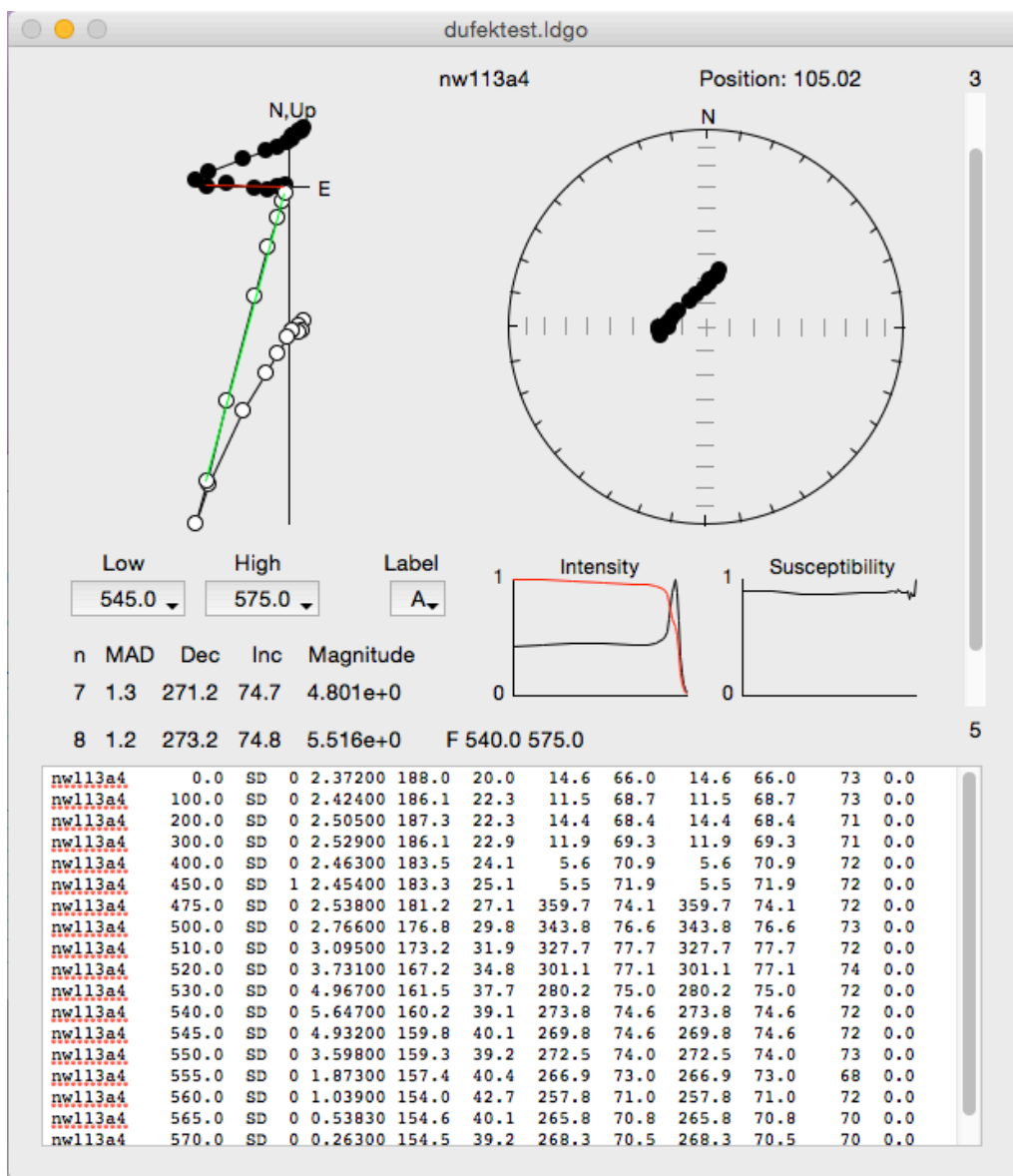


## MacPaleomag4.1 (May 2016)

This version of the program implements two major changes. The first is the ability to read in an existing PCA file and display and modify the existing picks. The second change is to allow viewing of the demagnetization data in two modes, either always zoomed in (with the lowest step shown always representing the start of the PCA fit as in MacPaleomag2.1) or showing all the data. Unfortunately, there is one feature that works less well in the latest version and that is the behavior when using the trackpad. A two-finger trackpad swipe now generates many events and can't be handled as easily. So I recommend using an attached mouse with a mousewheel. I've implemented some code that improves the behavior with the trackpad but it's still not optimal.



The display screen now shows the existing PCA record below the settings for the current PCA, controlled by the bevel buttons or mousewheel events over the Zijderveld plot.

