Physics MRI Research Centre

Universal Sorter

VERSION 4

User's Guide

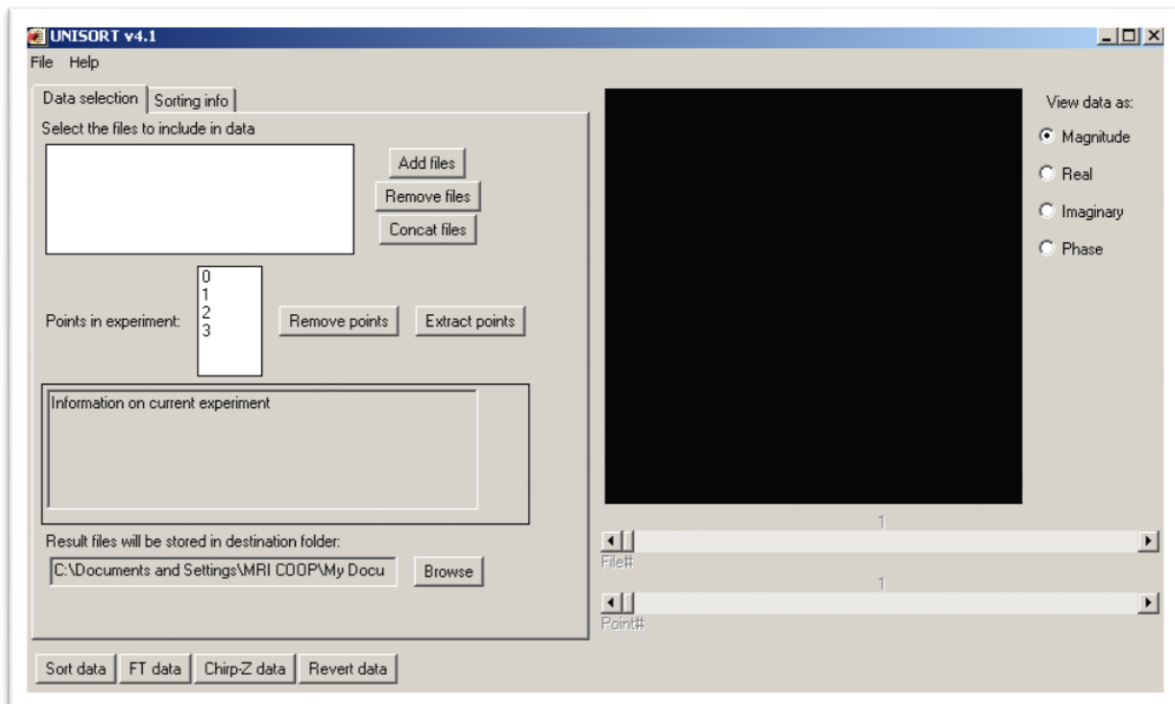Last Updated April 2011 by Jim Stevens

Introduction

The Universal Sorter is an IDL program which is used to process data acquired using any of the SPRITE-based sequences on the Tecmag and Resonance Instruments consoles. It can extract multiple-point data from NTNMR files, and it can easily sort data acquired using any of the most commonly used Spiral-SPRITE and Conical-SPRITE sequences. For newly designed sequences whose use has not become widespread, the program can read in a user-provided gradient table and sort the data anyway.

This guide explains how to use the Universal Sorter to process data quickly and easily. This applies equally to the IDL version running on the Macintosh computers, and to the version running under the Virtual Machine on the PCs running the consoles. On the Macs, the Universal Sorter can be started by entering "unisort" on the IDL command line. On the PCs, there should be an icon on the desktop which will start the IDL VM.

Unisort – Data Selection

When Unisort launches, the program will be on the "Data Selection" tab, where most of the file and point manipulations are done. The preview window on the right will show a basic rendering of whatever data is loaded, and is blank to start. Begin by adding files to the experiment with the "Add files" button.

Once data has been loaded into Unisort, new files can be added to the experiment, files can be concatenated together to form a single file, and points can be removed or extracted from the experiment. Through all of these changes, the preview window on the right, and the Information box toward the bottom should be updated to reflect the "shape" of the data (number of dimensions, size of each dimension, number of points acquired, etc).

