MECHANICAL DIGITIZING FOR PALEONTOLOGY - NEW AND IMPROVED TECHNIQUES

Heinrich Mallison, Alexander Hohloch, and Hans-Ulrich Pfretzschner

ABSTRACT

Three-dimensional digitized representations of bones offer several advantages over real bones or casts. However, creation of 3D files can be time consuming and expensive, and the resulting files are difficult to handle due to their size. Mechanical digitizing was hitherto limited to large bones. Here, new and improved data collection techniques for mechanical digitizers are described, facilitating file creation and editing. These include:

- Improvements to the in-program digitizing procedure, reducing time and financial demands.
- Specifics for an easy to assemble and transportable holder for small fossils.
- A significant increase in the size range of digitizable bones, allowing both exact digitizing of bones only a few centimeters long and bones larger than the range of the digitizer. This increase allows the study of assemblages including both small and large bones.
- Complex shapes such as costae and vertebrae can now be digitized with ease.
- Step-by-step directions for digitizer and program use to facilitate easy acquisition of the techniques.

3D-files of fossils digitized with these methods can be added to online databases easily, as small-scale preview and complete files. The file formats are common and the file sizes relatively small in comparison to CT or laser-scan data. Pointcloud files can be used interchangeably with laser-scan files of similar resolution. Other possible uses for mechanical digitizing data are described.

Additionally, techniques to extract and edit comparable data from CT scans are briefly described. CT-based data is used to check the accuracy of mechanically digitized data.

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INTRODUCTION

In recent year, digital files have increasingly been used for scientific research instead of real bones or casts. Currently, the most common way of obtaining a digital representation of a specimen is computer assisted tomography (CT) (see e.g., Zuo and Jing 1995; Gould et al. 1996; Knoll et al. 1999; Stokstad 2000; Golder and Christian 2002; Ridgely and Witmer 2004, 2006; Sereno et al. 2007; Witmer and Ridgely 2008). These digital images can consist of cross sections, but usually are three dimensional models of internal shapes of an object, e.g., in order to assess as yet unprepared specimen or depict internal structures without damaging the object (e.g., Witmer and Ridgely 2008). Models of external shapes can be used to rapid prototype (RP) scaled models or exhibition copies, because the high accuracy of CT scans justifies the high costs of CT scanning and RP. This technique also allows mirroring of specimen or combining several partial specimens into one complete individual or bone. Neutron tomography (NT) has also been tested (Schwarz et al. 2005), with mixed results.

Another method to obtain 3D files is laser scanning, either from three perpendicular views or with a surround scan. Alternatively, repeated scans can be taken at many angles and combined in the computer. An extensive project at the Technische Universität Berlin used laser scanners to digitize complete mounted skeletons and skin mounts (http://www.cv.tu-berlin.de/menue/ abgeschlossene_projekte/ 3d_rekonstruktion_von_dinosauriern/ fruehere_arbeiten/brachiosaurus_brancai/, see also Gunga et al. 1995; Gunga et al. 1999, Bellmann et al. 2005; Suthau et al. 2005; Gunga et al. 2007; Gunga et al. 2008). Bates et al. 2009 also employ such laser scans, albeit apparently at a lower accuracy. Also, some of the dinosaur skeletons mounted in the MFN exhibition were high resolution laser scanned as separate elements by Research Casting International (www.rescast.ca) during the museum renovation in 2006/2007.

All three methods produce vast amounts of data, depicting the object in very high detail. When such high resolution is not needed, the large file size becomes cumbersome. As long as only exter-nal surfaces are of concern, mechanical digitizing provides a cheap and fast alternative (Wilhite 2003a, 2003b), delivering small files of sufficient accuracy for most applications. Mechanical digitizing means creating a computer representation of a physical object by means of using an apparatus that samples 3D landmarks on the object's surface through touching it. Other techniques involving digitizing were used by Goswami (2004) and Bonnan (2004), who focused on specific bone landmarks. In contrast to our methods, these do not produce complete 3D images of bones and will not be addressed here. Similar in handling and data output to the methods described here is the sonic digitizer used by Hutchinson et al. (2005). It is limited to collecting point data, but provides a large range of up to 14 feet, albeit at slightly lower accuracy.

Here we detail improvements for digitizing techniques for dinosaur bones as described by Wilhite (2003a, 2003b), expanding the size range of suitable bones for the method significantly, both for larger and smaller specimens. New methods also allow complex shapes to be digitized with relative ease, and remove the need to edit the digitizing data in other programs before use. Also, the extraction of surface data from CT data in AMIRA 3.11® and the subsequent editing is described briefly. This CT based data is used to evaluate the accuracy of mechanical digitizing data.

Fossils (vertebrate or invertebrate) digitized with the methods described here can easily be added to online databases, instead of or alongside with photographic images. Most databases, such as the database of the New Mexico Museum of Natural History (Hester et al. 2004) or the American Museum of Natural History (http:// paleo.amnh.org./search.php) can easily accommodate small-scale previews as well as complete files, since the file formats are common and the file sizes relatively small in comparison to CT or laser scan data. Stevens and Parrish (2005a, 2005b, www.dinomorph.com) used several files created during this project for modeling *Brachiosaurus* in Dinomorph™. The University of Texas runs another digital library (http://www.digimorph.org/ index.phtml) based on high-resolution CT scans. Objects digitized via dense point clouds as described herein could conceivably be added to

this database as stereolithographies (*.stl files), provided sufficient resolution is obtained. For most applications, pointcloud files created with the Microscribe® can be used interchangeably with laser scan files of (or reduced to) similar resolution. The digital files can also be used to rapidly test possible skeletal assemblages, joint mobility ranges (Wilhite 2003a, 2003b), inter- and intraspecific variation (e.g., Wilhite 2005). Virtual skeletons created from them in CAD softwares such as Rhinoceros® can be an aid in planning museum mounts.

Another possible application is rapid prototyping. Scale models of bones can be produced at almost any scale, as well as molds for casting, or negatives of the bones that can serve as storage casts or as mounting racks for museum exhibition. High resolution rapid prototyping or 3D printing (600dpi) calls for CT or laser scan data, due to the ability to exactly create surface textures, but at lower resolutions (300dpi), accurate NURBS or STL objects from mechanical digitizing are of sufficient quality to create exhibition copies of fragile specimens or mirror images to replace missing elements in skeletal mounts. Research Casting International (www.rescast.ca) used full scale 3D prints of the exhibition skeleton of the MFN *Kentrosaurus* to construct the armature that was used for the new mounting of the skeleton in 2007.

Our methods probably work well for a plethora of disciplines aside from vertebrate paleontology, such as archeology. However, aside from a single trial using a fossil vertebrate footprint, we developed them solely on vertebrate body fossils. Researchers from other fields are encouraged to experiment with mechanical digitizing, and to adapt and improve upon the methods described here.

MATERIALS

Institutional abbreviations

IFGT Institut für Geowissenschaften, Eberhard-Karls-Universität
Tübingen, Tübingen (GER). Formerly Geologisch-Paläontologisches Institut Tübingen (GPIT)

GPIT IFGT collection numbers

MB.R. collection numbers of MFN

MFN Museum für Naturkunde – Leibnitz-Institut für Evolutions- und
Biodiversitätsforschung an der Humboldt-Universität zu Berlin, Berlin (GER) (also

abbreviated HMNB, MN, or HMN in literature)

JRDI Judith River Dinosaur Institute, Malta, MT (USA)

Computer software

(1) McNeel Associates 'Rhinoceros© 3.0 NURBS modeling for Windows®'

Rhinoceros 3.0® is a NURBS based CAD program. Versions 2.0, 3.0, and 3.0SR4 (Service Release 4) were used to obtain and process digital data. Version 4.0 is available, but was not used here. All digitizing methods described here were tested and can also be used in Version 4.0.

