

This discussion paper is/has been under review for the journal Solid Earth (SE).
Please refer to the corresponding final paper in SE if available.

GrainSizeTools: a Python script for estimating the dynamically recrystallized grain size from grain sectional areas

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Received: 3 October 2014 – Accepted: 3 November 2014 – Published: 27 November 2014

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Published by Copernicus Publications on behalf of the European Geosciences Union.

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Paleopiezometry and paleowattometry studies, required to validate models of lithospheric deformation, are increasingly common in structural geology. These studies require a numeric parameter to characterize and compare the dynamically recrystallized grain size of natural mylonites with those obtained in rocks deformed under controlled conditions in the laboratory. We introduce a new tool, a script named *GrainSizeTools*, to obtain a single numeric value representative of the dynamically recrystallized grain size from the measurement of grain sectional areas (2-D data). For this, it is used an estimate of the most likely grain size of the grain size population, using an alternative tool to the classical histograms and bar plots: the peak of the Gaussian kernel density estimation. The results are comparable to those that can be obtained by other stereological software available, such as the *StripStar* and *CSDCorrections*, but with the advantage that the script is specifically developed to produce a single and reproducible value avoiding manual steps in the estimation, which penalizes reproducibility.

1 Introduction

Dynamic recrystallization was defined by Stunitz (1998) as “the reconstruction of crystalline material without a change in chemical composition driven by strain energy in the form of dislocations”. Two mechanism of dynamic recrystallization have been identified (see a review in Urai et al., 1986 and references therein): (1) grain boundary migration (Poirier and Guillopé, 1979) and (2) progressive subgrain rotation (Poirier and Nicolas, 1975). The activation of these recrystallization mechanism depend on several factors, such as temperature, pressure, strain rate, presence of fluids, etc., and the interaction between these mechanism, to a greater or lesser degree, produces three easily identifiable types of dynamic recrystallization microstructures: (1) bulging recrystallization (or BLG), (2) subgrain rotation (or SGR); and (3) grain boundary migration (or GBM) (see Stipp et al., 2002 for details). The determination of the recrystallized grain size

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distribution in a deformed polycrystalline aggregate is one of the increasingly common tasks in structural geology and tectonics that study crystal plastic deformation in rocks at the microscale. Although there is no universally accepted model to explain the relationship between dynamically recrystallized grain size and deformation conditions (see De Bresser et al., 2001; Austin and Evans, 2007; Shimizu, 2008; Platt and Behr, 2011), it is clear that the dynamically recrystallized grain size is a key variable to determine the mechanical properties of dynamically recrystallized rocks. Experimental studies have demonstrated that dynamically recrystallized rocks evolve to a stable dynamically recrystallized grain size value during deformation by dislocation creep (Means, 1983; Pieri et al., 2001; Barnhoorn et al., 2004; Stipp et al., 2006). These steady-state dynamically recrystallized grain size have also been inferred in natural mylonites (e.g. Michibayashi, 1993; Herwegh et al., 2005). However, it is not well known whether this stable dynamically recrystallized grain size is represented by a single value of grain size or, most probably, by a stable continuous range of grain sizes with a particular distribution (normal, log-normal or others) and properties.

The observations outlined above led some authors to relate the dynamically recrystallized grain size (D) with the magnitude of the applied stress (i.e. the flow stress) with a relation of the type $D = A\sigma^{-m}$, where A and m are material and mechanism-specific constants (Luton and Sellars, 1969; Nicolas and Poirier, 1976; Twiss, 1977; Gillopie and Poirier, 1979; Ross et al., 1980; Schmid et al., 1980; Rutter, 1995; Stipp and Tullis, 2003) or with the rate of mechanical work (Austin and Evans, 2007); in other words, to use the dynamically recrystallized grain size as a paleopiezometer or paleowattometer respectively. Since there are no measures so far taken in situ within the lower crust or the lithospheric mantle (see Kozlovsky, 1987; Emmermann and Lauterjung, 1997 for the current limits reached so far), the paleopiezometry and paleowattometry studies in ancient exhumed mylonitic rocks are the key to constrain the theoretical strength profiles estimated for the lower crust and the lithospheric mantle, and therefore, to validate the models of lithospheric deformation.

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a particular distribution of grain sizes) and (2) grain shapes close or not too far from the simplest shape (i.e. sphere). Under such circumstances, there are several advantages to estimate the actual dynamically recrystallized grain size from a thin section (see Royet, 1991; Higgins, 2000).

In this work, we first review the available methods used to estimate the grain size from two-dimensional area section data and establish a set of instructions as robust as possible leading to a single numeric value that represents the dynamically recrystallized grain size. The second aim is to write a script implementing this protocol, checking that it provides reliable and reproducible results. Although there is free software available to estimate the dynamically recrystallized grain size based on 2-D approach and stereological considerations, such as *StripStar* (Heilbronner and Brun, 1998) or *CSD-Corrections* (Higgins, 2000), they are not open source and cross-platform (e.g. *CSD-Corrections*), they require many steps and the use of more than one software package to obtain the final results (e.g. *StripStar*), and, most important, they are not specifically designed to generate a single numeric value from the grain population under study. Our goal is to create a script meeting the following criteria: (i) it is written in a free and easy to read programming language that runs on all different platforms (Windows, Mac OS X, Linux, Unix), (ii) the use of the script does not require any knowledge of programming to use (i.e. user-friendly), (iii) provide a free and open source code organized in a modular way making it easier to modify, reuse or extend by anyone with programming skills if necessary; and (iv) the script must produce by itself the result required and ready-to-publish figures (i.e. there is no need of other software to produce figures or further treatment of data).

2 Grain size from sectional grain areas in ideal monodisperse distributions

To obtain a grain size value from a thin-section it is necessary to choose a correct parameter to describe the two-dimensional size of the grains. There are several parameters, such as the feret maximum length, the ellipse major or minor axis, etc. (see Hig-

gins, 2006; Heibronner and Barret, 2014). When particles are expected to be spherical or close to a spherical shape (near-equant objects), its 3-D size can be uniquely characterized by their diameter (or the average diameter if they are not perfect spheres). In this case, we think the best way to proceed is to convert the cross-sectional areas of each individual grain into an individual 1-D length, the diameter (d) of the grain, via the equivalent circular diameter (Heilbronner and Brun, 1998; Herwegh, 2000; Berger et al., 2011):

$$d = 2\sqrt{\frac{\text{area}}{\pi}} \quad (1)$$

Now consider the simplest grain size distribution in which all grains have similar shape (i.e. spheres) and size, this is called a monodisperse distribution. When a monodisperse system of grains is cut randomly, as in a thin section, the cut-section effect occurs, i.e. the intersection plane rarely cuts exactly through the centre of each grain (our pseudo-spherical particles) (Fig. 1). Therefore, the diameters obtained from the sectional areas are a population of apparent diameters that can theoretically vary between zero and the actual diameter of the grains (Fig. 1). In perfect monodisperse populations, the maximum diameter obtained from the data set would be the closest to the actual diameter and the accuracy of the grain size estimation only depends on choosing an appropriate sample size for the accuracy we are looking for (see Appendix A for details). Unfortunately, and leaving aside that most if not all natural mylonites show a continuous dynamically recrystallized grain size range instead of a unique grain size, this is an oversimplification and in dynamically recrystallized samples it is not trivial in many cases to distinguish sections of true recrystallized grains from those which are not or, in some cases, to distinguish a grain boundary from a sub-grain wall. This means that it is common to include within the data set grains with sizes (apparent diameters) larger than the actual recrystallized grain size. The inadvertent introduction of outliers can produce unreliable results in the estimate if we consider only the maximum value.

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(as long as the bin size/width established is not too large to produce misleading results) (see later). The modal interval is one of the statistical parameters commonly used to characterize the dynamically recrystallized grain size from population of apparent diameters but also from the derived 3-D grain size distributions (e.g. Berger et al., 2011).

