

Contents

1 ASCII / Terminal GUI	2
1.1 User's Manual	2
1.1.1 Settings	2
1.1.2 Extracting sweeps from the DAQ	6
1.1.3 Organizing Sweeps (Directory Sorter)	8
1.1.4 Averaging Sweeps	9
1.1.5 Signal Extraction	11
2 Toolchain: NMR_Visualizer.py	16
2.1 nearest	16
2.2 add entry	16
2.3 return persistence df	17
2.3.1 path	17
2.4 gui baseline file preview	17
2.4.1 filename	17
2.4.2 delimiter	17
2.5 gui raw sig file preview	17
2.5.1 rawsigfilename	17
2.5.2 delimiter	17
2.5.3 vnaVmeType	17
2.6 gui file fetcher	18
2.6.1 RAWSIG_Path	18
2.6.2 Baseline_Path	18
2.6.3 vnavmetype	18
2.7 VME frame aggregator	18
2.7.1 RAWSIG_Path	18
2.7.2 Baseline_Path	18
2.8 VNA frame aggregator	19
2.8.1 RAWSIG_Path	19
2.8.2 Baseline_Path	19
2.8.3 vnavmetype	19
2.9 VME File parser	19
2.9.1 filename	19
2.10 VNA File parser	20
2.10.1 filename	20
2.11 (Z) Impedance Converter	20
2.11.1 df	20
2.12 Curve Integrator	20
2.13 Ellie's Lorentizan Raw-Sig Fitting	20
2.14 General Fitting Function	20
2.14.1 df	20
2.14.2 start	20
2.14.3 finish	21
2.14.4 fitname	21
2.14.5 **kwargs	21
2.15 General Graphing Function	22
2.15.1 df	22
2.15.2 s	23
2.15.3 f	23

2.16 **kwargs	23
3 Clerical Tools	24
3.1 DAQ Muncher	24
3.2 Directory Sorter	25
3.3 Sweep Averager	25
3.4 Global Analysis	25
4 (deprecated) Tkinter GUI: gui.py	25
4.1 User's Manual	25
4.2 DAQ Extractor	26
4.3 Sweep Sorter	26
4.4 Directory Averager	27
4.5 Signal Analysis	27
4.5.1 Data Selection and Binning	29
4.5.2 Dataset Fitting	30
4.5.3 Automation	33

Introduction

This document will cover basic user operation of the VNA/VME NMR Visualizer toolchain, the GUI that comes with the Visualizer's toolchain, and the technical breakdown of each file. The GUI was designed so that the user would never need to interface with the raw code. However, given feature-bloat, and semi object-oriented structure, code stability may become an issue.

1 ASCII / Terminal GUI

With the release of python 3.9.1 the graphical interface that I wrote to wrap around this toolsuite broke. In order to overcome that, I wrote a second text-based front-end that the end user simply runs from the terminal.

1.1 User's Manual

The following is a how-to guide, and provides the user with an overall understanding of the capabilities and limitations of the ASCII terminal interface with the NMR toolsuite.

1.1.1 Settings

The settings file titled: *variablenames.py* is a python file that is imported in every module of the toolsuite. Here, the variables within *variablenames* are readily accessible, and reduces the presence of repeated strings throughout the toolsuite. Not only does this centralize the strings, and minimize the toolsuite. The file is well organized and commented to delineate what variables go with which module of the toolsuite. The following unnumbered sections will itemize the settings and their correspondence with the toolsuite.

DaqExtractor and Sweep Averager Settings

Variable	Default	Setting
dmsa_time_colname	“Time”	Name of the Timecolumn
dmsa_primary_thermometer_colname	“CCX.T3 (K)”	Name of the thermistor you trust most
dmsa_secondary_thermometer_colname	“Vapor Pressure Temperature (K)”	Name of the thermistor you trust second most
dmsa_magnet_psu_amperage_colname	“Magnet Current (A)”	Name of the magnet powersupply current
dmsa_sweep_centroid_colname	“Central Freq (MHz)”	name of the central sweep frequency
dmsa_sweep_width_colname	“Freq Span (MHz)”	name of the frequency span column
dmsa_system_status_colname	“NMR Status”	terminal column of data in dataframe – the rest is assumed to be nmr data
dmsa_system_status_nulls	[‘—’]	entries in nmr data that aren’t interesting
dmsa_system_null_status_directory	‘null_status’	where uninteresting sweep data goes
dmsa_terminal_colname	‘NMR Data’	name of the state of the experiment (te/ enhanced/baseline)

The daq extractor and sweep averager settings are **the most important** settings to know while analyzing NMR sweeps. Upon receiving a raw csv from the DAQ, the DaqExtractor “sets the tone” for the NMR signal analysis. Once the DAQ file has been extracted, it is difficult to inject additional DAQ data-streams until the *signal-analysis* portion is complete. On the execution of the DAQ Extractor, (which produces the .ta1 files) the extractor uses the stipulated settings from *variablenames.py*, and extracts the according entries from the appropriate DAQ columns. Once the .ta1 files are written, it’s difficult to switch out their primary and secondary thermistor values with those from the raw DAQ file. **It’s easier and faster to complete a signal analysis, and then use the timestamps from the global analysis files as “keys” to grab the alternate thermistors the user wants from the DAQ file.** A tool to do this has been written, and can be found in *./utilities/visualize_drift.py* under the function: *main_df_column_merger()*

Regardless, the signal analysis process begins with extracting the sweeps from the DAQ Extractor, and these settings set-the-tone for the down-stream analysis, so choose them carefully.

NMR Analyzer Settings

Variable	Default	Setting
na_primary_thermistor_name	dmsa_primary_thermometer_colname	Specifies the most trusted thermistor
na_secondary_thermistor_name	dmsa_secondary_thermometer_colname	Specifies the second most trusted thermistor
na_vme_yaxis_default	“Potential (V)”	Specifies the default y-axis
na_vme_xaxis_default	“MHz”	Specifies the default x-axis
na_global_analysis_headers	[“name”, “material”, “time”, “dtype”, “blpath”, “rawpath”, “xmin”, “xmax”, “sigstart”, “sigfinish”, “blskiplines”, ‘rawsigskiplines’, ‘B’, ‘T’, dmsa_primary_thermometer_colname, dmsa_secondary_thermometer_colname, “TEvalue”, “data_area”, “ltzian_area”, “data_cal_constant”, “ltzian_cal_constant”, ‘a’, ‘w’, ‘x0’ , “lorentzian chisquared (distribution)”, “ σ (Noise)”, “ σ (Error Bar)”, “lorentzian relative-chisquared (error)”, “Sweep Centroid”, “Sweep Width”, ‘e_f0’, ‘e_w’, ‘e_kmax’, ‘e_theta’]	Specifies the headers for the global analysis file

The NMR Analyzer settings are the settings for the back-end of the signal analyzer. Although the user will only interface with this python file indirectly through the GUI, settings can be adjusted. The primary and secondary thermistors should be specified in the DAQ-extractor settings level. The default vme x and y axis defaults have corresponding hard-coded VNA values as well. These will be updated in a future release. Take care to not edit the *global.analysis_headers* as the header-order corresponds to other hard-coded variables within the analyzer’s methods (like the order in which information is written to the global analysis file - you don’t want thermometry data where the magnetic field belongs).

TKinter GUI settings

Variable	Default	Setting
gui_primary_thermistor_name	dmsa_primary_thermometer_colname	Specifies the most trusted thermistor
gui_secondary_thermistor_name	dmsa_secondary_thermometer_colname	Specifies the second most trusted thermistor

Deprecated since January 5, 2021, but shouldn’t change, should tkinter magically begin working again.

ASCII GUI settings

Variable	Default	Setting
agui_primary_thermistor_name	dmsa_primary_thermometer_colname	See above
agui_secondary_thermistor_name	dmsa_secondary_thermometer_colname	See above
agui_allowable_file_extensions	[‘.ta1’, ‘.slp’, ‘.csv’]	file extensions the ascii gui is permitted to see
agui_vnavme_default	‘vme’	default mode / file interpretation
agui_xname_default	na_vme_xaxis_default	Specifies the default y-axis
agui_yname_default	na_vme_yaxis_default	Specifies the default x-axis
agui_impression	False	Gives impression of the various components of the data.

The *primary* and *secondary* thermistors should reflect the current data being analyzed. The *allowable file extensions* are used to filter the files out of custom file navigator that the user will use to select files and directories. The *vnavme* default is the default file-interpreting mode that the entire toolsuite is geared towards, In a future release, the program will automatically switch file parsers based on the file extension. Similarly with the back-end’s *vme x,y axis defaults* there are hard-coded VNA counterparts, in a later release, those variables will be pre-defined here.

Global Interpreter settings

Variables	Default
gi_primary_thermistor	“CCX.T3 (K)”
gi_secondary_thermistor	“Vapor Pressure Temperature (K)”
gi_time	‘time’
gi_lorentzianarea_results	“Lorentzian Area”
gi_scaled_polarization	“Scaled Polarization (%)”
gi_uncert_in_scaled_pol	“Uncert in Scaled polarization”
gi_integrated_data_area_results	“Integrated Data Area”
gi_ltz_area_results	“Lorentzian Area”
gi_bviaI_results	‘B via I (T)’
gi_primary_thermistor_results	gi_primary_thermistor
gi_secondary_thermistor_results	gi_secondary_thermistor
gi_centroid_results	“sweep centroid”
gi_width_results	“sweep width”
gi_te_results	“TEvalue”
gi_teviax0_results	‘TE via x0’
gi_tebest_results	“TE Best”
gi_te_uncert_results	“TE Uncert”
gi_rsq_results	“Reduced Relative Chi-Square”
gi_centroidlabel	‘x0’
gi_lorentzianarea	“ltzian_area”
gi_dataarea	“data_area”
gi_relchisq	“lorentzian relative-chisquared (error)”
gi_centroid	“Sweep Centroid”
gi_width	“Sweep Width”
gi_TE	“TEvalue”

The primary and secondary thermistor settings reflect the user-selected thermistors present in the global analysis file that the global-interpreter is reading from. By default, CCX.T3 and the Vapor pressure are being used, but this should be changed every time the user wants to look at a separate thermistor data-sets during a TE calibration (which is what the global interpreter is designed to do). Variables with “results” in their name are generally non-sensitive to

user-editing, but I would encourage the user to exercise caution, taking note of what settings are currently deviating from the defaults, and returning them back to normal should the tool-suite suddenly cease working.

1.1.2 Extracting sweeps from the DAQ

Extracting sweeps from the DAQ requires the user to ask themselves first and foremost: What thermistors are most representative of the target temperature? In analyzing NMR sweeps in the context of polarized target work within the Slifer Lab, calculating a good Thermal Equilibrium calibration constant is *contingent* on a stable temperature. A quick plot using the omni-view function from the Slifer-Cal Toolsuite can give us insight into what occurred during the cool-down. That toolsuite can be found here: [here](#)* With documentation located [here](#)[†].

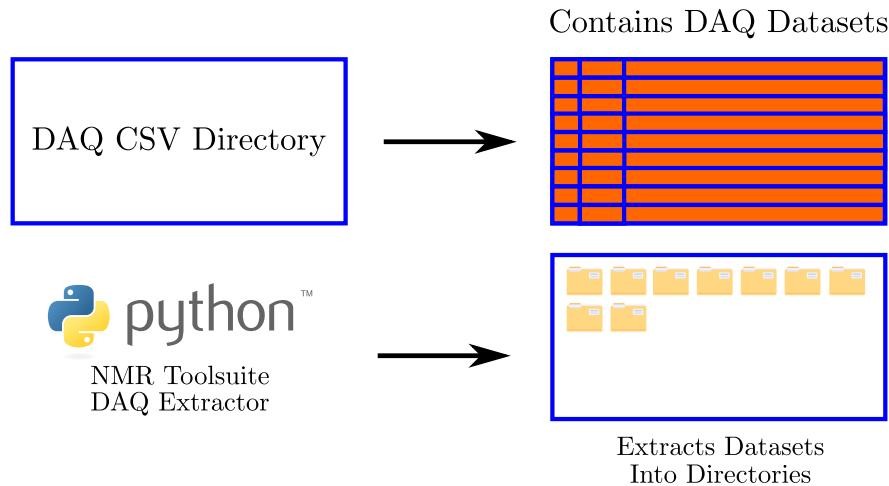


Figure 1: The DAQ extractor reads DAQ csv files then extracts the NMR sweeps, select thermistors, and magnet amperage writing that information in a custom file type that is categorized into special sub-directories. All the program needs to do this is the DAQ .csvs.

