MorphCol Supplement #8 – Repeatability Test with AMOR2

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History

AMOR was extended to AMOR2 by adding a motor-zoom (Diploma study of Sebastian Stapfer, 2007), which however, needed additional improvements and corrections (Nachbesserung DA Stapfer, finished on 23.12.2007). The new system needs now tests about the precision and performance of AMOR2 in the single-object and automeasurement modi. The tests and their results are described in the present report.

Re-analysis of variation in shape and size due to repeated automatic positioning of a single microfossil into the same position using the Auto-Zoom in AMOR2

Similar experiments were done as described in MorphCol supplements #3 and #5 in order to test the precision of outline measurements using the combined effects of the Sony DXC-390P video camera, automated orientation, the automated zoom function of AMOR2 together with the fine calibration described in MorphCol supplement #7.
The goal was to compare the precision when using AMOR2 with manual positioning of the same speciment on the Macintosh system, and to verify the fine calibration for AMOR2.

Experimental setup:

Specimen: 502_0100CCK0201 was used for this experiment (=same specimen as in MorphCol supplement #3, #5, and #7). The specimen was remounted in keel view into the center of field 30 of a new, empty slide (60 fields) for this test.
The imaging set up was the following:

AMOR2
Parameters a and be in file Programme/AMOR2/settings.ini were a=0.64732, b=0.0039901 (same as evaluated in MorphCol suppl. #5).
Camera: Sony DXC-390P
Cmount 1x
Leica MZ 6 binocular microscope using motorized zoom (zoom range from 0.63x to 4x).
Diaphragma opening at microscope set at 3
Achromat 1x objective
Cross-polarized light (new cross-polarizer from Volpi)
Illumination using Volpi 6000-1, light at 4 (fully open)

Imaging and orientation with AMOR2, single mode

Initialization, microscope moves to magnification 1.02 (value returned from AMOR2).

Sequence of operations:

Choose single mode
Sensibility=fine
Choose Magn=1.02

1 Autocenter
Autofocus
continue or increase Magn with sensibility=fine
Autotilt
Automagnificate
Autocenter

Autofocus
Capture (640x480 pixels, shift to 60 pixels, Tiff)
Reset
Goto 1 (repeat the procedure 15 times)

Autotilt was performed at various magnifications (see Table 1)
At the end, 15 images of the same specimen in tiff format were created, that were oriented at somewhat different magnifications and imaged at variable magnifications.
Note, that no autorotate was applied this time (in contrast to the repeatability test described in MorphCol supplement #5). Outlines should therefore be more similar to those performed on the Macintosh based system described in MorphCol supplement #3.

Image No.	Mag of image, (read in AMOR2)	Mag during autotilt	Zoom pos (mm) during autotilt
1	1,91x	autotilt @ 1,02x	
2	1,93x	autotilt @ 1,04x	16,0 mm
3	1,93x	autotilt @ 1,04x	16,0 mm
4	1,86x	autotilt @ 1,02x	16,0 mm
5	1,95x	autotilt @ 1,02x	16,0 mm
6	1,91x	autotilt @ 1,25x	22,5 mm
7	1,95x	autotilt @ 1,25x	23,0 mm
8	1,90x	autotilt @ 1,59x	31,0 mm
9	1,95x	autotilt @ 1,59x	31,0 mm
10	1,91x	autotilt @ 1,61x	31,0 mm
11	1,90x	autotilt @ 1,90x	37,0 mm
12	1,86x	autotilt @ 1,62x	31,5 mm
13	1,93x	autotilt @ 1,70x	17,0 mm
14	1,97x	autotilt @ 1,79x	35,0 mm
15	1,91x	autotilt @ 1,62x	31,5 mm

Table 1. Results during the repeatability test with AMOR2, single sample mode. Column 1=Image number. Column 2 indicates the magnification at which the image was captured (reading from the AMOR2 program). Column 3 indicates the magnification where the specimen was tilted (reading from the AMOR2 program). Column 4 indicates the mm readings at the zoom-wheel of the microscope.

Post-Processing:

Image convertion from Tiff files to raw files was done using Nih-Image 1.61 macro *Automate* (P for processing, R for saving to raw file format).

Conversion of magnifications:

In order to correct for the fine deviations between Magn values returned by AMOR to those read on the motorized zoom-wheel, program MagCorr1.out was applied to the magnifications read from AMOR2 for each individual image (see MorphCol supplement #7, and Figure 1 below).

Outline extraction and processing of outline coordinates:

Outline extraction on the black and white images was done using program Trace_AMOR1_batch.out, which was previously calibrated for the AMOR-Sony camera system (see Figure 1 below). This calibration uses the following equations for pixel to µm conversion (see MorphCol Supplement #4):

$$XPrec = 0.12986 * MAG + 0.000223 \qquad r^2=1.000$$

$$YPrec = 0.15742 * MAG - 0.00023756 \qquad r^2=1.000$$

Thereafter the outlines were interpolated to 250 points (cartesian coordinates) using program Sprep53.out. The x,y coordinates were the plotted on top of the figures shown in MorphCol supplement#3 (Mac system, manual orientation, manual zoom, Kappa camera), supplement#5 (PC system, first version of AMOR, automated orientation, Sony camera, manual zoom), and for AMOR2 (PC based, using automated orientation, Sony camera, motorized zoom with fine calibration).