5 The other statistical parameter commonly used to characterize the dynamically recrystallized grain size is the mean of the population, although the median was also used (see Ranalli, 1984). As can be seen in Fig. 2, if the population size is representative of the sample, the actual diameter is 1.28 times the mean of the entire apparent diameter population (or the mean 0.79 times the actual diameter). This is the reason why the
10 the mean dynamically recrystallized grain size obtained with 1-D methods is sometimes multiplied by a factor (or constant) to estimate the actual size. As discussed later this approach is not optimal to reach reproducibility when outliers exist and can lead to large errors in estimating the actual dynamically recrystallized grain size. In the case of the area-weighted diagrams (Fig. 2b) the distribution show similar features, although
15 as expected, the frequency of the apparent diameter intervals close to the actual grain size is more pronounced than in the number weighted approach. Another remarkable difference is that the area-weighted mean grain size is closer to the actual grain size (specifically 0.96 times) than the mean grain size. The area-weighted mean grain size has the same limitations as the use of the mean grain size.

20 It is important to highlight that the estimation of the modal interval compared to the mean or the area-weighted mean has the constrains inherent to the use of histograms and bar plots: (1) it is necessary to define the same left edge of the bin and the same bin size/width (or number of classes) to yield reproducible results in similar populations, and (2) they are not smooth. To use this approach (i.e. find the most likely dynamically
25 recrystallized grain size of the distribution) over the mean or the area-weighted mean, it would be useful to overcome these constrains. The issue of the left edge of the bin is easy to solve. Although in practice the actual left edge of the bin is set by the optical and image resolution limitations of the technique applied (Higgins, 2006), which means that it can vary across different studies, we know that the actual theoretical left edge of the

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bin is zero and we can set this limit at zero to improve reproducibility. The problem with the discrete nature of histograms and bar plots is inherent to the technique, and means that we obtain a modal interval instead of a single value, while at the same time the size of the interval depends on the bin size chosen. To convert this interval into a single value we have to choose which value within the interval is the best. Some software's (e.g. *CSDCorrections*) used the middle value, but as shown in Fig. 3 it is impossible to know whether the actual diameter corresponds to the upper limit of the modal interval (as in examples of Fig. 2a and b), any other value within the modal interval or even within the modal interval, since in real cases we do not know the actual dynamically recrystallized grain size we are looking for and therefore do not know if the selected bin size is a perfect multiple of the same.

The other critical factor to consider is the bin size/width. This parameter is directly related with the precision of the grain size estimation since it is assumed that the actual dynamically recrystallized grain size is within the modal interval obtained or close to the same (Fig. 3). If large bin sizes are selected, a gain or a loss of accuracy can occur but always at the cost of precision. On the other hand, if a small bin size is selected, then misleading results are more likely (e.g. the bin size must not exceed the measurement uncertainty in data). To yield producible results it would be necessary to implement an automatic process – an algorithm – that sets an optimal bin size based on the features of the population under study.

3 The Gaussian kernel density estimator as an alternative to the histogram

To overcome some of the inherent problems in the use of histograms we can use an alternative approach in the case of the number weighted approach: the Gaussian kernel density estimator or Gaussian kde. The Gaussian kde is, as the histogram, a non-parametric density estimator but it is smooth and independent of end points (Fig. 4). The interpretation of the data distribution still depends on the bandwidth chosen (the equivalent to the histogram's bin size/width), which strongly influences the shape of the

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Gaussian kde and, therefore, the location of the peak value. It is therefore necessary to implement a reliable method to perform this task. In any event, there are plenty of methods to find the optimal kernel bandwidth in literature depending on the expected features of the data set (see Scott, 1992; Turlach, 1993; Bashtannyk and Hyndman, 2001). The use of the Gaussian kde also has the advantage that it does not provide an interval, as in the case of using histograms, but a unique value (the peak value) that represents the most probable value of dynamically recrystallized grain size in a population of grains (see examples in Fig. 2c and e). This prevents having to choose which one is the most representative value of the actual dynamically recrystallized grain size within the modal interval, which as shown in Fig. 3 is impossible to know.

In summary, the assumptions and key features of the model to find the actual recrystallized grain size from 2-D data (sectional areas) and to implement within the script are:

- All dynamically recrystallized grains are near-equant objects approaching spherical shape. The grains can therefore be characterized solely by their diameter (or average diameter) using the equivalent circular diameter from their areas.
- There will be outliers and some measurement errors within the data set.
- Dynamic recrystallization results in a stable grain size – a steady-state microstructure – for a particular mineral phase. The stable recrystallized grain size can be represented by a single value: the actual grain size in case of monodisperse distributions and the most likely grain size in case of continuous grain size distributions. It is assumed that in the case of “equilibrium”, a continuous grain size distributions would fit a log-normal distribution (see later).
- The Gaussian kernel density estimator is a useful non-parametric tool and has several advantages compared to histograms.

4 The GrainSizeTools script

The script is written in Python, a general-purpose high-level interpreted programming language characterized by a clear syntax and ease of learning. The main advantages of Python language are: (i) it is free and open-source, (ii) the underlying computer language run on all different platforms (Windows, Mac OS X, Linux or Unix), (iii) there are a large number of open and freely available scientific libraries providing an interactive environment for algorithm development, data analysis, data visualization and numeric computation; and (iv) due to the preceding points, particularly the last one, the use of Python is becoming increasingly popular in academia and in science in general.

The *GrainSizeTools* script can be downloaded from <https://sourceforge.net/projects/grainsizetools/> and requires the three following scientific Python libraries: Numpy, Scipy (Oliphant, 2007) for data analysis, and Matplotlib (Hunter, 2007) for plotting. The script produces several types of output, allowing to save the graphical output as bitmap (8 file types to choose) or vector images (5 file types to choose). Although the script is designed to produce figures ready for publication, they can be easily customise within the Matplotlib environment (i.e. when the figure is showed by the script and prior to save it as a file) or by post-editing the vector image in vector-graphics applications such as Adobe Illustrator, ACDSsee Canvas, Inkscape or similar. Another important point is that to use the script there is no need for prior knowledge of the Python language. The steps to estimate the recrystallized grain size are easy to achieve and a quick tutorial can be found online (<http://sourceforge.net/p/grainsizetools/wiki/Home/>).

4.1 A brief description of the script

The script is organized in a modular way using Python functions. This facilitates to modify, reuse or extend the code and allows specifications of each function. In the specifications, the user will find the assumptions made, the conditions that must be met for the inputs and the result/s obtained for each one.

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The script can be divided into three main parts or functions with intuitive and self-explanatory names:

The first part is a function called “importdata” responsible for loading the data set into memory for subsequent manipulations. The data has to be previously stored in a text file such as txt (a data on each line) or csv (comma-separated values). This file is previously created with the image analysis software used to measure the sectional areas of the grains.

The second part is a function called “CalcDiameters” that returns an array of the diameters calculated from the sectional areas assuming that the grains are near-equant objects. In the event that the grains slightly depart from near-equant objects, the value would represent the diameter of a sphere of equivalent volume. If applicable, it also allows to correct the diameters calculated by adding the perimeter of the grains not previously included in the image analysis.

The third part is a function called “findGrainSize” that returns the number and area-weighted plots, the location of the Gaussian kernel density estimator peak, the modal intervals and their middle values produced by both approaches and other relevant information such as the bin size and the Gaussian kde bandwidth estimated.

