

PQL II – Data Viewing Program

PQL II (PASSCAL Quick Look) is a seismic trace viewing program and the application of choice at PASSCAL for viewing time-series data in mini-SEED, SEG-Y, or SAC format. PQL II, as the name implies, is the second generation of PQL. Both generations of code were written by Richard Boaz (Boaz Consultancy). PASSCAL staff support the code on several platforms including MAC OS X, LINUX, and SOLARIS.

The program automatically detects SEG-Y, SAC, mini-SEED, AH trace file formats and endian-type. Functions include trace viewing in both time and frequency modes, displaying header information, sorting, gap and overlap detection and display, use of filters, a variety of transform options, marking and saving picks, and postscript printing.

Within this document:

Commands, Top level menu buttons, and General scripts are in bold.

Command-line usage is highlighted yellow

Second level menu are italicized.

[URLs and email addresses are blue.](#)

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Installing PQL

Install PQL II by going to the PASSCAL download page:

<http://www.passcal.nmt.edu/content/software/package-downloads>

Or to directly to the PQL download area:

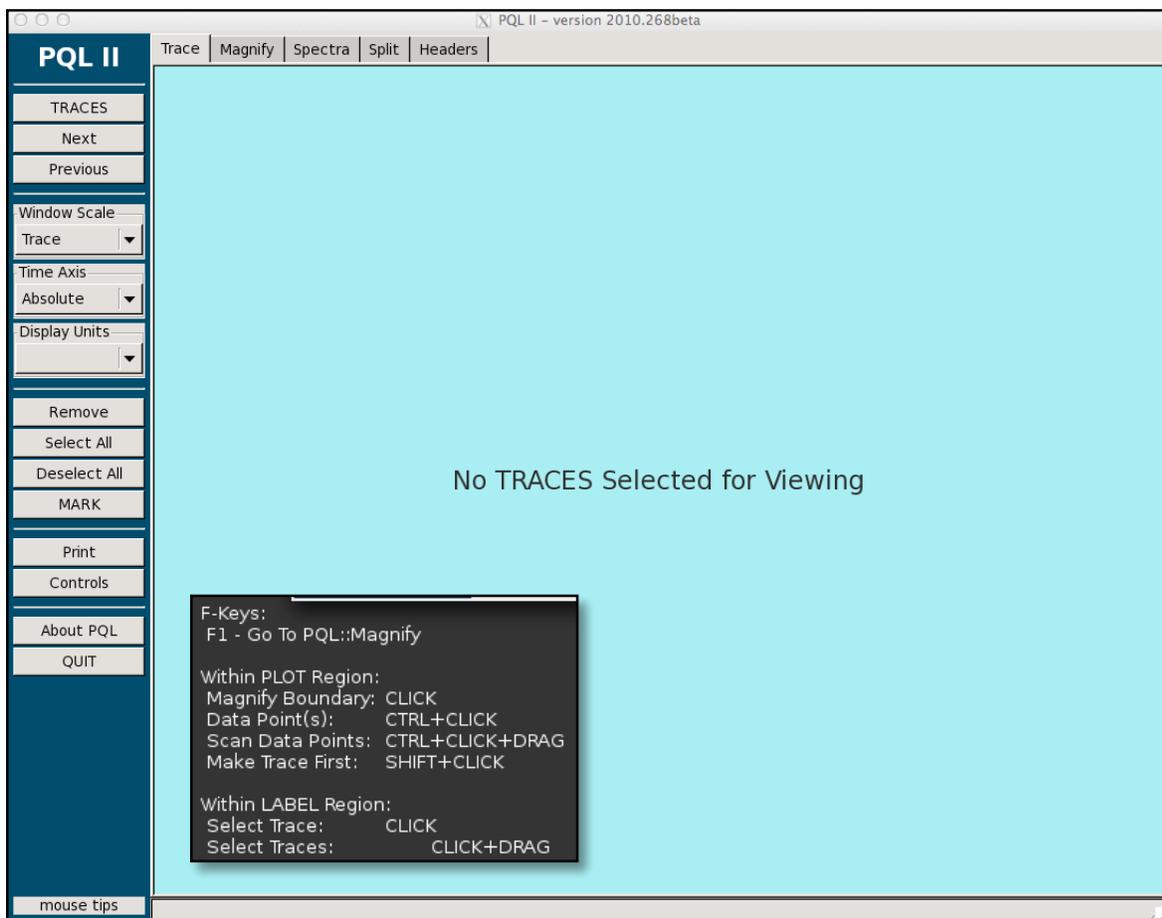
<http://www.passcal.nmt.edu/ftp/software/pql/>

Note: The PASSOFT (PASSCAL) software package needs to be installed before installing the PQL II software package.

Getting Started with PQL – Broad Overview of Functions

To use PQL II, either select the pql icon from the computer system dock or enter the program name on the command line to bring up the GUI:

```
>> pql
```



If using a laptop, consider starting PQL using the `-l` flag. Typing `pql -l` will start PQL in low-resolution mode which better interprets the size of the screen.

There are five tabs at the top of the GUI defining the top-level functions of the program.

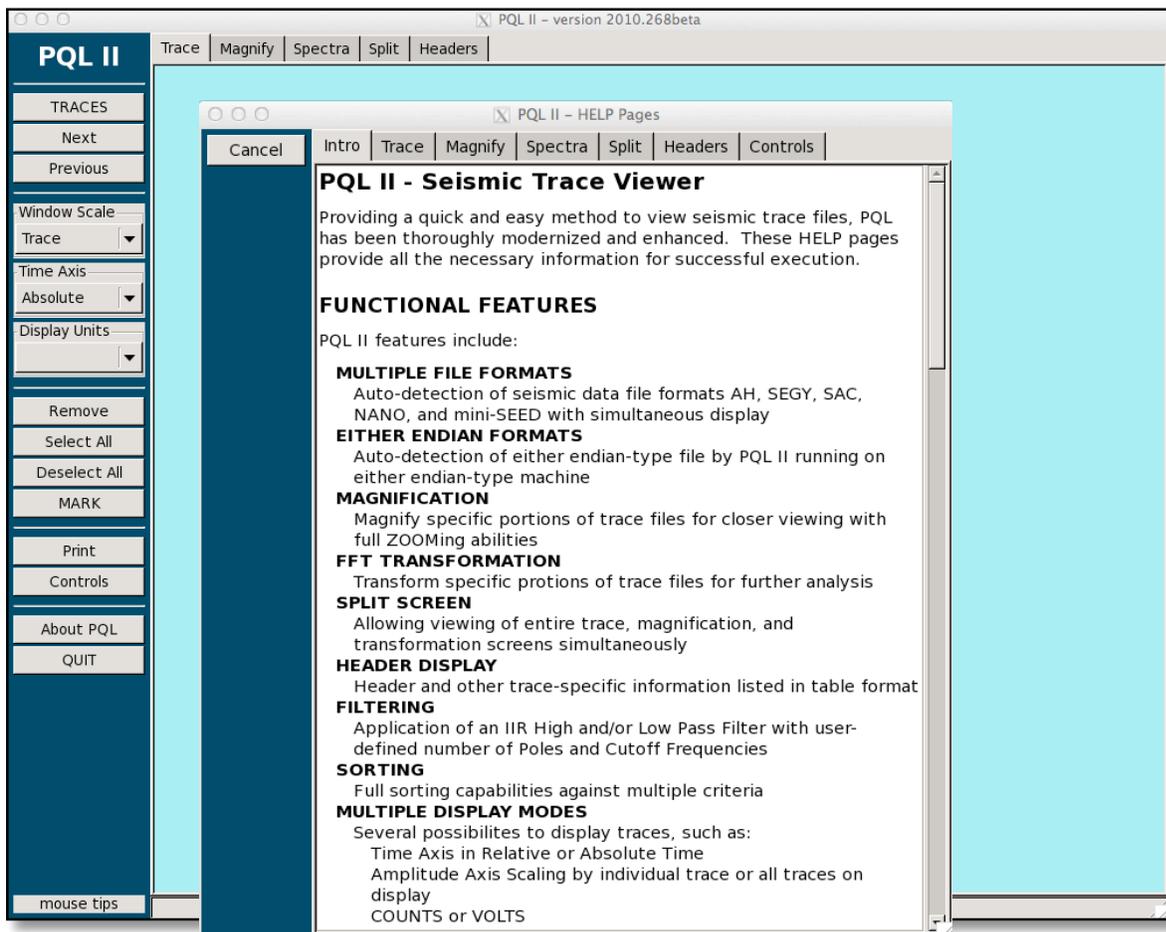
Trace	View individual traces.
Magnify	Zoom In and Out on selected areas of the trace.
Spectra	Transform and display selected areas of the trace.
Split	Display multiple views simultaneously.
Headers	View selected header information.

