

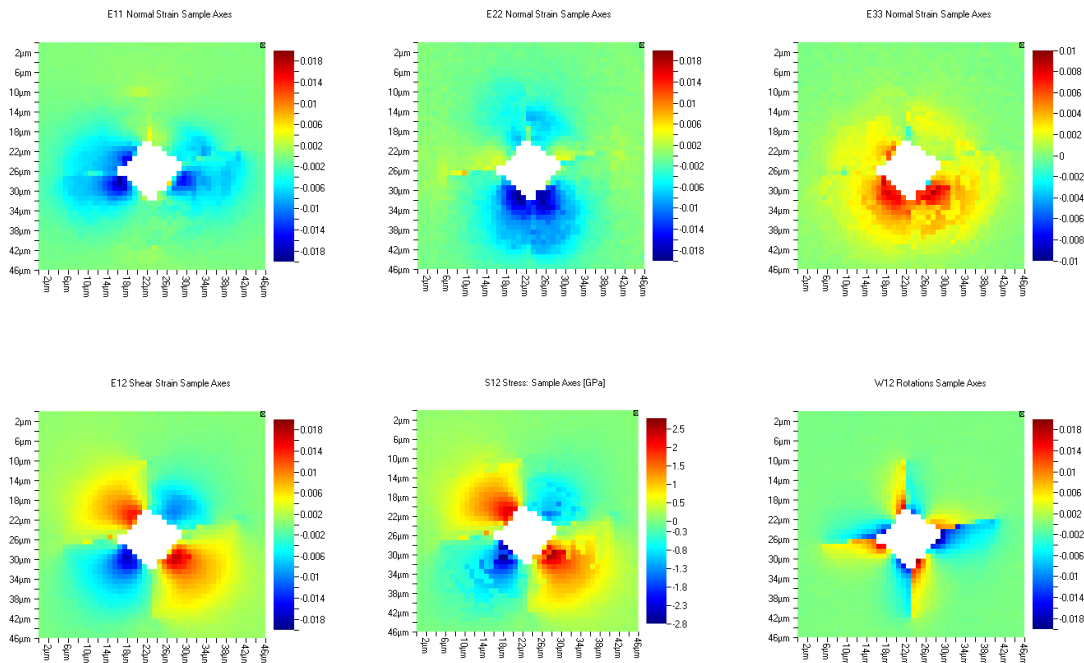
Strain measurement using HR_EBSD: Polycrystals

Tutorial #2: By Dr. David Dingley

Introduction,

I finished my first tutorial with an example of strain measurement using Cross correlated EBSD (EBSD). The sample was single crystal silicon which had been deformed by a micro-hardness indent. There were two issues in the example, the strain state of the reference pattern needed for the cross correlation and the magnitude of the strains surrounding the indentation. I did not go into details in the last tutorial as that was more fitting for this tutorial as it brings up some current issues of a complex nature.

I show the maps of the strains rotations and stresses surrounding the indent again to set the flavor of what is included here.



Normal strains, shear strains shear stress and rotations as examples of absolute strain measurement

There is no problem in this example of determining a point to act as the reference point that is strain free. The pixel in the top right hand corner coloured black is just one of many that could have been chosen. It is far from the deformation zone and the uniform colouration surrounding it shows that the strain reduced to this level well before it.

So what about the magnitude of the strains? Regard the map of the shear strain component ϵ_{12} (bottom row left). It is very symmetric with shears on opposite faces across the indent are the same whilst those on adjacent faces have opposite sign. This is fine. But let us look at the magnitudes The peak magnitude of the positive shear strain is 0.018 (1.8%) and the peak negative strain is also 0.018. This is a very large elastic strain and many materials scientists would say that the sample must have

fractured and the strain released. The experiment says that it hasn't. Is this reasonable. Well in this case of silicon where no dislocation activity is possible at low temperature and under the circumstances of an indentation, such a strain is expected. Finite element calculations are in support. We might also examine the other maps and note just how perfect the results appear for the measured rotations where the maximum is just 1 degree and for the shear stress σ_{12} where the maximum stress is 2.8GPa. The two fold symmetry seen in the ϵ_{11} and ϵ_{22} maps is due to the relative orientation of the diamond indenter and the crystal orientation. Only the ϵ_{33} map shows any significant deviation from symmetry.

These strains are calculated on the assumption that within the diffraction volume the normal stress is zero. Whereas this must be true for the very near surface regions it may not be for the entire volume. One of the problems associated with this observation here is that as it is actually the stress normal to the free surface that must be 0 then as the surface is actually tilted away from the bulk normal and we take the bulk normal as the one we set to 0 stress, then we may well have introduced some error in the measured ϵ_{33} component. The precise map then depends on the surface rotations (Vaudin, M. D., Stan, G., Gerbig, Y. B., & Cook, R. F. (2011). High Resolution Surface Morphology Measurements using EBSD Cross-Correlation Techniques and AFM. *Ultramicroscopy*. Elsevier. doi: 10.1016/j.ultramic.2011.01.039), which unfortunately we do not have for this particular experiment.

The polycrystalline case.

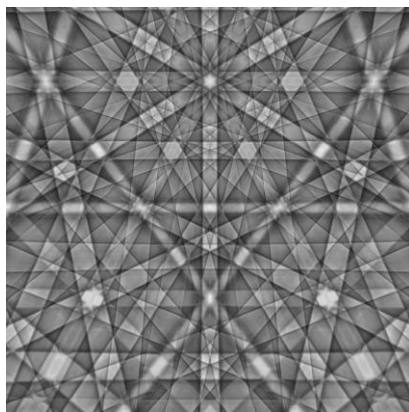
The applications of the HR EBSD technique have recently been concerned with polycrystalline samples. There is no problem in studying recrystallized or annealed samples where we might be interested in residual grain boundary strains for example but there will be a problem once plastic deformation has been induced and dislocations are distributed throughout the grains. (Already half a dozen papers have been written on the subject and some are, I am sorry to say, not all that helpful). Here is the gist of the problem.

If, for example, the point at which the reference pattern was recorded was not in a zero strain state but in uniaxial tension then this would still be regarded by the software as the zero strain state and every subsequent measurement would thus be in error. To determine the absolute strain state we would have to subtract from every measurement the tensile strain at the reference point. But as we do not know the strain state of the sample element from which the reference pattern was taken we can not do this. The same argument applies for any other strain component that was not zero at the reference point.

There is no answer to this problem at present. But there will be one soon. We are very close. It is not the principle of how to overcome this problem but its execution. The currently proposed solution is to simulate an EBSD pattern of the same crystal and orientation and impose in the simulation zero strain. We then compare the simulation with the EBSD pattern from the specimen.

The simulation has to be pretty good though as if it differs from the experimental pattern significantly the cross correlation will compare dissimilar features in the actual and simulated patterns leading to spurious measurements. Even an unstrained experimental pattern can then appear distorted when compared with the simulation. Fortunately, very good EBSD simulations are now becoming feasible due to the

eHRelient work of Winkelmann (2006) whose computer program is currently available commercially from Brüker (There is also free version available at www.bruker-axs.de). Below, is a simulation kindly forwarded by TB Britton of Oxford University, and produced when the software was freely available through Dr. Winkelmann directly. For a full description and even improved simulations see Winkelmann 2010. The pattern is of a titanium base alloy.



