

# Memorandums on Old Type Programs with GMT 6 (GMT 5) (eight programs contained in pmagm302.tar.gz)

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February 12, 2025

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# 1 System environment and installation

## Linux, gcc, and GMT

Eight programs contained in "pmagm302.tar.gz" use classic mode of GMT 6 tools (Wessel et al. 2019) via system calls to draw PostScript figures. The classic mode of GMT 6 modules are equivalent to those of GMT 5 (Wessel et al. 2013). Hence, the programs work only on the Linux system in which either GMT 6 or GMT 5 are installed. The programs also use the PostScript viewer Evince which has a function to watch file, i.e. redraw the figure if the PS file is altered. They are now working on "Ubuntu 22.04" in which "gcc 11.4.0", "evince 42.3", and "GMT 6.3.0" are installed. Other Linux environment should be OK as long as GMT 6 (or GMT 5) and Evince are installed. Some of the numerical algorithm used in the programs are adapted from those of Press et al. (1992).

Here, only the C sources are provided, which should be compiled by gcc. The programs are working on terminals in which TC shell "tcsh" is used as a login shell, but using other shell is probably OK. Use these programs at your own risk, although any problems have never been encountered. Nevertheless, you should be familiar with the minimum level of Unix commands such as "ps" and "kill" in case freeze of program occurs and "Ctrl+C" does not work.

## Installation

Put "pmagm302.tar.gz" at a certain directory and extract by

```
tar xvfz pmagm302.tar.gz
```

"pmagm302" directory is created and enter to this directory by

```
cd pmagm302
```

Then compile the source files by

```
make
```

Executable files will be created under "pmagm302/bin" directory. Copy them to your usual binary directory such as /usr/local/bin, etc. Each source directory, such as "pmagm302/pdemag-src", contains one or more test data files which are usually named as "t-\*.d" (some exceptions are "\*.dmg" or "\*.drc").

## Starting the program

Typing only the program name shows its usage to the display as the following example.

```
Usage: histo file [-Ww -Xmin/max -Ymin/max -C[N][L] -S -H]
```

Starting the program with the option "-H" (or, "-h") shows a simple help message as the example below. The message can be cleared by pressing "Q" (or, "q").

```
HELP MESSAGE OF HISTO
```

```
  Histogram of scalar data V1.21, H. Tanaka, 2021,2018.
```

```
  Optional approximation by normal or log-normal distribution curves  
  and statistical test of Chi-2 and Kolmogorov-Smirnov tests.
```

```
Usage:
```

```
  histo file [-Ww -Xmin/max -Ymin/max -C[N][L] -S -H]
```

```
Options:
```

```
  -Ww          -- bin width w
```

```
  -Xmin/max    -- range of min and max for x-axis
```

```
  -Ymin/max    -- range of min and max for y-axis
```

```
                (options X/Y alter only the graph appearance)
-C[N][L]  -- curves of normal(N)/log-normal(L) distributions
-S        -- Chi-2 and K-S tests to normal/log-normal
           distributions (depends on params in C-option).
-H        -- help message
```

Input file:

```
# comment line with # (or %) at the beginning at any places
# one datum per line at 1st column
x1 [y1, z1, .. -- any extra data are ignored]
x2
.
.
```

Output file:

```
PS graph of histogram is created with the name "file.ps".
When S option, results of statistical test are written to stdout.
(Press Q to Quit)
```

In the following sections, typical application of the programs are illustrated by using the test data files "t-\*.d" contained in each source directory "pmagm302/\*-src".

## 2 Statistical test: Test of distribution

### 2.1 Test of one data set by histo

"histo" compares a data set to normal or log-normal distributions based on the Chi-square and Kolmogorov-Smirnov tests (ex., Hoel 1971).

The test data files t-histoN.d and t-histoL.d include normal and log-normal distributed random data, respectively. Supposed mean and standard deviation are 60 and 20 for both data, but in the latter  $y = \log x$  is distributed as the normal distribution. Recommended way to use "histo" is as the followings. First type as

```
histo t-histoN.d
```

Then overall statistics are shown to the display as

```
Histogram and distribution test of t-histoN.d.
```

```
PS file: t-histoN.ps
```

N	Mean	Stdev	Max	Min
285	61.87	20.99	116.6	10.43

As the PostScript figure of the histogram is created, open it using Evince as

```
evince t-histoN.ps &
```

Using the ability of Evince to watch the PS file renewed, you can rerun "histo" with various options and see the redrawn figure as

```
histo t-histoN.d -Cnl -s >result.txt
```

You see the redrawn histogram with two fitted curves of normal and log-normal distributions. Results of the statistical test written in result.txt are below.

```
Histogram and distribution test of t-histoN.d.
```

```
PS file: t-histoN.ps
```

N	Mean	Stdev	Max	Min
285	61.87	20.99	116.6	10.43

```
Chi-square Test for normal distribution.
```

nbin	df	Chi2	p
4	1	1.358	0.2439
5	2	3.965	0.1377
6	3	0.958	0.8114
7	4	5.046	0.2826
8	5	2.747	0.7389
9	6	3.095	0.7969
10	7	5.632	0.5834
11	8	2.660	0.9539
12	9	10.537	0.3088
13	10	4.786	0.9050
14	11	8.116	0.7029
15	12	10.000	0.6160
16	13	7.211	0.8910
17	14	15.095	0.3717
18	15	8.621	0.8965
19	16	21.200	0.1710
20	17	16.544	0.4857

Mean p	Stdev of p
0.5822	0.2822

Kolmogorov-Smirnov Test for normal distribution.

```
D      p
0.0430 0.6582
```

Chi-square Test for Log-normal distribution.

```
N      Mean      Stdev
285    62.64      26.63

nbin df      Chi2      p
  4   1    15.702  0.0001
  5   2    16.807  0.0002
  6   3    23.526  0.0000
  7   4    19.242  0.0007
  8   5    27.449  0.0000
  9   6    24.632  0.0004
 10   7    33.772  0.0000
 11   8    39.404  0.0000
 12   9    39.168  0.0000
 13  10    33.432  0.0002
 14  11    36.116  0.0002
 15  12    30.842  0.0021
 16  13    32.923  0.0018
 17  14    36.211  0.0010
 18  15    33.632  0.0038

Mean p      Stdev of p
0.0007      0.0011
```

Kolmogorov-Smirnov Test for Log-normal distribution.

```
D      p
0.0972 0.0085
```

Although it is obvious, the null hypothesis that the data are from a log-normal distribution was rejected. In the Kolmogorov-Smirnov test, estimation of the significance probability  $p$  is based on the approximation formula of Press et al. (1992).

## 2.2 Test of two data sets by histo2

"histo2" compares two data sets whether they are different distributions by using the Chi-square and Kolmogorov-Smirnov tests.