To curb costs we tried to use Rhinoceros 3.0® exclusively when developing new methods. Some data operations described here dealing with complex geometric shapes, however, require either a very high level of program knowledge, or are impossible in Rhinoceros®, and are thus easier performed in or require another software (position 3 below).

(2) TGS Template Graphics Software Inc. 'AMIRA 3.11' (time-limited evaluation version)

AMIRA 3.11 is a 3D visualizing and modeling system that allows creation of surfaces (3D bodies) from computer tomography (CT) data.

(3) Geomagic Corporation 'Geomagic Qualify 8.0®' (time-limited evaluation version)

Geomagic 8.0® is a suit of CAQ (computer aided quality assurance) program components that complement each other. Geomagic Studio 8.0® includes all parts, but the more limited Geomagic Qualify 8.0® is also sufficient. It was used for editing those files based on point cloud digitizing or CT scans.

Technical equipment

(1) Immersion™ 'Microscribe 3D'

(2) Immersion™ 'Microscribe 3GL' (on loan from the Institut für Zoologie der Rheinischen Friedrich-Wilhelm-Universität Bonn)

The Immersion Microscribe3D© ('Microscribe', 'digitizer') is a three-dimensional mechanical point digitizer. The digitizer is easily transportable, cost effective, and reliable. The GL version of the digitizer has a longer arm, allowing for a greater reach with only a negligible loss in accuracy. The input from the Microscribe® to the computer was controlled with the foot pedal provided together with the digitizer. Various desktop and laptop PCs were employed, the least powerful being a Pentium II PC with an 800MHz processor and 256 MB of RAM,

connected to the digitizer via a serial connection cable, or a USB cable in case of the Microscribe GL®.

Fossil material

HM and AH mechanically digitized over 100 bones in various institutions. For the description of the methods given here only the following are used:

IFGT:

GPIT 1 *Plateosaurus engelhardti*: dorsal 2, left ilium, left radius

GPIT 2 *Plateosaurus engelhardti*: left humerus, left pedal phalanx II-1

GPIT ?610 *Diplodocus* sp.: right metacarpal 3

JRDI:

JRDI 200 *Brachylophosaurus canadensis*: left dorsal rib

MFN:

MB.R.2246 *Giraffatitan (Brachiosaurus) brancai*: left calcaneum

MB.R.2912 *Giraffatitan (Brachiosaurus) brancai*: left scapula

MB.R.2249.R9 - R17 *Giraffatitan (Brachiosaurus) brancai*: left metacarpus and manual phalanges I-1, I-2, II-1, III-1, V-1

unnumbered *Dicraeosaurus* sattleri.: left scapulocoracoid, tibia, fibula, astragalus

Further materials

Vertebrae were in some cases stabilized by wrapping one half in aluminum foil or a plastic film and burying this half in a box of sand. Adhesive masking tape was used to provide a base for markings on the bones and as a visual aid during digitizing, and a specially constructed variable holder was used to stabilize most medium-sized and small bones. Some very small markings must be made on the bone for digitizing, and extensive marking can be necessary in some cases. We used painter's masking tape for this purpose, choosing high quality brands with small amounts of low-power glue. These always came off the bone without damaging it, but sometimes removed paint coats from plaster fillings of damaged bone areas.

GENERAL OUTLINE OF MECHANICAL DIGITIZING METHODS

Prerequisites

As digital representations of fossil bones will usually lack many features of the real specimen, such as surface rugosities and textures or discolorations indicative of breaks and deformation, maximum care must be given to the process of selecting specimens for digitizing. Especially those with deformations of the bone obvious on the real specimen but invisible on a digital representation must be avoided.

There are two possible aims when digitizing:

a) digitally constructing 'ideal', that is undeformed and complete bones from several partial or damaged specimen, or

b) digitizing individual specimens exactly, e.g., to obtain a digital representation of one complete animal.

For (a), as an absolute minimum, a specimen must either allow measuring of at least two characteristic dimensions and their relation to each other (preferably total length and proximal or distal width) or three distinctive landmarks that can be pinpointed with millimeter accuracy. Additionally, the specimen must possess a significant section of non-deformed and non-eroded bone surface to be digitized in correct relation to said characteristic dimension. For example, a complete articular end that has been shifted in relation to the long axis of the bone through compression is useless, as the exact orientation cannot be ascertained. Only if the correct three dimensional relations of the characteristic dimension and the area digitized can be ascertained, can several pieces be combined correctly. These requirements are far less strict than those commonly used for other studies (e.g., Wilhite 2003b), as the methods described here allow combining sections from several specimens to obtain artificial 'ideal' digital bones.

Regarding (b), any specimen can be used. However, for most applications using digital data, especially scientific study, it is advisable to use well-preserved material. In case of elements that exist as left and right copies, it is often better to mirror contralateral elements, than to use a badly preserved bone. Similarly, in elements with a bilateral symmetry, mirroring one well-preserved half may be better than using a badly damaged part, as long as the symmetry plane is obvious on the bone. Such data operations must, however, be clearly mentioned, best as a text entry in the digital file itself. Also, it is important to remember that dam-

FIGURE 1. Typical setup for digitizing: laptop, digitizer, and fossil holder. Note the position of the digitizer close to the fossil and away from the operator, so that the tip can be pulled instead of pushed.

age obvious on a real bone will usually not be easily visible on the digital file. Because digital files can be (and often are) widely shared between researchers worldwide, it is important to select well-preserved and typical examples. Otherwise, there is a risk that imperfect or unusual specimens will be accidentally treated as complete or normal.

General Overview of the Digitizing Procedure

Here, only a short description of the general process is given. Various versions of the basic procedure have different advantages and limitations, and are best suited for various kinds of fossils, as detailed in Appendices A and B. Step-by-step directions for program and digitizer use are given in Appendices C through E.

For digitizing we used Immersion™ Microscribe 3D digitizers. A Microscribe consists of a base plate, on which a four part arm is mounted. The base plate contains sockets for cables connecting the Microscribe to a PC. The position of the arm's tip is measured through the displacement of the joints between the various parts compared to the 'neutral' position, into which the machine must be put before it is switched on. By pressing a button on a foot pedal, the operator can determine when data on the tip's location is transferred to the

computer. Various commercially available Computer Aided Design (CAD) softwares can receive this data and transfer it into data points. We only used Rhinoceros®, which has the additional ability to automatically interpolate NURBS curves between the data points delivered by the digitizer. Figure 1 shows a typical setup of the digitizer and laptop along with a specimen (*Diplodocus* sp. GPIT ?160). It is possible to digitize large objects while sitting on the floor (Wilhite 2003b), often made necessary by the large weight and resulting immobility of specimens such as sauropod longbones. Working on a table as shown in Figure 1 is decidedly more comfortable and reduces worker fatigue, as it is much easier to work the foot pedal in this position. While this seems trivial, we found that prolonged digitizing in an uncomfortable position increases the likelihood of time-consuming errors significantly, and also increases the time required for digitizing specimens. The quality of the digitized data also decreases when the operator assumes an uncomfortable working position such as squatting on the floor. At worst, this can lead to cramps or jittering of the hand, making data acquisition impossible.