These tabs will be discussed in detail later within this document.

Hovering over the box labeled **mouse tips** brings up the dark-colored box shown above. This box shows the keyboard shortcuts available for PQL II. Hover the mouse over any menu button for a short description of the command.

How to get program Help

Click on the **Controls** button on the left sidebar to bring up a GUI for setting default controls and for program help. The **HELP** pages are organized by topic and provide extensive information on the usage of PQL II.



Loading Traces

Load traces from either the command line or by using the GUI as shown below. Typing **PQL -h** brings up a brief overview of command line usage for loading traces. Specify which traces to load; by DAS (loads all channels associated with the DAS), by channel or by date. Wildcards can be used in any of these instances.

For example, load all of the data from DAS EZ01 in the directory containing EZ01 mseed files by typing:

```
>> pql *EZ01*
```

Or load all the BH* channels in the directory containing EZ01 day_volumes by typing:

```
>> pql *BH*
```

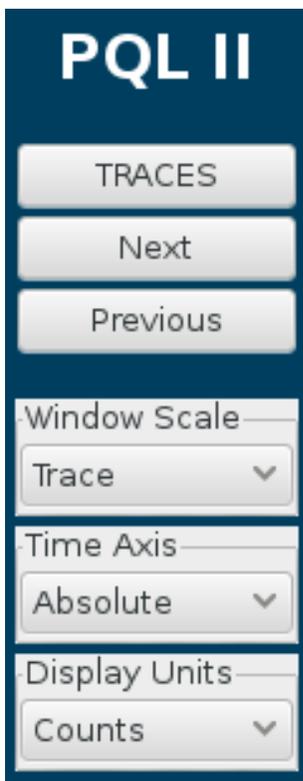
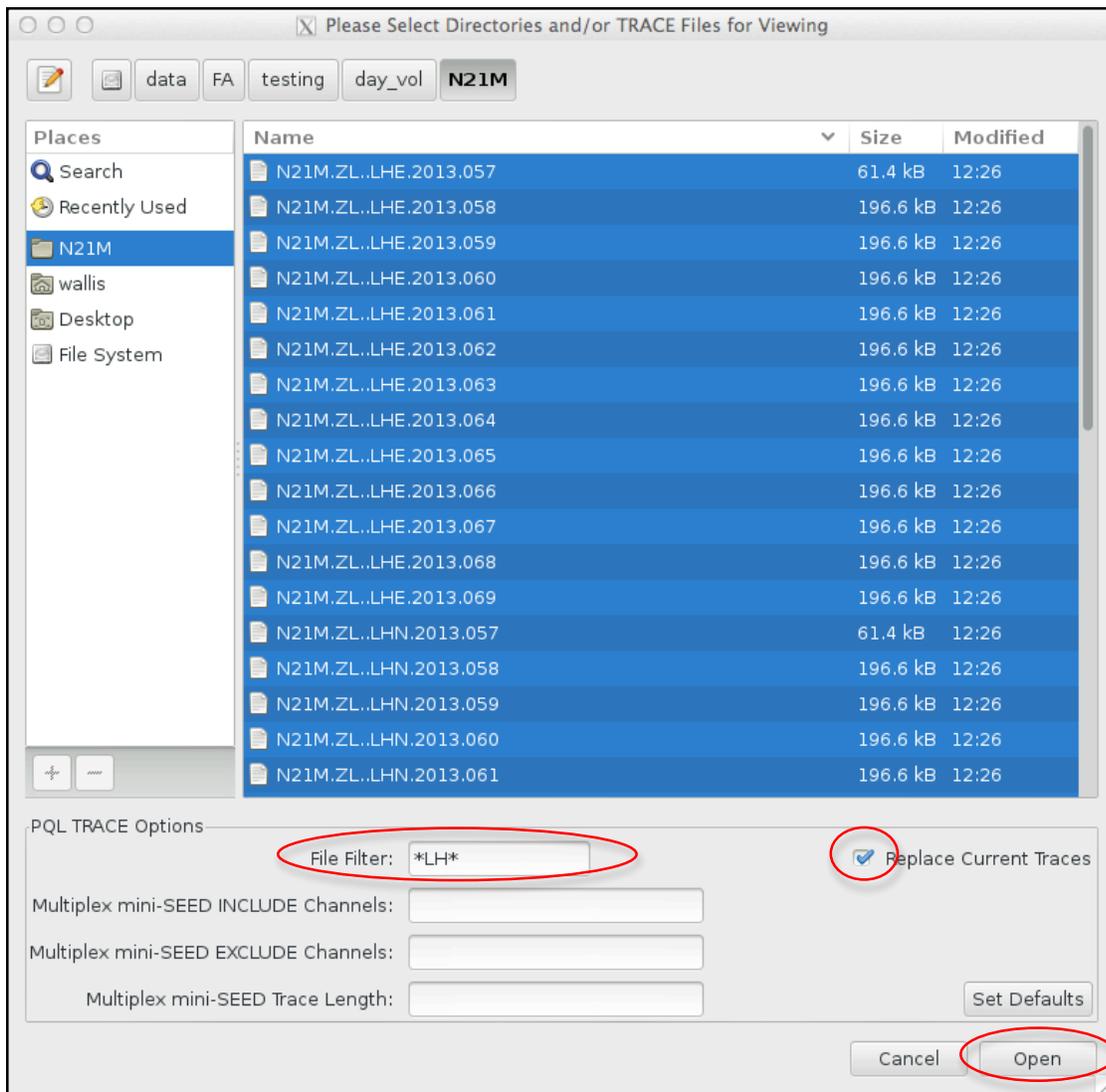
All of the data for a particular time span can also be specified within the directory containing day_volumes by typing:

```
>> pql *YYYY.DOY1 *YYYY.DOY2 *YYYY.DOY3
```

or specify certain channels (in the case all LH channels) for a particular time span within the day_volumes directory by typing:

```
>> pql *LH*YYYY.DOY1 *LH*YYYY.DOY2 *LH*YYYY.DOY3
```

Load traces for viewing by using the **Traces** button on the left sidebar in the main GUI. Navigate to a specific data directory and click **CTRL+a** to select all of the data in that directory. To narrow a selection use the **File Filter** box and wildcards to narrow the selection by station, channel, or date. Click the **Open** box to apply the file filter. Notice the **Replace Current Trace** check box. The default is checked and the program will replace the currently displayed traces with the newly selected traces unless this box is unchecked.