1. First, execute the *asciogui.py* file on the main branch of the github toolsuite:

```
(venv) [kb@EATX NMR_Toolsuite]$ python asciogui.py []
```

Figure 2: Simple virtual-environment using python to execute the asciogui program.

2. Then select the DAQ extractor option by entering the corresponding mode number, and pressing ENTER.

```
NMR Toolsuite options:
#####
# Mode   #   Functionality   #
#####
# 0    #   NMRAnalyzer   #
# 1    #   DAQExtractor   #
# 2    #   DirSorter     #
# 3    #   SweepAverage   #
# 4    #   GlobalInterpreter #
#####
What mode do you want the GUI in?
Enter number in table above: 1[]
```

Figure 3: This is the first stage that the user is greeted by in the ASCII Gui, I will later refer to this as the “Splash Screen”.

*https://github.com/Tristan-Anderson/Slifer_Lab_Thermometry

[†]<https://unh.box.com/s/k21gr1ta3zg6wepciuaejc7j0uom0b6>

3. The DAQ extractor will ask for a directory of .csv's or single .csv to extract into .ta1 files. Enter the respective directory by navigating with 0-n(d/f) per the instructions printed in the terminal. 'f' stands for file, and 'd' for directory. Selecting a file will immediately stop the selection process, whereas navigating with directories will not. Type "ok" to signal to the program to select the current working directory as your choice. If you need to navigate to the parent of the current working directory, enter "..", and you'll change directories accordingly.

```
oooooooooooooooooooooooooooo
@      DAQ Extractor      @
oooooooooooooooooooooooooooo
Extracts and organizes DAQ .csvs into .ta1 based on keywords found in variablenames.py and settings entered here, by the user.

### Pick directory or file to unpack ###
#####
# LinNUM #           Files          # Directories #
#####
# 0    # ~lock.global_analysis.csv#   .idea   #
# 1    #                         raw_data  #
# 2    #                         graph_data #
# 3    #                         __pycache__ #
# 4    #                         datasets  #
# 5    #                         .git     #
# 6    #                         graphs   #
#####
Current working Directory: /home/kb/research/wdirs/NMR_Toolsuite
Enter choice in the format of: 'LineNum(f/d)
ex: 1f
Enter Choice: []
```

Figure 4: Here the user selects a directory/single DAQ File to unpack. Select according to the instructions above.

4. Once the appropriate file(s) have been selected, *the user will then need to specify the location where to place the .ta1 files.*

```
### The current unpacking destination is  ###
oooooooooooooooooooooooooooo
@      Select a DIRECTORY to place files.      @
oooooooooooooooooooooooooooo
#####
# LinNUM #           Files          # Directories #
#####
# 0    # data_record_9-14-2020.csv #   old   #
# 1    # data_record_9-12-2020.csv #   #
# 2    # data_record_9-13-2020.csv #   #
# 3    # data_record_9-11-2020.csv #   #
# 4    # data_record_9-15-2020.csv #   #
# 5    # data_record_9-10-2020.csv #   #
#####
Current working Directory: /home/kb/research/wdirs/NMR_Toolsuite/raw_data/raw_data
Enter choice in the format of: 'LineNum(f/d)
ex: 1f
Enter Choice: []
```

Figure 5: When selecting multiple DAQ files (by choice of directory), each respective directory will be named according to the file it came from (minus an extension). This is where the DAQ interpreter will dump the extracted NMR sweeps (.ta1 files).

5. Once the directory has been selected to place the extracted information from the DAQ, the program will then prompt the user with a series of options. Having already completed the first two, the next option would be to extract the data. Press 2, ENTER, then the program will be on it's way, using multiprocessing if supported.

```

Path accepted.
#####
# option# #      name          #           describers      #
#####
#   0   # updateSelection #   Select file, or directory to unpack   #
#   1   # updateDestination #  Select destination to place unpacked data  #
#   2   # extractData     # Extract current selection into analyzeable files #
#####
Enter option number: 0

```

Figure 6: Two options are present in case the user made an error during the file selection process. To exit this loop, pop a ^ C or CTRL-C or BREAK, afterwards pressing ENTER. You will return to the toolsuite's splash screen.

1.1.3 Organizing Sweeps (Directory Sorter)

Now that you have extracted the NMR sweeps from the DAQ files, it is time to decide if you want to average the NMR sweeps. The first step in averaging sweeps is chronologically ordering them with the Directory Sorter. This ordering then allows the Sweep Averager covered in the next section to read each file in a single directory, and determine a directory's average.

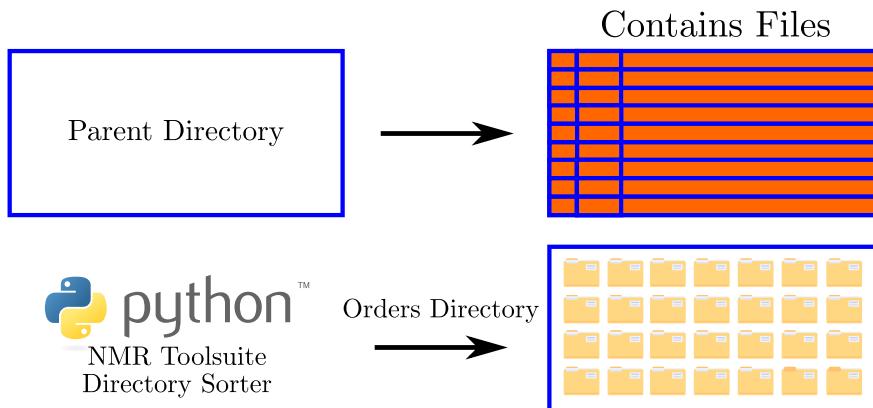


Figure 7: The directory sorter works by reading the timestamps of the .ta1 files. It catalogues these files by moving them into automatically created and named directories.

1. To use the Directory Sorter, select the Directory Sorter option from the NMR Splash Screen.

```

NMR Toolsuite options:
#####
# Mode #  Functionality #
#####
#   0   #  NMRAnalyzer   #
#   1   #  DAQExtractor  #
#   2   #  DirSorter      #
#   3   #  SweepAverage   #
#   4   #  GlobalInterpreter #
#####
What mode do you want the GUI in?
Enter number in table above: 2

```

Figure 8: NMR Splash screen selecting the Directory Sorter option.

2. Next, the user must guide the program to a directory containing just .ta1 files.

Figure 9: Initial screen of the Directory organizer.

3. Once that directory has been selected, the user can choose to shelf, or unshelf files present in the directory.

```
You selected /home/kb/research/wdir/NMR_Toolsuite/nice/data_record_9-10-2020/null_status/ which is a Directory
#####
# option# # name      #           describers      #
#####
#   0  # shelf    #   Organize the current directory per the user selected time-stamp      #
#   1  # unshelf  # Move files/folders in first child directories out to their parent directory #
#   2  # settimestamp #   Set the width of time to organize directories with.          #
#####
Enter option number: █
```

Figure 10: **Shelfing** refers to the act of organizing files by their time-stamps, placing each file that falls within a user-defined time-interval into a single directory. **Unshelfing** Refers to the undoing of the *shelving* process, which moves all of the child directory’s contents, into their parent directory, deleting the empty child directories in the process.

4. After choosing the *shelf* option, enter the width of time that the program will shelf the data. Once the hours, minutes, and seconds have entered into the program, it will start sorting the dataset.

```
Enter option number: 0
Your choice was shelf returning...
Enter the number of seconds:
Please enter a number between 0 59 or press enter to skip: 15
Enter the number of minutes:
Please enter a number between 0 59 or press enter to skip: 3
Enter the number of hours:
Please enter a number between 0 23 or press enter to skip:
Sentinel received - ignoring and returning.
Shelving complete.
```

Name
0910_235016_2
0910_234701_2
0910_234346_2
0910_234031_2
0910_233716_2

Figure 11: On the left, the user has entered 3 Minutes, 15 seconds as a time-width to organize the sweeps. On the right, a traditional file-explorer shows a portion of the automatically named directories. All of which have been populated with the corresponding .ta1 files.

5. To exit, or go back, enter a BREAK or ^C into the terminal, then Press ENTER.

1.1.4 Averaging Sweeps

The user may want to average NMR sweeps should they find that the NMR signal is not discernible from the noise-floor. This is done by first organizing the sweeps into directories that the user would like to average. **The Sweep Averager averages DIRECTORIES** it is up to the user to properly organize the directories, and ensure data-integrity and continuity during this process. The key with averaging sweeps, especially when dealing with a TE Calibration data set is to average the sweeps enough so the signal is discernible, but not so much as to render the data-set statistically moot. The sweep averager has two modes: single, and nested. In single mode, the averager reads

all of the data in the current directory, and averages them producing a file in the current directory. In nested mode, the averager reads all of the data in the child directories of the working directory, averages that data, then writes each directory's average to a file in the parent directory. Hopefully the following figure may clarify this description.

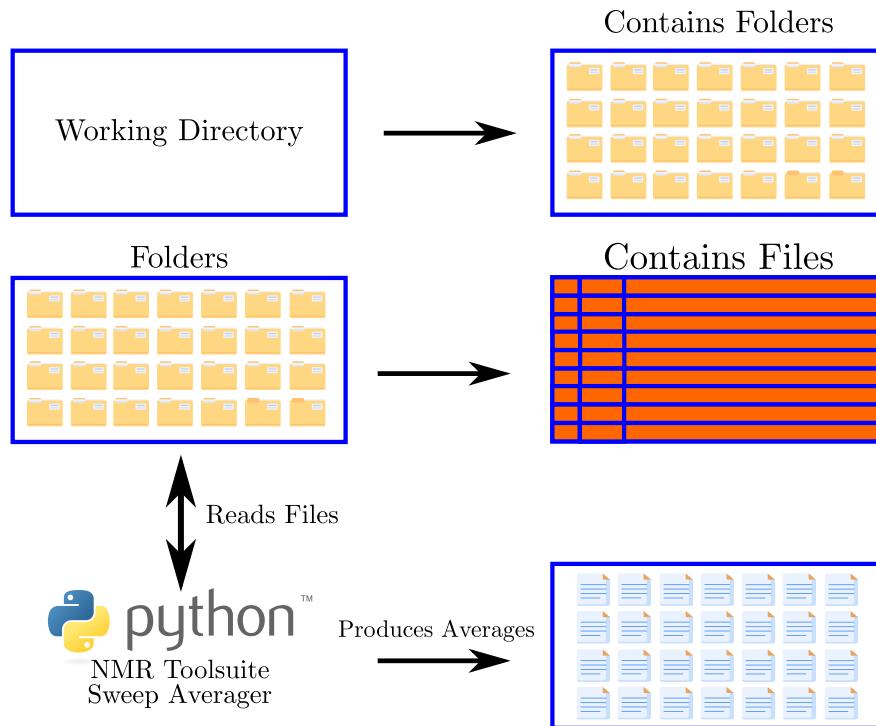


Figure 12: File icons courtesy of FlatIcon.

1. First, select SweepAverage option on the NMR Toolsuite splash screen. Then, choose the update location option.

```
#####
# option# #      name      #           describers      #
#####
#   0   # updatelocation # Select directory for averaging #
#   1   #   execute     # Start the averaging process  #
#####
```

Figure 13: In a future release, the user can simply select ‘execute.’ The program will detect whether a path to a data-set directory has been entered into the program. If the program has not been given a path to run average the directories, it will ask the user for one.

