Inter-laboratory Comparison of Data Analysis: The Interpretation of NRM Demagnetisation Curves

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Introduction

One of the main tasks in archaeomagnetic investigations is the identification of characteristic remanence directions (ChRMs). In many cases this means progressively demagnetising and measuring the natural remanent magnetisation (NRM), then determining the direction of the demagnetisation vector considered representative of the ChRM. The approach adopted is fairly standard within the AARCH network (and the archaeomagnetic community in general), and involves principal component analysis (PCA) via orthogonal vector projections (so-called Zijderveld plots) or great-circle analysis of vector end-point projections. Interpretation of such data is largely subjective, and in addition there is a wide range of computer software commonly in use.

In order to compare the analytical techniques in use within AARCH a set of demagnetisation data was compiled from 2 archaeomagnetic sites studied by the Madrid Lab and sent to each of the other labs for analysis. In total, 10 laboratories participated in the exercise. They are numbered 1 to 10 in order to preserve anonymity. The sites were chosen on the basis of their NRM component structure: one represents a "simple" NRM and the other a "complicated" NRM.

The data set

"Simple": Cartuja (C1B-C5A, 5 specimens)

The specimens were taken from bricks of a (~100 AD) Roman pottery kiln. On stepwise demagnetisation up to 100 mT they exhibit a simple NRM structure.

"Complicated": Yuste (Y11A-Y53B, 14 specimens)

The specimens were taken from 4 bricks of a modern (1959 AD) bread oven. On stepwise demagnetisation up to 700 °C they exhibit a complex, multi-component NRM.

For both sites the specimen code A or B refers to the relative position of the specimen with respect to the brick surface – A being nearer to the surface (and hence the source of heating) than B. This is significant in the Yuste specimens.

Different computer software uses different data file formats. After much trial and error(!), the data were provided as a spreadsheet containing declination, inclination and intensity at each demagnetising step. Declination and inclination were given in geographic co-ordinates. Each laboratory was charged with transforming this data into the necessary format for their respective software.

Results

Cartuja

The ChRMs defined by the 10 participating laboratories are shown in Table 1 and in Appendix 1, in all cases determined by PCA. A site-mean value has been calculated considering each specimen direction as independent, shown in Figure 1. This has been done for comparative purposes only. As would be expected, the results from the 10 labs are in close agreement at both specimen and site level and the mean site directions are statistically indistinguishable.

The main difference appears to be from which demagnetisation field the ChRM direction should be calculated, and whether the fitted direction is forced through the origin - although not all labs provided all of this information. Figure 1 shows specimen C2A, which gave the greatest variation in the determined ChRM. Using the 10-100 mT or 25-100 mT AF range, and forcing or not forcing the fit through the origin, produces a variation similar to that seen in the directions produced by each lab. It should be stressed that despite these differences, the “site-mean” results for each lab are statistically indistinguishable. For the case of simple archaeomagnetic analyses there is a uniformity of interpretation that implies a good reproducibility across the participating labs.