Preparation of specimens: Some markings must be made on the specimens before digitizing can take place. We placed masking tapes of different manufacture on them, on which we drew the required markings with felt tip pens. Although we never caused any damage to specimens this way, it is theoretically possible that the masking tape damages the bone surface. Thus, curatorial personnel should always be involved in the decision what tape to use, and where and how to apply it. Extremely delicate specimens should therefore be marked as little as possible. We recommend removing any tape from the bones as soon as possible.

If it is impossible to put masking tape on a specimen, digitizing it with point clouds or NURBS curves is still possible. Point clouds that partly overlap can be aligned manually in Rhinoceros® after digitizing. However, recalibration is impossible, unless there are at least three distinct and very small landmarks on the bone that can be used instead of markings. Not being able to recalibrate the digitizer creates a large risk of errors in the final file. Also, digitizing may take more time, and more erroneous curves may be created, if the bone cannot be marked in places difficult to digitize. NURBS digitizing without markings on the bone requires making a mental mark of curve starts and paths, to avoid drawing curves that intersect, leave large
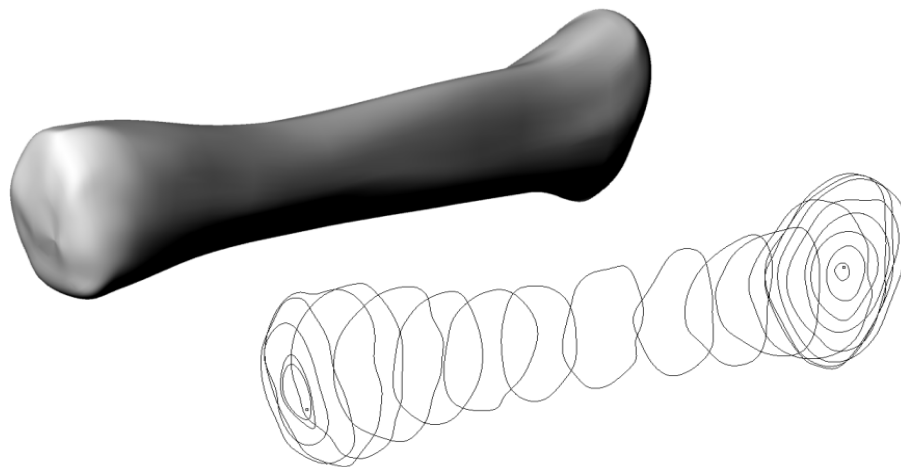
FIGURE 2. A digital bone (GPIT 1 *Plateosaurus engelhardti* left radius) and the curves and points used to create the loft. Note the sub-parallel arrangement of the curves. This digital bone is a NURBS body (closed surface), displayed in rendered view. Length of the bone 214 mm.

gaps, or otherwise results in errors in the final digital surface. This is possible even for large specimens, but requires extreme concentration, which increases worker fatigue. Additionally, the likelihood of erroneous curves increases, requiring additional time for correction both during digitizing and editing. We have successfully tested digitizing a sauropod metacarpal without markings.

Data acquisition: The easiest way to obtain 3D data of large bones with the Microscribe is by storing curves, not points, as detailed by Wilhite (2003b). Both curves and surfaces in Rhinoceros® are created as NURBS object. NURBS stands for non-uniform rational B-spline. Constructing a surface is easy when using a loft function on curves, which creates a NURBS surface. Even more comfortable is lofting a 'closed loft', leading directly to a closed 3D body, which is the method used most extensively here. Point clouds cannot be surfaced without much effort in Rhinoceros 3.0®. The current version Rhinoceros 4.0® allows meshing point clouds directly, but the process is error-prone and less accurate than in Geomagic®.

The process of digitizing with NURBS curves is best described as the electronic equivalent of wrapping sub-parallel wires around the bone, then pulling a cloth tight around the wires. See Figure 2 for an example of a digital bone (left radius of *Dicraeosaurus sattleri* MB.R.2622) and the curves used to create it. The curves are obtained by entering a simple command into Rhinoceros®, placing the tip of the digitizer on the bone at the start point of the intended curve, pressing down the foot

pedal, and moving the digitizer tip over the bone until the desired end point of the curve is reached. Then, the foot pedal must be released. Neighboring curves must be of similar length and should be roughly parallel. Large differences in length or separation tend to produce artifacts in the final surface. Also, curves may not cross each other.

Curves are placed at intervals at the operators' discretion and should be closely spaced where the morphology of the bone exhibits important features or where the topology changes abruptly, e.g., near cristae or at the articular ends. Relatively simple surface areas like shafts of longbones or scapular blades require few curves. The operator's judgment on the placement is one of the key elements that determine the accuracy of the digital bone.

If a bone cannot be represented by one set of sub-parallel curves due to its shape, it can be digitized by joining several partial surfaces or bodies together. Separate curve sets must be digitized for each part.

To reduce post-digitizing workload and achieve the most accurate results, closed curves reaching 360° around the bone are best. If a bone cannot be digitized with closed curves, due to its size or a fixed mounting that makes reaching all around it impossible, partial curves can be drawn and joined into closed curves.

Alternatively, a point cloud can be collected with the digitizer. Figure 3 shows point clouds of the lower left hind limb of the mounted *Dicraeosaurus* from the MFN (unnumbered) and the 3D files created from them. Point cloud digitizing is a
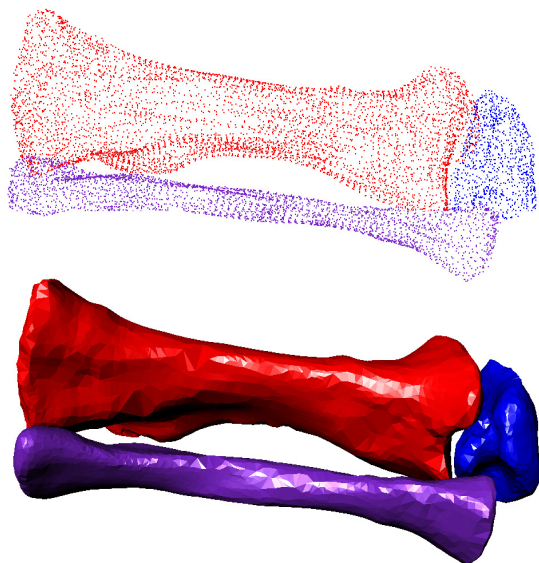
FIGURE 3. Lower hind limb of *Dicraeosaurus sattleri* (MFN unnumbered). (1) pointcloud file. Each bone was digitized in a different layer, indicated by different colors. (2) Low-resolution polygon mesh file created from the point clouds in Geomagic®. These meshes were not subjected to any editing. Length of the tibia 790 mm.

method usually more time consuming than digitizing curves, as the full surface of the bone must be densely sampled. On the other hand, hardly any planning ahead is required, and there is no need to mark the bone extensively, saving time especially when a complex geometry renders curve-planning difficult. It is best used for small bones of complex shapes, or for rough representations of large bones at low resolution.

Surface creation: A surface is created from curves as a NURBS surface, a 'loft', through a single command. If, which is most advisable, the entire surface is to be created in one piece (from closed curves), two points are also needed, one at each end of the bone. This will result in a closed body (resembling a deformed balloon) instead of an open surface (resembling a deformed tube).

