The problem of strain-marker centers and the Fry method

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Abstract—The Fry method and its variants will underestimate finite strain when applied to strain markers deformed heterogeneously at marker scale, despite homogeneous behavior at a population scale. This difference results from the post-deformation centers not coinciding with the original pre-deformation centers. The amount of error may rapidly approach 50% for small strains in ideal cases, but is likely to be in the range of 20–30%.

INTRODUCTION

AS ORIGINALLY conceived, the Fry method was developed to measure strains from isotropic anticlustered distributions of strain markers that had been homogeneously deformed (Fry 1979, Hanna & Fry 1979). In subsequent implementations, this robust technique has been applied to marker populations that were believed to have deformed at a sample scale in a statistically homogeneous manner (Cobbold *et al.* 1971). Measured markers have included ooids (Fry 1979), porphyroblasts (Lacassin & van den Driessche 1983), grain aggregates (Schwerdtner *et al.* 1983), chondrules (Cain *et al.* 1986), quartz grains (Dunne *et al.* 1988) and salt domes (Rönnlund & Koyi 1988). The effects of the degree of marker anticlustering, size and shape, and inhomogeneous deformation to the method have been examined and, in some cases, resolved (Crespi 1986, Onasch 1986, Erslev 1988).

A tacit assumption in many of the previous studies has been that the centers of deformed strain markers are the same centers as in the undeformed markers. However, marker-scale heterogeneous deformation can cause the final and original centers to differ in position relative to marker boundaries. For example, deformation could be a heterogeneous concentration of dislocation creep (chondrules), localized transgranular dissolution (quartz grains) or heterogeneous body flow (salt domes). All of these markers lack characteristic predeformational centers that can be identified after straining. Thus, the final centers are determined by qualitative observation or by a centroid calculation, and may not coincide with the sites of original centers. The purpose of this paper is to demonstrate that the Fry method will underestimate finite strain in situations where the final centers of the deformed strain markers do not coincide with original centers.

EXAMPLES

The following examples illustrate the effects of center migration, and have three common characteristics: (1) originally circular grains; (2) a mechanism for heterogeneous deformation by transgranular dissolution; and (3) strain is accommodated entirely by volume loss. It is emphasized that the results are applicable to more complexly shaped objects, other deformation mechanisms, and other strains.

Deformation in columns of circular grains

Consider two simulations where circular grains are deformed, so as to examine the behavior of grain centers (Fig. 1). In the first case (Fig. 1a), strain is distributed equally between grain contacts, so that deformation is uniform on both sides. Consequently, the final centers have the same locations as the original centers and the Fry method yields the correct finite strain.

In the second case (Fig. 1b), the strain is concentrated along alternate grain contacts, representing the end-
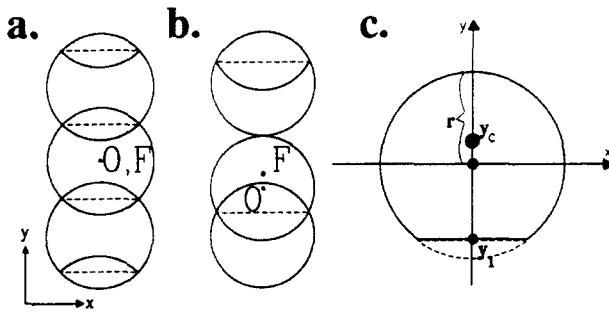
Fig. 1.(a) Three originally circular grains truncated (dashed lines) so that original (O) and final (F) centers coincide. (b) Grains heterogeneously truncated at alternate grain contacts (dashed line) so final center (F) differs from original center (O). (c) Truncated circular grain of radius r with co-ordinate origin at pre-deformational center, truncated edge at y_1 and new center at y_c. Dashed segment is removed portion of grain.

