Demag_GUI Usage and Tips (Version 4.0)

Installing

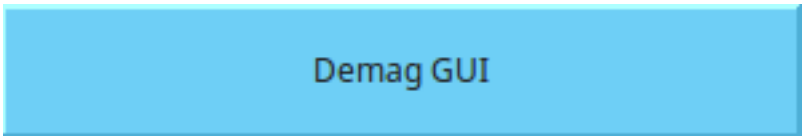
After downloading the PmagPy repository from github, to run this version of demag_gui it is necessary to download a working version of python (preferably python 2.7), the latest version of the visualization library wxpython on your archatecture, and the basic scientific libraries part of the scipy project.

Launching

The Gui may be launched either with the command line by going to the directory containing demag_gui.py and running it with:

```
python ./demag_gui.py
```

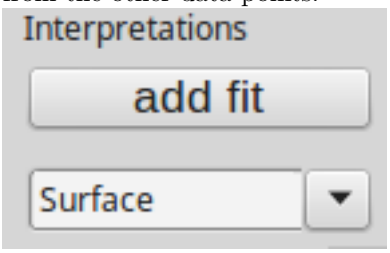
If you have QuickMagIC already running you can launch demag_gui by just clicking on the demag_gui button in the main window shown below. **Note:** on OSX it is recomended to launch through the QuickMagIC program as on wxpython 2.9 the drop down boxes seem to behave better when launched in this manner:



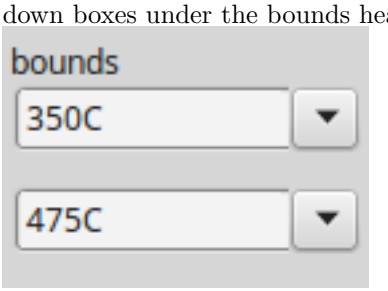
Interpretation of Specimen Data

Adding Interpretations:

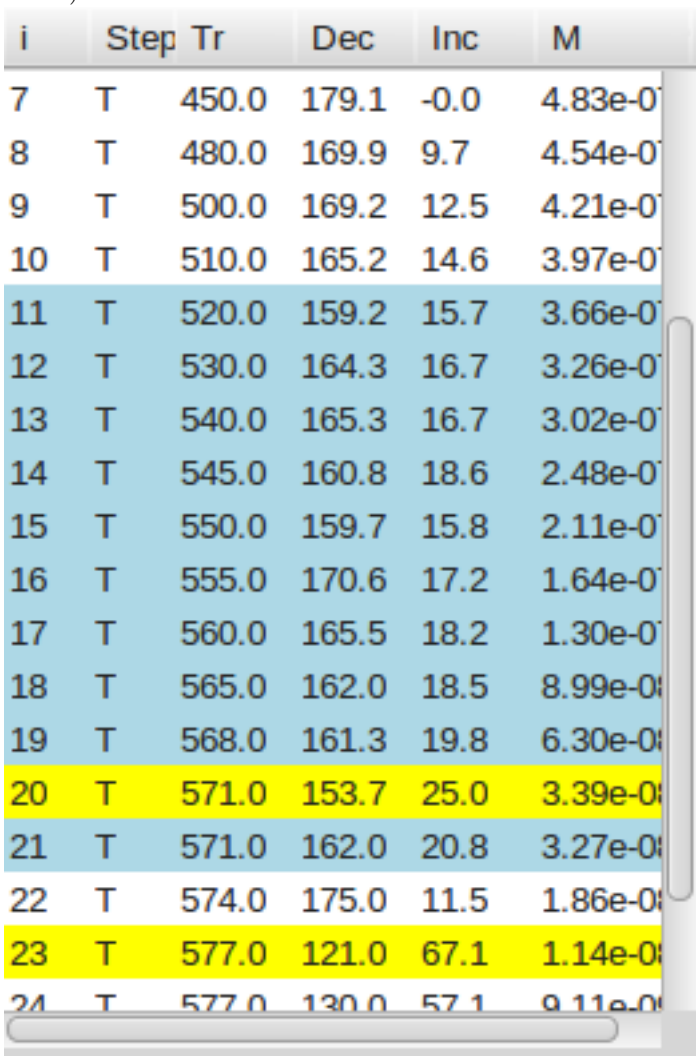
You can analyze specimen component data by adding fits with the add fit button. Additionally you can select the fit you would like to edit or view by using the drop down box under the add fit button. Once you have selected a fit the shape of the selected fit's data points will turn to a diamond shape to distinguish them from the other data points.