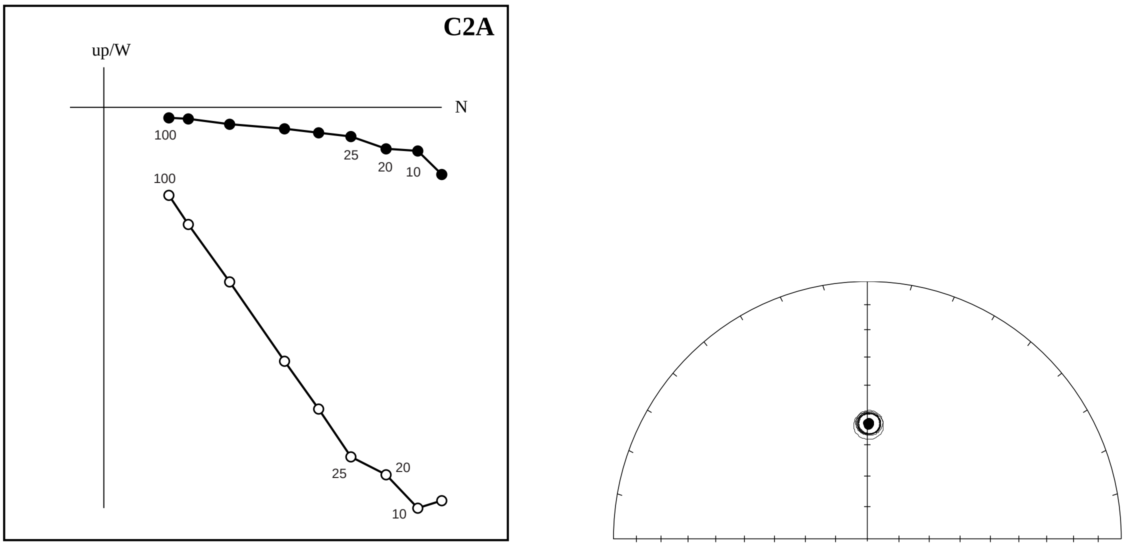

Figure 1. Zijderveld plot for specimen C2A and group mean directions and α_{95} (Cartuja).

<u>Yuste</u>

The ChRMs defined by the participating laboratories are shown in Table 2 and in Appendix 2. Most labs quoted the “ChRM”, whilst others calculated both “high” and “low” temperature directions. For the latter the “low” temperature direction has been taken as the ChRM on the basis that it represents the archaeomagnetic direction associated with partial heating of the sampled bricks of the oven. A site-mean value has been calculated treating each direction as independent. As before, this is for comparative purposes only.

There is much more variability in the interpretation of the Yuste specimens, in the method used to calculate the ChRM and in the acceptance or rejection of particular specimen directions. Eight of the 10 labs used PCA, whereas 2 used a combination of PCA and great-circle analysis. Only 2 labs accepted all 14 directions and 1 lab only accepted 4 of the directions. The most commonly rejected specimens were the B specimens, which come from further away from the kiln combustion chamber and preserve a greater part of the “primary” NRM associated with the original production of the bricks (eg. Y53B, Figure 2).

Despite this variability there is reasonable agreement at specimen and site levels. For specimens whose NRM is dominated by the ChRM component (eg. Y11A, Fig. 2) the agreement is very good, and as the “primary” NRM component becomes relatively more important the degree of agreement falls. This is due to the different interpretations of the remanence vectors, and to the definition of the ChRM components (eg. temperature range used in its calculation, PCA vs great-circle analysis). The site mean directions calculated for each set of laboratory ChRMs are comparable (Figure 2) and close to the expected direction for the site (Dec=351.1º, Inc=56.5º). The expected direction falls within the α_{95} limits for 9 of the 10 labs. The exception is lab 5, which only accepted 4 of the specimen ChRM directions. Lab 7, one of only two labs to accept all 14 ChRM directions, yielded the mean direction closest to the expected field value.