member case for deformational asymmetry, and the final centers differ in location from the original centers because of the asymmetry. For a grain truncating along one side (Fig. 1c), the deformation does not change the x-co-ordinate for the grain center, but causes the center to move along the y-axis away from the migrating edge. The y-co-ordinate for the post-deformation center (y_c) can be computed from the centroid,

$$y_c = \frac{\int\int y \, dx \, dy}{\int\int dx \, dy}. \tag{1}$$

Integrating (1) for the truncated grain in the case where more than half of the original disk remains $(-r \le y_1 \le 0)$, as shown in Fig. 1(c), yields

$$y_c = \frac{\frac{2}{3}(r^2 - y_1^2)^{3/2}}{y_1(r^2 - y_1^2)^{1/2} + r^2\left[\pi - \cos^{-1}\left(\frac{-y_1}{r}\right)\right]}, \tag{2}$$

where r is the grain radius, and y_1 is the y-co-ordinate for points along the truncated edge of the grain. For the case where less than half the original grain remains $(0 \le y_1 < r)$ integrating (1) yields

$$y_c = \frac{\frac{2}{3}(r^2 - y_1^2)^{3/2}}{-y_1(r^2 - y_1^2)^{1/2} + r^2 \cos^{-1}\left(\frac{y_1}{r}\right)}. \tag{3}$$

y_c is the post-deformation center commonly used in the Fry method unless a feature such as an ooid accretion center defines the original center. If y_c is used, strain magnitude may be underestimated because final centers are further from the truncated edge and each other than the original centers (Fig. 1b). For the end-member case, where only alternate grain boundaries are deformed, the actual percentage shortening would be

$$S = \frac{\Delta y_1}{2r} \times 100, \tag{4}$$

whereas the apparent shortening percentage is

$$S' = \frac{\Delta y_1 - \Delta c}{2r} \times 100, \tag{5}$$
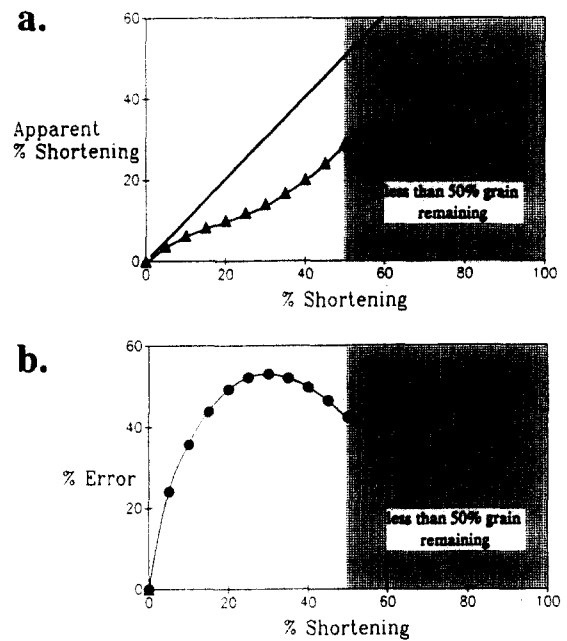

Fig. 2.(a) Actual percentage shortening vs apparent percentage shortening (equations 4 and 5 in text) for geometry in Fig. 1(c). The solid line illustrates case of apparent and actual shortening being equivalent with no underestimation. (b) Percentage error from underestimation as a function of actual shortening (equation 6 in text).

where Δy_1 is the change in grain width parallel to the y-axis from truncating the grain bottom, and Δc is the distance between the pre- and post-deformation centers. The error in the estimated strain is

$$\frac{S - S'}{S} \times 100. \tag{6}$$

The error in strain measurement increases rapidly for small strains (Fig. 2). For example, strain may be underestimated by 50% for an actual shortening of 20% (Fig. 2b).

