Thellier_GUI Tutorial

December 31, 2012

1 Introduction

This tutorial describes the Thellier_GUI and its embedded tools. Detailed explanation on the algorithms and methods of calculations can be found in Shaar and Tauxe (2013). The GUI was designed for Mac users, and it supports also PC and Linux platforms. The GUI is part of PmagPy software. It is a Python open code, and can be downloaded from PmgPy homepage (`http://earthref.org/PmagPy/cookbook/`).
The Thellier_GUI is a tool for viewing, analyzing, and interpreting the results of Thellier-type experiments. The supported protocols are : ZI (the "Coe protocol", Coe, 1967); IZ (the "Aitken et al., 1988), and IZZI (Tauxe and Staudigel 2004). Any other protocols will be supported on demand.
The required input of the program is measurements data file converted to MagIC format. For details on the MagIC format see `http://earthref.org/PmagPy/cookbook/` (Chapter 3). For support in converting measurements files to MagIC format contact Ron Shaar (rshaar@ucsd.edu) or Lisa Tauxe (ltauxe@ucsd.edu).

This tutorial is arranges as follows: In section 2 the front panel is described. In section 2 we provide explanation of all the options in the menu bar arranged in the order of their appearance.

2 Options and tools

The GUI includes the following options:

- graphical display of the data: Arai plot, Zijderveld plot, equal area plot, M-T plots, TRM acquisition plots.
- calculating remanence anisotropy tensors.
- calculating non-linear TRM effects.
- manual interpretation of specimens and samples by choosing temperature bounds for best-fit line.
- automatic procedure for calculating paleointensities using given experimental requirements (i.e. selecting criteria, and method of sample mean calculation).
- calculating paleointensity statistics.
- producing tables with the results for publishing.
- producing figures of Arai/Zijderveld/Equal-area plots for publishing.
- producing paleointensity curves: field intensity or VADM versus age.
- a built-in field-test (Thellier optimizer).

3 Thellier_GUI panel

select specimen window:

- **Specimen:** choosing a specimen from a list of all the specimens sorted by name.
- **previous/next:** buttons to move forward and backward in the specimens list.

select temperature bounds window:

- **T min/T max:** buttons to manually select temperature bounds.
- **save/delete:** save or delete currently displayed interpretation.

specimen results:

- **B_lab:** laboratory field in units of μT.

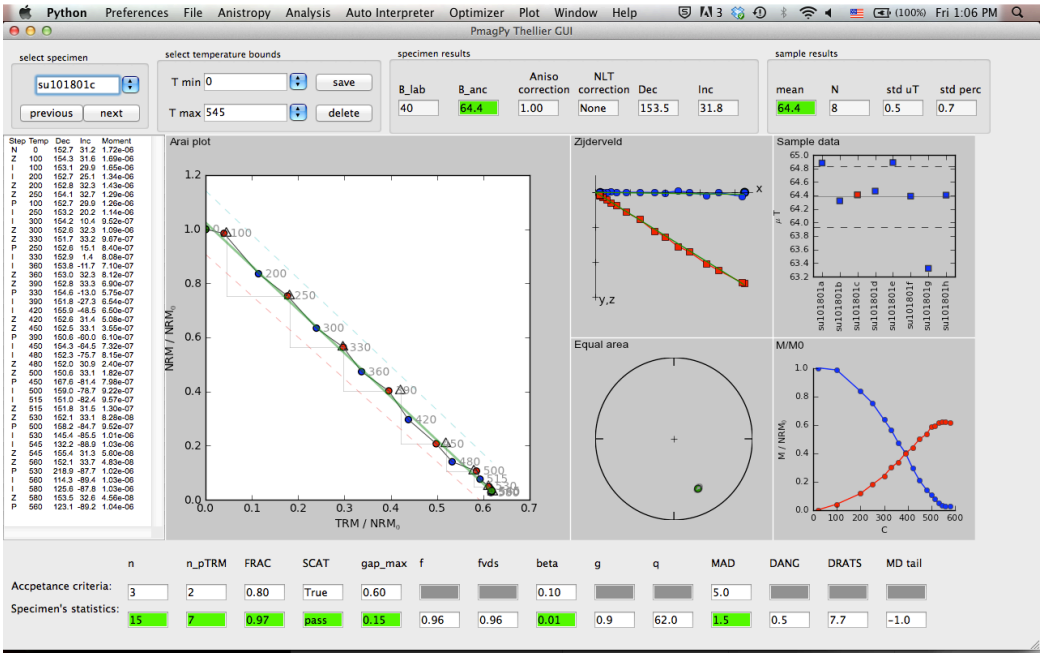

Figure 1: Thellier_GUI main panel

- **B_anc:** specimen's paleointensity in units of μT.
- **Aniso Correction:** anisotropy correction factor.
- **NLT Correction:** Non-Linear TRM (NLT) correction factor.
- **Dec/Inc:** Ancient declination/inclination calculated by PCA of the NRM in the selected temperature bounds.