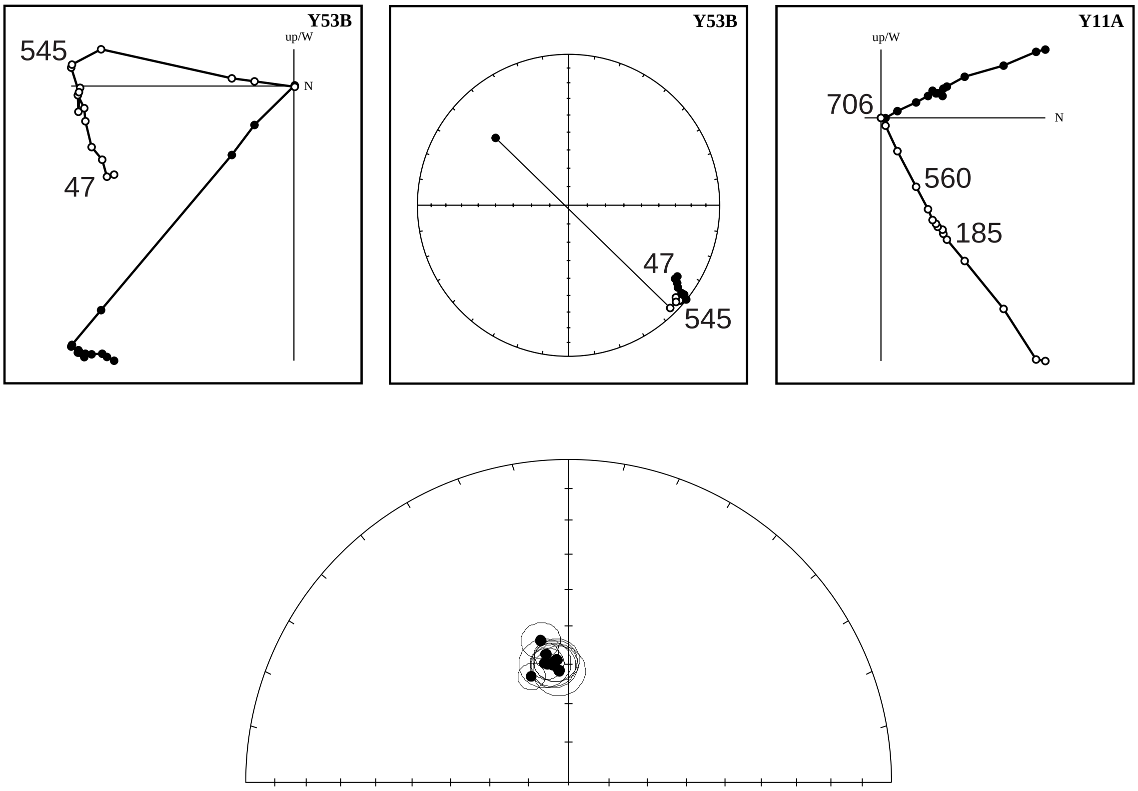

Figure 2. Zijderveld and stereographic plot of Y53B, Zijderveld plot of Y11A and group mean directions and α_{95} (Yuste).

Summary

There are differences in interpretation and in the acceptance or rejection of calculated directions for complex NRMs. This is unsurprising, considering that the analysis of NRM vectors is predominantly visual, so a large degree of subjectivity is expected. The (apparent) diversity of intepretation and use of rejection criteria is typical of that seen across the archaeomagnetic (and palaeomagnetic) community. However it is important to stress that within this variability the results obtained are consistent and comparable, and the calculated site directions are in agreement with the expected directions. Incorporating great-circle analysis of complex (eg. partially-heated) NRMs allows the definition of otherwise unresolvable components. The results from both Yuste and Cartuja indicate that there is a high level of consistency amongst the participating labs, which is encouraging with respect to the concept of network/methodalogical standardisation and calibration.