When digitizing point clouds, curves can be hand-built from suitable points, but this method is usually not advisable due to the high amount of work involved. Instead, current versions of Rhinoceros® can produce polygon meshes directly from point clouds. These usually require a few minutes' to half an hour's work of editing to remove artifacts and mesh errors, but this method allows accurate digitizing of small and complex shapes, such as

small to mid-sized vertebrae. Figure 4 shows the left humerus of GPIT 1 as a point cloud file, the resulting mesh in Geomagic®, and the final file produced by manual editing of the mesh. Both the initial meshing and all editing are, however, best accomplished in Geomagic®. Unfortunately, when Rhinoceros® is used to create the mesh, the resulting 3D bodies are often smaller than the volume covered by the original point cloud, producing significant errors in the surface shape. Also, Rhinoceros® tends to produce more meshing errors near sharp bends in the surface geometry than the Geomagic programs suite (Figure 5). Additionally, as opposed to Geomagic®, Rhinoceros® does not offer an option to preserve the edges of meshes when reducing their polygon number. This results in 'digital erosion' of sharp edges. Digitizing bones via point clouds may require more effort than via curves, but is decidedly cheaper than CT or laser scanning.

Mobile fossil holder: Accuracy is paramount when digitizing fossils, as even slight aberrations of the digital curves can lead to significant shifts of volume or appearance. A slight unnoticed rotation of the specimen during digitizing may lead to a misinterpretation of range of movement of joints that include the articular ends of the bone. Mass estimates of complete animals may be off by significant amounts if bones of the pelvis girdle are misshaped or longbones gain or lose length or volume through errors during digitizing. More common than unnoticed errors are significant movements of the specimen due to unstable placement or physical contact. Especially small bones will shift at even the slightest touch while curves are being drawn, invalidating the last curve drawn and requiring time-consuming recalibration. A common method to avoid this is placing the specimen either in sandboxes, where they are often still prone to shifting and the sand is likely to get into the computer and digitizer, or to fix them with Play-Doh® or similar deformable substances. Since various chemicals damaging to fossil bone may leak from these materials, their use is problematic. Also, 360° reach around the fossil is not possible. A construction drawing of the holder is available on request.

To solve these problems a variable holder was designed. It can be separated into small pieces and quickly reassembled. Figure 6 shows the holder in the minimum configuration with an unnumbered GPIT *Diplodocus* metacarpal and the extension parts used for larger bones. This construction kit setup makes the holder easy to stow
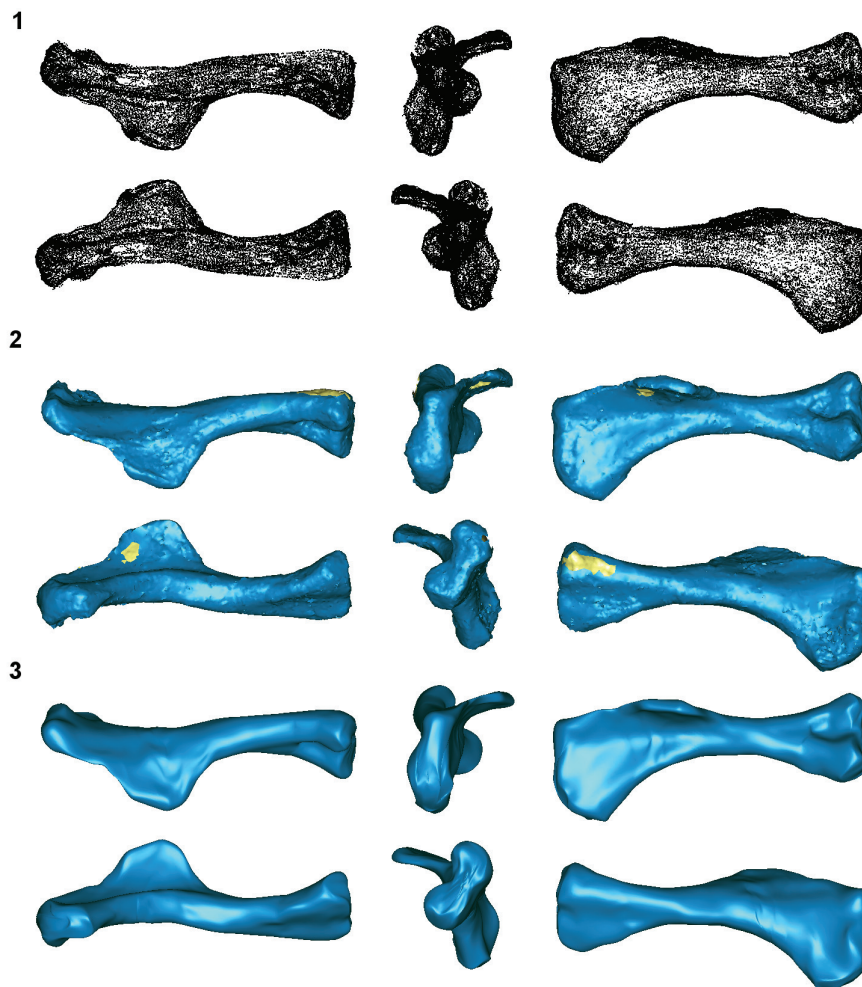
FIGURE 4. GPIT 2 *Plateosaurus engelhardti* left humerus (length 351 mm) point cloud based 3D file creation example. Clockwise, starting top left: lateral, proximal, cranial, caudal, distal, and medial views (terms refer to standardized in vivo position, assuming parasagittal posture). (1) Point cloud from mechanical digitizing. (2) Initial mesh as created in Geomagic®. Note the large holes and many small surface errors. (3) Final edited mesh. Small surface errors were deleted and the resulting holes as well as the large holes were closed with curvature-based filling.

and transport. It consists of a base plate made from heavy polyurethane, custom made metal holders that can be placed at variable intervals on the base plate as desired, and commercially available plastic contour gauges supported by the metal holders. On these, the bones rest stably, are well supported, and resist shifting even when bumped. Using smoother plastic gauges instead of metal holders avoids the risk of scratching the bone. The base plate is split into four parts. These parts can be stuck together as needed in order to accommodate large bones, but are not cumbersomely large when used for small bones. The smallest possible assemblage, sufficient for objects up to the size of sauropod metatarsals or hadrosaur humeri (ca.

10x10x35 cm), weighs approximately 3 kg, the largest tested assemblage, sufficient even for sauropod pubes and radii, weighs about 8 kg. Theoretically, the holder can hold even larger bones, if a sufficient number of contour gauges are used to support the bones.