2. Once the program has accepted the path, it will prompt the user to decide whether or not the path selected was a nested directory that contained child directories, or just a single directory making files therein to be averaged.

```
#####
# option# #      name      #           describers      #
#####
#   0   # nested   # Avarage sweeps in a nested directory, naming avg sweep after parent directory #
#   1   # directory #           average single directory into a single file
#####
Enter option number: [ ]
```

Figure 14: Here the user tells the program how to average the current selection. There are two options, one is to average the files within a single selected directory, and the other is to average the child directories (most likely created by the sweep sorter).

3. The Sweep Averager will then average the sweeps, needing no further input from the user.

1.1.5 Signal Extraction

Extracting an NMR signal from the custom Versa Module Eurocard (VME) board, or Vector Network Analyzer (VNA) is a step-by-step process. Good signal extraction begins during the experiment. First, a baseline - or the natural q-meter circuit response is measured by the VME/VNA board. Then, the target material is placed within the q-meter coils, and it polarizes (Per Chapter 2, Section 2 [here](#)[‡] For more information on the experimental setup, see Chapter 3, Section 2) This polarization is detected via a frequency-dependent NMR Absorption spectra, and measured for the VME as a Voltage, or for the VNA as the real and imaginary components of the S11 component in q-meter circuit. The second step to NMR signal extraction is to remove the q-meter's natural response from the NMR absorption spectra. For a more ideological discussion on the signal extraction process see Chapter 4 [here](#)[‡].

Now, with that data recorded, this toolsuite is prepared to analyze each spectra. In theory, the difference between these two spectra should result in an NMR spectra that is just a result of nuclear spins. The NMR Signal Extraction tool-suite just needs the path of the Baseline, and the path of the Raw NMR Signal.

1. Begin by selecting the NMR Analyzer option on the splash screen of the NMR toolsuite.

```
NMR Toolsuite options:
#####
# Mode   #   Functionality   #
#####
# 0     #   NMRAlyzer      #
# 1     #   DAQExtractor    #
# 2     #   DirSorter       #
# 3     #   SweepAverage    #
# 4     #   GlobalInterpreter#
#####
What mode do you want the GUI in?
Enter number in table above: 0
```

Figure 15: Select the NMR Analyzer functionality of the toolsuite by pressing '0' followed by ENTER.

2. Then, navigate to the path of the **baseline** with the ASCIIGUI's file-explorer.

```
#####
# LinNUM #   Files          # Directories #
#####
# 0   # 914_550pm_baseline_average.tal # 550pm  #
# 1   # 914_2pm_baseline_average.tal  # 2pm    #
# 2   # 914_415p_baseline_average.tal # 315pm  #
# 3   # 914_315pm_baseline_average.tal# 415pm  #
# 4   #                           # 610pm  #
#####
Current working Directory: /home/kb/research/wdirs/NMR_Toolsuite/datasets/sep_2020/data_record_9-14-2020/Baseline
Enter choice in the format of: 'LineNum(f/d)
ex: 1f
Enter Choice: 0f

### Baseline path updated ###
```

Figure 16: The user enters the baseline of their choice.

3. Next, the user will need to select a raw signal file that contains an NMR spectra. The program automatically changes the current working directory to the parent directory of the previous selection. From here, the user then needs to navigate to the raw-signal path.

[‡]<https://unh.box.com/s/ommw56pj5s8ve6afaog3sei9i9bh7z23>

```
### Update Raw Signal ####
Current working directory: /home/kb/research/wdirs/NMR_Toolsuite/datasets/sep_2020/data_record_9-14-2020
#####
# LinNUM #          Files          #      Directories   #
#####
# 0   # 15_Ellie TE calibrated ENHANCED d-Prop.csv   #           TE      #
# 1   # 15_628p-630p TE calibrated ENHANCED d-Prop.csv #       Baseline   #
# 2   #          14_Lab_dprop_TE.csv                  # 914_701a_to_915_405p_enhanced #
# 3   #          14_9_14_1900_dprop_TE.csv            # 515pte    #
# 4   #          14_Ellie_dprop_TE.csv                # 700pte    #
# 5   # 15_LAB TE calibrated ENHANCED d-Prop.csv     # 408pte    #
# 6   #                                         # no_nmr_status #
# 7   #                                         # Polarization  #
#####
Current working Directory: /home/kb/research/wdirs/NMR_Toolsuite/datasets/sep_2020/data_record_9-14-2020
Enter choice in the format of: 'LineNum(f/d)
  ex: 1f
Enter Choice: 
```

Figure 17: Navigate to the raw-signal path.

4. After the program has accepted the user's input to the rawsignal path, The program will request what type of target-material is the NMR spectras containing. Enter the material type then continue.
5. Then, the program will request that the user name the current instance of the program. Think of it as a human-readable name to label the current analysis session.

```
### Current instance name: 20210215_11201613406033 Instance ####
Input new instance name: 
```

Figure 18: By default, the instance-name will be the timestamp of the initial execution of the Signal Extraction toolsuite.

6. Once the instance has been given a name, the graph will be displayed in a popup window, and the terminal will contain options to modify the signal. **If the user wants to re-bin the data, make sure the re-binning is done first.**

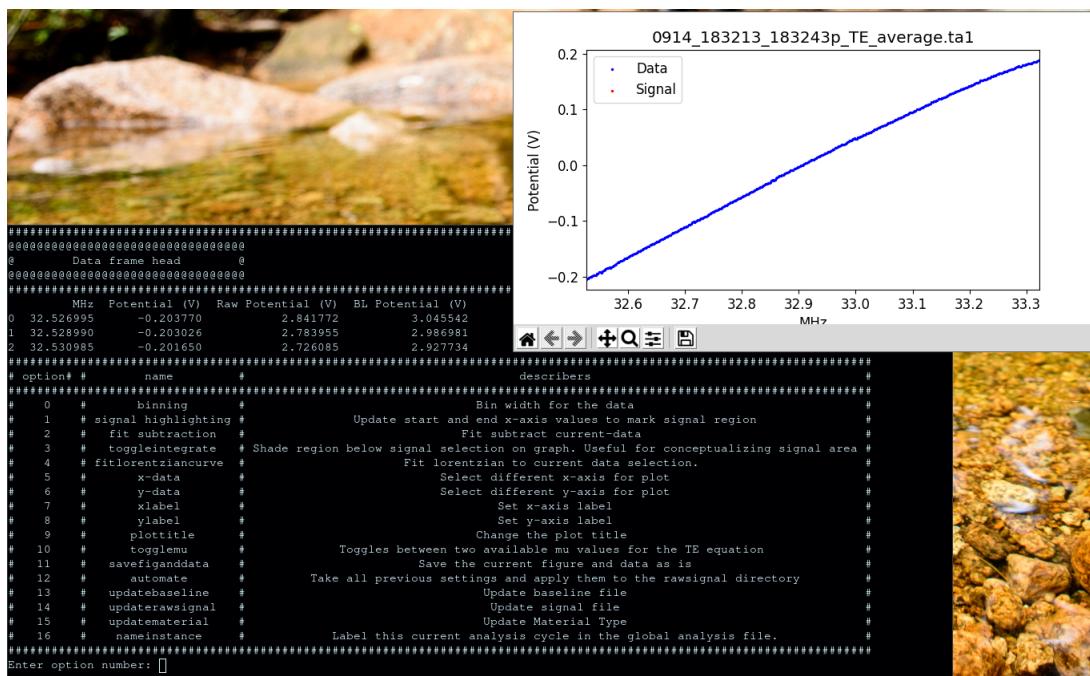


Figure 19: The terminal displays the available signal-extraction options.

7. We will now bin the data. Press the option number, then ENTER.

```

#####
# option#   name                                describers
#####
# 0   #   binning                                Bin width for the data
# 1   #   signal highlighting                   Update start and end x-axis values to mark signal region
# 2   #   fit subtraction                         Fit subtract current-data
# 3   #   toggleintegrate                      Shade region below signal selection on graph. Useful for conceptualizing signal area
# 4   #   fitlorentziancurve                    Fit lorentzian to current data selection.
# 5   #   x-data                                 Select different x-axis for plot
# 6   #   y-data                                 Select different y-axis for plot
# 7   #   xlabel                                Set x-axis label
# 8   #   ylabel                                Set y-axis label
# 9   #   plottitle                             Change the plot title
# 10  #   tooglemu                            Toggles between two available mu values for the TE equation
# 11  #   savefiganddata                      Save the current figure and data as is
# 12  #   automate                            Take all previous settings and apply them to the rawsignal directory
# 13  #   updatebaseline                      Update baseline file
# 14  #   updatersignal                        Update signal file
# 15  #   updatematerial                      Update Material Type
# 16  #   nameinstance                         Label this current analysis cycle in the global analysis file.
#####
Enter option number: 0
Your choice was binning returning...

### Current binning is 1. ***
Please select new binning
Enter bin width: 3

```

Figure 20: Here, the user selected a bin width of 3.

Note the updated current settings on the following output which reflect the entered current binning.

```

Enter bin width: 3
#####
@          Current Settings:      @
#####
@          Current Binning: 3
@          Current mu: PROTON
@          Current Baseline File: /home/kb/research/wdirs/NMR_Toolsuite/datasets/sep_2020/data_record_9-14-2020/Baseline/914_550pm_baseline.tal
@          Current Raw-Signal File: /home/kb/research/wdirs/NMR_Toolsuite/datasets/sep_2020/data_record_9-14-2020/TE/914_629_700p/0914_183243p_TE_average.tal
#####
@          Data frame head      @

```

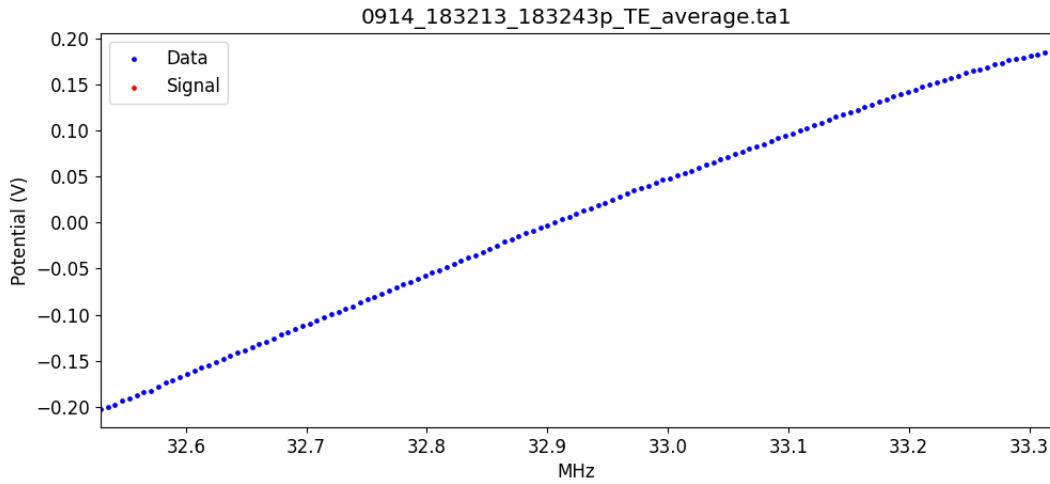


Figure 21: Caption

8. Now, notice how the NMR Spectra does not look like an NMR signal. This is because the baseline taken for this spectra did not perfectly capture the natural response of the q-meter, so a fit subtraction is needed to remove the upward trend. I also think I see a region of data where I anticipate the signal, so, I will need to highlight that region with the signal-highlighting option.
9. Now that the signal is highlighted, it is time to do a fit subtraction on the signal. Select the option and continue.