Adding and Removing Points

The data in a multi-point acquisition can be manipulated point by point. Any points removed from the experiment will be removed consistently from each file in the current experiment (eg: points 4, 5 and 6 might be removed from all twelve files currently loaded).

Remove points: select the points to be removed from the experiment and click on the "remove points" button. *Only points not selected will remain in the experiment.*

Extract points: select the points to be kept and click on the "extract points" button. *Only those points selected will remain in the experiment.*

These two methods of achieving the same effect are provided to match up with different user's perspectives on how they are managing multi-point acquisitions.

File Manipulation

File Loading

Unisort will open any of the following file types:
- Riimage (*.rii, *.riImage)
- NTMR (*.tnt)
- Bruker
- BYTE (*.dat)

Additionally, any of these files can be loaded if they are multi-point or single point files. Multiple files can be loaded at the same time, as long as they have compatible dimensions. For any set of files from the same acquisition this should not be a problem, but if there are different dimensions to the data, or different numbers of points the data cannot be viewed or operated on at the same time. *Warning: it is completely possible to load files of similar dimensions that are not related. The user is responsible for how they choose to combine data in this way.*

There is a special case where SPRITE data is loaded and the files will be of different sizes. In this case you will be prompted to concatenate the files (see below).

Filename Sorting

When multiple files are loaded into Unisort, they are automatically sorted, regardless of the order they were selected in. The algorithm that is used was chose because it is compatible with almost all file numbering formats. There are some file numberings that will not work properly with this system though; it is recommended that those files be renamed to match the conventions for file numbering.

Filename formats that will be sorted correctly: Any files that match this format will be sorted properly:

[any file name]+[any numbers or symbols][**filenumber].[file extension]**

So for example: somefile_X_C_1.riimage, somefile_X_C_2.riimage …, _C_27.riimage would be sorted properly even though files 1 and 2 do not have a leading '0'. Files that are numbered: 1,2,3,4,5,6,7,8,9,10,11 … would all be sorted properly, as would files numbered 01,02,03,04 …, 10, 11, 12 … be sorted properly. The file number **MUST** be the last part of the filename before the extension though.

File Locations

Unisort has been updated to make finding files and quickly saving changes to file easier on the user. There are some options to change the default behavior (see the Options section), but in general, this is how Unisort behaves:

Source location: When attempting to add files to the experiment, the dialog will open in the last folder that data was opened from. When Unisort is first run, it will start opening files in its default location which can be changed in the Options menu.

Destination location-\output\: One behavior is that the data will be saved in an "output" directory immediately off of where the data was added from. When multiple operations are done on the same set of data, there may be nested output folders (eg: source\output\output\output\) depending on the environment.

Destination location-default: Another behavior is where a standard output folder is selected. This can be chosen in the options menu, or manually updated. This method creates a kind of "dump" folder where users can retrieve their sorted data and file it appropriately afterward.

Destination location-manual update: There is a "destination folder" button and display at the bottom of the Unisort window. This shows where files will currently be saved to. The "browse" button allows the user to manually set a folder to save data into. Note that this will not change the default behavior or folder of Unisort; this only affects the next saving operation.

File Saving

The data in an experiment can be saved at most stages of operating on it in Unisort (not during a transformed preview). The data can be saved in one of 3 main ways, all of which are accessible from the "File" menu:

Save (current format): The default saving option. If this is an image file, it will be saved in the same format, in the default output location. Information such as if the file has been concatenated or sorted will be stored in the header information, as well as indicated by markers on the file name (_C for concatenation, _S for sorted). As a special case, if a multi-point file has been stripped down to a single point, that will be indicated by _X[point number] being appended to the file name as well. *Pressing Ctrl+S* will do this kind of save if it is available. If there are multiple files in the experiment, they will all be saved with the specified updates.