The two test data files t-histoN.d and t-histoL.d are the same as those in histo-src directory. Another data file t-histoN2.d includes another series of random data of normal distribution with the same mean and standard deviation. To see the two histograms of the data sets, run "histo2" without any options as

```
histo2 t-histoN.d t-histoL.d
```

Then overall statistics of the two data sets are shown to the display as

Histograms and common distribution test of t-histoN.d and t-histoL.d.

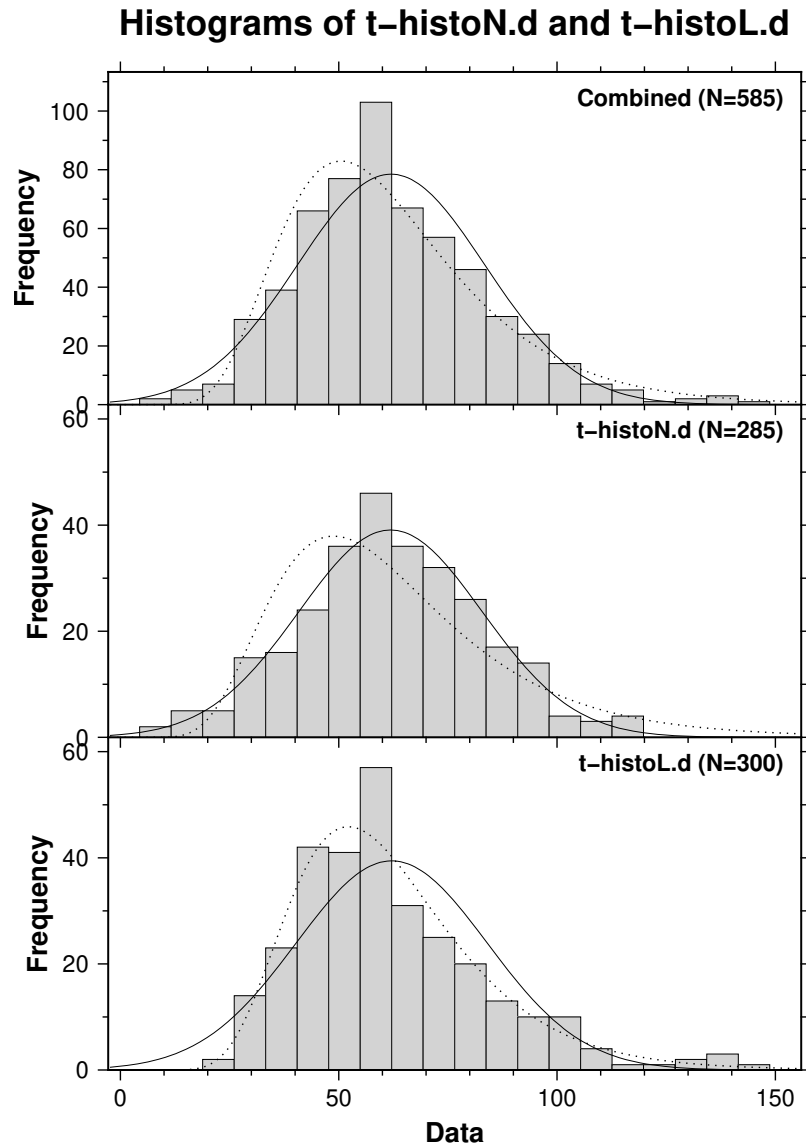
```
PS file: t-histoN-t-histoL.ps

      N      Mean      Stdev      Max      Min      File
Data1: 285    61.87    20.99    116.6    10.43    t-histoN.d
Data2: 300    62.13    21.90    142.7    25.46    t-histoL.d
```

You can see the PS file with PostScript viewer Evince. To carry out the statistical tests, to draw fitted curves of normal/log-normal distributions, and to add another histogram of the combined data, type as

```
histo2 t-histoN.d t-histoL.d -cnl -t -s >result2.txt
```

and the next figure is obtained.



Results of the statistical test written to result2.txt is quite lengthy because with “-Cnl” option each data set was compared to both normal and log-normal distributions. In the followings, only the initial part of the output is shown, in which the null hypothesis of the same distribution was not rejected with the significance level of 5% in spite of different random sources of the data.

Histograms and common distribution test of t-histoN.d and t-histoL.d.

PS file: t-histoN-t-histoL.ps

	N	Mean	Stdev	Max	Min	File
Data1:	285	61.87	20.99	116.6	10.43	t-histoN.d
Data2:	300	62.13	21.90	142.7	25.46	t-histoL.d
Total:	585	62.00	21.44	142.7	10.43	--

Chi-square Test for a common distribution of two data.

nbin	df	Chi2	p
4	3	2.362	0.5007
5	4	5.816	0.2133
6	5	4.438	0.4882
7	6	9.534	0.1457
8	7	6.783	0.4518

9	8	11.946	0.1536
10	9	9.634	0.3809
11	10	15.135	0.1272
12	11	21.342	0.0300
13	12	14.314	0.2811
14	13	24.622	0.0259
15	14	23.400	0.0541
16	15	19.090	0.2097
17	16	35.486	0.0034
18	17	26.148	0.0718
19	18	34.556	0.0107
20	19	32.908	0.0246

Mean p    Stdev of p  
0.1866    0.1743

Kolmogorov-Smirnov Test for a common distribution of two data.

D	p
0.1039	0.0798

...

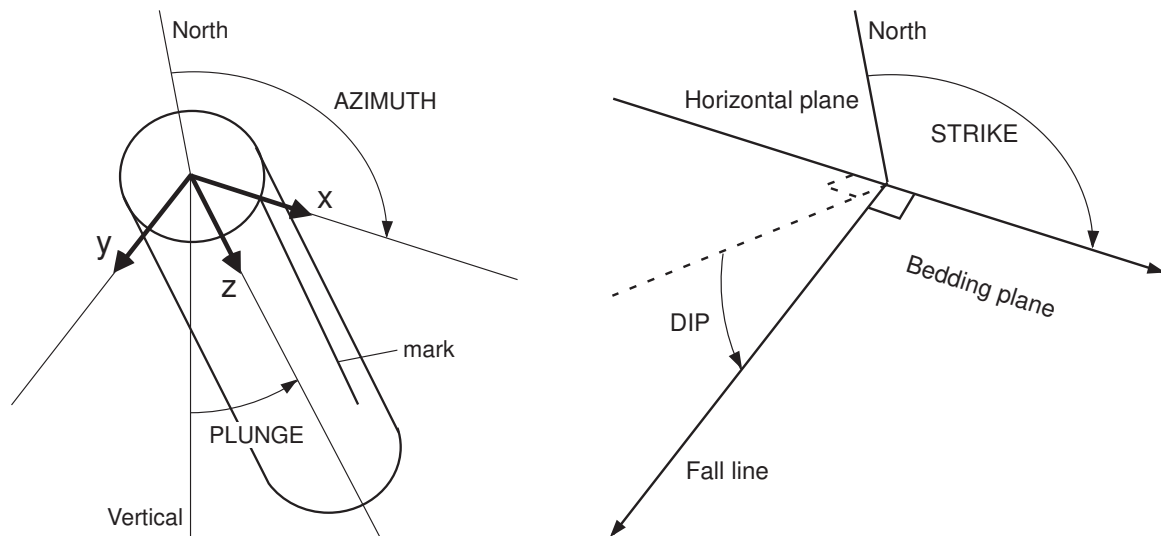
...