The protocol in the script to do this is explained below:

As portrayed above and shown in Fig. 3, choosing a different bin size (or number of classes) could lead to a different interpretation of the data distribution and, therefore, different results. To ensure reproducibility, the idea behind the script is that for similar populations similar bin sizes need to be used. For this, the idea is to avoid as far as possible manual data manipulation steps and use an automated process, this is, to find an algorithm that estimates on its own the optimal bin size. Although there is no best number of bins, there are some guidelines or rules of thumb to determine the optimal number of bins. *GrainSizeTools* implements two of the most commonly used rules of thumb to find the optimal number of bins: the Scott rule (Scott, 1979) – based on the sample SD – and the Freedman–Diaconis rule (Freedman and Diaconis, 1981) – based on the sample interquartile range. The rule used by default within the script

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is the Freedman–Diaconis rule since it is less prone to outliers in comparison to Scott rule. In principle, it is unreasonable that the bin size exceeds the uncertainty of the data acquired during the calculation of apparent diameters from the measured grain areas, around 4 % according to Berger et al. (2011). Because the actual diameter of the grains is unknown when we applied for the first time “findGrainSize” function, it is impossible to know if the bin size estimated is lower than the 4 % error limit. For this, the user can set later, if necessary, a larger user-defined bin size based on the assumed error during data acquisition and the actual dynamically recrystallized grain size estimation obtained in the first try. The same rules applies for the area-weighted approach, based on Herwegh (2000), that uses the sum of the areas respect to the total area (area percentages) of cross-sectional shapes for each grain size interval defined. This allows the comparison between distributions in number and area-weighted plots in order to obtain complementary information about the data set. The script returns the modal intervals and the middle values of the modal intervals in both cases. It also returns the area-weighted mean of the data set.

The script also implements the Gaussian kernel density estimator within the number weighted plot. It finds and returns the peak value of the kde function; this is, the most likely value of dynamically recrystallized grain size according to the number weighted approach. To estimate the optimal bandwidth of the Gaussian kde we use the Silverman rule of thumb method (Silverman, 1986), since such method works well for univariate systems with unimodal densities (Turlach, 1993; Bashtannyk and Hyndman, 2001). The implementation also allows to use the Silverman rule multiplied by a constant to modify the bandwidth for comparative purposes.

5 Testing the mean, the modal intervals and the Gaussian kde peak

Ideal monodisperse grain populations, such as described in Sect. 2, do not exist in natural or experimentally deformed samples. In fact, in grain size studies of dynamically recrystallized mylonites it is extremely uncommon – if they exist – to observe

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As shown in Fig. 6, in bimodal (or multimodal) cases the weighted area approach allows the user to know which of the two populations of grain size represents the pre-dominant phase in volume (i.e. the volumetric contribution), which matters for rheology considerations (Herwegh, 2000; Berger et al., 2011). This is because the number weighted approach tend to place the modal interval in the population of smaller grain size even when it is not the main phase, especially when the difference in grain size between the two populations is small (Fig. 5a and b). As expected, the mean values in these cases produce meaningless results. In contrast, the modal intervals (i.e. the local maximums) or the local Gaussian kde peaks reflect the actual size (or the theoretical most common size in case of a two or more continuous grain size distributions) of different grain populations.

As in a previous example (see Fig. 5a), Fig. 6a shows that in systems with discrete values of grain size (uni- or multimodal) the Silverman rule tends to smooth excessively the population of apparent diameters of grains. We found – based on empiricism – that the Silverman rule multiplied by $1/3$ yields best estimates (i.e. best accuracy) in these cases.

5.2.2 Log-normal dynamically recrystallized grain size distributions

Skewed distributions are particularly common in nature and often continuous distributions closely fit a log-normal distribution (Limpert et al., 2001). As an example, grain size ranges in sediments or non-deformed igneous rocks are typically log-normally distributed. It is rather common in dynamically recrystallized rocks that the 2-D or the derived 3-D dynamically recrystallized grain size distribution plots show long tailing distributions skewed to the right (see examples in Heilbronner and Bruhn, 1998; Heilbronner and Tullis, 2006; Berger et al., 2011; Heilbronner and Barret, 2014), which fits with the typical properties of this type of distribution. Based on these examples, it seems that at least some dynamic recrystallized mylonites reach a log-normal distribution of dynamically recrystallized grain size for a specific mineral phase (e.g. Ranalli, 1984; Michibayashi, 1993).

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A random variable x – in our case x is the diameter of the grain – is said to be log-normally distributed if $\log(x)$ is normally distributed (Fig. 7). Continuous log-normal distributions have two features, only positive values are possible for the variable and the distribution using a linear scale is skewed to the right (Fig. 7). Although log-normal distributions can be characterized by different parameters, we will use the scale (denoted as μ^*) and shape (denoted as σ^* or s^*) since they describe the data directly at their original linear scale (Limpert et al., 2001). As noted in Fig. 7 they correspond with the “back-transformed” values of mean (μ) and SD (σ) of the $\log(x)$ distribution and they are referred as the geometric mean or median (μ^*) and the multiplicative SD (s^*) respectively (Limpert et al., 2001). The multiplicative SD (s^*) controls the shape of the log-normal distribution (Fig. 8). Thus, if s^* takes a value of 1 we obtain a normal (Gaussian) distribution. However, if it takes much larger values, the shape of the log-normal distributions becomes increasingly skewed to the right (Fig. 8). In general most s^* values measured in nature range from 1.4 to 3 (Limpert et al., 2001).

To test the Gaussian kde peak estimator with log-normal dynamically recrystallized grain size populations it is necessary to simulate a set of random different log-normal populations. Because there are no previous studies showing the typical features of continuous log-normal distribution of grains in recrystallized mylonites, we need to assume, based on the dynamically recrystallized grain size plots appearance in previous studies, a range of shape and scale parameters to simulate a finite number of log-normal distributions. With this in mind, the shape parameter in recrystallized mylonites probably ranges between 1.3 and 2.0 (cfr. Fig. 8 with previous dynamically recrystallized grain size studies in mylonites). To set a range of scales the same principle applies. Hence different scale values (up to 38) will be tested to obtain a range that yields a reasonable set of representative log-normal distributions of dynamically recrystallized grain size. With these constrains, we randomly generate populations of spherical grains with different values of mode (i.e. the grain size value we are looking for), shape and scale. Then, the cut-section and the intersection-probability effects are applied to the actual population to simulate a 2-D distribution of apparent diameters, and finally

the Gaussian kde peak location is calculated. One hundred trials were generated in each simulation with pre-defined features. Ultimately, different statistical parameters are calculated to see how the parameters affect the estimations. It was also checked how a modification of the Silverman rule bandwidth estimator affects the Gaussian kde peak estimations.

The results obtained indicate that the behaviour of the Gaussian kde peak estimator is complex since it depends, to a greater or lesser extent, on the three variables considered (Fig. 9). Firstly, the estimations can be slightly over- or underestimate the actual value of the most probable grain size, although always with a theoretically reasonable accuracy. The precision and hence the reproducibility of the estimations – which is the key in this study – also depends on the considered variables. We observe that the higher the scale and the smaller the grain size the lower is the precision (Fig. 9a and b). Something similar occurs with the shape parameter although the changes are not as noticeable (Fig. 9c). The highest 2-sigma absolute error obtained for the Gaussian kde peak in all simulations performed was ± 2 ($\pm 5.4\%$ in relative error). Most of simulations yield relative 2-sigma errors below $\pm 4\%$, so theoretically the Gaussian kde peak estimator seems a robust estimator. However, the simulations performed warn that in case of a continuous log-normal population of dynamically recrystallized grain sizes in which the most probable dynamically recrystallized grain size is small (say smaller than 30 microns) and with a large range of dynamically recrystallized grain size (say higher than 100 microns), special care should be taken using the Gaussian kde peak estimator. In this case it would be desirable to use more than one parameter, such as the mean or the area-weighted mean, to compare between mylonites. Lastly, in the cases tested the modified version of the Silverman rule used in discrete models (the rule multiplied by $1/3$) yielded worse accuracy and precision.

Although it is likely that real dynamically recrystallized grain size populations in mylonites are within the limits of the cases tested, it is unknown – because of the lack of previous studies on this matter – whether the scales and shapes considered are realistic in some, or maybe in most, cases. Consequently we think the best way to

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test the reliability of the Gaussian kde estimator against other parameters is using real samples and compare it with the other parameters available (see Sect. 7 below). While the simulations performed have a lot of limitations due to all the assumptions made and the error data obtained have to be carefully considered, these simulations yield useful information since they allow us to understand how different parameters of the population affect the estimation.