Simulated EBSD pattern (*Winkelmann software*) supplied by TB Britton

What is of fundamental importance in the procedure is that the pattern center, x^* , y^* , and the specimen to screen distance z^* (together called the camera parameters) must be the same in the simulation as those under which the real EBSD patterns were recorded. A few simple experiments show that the sensitivity of strain measurement is such that even a fraction of a pixel error between pattern centre values completely invalidates the measurement (Villert, S., Maurice, C., Wyon, C., & Fortunier, R. (2009). Accuracy assessment of elastic strain measurement by EBSD. *Journal of microscopy*, 233(2), 290-301. doi: 10.1111/j.1365-2818.2009.03120.x).

This is discussed in some detail in the last part of this tutorial. At this stage of development of the EBSD technique it is not possible to know the experimental pattern centre to the required precision so that any papers purporting to use this technique without at the same time proving they know the experimental pattern centre to a fraction of a pixel must be read with great caution. This is the basis of the controversy about using the technique.

For samples deformed beyond the elastic limit therefore where dislocations are spread throughout the crystals we cannot at the moment produce strain maps where we are absolutely confident in the absolute values shown. However we can still be confident in relative values. They will be relative to the strain present at the point the reference pattern was recorded and relative to each other. To maximize the usefulness of the technique in these cases we must therefore explore ways in which we can locate areas in a sample, or in a particular grain in the polycrystalline case, where we can be confident that the strain is at least small. (We should perhaps note here that in applications of the technique where plastic strain effects are measured such as in mapping High Resolution Kernel Average, (HR KAM), the strain gradient and the GN dislocation density, absolute knowledge of the camera parameters is not needed as they depend only on relative measurements so are thus independent of the actual strain in the reference pattern.

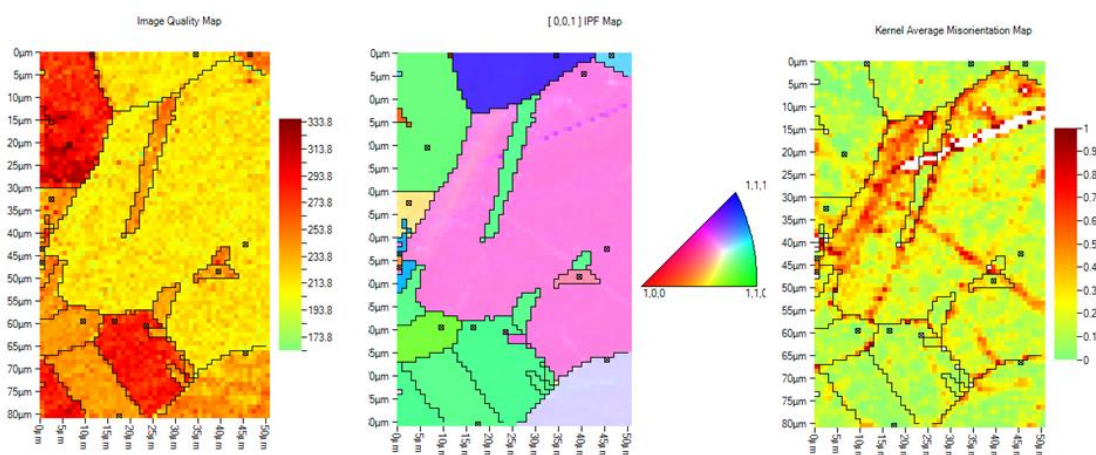
Seeking low strain regions.

First of all we have to accept that at the moment we cannot know the absolute strain with the accuracy anything like the precision to which we can determine it. Let us make clear the difference between accuracy and precision. Accuracy is a measure of how close we are to the true value. Precision is a measure of the random error in the measurement. The random error may be very small but systematic errors, e.g. the reference pattern is not one depicting zero strain, may result in the measured value being far from the true value.

However, not to despair, even if we do not know the accurate strain state of the zone from which we recorded our reference pattern, the *difference* in strain of any other point with respect to it remains known to the stated precision of the technique simply because we use the same reference point for each comparison. The proven precision of the Crosscourt 3 program is 1 part in 10000.

To demonstrate how I examine strained samples in such circumstances I include here an example of the mapping of the strain distribution in lightly deformed polycrystalline copper. I take you stage by stage through my reasoning process.

The data shown below was obtained by performing a normal OIM scan over the selected area and at each point of the scan a full resolution, 1K x 1K image of the EBSD pattern was recorded. The first output from the software is the standard maps you would expect in any EBSD package; image quality map, IPF map, confidence index map and fit map. To these standard maps we have added another, Kernel Average Misorientation (KAM) map. This map, originally introduced by TSL, has a value for each pixel equal to the average disorientation that pixel has with its neighbours. We show first the IQ, IPF and the KAM maps, the first two using Edax_TSL OIM analysis software, c/o Oxford University, the third calculated by Crosscourt.



IQ, IPF and KAM maps.

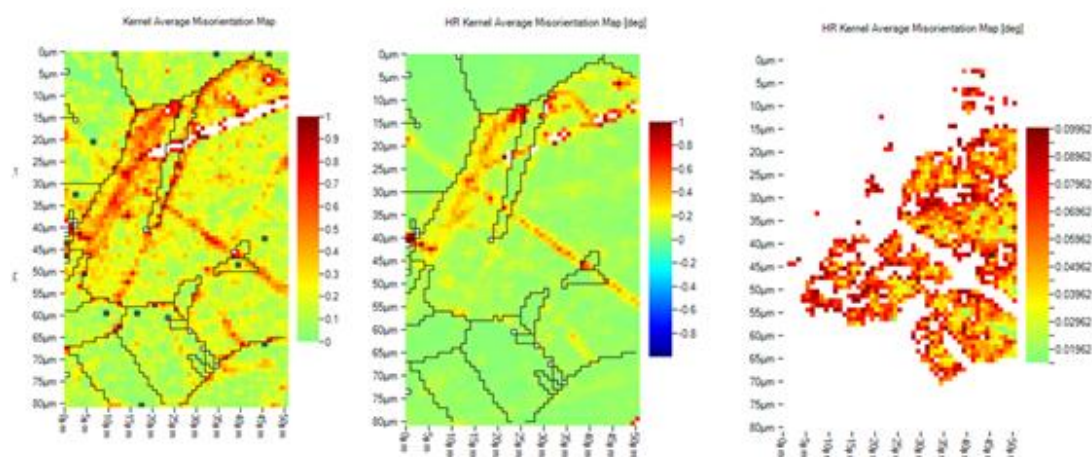
The KAM map has had a threshold applied to omit all values above 1 degree.