Once you have selected the desired fit you can edit its bounds using the drop down boxes under the bounds header

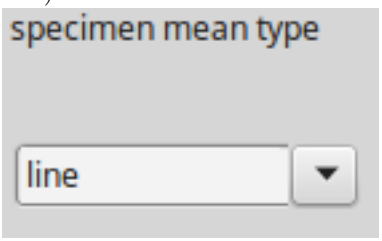


Alternativly you can double click the list of measurement steps on the left to pick out the bounds of your interpertation. The included steps in the currently selected interpertation are shown in blue on this list and measurement steps marked bad are shown in yellow. (This method of selecting bounds is recomended for mac users who have in the past experinced problems with the drop down boxes)

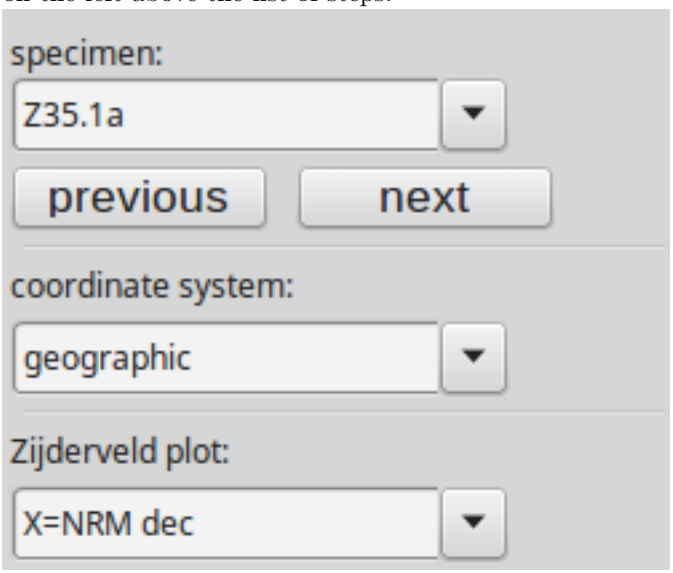


i	Step	Tr	Dec	Inc	M
7	T	450.0	179.1	-0.0	4.83e-0
8	T	480.0	169.9	9.7	4.54e-0
9	T	500.0	169.2	12.5	4.21e-0
10	T	510.0	165.2	14.6	3.97e-0
11	T	520.0	159.2	15.7	3.66e-0
12	T	530.0	164.3	16.7	3.26e-0
13	T	540.0	165.3	16.7	3.02e-0
14	T	545.0	160.8	18.6	2.48e-0
15	T	550.0	159.7	15.8	2.11e-0
16	T	555.0	170.6	17.2	1.64e-0
17	T	560.0	165.5	18.2	1.30e-0
18	T	565.0	162.0	18.5	8.99e-0
19	T	568.0	161.3	19.8	6.30e-0
20	T	571.0	153.7	25.0	3.39e-0
21	T	571.0	162.0	20.8	3.27e-0
22	T	574.0	175.0	11.5	1.86e-0
23	T	577.0	121.0	67.1	1.14e-0
24	T	577.0	130.0	57.1	9.11e-0

You may notice that the fit will be given a generic name such as *Fit 1* you can change the name of the fit from default by typing into the drop down box containing fits then pressing enter. You can anchor your interpertation or preform a plane fit using the drop down box under specimen mean type (default: line).



Coordinate Systems available as well as orrientation of Zijderveld are available on the left above the list of steps.



The properties of the current interpertation can be seen in the upper center of the GUI in a large box labeled specimen mean statistics.

Flagging Bad Measurment Data

You can set acceptance criteria to a pmag_criteria table by using Analysis/"Acceptance Criteria"/"Change Acceptance Criteria". If any measurement steps are bad you can flag them as such by right clicking on the list of measurement steps to the left of the GUI. If you flag a step bad that you would later like to restore you can simply right click on it again and it will be flagged as good again.

Plot Interface

The 4 plots that take up the majority of the center of the GUI are where you will see your data and interpertations displayed. In addition they have a new and somewhat unintuitive interface which likely needs explination. The zijderveld and the 2 equal area plots are by default set to zoom when you left click and drag your left mouse button you will zoom to the dragged out rectangle (currently equal area plots do not draw this rectangle as you drag your mouse but still zoom). On the zijderveld plot it is possible to switch between zoom and pan functionallity by right clicking, once in pan mode the mouse will turn into a hand allowing you then to click and move around the plot. On both the zijderveld and equal area plots if you wish to return to the origional plot simply click the middle mouse button to return to home position. **Note:** in the absence of a middle mouse button pressing both right and left mouse buttons at the same time works on most laptops in the case of macbooks clicking with two fingers should work, and if using apples magic mouse we recomend you download the MagicPrefs program which will allow you to configure your mouse however you prefer. Lastly when mousing over the equal areas if you end up over the top of a interpertation plotted there you can double click on it to switch the specimen and current interpertation to the clicked interpertation.