6 How many grains are needed to achieve reproducibility?

Before to proceed and test the script in natural samples and against other software available, it is necessary to deal with the issue of how many grains are needed to achieve reproducibility. This is a non-trivial question as for comparison of different studies it is a necessary condition to have reproducibility. Previous studies state that more than 500 grains are necessary (Heilbronner and Bruhn, 1998; Heilbronner, 2000) or a number of 200–250 grains (Berger et al., 2011) for dynamically recrystallized grain size analysis. Since these studies did not explicitly address how they estimated the minimum number of grains needed for dynamically recrystallized grain size analysis, we assume these numbers rely solely on practical experience and are not derived by some theoretical underlying principle. With the aim of solving this issue and as a first approach, we have implemented a Monte Carlo simulation to determine the minimum necessary sample size from a theoretical point of view in the case of monodisperse population of grains (see Appendix C). In this case, the given condition is based on the typical uncertainty of measurements. Berger et al. (2011) found that when repeating the measurement in the same targeted grain the error margins in the diameters calculated ranged between 1 and 4%. Taking the 4% error margin, our goal is to find the minimum number of grains needed so that if the measurement are repeated a number of times, nearly 95% (2-sigma) or 99% (3-sigma) of the time the mean calculated shows a variation equal or less than 4%. In other words, the error that is obtained due to technical limitations when we estimate the apparent diameters from the images

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(~ 4 % for targeted grains) is larger than the error obtained when the statistical methods to obtain a value representative of the grain size 3-D population from the 2-D data are applied.

As can be deduced from the plots showed in Fig. 10, this condition is satisfied for monodisperse populations of spheres when the number of measured grains is 203 in the case of σ_2 or is 455 grains in the case of σ_3 . These values were calculated assuming a perfectly monodisperse population of grains. This means that due to different sources of error and that the common event of reaching a continuous range of grain size instead of a unique value in real samples, the minimum sample size should be always higher than those shown here.

To set a more reliable minimum number of grains needed to achieve reproducibility it is necessary to use the same criteria applied in the previous simulation but using grain populations with a continuous range of dynamically recrystallized grain size. However, due to the infinite number of possible continuous distributions to consider the task seems impossible to accomplish, at least until we have a reliable knowledge about the type and parameters that characterize the dynamically recrystallized grain size continuous distributions in real mylonites. To overcome this situation, a large data set of natural dynamically recrystallized deformed rock can be used. The strategy – known as bootstrapping – is to perform a random resampling of the data set chosen and see how the sample size affects the results of the parameters that characterize the population of dynamically recrystallized grain sizes by comparing this to the results obtained using the whole population. For this, we use a population of dynamically recrystallized quartz grains measured in a natural deformed granite, sample MAL-05 (see below for details; Sect. 7) with a population of 2945 grains. It is assumed that this large number of grains contains all the information necessary to fully characterize the recrystallized grain size.

Following the same principle as in the above Monte Carlo simulation (see Appendix C for details), we found that the mean obtained from a large number of random samples has an error less than 4 % when the sample size is 428 for σ_2 (~ 95 % of the time) or 954 for σ_3 (~ 99 % of the time) (Fig. 10). It needs to be taken into account that

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if anyone performs the same simulation they would probably obtain slightly different results. The reason for this is that the coefficient of variation line is nearly parallel to the x axis when approximate to the value of 4 % and have an arbitrary noise due to the stochastic nature of the simulation (see the inset in Fig. 10d). This produces a range of values instead of a unique value. To overcome this, we performed ten simulations and with the results obtained it was estimated the Bayesian credible intervals (i.e. the true value falls within the credible region 95 % of the time), which were 421 to 428 grains in the case of the 2-sigma example and 943 to 954 grains in the case of 3-sigma example. The higher values of these credible intervals were taken as the minimum sample size.

7 Testing the script for reproducibility and against other software available

To test whether the script yields reproducible results and to compare it to other software available, it was used a data set from a natural mylonitic granite sample (named MAL-05) deformed in a crustal-scale extensional shear zone, the Vivero fault (Lopez-Sanchez, 2013). The granite is a coarse-grained two-mica granite with quartz (~ 35 %), feldspar (microcline and plagioclase; ~ 60 %) and muscovite plus biotite (\leq 5 %) as main constituents. Mylonitic samples show quartz aggregates with a complete or quasi-complete dynamic recrystallization dominated by a subgrain rotation mechanism (Fig. 11) (Lopez-Sanchez, 2013). In contrast, feldspar show cataclasis with syntectonic crystallization of very fine albite-oligoclase, K-feldspar and biotite grains along fractures as well as at the feldspar rims (Lopez-Sanchez, 2013). The thin-sections were cut parallel to the mineral and stretching lineation and perpendicular to the mylonitic foliation (XZ sections). The procedure to acquire and measure the areas of the dynamically recrystallized grain sizes is summarized in Table 1.

The strategy to check reproducibility was as follows: dynamically recrystallized grain size areas were measured and their apparent diameters derived from four different locations of the same deformed sample MAL-05 (belonging to two different thin sections). Assuming that there are no differences in the dynamically recrystallized grain

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regardless you consider 2-D or the derived 3-D dynamically recrystallized grain size distribution yields comparable results.

The script is written in Python, a cross-platform programming language, and is free and open source. To use the script no previous knowledge of the Python language is necessary. The results are somehow similar to those obtained with the stereological software packages *StripStar* and *CSDCorrections* choosing similar statistic parameters. The main advantages of the script for paleopiezometer or paleowattometer studies are that it is specifically developed to yield a single and reproducible value from a population of apparent diameters avoiding the non-automated steps in the other implementations. This approach improves previously available methods because: (i) the bin size and the bandwidth of the Gaussian kde is based on the population features, so it prevents the user to manually choose the number of classes (or bin size/bandwidth) which penalizes the reproducibility, and (ii) it uses a continuous non-parametric density estimator – the Gaussian kernel density estimator – instead of a discrete one to find the most likely dynamically recrystallized grain size of the distribution, which improves reproducibility.

The results produced by the script are different to those obtained in the past aiming to establish a correlation between dynamically recrystallized grain size and differential stress in experiments, which mainly used logarithmic and square root grain size using 1-D methods. Therefore, the results obtained by the script requires a calibration to be used as an absolute estimator of the differential stress. For this goal it can be used as an approximation the empirical conversion matrix reported in Berger et al. (2011). Specifically, the correction factor for the area-weighted mean or the correlation factor established for the *StripStar* software in case the Gaussian kde peak value is used (see Table 5 in Berger et al., 2011). Additionally, the results of the script can be used as a relative paleopiezometer or paleowattometer by comparing the dynamically recrystallized grain size in two or more mylonite samples.

Since the widely used 1-D methods suffer from several limitations, establishing a correlation factor between different methods and statistical parameters is not an optimal

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where R is the radius of the sphere, r_1 and r_2 the lower and upper limits of the apparent section interval defined, and P the probability to cut sections within the interval defined. If we take a sphere of unit radius the equation simplifies to:

$$P(r_1 < r < r_2) = \sqrt{1 - r_1^2} - \sqrt{1 - r_2^2} \quad (\text{A2})$$

5 Our aim is to find the number of grains needed to know with a certainty of 99 % that at least one of the grains measured in our data set have a size similar or with an error less than 4 % compared to the actual size. Assuming a sphere of unit radius and according to the equation shown above, we calculate for simplicity the opposite, this is, the probability that all sections obtained have a diameter shorter than 0.96 (an
10 apparent diameter shorter or equal than 4 % with respect to the actual size) is:

$$P(0 < r < 0.96) = \sqrt{1} - \sqrt{1 - 0.96^2} = 0.72 \quad (\text{A3})$$

If we increase the sample size (i.e. the number of random cuts), the probability that at least one random section show lengths larger than 0.96 follows the equation:

$$P_{\text{total}} = (1 - P^n) \quad (\text{A4})$$

15 where n is the number of random cuts (i.e. the sample size) and P_{total} the probability that at least one apparent section is larger than 0.96 for any given n . Then we have to find when at least one of the lengths of the sections randomly cut is larger than 0.96 with a certainty of 99 %. In doing this, we find that when the sample size is 15 the P_{total}
20 is 99.28 %. This means that when we measure just 15 grains, the chance of finding a section whose diameter has an error less than 4 % the actual size of the grains in a monodisperse system is greater than 99 %.