We now approach the cross correlation procedure and as discussed above we have to select a reference point in each grain so that all strain, rotation and stress values subsequently calculated will have values with respect to those points. I have found it best to allow the computer to select the reference points and I have used the selection

criterion as the point in each grain that has the smallest KAM values. I could have used best image quality, fit parameter, confidence index parameter or I could have selected the points manually. I am seeking the point in each grain which is likely to be under minimum or even better, zero strain.

Internal strains often show rapid change from point to point and if they go significantly beyond the elastic limit they will typically include dislocations within the sample volume and this will be manifest by crystal rotations and a higher value of the KAM. Thus, ideally, the software should search for regions where the KAM is small over as large an area as possible. However, because of the low precision in orientation measurement using the Hough transform to measure orientation, the standard KAM is noisy so that we in fact use only the lowest KAM value in our initial reference point selection and ignore the area over which it extends.

Below is shown a standard KAM map in which the pixel with minimum cross correlation value in each grain is indicated by a cross within the pixel.

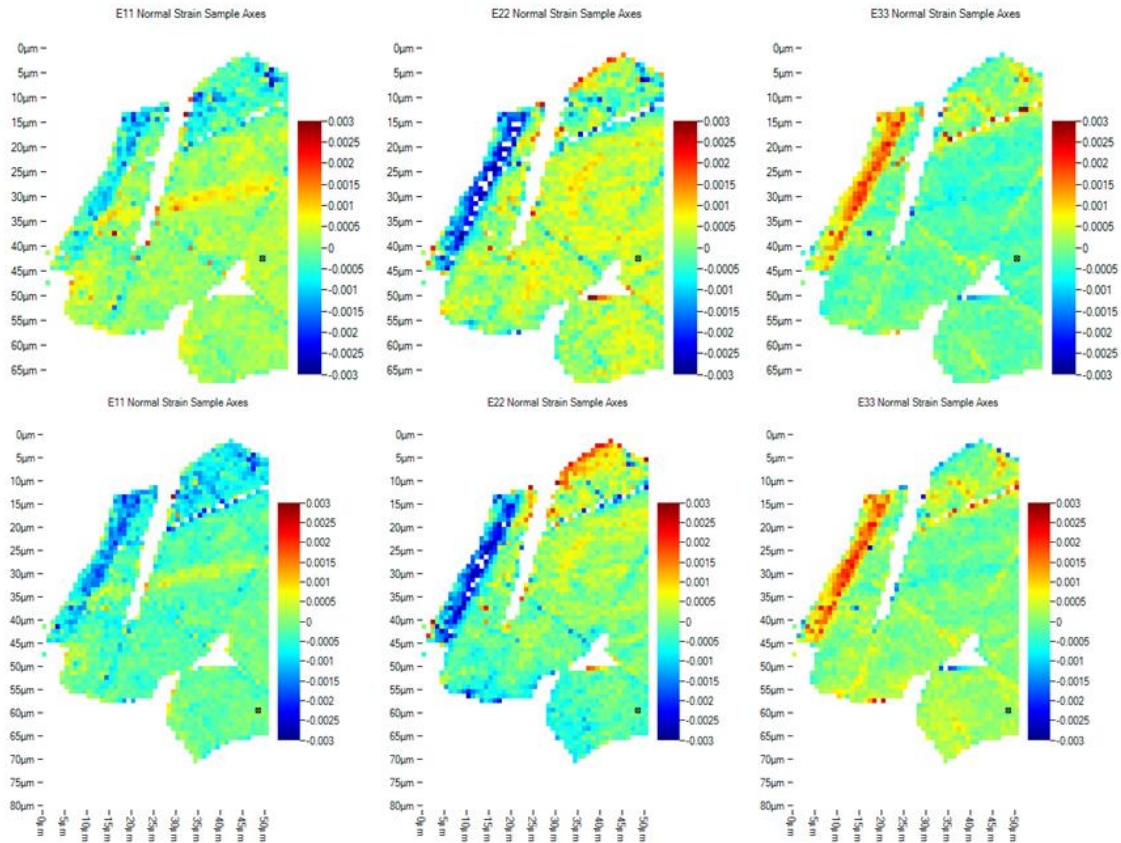


Left; Standard KAM, middle; high resolution KAM filtered at the 1 degree level right; high resolution KAM for central grain filtered at the 0.1 degree level.

Next to it is a high resolution KAM map calculated using the cross correlated data, and the corresponding reference point in each grain. It is immediately obvious that this map is far less noisy than the normally produced KAM map. It is simply a consequence of being able to measure disorientations 100 times more precisely using the cross correlation data. However, we are still searching for a large region in each grain that contains only small KAM values. We will then use a pixel within such a region as a new reference point for the grain. The display default value for the colour range in the KAM map of 1 degree is too large to show this clearly so that in the last of the three images the colour range is reduced to 0.1 degrees. I have selected just the large central deformed grain for this part of my analysis. All white pixels within this grain have KAM values greater than 0.1 degrees. The largest area with minimum strain is now more easily identified. It is the green area located towards the bottom right corner.

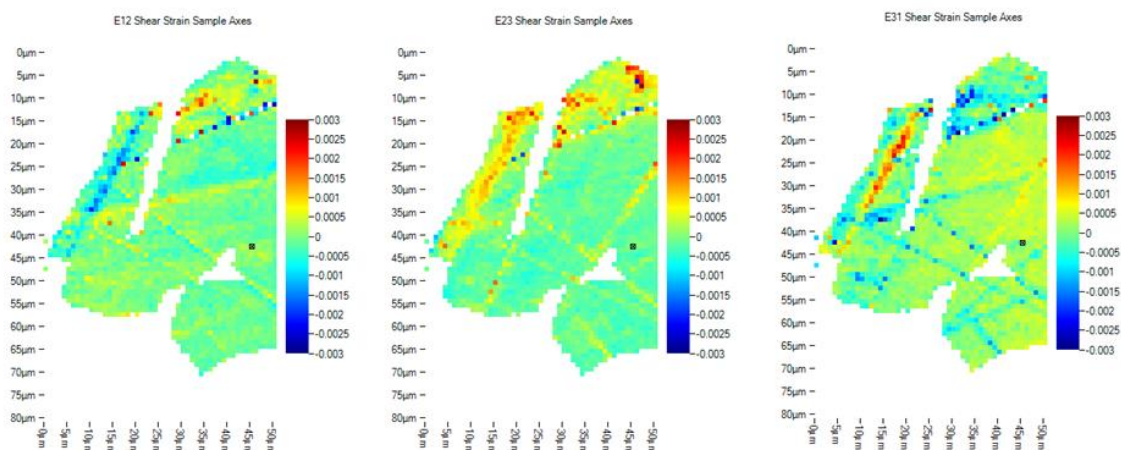
The KAM in this zone is 0.02 degrees. The area extends 5 microns by 1 micron. Although, we do not know whether the strain in this zone is zero, the probability is it is very low. We thus redraw the strain maps via a menu option using one of the pixels

in the green region as the new reference point. In the resulting map the strain values in this pixel are reduced to zero and the strain values for all other pixels are adjusted by subtracting from their strain values the original values of the new reference point. We compare below the strain maps of a single grain as calculated using the automated selection of the reference point and those calculated using the new reference.