Pervasive transgranular deformation

Consider a simulation where circular grains are deformed in a homogeneous displacement field (Fig. 3) described by

$$\begin{aligned} x' &= x \\ y' &= y(1 + e), \end{aligned} \tag{7}$$

where (x', y') are the co-ordinates for final positions, (x, y) are co-ordinates for initial positions and e is the elongation. The simulation consists of variably-sized, close-packed grains (Fig. 3a), subjected to 40% shortening $(e = -0.4)$ by transgranular dissolution with volume loss (Fig. 3b), which causes truncation between grains at all interpenetrating contacts.

The normalized Fry method (Erslev 1988) was used to determine strain in the simulation. The pre-deformational centers yielded the correct strain ratio of 1.68 (Fig. 3c), whereas the calculated centroids yielded a lesser strain ratio of 1.40 (Fig. 3d), corresponding to 29% apparent shortening or 28% error (Fig. 2b). This
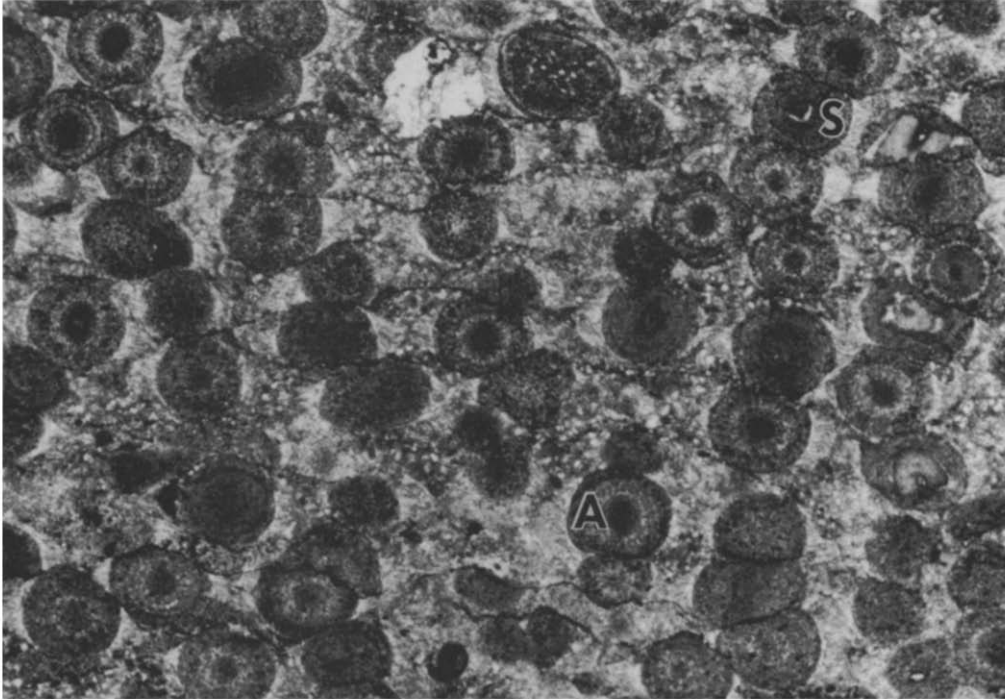
Fig. 4. Photomicrograph of deformation style in oolitic limestone (A—asymmetrically deformed grain, S—symmetrically deformed grain).

error could be achieved by an average imbalance of only 5-10% in truncation of opposing grain boundaries with respect to the original centers. Greater shortening imbalances between grain boundaries for loose-packed, variably-sized grains are possible than for the close-packed populations because the loose-packed grains are less strongly anticlustered (Fry 1979, Crespi 1986).

Deformation in an oolitic limestone

An oolite sample is used to illustrate that the Fry method underestimates strain for data from real rock samples (Fig. 4). The advantage of using ooids for this example is that strain determined from their accretion centers, which are assumed to be original centers, can be compared directly to strain determined from calculated centers.