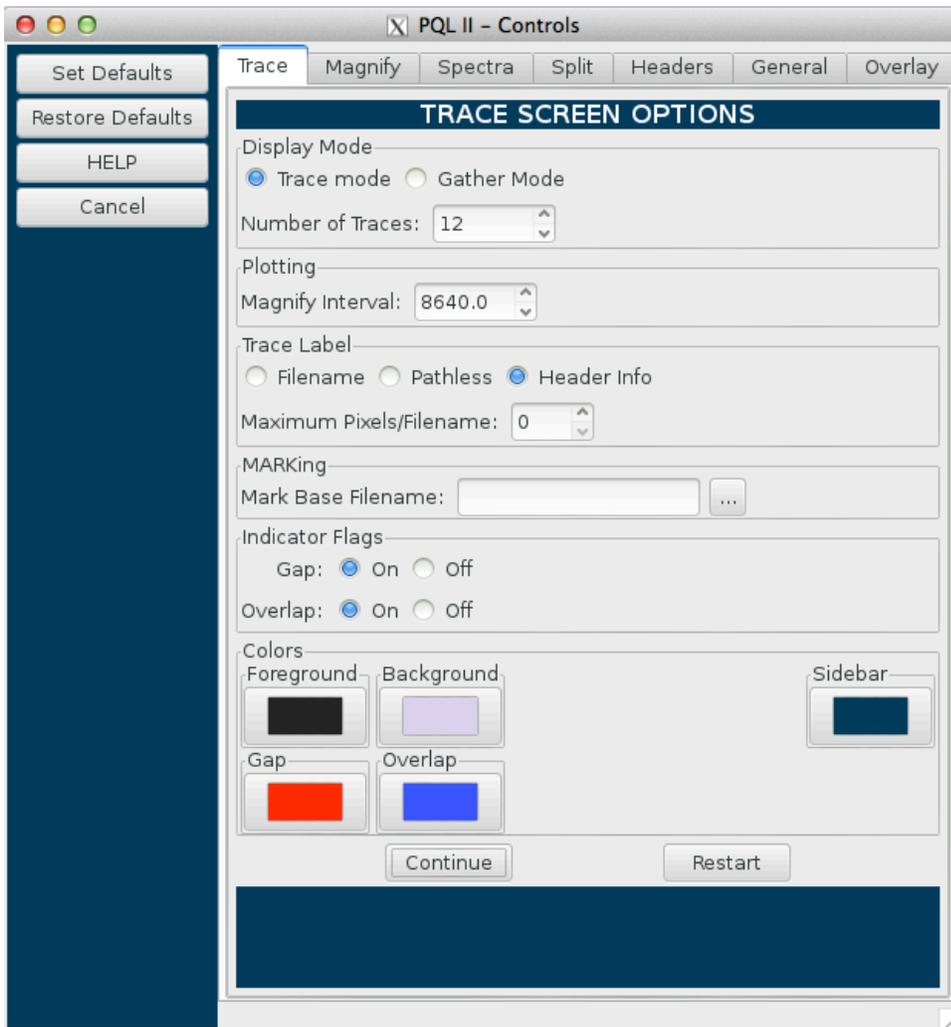
Once the traces are loaded they will be displayed in the main window with the **Trace** tab selected. The number of traces displayed is set in the **Controls** window (discussed below). The default number of traces is 12. If more than 12 traces have been loaded, additional traces will be displayed on subsequent windows. To navigate through the traces use the **Next** and **Previous** buttons immediately below the **TRACES** button in the sidebar.

Control how the traces scale by selecting the **Window Scale** toggle button on the left of the GUI. This toggles between **Window** (uses the maximum and minimum values of all traces displayed in the window) or **Trace** (uses the maximum and minimum values of each individual trace).

Just below the **Window Scale** toggle is the **Time Axis** toggle button. Toggle between **Absolute** (uses the absolute start times defined by the headers of all traces on display) and **Relative** (uses the maximum length in seconds of all traces on display).

Further customize the trace display by selecting the **Display Units** toggle, found just below the **Time Axis** toggle. Choose **Counts** for mini-SEED data, **Volts** for AH, SAC, and NANO formatted data, or **Both** for SEGY data. If, for example, mini-SEED data is loaded, the only option available is **Counts**.

Customize the viewing of selected traces by clicking on the **Controls** button in the sidebar, which will bring up a Controls window. Select the **Trace** tab at the top of this new window to show the customization options. Options include viewing in either trace or gather mode, the number of traces to display on one screen, magnification interval (default is 10% of the trace length), options for how to display the trace label, turning indicator flags on or off for gaps and overlaps and the colors you would like to use for each, as well as background and foreground display colors. The screen below shows the default settings.



Options for **Magnify**, **Spectra**, **Split**, and **Headers** are discussed within the appropriate sections below.

Setting Some General Use Defaults

The second to the last tab on the Control Window (shown above) is the **General** tab. Use this tab to customize a few basic options. Use the **Edit...** button in the center of the window below the

SORT Definitions heading to set the trace sort criteria. Click the **New Sort** button to sort the data. An example to start with:

Criteria #1: Absolute Start Time (Ascending)

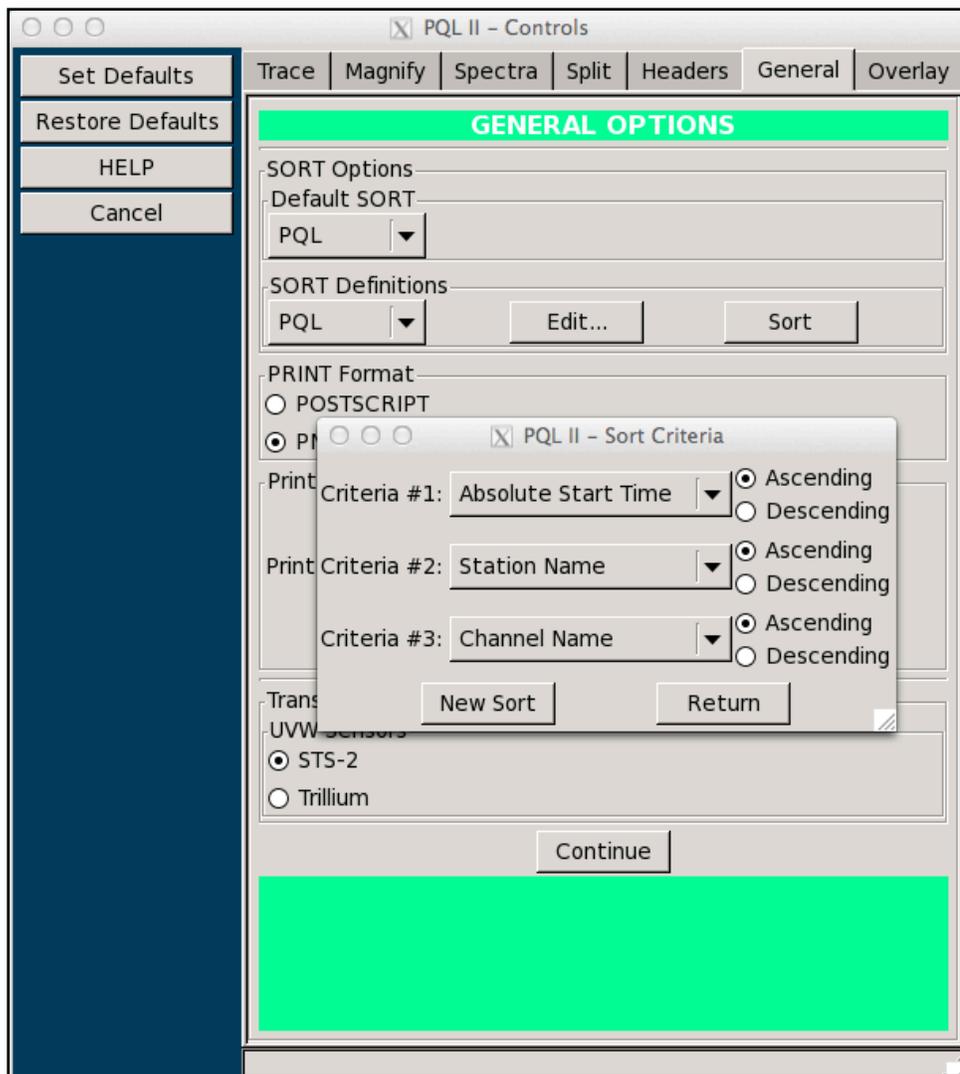
Criteria #2: Station Name (Ascending)