The rest is omitted.

...

### 3 Analysis of paleodirections

#### 3.1 Orientation and bedding tilt correction



Figures above illustrate the systems of core orientation and bedding attitude, which are used throughout the programs including those in another set "pmagt401.tar.gz".

In the orientation system (left figure), x-axis is in the horizontal plane. Azimuth of x-axis is measured clockwise from the north. Looking toward +x direction, y and z-axes are rotated clockwise by the angle plunge. This orientation system is applicable ONLY to the orientation device supplied by Natsuhara Giken.

For the bedding attitude and its tilt correction (right figure), a standard system is used. Bedding strike is measured clockwise from the north. Looking toward the measured strike direction, dip angle is positive when the bedding plane is inclined clockwise. Note that the bedding plane of (*strike*, *dip*) is equivalent to (*strike* + 180°, -*dip*).

#### 3.2 Three steps analyses of paleodirectional data

Paleodirectional data are analyzed in three steps according to the hierarchical treatment in paleomagnetism. "pdemag" calculates the sample-mean remanence directions, and then "pdirec" calculates the site-mean paleodirections and VGPs, and lastly "pstat" or "psvar" estimate the overall Fisher statistics. Naming of the data files is arbitrary with or without a file name extension. To avoid confusion, however, we use "\*.dmg" and "\*.drc" for the input files to "pdemag" and "pdirec", respectively. For the input files to "pstat" and "psvar", we use "\*.d".

Prepare the input data files to "pdemag" by a text editor (for users of Natsuhara Giken Spinner Magnetometer 2000, transfer programs "sp2m" and "\_sp2m" are available in "pmagt401.tar.gz"). The input files should be distinct to each site (ex., "site1.dmg", "site2.dmg", ... etc). Core orientation data can be omitted, in which case zero is assigned.  $\chi$ -step data can be included to each line. The file format is as the followings.

```
# site1.dmg -- name of this file (lines beginning with '#' are comments)
$ sample1-1 [azimuth plunge [strike dip]]
  step0 mag0 inc0 dec0 [chi0]
  step1 mag1 inc1 dec1 [chi1]
  ...
  ...
$ sample1-2 [azimuth plunge [strike dip]]
  step0 mag0 inc0 dec0 [chi0]
  step1 mag1 inc1 dec1 [chi1]
```



```
...
...
```

The output file from "pdemag" becomes the input file to "pdirec". When analyzing more than one site from multiple input files, you can assign the same output file so that it contains results from multiple sites as a group (ex., "groupA.drc"). You can also create several output files to discriminate different site groups (ex., "groupA.drc", "groupB.drc", ... etc). Before analyzing the "\*.drc" files by "pdirec", you should edit the file so that the site locations are included in the lines beginning with '\$' (they can be omitted for second and following sites if they are the same). The file format will be as the followings where the '#' line, Slat, and Slon are inserted by the user.

```
# groupA.drc -- name of this file
$ site1.dmg Slat Slon
sample1-1 inc1-1 dec1-1 ...
sample1-2 inc1-2 dec1-2 ...
...
...
$ site2.dmg [Slat Slon]
sample2-1 ...
sample2-2 ...
...
...
```

The output file from "pdirec" becomes the input file to the last analyses by "pstat" or "psvar". You can include results from several groups into one file. The followings are the file format which is common for both programs. The '#' line is inserted by the user.

```
# pmagstudy.d -- name of this file
$ groupA.drc
site1.dmg inc1 dec1 ...
site2.dmg inc2 dec2 ...
...
...
$ groupB.drc
siteB1.dmg ...
siteB2.dmg ...
...
...
```

### 3.3 Sample-level analysis by pdemag

"pdemag" analyzes results of step-wise demagnetization and determines the sample-level remanence directions. The algorithm of fitting a line or a great circle to the data is the principal component analysis (PCA) which is simplified from that of Kirschvink (1980). In the automatic mode, the PCA seeks only the remanence component in the highest steps. In the manual mode of PCA, however, any remanence components can be determined.

Three test data files, "site1.dmg", "site2.dmg" and "site3.dmg", are contained in the directory "pdemag-src". They are the data of normal, reversed and transitional directions, respectively, from the Taupo Volcano, New Zealand (Tanaka et al. 1996). The followings are typical procedure of the analysis.

```
pdemag site1.dmg
Progressive demagnetization from site1.dmg
NT10012AF
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q?
```

The PS (PostScript) figure of Zijderveld diagram is shown by "Evince". Type command **L** (or **I**) for the line fitting by PCA. The PS figure is redrawn with the best fitted line and the next message is shown on the display.

```
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q? l
Range,I,D,Mad,Thd: 0-80 -35.5 353.1 1.8 0.8 (Madc=5.0, Incl Org, IN SITU)
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q?
```

To write this result to a file with user specified name, use command **W**. Here, let the file be called "groupA.drc", and type as

```
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q? w
Output file name? groupA.drc
A new file groupA.drc is opened
PCA line results were written to groupA.drc.
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q?
```

Proceed to the next sample by command **+** as

```
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q? +
NT10033AF
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q?
```

The remanence direction of this sample seems to be very different from the previous one, and the data points projected on the equal-area plot seem to form a circular path. So, let's analyze the data by GTC (great circle) PCA by command **G** as

```
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q? g
Range,Ip,Dp,Mad: 0-80 24.3 310.8 3.9 (Madc=5.0, IN SITU)
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q?
```

Fit of the GTC to the data points seems to be quite high. Save the result to "groupA.drc" by command **W** as

```
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q? w
GTC results were written to groupA.drc.
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q?
```

The result was appended to the file "groupA.drc". Continue the analysis to the last sample. At any time, typing the command **H** shows simple help to guess the purpose of each command as

```
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q? h
Commands:
+-next, --back, 0-first, 9-last, Core, in-Situ, Bed-corrected,
Line-pca, Gtc-pca, critical-Mad, oRigin-on/off, Anchor-on/off, auTo-on/off,
Delete-results, Write-results, Psfile, eNlarge-scale, annOtate-on/on2/off,
Equal-area, Zijderveld, Help, Quit
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q?
```

After quitting the program by command **Q**, proceed the similar analysis to other test data files "site2.dmg" and "site3.dmg". Here, let's assign the same file name "groupA.drc" to the output file. The followings are some messages after starting the analysis of "site2.dmg".

```
pdemag site2.dmg
Progressive demagnetization from site2.dmg
NT54011AF
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q? l
Range,I,D,Mad,Thd: 0-80 62.1 168.6 1.8 0.3 (Madc=5.0, Incl Org, IN SITU)
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q? w
```

```

Output file name? groupA.drc
An old file groupA.drc is opened to append.
OK? (Y or Rtn/N) y
PCA line results were written to groupA.drc.
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q?