sample results:

- **mean:** sample mean in units of μT.
- **N:** number of specimens in the sample used for calculating the mean, in units μT.
- **std uT:** standard deviation of the sample mean.
- **std perc:** standard deviation of the sample mean decided by the mean, units of percentage.

main panel:

- **measurements text panel:** four columns listing the measurement data: Step: "N" for NRM, "Z" for zero field step, "I" for infield step, "P" for pTRM check, and "T" for tail check. Temp: temperature in C
  Dec: declination
  Inc: inclination
  Moment: magnetic moment in units of Am^2

- **Arai plot:** Arai plot normalized by NRM_0. blue circles are zero field steps, red circles are infield steps, triangles are pTRM checks, blue squares are tail checks. Temperatures are displayed near data points. pTRM checks and tails checks are connect to the temperature in which they were carried out. Temperature bounds and best fit line are marked in green. 'SCAT box' is marked with dashed lines.

- **Zijderveld plot:** A Zijdrveld plot of the NRM step. The x axis is rotated to the direction of the NRM .blue is the x-y projection, red is x-z projection.

- **Equal area plot:** An equal area projections of the NRMs (circles) and the pTRMs (triangles). solid symbols are positive inclination. open symbols are negative inclinations.

- **Moment-temperature plot:** NRMs are in blue, pTRMs are in red.

- **sample data:** If at least two specimens have a saved interpretation, then their values are displayed on this plot. The mean $\pm$ standard deviation of the mean are marked as horizontal lines. The current specimen in marked in red.

paleointensity statistics:

- The bottom of the main panel include the values of the paleointensity statistics. The first line is the threshold values (empty if N/A). The second line is the specimen's statistics. For details on each of the parameters see Appendix A1 in Shaar and Tauxe (2012).

4 Thellier_GUI Menu bar

Menu bar: Preferences

- **Set preferences:** Open a dialog window for customizing the display of the GUI.
  - **GUI appearance:** change the size of the display. Default is 1 (not supported yet - to be done).
  - **Arai plot:** switching on/off the temperatures display and the arrow connecting the pTRM-check (and tail check).
  - **Zijderveld plot:** switching on/off the temperatures display .
  - **equal area plot:** switching on/off the temperatures display, and the pTRM directions (i.e. the triangles).
  - **non-linear TRM plot:** As there is only room for 5 plots in the GUI, the user can choose which plot to show in the top right corner of the GUI: TRM acquisition experiment, and M/M0 plot.

When clicking on the OK button, a file dialog will appear, the preference file must be saved in PmagPy folder.

Menu bar: File

- **Open MagIC project directory:** Open a dialog window for choosing a new project directory. A project directory must includes a file called magic_measurements.txt with all the measurements converted to MagIC format.
- **Add a MagIC project directory:** Add additional MagIC directories to the current display.
- **Open MagIC measurement file:** Open a dialog window for choosing a new magic measurement file. This file can have any name, but it must be a MagIC formatted measurement file.
- **Open all MagIC project directories in path**. Open a dialog window for choosing a directory. All the folders in this directory are inspected, and all the MagIC folders (A folder with a file named magic_measurements.txt) are added to the GUI. This option is useful when compiling together data from different sources.

- **Save plot:** save the current display of the Arai plot, Zijderveld plot, Equal area projection, and M-t plot. The default options for saving the figures are pdf,svg, and eps. To save in another format the appropriate suffix should be added to the file name (python supported formats are emf, eps, pdf, png, ps, raw, rgba, svg, svgz)