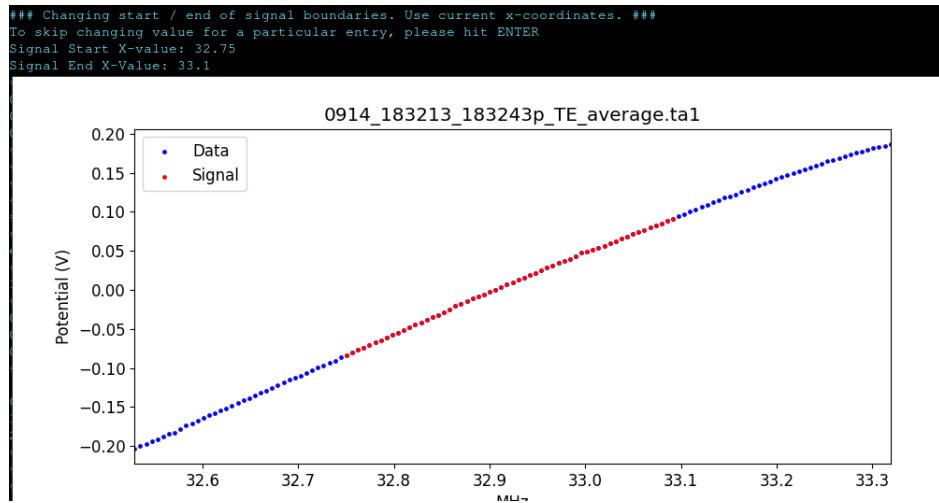


Figure 22: Notice the two bumps? One is at about 32.875 and the other is at about 32.99. These are likely signal artifacts.

10. There are 7 different types of fit subtractions. Most fit subtractions will be covered by the polynomials, or sine functions. If you're fitting the raw NMR Signal (accessible through the y-data) the Lorentzian fit subtraction methods may also be useful. For this dataset, I will select the third order polynomial.

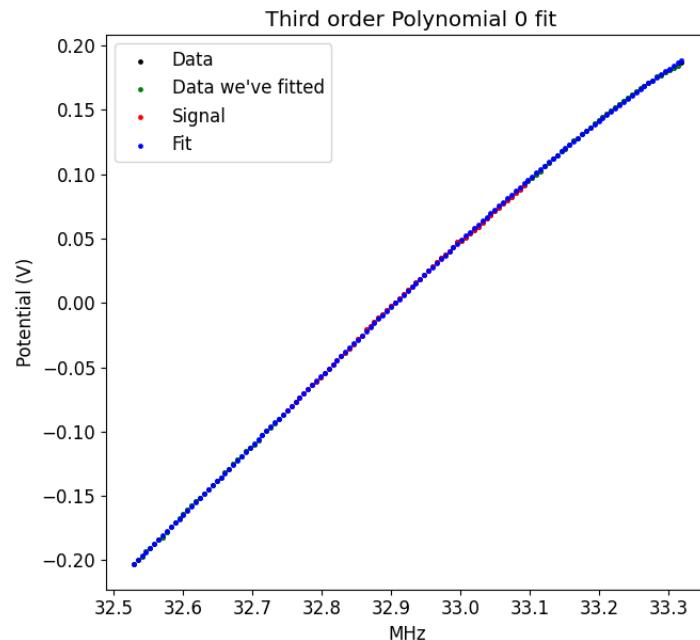


Figure 23: Visually, it looks like the fit of the third order polynomial about the signal region is good.

```
#####
# option# #           name          #      describers   #
#####
# 0   #           Sin            #      sin          #
# 1   #           Third order Polynomial #      third_order #
# 2   #           Fourth order Polynomial #      fourth_order #
# 3   #           Fifth Order Polynomial #      fifth_order #
# 4   #           Sixth Order Polynomial #      sixth_order #
# 5   #           True Lorentzian    #      lorentzian_ellie #
# 6   # Lorentzian (absorbtion/dispersion) # absorbtion_dispersion_ellie #
# 7   #           Cancel Fit       #      Cancel Fit   #
#####
Enter option number: 1
Your choice was Third order Polynomial returning...
CHI SQUARED VALUES FOR EACH FIT
#####
# Fit #      sin          # 3.6917269768204062e-06 #
# Fit #      third_order # 3.5399031238242776e-06 #
# Fit #      fourth_order # 2.1536423309483564e-05 #
# Fit #      fifth_order # 3.441051393447855e-06 #
# Fit #      sixth_order # 2.4213628538447786e-06 #
# Fit #      lorentzian_ellie # FITTING ERROR #
# Fit #      absorbtion_dispersion_ellie # 193624039.08459774 #
#####
# option# #   name          #      describers   #
#####
# 0   # approve  #   The fit looks good, let me see the fit subtraction
# 1   # disapprove #   The fit looks bad, let me redo it.
# 2   # cancel   # Cancel the fit subtraction, and do not change the graph
#####
Enter option number: 1
```

Figure 24: In the terminal, the program will ask for the user to approve, or disapprove the fit, I will approve it.

11. Next, if the current displayed dataset needs an additional fit subtraction, make sure to repeat the last few steps to carry out an additional fit subtraction.
12. After the fit subtraction is done, the user can choose to shade the region of data under the highlighted signal region by selecting the option *toggleintegrate*.
13. Once selected, it becomes clear what the program is integrating. Next, the user can adjust/adapt the axis labels, plot-title, or change out the TE calibration equation. I know that this particular NMR spectra was taken from a deuteron target material. I will toggle the proper mu accordingly to reflect an accurate deuteron TE calculation.

```
Current mu is proton
#####
# option# #   name          #      describers   #
#####
# 0   # proton  # Proton Mu #
# 1   # deuteron # Deuteron Mu #
#####
Enter option number: 1
```

14. Should the dataset being analyzed is from a proton, the option (#4) *fitlorentziancurve* is used to fit a lorentzian curve to the clean NMR spectra. **Select this should you be analyzing proton nmr data.**
15. Since what I have done is all I needed to do during this signal extraction session, I am ready to automate the signal extraction process. All that is needed for this is simply enter the option to automate, and the program will do the rest.

```
Enter option number: 12
Your choice was automate returning...
ID: 2 : 1 of 5 [20.0%] ETA: 2.1 s
ID: 6 : 1 of 5 [20.0%] ETA: 2.1 s
ID: 3 : 1 of 5 [20.0%] ETA: 2.1 s
ID: 4 : 1 of 5 [20.0%] ETA: 3.4 s
ID: 0 : 1 of 5 [20.0%] ETA: 3.4 s
ID: 1 : 1 of 5 [20.0%] ETA: 3.4 s
ID: 7 : 1 of 5 [20.0%] ETA: 3.6 s
ID: 5 : 1 of 5 [20.0%] ETA: 3.9 s
ID: 8 : 1 of 9 [11.111118%] ETA: 8.0 s
ID: 6 : 2 of 5 [40.0%] ETA: 1.6 s
ID: 3 : 2 of 5 [40.0%] ETA: 1.7 s
ID: 2 : 2 of 5 [40.0%] ETA: 1.7 s
ID: 3 : 3 of 5 [60.0%] ETA: 1.1 s
ID: 5 : 2 of 5 [40.0%] ETA: 2.4 s
ID: 0 : 2 of 5 [40.0%] ETA: 2.4 s
ID: 2 : 3 of 5 [60.0%] ETA: 1.1 s
ID: 7 : 2 of 5 [40.0%] ETA: 2.6 s
ID: 1 : 2 of 5 [40.0%] ETA: 2.6 s
ID: 4 : 2 of 5 [40.0%] ETA: 2.6 s
ID: 8 : 2 of 9 [22.22222%] ETA: 6.2 s
ID: 6 : 3 of 5 [60.0%] ETA: 1.3 s
ID: 2 : 4 of 5 [80.0%] ETA: 0.5 s
ID: 5 : 3 of 5 [60.0%] ETA: 1.5 s
ID: 7 : 3 of 5 [60.0%] ETA: 1.5 s
ID: 3 : 4 of 5 [80.0%] ETA: 0.6 s
ID: 8 : 3 of 9 [33.33333%] ETA: 4.7 s
ID: 0 : 3 of 5 [60.0%] ETA: 1.6 s
ID: 1 : 3 of 5 [60.0%] ETA: 1.7 s
ID: 4 : 3 of 5 [60.0%] ETA: 1.7 s
ID: 6 : 4 of 5 [80.0%] ETA: 0.7 s
ID: 7 : 4 of 5 [80.0%] ETA: 0.7 s
ID: 2 : 5 of 5 [100.0%] ETA: 0.0 s
ID: 5 : 4 of 5 [80.0%] ETA: 0.7 s
ID: 8 : 4 of 9 [44.44444%] ETA: 3.9 s
ID: 3 : 5 of 5 [100.0%] ETA: 0.0 s
ID: 0 : 4 of 5 [80.0%] ETA: 0.8 s
ID: 7 : 5 of 5 [100.0%] ETA: 0.0 s
ID: 4 : 4 of 5 [80.0%] ETA: 0.8 s
ID: 1 : 4 of 5 [80.0%] ETA: 0.8 s
ID: 6 : 5 of 5 [100.0%] ETA: 0.0 s
ID: 5 : 5 of 5 [100.0%] ETA: 0.0 s
ID: 8 : 5 of 9 [55.555556%] ETA: 2.9 s
ID: 1 : 5 of 5 [100.0%] ETA: 0.0 s
ID: 0 : 5 of 5 [100.0%] ETA: 0.0 s
ID: 4 : 5 of 5 [100.0%] ETA: 0.0 s
ID: 8 : 6 of 9 [66.66667%] ETA: 2.1 s
ID: 8 : 7 of 9 [77.7778%] ETA: 1.3 s
ID: 8 : 8 of 9 [88.8889%] ETA: 0.6 s
ID: 8 : 9 of 9 [100.0%] ETA: 0.0 s
```