```

It is asked if you do not mind to append the results to an existing file.

Some samples contained in "site2.dmg" have only two data points due to blanket AF demagnetization. By typing command **L**, "pdemag" gives the anchored remanence direction including the two data points, i.e. the mean of the NRM and the single demagnetized direction. To exclude the NRM direction and obtain the true blanket demagnetized direction, turn off the automatic analysis by command **T**. Then assign the same step numbers to the question "i1,i2?" which are "1 1" in this case. The procedure is shown as below.

```

+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q? +
NT54061AF
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q? 1
Range,I,D,Mad,Thd: 0-20 65.1 165.2 1.3 0.1 (Madc=5.0, Incl Org, IN SITU)
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q? t
(Auto off) 0- 1: i1,i2? 1 1
Range,I,D,Mad: 20-20 64.3 164.5 -1.0 (Auto off, Anchored, IN SITU)
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q?

```

You can also type command **T** beforehand and then determine the single step remanence direction as

```

+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q? +
NT54061AF
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q? t
au"T"o analysis was turned OFF.
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q? 1
(Auto off) 0- 1: i1,i2? 1 1
Range,I,D,Mad: 20-20 64.3 164.5 -1.0 (Auto off, Anchored, IN SITU)
+,-,0,9,C,S,B,L,G,M,R,A,T,D,W,P,N,O,E,Z,H,Q?

```

When all results from the three "site\*.dmg" files are saved to the "groupA.drc", this file becomes the input file to the next-step site-level analysis by "pdirec". One more data file for "pdemag" is included in the "pdemag-src" directory; "t-chidat.dmg". This file contains examples with  $\chi$ -step data.

### 3.4 Site-level analysis by pdirec

In the previous section, program "pdemag" created a data file "groupA.drc" which contains sample-mean remanence directions from three sites. Program "pdirec" reads this file and calculate the site-mean paleodirection for each site. However, you need to put site locality, latitude and longitude, at the end of the line beginning with '\$'. Before editing "groupA.drc", try to let "pdirec" read the file, and the results are as below.

```

pdirec groupA.drc
** Missing site locale of site1.dmg. Set to (0N,0E). **
** Missing site locale of site2.dmg. Set to previous site. **
** Missing site locale of site3.dmg. Set to previous site. **
Paleodirections from groupA.drc
site1.dmg (IN SITU)
+,-,0,9,8,1,C,S,B,U,M,D,R,I,W,P,H,Q?

```

The equal-area plot of field directions seems to be OK but the VGP position is strange. This is because the program set (lat=0N,lon=0E) to the locality. Hence, including the information of the site locality is mandatory at least for the first site. Site localities can be omitted for the following sites if they are the same as the first one. Here, let's proceed with another file "groupAa.drc" (in directory "pdirec-src") in which the site information was written beforehand.

```
pdirec groupAa.drc
Paleodirections from groupAa.drc
site1.dmg (IN SITU)
+,-,0,9,8,1,C,S,B,U,M,D,R,I,W,P,H,Q?
```

Before proceeding, you may type command **U** because the site is in the southern hemisphere.

```
+,-,0,9,8,1,C,S,B,U,M,D,R,I,W,P,H,Q? u
```

Now the site locality is shown with a star in the equal-area plot of VGPs. Write the results of the Fisher statistics to a file by command **W**. Here, let the file name be "pmagT.d" as

```
+,-,0,9,8,1,C,S,B,U,M,D,R,I,W,P,H,Q? w
Output file name? pmagT.d
A new file pmagT.d is opened
Results were written to pmagT.d.
+,-,0,9,8,1,C,S,B,U,M,D,R,I,W,P,H,Q?
```

Proceed to the next and the last sites, then quit as

```
+,-,0,9,8,1,C,S,B,U,M,D,R,I,W,P,H,Q? +
site2.dmg (IN SITU)
+,-,0,9,8,1,C,S,B,U,M,D,R,I,W,P,H,Q? w
Results were written to pmagT.d.
+,-,0,9,8,1,C,S,B,U,M,D,R,I,W,P,H,Q? +
site3.dmg (IN SITU)
+,-,0,9,8,1,C,S,B,U,M,D,R,I,W,P,H,Q? w
Results were written to pmagT.d.
+,-,0,9,8,1,C,S,B,U,M,D,R,I,W,P,H,Q? q
```

By command **D**, you can exclude a direction which is the most apart from the mean. However, eliminating an anomalous direction should be avoided unless you obtain a positive outlier statistical test and find a good physical reason (outlier test is available by "tmeandir" contained in another archive "pmagt401.tar.gz").

Now, the file "pmagT.d" becomes an input file for the last-step analysis by "pstat". Two more data files for "pdirec" are included in the "pdirec-src" directory; "t-taupo.drc" and "t-mm88.drc". The former contains decent number of sites from the Taupo Volcano. The latter is the test data of McFadden & McElhinny (1988) to demonstrate the combined analysis of lines and GTCs. The latter also contains a case in which the data are all GTCs and no lines.