Save as Byte: The data will be saved in the BYTE format, which is compatible with Acciss and Jaims for example. There is no header information in this format, but the file changes will still be shown in the file name as for the normal save. Note that if BYTE data was loaded, the normal save will preserve that format when saving. Also of note, BYTE is not compatible with multi-point formats. *While it is possible to save a multi-point file in Unisort, it is not a recognized type that Acciss or Jaims will recognize.*

Split by Points: If this is chosen from the "file" menu, a multi-point file will be split into a separate file for each point. If, for example, a set of six files with 10 points each was saved in this way, then 60 single point files would be generated in the output folder. The split files will each be tagged in their file name to indicate which point and file they originated from ([filename with number]_X[point number].[file type]).
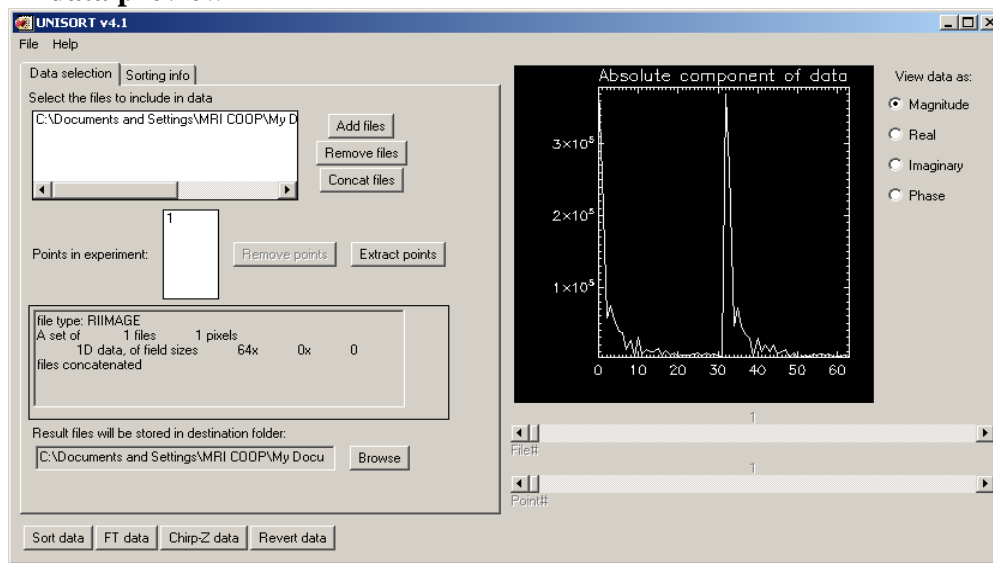
Concatenating Files

If multiple files have been loaded into Unisort (if they have, then they are of compatible dimensions), then they can be concatenated together. This feature is provided to assist with some Double Half-K file acquisitions that need to be manually concatenated. There are no other known uses at this time, but Unisort is designed with the expectation that the user will apply these methods in a manner appropriate to their data.