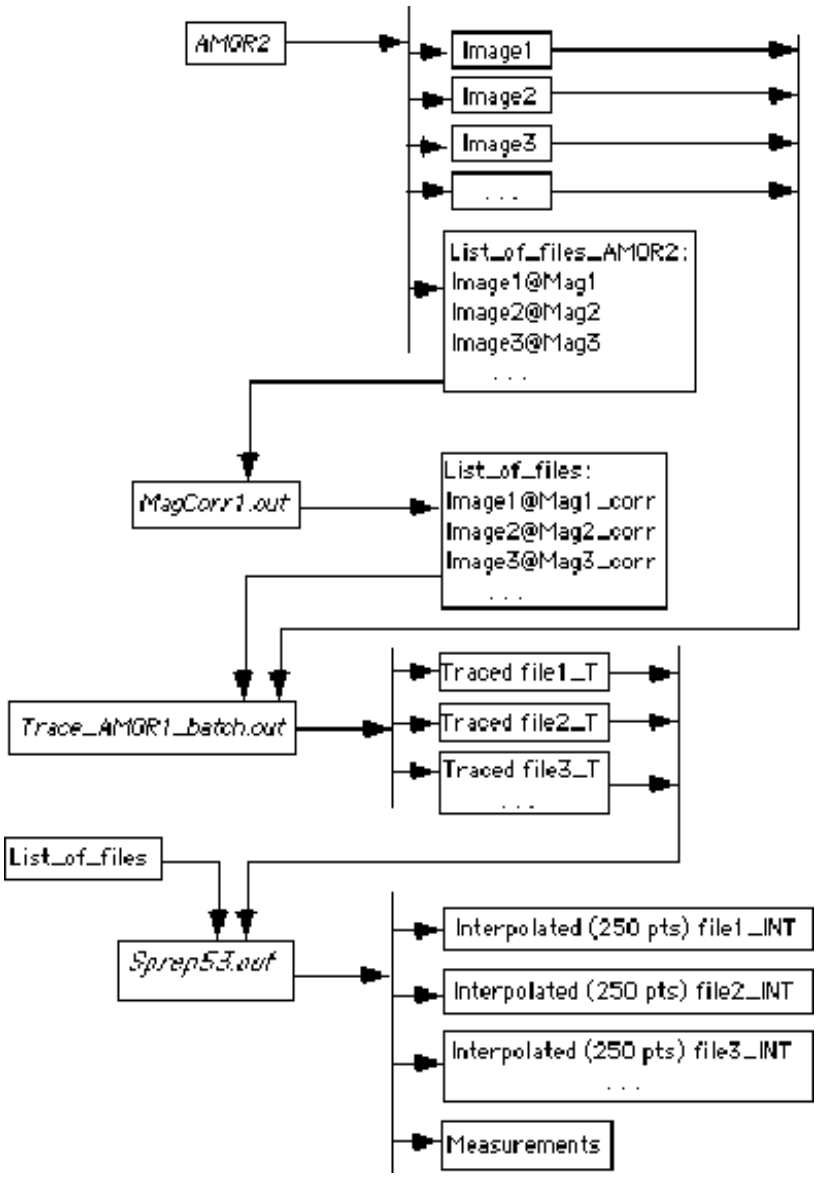

Figure 1. Flow-scheme for the present test.

Results:

Precision of automated orientation using AMOR Stage V:

Figure 2 illustrates, that the degree of overlap after orientating the same specimen 15 times into the same orientation using AMOR2 (in single mode) is nearly perfect.

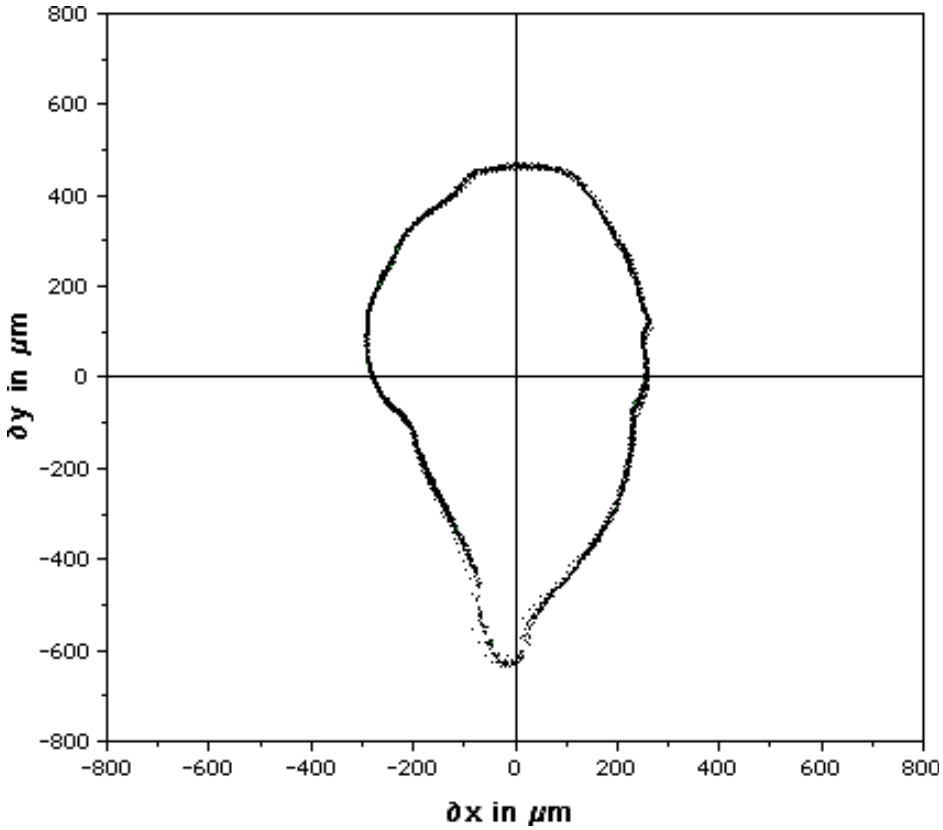

Figure 2.
Cartesian coordinates (in µm) of outlines from specimen No. 502_0100CCK0201 after 15 x orientation using AMOR2, including the fine calibration. Each outlines has 250 points after interpolation with Sprep53.out.

In Figure 3 the data are compared to an earlier repeatability test using the same specimen, but applying the previous version of AMOR (single mode), without motorized zoom (described in MorphCol supplement #5). Besides, that there is an angular offset due to autorotate operation in the earlier test, the outlines show good coincidence.

Figure 4 illustrates the comparison of the present measurements with those done on the same specimen but using the original Macintosh-based imaging system. In that system the specimen was oriented by manual manipulation with the hemispherical stage, imaging was through a Kappa camera, and zooming was also done manually at the microscope.

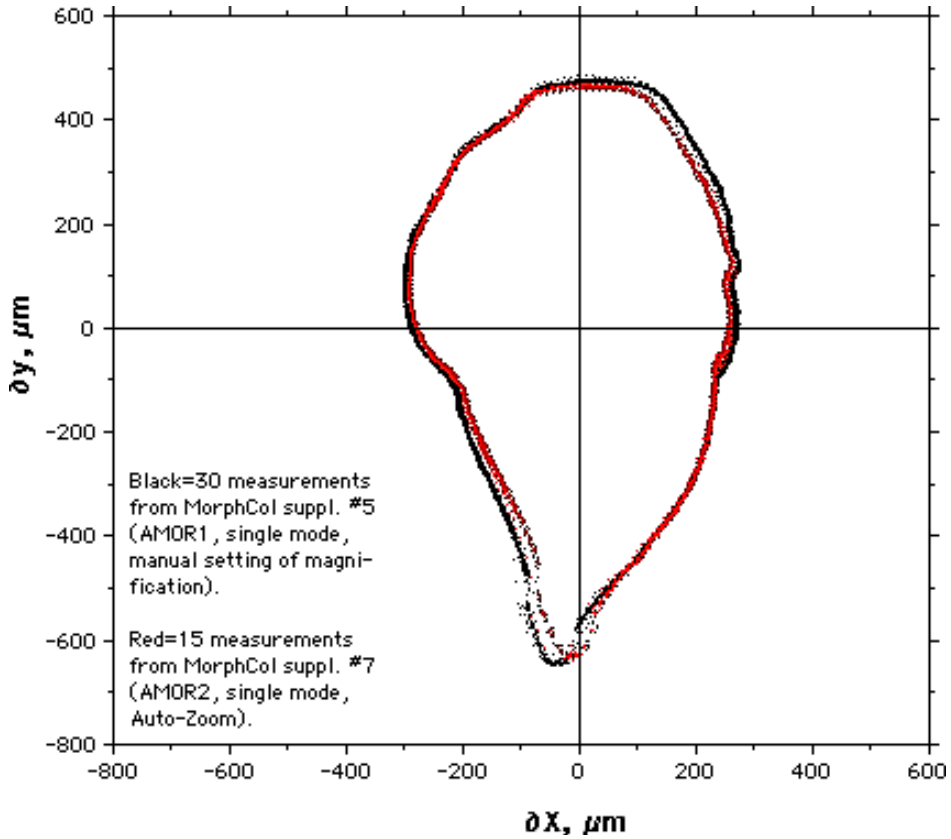

Figure 3. Comparison of the present results (black) with those shown in MorphCol supplement #5 (in red) (i.e. using the first version of AMOR, single mode, with Sony camera, with manual zoom cntrol). The angular offset between the two data sets occurs because in supplement#5 autorotation was done after tilting, whereas in the present test no autorotation was done. Also note, that between these two tests the specimen was displaced into a different slide and into a different field, which caused minimal variation in the shape of the outlines.