### 3.5 Group-level analysis by pstat

Using the file "pmagT.d" which was created in the previous section, "pstat" analyzes the group-level Fisher statistics and determines the grand-mean paleodirection or paleomagnetic pole. Type as

```
pstat pmagT.d
Fisher statistics from pmagT.d
groupAa.drc
+,-,0,9,C,G,U,A,V,D,R,S,X,P,H,Q?
```

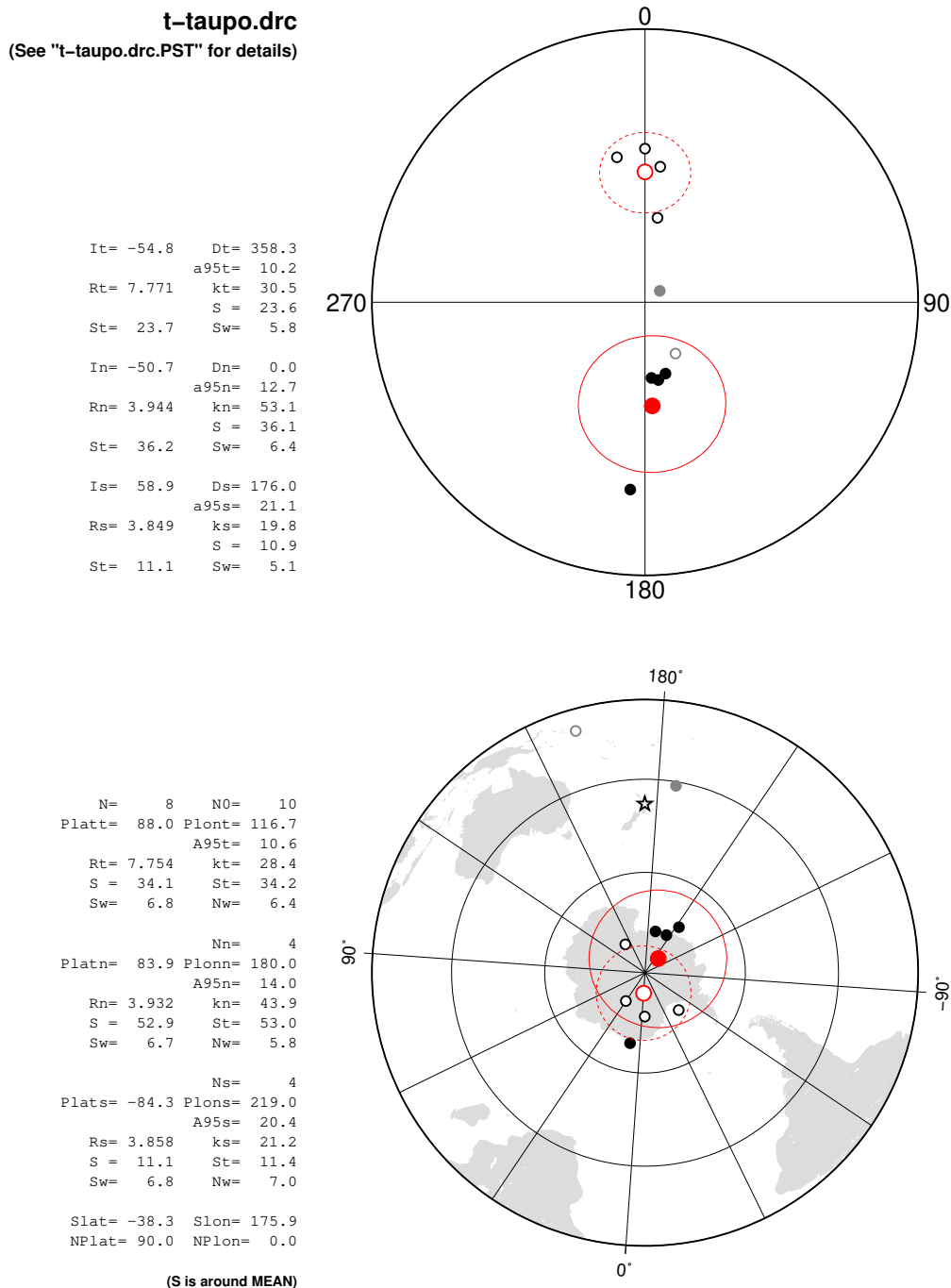
Equal-area plots of paleodirections and VGPs are shown, in which the  $\alpha_{95}$  of the mean VGP is very large of  $93^\circ$ . This is because the data are from only three sites and one is transitional. "pstat" calculates the mean VGP after flipping the reversed directions. The site-mean paleodirection is judged to be reversed if its VGP position is in the southern hemisphere. Using the command **D**, you can exclude the most apart transitional pole and recalculate the Fisher statistics as

```
+,-,0,9,C,G,U,A,V,D,R,S,X,P,H,Q? d
```

Now the  $\alpha_{95}$  of the mean VGP is reduced to  $57^\circ$ .

"pstat" automatically writes the Fisher statistics to a text file named as "\*.PST" which is "groupAa.drc.PST" in this case. The "\*.PST" file is overwritten every time the equal-area plot is redrawn. In the "\*.PST" file, N0 is the total number of the sites and those under column "N" indicate the numbers actually used in the statistics. S is the angular dispersion of field (VGP) around the mean direction (pole) or a specified direction (pole), and which is used is indicated under column "Center\_ASD". St, Sw, and Nw are between-site dispersion, within-site dispersion, and the mean of the sample numbers used at each site. The results under title "ADP Field:" are those transformed to the axial dipole field coordinates (Hoffman 1984).