Menu bar: anistropy

- **Calculate anisotropy tensors:** The program calculates the anisotropy tensor. The supported measurement protocols are: ATRM in six positions (with options of baseline measurement and alteration check), AARM in 9 or 15 positions (see Tauxe, 2010 for details). A baseline measurement for each warm step is required. The program calculates the 6-element anisotropy tensor, eigenvectors, eigenvalues, and F-tests. The results are listed in MagIC files called "rmag_anistropy.txt" and "rmag_results.txt". The log file is saved in rmag_anisotropy.log. The program uses some health tests to distinguish between anisotropic and statistical isotropic specimens:
  - **F-test:** if the F-test is less than the 95% threshold value for anisotropy, then a warning will appear in the rmag_anisotropy.log, and the anisotropy tensor is set to an identity matrix.
  - **alteration check** - atrm only (optional): The threshold value is given in units of percentage ($100 \cdot (M_1 - M_2)/max(M_1, M_2)$), where M_1 is the ATRM measurement and M_2 is the alteration check measurement. If the alteration check exceeds the threshold value, then an Error message will appear in the log file, and the anisotropy tensor will be set to identity matrix. If no value is inserted by the user in the window, then the alteration check is ignored.
  - **Antiparallel diff** - atrm only (optional): The threshold value is given in units of percentage ($100 \cdot (M_1 - M_2)/max(M_1, M_2)$), where M_1 is an ATRM measurement and M_2 is ATRM measurement in the antiparallel direction (i.e. +x and -x, +y and -y, +z and -z). If the Antiparallel diff exceeds the threshold value, then an Error message will appear in the log file, and the anisotropy tensor will be set to identity matrix. If no value is inserted by the user in the window, then this check is ignored

- **Show anisotropy calculation Warining/Errors:** The warnings and errors of the anisotropy tensor calculation. These errors/waring are also listed in " rmag_anisotropy.log".

Menu bar: Analysis

- **Acceptance criteria:**
  - Set Accpetance criteria to default: reset acceptance criteria to default values.
  - Change acceptance criteria: open a dialog box for setting acceptance criteria and sample's calculation methods . For details on each definition in this dialog box see Appendix A1 in Shaar and Tauxe (2012).
  - Import criteria file: open criteria from an existing an pmag_criteria.txt file.

  The acceptance criteria are saved in a MagIC file called "pmag_criteria.txt".

- **Import previous interpretation ('redo file'):** open a previously saved "redo file" that includes previous interpretations. The "redo file" is tab-delimited txt file with three fields. the first field is specimen name, the second is minimum temperature bound (in Kelvin, whereas NRM is 273), and the third field is the maximum temperature bound.

- **Save current interpretation:** save the current interpretations and create the following files in the project directory:
  - thellier_GUI.redo: A redo file that includes the temperature bounds of all the saved interpretation. wee above.
  - thellier_GUI.specimens.txt: A text file that includes the interpretation of all the saved specimens, and the values of their paleointensity statistics. The first three lines are the acceptance criteria defined at the time the data was saved. The rest of the file is a list of the specimen's data sorted by specimen's name. The last columns is Pass/Fail - if the specimen fail the criteria, the list of the failed parameters is given. This file is useful for preparing the final table for publication.

  - thellier_GUI.samples.txt: A text file that includes the statistics of the samples. All the samples are included in this list regardless the sample's acceptance criteria. This file is useful for preparing the final table for publication.

- **Clear all current interpretation:** clear all the saved interpretations.

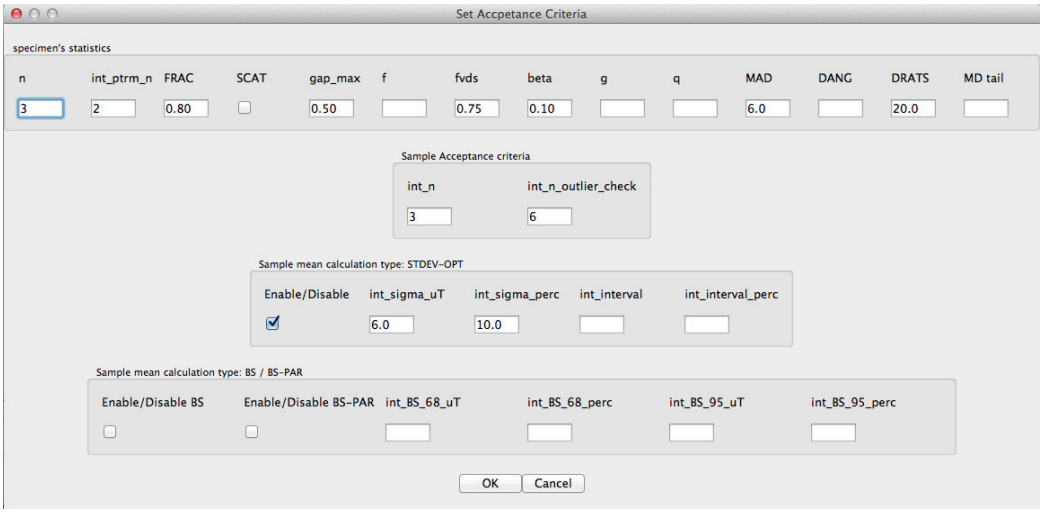

Figure 2: Setting acceptance criteria and sample's mean calculation method. For explanation on each parameter see Appendix in Shaar and Tauxe (2012)