Criteria #3: Channel Name (Ascending)

Click the **Return** button to return to the General options window.

Selecting the **Sort** button after editing the sort criteria will sort the headers and loaded traces into the requested order.

Other options to set here are *PRINT Format* as Postscript or PNG, Resolution and Paper size for *Printing* as well as selecting the type of sensor for *Transform options*. Be sure to click on the **Set Defaults** button at the top left corner of the window to save your options before moving to another tab.



Selecting Traces and Navigating Though the Trace Windows

Navigate to the next or previous screen of traces by clicking on the **Next** or **Previous** buttons in the sidebar of the GUI directly below the **Traces** button. Click the Next or Previous buttons and then go back to the original screen to have the traces show correctly.

Selecting Traces

Select All or **Deselect All** of the traces by clicking on the appropriate buttons in the sidebar of the GUI. Alternatively, select one or more traces by simply clicking on the trace label to select and clicking again to deselect.

Removing Traces

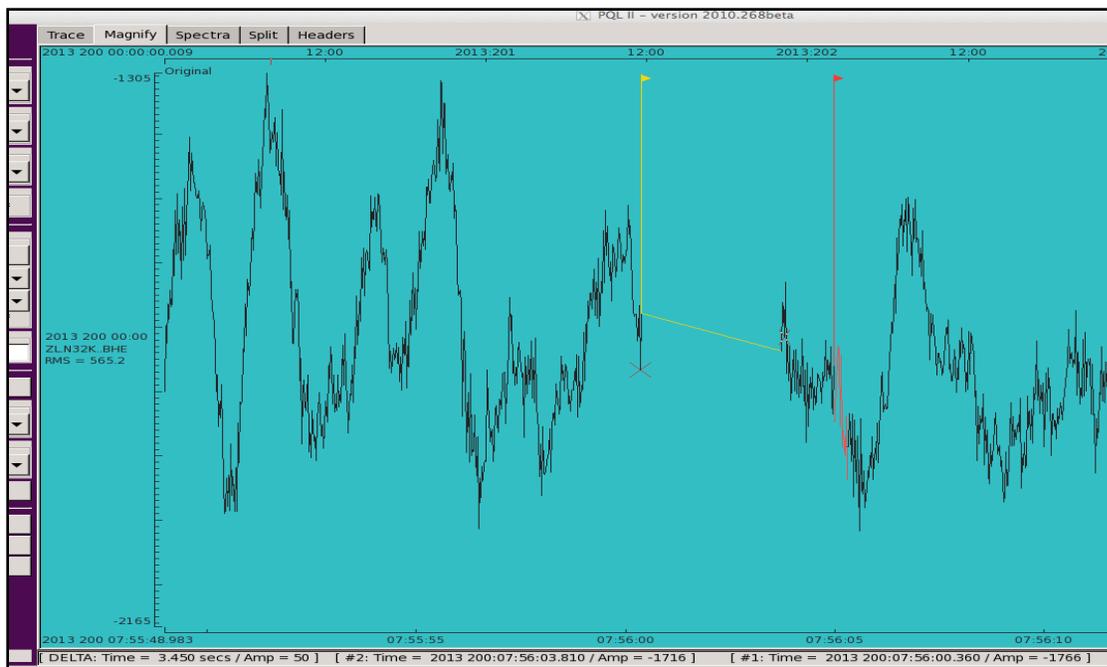
To remove a loaded trace simply select the trace and click on the **Remove** button to the left of the GUI. Click the Next or Previous buttons and then go back to the original screen to have the traces show correctly.

Selecting a Time Window to Magnify or Transform the Trace

To magnify or transform a trace, select a time window. Click on the trace to define the time window. Click the **Deselect All** buttons at the left of the GUI to deselect the time window or remove a stray click mark. The **Remove** button will do two things. If a trace or traces are highlighted the **Remove** button will remove them from the display. If no traces are highlighted and an area to magnify is selected, the **Remove** button will remove the vertical lines in a similar manner to the **Deselect All** button.

Getting Time and Amplitude from the Trace Display

To obtain the time and amplitude of a specific point on the trace, **CTRL click** on the point and the time information will be displayed in the status bar at the bottom of the GUI. To obtain the delta time between two events, **CTRL click** on each event and the delta time between the points as well as the time and amplitude of each point is displayed in the status bar. The example below shows the length of a data gap.

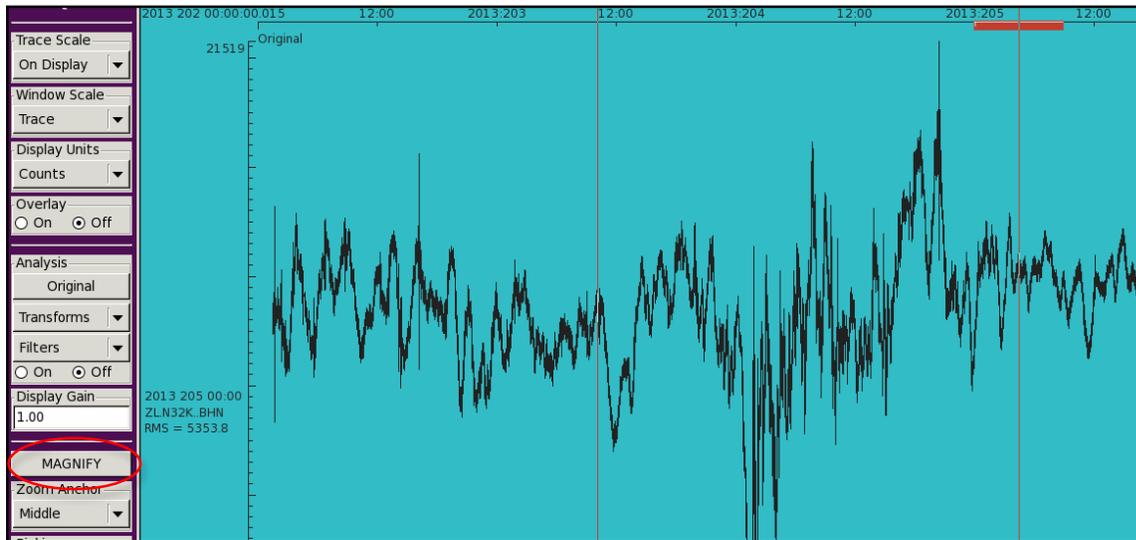


Magnifying Traces

PQL has a variety of ways to get a closer look at the traces.