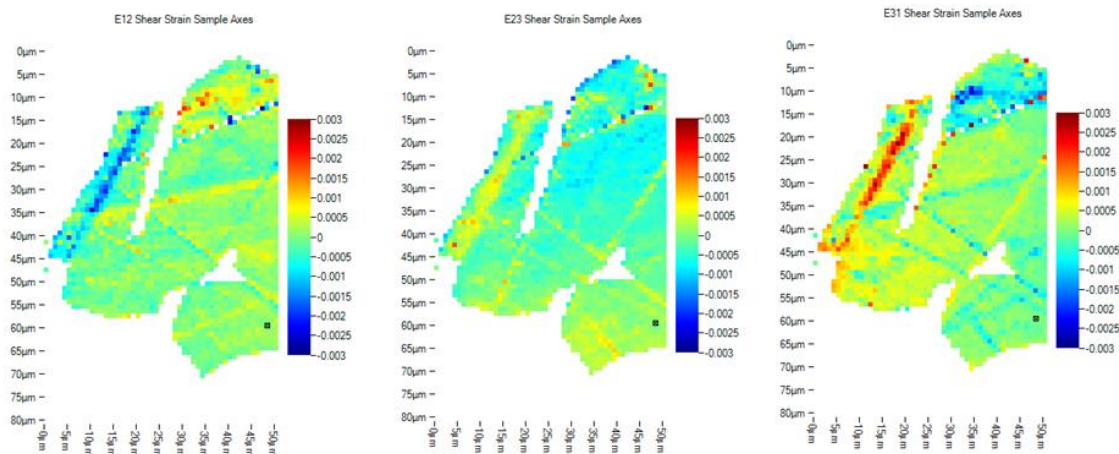


Upper maps-normal strains maps using auto selected reference point. Lower maps - corresponding maps of normal strain using the new reference point. Reference points are marked x.

We can do the same thing for shear strains.



Shear strains maps using auto selected reference point. Reference point at x.



Shear strains maps using manual selected reference point. Reference point at x.

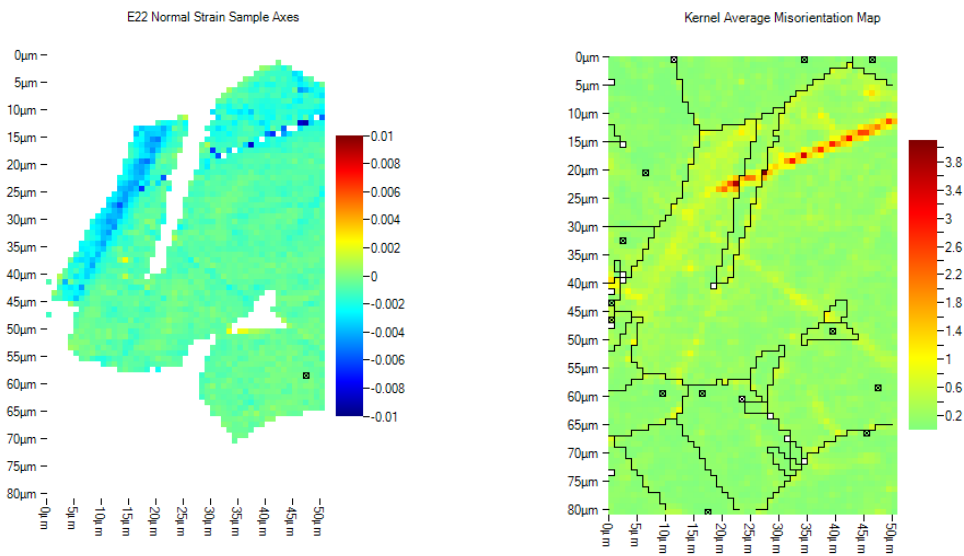
We do not in fact know which is the more accurate set of maps. But the criterion I have chosen here gives me a greater confidence that the set determined using a manually selected reference point on the basis of a small KAM value within an area of small KAM values, is closer to the true values.

That leaves us with the interesting observation which in the several studies I have made, appears quite frequently. It is that some of the strain values are significantly larger than the elastic limit. This is problem 2 I referred to above. In all of the maps I have ranged the color scale to include strain values between plus minus 0.003, i.e. approximately 3 times the bulk elastic limit. Any pixels above this value are white in the maps. (Remember the above maps are for just the one large and most deformed grain observed in the scan).

Most of the strain maps show a distribution of strain that is reasonable, i.e. they show a range of strains going approximately equal from positive to negative albeit that the range exceeds the elastic limit. However, there is one region that merits further examination. It is the stripe of high strain running parallel to the top left grain boundary. It is clearly seen as a large compression (dark blue) in the map of the normal component strain ϵ_{22} and in tension in the map for the ϵ_{33} component. In the map ϵ_{22} , as well as the large compressive strains, there are, at the same time, some regions of large tensile strain close to the upper grain boundary. The apparent strain range within the sample is -0.003 to +0.002. Because the strain range swings from + to - we can not explain away the large values on the basis that the reference point strain is not actually zero. This is because, if we reduced the maximum value (-0.003) of the compressive strain to say -0.001 we would have to raise all other values by +0.002 so that the maximum tensile value would increase to +0.004 an even greater strain than before and now 4 times the macroscopic yield point. Thus, if we are to doubt that the observed strain values of 2 to 3 times the yield strain are valid, then we have to find some alternative explanation for it.

I have repeated this map below and set the maximum strain value shown to 0.01, 10 times the elastic limit. Any pixels showing this level of strain must be highly suspect. They will appear dark red or dark blue. In fact, there are some but as we can see they

are contained in what appears to be a deep scratch running across the grain. The scratch is more clearly depicted in the high resolution KAM map which I also repeat here for a direct comparison with the strain map.

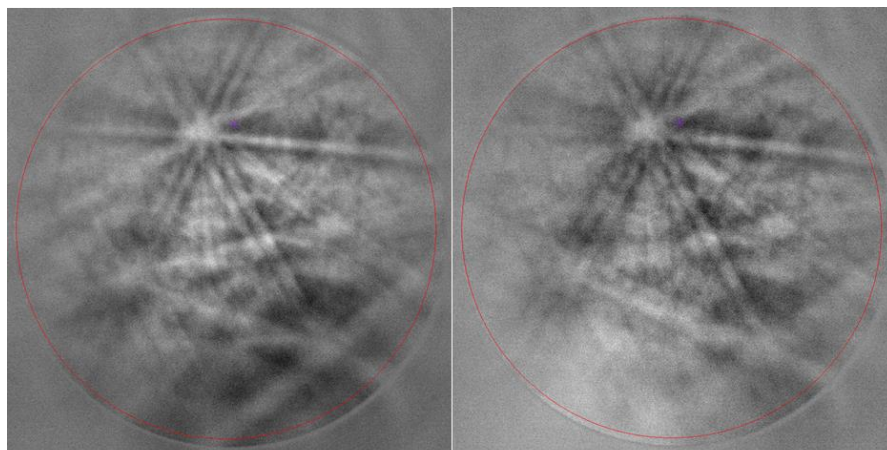


Normal strain map ϵ_{22} for large grain.