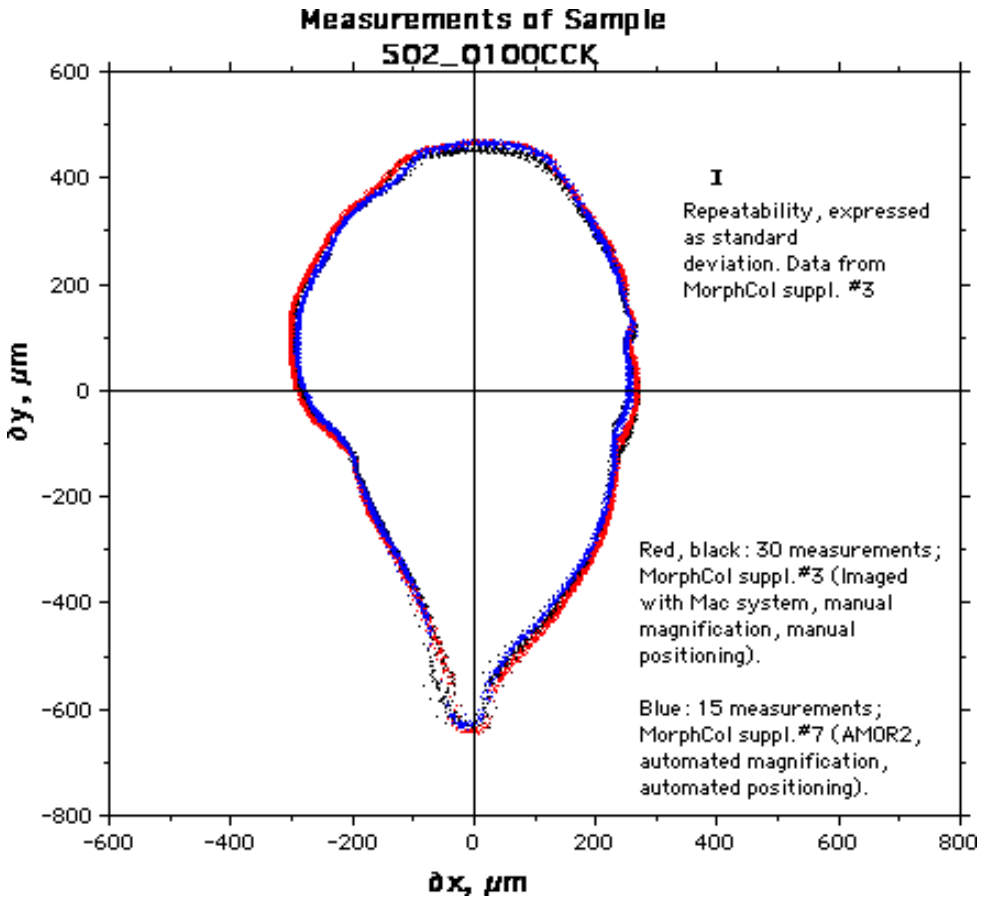

Figure 4. Comparison of measurements of the same specimen between AMOR2 (single mode, in blue) and the original Macintosh based imaging system, where orientation and zooming was done manually (red and black). There is good overlap between the two sets of measurements, which confirms the applicability of the pixel to micrometer conversion in Trace_AMOR1_batch.out and the correction for magnification for AMOR2 done with program MagCorr1.out in MorphCol supplement#7.

Mag-Test: Imaging and orientation with AMOR2 in single measurement mode at various magnifications from 0.65x through 2.59x

This test series was done in order to confirm the correct conversion of pixels in micrometers at various magnifications of the motorized zoom in single measurement mode of AMOR2. Again, the same specimen as above (e.g. specimen 502_0100CCK0201, which was re-positioned in field 30 of another slide), was used for this test.
The following protocol was applied in AMOR2 for this test:

1.) Launch AMOR2, complete initialization steps (stage moves into horizontal position, the zoom motor moves to zoom position at 1.02).
2.) Select single mode operation, move to field No. 1 of the slide, center the first field (if necessary use the x- and y translation buttons in fine mode to go to the center of field No. 1).
3.) Move to an arbitrary field in the slide, fine-adjust x and y if necessary, Autocenter.
4.) Enter field 30, where the test specimen is located.
5.) Autocenter, Autofocus.

6.) Select new magnifcation, at which x- and y autotilting should be done (1.62x is a good magnification for tilting operations).
7.) Autocenter, Autofocus, Autotilt.
8.) Select magnification, at which image shall be stored (choose one of the raster positions indicated, e.g. 0.63x, 0.80x, ..., 4.00x; the readout of the magnification in AMOR is then 0.65x, 0.81x, ..., which must be corrected prior to outline extraction with program MagCorr1.out).
8.) Save the image (expand to 640x480 pixels, 60 pixels from left border) (do not autorotate).
9.) Reset.
10.) Goto 3 and repeat steps 3 through 10 until all magnifications were tested.
11.) To abandon quit the single specimen mode, and quit AMOR2.

After imaging, all magnifications read from AMOR2 were corrected with program MagCorr1.out. Then, Trace_AMOR1_batch.out was applied with the corrected magnifications. Thereafter, the traced outlines were fed into Sprep53 for final transformation and interpolation at 250 points, as indicated in the flow scheme in Figure 1.
The tilt magnifications at each run are indicated in Table 2. The results of the magnification test is illustrated in Figure 5. Detailed analysis has confirmed a very good coincidence of the 8 outlines from the Mag-Test with all other tests in the present report (not illustrated here).

Run#	Image name	Mag of image (read in AMOR2)	Mag during auto tilt (in AMOR2)
1	0001r	0.65x	1.62x
2	0002r	0.81x	1.62x
3	0003r	1.02x	1.62x
4	0004r	1.29x	1.62x
5	0005r	1.62x	1.62x
6	0006r	2.04r	1.62x
7	0007r	2.30x	1.62x
8	0008r	2.59x	1.62x

Table 2: Details of the Magnification test in AMOR2 (single sample mode). The image mag in run#7 and 8 were set using the fine sensibility mode.