The fragility of the specimen strongly influences the ideal setup. More gauges mean better support, fewer gauges mean better access. The longest bone digitized during this project was a *Brachylophosaurus* rib from the JRDI. The excellent preservation and hardness of the bone allowed using only four gauges (Figure 7). On the other hand, the ribs of the *Plateosaurus* skeleton GPIT 1 could not be supported on the holder due to their
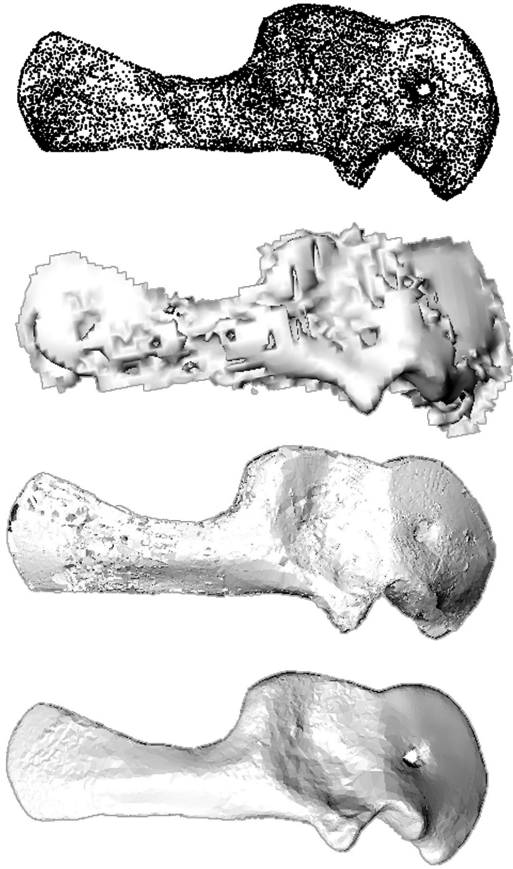
FIGURE 5. *Dicraeosaurus sattleri* (MFN unnumbered) left scapula. (1) point cloud file as digitized. (2) Polygon mesh created in Rhinoceros®. Note the massive meshing errors along the edges of the bone and on thin surface parts. (3) Polygon mesh created in Geomagic®. Note the drastically lower number of meshing errors and the smaller triangle size along the bone edges. Meshing has also closed the coracoid foramen. (4) Finished 3D surface based on (3) after editing in Geomagic®. Length of the scapula 1067 mm.

FIGURE 6. Minimum configuration of the fossil holder with a *Diplodocus* sp. Metacarpal 3 (GPIT ?610). The bone has been marked for digitizing with coordinates (Y and O, X is hidden from view), seam line, some curve paths, and end points. On the right and on top extension parts and double-wide contour gauges are shown.

FIGURE 7. Digitizing a *Brachylophosaurus canadensis* rib (JRDI 200, length 1048 mm). Note the extensive markings on the bone. The finished 3D file is visible on the laptop screen.

fragility. Close enough spacing of the gauges would have made access to the lower side impossible. Curatorial personnel should always be included in the decision on what setup of the holder is employed.

Size range: The lower end of the size range of objects that can be digitized accurately is defined less by dimensions, but rather by the necessity to keep the object perfectly immobile without obscuring a large part of its surface. The smallest bones that we were able to digitize were less than 5 cm long, held in place on the table with two fingers, and digitized using point clouds. NURBS curve digitizing usually works well for objects with a
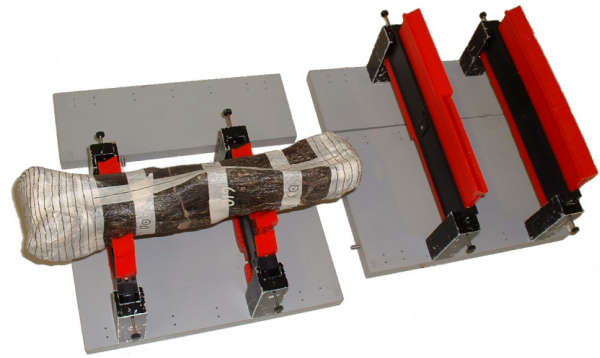
length greater than 10 cm. Similarly, the maximum size is not defined by greatest (or least) extension, but rather by the complexity and size of the surface area. The larger and/or more complex in shape a bone is, the more recalibrations of the digitizer will be necessary to sample it sufficiently. For example, a 50 cm long sauropod vertebra may require more recalibrations than a 2 m long sauropod scapula. Each recalibration decreases the accuracy of any digitizing taking place after it. While in theory the size range is unlimited, our experience shows that

recalibrating more than five times should be avoided. However, this number is not a hard limit, and there is no single bone in any extant or extinct vertebrate that is too large for the methods described here. Digitizing very large objects usually results in a reduced absolute, but not necessarily relative accuracy.

Manpower requirements: Normally, one person can transport the equipment and digitize bones alone. The digitizer and the fossil holder together fit into a standard suitcase, and weigh less than 20 kg. When digitizing very large bones it may be difficult for one person to operate both the digitizer arm and the foot pedal, especially if it is necessary to step around a mounted bone during digitizing. A second person should then be employed to operate the foot pedal. In this study, only a scapula of *Giraffatitan (Brachiosaurus) brancai* (MB.R.2912), mounted vertically, made a helper necessary.

Digitizing time requirements: The time needed for digitizing depends significantly on the expertise of the person operating the digitizer. Generally, between 5 and 20 minutes suffice to digitize a small or medium sized bone of simple geometry, such as a longbone, metatarsal, pelvic bone, or rib. Very large bones (over 1 m length) or complex shapes (vertebrae, skull elements) may take several hours, although usually 30 minutes are sufficient. Post-digitizing editing may require several hours. Normally, though, simple bone shapes will not require editing at all, while editing complex shapes can usually be completed within 15 minutes. Polygon meshes based on point cloud data are easier to edit in Geomagic®, which usually takes a few minutes only, than in Rhinoceros®, which may take up to half an hour. Overall, the techniques allow digitizing and final editing of virtual bones as fast as or even faster than extracting and editing virtual bones from CT data. Considering that CT scanning involves wrapping and transporting the specimens, plus time for the actual scanning, mechanical digitizing is decidedly faster.

EXTRACTING VIRTUAL BONES FROM CT DATA

One of the two most detailed and expensive techniques of creating 'virtual' bones is high-resolution computer tomography (HRCT, short CT) scanning specimens. This allows maximum resolution, far higher than required for most uses, similar to high resolution laser scans of individual bones. The former technique has the advantage of allowing the study of internal structures and does not suffer from 'blind spots', as X-rays penetrate the material. Even surfaces completely blocked from view such as deep cavities and recesses on skulls are faithfully reproduced in the virtual bones. Virtual bones from both methods can be assembled into virtual skeletons either simply based on their own shapes, much as it is possible for real bones. Drawings, photographs, or measurements of mounted skeletons can be of help, but are rarely required, since the high-resolution virtual bones provided by both methods contain all the information needed for assembly. One drawback of these methods is the relatively large file size. Both Rhinoceros® and the Geomagic® program suite offer options for reducing the number of polygons in each mesh, reducing the file size proportionately. The latter program offers the additional option of preserving the outside contours better and thus should be preferred. While reducing the mesh number decreases file size, the resulting virtual bones lose accuracy, and the reduction should not be taken too far. On average, a reduction to 2.5 to 10% is the maximum tolerable, depending on bone size and shape. Delicate structures may start losing shape at 20% reduction already (i.e., 80% of the original size).