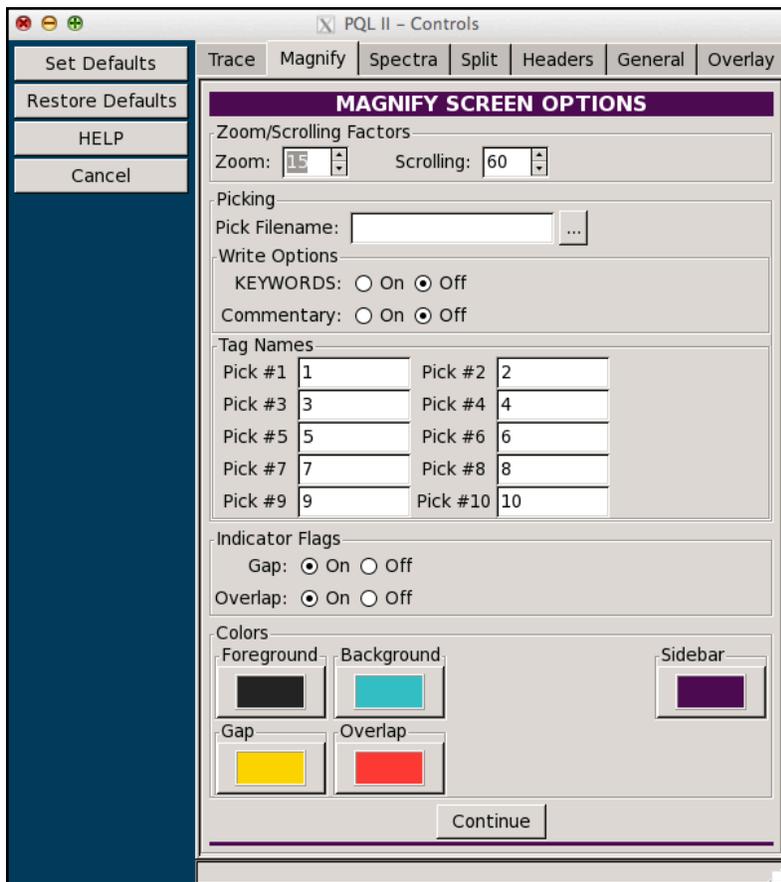
Click on the trace label to select the trace or use the **Select All** button at the left side of the GUI. Once the trace(s) have been selected, click on either side of the area of interest to select a time window and then click the **Magnify** tab at the top of the GUI to zoom in one level. To magnify an area of interest further, click on each side of the area of interest and then click on the newly revealed **Magnify** button in the left sidebar.

Remember to select the trace labels or nothing will be magnified.



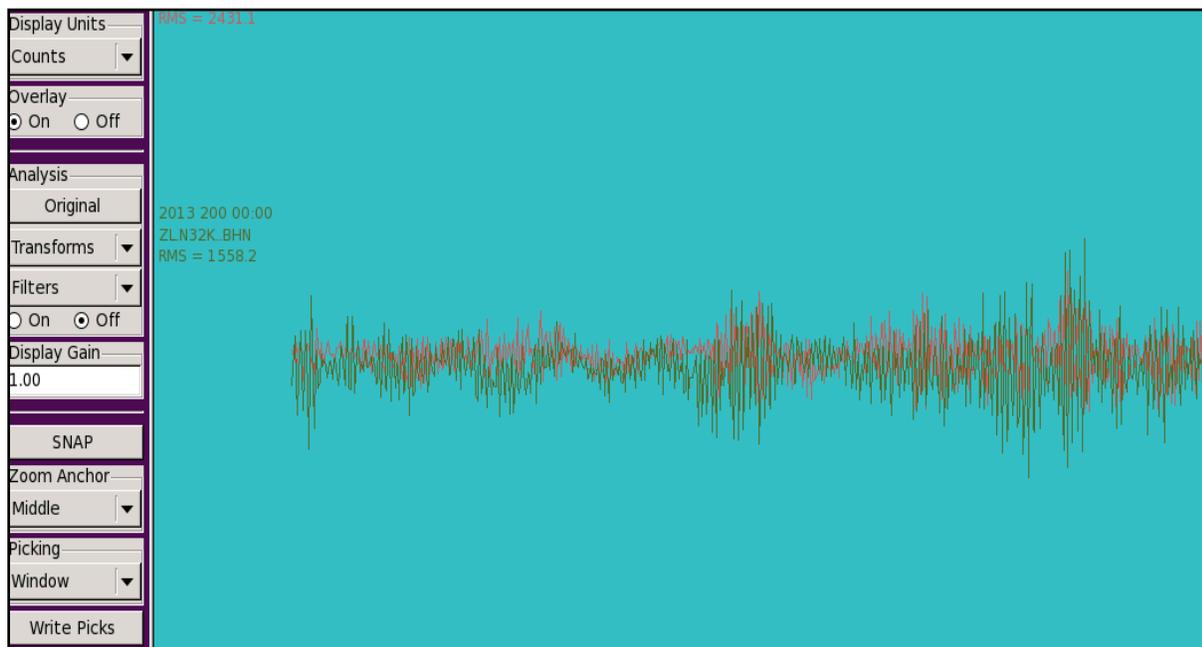
Another way to magnify the trace further is to click anywhere on the trace and drag to the right. Dragging to the left shrinks the size of the trace. The trace can also be magnified by using the up arrow keys or pushing the flywheel on the mouse forward. Reversing any of these actions will shrink the trace. To restore the original trace, click on the **Trace** tab at the top of the GUI. Select the **Split** tab at the top of the GUI to get a view of the entire trace in the same screen as the magnified area.

Modify the zooming speed (higher number if faster) and the scrolling distance (as a percentage of the screen) by clicking on the **Controls** button in the sidebar on the left side of the GUI and then selecting the **Magnify** tab at the top of the **Controls** GUI.