When opening SPRITE acquisitions, it is often the case that a 2D or 3D image is split into many files of different sizes. If a set of files is opened, and the files are of different sizes, the user will be prompted to concatenate them together. It is recommended that all files from a single acquisition are loaded at one time and concatenated, although they could be loaded in batches and concatenated. Typically, the SPRITE data would then be sorted to generate the 2D or 3D image. In any case, the new data will be saved in a filename based on the first file in the set of files concatenated together.
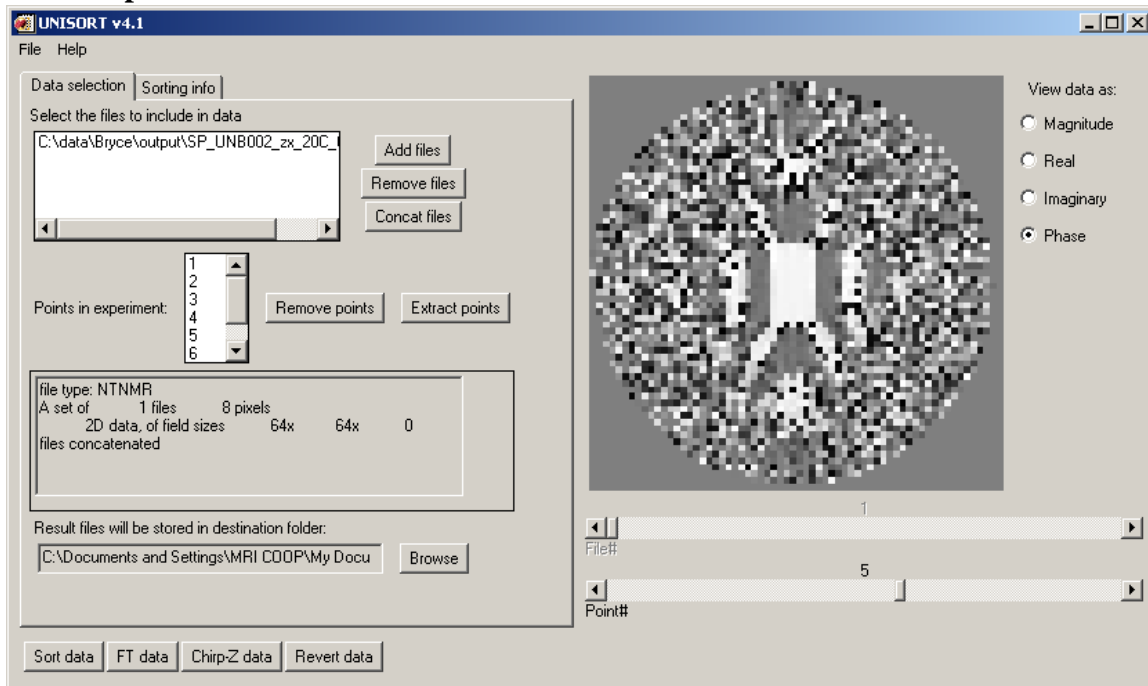
Preview Window of 1D, 2D and 3D images

On the left of the Unisort window, there is a preview area to see a general view of what the data currently looks like. If there are multiple files or points, they can each be seen by using the sliders just below the preview. The intention of this preview is not to provide advanced image manipulations tools, but simply to confirm that the data is looking as expected based on what the subject of the acquisition was. Below are some examples of 1D, 2D and 3D images. Note that in the case of a 3D image, a centre slice through the Z axis is displayed. This may not be useful if the data is uniform across the Z axis.
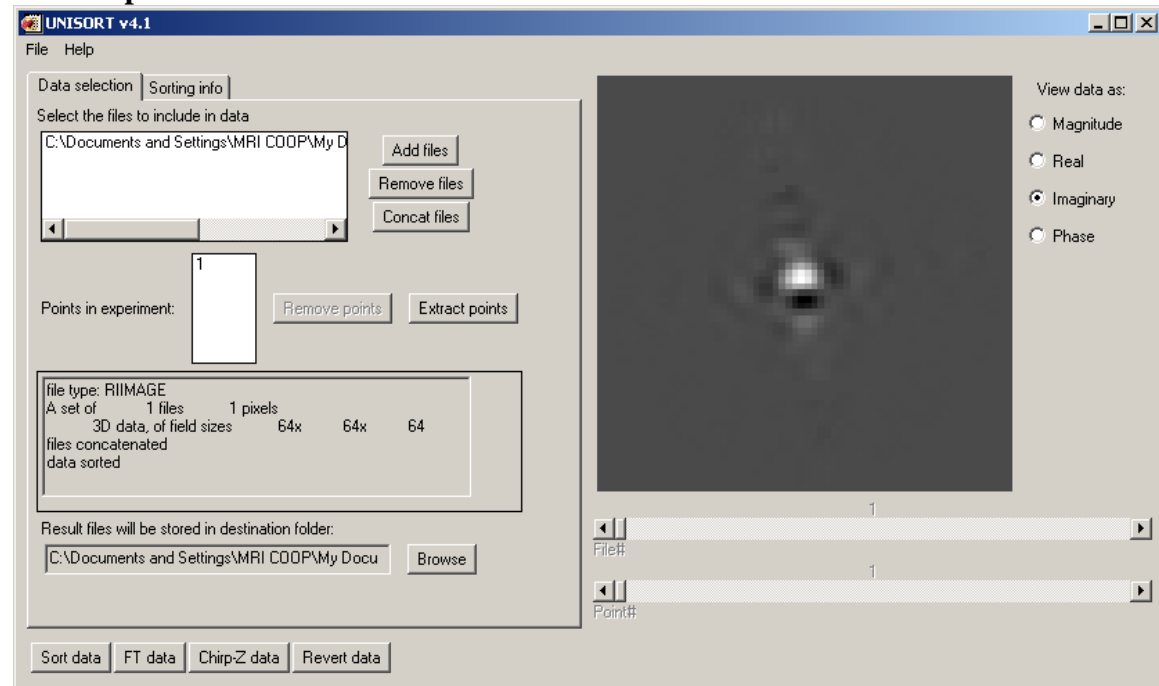
1D data preview