For data extraction, the files of one scan are loaded into AMIRA 3.11®. Then, a 'LabelVoxel' module is created and applied to the data. Here, up to four different areas of density can be defined. A histogram is helpful for interpreting the data and deciding where to set the borders. It is possible, e.g., to remove or include plaster fillings by choosing different settings. Now, an 'OrthoSlice' module can be created to view cross sections. In order to keep the computing time and memory requirements low, the re-labeled data should be cropped to contain no unnecessary space, e.g., empty space under or above the bones. Large bones should be cropped out so that each bone is treated separately. Since the original data is still present in unaltered form, after extraction of the first bone it can simply be 'labeled' again and the next bone treated. To each cropped set of labeled data, a 'SurfaceGen' module is attached and executed. This creates a polymesh surface, which can be saved as a number of different formats, e.g., ASCII stereolithography (*.stl). The resulting files are highly detailed and accordingly huge. A longbone can easily have 10 million polygons and exceed 1 GB in file size. To reduce the size, it is useful to load the files into Rhinoceros® and re-save them as binary STL files, which have a significantly smaller size without any data loss. Reducing the

number of polygons, on the other hand, results in a less accurate representation of the surface. Usually a reduction to 20% is hardly noticeable to the human eye if a bone is displayed at full-screen size. Therefore, a slight to generous reduction may be acceptable depending on the planned use of the data. As mentioned above, this is best done in Geomagic®, as this program has an option to 'preserve edges', guaranteeing a minimum of shape change during polygon reduction. AMIRA 3.11® also offers this option, here called 'Simplifier'. 'Preserve slice structure' is the equivalent to the edge preservation option in Geomagic®.

ACCURACY OF
MECHANICAL DIGITIZING DATA

Any 3D file is only of use if it mirrors the original object accurately enough for the investigation at hand. As described above there exists an inverse relationship between accuracy and file size. The smaller files produced from mechanical digitizing offer the benefit of easier handling over the large files from laser or CT scanning, but is their accuracy sufficient for e.g. skeletal reconstructions or rapid prototyping of scale models? In order to test this, a number of mechanical digitizing files were compared to the high-resolution CT based files scaled down to the same final size as the mechanical digitizing files. The following virtual bones of GPIT1 *Plateosaurus engelhardti* were used in order to cover different sizes and shapes: left humerus, left ilium, second dorsal vertebra. Additionally, the pedal phalanx II-1 from GPIT 2 *Plateosaurus engelhardti* was digitized. The files were imported into Geomagic® and aligned automatically with the 'Best fit' option. A 3D comparison analysis was performed, creating a 3D map of the surface pair, in which distance between the surfaces at any point is displayed by varying colors. The program also calculates the maximum, average, and standard deviations. Note that the actual errors of the mechanical digitizing files are probably smaller than determined by the program, because the alignment was not optimized for minimal deviation. Geomagic® offers a variety of alignment options, but we considered it unnecessary to test which one offers the smallest deviation values.

Test files

Ilium: The CT data of the left ilium consisted of 1778 slices, of which 889 (every second) were used to extract the file. The reduction was made necessary by the fact that each slice of 0.5 mm thickness overlapped the neighboring files by half

that amount, which for unknown reasons created massive artifacts (wrinkling) in the finished surfaces. The scan of the ilium also included the right fibula, totaling a data volume of 894 MB at 516 kB per file. From it, an STL file in ASCII format with 203 MB was extracted. This file, which still included pieces of the fibula and internal 3D bodies in the ilium, was edited to gain the maximum resolution STL file of the ilium in Rhinoceros®, having shrunk to 47 MB by removal of the excess data and saving in binary STL format. One deep pit stemming from obvious damage was removed by manual editing. The file has 977244 triangles and was reduced in Geomagic® to 89816 (9,19%) to achieve the same file size as the point cloud file.

The point cloud data consisted initially of 44865 points, which were meshed into a surface with 89816 polygons. This was edited manually to remove some obvious artifacts along sharp edges, where curvature-based filling was applied. Also, various small artifacts on flat surfaces were removed. The files size is 4,33 MB.

For the 3D deviation comparison a display scale was selected that details deviations of between +/- 0.5 mm and +/- 5 mm. Deviations smaller than half a millimeter we assume to be irrelevant. Deviations up to 2.5 mm are tolerable, and for values up to 5 mm (~ 1% of greatest length of the ilium) it is important where they occur. If strong deviations are limited to damaged areas of the bone, they can be ignored outright. On the other hand, several millimeters of deviation over larger areas are unacceptable. Any deviation greater than half a centimeter can only be tolerated if it has no influence on the likely shape of the undamaged bones, i.e., if it occurs due to damage of the specimen. The likeliest scenario for such a deviation is a tiny, deep hole in the bone that must be passed over with the digitizer.