Menu bar: Auto Interpreter

- **Run Thellier auto interpreter:** Run *Thellier_auto_interpreter* using the current acceptance criteria and sample's mean calculation method.

- **Open auto interpreter output files:** Open a dialog window to see the Thellier_interpreter output filed (see below).

- **Open auto interpreter Warnings/Errors:** Open a window with Warning and Errors of the Thellier_auto_interpreter (see below).

Menu bar: Optimizer

- **Run Thellier Optimizer:** open a series of dialog windows for running thelier_optimizer_2D.

5 Thellier auto interpreter

Thellier_auto_interpreter output files

The Thellier_auto_interpreter is an automatic interpretation of the data. The guiding principles for the algorithm are the paleointensity statistics saves in pmag_criteria.txt. For the definition of each parameter see Shaar and Tauxe (2012).
Thellier_auto_interpreter produces the following output files in a directory named "thellier_interpreter":

- **thellier_interpreter.log**
  A log file. Each line in the log file starts with-I- (Information), -W- (Warning), or -E- (Error). The first massages include general messages and acceptance criteria. Then, each trial (a pair of temperature bounds) is given, for example:
  -I- specimen su100301a (200-500) FAIL on: specimen_frac= 0.799844,
  -I- specimen su100301a (200-515) PASS
  The end of the log files include the samples mean calculation.

- **thellier_interpreter_specimens_bounds.txt:**
  A summary file that lists the minimum and the maximum of the 'acceptable interpretation' (for specimens that have at least one 'acceptable' interpretation). The first four lines in the file are the acceptance criteria used. The next line is a header, and then the data for all the specimens: sample name, specimen name, anisotropy correction factor, anisotropy correction type, NLT correction factor, lab field (uT), minimum 'acceptable' interpretation, maximum 'acceptable' interpretation, and Warning. This file is useful for inspecting the behavior of the dataset in general.

- **thellier_interpreter_all.txt** A file that contains all the accepted interpretations (temperature bounds, paleointensity values, and statistics) for all the specimens. There may be more than one 'acceptable' interpretation for each specimen.

- **thellier_interpreter_STDEV-OPT_specimens.txt:**
  A list of the specimen's interpretations that were chosen by STDEV-OPT algorithm to produce the sample's mean, and the paleointensity statistics. This information is useful for generating a table for a publication.

- **thellier_interpreter_STDEV-OPT_samples.txt**:
  A summary file with all the samples that passed the criteria. The first four lines are the acceptance criteria used in the interpretation. Then, the following information is given: sample name, number of specimens used in the calculation, the paleointensity in units of μT, standard deviation of the sample mean in units of μT, standard deviation divided by the mean in units of %, Interval of accepted sample means in units of μT, Interval of accepted sample means divided by the sample's mean in units of %, Warning.This information is useful for generating a table for a publication.

- **thellier_interpreter_STDEV-OPT_redo** A "redo" file (see "analysis" menu option). This is a tab-delimted text file with three fields: the first field is specimen name, the next is minimum temperature bound (in Kelvin, whereas NRM is 273), and the third field is the maximum temperature bound.

- **thellier_interpreter_BS_samples.txt** A summary file with all the samples that passed the criteria in the bootstrap method (only if BS method is used for sample calculation).

- **thellier_interpreter_BS-PAR_samples.txt** A summary file with all the samples that passed the criteria in the parametric bootstrap method only if (BS-PAR method is used for sample calculation).

6 Thellier_optimizer_2d

Thellier_optimizer_2d is a built-in self test for the consistency of the data among 'test groups' (see Shaar and Tauxe, 2012 for details).
The Thellier_optimizer_2D requires definition of **'test groups'**, **'test functions'**, and **'fixed_criteria'**.

Test groups

Test groups include samples that are expected to give similar paleointensity results. The test groups are defines in an "er_sample" file (tab delimited). The first line in this file is:
tab er_samples.
The next line is the header, which must include at least the following:
er_sample_name er_group_name.