	name	material	time	dtype	...	e_F0	e_w	e_max	e_theta
0	dPropTrityLE_S0	0x6e63TritylDPrp	2020-09-14 18:32:27	vme	...	None	None	None	None
1	dPropTrityLE_S1	0x6e63TritylDPrp	2020-09-14 18:55:59	vme	...	None	None	None	None
2	dPropTrityLE_S2	0x6e63TritylDPrp	2020-09-14 18:58:31	vme	...	None	None	None	None
3	dPropTrityLE_S3	0x6e63TritylDPrp	2020-09-14 18:29:57	vme	...	None	None	None	None
4	dPropTrityLE_S4	0x6e63TritylDPrp	2020-09-14 18:48:59	vme	...	None	None	None	None
5	dPropTrityLE_S5	0x6e63TritylDPrp	2020-09-14 18:49:59	vme	...	None	None	None	None
6	dPropTrityLE_S7	0x6e63TritylDPrp	2020-09-14 18:45:31	vme	...	None	None	None	None
7	dPropTrityLE_S8	0x6e63TritylDPrp	2020-09-14 18:51:31	vme	...	None	None	None	None
8	dPropTrityLE_S9	0x6e63TritylDPrp	2020-09-14 18:55:31	vme	...	None	None	None	None
9	dPropTrityLE_S10	0x6e63TritylDPrp	2020-09-14 18:37:59	vme	...	None	None	None	None
10	dPropTrityLE_S12	0x6e63TritylDPrp	2020-09-14 18:50:27	vme	...	None	None	None	None
11	dPropTrityLE_S13	0x6e63TritylDPrp	2020-09-14 18:53:59	vme	...	None	None	None	None
12	dPropTrityLE_S14	0x6e63TritylDPrp	2020-09-14 18:58:59	vme	...	None	None	None	None
13	dPropTrityLE_S15	0x6e63TritylDPrp	2020-09-14 18:33:31	vme	...	None	None	None	None
14	dPropTrityLE_S16	0x6e63TritylDPrp	2020-09-14 18:47:31	vme	...	None	None	None	None
15	dPropTrityLE_S18	0x6e63TritylDPrp	2020-09-14 18:40:27	vme	...	None	None	None	None
16	dPropTrityLE_S19	0x6e63TritylDPrp	2020-09-14 18:53:59	vme	...	None	None	None	None
17	dPropTrityLE_S20	0x6e63TritylDPrp	2020-09-14 18:44:59	vme	...	None	None	None	None
18	dPropTrityLE_S21	0x6e63TritylDPrp	2020-09-14 18:44:27	vme	...	None	None	None	None
19	dPropTrityLE_S22	0x6e63TritylDPrp	2020-09-14 18:45:59	vme	...	None	None	None	None
20	dPropTrityLE_S24	0x6e63TritylDPrp	2020-09-14 18:30:59	vme	...	None	None	None	None
21	dPropTrityLE_S25	0x6e63TritylDPrp	2020-09-14 18:30:27	vme	...	None	None	None	None
22	dPropTrityLE_S26	0x6e63TritylDPrp	2020-09-14 18:29:27	vme	...	None	None	None	None
23	dPropTrityLE_S27	0x6e63TritylDPrp	2020-09-14 18:42:27	vme	...	None	None	None	None
24	dPropTrityLE_S28	0x6e63TritylDPrp	2020-09-14 18:48:27	vme	...	None	None	None	None
25	dPropTrityLE_S30	0x6e63TritylDPrp	2020-09-14 19:00:43	vme	...	None	None	None	None
26	dPropTrityLE_S31	0x6e63TritylDPrp	2020-09-14 19:00:59	vme	...	None	None	None	None
27	dPropTrityLE_S32	0x6e63TritylDPrp	2020-09-14 18:38:27	vme	...	None	None	None	None
28	dPropTrityLE_S33	0x6e63TritylDPrp	2020-09-14 18:32:59	vme	...	None	None	None	None
29	dPropTrityLE_S34	0x6e63TritylDPrp	2020-09-14 18:37:31	vme	...	None	None	None	None
30	dPropTrityLE_S35	0x6e63TritylDPrp	2020-09-14 18:54:27	vme	...	None	None	None	None
31	dPropTrityLE_S37	0x6e63TritylDPrp	2020-09-14 18:40:59	vme	...	None	None	None	None
32	dPropTrityLE_S38	0x6e63TritylDPrp	2020-09-14 18:39:31	vme	...	None	None	None	None
33	dPropTrityLE_S39	0x6e63TritylDPrp	2020-09-14 18:53:31	vme	...	None	None	None	None
34	dPropTrityLE_S40	0x6e63TritylDPrp	2020-09-14 18:31:31	vme	...	None	None	None	None
35	dPropTrityLE_S41	0x6e63TritylDPrp	2020-09-14 18:59:59	vme	...	None	None	None	None
36	dPropTrityLE_S42	0x6e63TritylDPrp	2020-09-14 18:41:31	vme	...	None	None	None	None
37	dPropTrityLE_S44	0x6e63TritylDPrp	2020-09-14 19:54:59	vme	...	None	None	None	None
38	dPropTrityLE_S45	0x6e63TritylDPrp	2020-09-14 18:28:59	vme	...	None	None	None	None
39	dPropTrityLE_S46	0x6e63TritylDPrp	2020-09-14 18:38:59	vme	...	None	None	None	None
40	dPropTrityLE_S47	0x6e63TritylDPrp	2020-09-14 18:52:27	vme	...	None	None	None	None
41	dPropTrityLE_S49	0x6e63TritylDPrp	2020-09-14 18:42:59	vme	...	None	None	None	None
42	dPropTrityLE_S50	0x6e63TritylDPrp	2020-09-14 18:43:31	vme	...	None	None	None	None
43	dPropTrityLE_S51	0x6e63TritylDPrp	2020-09-14 18:41:59	vme	...	None	None	None	None
44	dPropTrityLE_S52	0x6e63TritylDPrp	2020-09-14 18:51:59	vme	...	None	None	None	None
45	dPropTrityLE_S54	0x6e63TritylDPrp	2020-09-14 18:59:37	vme	...	None	None	None	None
46	dPropTrityLE_S55	0x6e63TritylDPrp	2020-09-14 18:59:27	vme	...	None	None	None	None
47	dPropTrityLE_S56	0x6e63TritylDPrp	2020-09-14 18:51:59	vme	...	None	None	None	None
48	dPropTrityLE_S56	0x6e63TritylDPrp	2020-09-14 18:51:29	vme	...	None	None	None	None

Figure 25: Multi-Processing parallelization results in a lot of text printed to the console. Each line printed here represents a single NMR spectra successfully analyzed. 49 NMR spectra were analyzed in just over 2 seconds on a 16 core processor.

Figure 26: After a successful analysis of an entire dataset, the program will print out the results array, and then save it after the user presses enter.

2 Toolchain: NMR_Visualizer.py

Here's the technical documentation

2.1 nearest

```
nearest(test_val, iterable):
```

This function returns the nearest value to *test_val* in the iterable data structure *iterable*. This is used to determine the closest value to a user's selection of signal-region highlighting, and sometimes used to locate data in a parrell data structure that wasn't perfectly indexed.

2.2 add entry

```
add_entry(*rowvals, **kwargs):
```

Adds an entry to the `global_analysis.csv` that is produced with analysis using the GUI and some special uses of the toolchain. The function adds a line to `.csv` if it exists. If the `csv` does not exist, an empty one will be created then the entry will be added to the new file. Two minor sub-functions are folded into the `add_entry` function:

gen-persistence(path,columns)
Creates CSV file at *path* with columns *columns*

get_persistence(headers, fname)

Reads the global_analysis.csv. If that file does not exist, it will make one. The function returns either the successfully read data frame, or an empty one ready to populate.

*rowvals

Expects a list of values to zip with “headers” kwarg passed on function call. Rowvals is mandatory.

**kwargs

The *headers* keyword argument is used in the **add_entry** name space is particular to where it is called from. **add entry** requires the user to ask them self: “What do you want to save?” and you must pass the row-values and headers accordingly

2.3 return persistence df

`return_persistence_df(path):`

Reads and returns data frame object at *path*. This is used to read the global_analysis file

2.3.1 path

Path either absolute, or path relative to current working directory.

2.4 gui baseline file preview

`gui_bl_file_preview(filename, delimiter):`

Looks at the first 200 lines of the baseline file and delivers a small preview for the user to view during file selection.

2.4.1 filename

Path either absolute, or path relative to current working directory.

2.4.2 delimiter

Delimiter for the file to be read, generally ‘t’ for this application, but ‘is here if you need it’.

2.5 gui raw sig file preview

`gui_rawsig_file_preview(rawsigfilename, delimiter, vnaVmeType)`

Looks at the first 200 lines of the raw signal file and delivers a small preview for the user to view during file selection.

2.5.1 rawsigfilename

Path to the raw signal file. Either absolute, or path relative to current working directory.

2.5.2 delimiter

QoL. Generally the delimiter is ‘t’, but it can be easily changed to accomodate the file format.

2.5.3 vnaVmeType

Used to switch between file interpreters.

2.6 gui file fetcher

```
gui_file_fetcher(RAWSIG_Path, Baseline_Path, vnavmetype, impression=False, binning=1, blskiplines=4,
    rawsigskiplines=4):
```

Fetches appropriate data from *RAWSIG_Path*, *Baseline_Path* with the appropriate file interpreter for the VNA/VME types (.s1p, .ta1)

2.6.1 RAWSIG_Path

An absolute or relative path to the raw signal file

2.6.2 Baseline_Path

An absolute or relative path to the baseline signal file

2.6.3 vnavmetype

A string either ‘VNA’ or ‘VME’ that determines which file interpreter to use when reading signal files.

impression

A boolean keyword argument that can be toggled to save a graph/impression of the S11 parameters and Re/Im of Z for the VNA data.

binning

Bin-width in datapoints.

blskiplines

Number of lines to skip before reading the baseline data like a seperated-value

rawsigskiplines

Number of lines to skip before reading the raw signal data like a seperated-value

2.7 VME frame aggregator

```
vme_frames(RAWSIG_Path, Baseline_Path, binning=1, blskiplines=4, rawsigskiplines=4)::
```

Collects and parses data from a .ta1 file, getting both the raw signal dataframe and baseline dataframes. The data can be re-binned with a bin-width of *binning*. No impression is available in this function.

2.7.1 RAWSIG_Path

An absolute or relative path to the raw signal file

2.7.2 Baseline_Path

An absolute or relative path to the baseline signal file

binning

Binwidth in datapoints

blskiplines

Number of lines to skip before reading the baseline data like a seperated-value

rawsigskiplines

Number of lines to skip before reading the raw signal data like a seperated-value

2.8 VNA frame aggregator

```
vna_frames(RAWSIG_Path, Baseline_Path, impression=False, title="", z_im=False, binning=1, blskiplines=4,
           rawsigskiplines=4):
```

Collects and parses VNA data from a .s1p file, getting both the raw signal dataframe and baseline dataframes. The data can be re-binned with a bin-width of *binning*. An impression (plot) of the real and imaginary parts of S11 and z (impedance) can be saved to the current working directory by toggling *impression*.

2.8.1 RAWSIG_Path

An absolute or relative path to the raw signal file

2.8.2 Baseline_Path

An absolute or relative path to the baseline signal file

2.8.3 vnavmetype

A string either ‘VNA’ or ‘VME’ that determines which file interpreter to use when reading signal files.

impression

A boolean keyword argument that can be toggled to save a graph/impression of the S11 parameters and Re/Im of Z for the VNA data.

binning

Bin-width in datapoints.

blskiplines

Number of lines to skip before reading the baseline data like a seperated-value

rawsigskiplines

Number of lines to skip before reading the raw signal data like a seperated-value

2.9 VME File parser

```
vme_file_parser(filename, skiplines):
```

Breaks down a VME (.ta1) file (at *filename*) line-by-line (skipping *skiplines* lines) and stores sweep information into a pandas dataframe, returning the dataframe to the caller.

2.9.1 filename

Absolute or relative path to file.

skiplines

Type int keyword argument that tells the file parser to skip the first *skiplines* lines.

2.10 VNA File parser

```
vna_file_parser(filename, skiplines=4)
```

Breaks down a VNA (.s1p) file (at *filename*) line-by-line (skipping *skiplines* lines) and stores sweep information into a pandas dataframe, returning the dataframe to the caller.

2.10.1 filename

Absolute or relative path to file.

skiplines

Type int keyword argument that tells the file parser to skip the first *skiplines* lines.

2.11 (Z) Impedance Converter

```
get_z(df):
```

Does a change of basis between the Re/Im S11 components, and the Re/Im parts of the impedance. Returns df with “MHz”, “Z_re”, and “Z_im” columns.

2.11.1 df

Requires a pandas dataframe with columns: “MHz”, “Re(S11)”, “Im(S11)” columns.

2.12 Curve Integrator

```
integrate_curve(start_index, end_index, df=None, x="MHz", y="Z_re"):
```

Returns the trapezoidal Riemann integration of the data points between *start_index*, *end_index* in *df*. Will implement better quadrature techniques soon (sum of two Riemann schemes).

2.13 Ellie's Lorentizan Raw-Sig Fitting

```
absortion_dispersion_ellie(f, f0, w, kmax, theta):
```

See NMR Model in Box for mathematical explanation and justification.

2.14 General Fitting Function

```
gff(df, start, finish, fitname, **kwargs):
```

A general fitting function for this NMR toolchain. Requires a pandas dataframe *df*, a start *start* and end *end* index, as well as a hard-coded fitname *fitname* to fit to column *y* in *df*. This function operates by array index, and not by numerical values. Consult the **nearest** function to get array indexes. Fits the data around the signal, where the signal is selected by index placement within the column of the dataframe. Within this function, the signal is generally within: *ydata*[*s:f*].

2.14.1 df

Pandas Dataframe. A non-empty pandas dataframe.

2.14.2 start

Int. The start index in *df* of the region that should be ignored during the fitting.

2.14.3 finish

Int. The end index in *df* of the region that should be ignored during the fitting.

2.14.4 fitname

String. The human readable function name used to label types of fits. Accessable in the command line.

2.14.5 **kwargs

```
y="Z_re", x="MHz", preview=False, pltttitle=' ', fit_sans_signal=False, function=[], fit_bounds=[], sf=None,
ff=None, savefit=False, filename="UNNAMED_GRAPH", binning=1, xmin=None, xmax=None, gui=False,
automated=False, p0=None, bounds=[[[-numpy.inf, -numpy.inf, -numpy.inf, -numpy.inf
], [numpy.inf, numpy.inf, numpy.inf, numpy.inf]]]
```

y

Str. Name of the column in *df* containing dependent values to model with respect to *x*.

x

Str. Name of the column in *df* containing independent values to map onto *y*.

preview

Boolean Flag. Pyplot.show's the figure before continuing. Useful in the command line.

pltttitle

String. User specifiable title to the proof-plot this generates

fit_sans_signal

Boolean Flag. Fits *y* data ignoring all data in region: ydata[start:finish]

function

List of Strings. The hard-coded function name to fit with scipy optimize curvefit. Must be parallel to each tuple in *fit_bounds*, or must be len 1 to apply single function to all x-ranges in *fit_bounds*

fit_bounds

An array of tuples [(x1s, x1f), ..., (xns, xnf)]. X-ranges to fit each function in *function* with. Will zip *fit_bounds* with *function*. Must be equal length as *function*, unless len(*function*) is 1.

sf & ff

Integers. If sf, and ff parameters are not assigned a value during this functions invocation, the function will default to fitting *everything except the signal*.