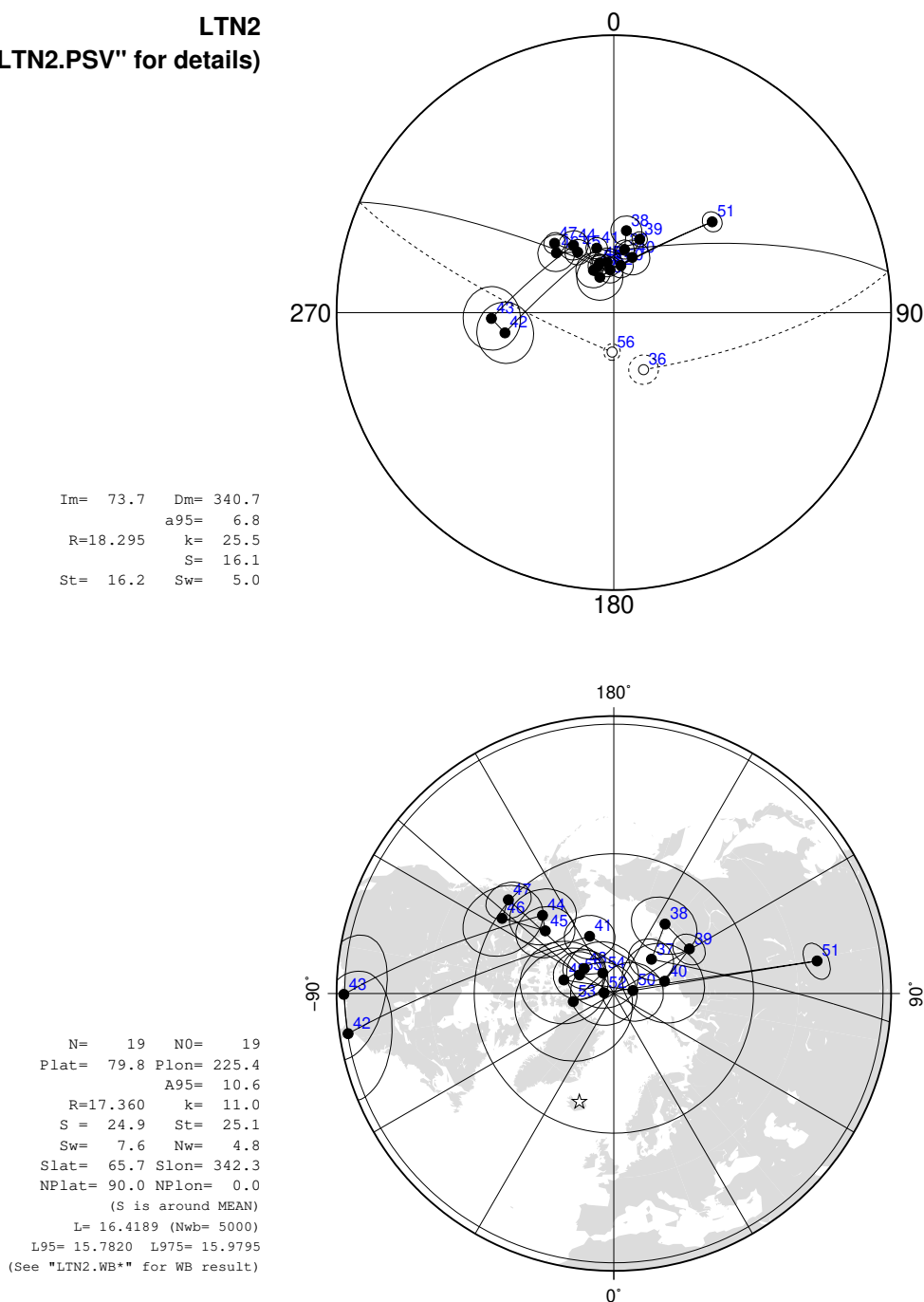
Directory "pstat-src" contains a test data file "t-taupo.d" which was created from "t-taupo.drc" (test data for "pdirec"). File "t-taupo.d" contains decent number of site-mean directions from the Taupo Volcano. You may try them out to find how the various commands of "pstat" work and also survey various statistics contained in the "\*.PST" files. The next figure shows an example of PS figure from "t-taupo.d" in which two transitional sites are excluded and polarity is separated by command V.



### 3.6 Analysis of sequential lava sites by psvar

"psvar" is basically the same program as "pstat" but it is aimed to study the series of paleodirections from lava successions. The input file should be the output from "pdirec", but you need to edit it so that the flow-mean directions are stratigraphically ordered from the lowest to the highest positions. You also need to group the flow-mean directions with "\$ Group-name" line according to the polarities of the lava groups (see the test file "t-iceland.d" in directory "psvar-src"). "psvar" draws the VGP paths on the equal area plots and automatically writes the Fisher statistics to a file "\*.PSV" in overwrite mode, where "\*" is the "Group-name". Command **W** carries out the serial correlation test of Watson & Beran (1967) and write the results to three separate files "\*.WB", "\*.WB0", and "\*.WB1". The next figure is an example of VGP paths from "t-iceland.d" in which the data are taken from Tanaka & Yamamoto (2016).

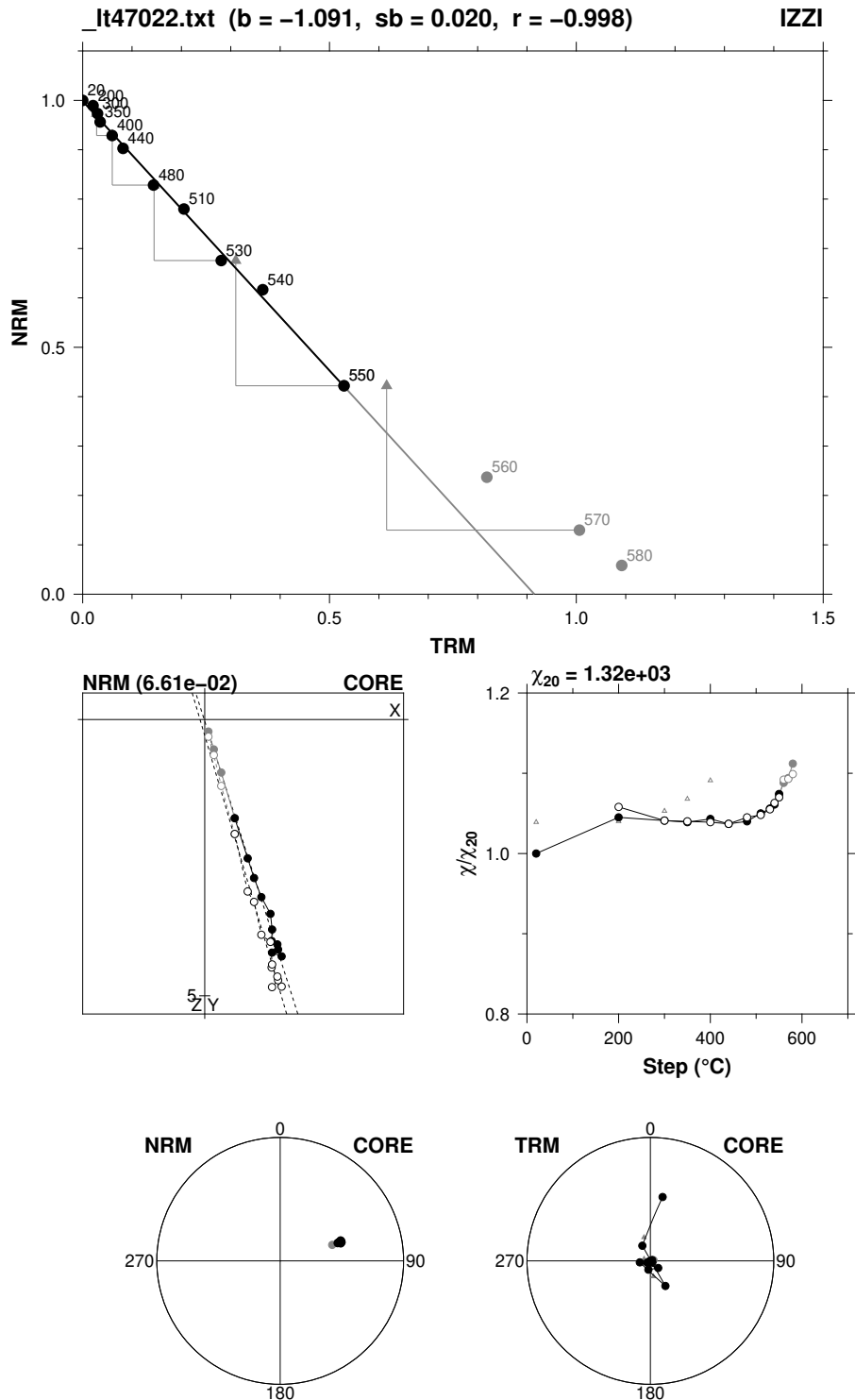
**LTN2**  
(See "LTN2.PSV" for details)



