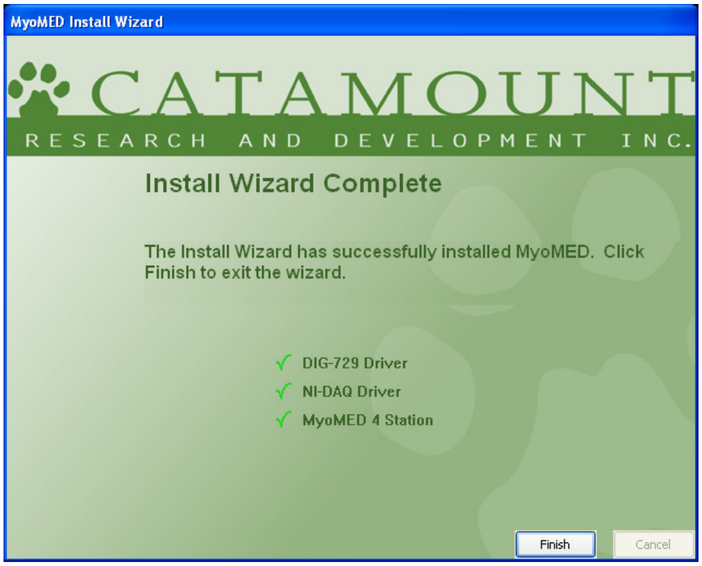


MyoMED has been successfully installed.

Click the Finish button to exit this installation.

Click **Finish** to close this window and the screen shown in Figure E-15 will appear.

*Figure E-14 – Installation Wizard Complete*



Install Wizard Complete

The Install Wizard has successfully installed MyoMED. Click Finish to exit the wizard.

✓ DIG-729 Driver
✓ NI-DAQ Driver
✓ MyoMED 4 Station

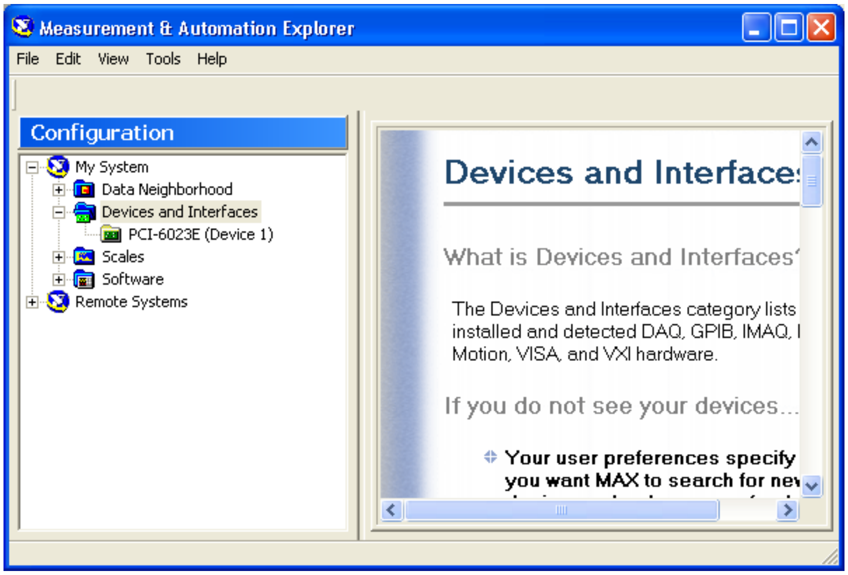
The computer must be restarted before the MyoMED software can be used. Click **Yes** to restart the computer now and **No** to restart at another time. After the computer has restarted, start the **Measurement and Automation** program by clicking on the appropriate shortcut icon on the desktop. The screen shown in Figure E-16 will appear.

*Figure E-15 – Restart Needed*

Before you can use MyoMED, you must restart your computer. Restart the computer now?

From the **Configuration** window on the left side, expand the **Devices and Interfaces** folder by double clicking on it.

*Figure E-16 - Measurement and Automation Explorer*

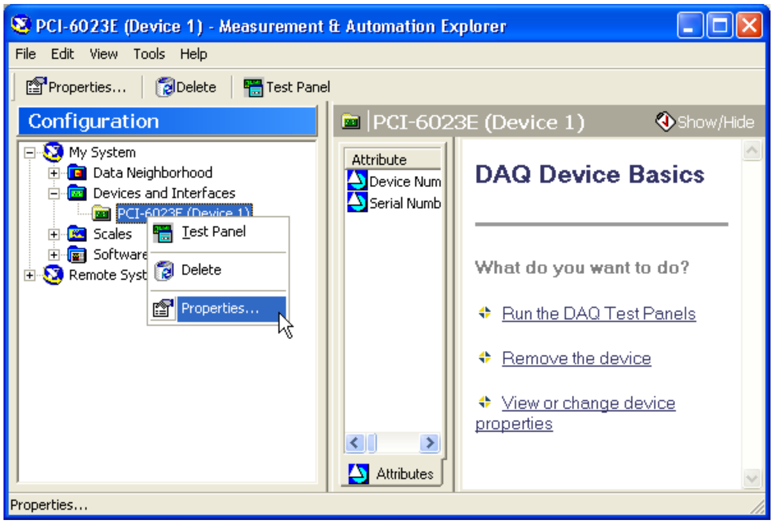


The Devices and Interfaces category lists installed and detected DAQ, GPIB, IMAQ, I Motion, VISA, and VXI hardware.

Your user preferences specify you want MAX to search for nev

Right click on **PCI-6023E (Device1)** and the menu shown in Figure E-17 will appear. Click **Properties…** and the screen shown in Figure E-18 will appear.

*Figure E-17 – PCI-6023E Properties*



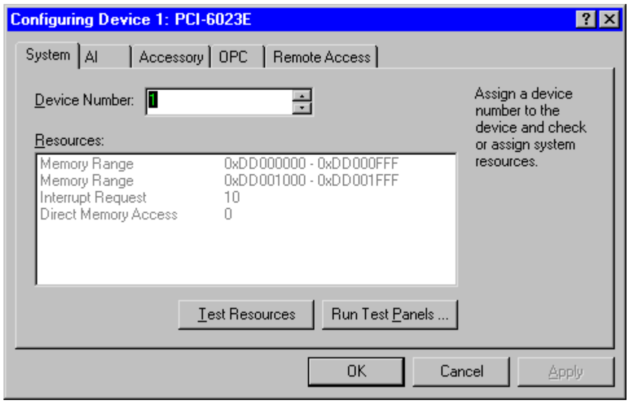
DAQ Device Basics

What do you want to do?

- Run the DAQ Test Panels
- Remove the device
- View or change device properties

Click the **Test Resources** button and the screen shown in Figure E-19 will appear.

*Figure E-18 - Configuring Device 1: PCI-6023E*



Device Number: 1

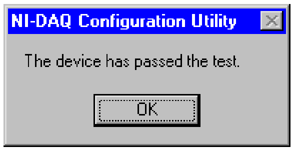
Resources:

| | |
|---|---|
| Memory Range | 0xDD000000 - 0xDD000FFF |
| Memory Range | 0xDD001000 - 0xDD001FFF |
| Interrupt Request | 10 |
| Direct Memory Access | 0 |

Assign a device number to the device and check or assign system resources.

Click **OK** to close this window. Close the screen shown in Figure E-18 by clicking **OK** and the screen shown in Figure E-16 will appear. Close this screen by selected **File | Exit**. The DIG-744 (NI-DAQ) card and its drivers should now be installed correctly.

*Figure E-19 – NI-DAQ Configuration Utility*



The device has passed the test.