If sf and ff parameters are assigned a value during this function's invocation, the function will fit data in the following slices:

- Region 1: (xdata[sf:start], ydata[sf:start]);
- Region 2: (xdata[finish:ff], ydata[finish:ff])

If fit_sans_signal is True, *sf* and *ff* are used to narrow the fit region to the left and right of the peak, the fitting regions to the left and right of the signal will be narrowed from the ends of the dataset. This ASCII ‘art’ may help illustrate.

```

#      (sf index)  (start index)    (finish index)  (ff index)
#           |           |   --  |           |
#           |           |   --  |           |
# not fitting| fitting | -----| fitting | not fitting
#           V           V --  --- V           V
# -----|++++++|-----|++++++|-----
# sf region |           | SIGNAL |           | ff region

```

savefit

Boolean. Saves the proofing plot produced by *gff*.

filename

String. Custom filename for the plot written to disk by *savefit*.

binning

Int. Helps scale individual points for the scatter plots.

xmin

Number. Matplotlib pyplot's graph window minimum x

xmax

Number. Matplotlib pyplot's graph window maximum x

gui

Boolean flag. Used to return figure to display in tkinter GUI.

automated

Boolean used to help user troubleshoot fitting routine when GUI automates sweep-extraction. Prints warning when *y* is not found in *df*. This can happen due to a bad y-fit on a particular sweep.

p0

Array of numbers. Initial points used to find absorption/dispersion parts of the lorentzian-shaped raw signal. Used only during fitting of absorption/dispersion lorentzians.

bounds

2-D array of numbers. Fit parameter bounds (coersion) passable in the command line that helps encourage least-squares fitting routine to model the data.

2.15 General Graphing Function

```
ggf(master, s, f, **kwargs):
```

General graphing function for the

2.15.1 df

Pandas Dataframe. A non-empty pandas dataframe.

2.15.2 s

Int. The start index in *df* of the signal to plot.

2.15.3 f

Int. The end index in *df* of the signal to plot.

2.16 **kwargs

```
xmin=None, xmax=None, plttitle="", x="MHz", y="Z_re", xlabel="Frequency (MHz)", ylabel="Re(Z) Impedance [Ohms]", filename="", fit_marking=False, fit_bounds=[], noshow=True, binning=1, redsig=False, integrate=False, thermal_equilibrium_value=False, b=None, T=None, fitorentzian=False, edata=-1, gui=False, fitorentziancenter_bounds=None, automated=False, temu=up
```

x

Str. Dataframe column name containing the x data.

y

Str. Dataframe column name containing the y data.

filename

Str. The name of the file to save the graph to.

fit_marking

Boolean flag. Used for marking the data during fit subtraction.

fit_bounds

Array of x-tuples [(x1s,x1f),...,(xns,xnf)]. Used in tandem with *fit_marking* to highlight ranges

noshow

Boolean Flag. Used to turn off figure preview before saving graph.

binning

Int. A number used to size the points on the scatter plots.

redsig

Boolean flag. Highlight the user-selected signal region red.

integrate

Boolean flag. Used to shade the area under the user-selected signal region to provide a visual representation of the area underneath the graph.

thermal_equilibrium_value

Boolean flag. Calculates the Thermal Equilibrium value from the TE equation and places its value as text on the graph. Also finds calibration constant for plotted data. Only configured for the proton as of June 18, 2020.

b

Number. B, or the magnetic field used to calculate the TE equation.

T

Number. T, or the Temperature used to calculate the TE Equation.

fitlorentzian

Boolean flag. Fit a lorentzian to the data, and plot the fit, useful for fitting the proton NMR signal.

gui

Boolean flag. Used to return function to tkinter handler for GUI display.

clearfigs

Boolean flag. Used to free-up memory

fitlorentziancenter_bounds

Tuple, Numbers. Used to constrain center of the lorentzian fit within the user-selected signal region.

automated

Boolean flag. used to help user troubleshoot fitting routine when GUI automates sweep-extraction. Prints warning when y is not found in df. This can happen due to a bad y-fit on a particular sweep.

temu

Number. The Mu used in the TE equation.

edata

Pandas Dataframe. Use-able in the command line. A dataframe that contains data to plot over other data currently on the figure.

xmin

Matplotlib pyplot's graph window minimum x

xmax

Matplotlib pyplot's graph window maximum x

xlabel

Matplotlib pyplot's xlabel

ylabel

Matplotlib pyplot's ylabel

plttitle

Matplotlib pyplot's plot title

3 Clerical Tools

3.1 DAQ Muncher

Partitions a DAQ csv file line-by-line into separate (.ta1) files which analysis is done on.

3.2 Directory Sorter

Organizes Files for to be averaged or isolated from one-another based on timestep.

3.3 Sweep Averager

Averages DAQ Munched files within a single directory, or in a 2d file structure. (A directory with many 1-layer sub-directories)

3.4 Global Analysis

Takes the results from the analysis, and pulls together other useful system data-streams into a single plot.

4 (deprecated) Tkinter GUI: gui.py

THIS HAS BEEN NON FUNCTIONAL SINCE THE RELEASE OF Python 3.9.1!!!

Is a tkinter widget-based graphical user interface that connects the user with the toolchain.

4.1 User's Manual

The following packages are required for the GUI's execution, and toolchain usage. I would advise using a virtual environment, to keep your root python directory clean.

- datetime
- tkinter *
- glob*
- statistics *
- gc*
- shutil *
- matplotlib
- scipy
- numpy
- math *
- os *
- pandas
- tkinter
- gc *
- traceback *

The libraries with (*) should already be included with all but the most bare-bones python distributions.
When you execute the gui.py the following window will appear:

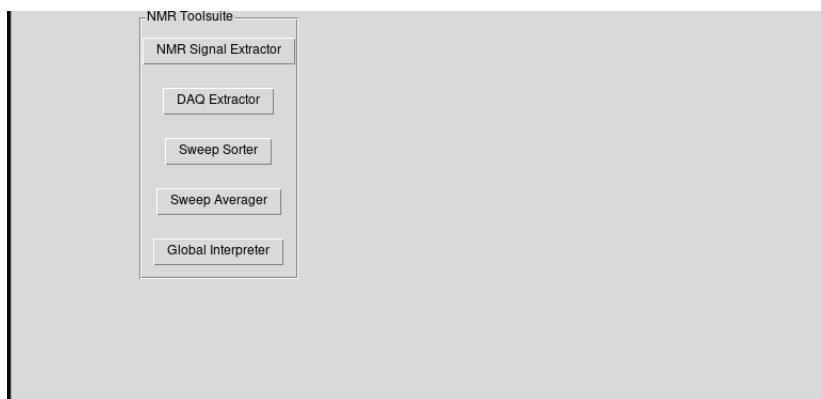


Figure 27: This is the beginning page in which the user is able to select any of the tools embedded in the tool-suite.

4.2 DAQ Extractor

Proceed by clicking the "DAQ Extractor" button on the NMR tool-suite splash screen. Here, is where the signal extraction process begins. The DAQ extractor takes a DAQ csv, with all of the telemetry, NMR sweeps, and produces a .ta1 file *for each row in the DAQ csv*. There is a 1:1 correspondence between the DAQ rows, and files the DAQ Extractor creates.

With this in mind, the DAQ Extractor has the capability to create directories and categorize each created .ta1 file into a particular directory. It does this automatically to avoid polluting the local directory with tens of thousands of files. The organizing process is controlled by the "NMR Status" Column within the DAQ csv; and a soft coded value within the python script itself.

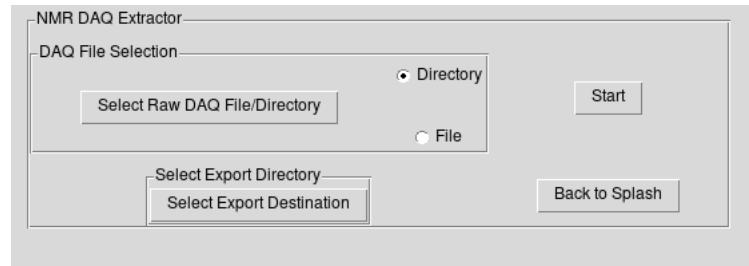


Figure 28: Caption

To operate this portion of the GUI, you must first select to process a single DAQ csv, or a directory of DAQ csvs. You can then select the Export directory, but the default directory for that is the local directory in which the program is executed. Below is an example of parsing data from the 2020 September experimental phase.

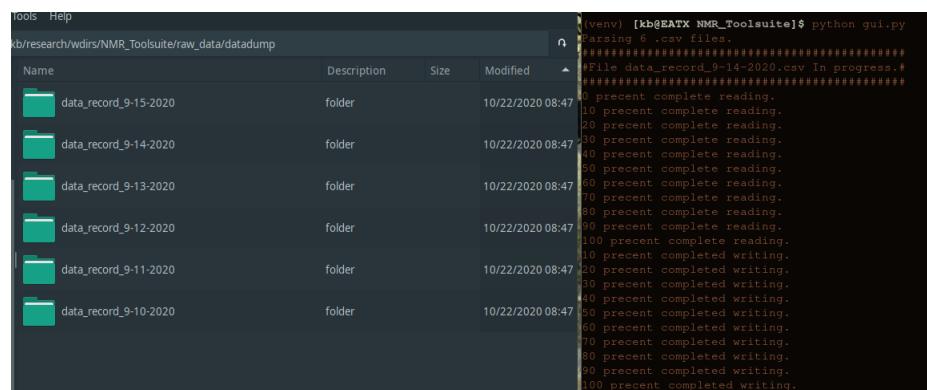


Figure 29: Caption

4.3 Sweep Sorter

Proceed by clicking the "Sweep Sorter" button on the NMR tool-suite splash screen. Here, is where you can further organize the enormous number of files into sub-directories for multi-sweep averaging, and time organization.

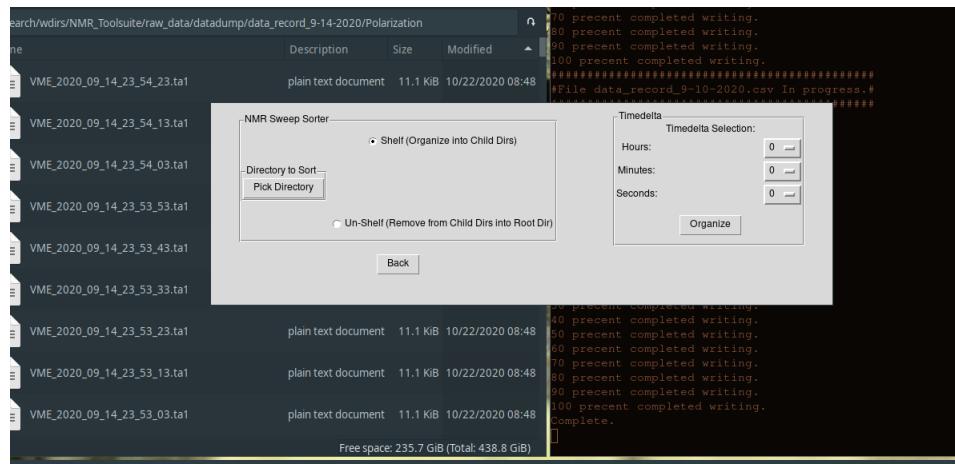


Figure 30: Caption

On the left hand side of the GUI the user is able to select a directory to organize. They can either “Shelf” or “Unshelf” the data which this program organizes for the user. On the right hand side of the GUI, the

4.4 Directory Averager

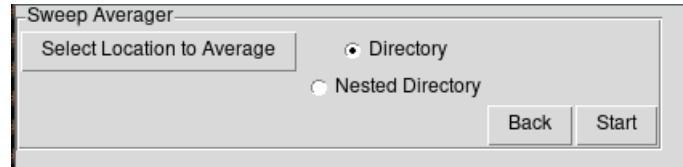


Figure 31: Caption

4.5 Signal Analysis

Proceed by clicking the “NMR Signal Extractor” button on the NMR tool-suite splash screen Here, the user is able to select the file type of the polarized target group’s NMR recording system. Currently, the DAQ output from the VME (using files generated with VME_ Extractor) and the VNA. To begin, I will click the ”Select Baseline” button, and select an adequate baseline file.