2D data preview

3D data preview

Magnitude, Real, Imaginary, Phase components of Preview

In the above examples, the data has been viewed by Magnitude, Phase, and Imaginary components respectively. These views are provided to show the complex data from an acquisition in different ways. These views are simplifications of the complex data by only

looking at the magnitude, real component, imaginary component or deriving the phase for each pixel of the image. Other programs provide better methods of looking closely at the images.

Sorting Data

The main function of Unisort is to sort data however. Once data has been loaded into an experiment, it can be sorted. If the data matches one of the common types of gradient tables for sorting, simply pressing the "Sort data" button at the bottom of the screen will sort the data. To determine if the data is one of the standard types, Unisort opens a file "unisort_types.txt". If the data matches one described in the file (represented in the list below) Unisort will show you the form that it matched and prompt if it is okay to proceed. This can be aborted and other options can be manually input instead.

Sequence description	Points in gradient table
64^2 Spiral-SPRITE, single interleaf, old version	2564
64^2 Spiral-SPRITE, single interleaf, new version	2565
64^2 Spiral-SPRITE, four interleaves, old version	2592
64^2 Spiral-SPRITE, four interleaves, new version (padded)	2596
64^2 Spiral-SPRITE, eight interleaves, old version	2580
64^2 Spiral-SPRITE, eight interleaves, new version (padded)	2600
64^2 Spiral-SPRITE, 64 interleaves (padded)	3264
64^2 Radial-SPRITE, 64 rays (padded)	2304
128^2 Spiral-SPRITE, single interleaf, old version	10495
128^2 Spiral-SPRITE, single interleaf, new version	10492
128^2 Spiral-SPRITE, four interleaves, old version	10460
128^2 Spiral-SPRITE, four interleaves, new version (padded)	10468
64^3 Conical-SPRITE, 39 Cones, newest version	63607
64^3 Conical-SPRITE, 39 Cones, older version	62505