(Another header "comments" is recommended).
The rest of the lines are the sample names and the group names. (see the example below).

fixed_criteria

fixed_criteria are the list of threshold values for paleointensity statistics, not including frac and β. When selecting Optimizer $\rightarrow$ Run Thelllier Optimizer, a criteria dialog window (Figure 2) is opened in order to set the "fixed_criteria".
The fixed criteria are saved in a file named "pmag_fixed_criteria.txt" in a folder named "optimizer".

Thellier_optimizer_2d Dialog window: Test functions and run definitions

Figure 3 show the Thellier_optimizer_2d dialog window.
The upper control buttons select the range of β and FRAC.
test functions are entered in the main text panel.
The button "Check function syntax" is used to check if the functions can be compiled. If the functions are valid the text window will show "PASS", otherwise it shows "FAIL".
The button "choose optimizer group file" opens a file dialog for choosing the er_sample file with the 'test groups'.
The button "Run optimizer" starts the optimizer.

Thellier_optimizer_2d output files

All Thellier_optimizer_2d output files are saved in a folder named "optimizer" in the project directory. Te output files are as follows:

- **optimizer_functions.txt:** This file saves the test functions as entered in the Thellier_optimizer_2d dialog window.
- **pmag_fixed_criteria.txt:**This file saves the fixed_criteria used by Thellier_optimizer_2d.
- **thellier_optimizer.log**: a log file.
- **thellier_optimizer_interpretation_log.txt.gz**: this log file includes information on all the iteration over all the specimens using all the sets of criteria. Since this is a big file, it is saved in a gzip compressed format.
- **optimzer_results.txt**: a summary files of the optimizer results. Each line includes the following: FRAC, beta, test-site name, name of sam-

ples that passes separated by :, sample's paleointensities in microT, arranged in the same order as samples' names, test-site mean, test site standard deviation, test site standard deviation divided by its mean.

- **pdf**: pdf files with colormaps showing the results of the test functions.
- **svg**: svg files with colormaps showing the results of the test functions.