Using Overlay Mode

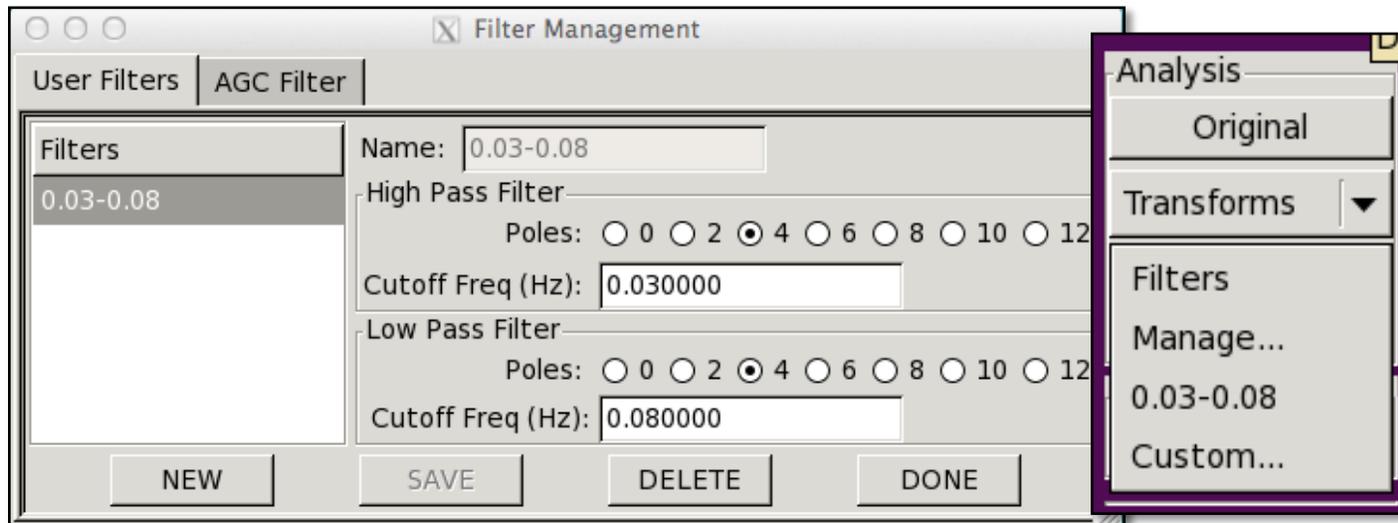
To overlay traces turn on this feature by clicking the **On** radio button in the *Display Units* section on the left of the GUI. Use the **Controls** window to select colors for the overlays.



Filtering data

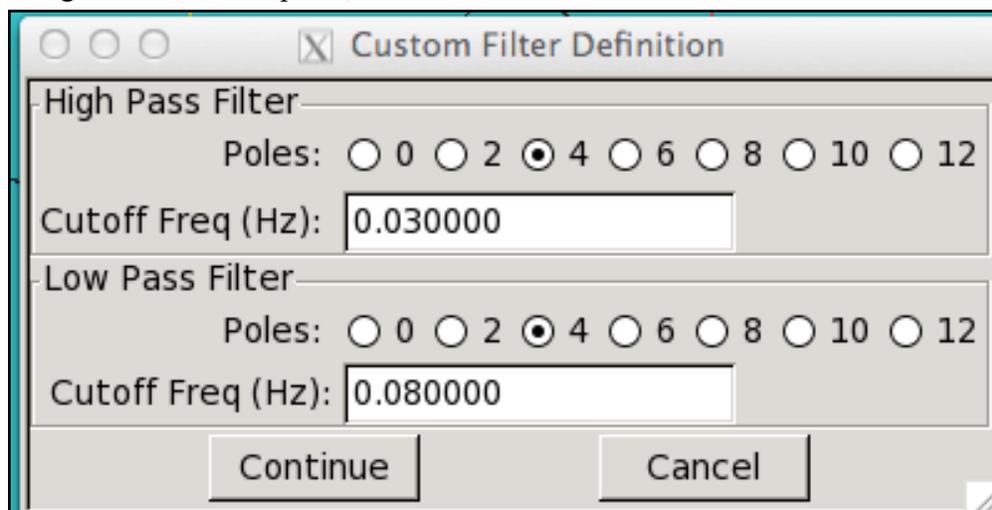
To filter the magnified traces, use the pull down **Filters** menu in the *Analysis* section on the left side of the GUI. The **Filters** pull down menu options include *Manage...*, *Custom...*, and any filters that had been previously customized. PASSCAL laptops have a number of default filters already set up.

The Manage option brings up a **Filter Management** window as shown below. Use this window to customize and save filters. In the example below the user is creating a new filter using 4 poles, a High pass cutoff frequency of 0.03 Hz, and a low pass cutoff frequency of 0.08 Hz. Once saved, this filter will be displayed on the **Filters** pull down menu.



Apply these filters by selecting the On radio button just below the **Filters** pull down menu. Once the specified transforms or filters have been viewed, revert to the original trace by clicking on the **Original** button at the top of the *Analysis* section.

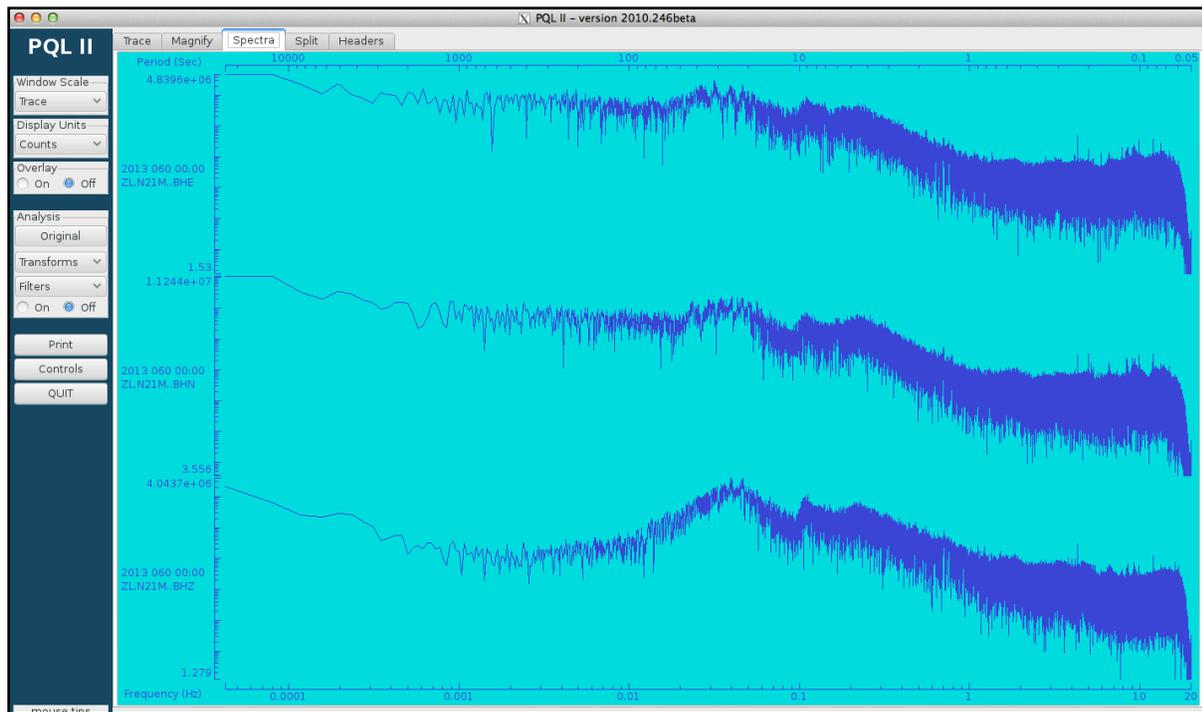
Using the *Custom...* option, a one time filter definition can be created.