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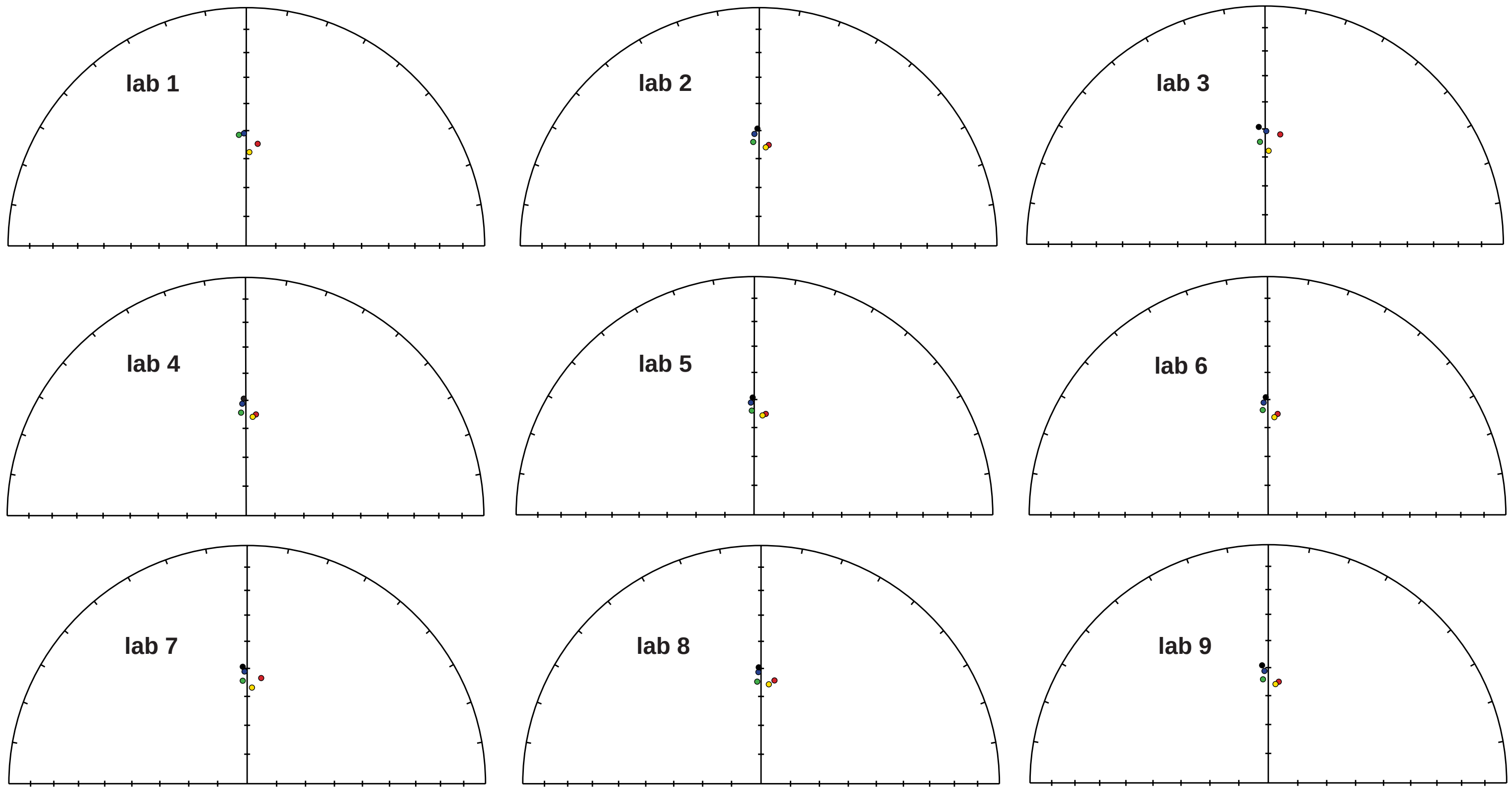
Table 1. ChRM directions for *Cartuja*, where PCA=principal component ananlysis, GC= great circle analysis, R=rejected.