Figure 8.1 shows the 3D deviation maps of the pointcloud based file compared to the CT file. Deviation ranges from nearly +5 mm to almost -15 mm, but values greater than 2.5 mm occur exclusively near cracks in the bone. The mechanical digitizing file preserves a different 3D body than the CT scan data in such places, because it is limited to gathering data at the air/solid boundary, while in the CT file some of the crack infill is missing, because the extraction threshold was set roughly at the bone/sediment boundary. Geomagic detects and ignores non-alignable areas, but the edges of these areas are assessed. Despite these, average deviation is below 0.5 mm.
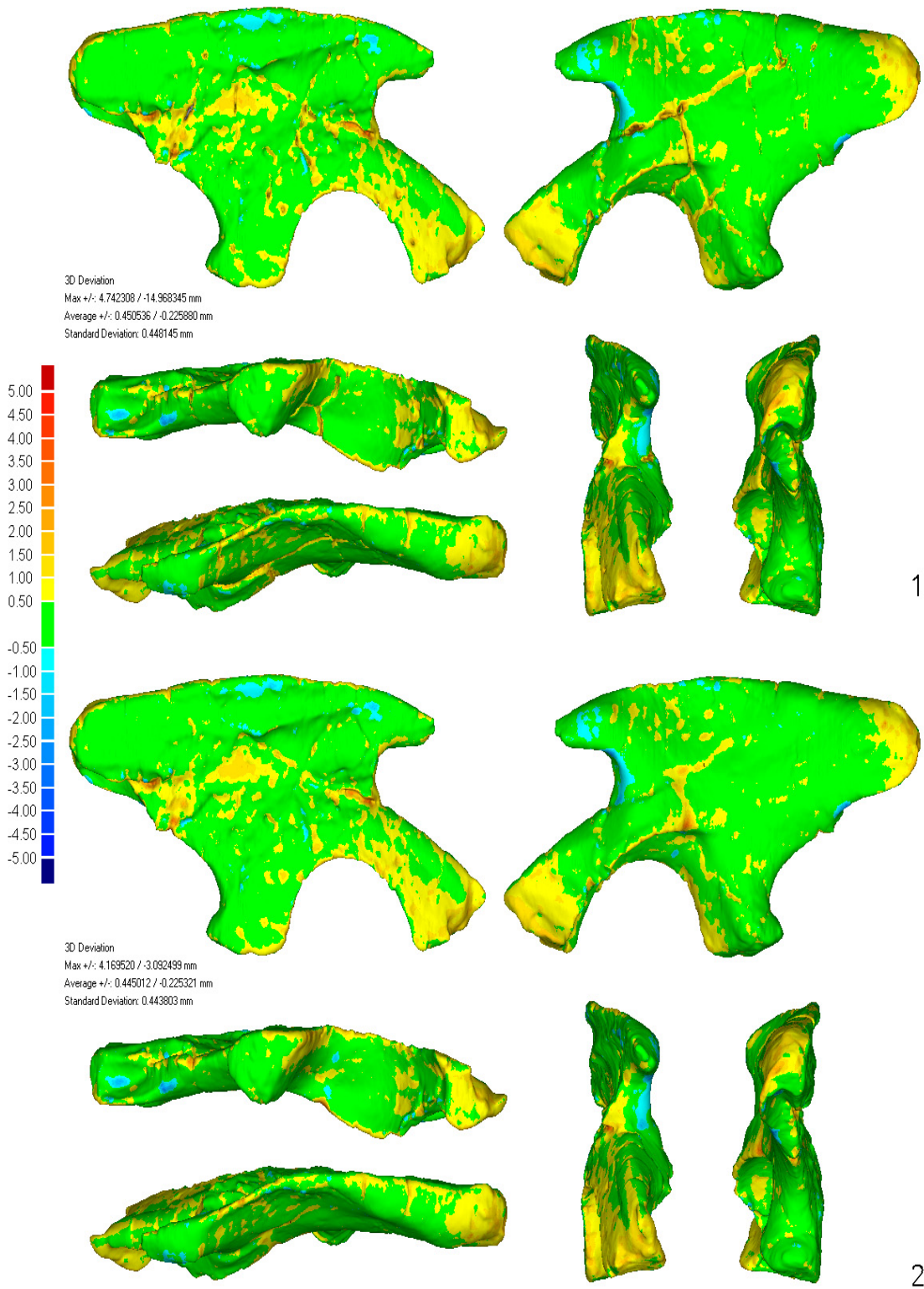
FIGURE 8. 3D deviation maps from Geomagic® of the left ilium of GPIT 1 *Plateosaurus engelhardti* (maximum extension 426 mm). (1) pointcloud-based file compared to unedited CT file. (2) pointcloud-based file compared to CT file in which all major cracks and holes were smoothed.
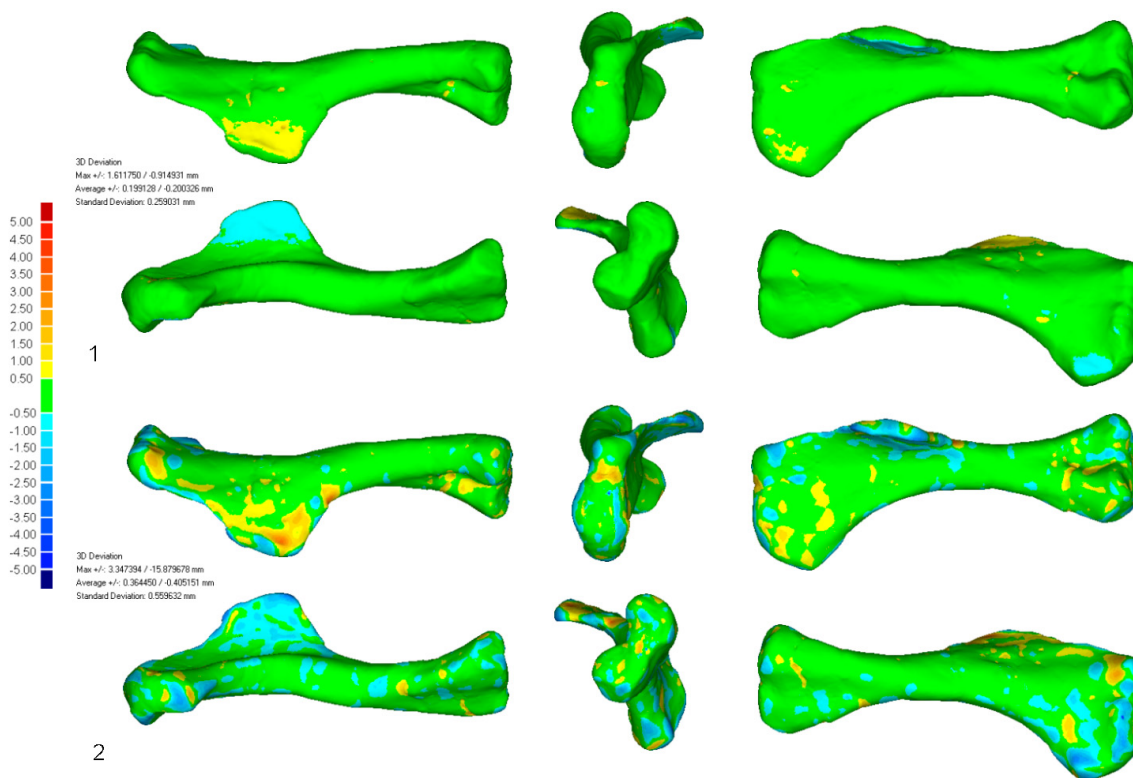
FIGURE 9. 3D deviation maps from Geomagic® of the left humerus of GPIT 1 *Plateosaurus engelhardti* (length 351 mm). (1) pointcloud-based file compared to CT file. (2) NURBS file compared to CT file.

To test how significant the influence of the shape differences caused by the cracks is, the CT based file was extensively edited to smooth the cracks over. This lead to the removal of further internal surfaces and created 43 holes in the outer surface, all of which were automatically closed by curvature-based filling. In all, the number of polygons dropped by 15.8% to 75658 polygons, reducing file size to 3,6 MB. 3D comparing this file to the point cloud file (Figure 8.2) resulted in a significant reduction of the maximum deviations (+4.12 mm / -3.1 mm). The average and standard deviations were little influenced, in contrast, due to the large undamaged surface areas, which outweigh the cracks.

Humerus: The humerus based on NURBS curves, created in roughly seven minutes, was lofted in Rhinoceros® with a loft rebuild option with 25 control points, and exported for comparison in Geomagic® as a polymesh file with 13764 polygons. The original NURBS file has a size of 1.27 MB.

The mechanical digitizing file with points consisted of 24640 points, with only a handful of obviously erroneous points. Digitizing time was roughly 10 minutes. Meshing in Geomagic® produced a surface with various small and two large holes. All could be filled with curvature-based filling without problems. The file was now manually smoothed, after which 49102 polygons remained. Figure 4 shows the original point cloud, the wrapped surface, and the edited final surface. The file size is 2.47 MB, nearly double that of the NURBS file.

The CT data of the left humerus stemmed from an earlier scanning opportunity and had a lower resolution than all later CT scans. The STL file extracted from 282 MB of raw data initially had a size of 359.202 MB (ASCII STL) and 1763876 polygons. It was reduced to 2.81% to match the 49524 polygons of the point cloud file. This operation alone required over 12 minutes calculation time on a 2.4 GHz PC with 2 GB of RAM and a 256MB graphics card.