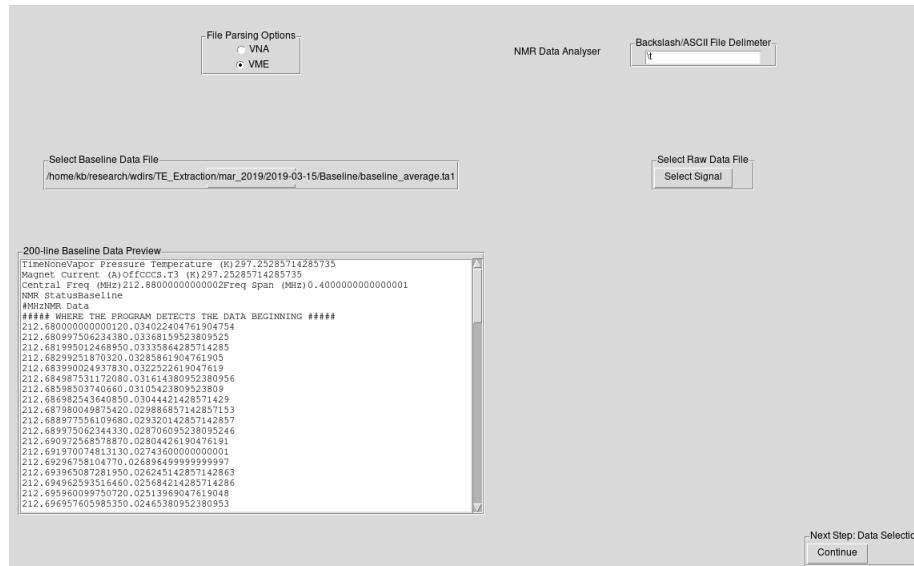


Figure 32: Once the file-dialogue has successfully selected a valid file, a 200 line file preview will appear.

And likewise for the signal file:

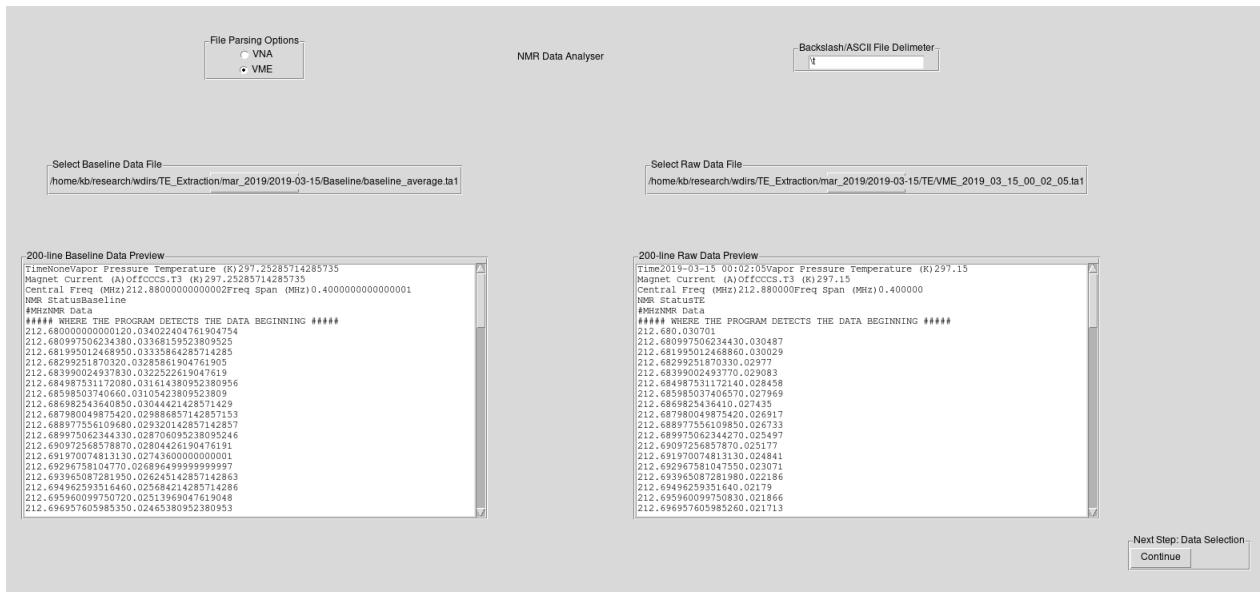


Figure 33: Caption

When these files have been selected, press the continue button.

4.5.1 Data Selection and Binning

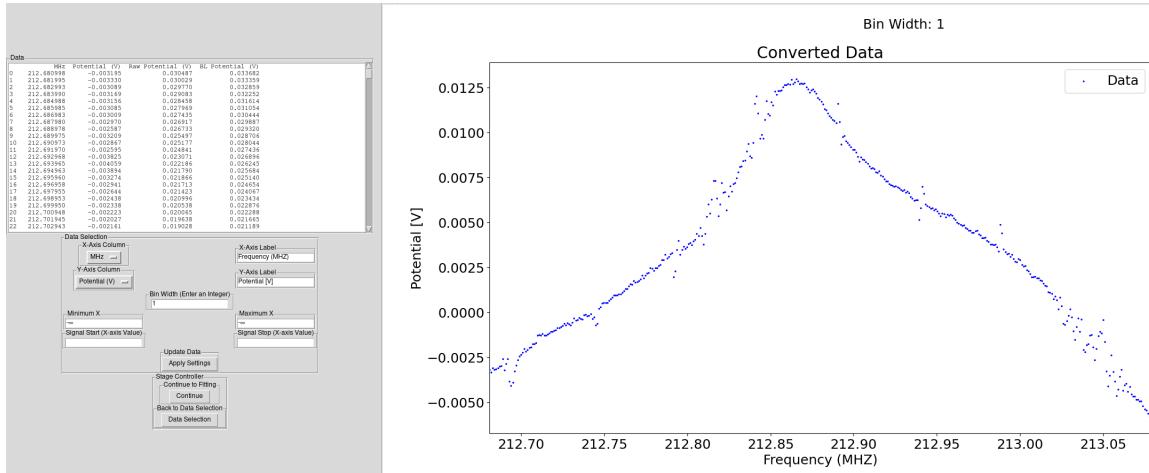


Figure 34: Data Selector

Figure 34 depicts a general impression of the data. For the VME's case, the axes are pre-labeled, and can be re-labeled if desired. Multiple channels of data are individually available for the VNA and VME. Unfortunately there is no functionality to plot multiple channels of data (on the y-axis) simultaneously. In the following table are the plot-able data-streams for each VNA⁸/VME measuring system. If selecting axis other than the default, be sure to update the graph by clicking the "Apply Settings" under the "Update Data" frame before carrying other settings, it is easy to think you are applying settings to one dataset, while actually making an adjustment on something historical!

Plot-able Datastreams (X/Y)

VME	Mhz	Potential (V)	Raw Potential (V)	BL Potential (V)			
VNA	Mhz	Z_re	Z_im	Raw Re(z)	Raw Im(Z)	BL Re(Z)	BL Im(Z)

When the axes are established, the user has the choice of selecting a bin width, which by default is 1 — showing every data point within the set. The bin width n determines how many raw data-points are being averaged to a single point on the plot.

Once the binning has been selected, and the graph has been updated with the "Apply Settings" button, the x-axis can be narrowed. By default, the plot will show all of the data, in ASCII this is represented by the infinity sign " $\pm \infty$ " under the "Minimum X" and "Maximum X". Changing this view window size **will truncate data outside of the viewing range**.

When the range of the x-axis has been determined, the user can select a region of interest (pictured: Signal Start/Signal Stop), by sandwiching their region between the boundaries of the region. In order to do this the user must identify where their region starts, and ends according to the x-axis, then fill in the "Signal Start (X-axis Value)" and "Signal End (X-axis Value)" entries accordingly. Press "Apply Settings" again to view the user selected regions.

⁸The VNA has some intermediate mathematical conversions that can be recovered by editing a line of NMR_Analyzer.py under function: `get_z()`

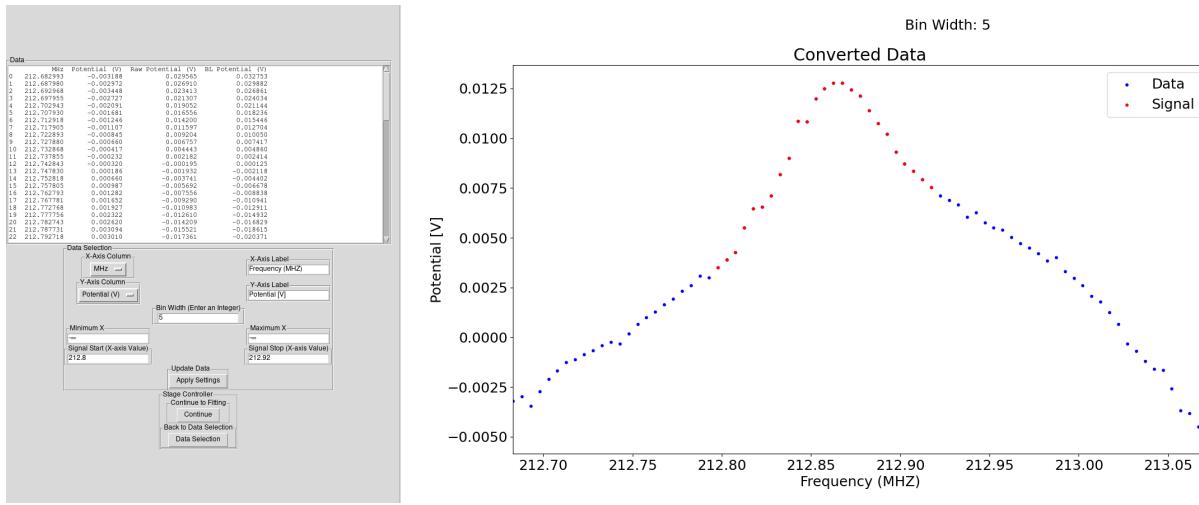


Figure 35: Caption

When the signal region has been highlighted, press "Continue" to advance to the fitting portion of the GUI.

4.5.2 Dataset Fitting

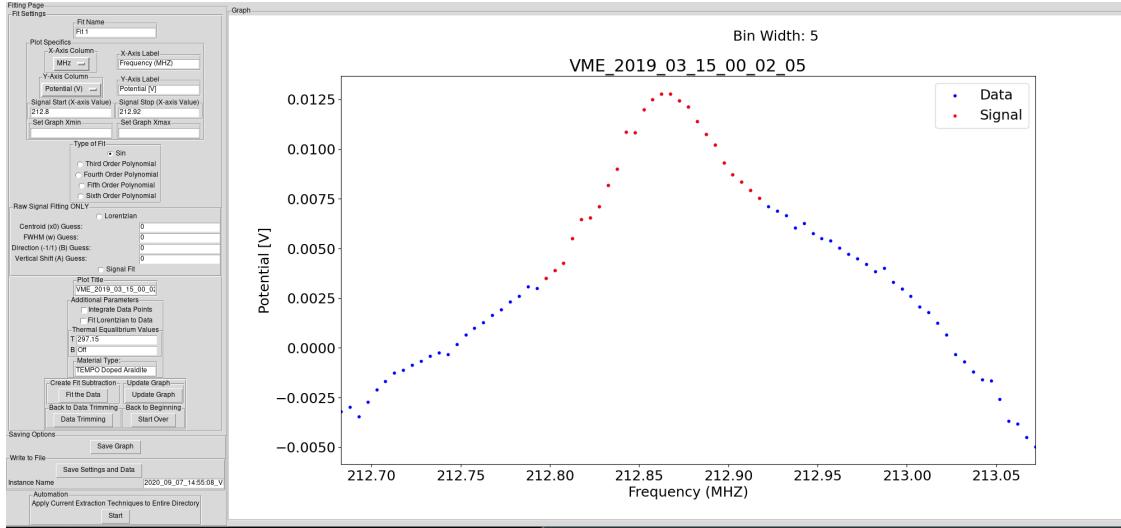


Figure 36: Caption

Here, the user is able to update the axes, re-highlight the signal, set a limit on what part of the data-set is visible, fit and subtract the background data around the shaded red region, fit the raw signal, update the graph title, display the Riemann integration of the data-set, fit a lorentzian curve to the data-set, update thermal equilibrium parameters (TE), track the material type, go back to a previous GUI window, completely restart the process, save the graph as displayed, save the data involved in generating the graph, and finally apply current signal-extraction techniques to other files in the raw-signal directory.