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Appendix B: A stochastic model to simulate grain size distributions (Monte Carlo approach)

To simulate the cut-section effect, it is considered a circle of unit radius (diameter = 2) and then generates a user-defined number of random cuts (depending on the sample size desired). For this, we use a Python built-in function called *random.random* that generates a random irrational (floating point) number between 0.0 and 1.0. This represents any possible cut from the centre of the circle to its edge (Fig. B1). Then, following the Pythagorean Theorem it is calculated the length of the section (also known as chord length) using the following relationship:

$$\text{section length} = 2\sqrt{1 - d^2} \quad (\text{B1})$$

The apparent diameters obtained can be corrected – if necessary – according to a selected diameter. The Python function implemented to simulate this effect is called *generateRandomSections* (see Supplement, *SourceCode_AnexoB.py* file). Because monodisperse systems are only affected by the cut-section effect, this Python function can be used to simulate perfect monodisperse systems. This process is repeated a number of times, as many as required to be reproducible within the level of confidence desired (see Appendix C). The data generated is stored and then plotted on a histogram (see Figs. 2, 5 and 6 within the manuscript for examples). According to the law of large numbers (or Bernoulli's law), if sample size is large enough, the Monte Carlo Simulation will produce the same results for a given accuracy obtained by the Eq. (A1) by Sahagian and Proussevitch (1998) showed in the Appendix A.

In the case of simulating a monodisperse data set with outliers (e.g. Fig. 5a and b) the procedure was as follows: first, it is established the grain size, the sample size and the ratio between the correct measures and the outliers. Once calculated the number of outliers that need to be added to the data set, the code generated a defined number of grains with a random size ranging between 1.01 to 1.5 times the recrystallized grain size defined (e.g. if the actual grain size is set to 100 microns, the outlier grains

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will range between 101 to 150 microns). The maximum limit has been set arbitrarily at 1.5 times. Then, for each random grain created a random section is generated and added to the data set (see function *generateSample_withOutliers* within the *SourceCode_AnexoB.py* file in the Supplement).

To generate a data set simulating uncertainty during measurement – as in the Fig. 5c and d within the text – there are two approaches. One assumes that the uncertainty of the data is independent of the size considered and the other assumes that the error measurement is size dependent. Studies showed that the last approach is the correct one (Gualda, 2006; Berger et al., 2011). Thus, Berger et al. (2011) carried out a study involving repeated measurement on several grains and found that the error in grain size varies between 1 and 4 % for targeted grains but up to 15 % for smaller grains; this is in part due to optimizing resolution for the targeted grain sizes, resulting in considerable errors for the smallest grain sizes. Taking this into account, the procedure created to simulate such uncertainty in the data set works as follows. First, it is established the grain size, the sample size and the uncertainty expected for the sectional areas. Then it is created a number of random sections defined by the user. To generate the uncertainty within the data set: (i) it is calculated the maximum absolute error taking into account the uncertainty desired, (ii) all the values below this maximum error margin are removed to prevent negative values within the data set during the addition of random errors (there is also a practical reason for doing this since the uncertainty obtained during measurements delimits the actual optical and resolution limitations of the technique applied), and finally, (iii) a random error between zero and the maximum absolute error estimated with a random sign (i.e. positive or negative) is generated and added for each value; it is assumed that the expected error has a normal (Gaussian) distribution, this is, it is most likely that the result is closer to the actual value than the extreme values defined (see function *generateSample_withUncertainty* within the *SourceCode_AnexoB.py* file in the Supplement).

To simulate the intersection probability effect in case of polydisperse populations, first we create a large population of grains (say a million) with a defined distribution and

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is calculated a modified version of the coefficient of variation (originally the SD divided by the mean; σ/μ). We use the sigma-2 and sigma-3 values instead of the SD (sigma-1). Based on the study of Berger et al. (2011), the errors in the diameter measurements are up to 4% for targeted grains. Therefore, the modified coefficient of variation has to meet the following condition:

$$2\sigma/\text{mean or } 3\sigma/\text{mean} < 0.04 \quad (\text{C1})$$

If the condition is not satisfied, the sample size is increased (with a step size defined by the user) and the process initiates once again until the condition is satisfied.

4. When the condition is satisfied, the sample size for the defined condition is reported and a number of plots showing the evolution of the mean, the SD and the modified coefficient of variation throughout the process of increasing the sample size are generated.

The code implemented to perform this task is shown in the attached file: *findSampleSize.py*

**The Supplement related to this article is available online at
doi:10.5194/sed-6-3141-2014-supplement.**

Author contributions. Marco A. Lopez-Sanchez designed the simulations, developed the Python code, interpreted the data and drafted the manuscript. Sergio Llana-Fúnez contributed with new ideas and tested the scripts independently during the preparation of the manuscript.

Acknowledgements. The study of the dynamically recrystallized grain size distribution in dynamically recrystallized rocks was undertaken during the last stages of the Ph.D. of the author and funded by research grant CGL2010-14890 from the Spanish Government and a Severo Ochoa doctoral fellowship (BP07-120) from the Principality of Asturias Government (Spain).

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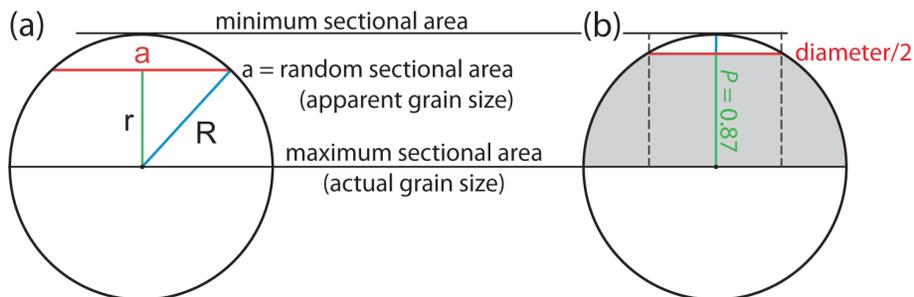


Figure 1. (a) Possible sections through a circle (sphere projection). R is the radius, a the section or chord length of a random section and r the apothem, this is, the distance from the centre of the circle to the midpoint of the section length. The chord length correspond with the apparent diameter and ranges between zero and the actual diameter of the grain when the section cuts through the centre of the circle. (b) Example showing an apparent section that correspond with the half of the actual diameter. The scheme allows to visualize that to obtain apparent diameters larger than the half of the actual diameter is most likely ($P = 0.87$) than the opposite.