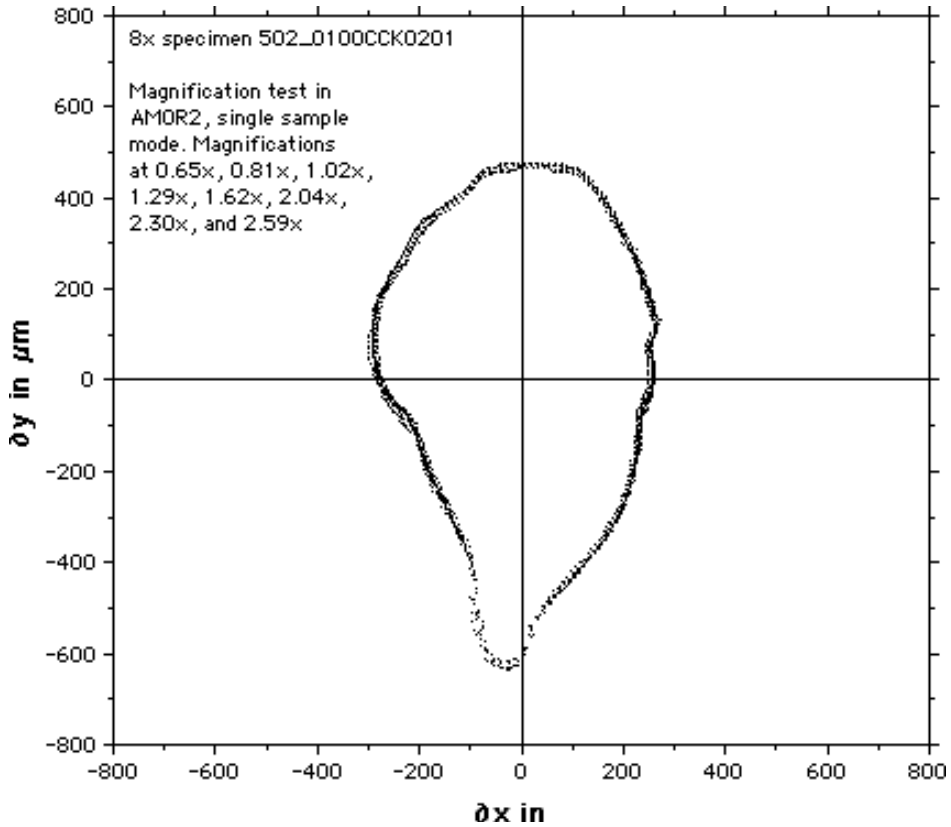

Figure 5: Mag-Test. Processed outlines after 8 times imaging the same specimen in AMOR2 (single mode operation) at 8 different magnifications.

Imaging and orientation with AMOR2 in auto measurement mode

The precisely same setup of AMOR2 was used for the following tests, however in auto measurement mode. The specimen was again 502_0100CC0201, placed in field No. 30 of the above slide. Light at the Volpi 6000-1 illumination was set to full open. The diaphragm was set to position 3. Cross-polarized light was used. All magnification readings indicated below were taken from within the program. The following protocol was found to give good working performance of AMOR2:

1.) Launch AMOR2, complete initialization steps (stage moves into horizontal position, the zoom motor moves to zoom position at 1.02).
2.) Select single mode operation, move to field No. 1 of the slide, center the first field (if necessary use the x- and y translation buttons to go to the center of field No. 1).
3.) Move to a second field, adjust x and y if necessary, Autocenter.
4.) Leave single mode (Quit).
5.) Start auto measure mode.
6.) Choose all settings, e.g.

Disable ratio
Polarized light
Error handling manually
Slide 60
Keel view
Selected range (fields 1 and 30 will then be selected)
Sample name 502_0100CCK, tif format
Autorotate **disabled** !
Expand to picture 640x480 pixels

Shift to 60 pixels from left border

7.) Run the automatic measurement

8.) After storage of the final image Return to 2.) and repeat all steps for a new automatic sample run. A total of 15 runs on the same specimen were done for this test

Run#	Image name	Mag of image, (read in AMOR2)	Mag during auto tilt (in AMOR2)
1	502_0100CCK3001	1,91x	1,01x
2	502_0100CCK3002	1,91x	1,02x
3	502_0100CCK3003	1,91x	1,01x
4	502_0100CCK3004	1,02x	1,02x
5	502_0100CCK3005	1,91x	1,02x
6	502_0100CCK3006	1,91x	1,02x
7	502_0100CCK3007	1,91x	1,02x
8	502_0100CCK3008	1,91x	1,02x
9	502_0100CCK3009	1,93x	1,02x
10	502_0100CCK3010	1,88x	1,02x
11	502_0100CCK3011	1,93x	1,02x
12	502_0100CCK3012	1,91x	1,02x
13	502_0100CCK3013	1,91x	1,02x
14	502_0100CCK3014	1,91x	1,02x
15	502_0100CCK3015	1,90x	1,02x

Table 3: Magnifications while imaging with AMOR in auto-measurement mode.

Table 3 shows the Runs, associated image files, magnifications during tilt operation, and magnifications at final imaging (all magnification readings fom within the AMOR2 program).

The resulting Tiff images were then processed to binary raw images using the automation macro in Nih-Image. The magnifications from AMOR2 exported to list_of_files were corrected using the MaCorr1.out program. Thereafter the outlines were extracted using Trace_AMOR1_batch.out, and the coordinates interpolated and transformed using Sprep53.out (see flow diagram in Figure 1). Figure 6 illustrates the results showing good coincidence of the 15 outlines after the experiment in auto-measurement mode.

