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 and install a working version of python (preferably python 2.7), the latest version of the visualization library wxpython on your architecture, and the basic scientific libraries that are part of the scipy project.

Launching

The GUI may be launched with the command line by navigating to the directory containing demag_gui.py and running it with:

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

If you have QuickMagIC already running or if you need to convert files to magic format you can launch demag_gui by just clicking on the demag_gui button in the QuickMagIC GUI, shown below. **Note:** on OSX it is recommended to launch through the QuickMagIC program as on wxpython 2.9 the drop down boxes seem to behave better when demag_gui is launched as a plug in:

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.
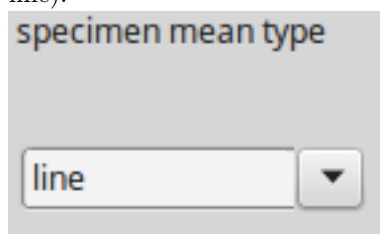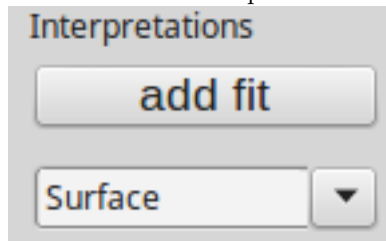
Once you have selected the desired fit you can edit its bounds using the drop down boxes under the bounds header
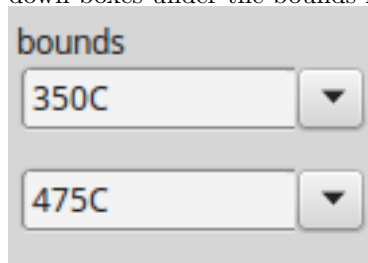
Alternatively you can double click the list of measurement steps on the left to pick out the bounds of your interpretation. The included steps in the currently selected interpretation. are shown in blue on this list and measurement steps marked bad are shown in yellow.

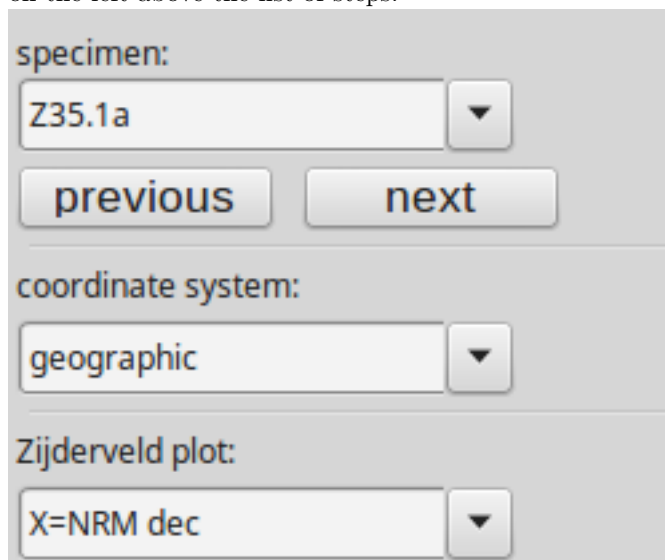| i	Step	Tr	Dec	Inc	M
7	T	450.0	179.1	-0.0	4.83e-0
8	T	480.0	169.9	9.7	4.54e-0
9	T	500.0	169.2	12.5	4.21e-0
10	T	510.0	165.2	14.6	3.97e-0
11	T	520.0	159.2	15.7	3.66e-0
12	T	530.0	164.3	16.7	3.26e-0
13	T	540.0	165.3	16.7	3.02e-0
14	T	545.0	160.8	18.6	2.48e-0
15	T	550.0	159.7	15.8	2.11e-0
16	T	555.0	170.6	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 interpretation. or preform a plane fit using the drop down box under specimen mean type (default: line).

specimen mean type

line

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

specimen:

Z35.1a

previous   next

coordinate system:

geographic

Zijderveld plot:

X=NRM dec

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

specimen mean statistics

dec	inc	n	mad	dang	a95
177.9	-44.8	5	3.2	17.8	

Flagging Bad Measurement 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 interpretations displayed. In addition they have a new and somewhat unintuitive interface which likely needs explanation. 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 functionality 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 original 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 recommend 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 interpretation. plotted there you can double click on it to switch the specimen and current interpretation. to the clicked interpretation.