Like the previous window of the GUI, every time a modification is made to the settings page on the left, the graph must be updated to accurately reflect the changes applied, please click the "Update Graph" button after setting changes have been made.

The plot specifics widget is very similar to the Data Selection and Binning panel. The x and y axes/labels may be changed, the signal region and plotting window can be narrowed, or widened, and intermediate datasets (i.e. baseline, raw signal... etc) can be selected. There is no binning on this GUI pane. Any change of these settings will not be displayed until the graph has been updated.

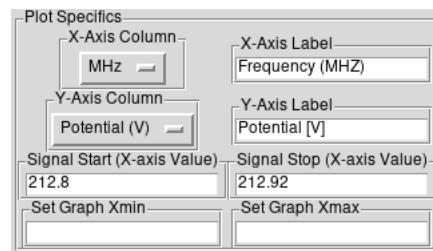


Figure 37: Caption

The user is able to then choose from a variety of functions to fit the data about the signal[¶]. The user should select which type of fit they think best resembles the background data, and click the "Fit Data"

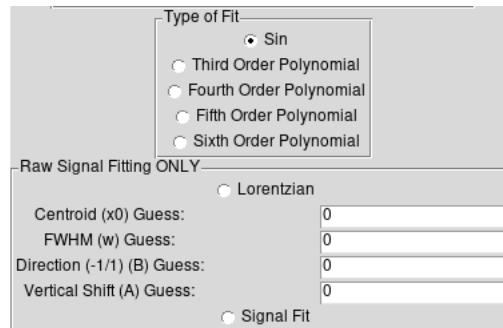


Figure 38: Caption

Upon a sucessful fit, the user will be presented with the fit imposed over the data:

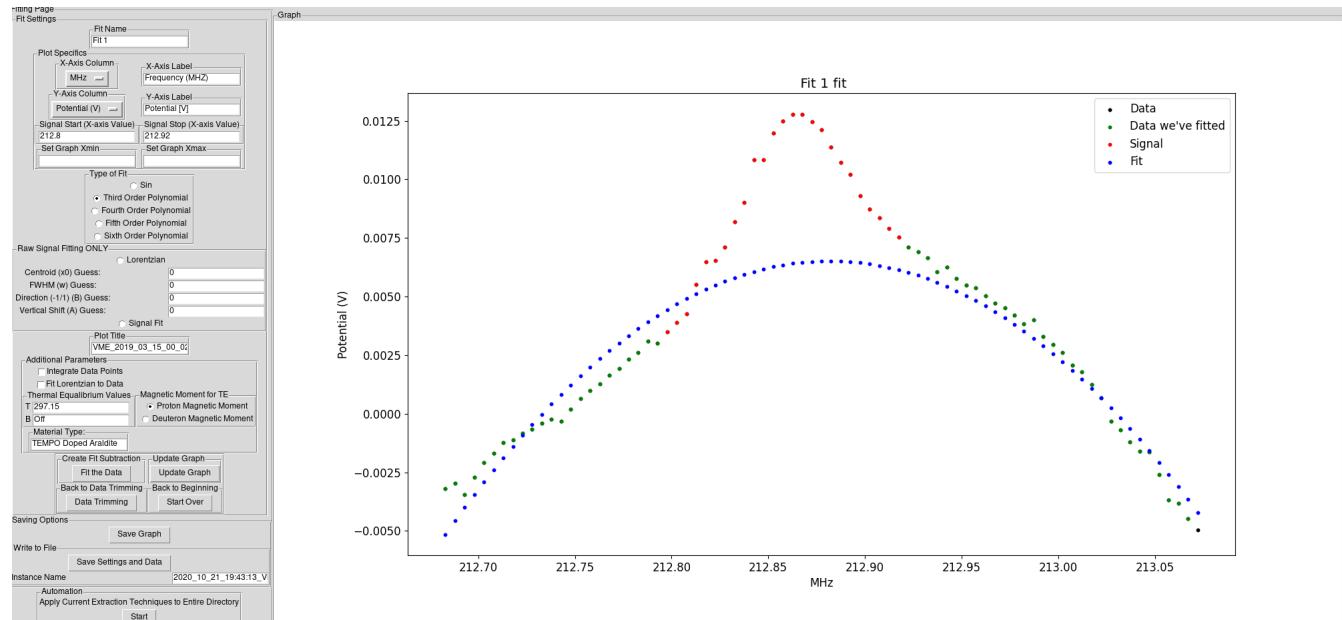


Figure 39: Note the dotted blue lines.

Upon a failed fit, the user will be presented with the signal graph with color-inverted data-points.

[¶]including raw signal fitting (Consult Ellie's NMR/Proton Model) which has not been successfully implemented yet into the gui due to least-squares fitting issues

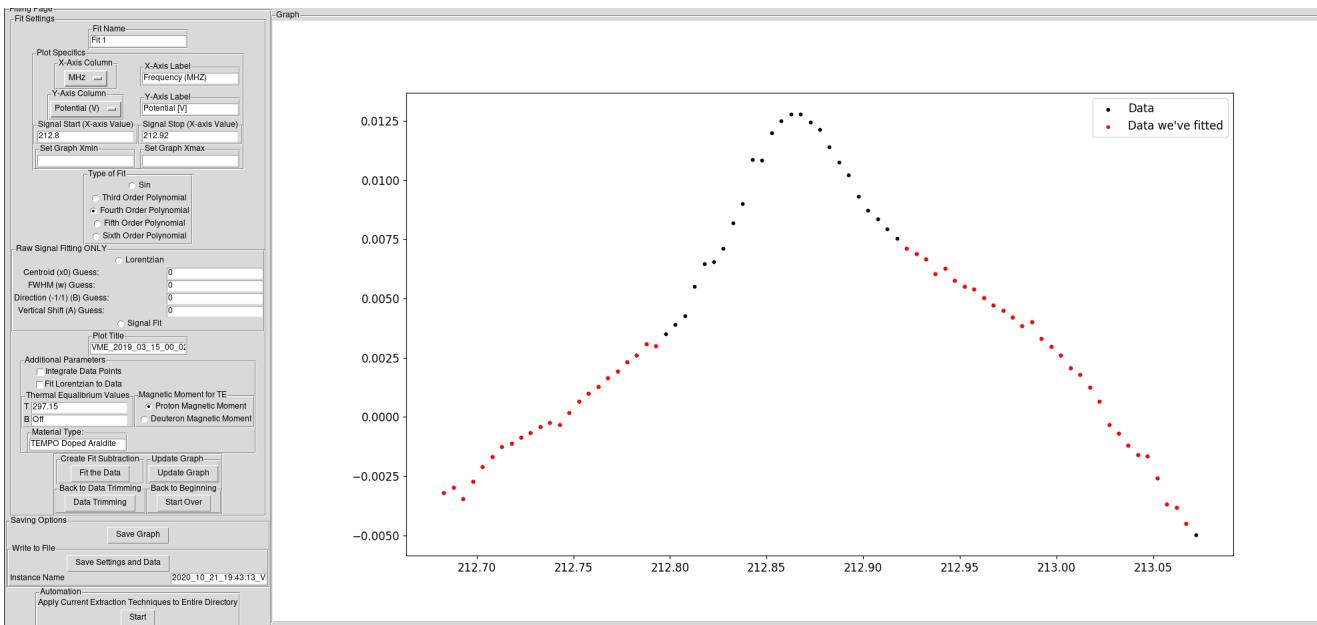


Figure 40:

To select the fit-subtracted dataset, change the y-axis column pull-down menu, to the fit-subtraction menu.

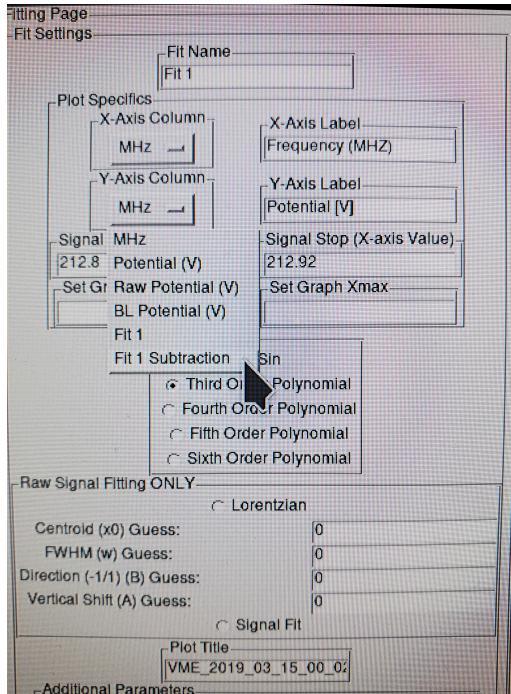


Figure 41: Apologies for the moiré. Remember to update the graph after selecting a new y-axis column.

In the following image, several parameters can be adjusted, this includes the plot title, numerical integration between the signal region (displayed as a shaded region below the signal selection), a lorentzian curve fit that captures the proton NMR, and lastly the TE Equation can have its reported temperatures and magnetic field manually adjusted. In the generated global analysis file, original values are preserved, but these user-inputs are stored as well.

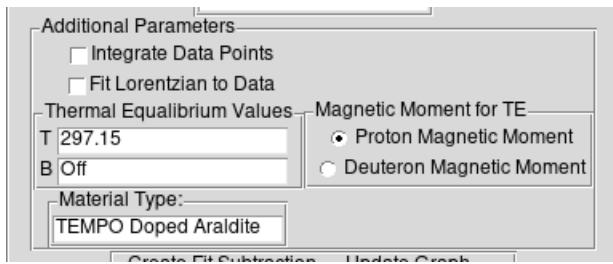


Figure 42: Caption

And at last, we arrive at the control-area of the fitting frame.

The grid of 4 buttons control the current frame and enable restarting the NMR signal extracting process. I'd like to guide your attention to the next 3 buttons, and instance name

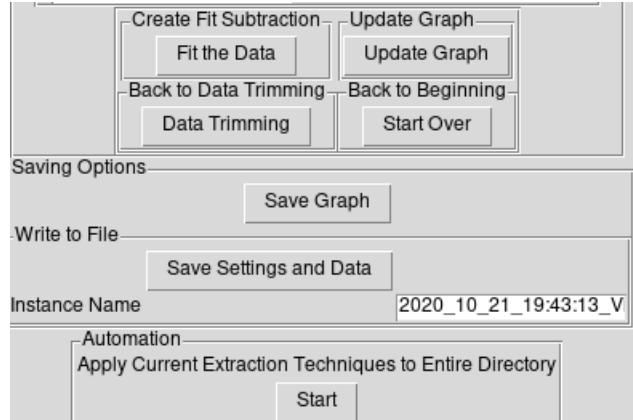


Figure 43: Caption

The “Save Graph” button will update the graph to reflect the current settings, then it will save the graph in local directory (where the program is being executed). The “Save Settings and Data” will save the data stored in memory pertaining to the current sweep being displayed.

4.5.3 Automation

The last and final part of the user-manual to this GUI is with automation. All you need to do to automate the signal extraction process is to press the automate-start button. The program will apply all of the settings which you have selected for this current session, and apply it to all of the other sweep signals within the directory from where you selected the current signal.