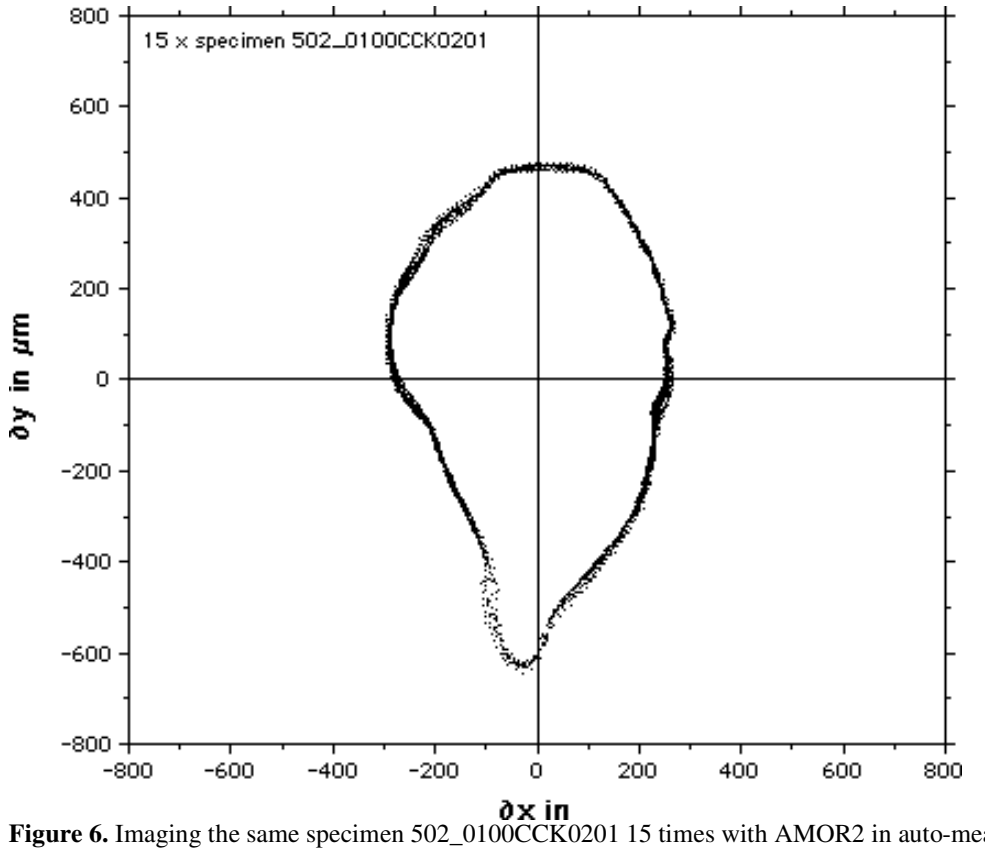

Figure 6. Imaging the same specimen 502_0100CCK0201 15 times with AMOR2 in auto-measurement mode. Note, that the specimen was replaced from the original slide into field No. 30 of another slide prior to imaging.

In Figure 7 this experiment is compared with the results from MorphCol supplement#3 (30x manual positioning with hemispherical stage on Macintosh-based imaging system), and suppl. #8 (15x positioning with AMOR2 in single mode, see sections above).

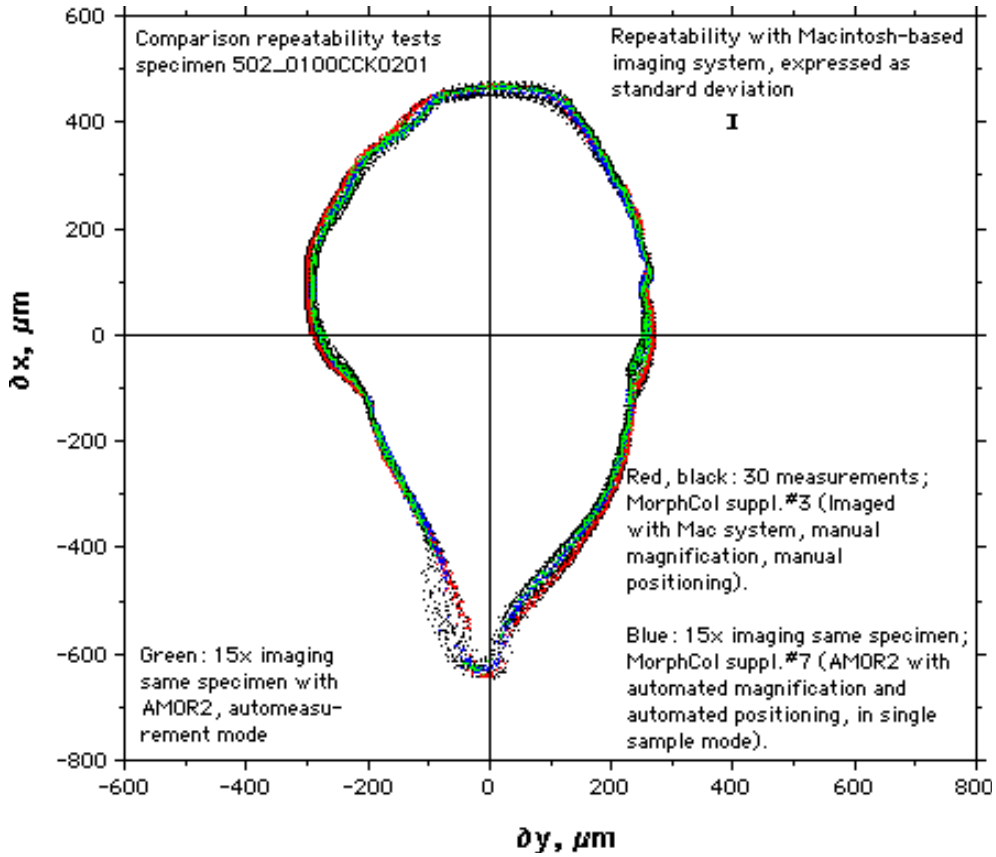

Figure 7. Comparison of results in different repeatability tests. Red (15 outlines) and black (15 outlines) points are from the manual positioning experiment using the hemispherical stage and the Macintosh based imaging system with the Kappa camera (see MorphCol supplemet#3). The indicated vertical bar of standard deviation is taken from that test. Green points (=15 outlines) were generated using the AMOR2 system (PC based, Sony camera) in single sample mode (see repeatability tests in section further above). Blue points (15 runs) represent outlines generated with the AMOR2 system in auto measurement mode. The specimen was not replaced between the AMOR2 tests in single- and automatic measurement modes. The slight deviation between green and blue outlines could be the result from slightly adjusting the polarizer position between the two experiments and changing room-light (imaging during evening versus imaging during full sunny day-light).

In general there is good visual agreement among the experiments, although results are not to 100% coincidential. Deviations between experiments in AMOR2 single sample vs automeasurement mode could have resulted due to different room light (imaging during evening light vs imaging during full sunny daylight), although it was attempted to keep room light dimmed. The slight deviations between outlines taken with the Macintosh-based imaging system and those taken AMOR2 are because the specimen was imaged within the original slide in the first case (specimen 1 in field No. 2), but removed and re-mounted to field No. 30 of another slide in the second series of experiments. For analysis of interspecimen shape- and size variation, however, all repeatability experiments show reasonably good coincidence of the outlines.

Error estimates using polar coordinates of the outlines

Error estimate were also carried out using the polar form of the outlines, similar to the analysis in MorphCol supplement #3 (Macintosh based imaging system). For this purpose the outlines of all tests [i.e. magnification test (8 outlines), single-object measurement (15 outlines), and automeasurement (15 outlines)] were combined together, which gives a total of 38 orientation tests on the same specimen. The 250 cartesian points of every interpolated outline were converted to polar coordinates using program *XY_to_PhiD1.out*. This conversion gives the ray argument Phi (in degrees, equiangular distances) and raylength Rho (in µm) for every point. The data of Rho and Phi are listed in Excel sheet "Master Ray (Rho, Phi) table" In that matrix the following abbreviations are used in the header:

PhiMagS01, RhoMagS01 for the Phi's and Rho's of the outline No. **01** during the **Mag**nification (**S**ingle-object) mode;

PhiRepA01, RhoRepA01 for the Phi's and Rho's of outline No. **01** during the **Rep**eatability test in **A**utomeasurement mode;

PhiRepS01, RhoRepS01 for the Phi's and Rho's of outline No. **01** during the **Rep**eatability test in the **S**ingle-object mode.

Statistical analysis (with Excel) the values in the ray table gave an average Rho of 340.341 µm over all 38 x 250 rays and a standard deviation of 87.197 µm over all 38 x 250 rays.