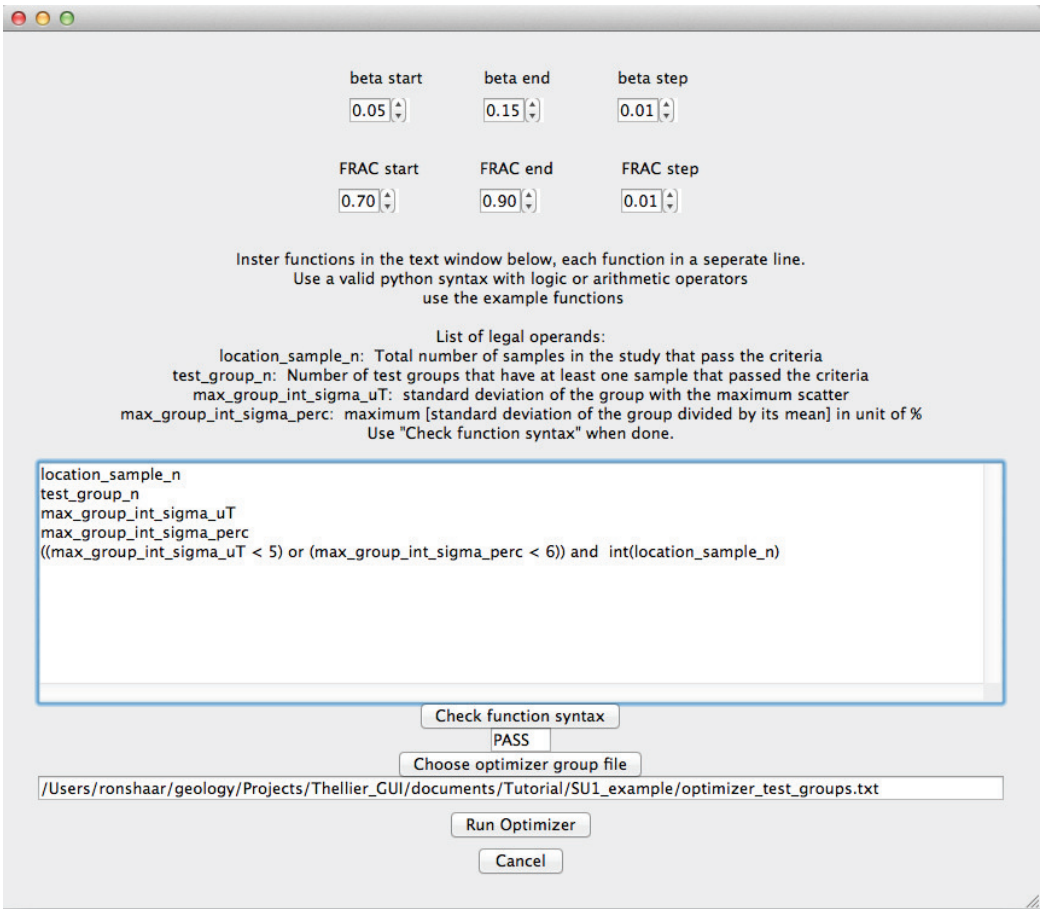

Figure 3: Thellier_optimizer_2D dialog window

7 Tutorial by example

7.1 Getting started

- If PmagPy is not installed yet on your computer follow the instructions in MagIC cookbook chapters 1 and 5: `http://earthref.org/PmagPy/cookbook/`).
- If PmagPy is installed, download the latest version of PmagPy from `https://github.com/ltauxe/PmagPy`.
- Download example data files for PmagPy from `http://earthref.org/PmagPy/Datafiles_2.0.zip` There are two folder located under the folder "thellier_gui": SU1_example and Tauxe_2006_example.

7.2 Case study 1: SU1_example

There are two ways to lounch the thellier_gui. From the MagIC GUI or from the Terminal window (Mac) command window (PC):

- **From the MagIC gui**: From the menu bar select "Analysis and Plots" → "Thllier type experiments" → Thellier guy program.
- **From the terminal window / Command window**: Open a new Terminal window (Mac) or command window (PC). Type "thellier_gui.py" and press enter. A choose directory dialog window will appear. Select the SU_1 project directory. click on the "choose" button.

7.2.1 Setting appearance

From the menu bar choose "Preferences" in order to set the desired appearance (see section 4). For example, uncheck the "show temperature" box in the "Zijderveld plot" static box. Click "OK". A message will appear telling you that you should save this file in the PmagPy directory. Click Ok, and save the new "thellier_gui_preferences.py" in the PmagPy folder.

7.2.2 Calculating anisotropy tensor

From the menu bar choose "Preferences" choose Anisotropy → calculate anisotropy tensor. A window will appear. Set the alteration check to 6% (write 6 in the window). and the anti-parallel difference to 6%. Click OK. New files names "ramg_anistropy.txt" and "rmag_results.txt" will be created. To see Errors and warning choose "Anisotropy" → Show anisotropy calculation Errors/Warnings. Errors are marked in red and must be carefully inspected.

7.2.3 Manual interpretation

Manual interpretation is the conventional approach of selecting temperature bounds for each specimen. In this example we manually interpret one sample, su100601.

- Set acceptance criteria: From the menu-bar choose Analysis → Acceptance criteria → Change acceptance criteria. A criteria dialog box will appear.

- In the first line (specimen's statistics) set the following values: int_n=3, int_ptrm_n=2, SCAT=false (unchecked), gap_max=0.5, f_vds=0.75, beta=0.1, MAD=6, DRATS=20. delete the values in the other boxes (empty boxes).
  In the second line (Sample's acceptance criteria) set the following values: int_n=3. delete the value in the other boxes.
  In the third row (Sample mean calculation method: STDEV-OPT) check the Enable/Disable box, and set the following values: int_sigma=6, int_sigma_perc=10. Delete values in the other boxes. click on the OK button.
  A message dialog will appear telling you the criteria that you chose are saved in a file name pmag_criteria.txt. The next time you will open the GUI in this project directory, these criteria will automatically be chosen. Click OK on the message box. The new acceptance criteria are now listed in the paleointensity statistics window at the bottom pf the main panel.

- Manual interpretation of sample su100601: choose specimens su100601a from the specimen list. choose temperature bounds from the Tmin/Tmax windows: 200 and 580. B_anc shows 60.2 in green, which means that

this interpretation passes the specimen's acceptance criteria. Now, change Tmax to 530. B_anc window change color to red, and also the fvds window (the row on the bottom of the GUI). This is an indication that the interpretation did not meet the criterion for fvds. Change Tmax to 580 (as before) and press "save" button. The interpretation in saved.