KAM map for all grains.

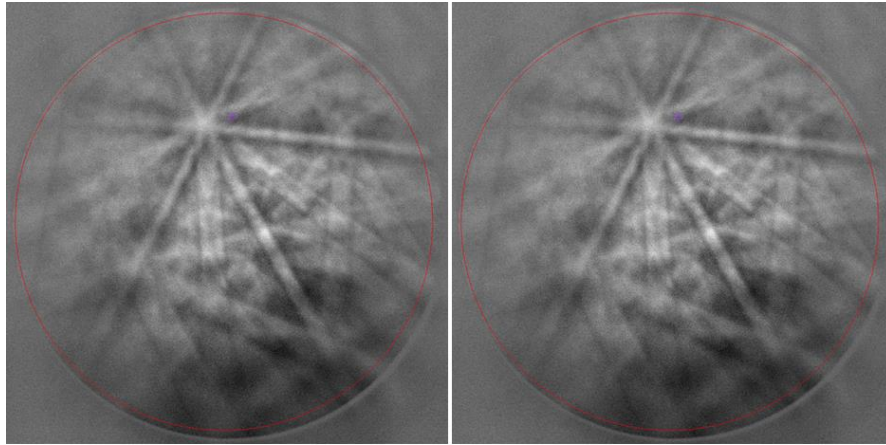
I am going to examine these two maps to discover whether there is something interfering with the strain measurement that would clearly invalidate the high strain measurements. I will use the data in the scratch to do this

I have pasted below the EBSD patterns obtained from different pixels within the upper scratch. Within the scratch the as measured strain values ranged from 0.001 to 0.01, up to 10 times the elastic limit. Surely this must give us a clue as to what is happening. Beneath each pattern is the recorded ϵ_{22} strain value.



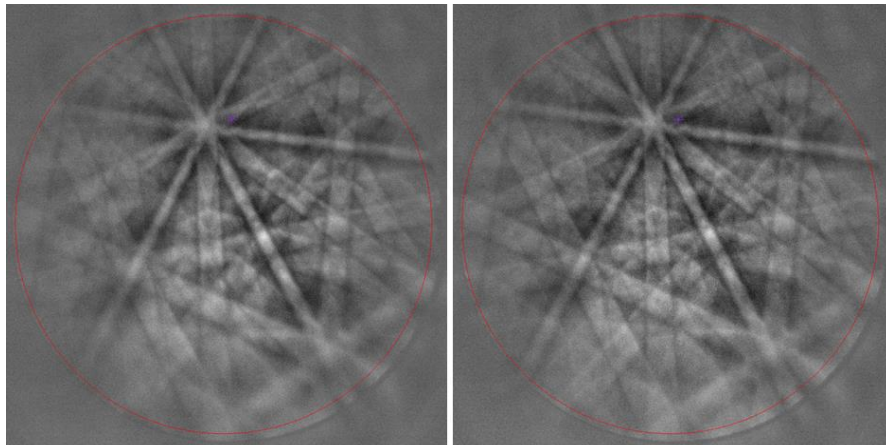
ϵ_{22} 0.03 normal strain (scratch)

ϵ_{22} 0.01 normal strain (scratch)



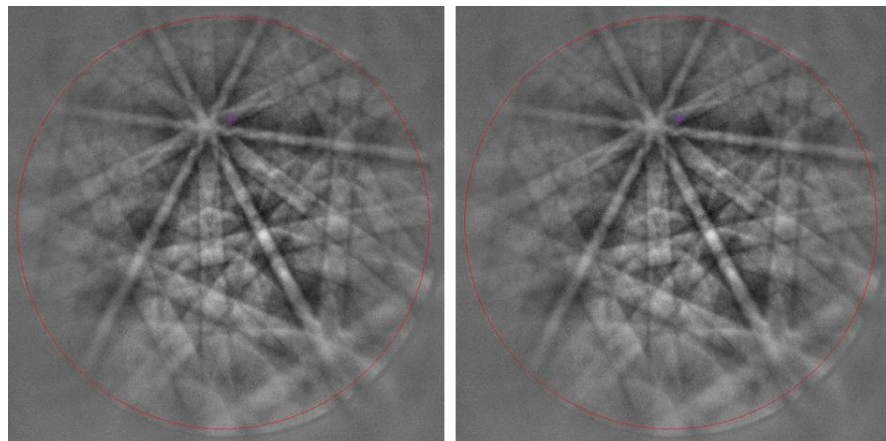
ϵ_{22} 0.009 normal strain (scratch)

ϵ_{22} 0.006 normal strain (scratch)



ϵ_{22} 0.003 normal strain (scratch)

ϵ_{22} 0.002 normal strain (scratch)



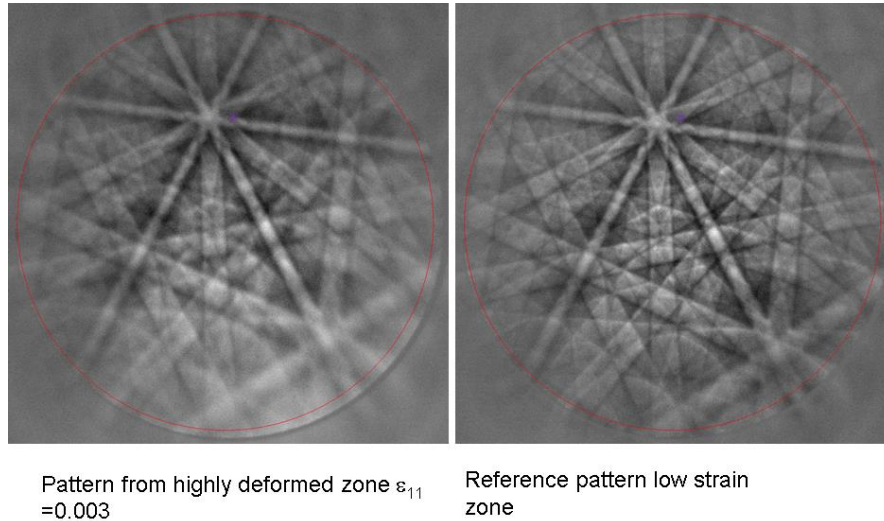
ϵ_{22} 0.001 normal strain (scratch)

Reference pattern

It is clear the extreme strain values are from very poor patterns. The first pattern clearly demonstrates that within the crystal volume extends contributing to the pattern, a column which theory suggests is probably of the size 20nm in diameter and 60nm into the specimen, one can indeed get orientation changes of a degree or more producing diffuse lines and/or overlapping patterns. The cross correlation procedure will be confused in such circumstances and is the reason for the inaccurate strain

values in the scratch. In different regions of the scratch higher quality patterns can be obtained as shown in the figure. The measured elastic strain values obtained from these patterns, included in the caption, are quite reasonable.