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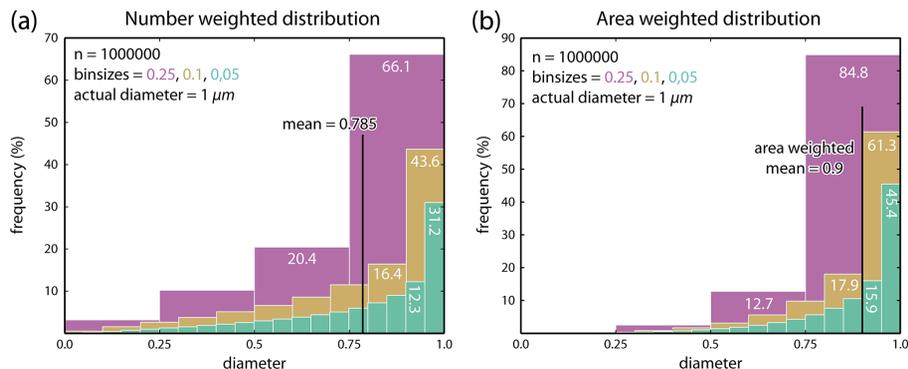


Figure 2. Grain size distribution plots producing by cutting a sphere of the same size randomly (monodisperse system). **(a)** Histogram of apparent diameters from a population of spheres of size 1 showing different number of classes or bin sizes. The actual diameter of the grain is always within the most frequent class of the histogram, the modal interval. Specifically in the upper limit of the same. The mean of the population is always 0.785 times the actual grain size for a representative sample size. **(b)** Same population as **(a)** but a bar plot showing the area percentages of equivalent diameters (i.e. the sum of the areas of the grains respect to the total for each grain size interval defined). The area-weighted mean of the population is 0.9 times the actual grain size for a representative sample size.

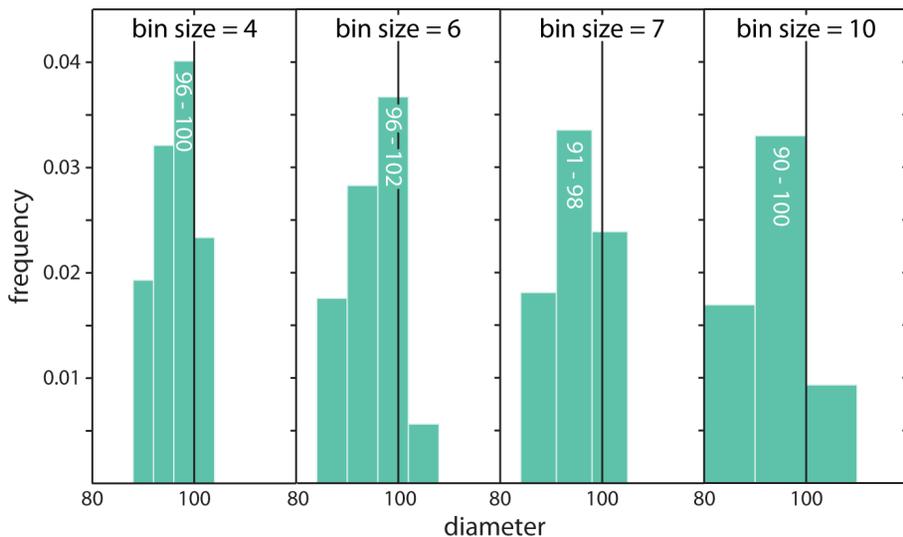


Figure 3. Plots showing the effect of choosing different bin sizes for the same data set. The monodisperse data set is formed by 5997 measures, the actual grain size was set in 100 and the absolute maximum uncertainty in measure within the data was set in ± 4 (4% of the actual size). For clarity, only the bins surrounding the actual grain size are showed. Because 4 and 10 are perfect multiples of 100, the upper limit of the modal interval coincides with the actual grain size. In this example, 4 is the best bin size since we know that the uncertainty within the data is the 0.04. Bin sizes higher than 4 do not produce best estimations and instead produces worse precision (i.e. wide intervals). In the case that the bin size is not a multiple of the actual grain size – the most probable scenario since we unknown the value we are looking for – the actual value may or may not be within the modal interval, although always close.

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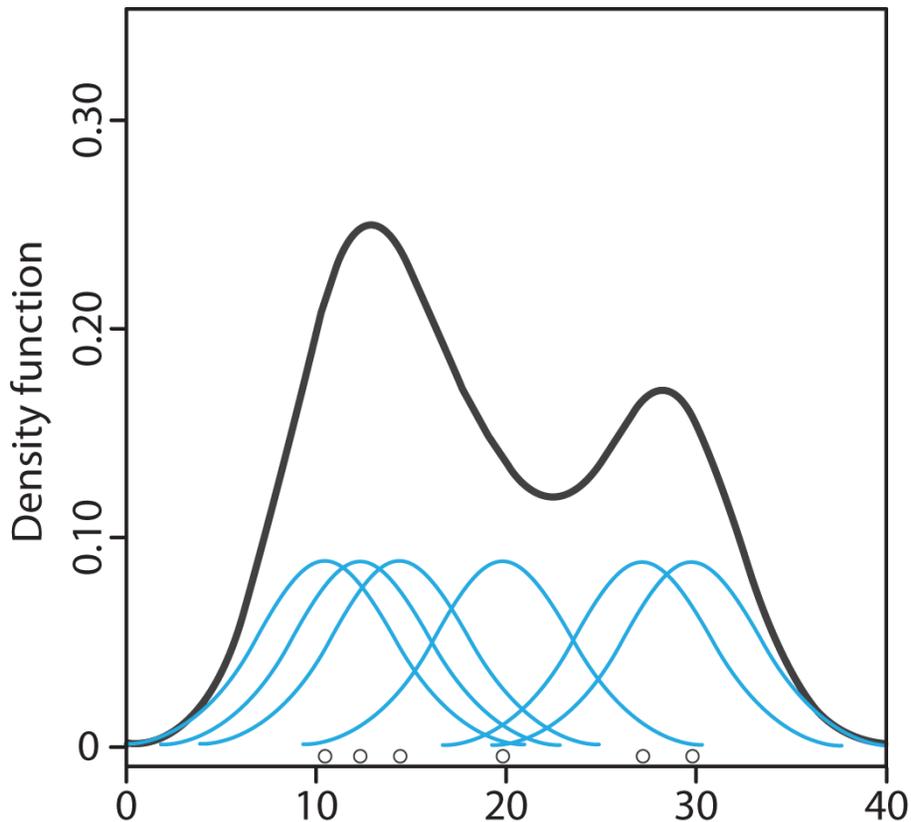


Figure 4. The Gaussian kernel density estimator is a function that stacks a Gaussian “bell curve” on top of each measurement and whose SD, determined by the local probability density, defines the bandwidth (the equivalent to the histogram’s bin size/width). This function is a non-parametric density estimator that, contrary to the histogram, is smooth and independent of end points.

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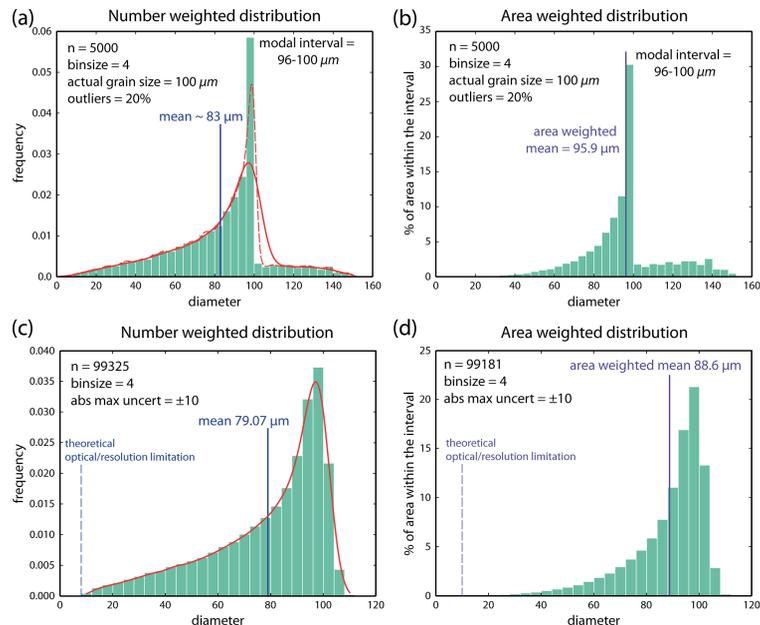
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Figure 5. (a, b) Number and area-weighted plots showing the distribution of apparent diameters of a population of spheres of size 100 in which the 20% of the data are outliers (not fully recrystallized grains; see Appendix B for details). (c, d) Number and area-weighted plots showing the distribution of apparent diameters of a population of spheres of size 100 with uncertainty in the measure. The maximum uncertainty during the outline of the grains was set in ± 10 (10% the actual size). This uncertainty limit also established a theoretical optical/resolution limitation of the measure (i.e. simulates that the technique does not allow grain measuring below the established limit). The distribution of apparent diameters no longer has an ideal *J-shaped* and there are apparent diameters above the actual value. The number weighted plots also shown the Gaussian kernel density estimator using the Silverman rule (continuous red line) and the Silverman rule multiplied by 1/3 (dashed red line) to estimate the bandwidth.