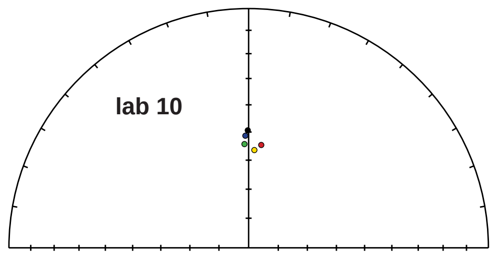
	Laboratory 1			Laboratory 2		
Specimen	**Dec**	**Inc**	**PCA/GC/R**	**Dec**	**Inc**	**PCA/GC/R**
C1B	358.8	51.0	PCA	357.8	51.2	PCA
C2A	6.3	54.5	PCA	5.8	54.9	PCA
C3A	1.8	57.6	PCA	4.2	55.9	PCA
C4A			R	357.1	54.0	PCA
C5A	356.2	51.4	PCA	359.4	49.2	PCA
	Laboratory 3			**Laboratory 4**		
Specimen	**Dec**	**Inc**	**PCA/GC/R**	**Dec**	**Inc**	**PCA/GC/R**
C1B	0.6	50.7	PCA	358.3	51.2	PCA
C2A	7.9	51.6	PCA	5.8	54.8	PCA
C3A	2.2	57.7	PCA	4.2	55.8	PCA
C4A	357.2	54.6	PCA	357.5	54.3	PCA
C5A	357.0	49.2	PCA	359.1	49.3	PCA
	Laboratory 5			**Laboratory 6**		
Specimen	**Dec**	**Inc**	**PCA/GC/R**	**Dec**	**Inc**	**PCA/GC/R**
C1B	358.1	51.1	PCA	358.1	51.0	PCA
C2A	6.4	54.9	PCA	5.8	54.9	PCA
C3A	4.6	55.5	PCA	4.0	56.2	PCA
C4A	358.5	53.9	PCA	357.4	53.7	PCA
C5A	359.2	49.2	PCA	359.2	49.1	PCA
	Laboratory 7			**Laboratory 8**		
Specimen	**Dec**	**Inc**	**PCA/GC/R**	**Dec**	**Inc**	**PCA/GC/R**
C1B	358.7	51.1	PCA	358.7	51.3	PCA
C2A	7.5	53.1	PCA	7.4	54.0	PCA
C3A	2.9	56.8	PCA	4.5	55.5	PCA
C4A	357.5	54.3	PCA	357.8	54.7	PCA
C5A	357.8	49.3	PCA	358.8	49.6	PCA
	Laboratory 9			**Laboratory 10**		
Specimen	**Dec**	**Inc**	**PCA/GC/R**	**Dec**	**Inc**	**PCA/GC/R**
C1B	358.0	51.1	PCA	358.3	51.3	PCA
C2A	5.8	54.8	PCA	6.9	54.3	PCA
C3A	4.2	55.8	PCA	3.4	56.3	PCA
C4A	357.1	54.1	PCA	357.7	54.2	PCA
C5A	357.0	49.1	PCA	359.5	49.3	PCA

Table 2. ChRM directions for *Yuste*, where PCA=principal component ananlysis, GC= great circle analysis, R=rejected. The Dec/Inc values for GC analysis refer to the direction of the pole of the fitted great circle traced by the vector end-points and not the ChRM direction.

	Laboratory 1			Laboratory 2		
Specimen	**Dec**	**Inc**	**PCA/GC/R**	**Dec**	**Inc**	**PCA/GC/R**
Y11A	336.5	53.8	PCA	334.0	59.7	PCA
Y12B	339.7	54.3	PCA			R
Y12A	359.2	54.0	PCA	345.6	62.5	PCA
Y13A	340.9	64.1	PCA	340.0	62.4	PCA
Y31B			R			R
Y31A	356.5	53.5	PCA	358.2	53.4	PCA
Y32A	344.9	63.5	PCA	7.4	51.2	PCA
Y33A	9.9	49.1	PCA	12.8	50.7	PCA
Y42B	0.1	72.2	PCA			R
Y42A			R	332.7	60.7	PCA
Y43A	57.8	74.5	PCA	344.2	59.1	PCA
Y52A	357.1	63.6	PCA	355.2	62.4	PCA
Y53B	7.7	68.0	PCA			R
Y53A	350.9	55.5	PCA	13.9	70.3	PCA
	Laboratory 3			**Laboratory 4**		
Specimen	**Dec**	**Inc**	**PCA/GC/R**	**Dec**	**Inc**	**PCA/GC/R**
Y11A	336.9	55.1	PCA	338.4	57.3	PCA
Y12B	16.8	49.8	PCA	345.5	-35.9	GC
Y12A	346.1	60.5	PCA	359.5	54.0	PCA
Y13A	338.6	61.1	PCA	332.9	-26.3	GC
Y31B			R			R
Y31A	359.1	54.3	PCA	32.0	-38.1	GC
Y32A	5.7	53.6	PCA	32.5	-37.8	GC