Let's now make a similar comparison, between an EBSD pattern taken in the deformation band at the upper grain boundary with the EBSD reference pattern. The maximum measured normal strain value from the pattern for ϵ_{22} is -0.003 (it is in compression).



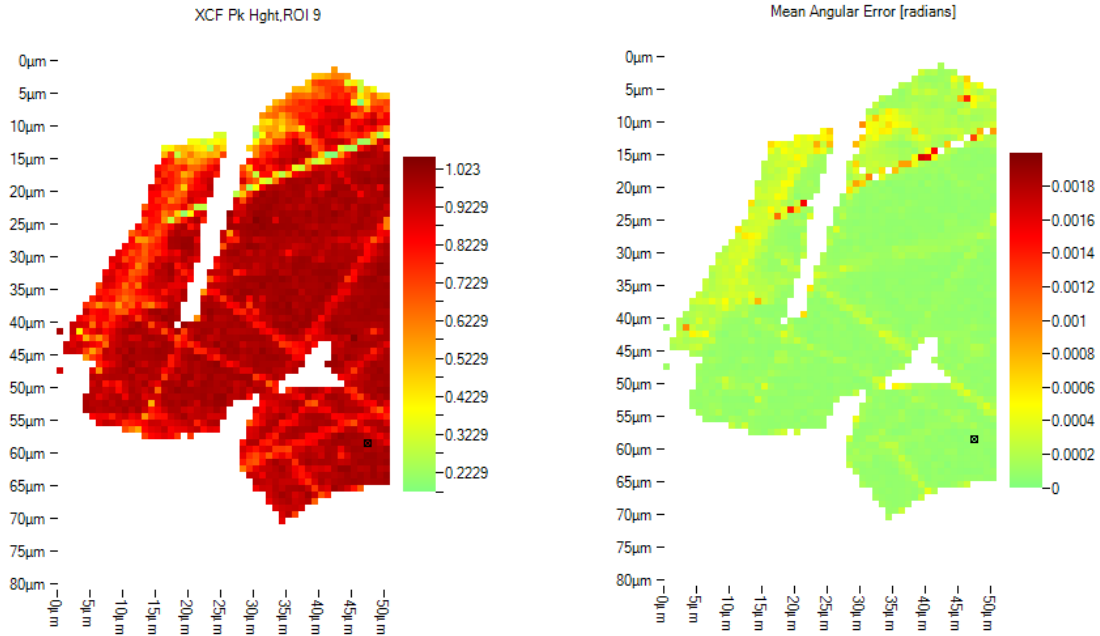
This is large but although the EBSD pattern from the deformed region appears more diffuse it is nothing like as diffuse as some of the patterns from the scratched region. The pattern from the deformed region is also rotated from the reference pattern but by less than 1 degree. This small rotation, which is extracted from the primary deformation matrix to allow elastic strains to be measured, is unlikely to affect the accuracy of the strain measurement. Rotations of up to 8 degrees are well within the scope of the technique. Hence, if an artifact is playing a role it has to be the diffuseness of the pattern from the deformed area. (Note this diffuseness results more from crystal rotations *within* the sample volume than to line broadening due to lattice parameter change). We already know from the high value of the high resolution KAM, that significant orientation changes exist between neighboring pixels in this band. These leads us to ask, is even this small amount of diffuseness observed in the pattern really enough to invalidate the strain measurement. It is not so obvious as in the case of the scratch but it is sensible still to ask the question. We have to find some quantitative measure to answer it.

Quantitative measures of unreliable strain measurements

There are two possible approaches:-

- 1) using the cross correlation peak height and
- 2) using the geometric mean error.

Two maps showing the distribution of these functions are shown below.



Cross correlation peak height and geometric mean angular error maps for a single grain.

The Cross correlation peak height is a measure of how well the EBSD image within a ROI from the reference pattern matches the corresponding image within the same ROI from the deformed pattern *after* it has been shifted so that the two images match best. The result is normalized against the peak height of the auto-correlation peak height of the reference pattern.

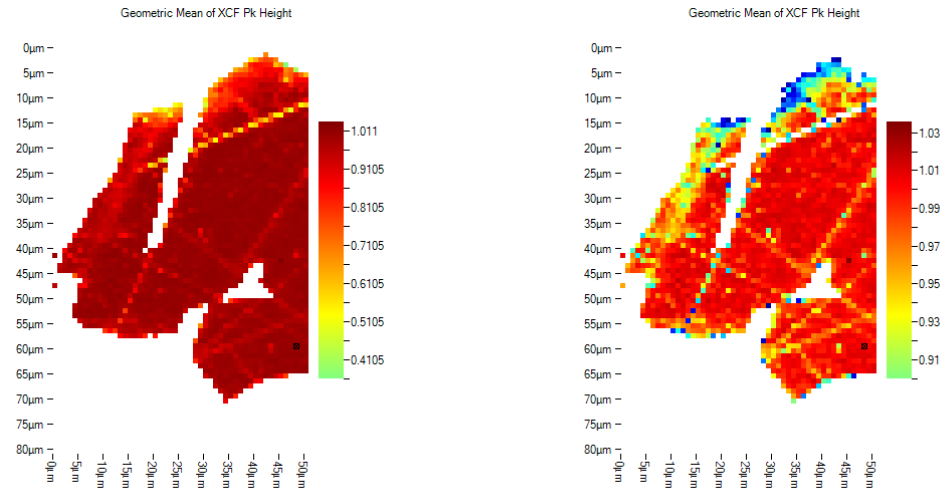
The Mean Angular Error (MAE) is the mean of the errors for each ROI, between the *as measured shift* of a particular ROI and the *shift predicted* from the finally calculated strain tensor for that same ROI. We will use this latter information later but first we will examine the Cross Correlation peak height.

If there had only been a uniform shift, i.e. rotation but no strain, between the reference pattern and the strained pattern then the peak height correlation value would be very close to 1 depending on the amount of shift. If one pattern was distorted however with respect to the other and no crystal rotation then the Peak Height value would decrease but still be very close to 1. Rotation within the sample volume causes diffuseness in the pattern and a significant lowering of the Peak Height value.

In the example above we show the cross correlation peak height map for one ROI. We can now see that there are in fact several scratches crossing the grain. In the upper and worst scratch the Peak Height values are very low and of the order 0.44. In other scratches they are closer to 0.7. In the region surrounding the reference pattern and for that matter in most of the grain the values are all above 0.9. In the deformation band they are mostly above 0.85 but a few points fall to 0.78.

We have found a way of combining all the cross correlation peak height data together. This entails multiplying together all the peak height values for all ROIs and dividing the result by the number of ROI followed by normalization. We call this the geometric mean HRF peak height. It has the effect of rapidly reducing the value if just one or

two regions are of poor quality. The relevant figures are shown below. In the left hand map we show values for all pixels in the grain. In the right hand map we have limited the scale to show only values between 1 and 0.9. All values with mean correlation less than 0.9 appear white. We see that all the values in the worst scratch have been eliminated as we would have expected from the quality of the EBSD patterns shown above for this region. However none within the deformation band are eliminated.