## 4 Paleointensity experiments by Thellier's method

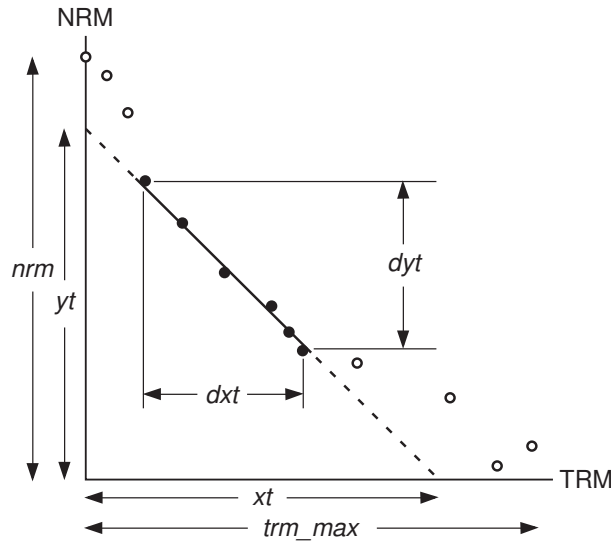
### 4.1 Analysis of Thellier results by pinte

"pinte" analyzes results of paleointensity experiments by Thellier's method (Thellier & Thellier 1959). "pinte" supports the data format from three protocols of the method; ZI (Coe et al. 1978), IZZI (Tauxe & Staudigel 2004), and IZ (Aitken et al. 1988). Three test data files for each protocol are contained in directory "pinte-src"; "t-zi.d", "t-izzi.d", and "t-iz.d". The data format should be common throughout a file. The protocol should be assigned at the beginning by "\$\$" line such as "\$\$ IZZI" (can be omitted for ZI). In the analysis of the Arai plot (Nagata et al. 1963), fitting of a linear line is carried out by manually selecting appropriate steps. The next figure is an example from "t-izzi.d" which is taken from Tanaka & Yamamoto (2016).



## 4.2 Parameters contained in "\*.PI" files

Considering the ongoing debate on the reliability of Thellier's paleointensity experiments, "pinte" calculates various parameters including those of circle fitting by Taubin method (Taubin 1991, Chernov 2012). All parameters, along with usual quality factors of Coe et al. (1978), are written to a file "\*.PI" where "\*" is the sample name. The "\*.PI" file is overwritten every time new analysis is carried out. The followings are summary of the parameters.



- NRM & TRM vectors at each step:
  - NRM and TRM: residual NRM and acquired TRM at each step, normalized by NRM intensity at 20°C  $nrm$ .
- pTRM tests:
  - PT/T: ratio of a tested pTRM to the original pTRM.
  - $dp/xt$ : ratio of the change of pTRM to the extrapolated total TRM  $xt$ .
  - DRAT:  $DRAT$  of Selkin and Tauxe (2000).
- MD tail tests:
  - $N2/N$ : ratio of tested NRM to the original NRM.
  - MDtl: MD tail normalized by the NRM intensity  $nrm$ .
  - MDtl/yt: ratio of MD tail to the extrapolated NRM intensity  $yt$ .
- Line & circle for the selected segment:
  - $b$ ,  $sb$ ,  $r$ : slope, its standard error, and a correlation coefficient, respectively, for the selected linear segment. Calculations of  $b$  and  $sb$  are based on Coe et al. (1978) which uses the method of York (1966).
  - $f$ ,  $g$ ,  $q$ : NRM fraction ( $dxt/yt$ ), gap factor, and quality factor, respectively, of Coe et al. (1978).
  - $a$ ,  $sa$ : y-intercept and its standard error of the fitted line.
  - $cdpt$ ,  $CDRAT$ : sum of  $dp/xt$  and  $DRAT$ , respectively, within the temperature range which covers the selected linear segment. The latter is  $CDRAT$  of Kissel and Laj (2004).
  - $fn$ :  $fn = dxt/nrm$ .



- fv, FRAC: NRM fractions of Tauxe and Staudigel (2004) and Shaar and Tauxe (2013), respectively. Both are based on the calculations of vector difference sum.
- Zstr: zigzag parameter  $z^*$  of Yu (2012).
- Z1, Z2: see the comments in cal\_zstar() in the C source file pi\_regres.c.
- kc, SSE: a measure of the curvature  $\vec{k}$  and sum of the squares of the errors  $SSE$ , respectively, of the fitted circle (Paterson, 2011).
- X0, Y0, rc: center and radius of the fitted circle.
- sse-line, sse-line2: sse-line is the  $SSE$  of the fitted line of Tanaka and Yamamoto (2016). sse-line2 is the  $SSE$  from which the contribution of the first data point of the selected segment is subtracted. sse-line2 is used for the second linear segment which is added to that of the first segment to obtain the total  $SSE$  of the two linear segments.
- Circles for the data points in selected/all ranges (TRM normalized):
  - parameters for the fitted circle are shown with \* for the Arai plot in which TRM is normalized by the maximum intensity of TRM *trm\_max*.
- Circle for selected data points normalized by (N[I1]-N[I2]) & (T[I2]-T[I1]):
  - parameters are shown with ' when NRM and TRM are normalized by *d<sub>yt</sub>* and *d<sub>xt</sub>*, respectively, over the selected linear segment. kc' is the  $k'$  of Cromwell et al. (2015) and Tanaka and Yamamoto (2016).
- Remanence direction of the selected segment:
  - MAD: maximum angular deviation *MAD* of Kirschvink (1980) of the fitted NRM vector which corresponds to the linear segment in the Arai plot.
  - theta: angular difference  $\theta$  between the free and anchored vectors fitted to the NRM over the selected steps (Tanaka and Kobayashi, 2003). theta is the same with  $\alpha$  of Selkin and Tauxe (2000).
  - devn, devl: devn is *dev* of Tanaka and Kobayashi (2003) which is the minimum distance of the fitted NRM vector from the origin divided by the extrapolated NRM *yt*. devl is the minimum distance which is normalized by the length of the fitted NRM segment  $\sqrt{d_{xt}^2 + d_{yt}^2}$ .

## 5 Miscellany: Circle fitting of X-Y data by pcirc

"pcirc" carries out circle fitting to 2-dimensional  $X$ - $Y$  data ( $N \geq 3$ ) by the method of Taubin (1991). This method seeks the circle parameter by minimizing the sum of the squares of "algebraic" distance  $r_i^2 - R^2$  not the "geometric" distance  $r_i - R$ , where  $r_i$  and  $R$  are the distance of a data point from the center and the radius of the circle, respectively. Although the algebraic fits are less accurate than the geometric fits, Taubin's method is one of those improved over the classical ones such as Kasa (1976) (see, Chernov & Lesort 2005). The programming code used is adapted from the C++ routines given by Chernov (2012).

