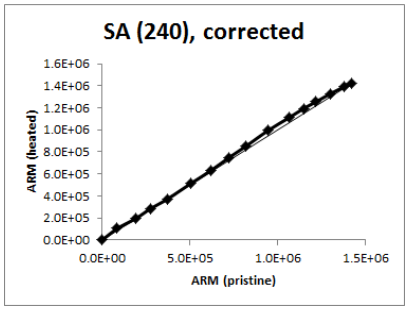
ARM test

Marilyn W.L. Monster

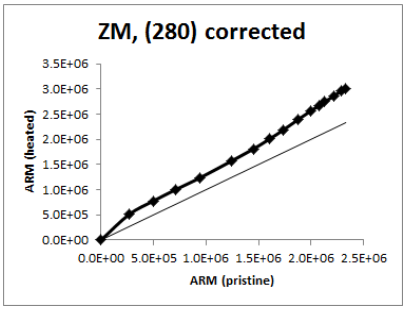
Introduction

The ARM test checks for (chemical or magnetic) alteration that is not visible in e.g. susceptibility-v-temperature plots (Kappabridge). ARM (anhysteretic remanent magnetisation) is a magnetisation gained by applying a bias field during alternating-field demagnetisation, so basically the AF equivalent of the pTRM your sample gains during an MSP experiment. You compare the ARM gained by an unheated (pristine) sample (plotted on the horizontal axis) to that gained by a sample that's been heated to the temperature used in the MSP experiment (plotted on the vertical axis).

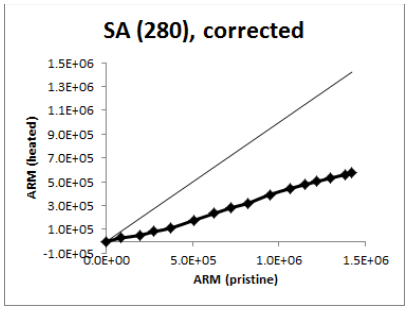
- If the ARM gained is the same for both samples, the MSP method should yield the **right answer** (unless progressive alteration occurs)
- If the heated sample gains more ARM than the unheated sample, you expect the MSP curve to be shifted upward and therefore to yield an **underestimate** (it crosses the *x* axis too soon)
- If the heated sample gains less ARM than the unheated sample, you expect the MSP curve to be shifted downward and therefore to yield an **overestimate** (it crosses the *x* axis too late)



Etna SA (240°C): ARM on ideal line; correct PI expected



Etna ZM (280°C): ARM above ideal line; underestimate expected



Etna SA (280°C): ARM below ideal line; overestimate expected

Preparing the samples

Per site:

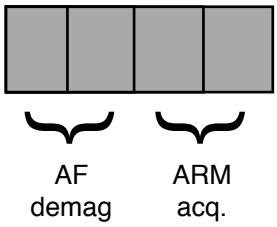
- One core remains pristine
- One core is heated to the MSP temperature (N.B.: this temperature may be different for different sites!)

These cores are then cut in four or more separate specimens. (It is also possible to use half or even quarter specimens, if little sample material is left.) Make sure there is an orientation arrow on your cores before cutting them!!! The orientation itself doesn't matter, but you need the arrow to align your samples in the robot cubes.

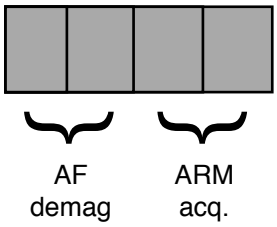
In order to be able to calculate the ARM gained, we AF demagnetise (in one axis only!!!) half the samples of each core and subject the other half to an ARM acquisition.

In summary:

Room temperature:



Heated to MSP temperature (in zero-field):



The specimens can then be weighed (very important!) and put into robot cubes. Make sure the samples are aligned the same way! (I.e. all samples from the same core should have their orientation arrows pointing in the same direction.)

The robot

The robot files for the AF demag and the ARM acquisition are the same in all but one respect: in the AF demag a bias field of 0 μT should be specified and in the ARM acquisition a bias field of e.g. 40 μT. Both measurements use type 5 (ARM acquisition) because we only want to demagnetise in the *x*-axis. Also make sure that in the ARM acquisition the robot takes four instead of eight samples at a time.

Always let someone else (e.g. Mark, Lennart, me) check your robot file! It's very easy to make mistakes.

Data analysis

See Excel worksheet. Basically what you want to do is isolating the ARM, so you average the *x* component of the two (or more) samples that have been AF demagnetised and the *x* component of the samples that have acquired an ARM. By subtracting the two, the ARM is isolated. This is done for both the pristine and heated samples. Make sure to normalise by weight before averaging!

The ARM gained by the heated specimens is then plotted against the ARM gained by the pristine samples. Ideally, these ARMs should be the same and the data points should plot on the diagonal.

Check **De Groot et al. (2012)** for the parameters used to correct for differences in NRM between the pristine and heated cores and for the amount of NRM lost.