Updating the standard set of sequences

The file "unisort_types.txt" can be updated to include other sequences, if they have had the appropriate gradient tables generated in GradTable. If the gradient tables are added to the folder "gradient_tables" and the specifications are added to the "unisort_types.txt" file, new sequences can be automatically detected by Unisort. If a sequence will be used often, this would make using Unisort much easier than manually inputting the information each time.
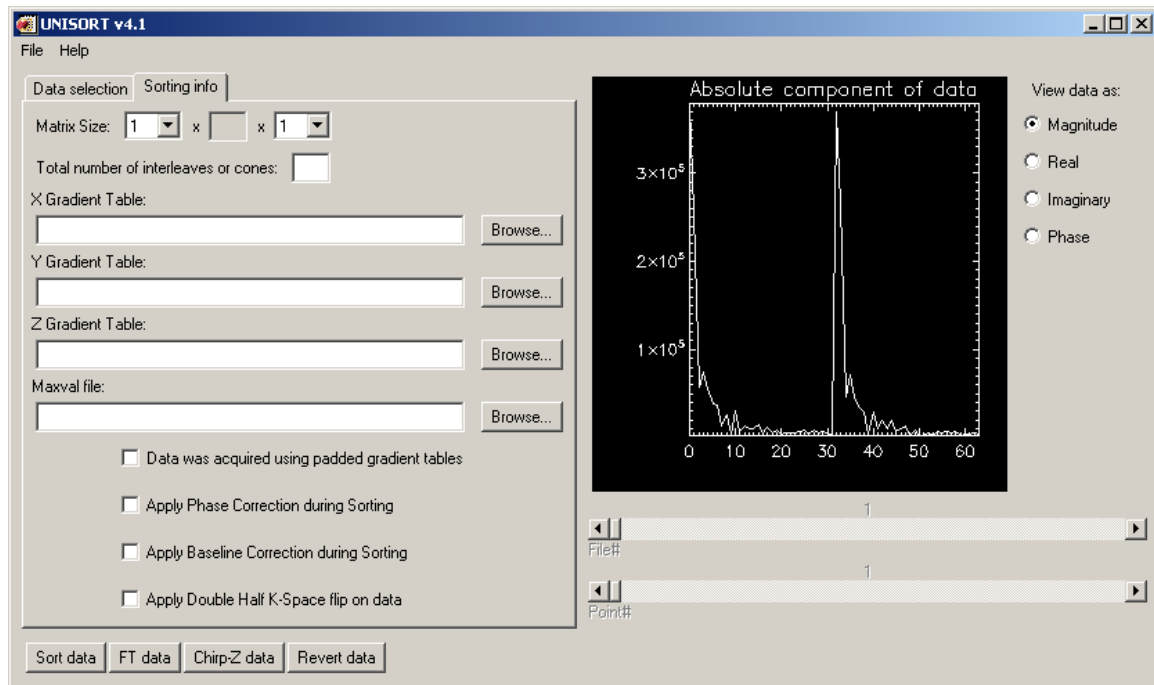
Updates to the "unisort_types.txt" file should be made according to the following pattern:
- Number of gradient table points
- Descriptive name
- Filename of X gradient table
- Filename of Y gradient table
- Filename of Z gradient table (or "none" if there is none)
- Filename of maxval file (or "none" if there is none)

- Number of interleaves/cones
- X gridsize ("0" means 1, "1" means 32, "2" means 64, "3" means 128)
- Z gridsize ("0" means 1, "1" means 32, "2" means 64, "3" means 128)
- Flag indicating whether gradient tables contains dummy points

Manual Sorting Parameters

If the data does not match one of the known sequences, or you wish to manually override the gradients used to sort, you can setup the sort in the "Sorting info" tab. Also, if there are specific changes to the sequence that you would like to make, they can be specified on the "Sorting info" tab.

Matrix Size
Here the size of the resulting image is specified. For 1D and 2D images, the first field needs to be updated. If it is a 3D image, the third field must be entered. *Note that if the total number of data values do not match the product of the X by Y by Z size of the image then sorting will not occur.*

Interleaves or Cones
This field must be filled in to determine the shape of the sequence. This value is determined by the gradient as it was built in GradTable.

X/Y/Z Gradient Tables
These fields are where the gradient files must be specified. If custom gradients are being used, then these are required. If it is not a 3D image, the Z gradient is not required. In most cases, a Maxval file is also required and should have been generated in GradTable.

Padded Gradient

If the data was acquired with a padded table, checking this option will adjust the results to reflect that. For custom gradients, please be aware of how the gradient was built before using a custom sorting sequence.

Perform phase correction

With some acquisitions on the Tecmag consoles there is a problem with the phase of the data; it changes periodically throughout the acquisition. Attempts to process this data usually result in severe artifacts from signal attenuation at the center of k-space. To correct this problem, each interleaf can have its initial phase set to zero by Unisort. Check this box to turn on this extra processing step.

Perform baseline correction

For data with a DC offset, Unisort can attempt to baseline-correct each interleaf by calculating the average value of the last eighth of the points on each interleaf, and subtracting that average from the entire interleaf. Check this box to enable baseline correction for the current dataset.