## File Menu

File	Plot	Analysis
Open		⌘O
Order File		
PCA File		
Print		⌘P
Print Rest		
Next		⌘N
Previous		⌘B

**Open:** Open an LDGO file (see info at end of document on producing an LDGO format file). Some error checking is implemented so, e.g. you will get a dialog if the header is missing (it looks for an underline) or if the number of columns is too few or if data are out of range. The parsing is by whitespace so spaces or tabs will do and no particular format (apart from the header and the right number of columns through all three coordinate systems - sus and vol columns are optional).

**Order File:** This menu option reads in a file with specimen names and stratigraphic heights. The file need not be sorted as this is handled internally. The file can also have more records or fewer records than in the LDGO file. All samples

with a matching record will be displayed in the order of stratigraphic height (displayed at top right of diagram). If you open a new LDGO file the program will try to use the existing heights file and if no matches are found it will invalidate the heights array (and the stratigraphic position will disappear).

*Note: I haven't tested this extensively with loading a PCA file. For example, I would be cautious about loading a PCA file and then an order file that had only a subset of the samples in the original PCA file.*

**PCA File:** Loads a PCA file (in the format generated by MacPaleomag). The default is to show the existing PCA with the selected component label. This existing PCA record is shown below the current selection. Both will be the same when you move to a new sample in the file but the existing record is static while you change the Low and High treatment steps for the current selection so that the two can be compared. Note that a PCA file (either new or existing) must be selected before the Analysis Menu is activated.

*Note: The elegant way to allow updating of a text file is to store the data in a direct access file. This is more complicated and so I've opted to still use a simple text file. The PCA records are stored internally in an array (which is updated as needed) and then this is written when the program quits. I've also implemented an autosave (every 10 minutes). This is written to PCAsave.pca in the current directory.*

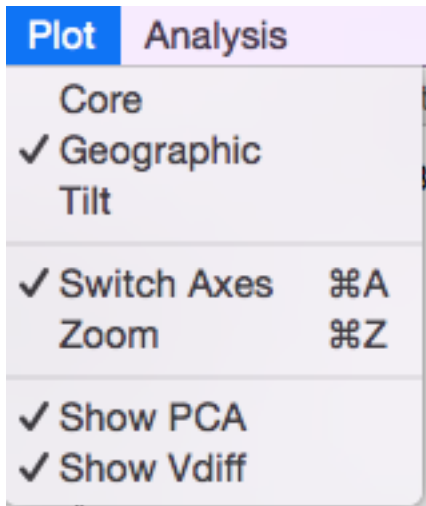
**Print:** This will print the current page or will allow saving the vector graphic output as a PDF file (with specimen name as the default). Print at 100% generates reasonable output.

**Print Rest:** This prints all records (also can be saved to multipage PDF). The file name default will be the LDGO file name(coordinates).pdf. The current settings (e.g. whether to zoom or not, whether to show the PCA fit) are used for the output.

**Next:** Keystroke shortcut to move to next sample

**Previous:** Keystroke shortcut to move to previous sample

### Plot Menu



**Core, Geographic, Tilt:** Select the coordinate system to view. The default is geographic.

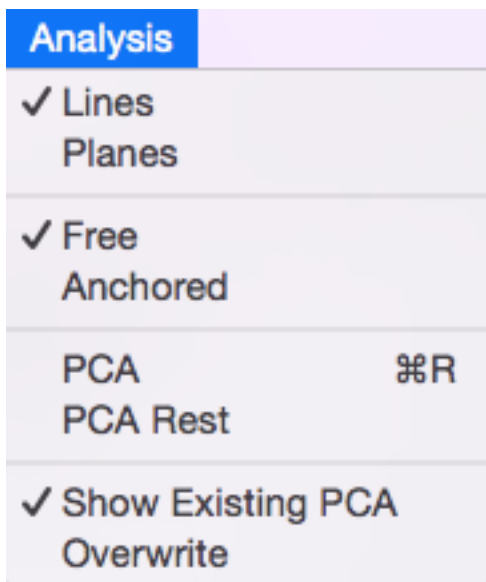
**Switch Axes:** Toggles the projection from N, Up vs E to W, Up vs N.

**Zoom:** This toggles between the two zoom modes. If unchecked, then all data will be displayed on the screen and in the PDF saved or printed. If checked, then the data block will be trimmed so that only data above the current Low treatment setting is displayed. The default is to show all data.

**Show PCA:** Toggle to plot PCA fit. On by default.

**Show Vdiff:** Toggle to plot decay of vector difference sum (in red) on the intensity plot. On by default.

### Analysis Menu



**Lines/Planes:** If lines is selected the PCA fit will be displayed on the Zidjeveld plot. The calculation uses the intensity of the vectors. If planes is selected the GC fit will be shown on the EQ plot (dark blue = lower hemisphere, light blue = upper hemisphere).