Using the test data "t-pcircl.d" which is contained in the directory "pcirc-src", type as

```
pcirc t-pcircl.d
```

Results of circle fitting are displayed as

Circle fitting of t-pcircl.d

PS file: t-pcircl.ps

N	X0	Y0	R	k	SSE
20	-0.001723	0.002424	1.009	0.9906	0.03228

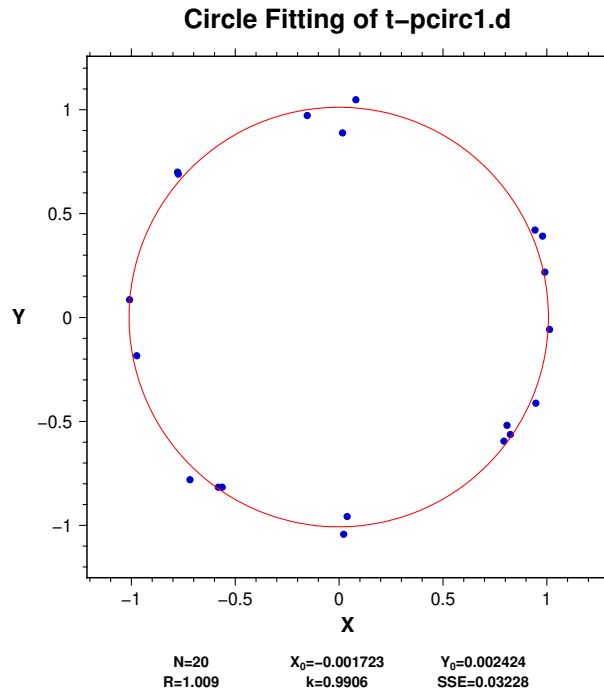
where  $(X_0, Y_0)$  and  $R$  are the circle center and the radius, respectively.  $k$  is a measure of the curvature extended from Paterson (2011) defined as,

$$k = \begin{cases} 1/R, & \text{if } \bar{X} < X_0 \text{ and } \bar{Y} < Y_0 \text{ (concave up),} \\ 1/R, & \text{if } \bar{X} > X_0 \text{ and } \bar{Y} < Y_0 \text{ (concave up),} \\ -1/R, & \text{if } \bar{X} > X_0 \text{ and } \bar{Y} > Y_0 \text{ (concave down),} \\ -1/R, & \text{if } \bar{X} < X_0 \text{ and } \bar{Y} > Y_0 \text{ (concave down),} \\ 0, & \text{if } \bar{X} = X_0 \text{ and } \bar{Y} = Y_0, \end{cases}$$

where  $(\bar{X}, \bar{Y})$  is the centroid of the data.  $k$  was introduced to evaluate Thellier's paleointensity results. Hence, ignore it when general data are fitted to a circle.  $SSE$  is the sum of the squares of the error, defined as,

$$\begin{aligned} SSE &= \sum_{i=1}^N Error_i^2, \\ &= \sum_{i=1}^N \left( \sqrt{(X_i - X_0)^2 + (Y_i - Y_0)^2} - R \right)^2. \end{aligned}$$

Figure below is the output PS file "t-pcircl.ps".



Using the watch ability of the PS viewer "Evince", you can observe the change of the appearance of the figure by re-typing "pcirc" with options. To see mainly the first quadrant of the circle with the marker of the center, and list out the input data on the display, type as,

```
pcirc t-pcirc1.d -x-0.2/1.2 -y-0.2/1.2 -c -1
```

You can see the enlarged part of the circle with the center marker in the PS figure. In the data list, "Error" mentioned above is also shown.

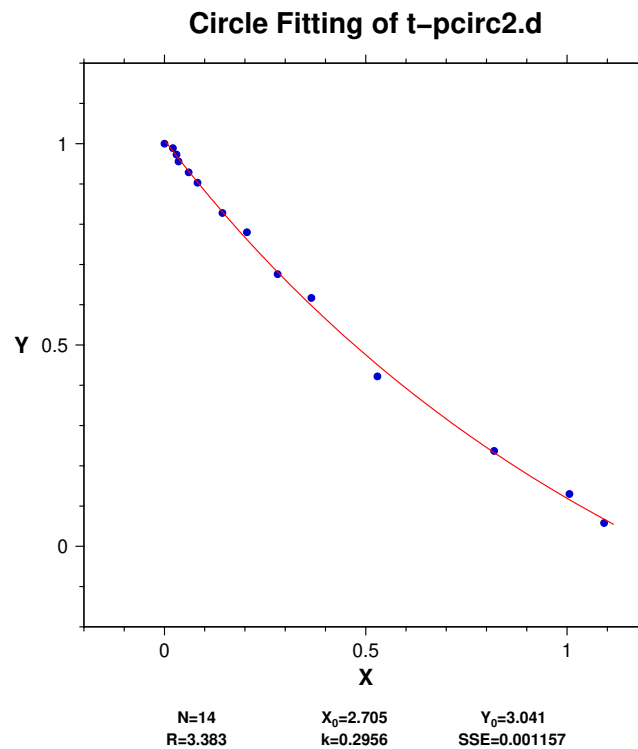
Two other files of test data "t-pcirc2.d" and "t-pcirc3.d" include paleointensity results of the Thellier's and Shaw's methods, respectively. Figure below is obtained by typing "pcirc" with option "-A" which draws an arc covering the span of the data, together with range options "-X" and "-Y" as,

```
pcirc t-pcirc2.d -x-0.2/1.2 -y-0.2/1.2 -a
```

The sign of  $k$  is positive because the arc is concave up. If you try another test data file "t-pcirc3.d" as,

```
pcirc t-pcirc3.d -x-0.1e4/1.5e4 -y-0.1e4/1.5e4 -a
```

the obtained "k" will be negative because the arc is concave down.



The last test data "t-pcirc4.d" contains only four data points (1.1,0.0), (0.0,0.9), (-1.1,0.0), (0.0,-0.9). The result from this file is as the followings.

Circle fitting of t-pcirc4.d

PS file: t-pcirc4.ps

N	X <sub>0</sub>	Y <sub>0</sub>	R	k	SSE
4	0.000	0.000	1.005	0.000	0.04010

This result illustrates a cautionary case in which the radius  $R$  of the fitted circle is slightly larger than the optimal value of 1. As mentioned before, the algebraic fits are less accurate than the geometric fits. Nevertheless, the former method is simple and accurate enough for at least paleomagnetic purposes.

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