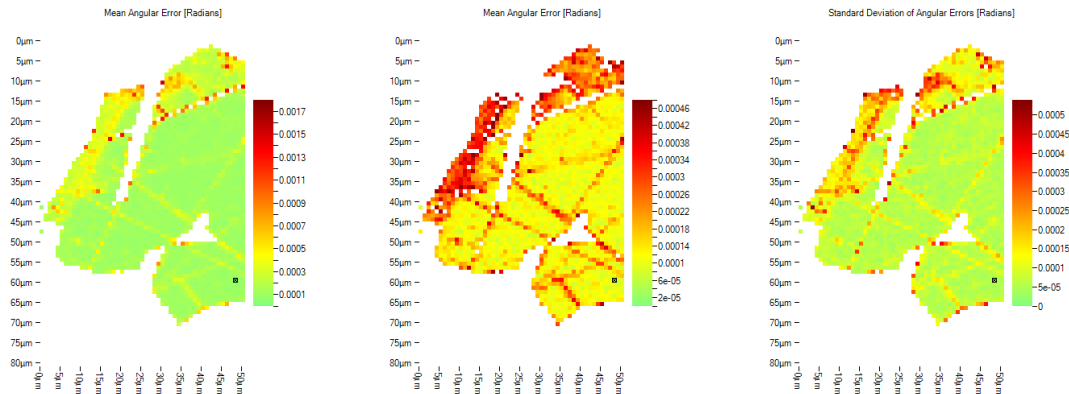


Geometric mean cross correlation peak height for the selected grain. Left full colour range, right, coloured pixels have a value greater than 0.9.

Thus, we note that using the geometric mean peak height function as a discriminator has not eliminated all regions where the strain values exceeded the macroscopic yield point. We obviously have gone part of the way of removing less certain data. But at what value should we set the peak height below which we are confident in the remaining data. Fixing the cut off value at 0.9 seems a bit arbitrary. Thus we need to take this further. We study next then what we call the mean angular error.

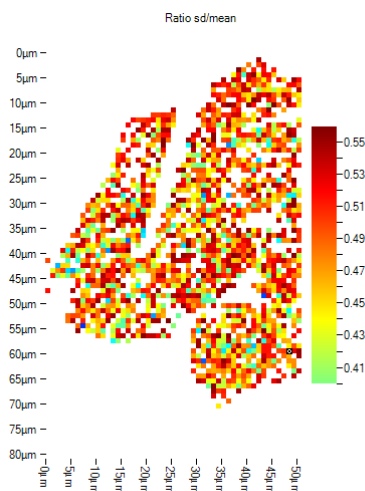
As mentioned above this is calculated from the angular error between the *as measured shift* of a particular ROI and the *shift predicted* from the finally calculated strain tensor. The calculated strain tensor is effectively the least squares fit of all the possible strain tensors obtained by combining different ROI. A map of the mean angular error is shown below. The colour range has been set in the left hand map at 0.0018 radians or $1/10$ degree. (The angular range extends only to 0.1 of a degree simply because elastic strains by their nature are small). In the centre map the maximum value has been reduced to 0.00054 radian or $3/100$ degree in order to see more clearly the distribution of the error. Most of the pixels in the deep scratch near the top of the grain have errors greater than 0.00054 and are shown white. In the main part of the grain very few have errors greater than this.

A third map shows the standard deviation of the error of this function calculated from the error measured for each region of interest. It is everywhere small and approximately equal to 0.5 times the mean value and this includes the values in the high strain band.



Maps showing mean angular error and standard deviation.

So what might we choose as a value for the error below which we have high confidence in the calculated strain values. We might start by looking to see if the standard deviation shows any systematic dependence on mean error. To do this we divide the former by the latter. The relevant map is shown below.



Map of ratio of mean angular error /standard deviation.

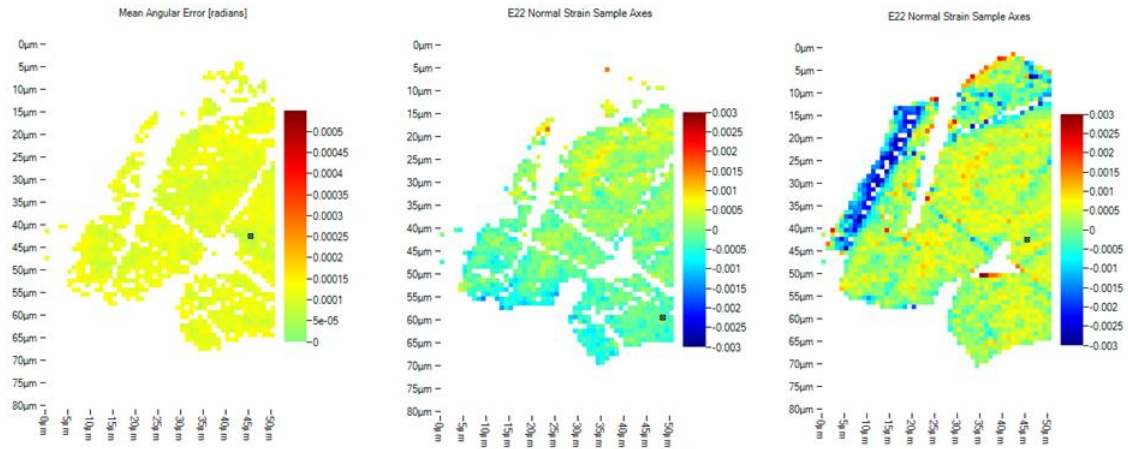
The limits are 0.58 to 0.40. It is seen that the ratio is pretty well randomly distributed with few pixels outside the range even in the deformation band region and scratch regions. Thus this is not a useful line to pursue.

We do know however, that we are safe to accept data in the low strain regions where little or no plastic deformation has occurred. The geometric mean error here is 0.00018 radians or $1/100^{\text{th}}$ of a degree.

This, therefore, gives us a safe and stringent limit for accepting data. We might say all data with a mean angular error greater than this is unreliable.