In order to estimate the deviation between the 38 outlines it is necessary to consider the variation in ray-length for each of the 250 points in the outlines. For this reason the values of Rho and Phi are plotted against ray number for each of the 38 outlines (see Figures 8 and 9). The Graph for Phi shows a straight linear increase of Phi with increasing ray number (Figure 8). The angular difference is between neighboring rays is very close to the theoretical value of 1.44°, which results from the division of 360° by 250 points per outline.
The Graph for Rho is illustrated in Figure 9. It shows, that the variation in ray-length is a function of the direction of the corresponding ray, i.e. of the ray number. The strongest variation occurs at ray no. 183, which corresponds to 263.52° (upper keel region of the shell). This strong variation is due to the nearly parallel direction of the outline and the corresponding rays in that region, which ends up in large differences between neighboring rays in that region. In this perspective the polar representation is not an ideal way to analyze of shape variation !

Mean ray lengths and 95% confidence intervals were estimated from the 38 outlines per ray number, also using Excel spreadsheets (see Figure 10). In addition, an absolute error was calculated, which is expressed as the difference between the smallest and the largest length per ray position n in each outline, i.e.

$$[\mathrm{Max}(\rho_{1,n},\rho_{38,n}) - \mathrm{Min}(\rho_{1,n},\rho_{38,n})]_{n=1,\ldots,250}$$

From these error estimates, which also vary strongly with ray number (see red curve in Figure 10) an overall mean error for all 38 outlines was estimated at 23.34794 µm. This is 6.86% of the mean of all rays of the 38 outlines. With other word, the average error in ray variation is ±11.7 µm or 3.43% of the average ray length (the average ray length is 340.341 µm, see above).

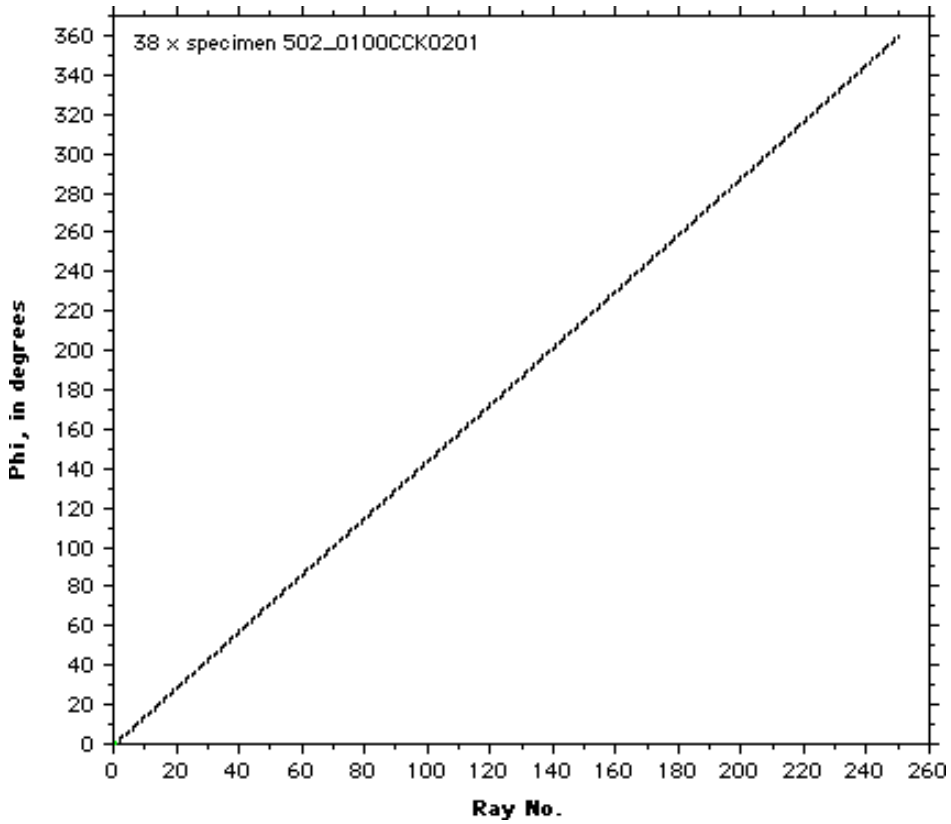

Figure 8. Plot of Ray numbers (1 through 250) versus Phi for all 38 outlines of specimen 502_0100CCK0201 imaged with AMOR2 in the present test series. The angular increment from one point to the next is very close to the theoretical value 1.44°.

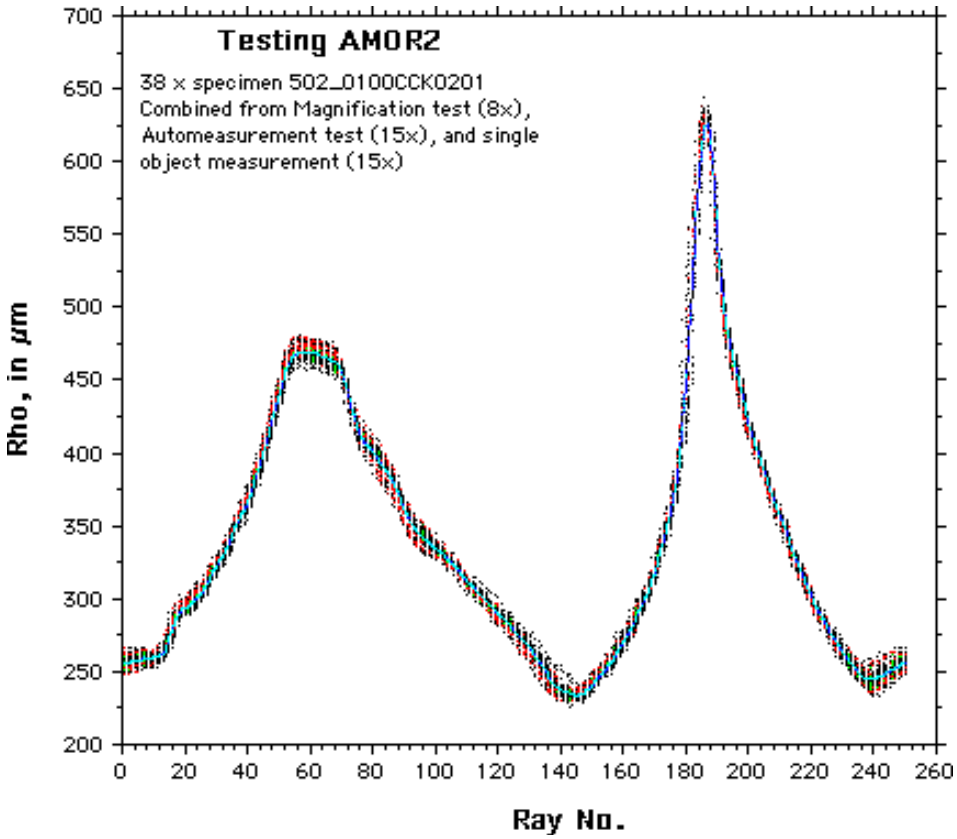

Figure 9. Raylength Rho as a function of the ray number (rays 1 through 250) for each of the 38 outlines taken with AMOR2. Black points represent the 8 outlines of the magnifcation test. Red points represent the 15 outlines taken during the repeatability test in auto-measurement mode. Green points represent the 15 outlines taken during the repeatability test in single-object mode. The cyan line represents the mean ray-lengths from all three test-series.