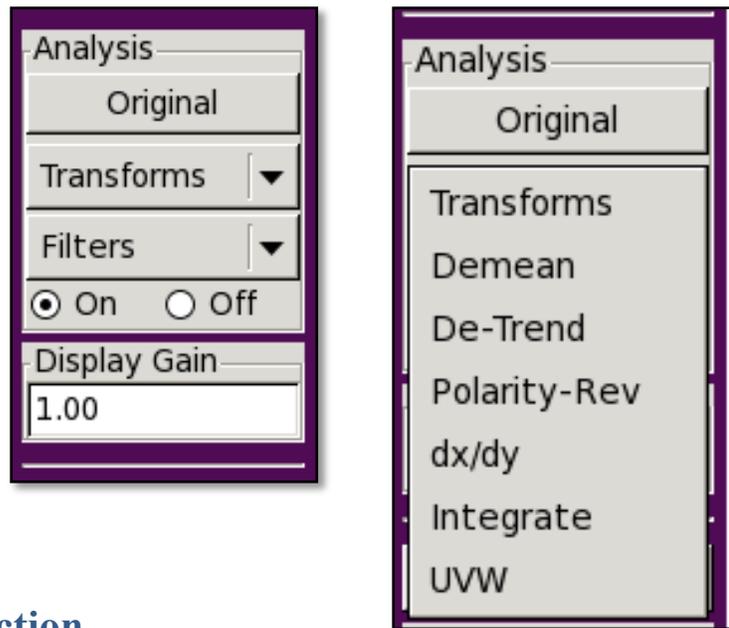
Displaying a Spectra

The Spectra screen displays a fast Fourier Transform (FFT) of the selected portion of a trace or traces. To display the spectra of selected traces, first pick a window on the trace or magnify screen and then click on the **Spectra** tab at the top of the GUI to display a spectra of the selected time window.

To customize the spectra display select click on the **Controls** button at the left side of the GUI and then select the **Spectra** tab at the top of the new GUI window. Using this window, a logarithmic or linear amplitude or frequency scale can be selected. Specify a minimum value and number of decades for the amplitude, a minimum and maximum value for the frequency, and choose foreground, background, and sidebar colors for the spectra display. Click on the **Continue** button at the center of the window to apply selections. Once the display is customized, click on the **Set Defaults** button at the left side of the window to save the defaults.



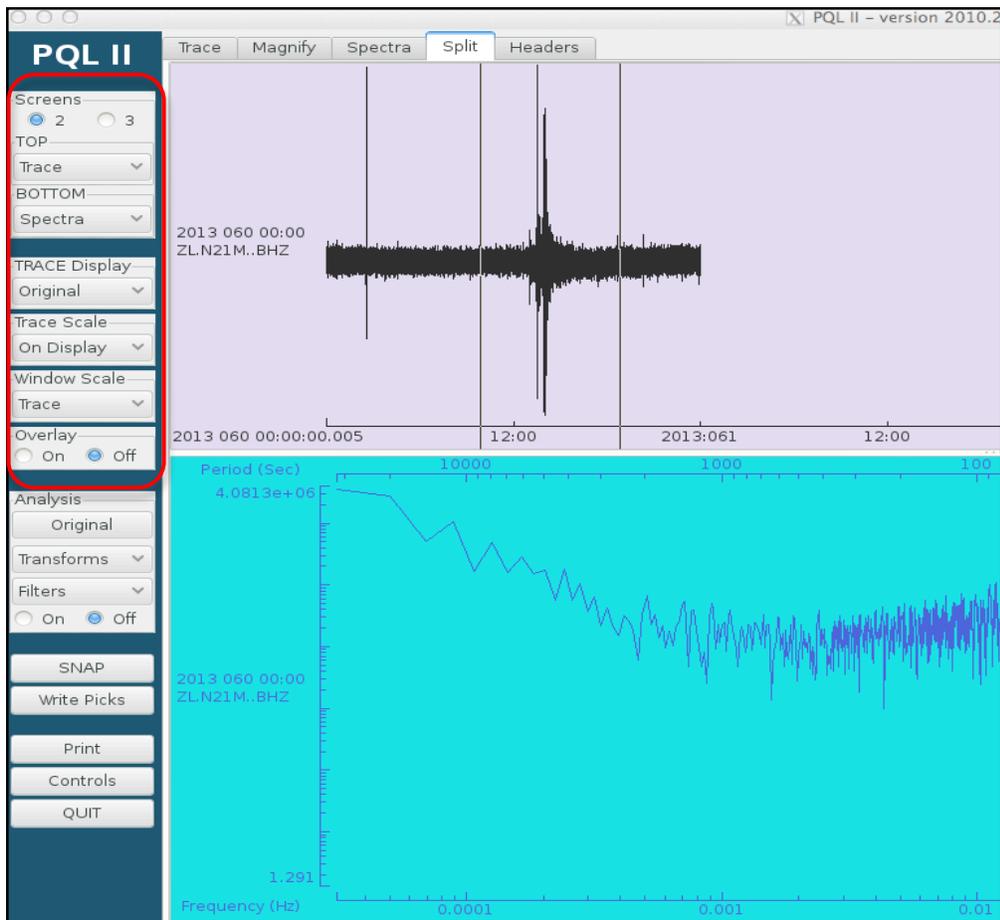
With a spectra displayed, it is possible to choose from a number of *Analysis* options. There is a **Transforms** pull down menu on the left side of the GUI from which the following calculations can be selected: *De-mean*, *De-trend*, *Polarity Reversal*, *Derivative (dx/dy)*, *Integrate*, and *UVW*. Be patient. These calculations may take a few seconds.



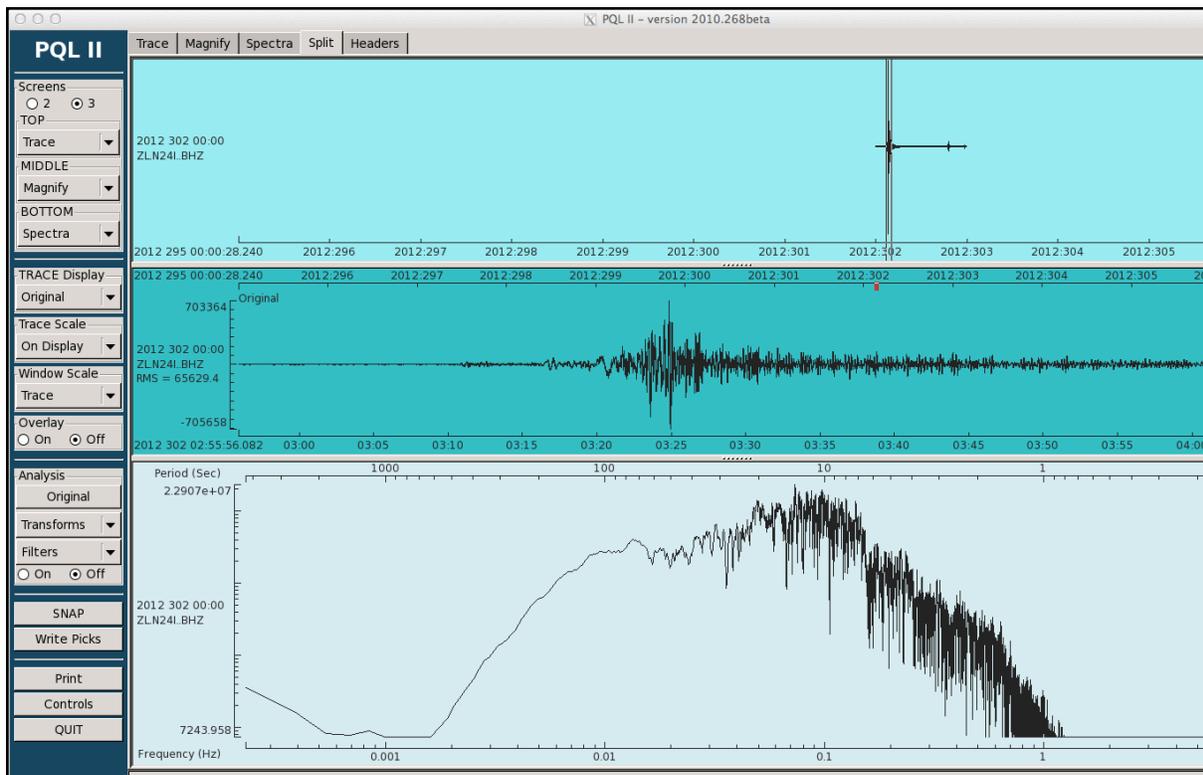
Using the Split Screen Function

The split screen function is accessed by clicking on the **Split** tab at the top of the GUI. This function is useful to help find the section of the trace being magnified and it can also be used to display the trace(s) and spectra in the same window.