Saving Specimen Interpretations

Once you have picked out your interpretations 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 interpretations to a redo file" to create this file type or you can just hit the save button next to add fit, this method is recommended as it prevents accidental pressing of the clear all interpretations button. **Note:** this file type does **NOT** load previous interpretations on start up you must go to the menu option Analysis/"Import previous interpretations 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 interpretations 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 immediately 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 alternatively you can save any of the plots individually. If you zoom on any of the plots the zoomed image will be saved not the origionally plotted image although the plot will redraw and reset it's zoom level. Some example images can be seen below:
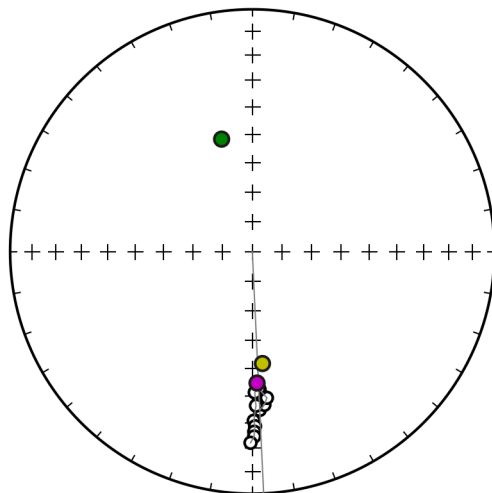
Zijderveld plot
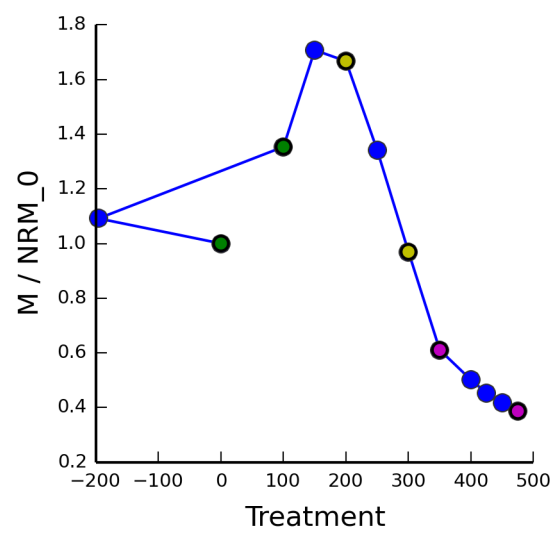X-axis rotated to NRM (177); NRM=3.93e-07 Am^2

150C

250C

-196C

350C

425C

475C

x

y , z
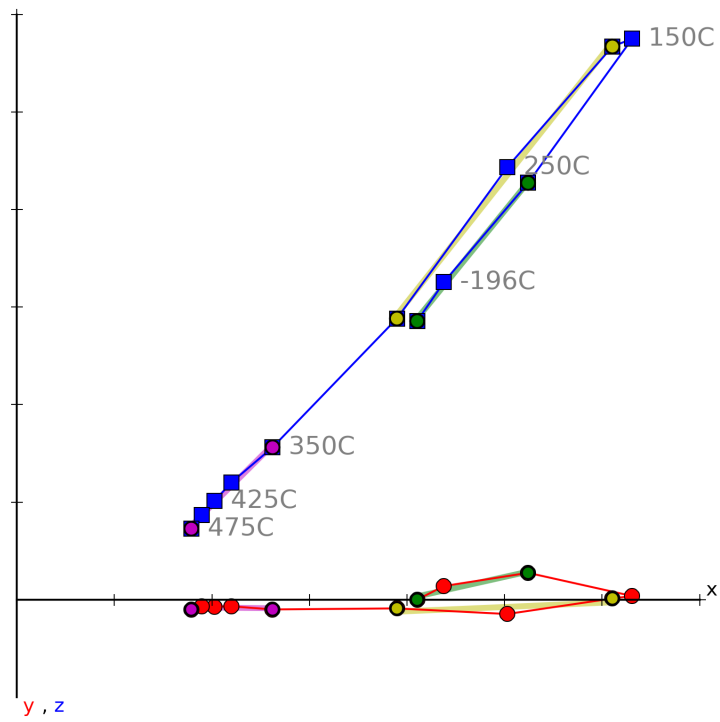
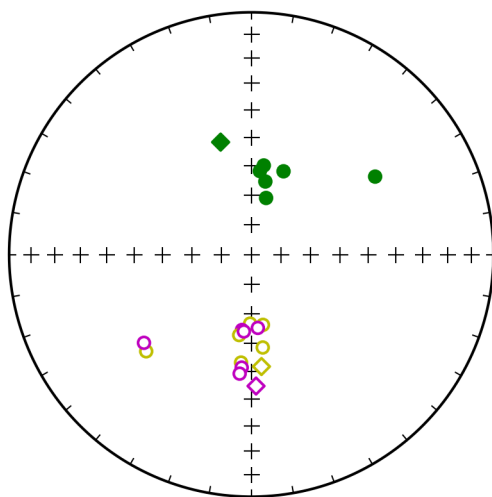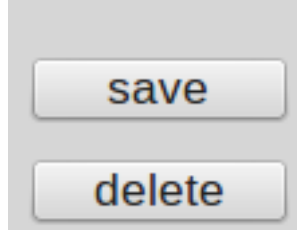**specimen: Z35.1a**