**Free/Anchored:** Type of PCA fit.

**PCA:** Save the PCA record (in all coordinate systems). The record is either appended to the existing records (if Overwrite is not checked) or replaces the existing record if Overwrite is

checked.

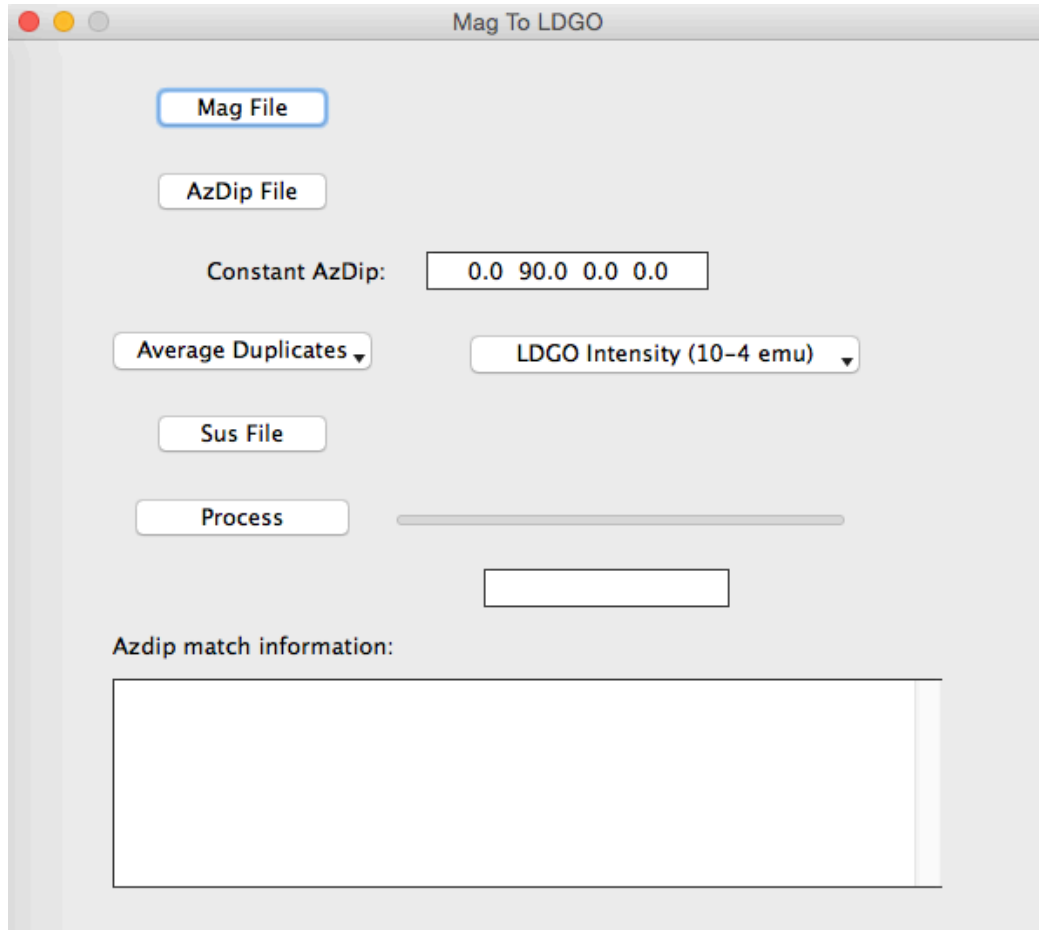
*Note: If multiple PCAs are available with the same component label, the first one is displayed on screen and this is also the record that will be replaced in Overwrite mode.*

**PCA Rest:** Process the entire data file using the current treatment levels and component label. If the selected treatment range does not exist for a specimen, the PCA will be calculated based on all data.

**Selecting the treatment range for PCA analysis:** The low treatment level for the PCA can be selected in one of two ways: via the "Low" bevel button or by zooming in. When the mouse is over the Zidjerveld plot the mousewheel controls the zoom level. The high treatment level for the PCA can be selected in one of three ways: via the "High" bevel button or by clicking on a point in the Zidjerveld plot or clicking on the EQ plot. Set the component label via the "Label" bevel button.

## Mag2LDGO (v1.3)

The MacPaleomag program is designed to view data stored in the Lamont (LDGO) format, which contains demagnetization data in sample, geographic and tilt corrected coordinates. Not all data acquisition programs store results in all coordinate systems and so Mag2LDGO is a simple conversion program to produce an LDGO format file.