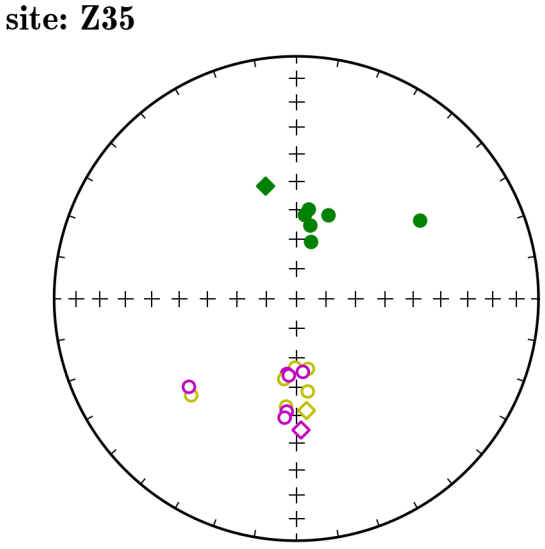
Saving Specimen Interpretations

Once you have picked out your interpertations you can save the session data in two different ways a .redo file or pmag tables. In addition you may save image files of the plots.

The .Redo File: You can use Analysis/"Save current interpertations to a redo file" to create this file type or you can just hit the save button next to add fit, this method is recomended as it prevents accidental pressing of the clear all interpertations button. **Note:** this file type does **NOT** load previous interpertations on start up you must go to the menu option Analysis/"Import previous interpertations from a redo file" to restore your previous session.

The Pmag Tables: By going to the menu File/"Save MagIC pmag tables" you can export your interpertations made in Demag GUI to the MagIC pmag tables which can then be used by other MagIC programs or uploaded to the MagIC database. You can export any or all of the 3 coordinate systems upon selecting this option and you may choose to save pmag_samples, pmag_sites, and pmag_results tables in addition to the pmag_speciemns table that is output. If you choose to output additional information you will be prompted by a pop up window for additional information. **Note:** this save format loads on start up of the GUI imediatly restoring your session, also selection of this option will overwrite your demag_gui.redo file in the working directory.

Images of Plots: Select the menu option File/"Save plot"/"Save all plots" to save all plots alternativly you can save any of the plots individually. Some examples can be seen below:



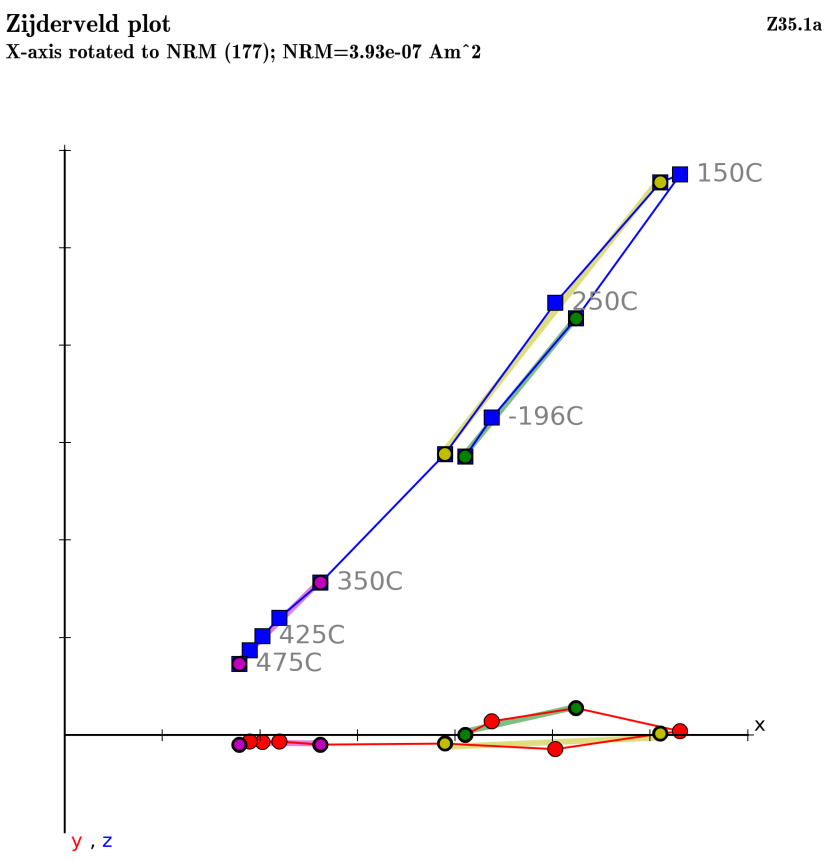


Figure 1: Zijderveld with 3 interpertations

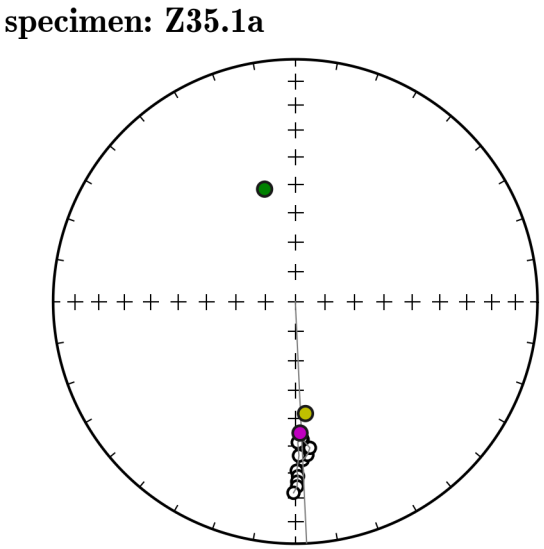


Figure 2: Equal Area plot of specimen data and interpertations

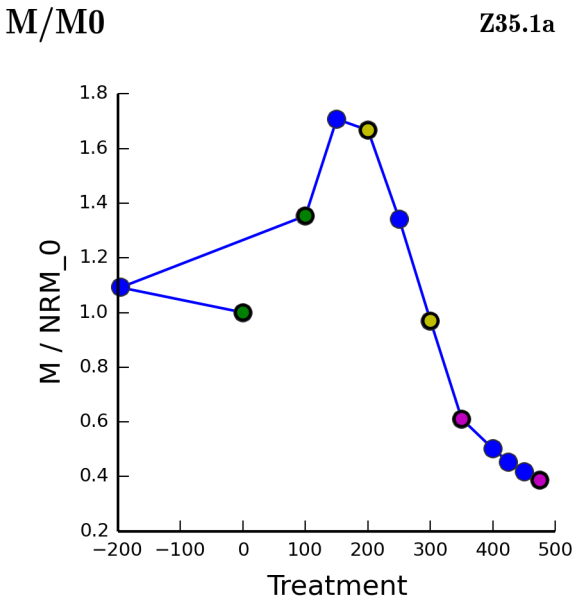
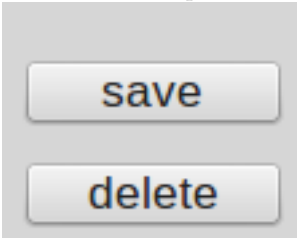


Figure 3: M/M0

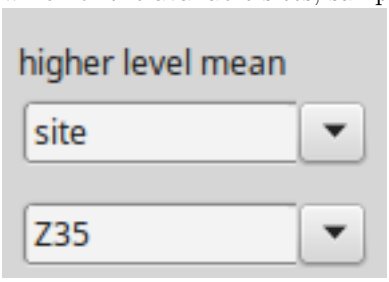
Deleting Specimen Interpretations

If you would like to delete a single interpertation select the one you wish to delete from the interpertation drop down box then click delete. Alternativly if you wish to clear all interpertations you may go to the menu option Analysis/"Clear all current interpertations".

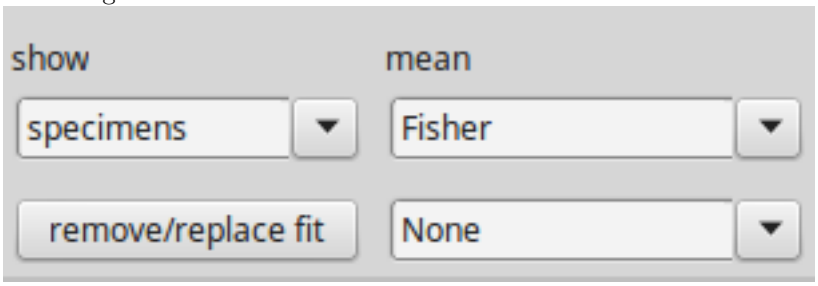


Higher Level Plots and Interpretation

The set of drop down boxes to the right of the interpertation data is there to determine what level you want to analyze in the higher level analysis options include: site, sample, location, and study. The drop down below this selects which of the available sites, samples, location, or studies you want to display.



You can then select how to group your data by using the drop down menu under the show header. You can select what kind of mean to take using the first drop down under the mean header. Which interpertations to use for the means can be selected under the second drop down menu. You can then use the remove/replace button to remove or replace the set of points belonging to the current specimen in the higher order mean.



You can view Fisher/Bingham statistics in the bottom left of the GUI.