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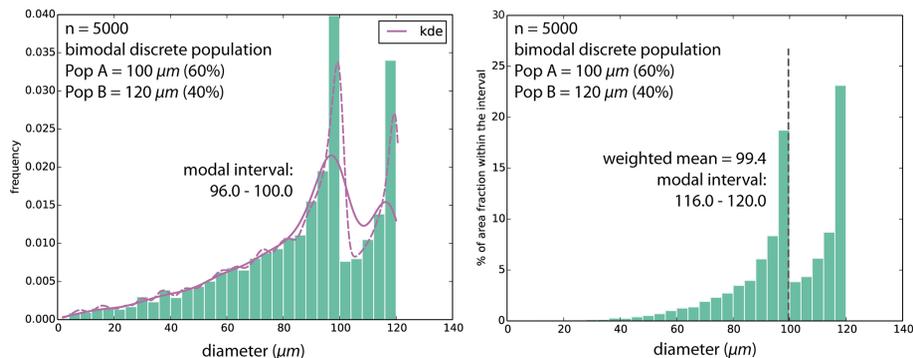


Figure 6. Grain size distribution plots of a bimodal discrete population consisting of a 60/40 % mixture of spherical particles with sizes 100 and 120 respectively. The contribution in volume is 46.5/53.5 % respectively. The two local maxima in both plots indicate the existence of two population of spheres with sizes specified by the local maxima's. Both plots show different modal intervals due to the different approach. The area-weighted plot locate the modal interval in the population that represents the major/main phase (i.e. the volumetric contribution). The number weighted plot shown the Gaussian kernel density estimator using the Silverman rule (continuous purple line) and the Silverman rule multiplied by 1/3 (dashed purple line) to estimate the bandwidth.

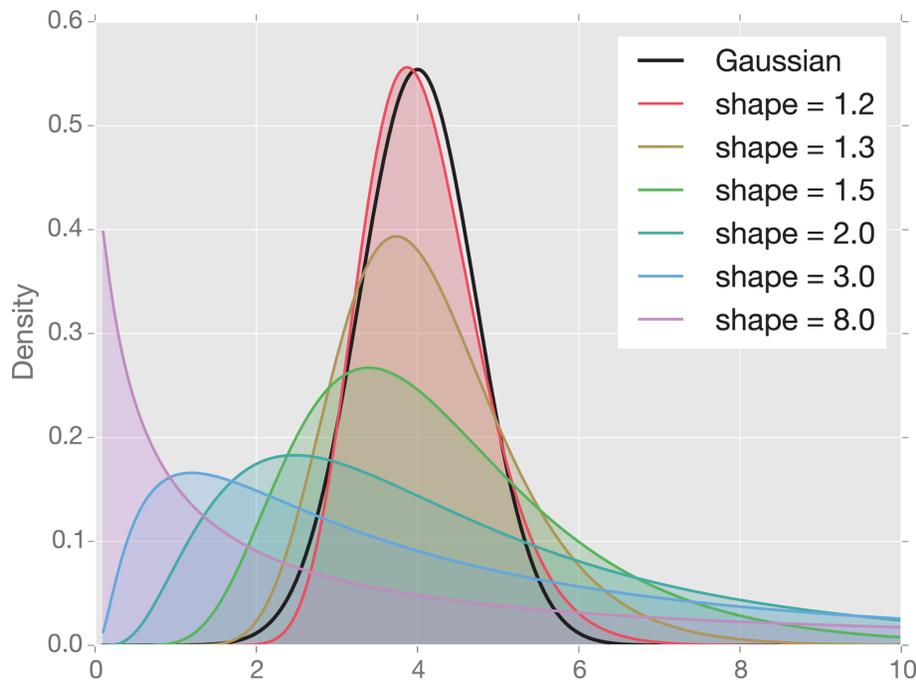
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Figure 8. Probability density functions of selected log-normal distributions with different shape values (σ^*) but same scale ($\mu^* = 4$) compared with a normal or Gaussian distribution (black). A change in μ^* affects the scaling in horizontal and vertical directions, but the essential shape σ^* remains the same. Note that for a same scale parameter the theoretical range of the grain size expected is different considering different shape parameters. Based on Fig. 4 in Limpert et al. (2001).

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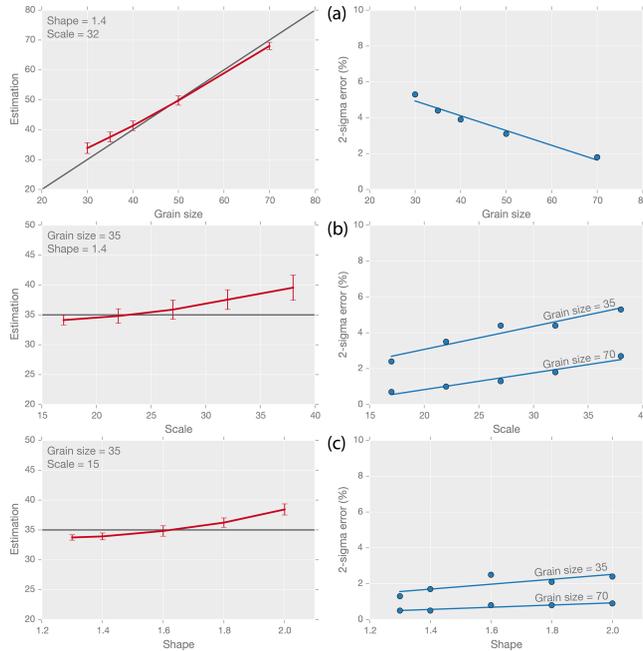


Figure 9. Results of the Gaussian kde peak estimator in the performed log-normal simulations. Each synthetic sample of apparent diameters have a sample size of 12 500 grains and the cut-section and intersection probability effects were taken into account. One hundred trials for each defined log-normal population of grains was performed. **(a)** Estimations using the grain size as variable and values of shape and scale fixed at 1.4 and 32 respectively. On the left, the results of the estimation (in red) respect to the expected (in black). Error bars correspond to the absolute 2-sigma error obtained. On the right, the relative 2-sigma errors respect to the mean (in blue). **(b)** Estimations using the scale parameter as variable and the grain size and the shape fixed at 35 and 1.4 respectively. On the left it is shown also the relative 2-sigma error considering the grain size as 70. **(c)** Estimations using the shape parameter as variable and the grain size and the scale fixed at 35 and 15 respectively.