- Click on the next button to choose the next specimen (su100601b). Before analyzing this specimen, press on the "previous" button, so you can see that your previous interpretation is saved. click on "next" to return again to specimen su100601b. Find temperature bounds that pass the criteria (for example 200,580). Make sure that all colors are green, and click on the "save" button. Go over all the other specimens in the sample (su10060a to su100601g). you will find that three specimens can pass: a,c, and g. Look at the Sample data figure (top right) it shows the saved interpretation for all the specimens in the sample, and the mean ± standard deviation of the mean.

- To save all your interpretation into files, choose from the menubar Analysis → Save current interpretation. Three files will be generated in the project directory:
  1. thellier_GUI.redo (the temperature bounds for each specimen):
  su100601a 473 853
  su100601c 473 853
  su100601g 473 853
  (notice that the temperature bounds are in Kelvin)
  2. thellier_GUI.specimens.txt (the paleointensity statistics for each specimen - according to the headers. It is easy to view the content of this file using Exel):
  su100601a su100601 61.7 200 580 40.0 1.07 1.01 15 8 0.77 0.87 0.89 0.14 0.02 N/A 0.63 N/A 5.11 4.14 PASS
  su100601c su100601 54.4 200 580 40.0 0.94 N/A 15 8 0.60 0.78 0.79 0.23 0.01 N/A 5.19 N/A 2.51 1.33 PASS
  su100601g su100601 58.4 200 580 40.0 1.00 1.01 15 8 0.70 0.83 0.85 0.19 0.02 N/A 2.80 N/A 3.12 1.96 PASS
  3. thellier_GUI.samples.txt (the paleointensity statistics of the samples):
  er_sample_name sample_int_n sample_int_uT sample_int_sigma_uT sam-

ple_int_sigma_perc
su100601 3 58.2 3.0 5.1

- You can save the Arai plot (or any other plots) from the File menu. Choose file → Save Plot → Save Arai plot. A file dialog window will appear. You can change the format of the figure in the bottom tab (pdf, svg, or png), but you can also save as other format by adding the appropriate suffix to the file name.

- close the GUI: File → Quit.

- Re-open the GUI like before (by writing the command "thellier_gui.py" in the terminal box) and choose the same working directory (SU1_example). Notice, that the criteria that you set before are automatically used. To import your previous interpretations and continue working on this dataset choose from the menu bar Analysis → import previous interpretation. Choose thellier_GUI.redo and click on the 'open' button.

7.2.4 Automatic interpretation - *thellier_auto_interpreter*

Instead of trying to find manually the most appropriate temperature bounds, the thellier_auto_interpreter allows a fast and consistent way to choose the temperature bounds for the specimens. For details see Shaar and Tauxe (2012).

- We will use the same acceptance criteria, which were set on the previous section..

- Choose from the menu bar Auto interpreter → Run Thellier auto interpreter. The interpreter will run approximately 30 seconds. When its done, a message window will appear saying that the interpreter finished successfully (if not, check for errors in the terminal window, or in a file name "thellier_interpreter.log" located in a folder name "thellier_interpreter". If the issue cannot be resolved send e-mail with the description of the problem to rshaar@ucsd.edu). Click OK in the message window.

- The automatic interpretations are automatically saved, and we can review them on the Arai plots. Lets look, for example, on the sample

we interpreted manually: su100601. Choose specimen su100601a from the specimens list. In a first look the choice seems strange because the automatic interpretation chose temperature bounds 0 and 580. A choice between 200 and 580 may seem more reasonable as it provides an nearly straight line. The sample data figure explains this issue. The thellier_auto_interpreter chooses the interpretations that minimize the standard deviation of the sample's mean. Six specimens from this sample passed the criteria, and the value of su100601a is much higher than the remaining five. So, the thellier_auto_interpreter chose the 'acceptable' interpretation with the shallowest slope. Go over the other specimens in the sample, and review the automatic interpretation. If you want, you can change the automatic interpretation, and save your own "manual" interpretation by choosing Analysis → Save current interpretation. Notice, that the output of thellier_auto_interpreter is sensitive to the choice of the acceptance criteria, and different criteria may lead to significantly different final results.

7.2.5 Choosing the optimal criteria - *thellier_optimizer_2D*

Shaar and Tauxe (2012) discuss a method to choose the optimal specimen's acceptance criteria. Here, we follow the example given in this paper. Shaar and Tauxe (2012) suggested using seven statistics for specimen's acceptance criteria. The choice of four of which is trivial, and the remaining three are MAD, FRAC and β. The thellier_optimizer_2D helps finding the optimal values for FRAC and β. The thellier_optimizer_2D required three types of inputs: 'fixed_criteria", "test_groups", and "test_samples", as decried below:

- The test groups are defined in an "er_sample" file. An example for this file is given in working folder SU-1 named "optimizer_test_groups.txt". Open this file in Excel to understand its syntax. The first line is a general header. The rest of the file include sample name, group name, and comments.