The accretion centers yielded a strain ratio of 1.68 via the Fry method (Fig. 5a). Some points obscure the central void of the Fry plot because strain is preferentially concentrated along some of the transgranular dissolution sites (Fig. 4), producing short chord lengths between those adjacent accretion centers. In contrast, the calculated centroids yielded a strain ratio of 1.42 via
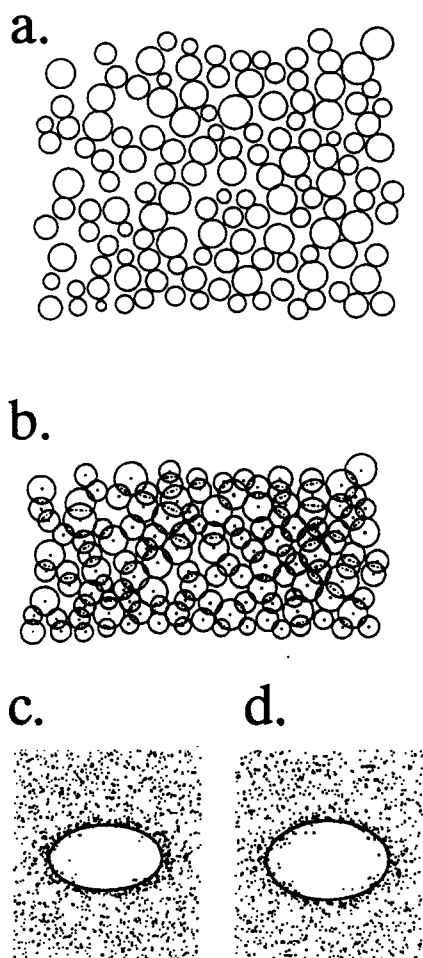
Fig. 3. Simulations of pervasive transgranular deformation. (a) Undeformed population of 135 close-packed circular grains. (b) Population (a) deformed by 40% vertical shortening with dots defining original centers and dashed lines as truncated grain boundaries. (c) Normalized Fry plot for (b) using original centers. (d) Normalized Fry plot for (b) using final calculated centers. Ellipses define chosen strain.
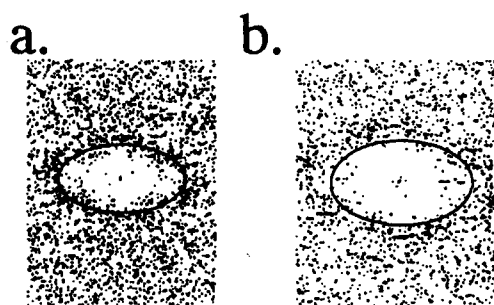
Fig. 5.(a) Fry plot for oolite sample using 236 accretion centers. (b) Fry plot for oolite sample using final calculated centers. Ellipses define interpreted strain.

the Fry method (Fig. 5b), which is a 25% error that requires about a 5% imbalance in grain truncation (Fig. 2).

DISCUSSION

In strain studies that use markers such as grain aggregates, some porphyroblasts, quartz grains, chondrules or salt domes, the pre-deformational centers are not defined by distinctive features. The only available centers for analysis are the calculated centroids. The above examples show that centroids will underestimate the finite strain when used in the Fry method, if the sample is deformed heterogeneously at marker scale.

Strain markers that lack clearly defined original centers should be examined for the effects of object-scale heterogeneous deformation before employing the Fry method. The heterogeneity may be manifested as transgranular dissolution, variations in dislocation densities, variations in the density of Tuttle lamellae, or localized recrystallization. In such situations, the Fry method or a variant can yield an underestimate for finite strain. As shown in the first example (Fig. 1) with strong anticlustering, the error will approach 50% even at small strains of only 20% shortening (Fig. 2). The second and third examples (Figs. 3, 4 and 5) demonstrate the maximum error for a given shortening can only occur where the strain is strongly heterogeneous at marker scale. Instead, smaller errors of 20-30% are more likely, even in less anticlustered populations with moderate to large strains where strain ratios exceed 1.5.

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