**Mag File:** This will bring up a dialog to select a file with remanence data. Although this is set up to read in a \*.mag format file, any text file with the appropriate data columns will work. The parsing is by whitespace so spaces or tabs will do and no particular format is expected apart from having the columns in the correct order. An example \*.mag file with columns labeled is shown below.

Sample	Treat	CSD	Int(emu)	Decl.	Incl.	Optional metadata string
hp017a4	0.00	0.3	2.169E-3	142.9	54.6	12/10/07;14:29;°C;0.0000;microT;jason;G34; 1
hp017a4	100.00	0.3	2.358E-3	144.3	55.4	12/11/07;10:39;°C;0.0000;microT;jason;G34; 1
hp017a4	200.00	0.2	2.370E-3	144.6	55.5	12/11/07;12:04;°C;0.0000;microT;jason;G34; 1
hp017a4	300.00	0.2	2.365E-3	145.3	54.8	12/12/07;09:26;°C;0.0000;microT;jason;G34; 1
hp017a4	400.00	0.3	2.269E-3	145.2	54.5	12/12/07;11:16;°C;0.0000;microT;jason;G34; 1

So a text file (with no header) with sample ID, treatment, CSD, Intensity, Dec, Inc will suffice. Pressing the "Process" button at this stage will produce an LDGO file with the appropriate header and directional data in all three coordinate systems the same (i.e. applying the constant orientation shown by default).

*Note: The Lamont format is a compact format and as a result the sample ID is limited to 10 characters.*

*Note: The output file will have the default name \*.ldgo. If this file already exists you will be prompted on whether to overwrite the file.*

**AzDip File:** This will bring up a dialog to select an orientation file. The orientation file has a simple 5 column format (again spaces or tabs will do) with sample ID, azimuth, dip, bedding strike, bedding dip.

hp016a	216.9	58.0	000.0	0.0
hp017a	214.8	38.0	000.0	0.0
hp018a	220.8	49.0	000.0	0.0

The convention used is that the azimuth/dip are the orientation in the direction of drilling (i.e. the sample +Z orientation) and bedding strike is such that dip is to the right of strike.

The sample orientation is matched to the demagnetization in two stages: 1) an exact match is sought, 2) if no exact match is found, the final character of the sample ID is stripped off and the search is repeated. So a single entry (e.g. hp017 would be used for specimens hp017a, hp017b etc.). Samples for which no orientation data are found will be listed in the text box.

A constant orientation record may be used by editing the text in the Constant AzDip box. An orientation record with "0 90 0 0" will result in the same data in sample, geographic and tilt corrected coordinates.

**Average Duplicates:** The default is to average duplicate measurements at the same treatment step.

**Intensity output:** The original Lamont data files stored intensities in  $10^{-4}$  emu (approximating the order of a single flux count) and so intensity values can be more easily scanned. This is the default: assuming that input intensities are in emu, the output will be in  $10^{-4}$  emu and nicely formatted. You may also select to leave the intensities in the same units as on input (output will be in exponential notation).

**Sus File:** Susceptibility data are often measured in conjunction with thermal demagnetization studies and the Lamont format has a column to accommodate the susceptibility values. This will bring up a dialog box for an optional tab-delimited text file with the susceptibility data. The file must contain a header record with column headings for the treatment steps. Each row contains sample ID, susceptibility values for

the corresponding treatment steps. Susceptibility entries need not be present for all treatment steps.

**Process:** Creates the Lamont output file. The structure of the output file is as follows:

```

/Users/Jeff/Document
LAT:  0.00  LON:  0.00
  ID      TREAT  I  CD      J      CDECL CINCL  GDECL GINCL  BDECL BINCL  SUSC  M/V
-----
nw113a4    0.0  SD  0  2.37200 188.0  20.0   14.6  66.0   14.6  66.0    73  0.0
nw113a4   100.0  SD  0  2.42400 186.1  22.3   11.5  68.7   11.5  68.7    73  0.0
nw113a4   200.0  SD  0  2.50500 187.3  22.3   14.4  68.4   14.4  68.4    71  0.0
nw113a4   300.0  SD  0  2.52900 186.1  22.9   11.9  69.3   11.9  69.3    71  0.0

```

The header may contain an arbitrary number of lines but the end of the header is denoted by underlines. The columns are:

TREAT = treatment level

I = Instrument code

CD = CSD (circular standard deviation)

J = Intensity in the specified units

CDECL, CINCL = declination, inclination in sample coordinates

GDECL, GINCL = declination, inclination in geographic coordinates

BDECL, BINCL = declination, inclination in tilt corrected coordinates

SUSC = susceptibility

M/V = mass or volume (not implemented)