Transformation preview

A simple set of data transformations are now provided by Unisort. The intention is to provide a preview of what the data will look like after it is transformed so the user can decide if the experiment is worth working with further. The preview data cannot be saved however, so that the user is required to use one of the more advanced programs to process the data properly. This is also done so that the transformations are done consistently by Jaims or Acciss for example.

Fourier Transform Preview

Pressing the "FT data" button will perform a simple Fourier transform on the data. If there are multiple files, every file will be transformed, and similarly all points in the experiment will be transformed. The preview window can still be used to look at the files/points individually, and see the magnitude, phase, etc. Saving is disabled on the preview, and the user **must revert the data to save the files as they were before the transformation.**
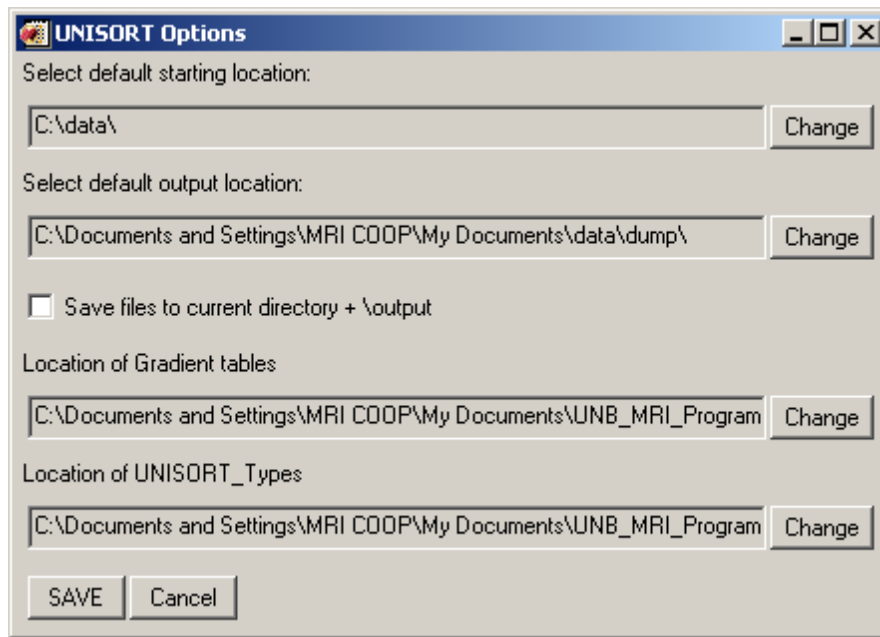
Chirp-Z Transform Preview

Pressing the "Chirp-Z data" button will perform a simple Chirp-Z transform on the data. If there are multiple files, every file will be transformed, and similarly all points in the experiment will be transformed. The preview window can still be used to look at the files/points individually, and see the magnitude, phase, etc. Saving is disabled on the preview, and the user **must revert the data to save the files as they were before the transformation.**

Revert Data

This feature is provided so that the data can be operated on as it was before either the Chirp-Z or Fourier transforms were performed. If, for example, the data had been sorted but not saved, the user could revert the data back to before it had been Fourier

transformed in order to save it in its sorted state. This will not "unsort" the data, and a message will be given if the user chooses to revert data that has not been transformed.

Options

Under the "file" menu, there is a button for "options." Choosing this will open up the dialog box shown above. This dialog is provided so the user can change some of the default behavior of the program without having to change the source code.

The **default starting location** is where data will initially be opened. Especially on shared computers, it is recommended that this is set to the location that acquired data is usually stored (eg: My documents, or desktop as is the convention for each machine).

The **default output location** is where files will be saved to by Unisort. The behavior can either be to save in an "\output\" folder off of where the data was loaded from (check the checkbox), or to a standard output folder. Again, it is recommended that a convention be established on shared computers so that each user knows where to look for their data. *The output folder can be manually overridden by selecting the output folder in the main window of Unisort.*

The last two boxes indicate the expected locations of the gradient tables and the unisort_types.txt file respectively. These should be setup when Unisort is installed and not changed unless the folder structure for Unisort is being changed. Unisort will attempt to verify that unisort_types.txt is in the location specified.