Once **Split** tab has been selected, some new options will appear at the left side of the GUI – see red outlined area below. Options include selecting from 2 or 3 screens and what to display in each of the screens. If the 2 screens button is selected, the options include toggling between Trace, Magnify, and Spectra for either the **Top** screen or the **Bottom** screen. If the 3 screens button is selected, there will be a screen with each of the choices above.



Notice that on the 3-screen display shown below, a dark bar (shown in red) in the second panel shows the location of the zoomed area in the first panel and the times selected for the spectra in the third panel.



Clicking on the **Trace** tab returns to the original view with all of the loaded traces.

Displaying Header Information

To check the header information of selected traces, click on the **Headers** tab at the top of the GUI. The header information will appear in the PQL window. The last two columns of the header information shows gaps and overlaps in the data and is a quick way to check for them.

Trace	Filename	Sensor ID	Network	Station	Location	Channel	Start Time	Length	SPS	Samples	File Type	Gain	Scale	Amplitudes	Gaps	Overlaps
	N21M.ZL.BHE.2013.060		ZL	N21M		BHE	2013 060 00:00:00.005	86399.975	40	3456000	mini-SEED	1	1.0000e+00	-180103 / 168674	0	0
	N21M.ZL.BHN.2013.060		ZL	N21M		BHN	2013 060 00:00:00.005	86399.975	40	3456000	mini-SEED	1	1.0000e+00	-147182 / 212886	0	0
	N21M.ZL.BHZ.2013.060		ZL	N21M		BHZ	2013 060 00:00:00.005	86399.975	40	3456000	mini-SEED	1	1.0000e+00	-35945 / 35439	0	0

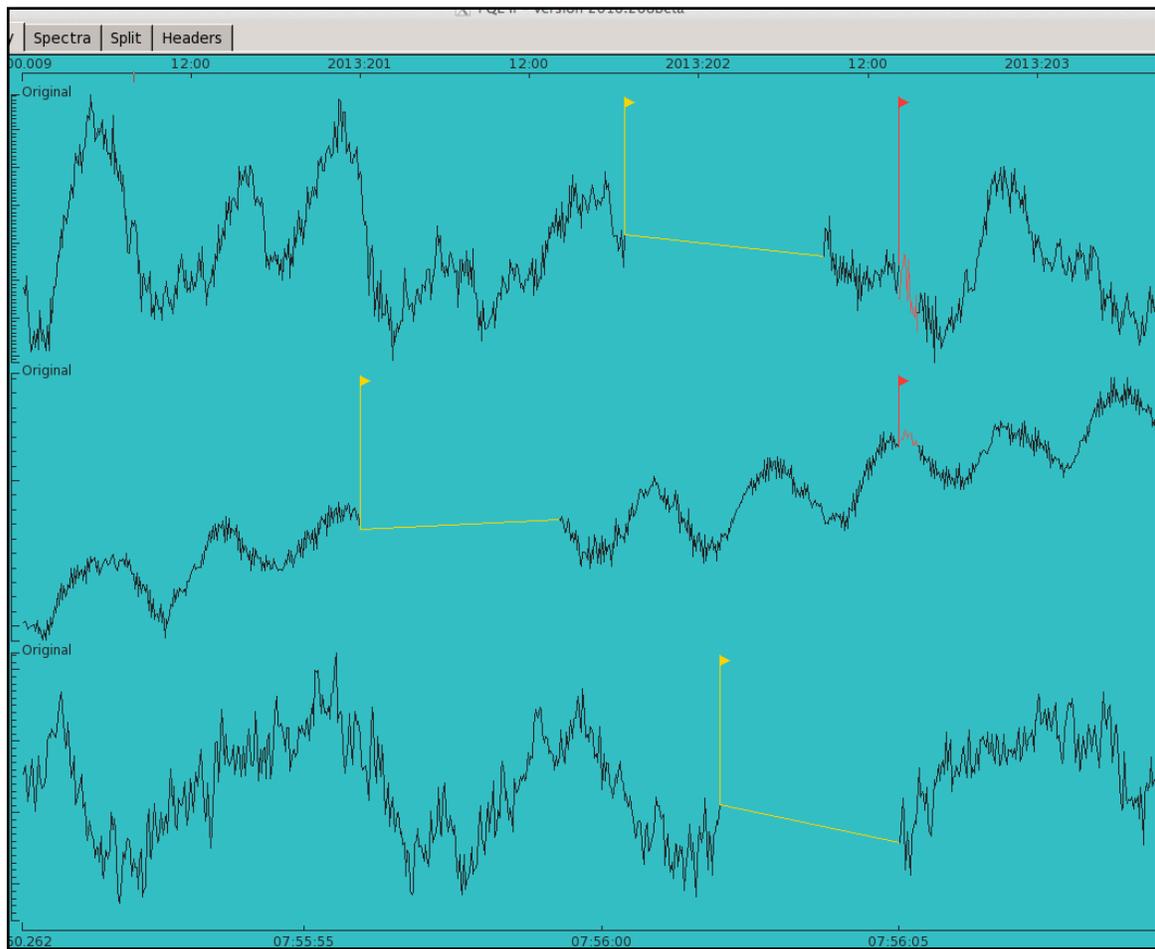
Set which fields of the header to display by clicking on the **Controls** button in the sidebar at the left of the GUI to access the **Controls** GUI. Select the **Headers** tab and toggle on or off the check boxes for each field. The default includes all fields.

Note: The gain displayed in the header information set to a default value of 1 and does not reflect any actual changes in gain.

Gaps, Overlaps, and Data Flagged as Timing Questionable

As mentioned above, determine if there are any gaps and overlaps by checking the header information. These can also be seen while viewing the data because they are color-coded. By

default, data gaps are colored yellow and data overlaps are colored red. The examples below show both a data gap (yellow flag) and a data overlap (red flag).



Caveats

If a GUI window is open no other program functions can be accessed until that additional window is closed.

If the Screen Locks Up

The program occasionally gets hung up or freezes. When this happens simply click on the **Quit** button on the left of the GUI (or xkill the program from a terminal) and re-load the data.

Implied File Size Limit

PQL II uses dynamic memory allocation when reading files. This could prove problematic as the computer memory is not always de-allocated when available. The result is that some large files can not be loaded. Either allocate maximum memory from the command line or split large miniseed files into smaller chunks using one of various options for **sdrsplrit**. See **sdrsplrit -h** for all the options. A basic rule of thumb is that **PQL** will not load files larger than 90MB.