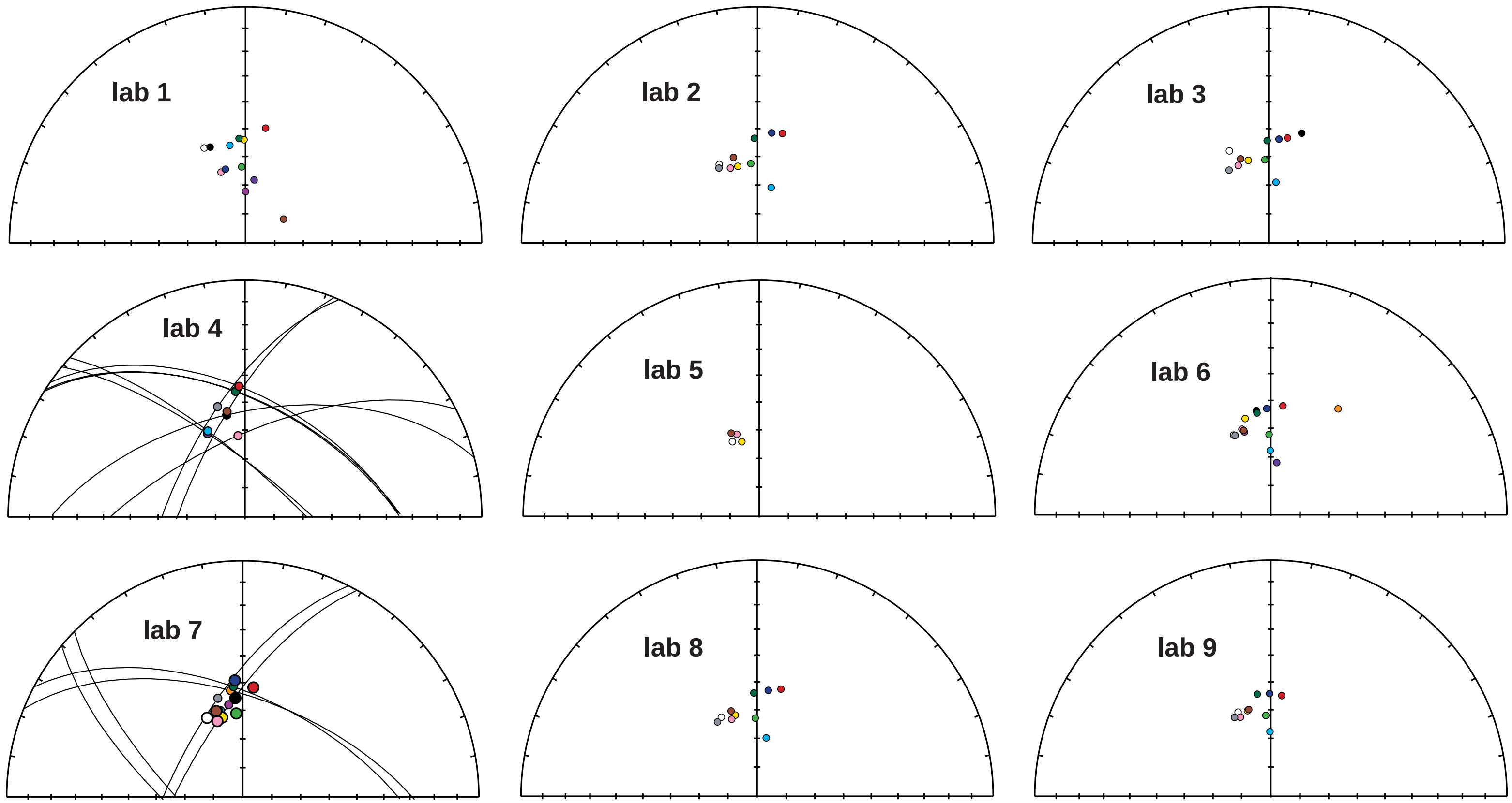
	Laboratory 3			Laboratory 4		
Specimen	**Dec**	**Inc**	**PCA/GC/R**	**Dec**	**Inc**	**PCA/GC/R**
Y33A	10.2	52.7	PCA	34.6	-39.5	GC
Y42B			R			R
Y42A	331.6	61.2	PCA	293.5	-26.7	GC
Y43A	341.6	59.2	PCA	292.2	-21.7	GC
Y52A	357.4	61.1	PCA			R
Y53B			R	39.3	-15.4	GC
Y53A	6.9	68.9	PCA	42.3	-14.7	GC
	Laboratory 5			**Laboratory 6**		
Specimen	**Dec**	**Inc**	**PCA/GC/R**	**Dec**	**Inc**	**PCA/GC/R**
Y11A	334.7	60.5	PCA	335.0	59.5	PCA
Y12B			R	352.1	53.3	PCA
Y12A	346.9	63.5	PCA	345.0	55.3	PCA
Y13A	340.3	62.5	PCA	341.3	58.6	PCA
Y31B			R	32.4	45.8	PCA
Y31A			R	352.3	54.2	PCA
Y32A			R	357.8	52.9	PCA
Y33A			R	6.3	51.7	PCA
Y42B			R	342.3	59.8	PCA
Y42A			R	335.8	59.8	PCA
Y43A	341.4	59.5	PCA	342.2	59.2	PCA
Y52A			R	358.8	62.2	PCA
Y53B			R	6.3	71.9	PCA
Y53A			R	359.4	67.8	PCA
	Laboratory 7			**Laboratory 8**		
Specimen	**Dec**	**Inc**	**PCA/GC/R**	**Dec**	**Inc**	**PCA/GC/R**
Y11A	335.7	59.9	PCA	335.7	59.9	PCA
Y12B	355.7	55.4	PCA			R
Y12A	345.4	61.6	PCA	344.9	60.8	PCA
Y13A	341.4	62.3	PCA	341.8	61.9	PCA
