

Using XPLORER

XPLORER DESIGN AND DEVELOPMENT PHILOSOPHY

We at dnaTools, Inc. developed this application to provide a platform independent tool for viewing chromatograms. Its primary function is to view, edit, extract sequences, trim, and align chromatograms. Other features and functions will be added in the natural evolution of XPLORER. The tool was designed to work primarily with chromatograms secondarily with text files. Enhancements and improvements are continually in process. Please forward to us comments and enhancement requests.

XPLORER is a Copyrighted program. Please do not reverse engineer the program and include portions of it in your own designs. Portions of the program can be licensed to developers, contact dnaTools, Inc. for details.

XPLORER uses a run time license to enable functionality. The demo license allows you to use all features within the View tab. Please contact dnaTools, Inc. to enhance your license or enable additional functionality.

View Tab

The View Tab is used to view chromatograms, search for base patterns, display statistical information about a selected base, and to screen the selected chromatogram for secondary peaks.

Open a Folder of Chromatogram --

1. Launch XPLORER
2. From the File Menu select Open
 - 2.1 Navigate to and Highlight a Folder of Chromatograms
 - 2.2 Select the Choose Button
 - 2.3 This will list the chromatograms with individual checkboxes in the File Pane.
3. Select one of the chromatogram checkboxes.
After understanding the browser, you may select as many chromatograms as you desire.

Screen for Secondary Peaks –

1. Select the Screen Button and leave the default values unchanged.
2. Select the Start Button.

A window appears at the completion of the screen function listing potential base positions of secondary structures.

Selecting any of the listed values will advance the display to that setting.

3. Refine the screen by increasing or decreasing the % of Peak value.
Reduce the potential peaks by increasing the % of Peak value.

Use the other Screen Parameters to increase the detection sensitivity.

Set the % of Peak value to 50, set the Slope value to 25, set the Standard deviation to 40.
Use these values as a starting point to detect smaller peaks.

Decreasing the Slope and Std. Dev. values allow for detection of shallower peaks.

Use the Next N feature to quickly step to potential secondary peaks that are represented by N's.

Data Button --

Select a Base or a waveform peak then select the Data Button.

This displays a table showing statistical information surrounding and about the base.

The beginning of the table shows five data points to the left and right of the selected base.
This allows visual analysis of the surrounding data points.

The table then displays the Left and Right Least Means Square Slope of the waveform.

The Standard Deviation of each base is then listed.

Use these data values to characterize waveforms for use in the screening feature.

Next N --

Select the Next N button to step to the next undetermined base.

Then use the Data button to analyze the data values surrounding the base.

Between the data values and the appearance of the waveform the base value can be determined.

This feature can be used to quickly step to potential secondary peaks.

Find --

Single and multiple chromatogram displays can Snap to the same Base position by selecting the Find... button and entering the desired base position.

Proteins --

The Proteins buttons allows you to select which taxonomy and reading frame to view.

Trim Tab

The Trim Tab is used to edit sequence text files, even if they are in the chromatogram.

SNP Tab

The SNP Tab is used to identify base call differences in chromatograms.

The SNP Tab applies an exact match aligner to the selected chromatograms.

Differences in base calls are highlighted with pink lines in the view pane.

Positioning the cursor by a pink line and clicking the mouse will draw a view rectangle.

Reposition the rectangle until it encloses the pink line.

View the base difference in the chromatogram pane.

Selecting an expansion arrow allows visual inspection of the selected area.

Inspect the difference for secondary peaks.

Closing XPLORER

From the File Menu select Close All then select Exit.

Closing XPLORER in this manner writes path information into a configuration file, so the next time XPLORER is opened it will maintain the same window size and file paths.

June 7, 2004

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