- To run the optimizer choose from the menu bar Optimizer → Run Thellier optimizer. click OK in the message dialog. The first step is setting the 'fixed_criteria". We choose for the specimen's criteria: n=3, int_ptrm_n=2,SCAT=checked, gap_max=0.6, MAD=5.0. We choose for the sample's criteria:int_n=3, int_n_outlier_check=6, EnableSTDEV-

OPT, int_sigme_uT=5, int_sigma_perc=6. The rest of the boxes should be empty. click OK. click OK on the message window that will appear.

- The thellier_optimizer_2D dialog window will appear. The first two rows of controls for choosing the range for β and FRAC. choose beta from 0.05 to 0.15 in steps of 0.1 and FRAC from 0.7 to 0.9 in step of 0.02.
  Inert the following functions to the text panel:
  study_sample_n
  max_group_int_sigma_uT
  ((max_group_int_sigma_uT <= 5) or (max_group_int_sigma_perc <= 6)) and int(study_sample_n)
  click on the "Check function syntax" button. If there are no typos, then the text box below the button should be PASS.
  click on the "Choose optimizer group file" button. A file dialog window will appear. choose the file "optimizer_test_groups.txt". Click the button "Run Optimizer" to start. The runtime using these parameter is about 8 minutes. ‘

- All the output files of the optimizer are saved in a folder named "optimizer" (see section 4.4). Compare the figures in the 'pdf' folder with Figure 7 in Shaar and Tauxe (2012).

- The figure in optimization_function_2.pdf suggest using β $\leq$0.10 and FRAC $\geq$0.79. Set these values as acceptance criteria, and run thellier_auto_interpreter.

7.3 Case study 2: DSDP/ODP submarine basaltic glass collections

This case study follows the second case study in Shaar and Tauxe (2012).

7.3.1 thellier_auto_interpreter

- Open a new Terminal window. Type "thellier_gui.py" and press enter. A choose directory dialog window will appear. Select the project directory: Tauxe_2006_example. click on the "choose" button.

- Set the acceptance criteria: From the menu-bar choose Analysis → Acceptance criteria → Change acceptance criteria. A criteria dialog box will appear. In the first line (specimen's statistics) set the following values: n=2, int_ptrm_n=2, SCAT=false (unchecked), gap_max=0.5, f_vds=0.2, beta=0.1, MAD=15, DRATS=30, DANG=15. delete the values in the other boxes (empty boxes). For the sample's acceptance criteria choose: int_n=2, Enable STDEV-OPT, int_sigme_uT=5, int_sigma_perc=15. Click OK.

- Choose from the menu bar Auto interpreter → Run Thellier auto interpreter. The automatic interpretation takes about 1.5 minutes.. A message dialog will appear when the program is done. With the "previous" and "next" buttons review the automatic interpretation.

7.3.2 Choosing the optimal criteria - *thellier_optimizer_2D*

- To run the optimizer choose from the menu bar Optimizer → Run Thellier optimizer. click OK in the message dialog. The first step is setting the 'fixed_criteria". We choose for the specimen's criteria: n=3, int_ptrm_n=2,SCAT=checked, gap_max=0.6, MAD=10.0. We choose for the sample's criteria:int_n=2,, EnableSTDEV-OPT, int_sigme_uT=5, int_sigma_perc=15. The rest of the boxes should be empty. click OK. click OK on the message window that will appear.

- The thellier_optimizer_2D dialog window will appear. The first two rows of controls for choosing the range for β and FRAC. choose beta from 0.05 to 0.27 in steps of 0.02 and FRAC from 0.30 to 0.86 in step of 0.02.
  Inert the following functions to the text panel:
  location_sample_n
  max_group_int_sigma_uT
  ((max_group_int_sigma_uT <= 5) or (max_group_int_sigma_perc <= 15)) and int(location_sample_n)
  click on the "Check function syntax" button. If there are no typos, then the text box below the button should be PASS.
  click on the "Choose optimizer group file" button. A file dialog window will appear. choose the file "er_test_groups.txt". Click the button "Run Optimizer" to start. The runtime using these parameter is about 20 minutes. Compare the results with Fig 10 in Shaar and Tauxe (2012)