Y31B	21.9	-33.9	GC			R
Y31A	27.7	-34.0	GC	358.2	53.9	PCA
Y32A	356.1	49.0	PCA	6.1	52.8	PCA
Y33A	5.5	51.5	PCA	12.5	51.6	PCA
Y42B	299.0	-21.1	GC			R
Y42A	296.7	-25.0	GC	332.0	60.8	PCA
Y43A	342.8	58.8	PCA	343.0	59.0	PCA
Y52A	355.5	60.9	PCA	358.8	62.9	PCA
Y53B	219.9	19.2	GC			R
Y53A	224.5	16.6	GC	8.8	69.6	PCA
	Laboratory 9			**Laboratory 10**		
Specimen	**Dec**	**Inc**	**PCA/GC/R**	**Dec**	**Inc**	**PCA/GC/R**
Y11A	333.8	58.6	PCA	331.2	60.1	PCA
Y12B			R			R
Y12A	344.8	59.2	PCA	346.2	63.1	PCA
Y13A	339.0	60.6	PCA	335.5	62.7	PCA
Y31B			R			R
Y31A	352.4	54.1	PCA	353.5	53.6	PCA
Y32A	359.4	54.2	PCA	358.1	47.9	PCA
Y33A	6.2	54.7	PCA	6.8	47.1	PCA
Y42B			R			R
Y42A	335.2	59.9	PCA	333.6	58.8	PCA
Y43A	345.6	58.6	PCA	334.1	56.6	PCA
Y52A	356.5	61.9	PCA	352.6	63.9	PCA
Y53B			R			R
Y53A	359.3	67.7	PCA	15.2	70.3	PCA

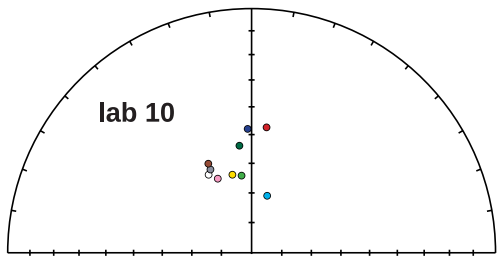




APPENDIX 1. Cartuja ChRM directions

key C1B C2A C3A C4A C5A





APPENDIX 2. YUSTE ChRM DIRECTIONS

key					
	Y11A(white)	Y12B	Y12A	Y13A	Y31B
	Y31A	Y32A	Y33A	Y42B	Y42A
	Y43A	Y52A	Y53B	Y53A	