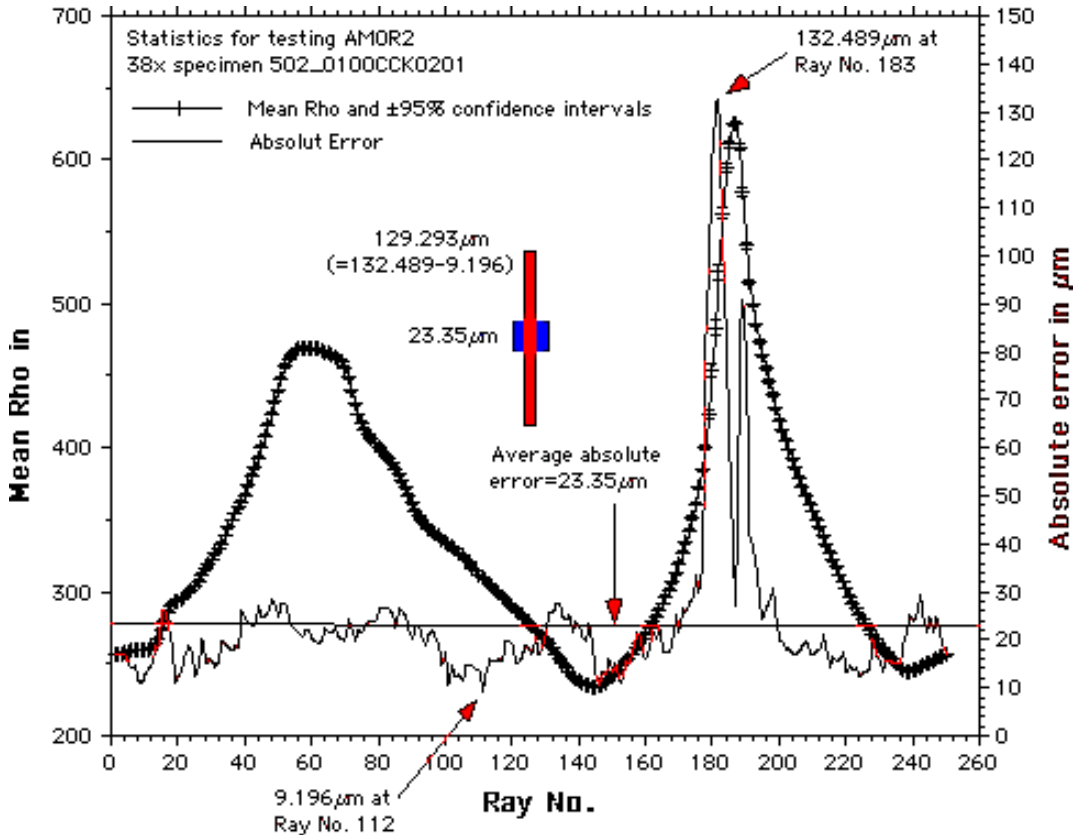

Figure 10. Black curve: Plot of the mean ray length Rho(n) as a function of ray number n, together with the ±95% confidence intervals about the means. The red curve illustrates the absolute error between outlines at each ray (n). The absolute error of Rho was calculated as follows: $[\mathrm{Max}(\rho_{1,n},\rho_{30,n}) - \mathrm{Min}(\rho_{1,n},\rho_{30,n})]_{n=1,...,250}$. The horizontal red line indicates the mean absolute error, averaged over all 250 rays for all 38 outlines.

Alternative error estimates of the outline variation using the enclosed area

As discussed in the above section, error estimates for outline variation based on polar coordinates depend on the direction of the local ray, which makes an overall error estimation more difficult. In order to overcome this difficulty an alternative shape variation estimate between the outlines is proposed, which is based on the enclosed area of each outline. Area estimates for each outline are provided in the measurements file of the *Sprep53* program. Simple statistics were calculated using Statistica (see Table 4). The standard error is 0.233% from the mean keel view area and 3.438% from the total range (=0.0263mm^2) of the 38 outlines.

N	38
Min	0.3763
Max	0.4026
Mean	0.38785
Std. Error (=68% CI)	0.0009042
Std. Dev. (=S)	0.0055738
Skewness	0.9570497
Kurtosis	0.8299401
First quantile (25%, Q_1)	0.3839
Third quantile (75%, Q_3)	0.3905
IQR (=Q_3-Q_1)	0.0066

Table 4. Statistics for the keel-view area measurements of the 38 outlines. IQR= Interquartile range. 68% CI=68% confidence interval (=standard error).

Figure 11 illustrates the frequency distribution of the keel-view measurements of the 38 outlines. The bin-width h was determined using the formula (after Keating and Scott, 1999):

$$h = [3.49 * \min(S, IQR/1.349)]/N^{-1/3} = 0.0050789$$

The frequencies obtained in this way are shown in Table 5 below. This analysis shows, that the variation in keel-view area measurements are very small in comparison to the total range of keel view area measurements from over 6000 specimens measured from Pliocene to Pleistocene specimens shown in Figure 10 of Knappertsbusch (2007).

Intervals in mm^2	Number of outlines
0.375 - < 0.380	1
0.380 - < 0.385	13
0.385 - < 0.390	14
0.390 - < 0.395	4
0.395 - < 0.400	5
0.400 - < 0.405	1

Table 5. Frequencies shown in Figure 11.

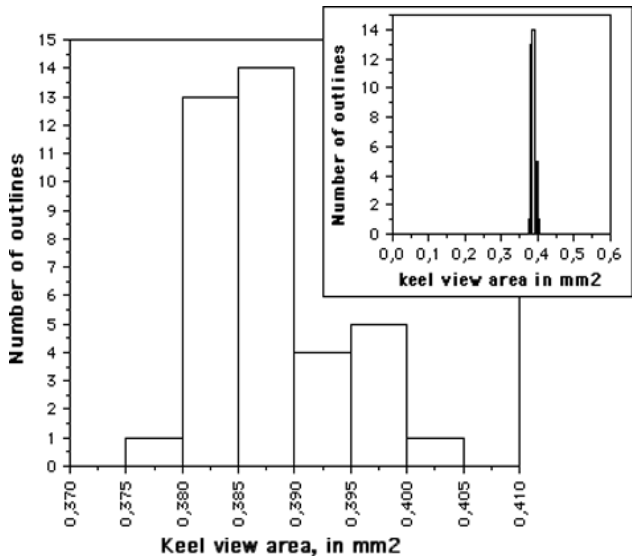

Figure 11. Diagram showing the frequencies of keel view area measurements (in mm^2) of the 38 individual outlines obtained with Sprep53.out program. The bin-width was determined at 0.005 mm^2 using the method described in Keating and Scott (1999). As a comparison the inset shows the same diagram but on a scale ranging from 0 to 6 mm^2 as applied in Figure 10 of Knappertsbusch (2007), where the range of keel view area measurements is shown for a large number of shells from menardiform globorotalids.