M/M0

Z35.1a

site: Z35

Deleting Specimen Interpretations

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


Higher Level Plots and Interpretation

The set of drop down boxes to the right of the interpretation. 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.
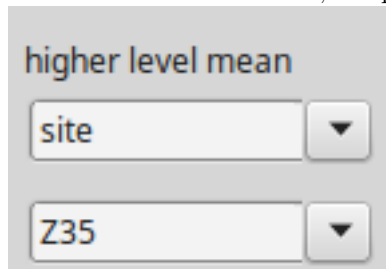
You can then select how to group your data by using the drop down menu under the show header. You can select what kind of mean to take using the first drop down under the mean header. Which interpretations to use for the means can be selected under the second drop down menu. You can then use the remove/replace button to remove or replace the set of points belonging to the current specimen in the higher order mean.
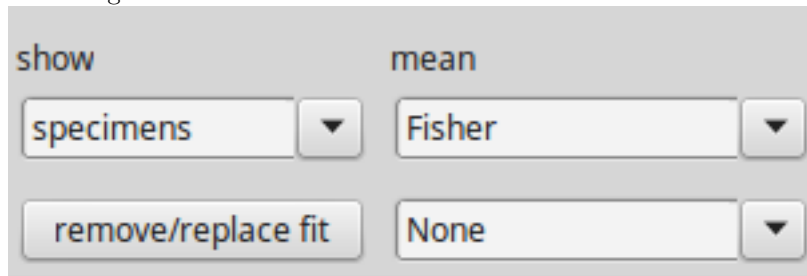
You can view Fisher/Bingham statistics in the bottom left of the GUI.

Fisher statistics:
dec: 183.9
inc: -54.0
alpha95: 48.1
K: 1.0
R: 6.8791
n_lines: 21
n_planes: 0

Interpretation Editor

In order to more easily view and edit specimen interpretation. data a separate specimen interpretation. editor has been created under the tools menu of the Demag GUI. This panel consists mostly of a log of all interpretations and their parameters from which you can select which interpretation. to view double clicking on the interpretation. in the list, the currently selected interpretation. is colored blue as shown in the image below. You can mark interpretations as bad which removes them from any fisher means or other high level means by right clicking on their entry in the list, all interpretations marked bad are colored yellow. Further you can highlight interpretations by singly clicking on the list and holding the shift or ctrl key (command key on mac) to select multiple interpretations this will allow you to delete or alter the characteristics of multiple interpretations at once without having to select each one in turn. This mass alteration is allowable using the the Name/Color/Bounds boxes to input new data then clicking the "apply changes to highlighted fits" button. You can delete highlighted fits using the "delete highlighted fits" button. The "add fit" button in the interpretation. editor adds a fit to the current specimen. In the case of interpreting large data sets you can reduce the number of items plotted on the equal area at the bottom of the editor and the number of entries in the log by using the display settings. The equal area plot on the bottom works just like

the higher level equal area on the main Demag GUI panel allowing you to select interpretations on it by double clicking and zoom by clicking and dragging.