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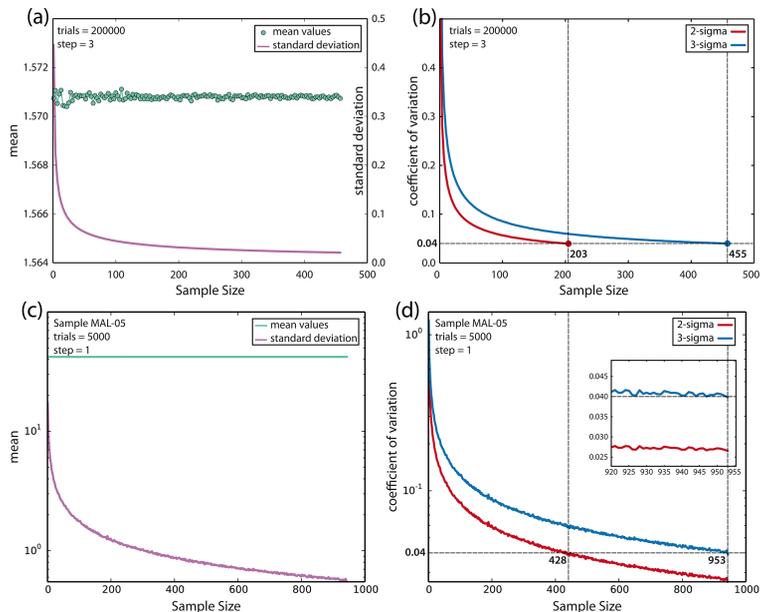


Figure 10. Results of the Monte Carlo simulations to find how many grains are needed to achieve reproducibility using a synthetic monodisperse population of apparent diameters **(a, b)** and a natural dynamically recrystallized mylonite **(c, d)**. **(a)** Evolution of the mean and the SD during the increasing of sample size. Note that the mean barely changes its value due to the large number of trials used in each sample size while the SD declined monotonically as we increased the number of samples. **(b)** Evolution of the coefficient of variation (σ/mean), using the sigma-2 and sigma-3 values during the increasing of sample size. The plot shows that when we measure 203 (for 2-sigma) or 455 (for 3-sigma) grains the variation of grain size estimations in each trial is less than 4 %, this is, less than the typical error found when repeating measurements of the same grain (Berger et al., 2011). **(c, d)** Same as above but using bootstrapping with a data set belonging to a natural mylonite (MAL-05). Note that for clarity the vertical axis have a logarithmic scale. The inset in **(d)** show a linear scale.

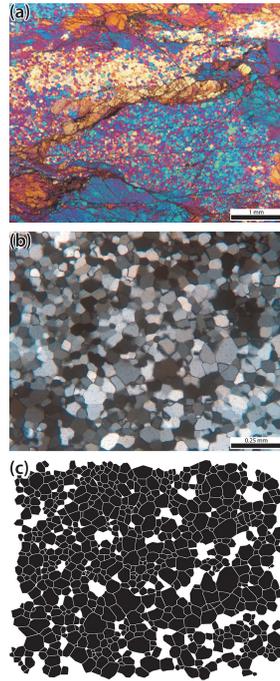


Figure 11. Quartz microstructure in sample MAL-05. **(a)** General aspect of Penedo Gordo mylonites under optical microscope (crossed polars, gypsum plate inserted). Note that original quartz grains are almost fully recrystallized and have a strong lattice preferred orientation. **(b)** Optical micrograph (crossed polars) showing the typical aspect of dynamically recrystallized quartz grains. **(c)** Quartz grain boundaries from micrograph **(b)**. This is the data set O2 in Fig. 13.

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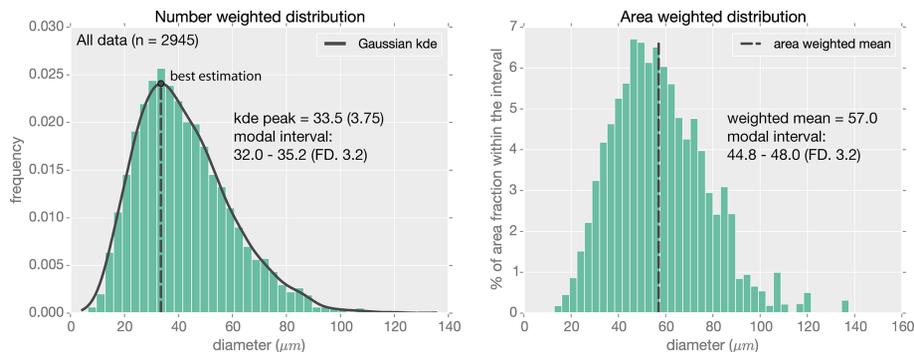
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Figure 12. *GrainSizeTools* script results using the full data set from the natural sample MAL-05. The best estimation is 33.5 microns.

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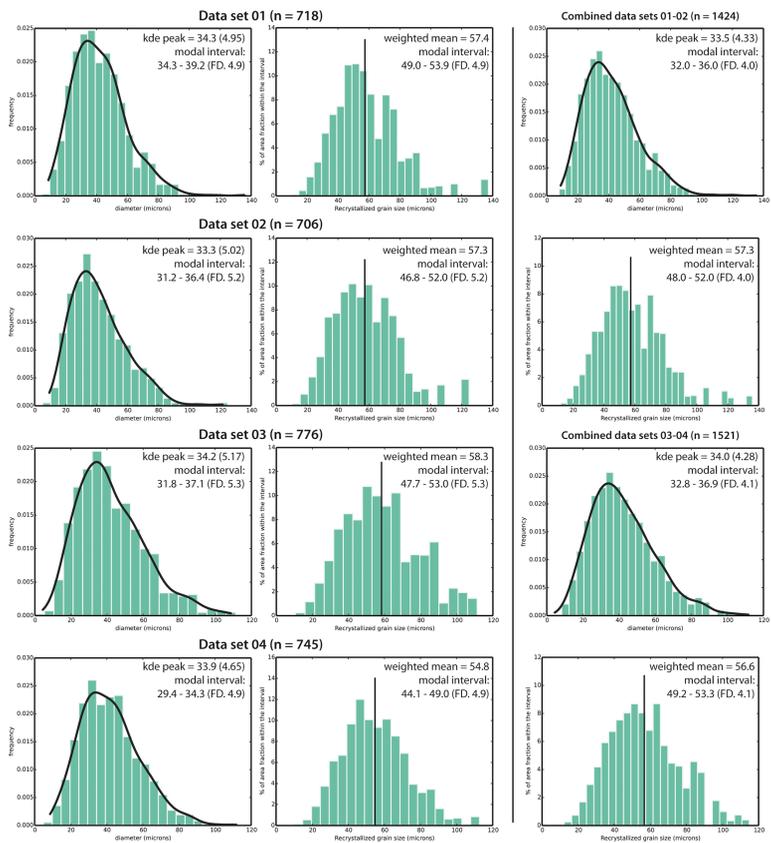


Figure 13. GrainSizeTools script results using different sub-data sets from the natural sample MAL-05 to test reproducibility.

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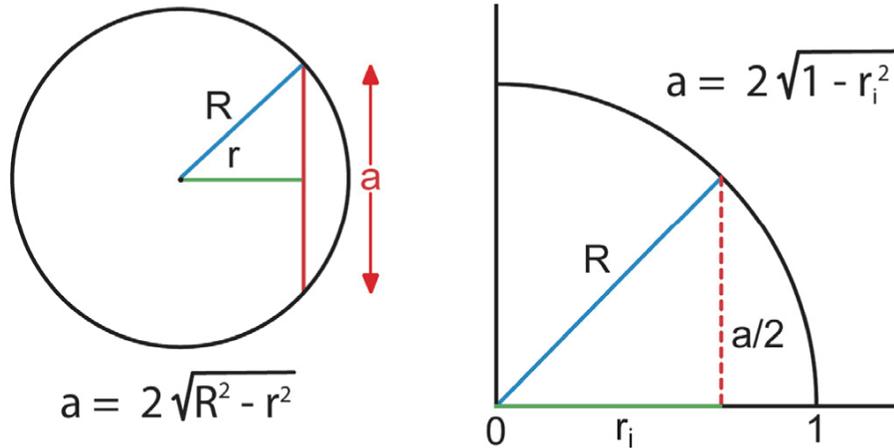


Figure B1. Model to generate apparent random sections through a sphere and calculate the apparent diameter. Following the Pythagorean Theorem, to calculate the chord or section length through a sphere we need to know the radius (R) and the apothem (r). Taking a sphere of radius 1, we generate random apothems (r_i) between 0 and 1 and then calculates and store the apparent diameters (from 2 to 0).

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