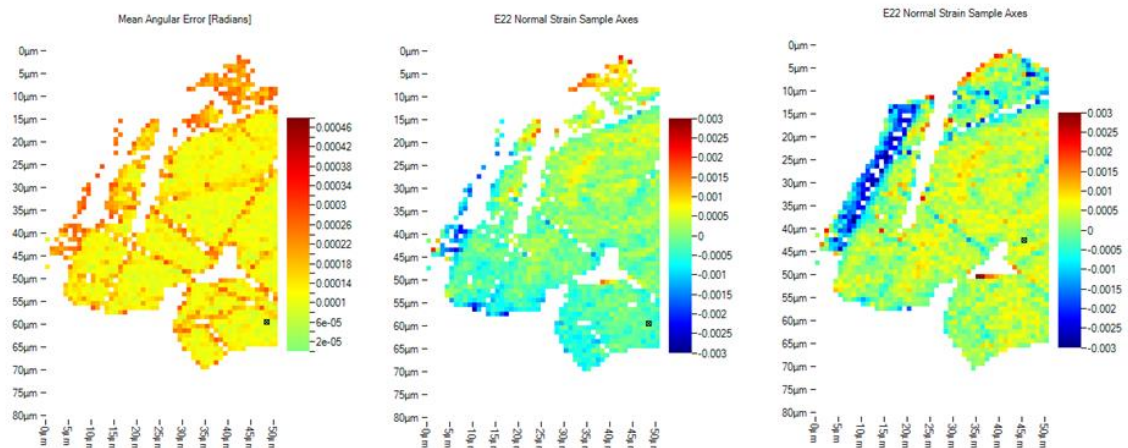
The mean angular error map to the left below is drawn to illustrate accepted data on this basis. All data with a mean angular error above 0.00018 radians has been rejected. All data above this error within the grain appears white. In the middle map this

criterion has been applied to the normal strain data map for ϵ_{22} . The previous ϵ_{22} map showing strain data irrespective of angular error is shown to the right for comparison.



Left Mean angular error map. *Middle* ϵ_{22} map rejecting all pixels with values greater than 0.00018 radians. *Right* ϵ_{22} map with no error filtering criteria.

Virtually all strain data accepted using this criterion, i.e. the middle map, has a value less than the macroscopic yield point. The result is that all data in the deformation band has been rejected. However, this criterion was the severest we could impose. A more reasonable value would be the angular error in the strain free region plus one standard deviation of this value. That puts the upper limit of angular error at 0.00026 radians. When this criterion is applied we obtain the corresponding maps shown below.



Left Mean angular error with cut off at 0.00026 radians. *Middle* Normal strain data ϵ_{22} with filtering of data with angular error greater than 0.00026. *Right*, normal strain data ϵ_{22} with no filtering for comparison.

More pixels are now included in the map. All data in the deep scratch remain rejected as do significant numbers in the finer scratches. However, the most important result is that using this more reasonable cut off level some pixels in the deformation band that pass the filtering process have strain values up to 0.002, that is nearly twice the macroscopic yield point. If we were to increase the error limit above the absolute minimum threshold to three times the standard deviation, i.e. to 0.00035 then nearly all the data within the deformation band becomes acceptable.

I think we now have a means of quantifying our confidence level for accepting and rejecting data. It is that given by the mean error plus one two or three times the standard deviation of the geometric mean. Thus alongside any strain results the error level used in accepting the data should always be given as in any other statistical based analysis.

Thus with regard to the particular example described here there are indeed many pixels which have strains greater than the elastic limit even at the most stringent one standard deviation limit. We should note in passing that this is not an impossibly high strain value as dislocation pile ups can produce strains much higher than this. Although we normally expect such strains to be relaxed by further dislocation activity, dislocation tangling in the deformation bands and the shortening of distances between the dislocation pinning points so increasing the force necessary to activate slip via the Frank Reed mechanism, may well allow for such large elastic strains.

Final notes on experimental procedure

I add a few further points that are required in experimental practice and with which current and future users of the technique should be familiar.

- 1 Because the reference pattern and the strained pattern necessarily originate from different regions of the specimen a correction for the shift in pattern centre is required. A shift in pattern centre will cause the entire pattern to be displaced by an amount exactly equal to the shift. Normally the shift is known because it is the movement of the SEM beam from the reference point on the specimen to the strain point. For example if the beam shift is 10 microns in the x direction and -15 microns in the y direction, the pattern centre values need to be corrected by exactly these amounts.
Of course the system first needs to be calibrated to determine the pixel shift value in the EBSD image for a 1 micron SEM beam shift on the specimen in both x and y directions. This calibration is very simple to do and is the first step undertaken in software installation. We need not worry unduly here about the details.
- 2 When the beam is moved in the y direction then because the specimen is tilted there will be a change in the specimen to screen distance i.e. a change in the z^* value. This will cause all points in the EBSD pattern to zoom hence there is this second order effect on measured shifts in the ROI. Again this is all taken care of in the Crosscourt 3 software so apart from knowing that this correction is necessary the software user need not be concerned with the rather tedious calculations involved.
- 3 It follows that in general use, each specimen must be mounted at a known tilt angle and if the angle is different from that at which calibration was made a corresponding correction needs to be made in the 'beam shift distance to shift in pattern centre'. If the specimen tilt axis is parallel to the X axis this

correction applies only to the y values. In addition if the specimen tilt axis is not coincident with the point viewed on the specimen there will be a corresponding change in the specimen to screen distance. If the distance between Y tilt axis and point viewed on specimen was 5 mm then to maintain the precision in strain measurement of 1 part in 10000 the tilt angle needs to be known to better than 0.2 degrees.

- 4 Likewise the specimen must be carefully aligned in the microscope so that an x shift of the beam moves the beam across the surface at constant height. Technically this means that the normal to the sample surface and y axis in the sample plane must both be at right angles to the SEM x beam shift. Otherwise the beam will move up or down the sample surface when the SEM beam is shifted in the x direction. This in turn means the pattern centre will move up or down the phosphor screen depending on the alignment error. This is a more difficult alignment to make. If the sample is flat and extends several hundred microns in the x direction then a possible misalignment might be detected by the SEM image going out of focus when the beam is scanned from one side to the other. Alternatively a scratch can be made in the sample surface to define the x direction. Then the sample can be rotated in the specimen holder until an x line scan moves the beam exactly along the line. This fix depends on being able to rotate the specimen about an axis normal to its surface when mounted in the microscope. It could be that special sample holders will have to be supplied as the precision of the technique improves beyond the 1 part in 10000 level.
- 5 The original software was written to enable strain measurements at 60nm spatial resolution on semiconductor devices. The area scanned was normally less than 3 microns. In that case these corrections are unnecessary at the 1 part in 10000 resolution. However more recently large scan areas are being made on polycrystalline samples and such corrections are essential. Fortunately, again, the corrections are taken care of automatically in Crosscourt 3. So the users of this program should have few problems.
- 6 All of these corrections are purely geometric and precise because they depend on the measured difference in beam position from the point at which the reference pattern was recorded to the point where the strain is being measured. The differences are accurately and precisely known because they are determined from computer controlled movement of the electron beam.
- 7 There has been some discussion in the literature on using a separate specimen from which a reference pattern could be obtained or a simulated pattern obtained. Recently in situ straining has been used together with the strain measuring software. All of these cases are problematic. I have already referred to the problem that if the pattern centre is not the same for patterns being compared to an accuracy of better than 1 pixel then phantom strains will be observed because of the errors thereby introduced. There is no way around this apart from finding a technique for accurately determining the pattern centre. I will defer my discussion on this point till a future tutorial as several groups are currently in the throes of finding such a method but none has been produced which is completely satisfactory at the time of writing.