Conclusions

The visual inspection of outline matching between Macintosh-based system (manual orientation) and the AMOR (PC based, motorized orientation) confirms good coincidence of outlines. Tests in single sample mode or auto-measurement mode of AMOR2 gave no large differences. No influence on the outlines was detected when AMOR2 was used at different magnifications. Room-illumination, however, was found to be important to the results as this can influence the threshold of grey-level separation during binarization of the live images. Too bright room light also can be critical during auto tilt, leading sometimes to non-decisive conditions, which causes tilting to endlessly loop or system hang. In

auto-measure mode AMOR2 works best at dimmed room illumination. AMOR2 is thus suitable for routine imaging of samples.

The average difference between the maximum ray length and the minimum ray-length for each ray and over the 38 specimens measured was 23.35 µm. This corresponds to an accuracy of AMOR2 of ±11.7 µm or 3.43% of the average ray length for all 38 tests in this experiment. Polar analysis of ray variation, however, is not an ideal way to measure global differences between outlines because it depends on the direction of the rays. A better global indication for measurement accuracy and repeatability the the mean, standard deviation and standard error (=68% confidence interval about the mean) of the areas of the 38 silhouettes. The analysis gave a standard error of 0.0009042 mm^2, which is 0.233% from the mean keel view area and 3.438% from the total range (=0.0263mm^2) of the 38 outlines.

Literature

Keating, J.P. and Scott, D.W. (1999). Ask Dr. STATS. Stats #25, Spring 1999, pp. 16-22.

Knappertsbusch, M. (2007). Morphological variability of Globorotalia menardii (planktonic foraminifera) in two DSDP cores from the Caribbean Sea and the Eastern Equatorial Pacific. Carnets de Géologie, Article 2007/04 (CG2007_A04).

Appendix

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      Program MagCorr
C
C     By Michael Knappertsbusch
C     Version 1.0, 5.2.2008
C
C     This program corrects the magnifications, that are determined and displayed
C     in AMOR2 (formula file Programme/AMOR2/settins.ini), into the correct values
C     at the zoom wheel of the Leica MZ6 microscope. The method is by segment-wise
C     linear interpolation (segments I through VIII) as described in section 3 of
C     Knappertsbusch (2008). Fine calibration of AMOR2. MorphCol Supplement #7,
C     4 February, 2008.
C
C
C     Input is file INPUT (i.e. an ascii text file called list_of_files, which AMOR2
C     generates and which contains the name of each image taken together with the
C     corresponding (AMOR2 calculated) magnification. The format of this information
C     is explained in the following example:
C
C           3001r,1.90
C
C     The first 4 characters indicate the specimen number in that slide (characters 1-2
C     are the field number, characters 3-4 are the specimen [usually 01 when working with
C     AMOR2]). The fifth character is a lowercase r, indicating a raw file format (required
C     by the program Trace_AMOR1_batch.out). The sixth charcter is a comma (can be used herein
C     as a delimiter between specimen number and magnification). The following four characters
C     indicate the magnification as calculated from AMOR2.
C
C
C     Output is file OUTPUT (the file containing the image file names and corresponding
C     corrected magnifications). The output file can the be imported into
```

```
C       program Trace_AMOR1_batch.out for outline extraction.

C       Variables:
C       X = Magnification returned by AMOR2
C       Y = Corrected magnification
C
C
        INTEGER N
        DOUBLE PRECISION X,Y
        CHARACTER*13 INPUT
        CHARACTER*20 OUTPUT
        CHARACTER*5 IMAGE
C
        WRITE(9,*) '***********************************'
        WRITE(9,*) '*                                 *'
        WRITE(9,*) '*           MagCorr               *'
        WRITE(9,*) '* Corrects the magnification      *'
        WRITE(9,*) '*        from AMOR2               *'
        WRITE(9,*) '*                                 *'
        WRITE(9,*) '* Version 1 from 2 February 2008  *'
        WRITE(9,*) '*    by Michael Knappertsbusch    *'
        WRITE(9,*) '*                                 *'
        WRITE(9,*) '***********************************'
        WRITE(9,*) ' '
        WRITE(9,*) '. . .Enter the "list_of_files" from AMOR2. . .'
        READ(9,5) INPUT
 5      FORMAT(A13)
C
C
C***    Generating an output file for the corrected magnifications:
C
        WRITE(9,*) '. . .Enter an output name. . .'
        WRITE(9,*) '             (max 20 chars)'
        READ(9,6) OUTPUT
 6      FORMAT(A20)
        OPEN(15,FILE=OUTPUT,STATUS='NEW')
C
C
C***    Write a header line for the output to the screen:
C
        WRITE(9,*) 'SPECIMEN #, MagAMOR2, Corrected Mag'
C
C
C
C***    Opening and reading the input file:
C
        OPEN(14,FILE=INPUT,STATUS='OLD')
        N=0                                             ! N=Counter for the files in list_of_files
 10     READ(14,*,END=100) IMAGE,X
        N=N+1
C
C
        IF (X.LT.0.81) THEN                             ! [X < 0.81; segment I ]
          Y=1.0625*X-0.060625
        ELSE IF ((X.GE.0.81).AND.(X.LT.1.04)) THEN ! [0.81 ≤ X < 1.04; segment II ]
          Y=0.8695652*X+0.0956521
        ELSE IF ((X.GE.1.04).AND.(X.LT.1.31)) THEN ! [1.04 ≤ X < 1.31; segment III ]
          Y=0.9259259*X+0.037037
        ELSE IF ((X.GE.1.31).AND.(X.LT.1.63)) THEN ! [1.31 ≤ X < 1.63; segment IV ]
          Y=1.1290323*X-0.2290322
        ELSE IF ((X.GE.1.63).AND.(X.LT.2.06)) THEN ! [1.63 ≤ X < 2.06; segment V ]
          Y=0.9302325*X+0.0837209
        ELSE IF ((X.GE.2.06).AND.(X.LT.2.57)) THEN ! [2.06 ≤ X < 2.57; segment VI ]
          Y=0.9803921*X-0.0196078
```

```
      ELSE IF ((X.GE.2.57).AND.(X.LT.3.26)) THEN ! [2.57 ≤ X < 3.26; segment VII ]
        Y=1.0144928*X-0.1072463
      ELSE IF (X.GE.3.26) THEN                   ! [3.26 ≤ X; segment VIII ]
        Y=0.9090909*X+0.2363636
      END IF
C
C
C***  Output:
C
      WRITE(9,50) IMAGE,X,Y                      ! Output of results to screen
      WRITE(15,60) IMAGE,Y                       ! Output of results to file
 50   FORMAT(A5,'      ,   ',F4.2,'  ,   ',F4.2)
 60   FORMAT(A5,',',F4.2)
      GOTO 10
C
C
 100  WRITE(9,*) ' '
      WRITE(9,*) '. . .',N,' magnifications corrected. . .'
      PAUSE 101
 101  CONTINUE
      STOP
      END
```