Figure 9 shows the 3D deviation maps for the pointcloud (Figure 9.1) and NURBS (Figure 9.2) files using the same scale as the ilium comparisons (+/- 0.5 mm to +/- 5 mm). Average deviation is ~ 0.2 mm for the point clouds file and ~0.4 mm for
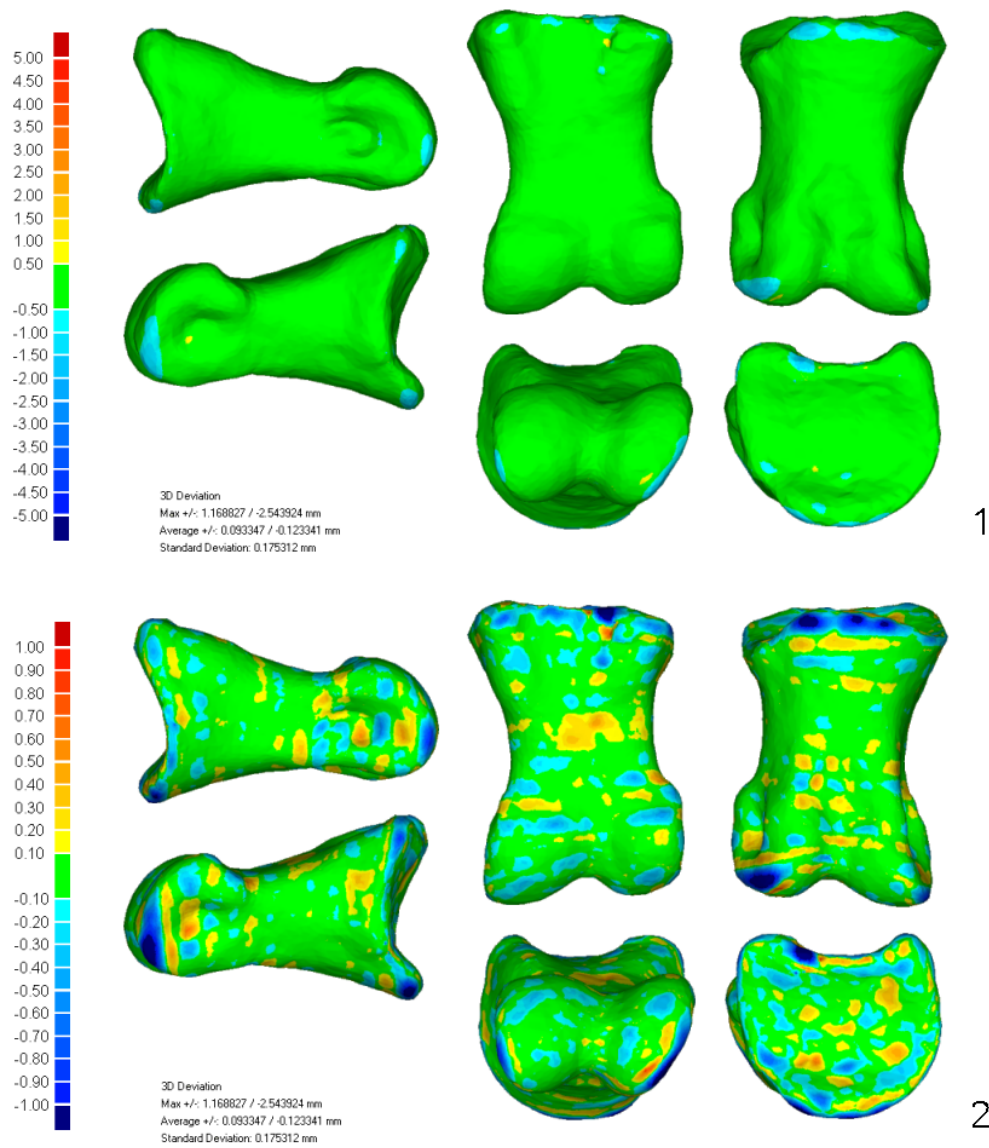
FIGURE 10. 3D deviation maps from Geomagic® of the left pedal phalanx II-1 of GPIT 1 *Plateosaurus engelhardti* (length 73 mm). (1) pointcloud-based file compared to CT file using 5 mm scale. (2) as (1), but using 1 mm scale.

the NURBS file. In contrast, maximum deviation is significantly different between the two files. While the point clouds file differs at most 1.61 mm in one small location on the humeral crest, the NURBS file shows larger areas of strong deviation along prominent edges. The extreme value of over 15 mm, however, is limited to a small spot, where apparently a lofting artifact creates a deep indentation in the loft file. Note that the large holes in the original mesh (Figure 4.2) do not result in large errors in the final surface due to the use of the curvature-based filling algorithm.

Pedal Phalanx II-1: The point cloud file, created in roughly four minutes, consisted of 9212 points after removal of erroneous points. The mesh created from it required some editing due to internal polygons. They were apparently caused by small errors during recalibrations, leading to a suboptimal fit between the point clouds created before and after recalibrations. The file size is 906 kB with 18540 polygons after smoothing. The NURBS file, a rebuild loft with 100 control points, was created in 10 minutes, most of which was spent taping and marking the bone. It has a size of 933 kb as a STL.
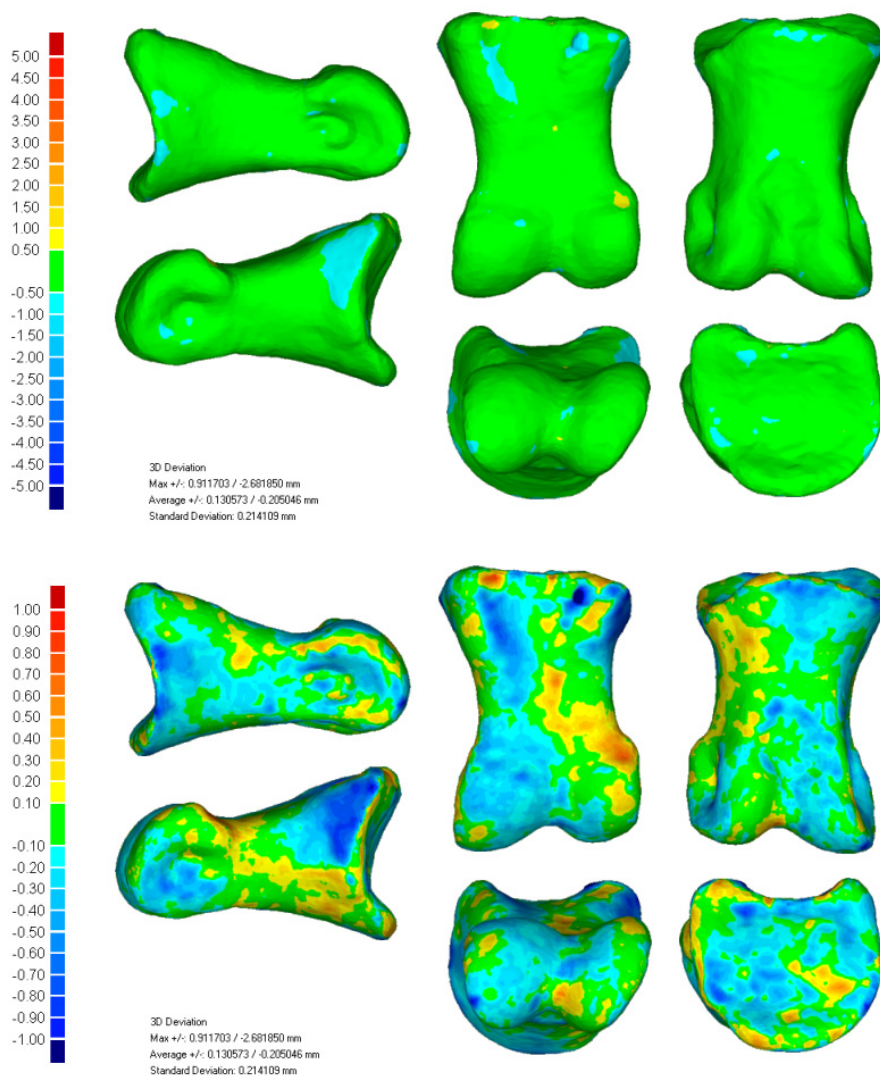
FIGURE 11. 3D deviation maps from Geomagic® of the left pedal phalanx II-1 of GPIT 1 *Plateosaurus engelhardti* (length 73 mm). (1) NURBS file compared to CT file using 5 mm scale. (2) as (1), but using 1 mm scale.

The left pedal phalanx II-1 was CT scanned along with various other small elements. Original size was 170054 polygons and 33.1 MB. After surface extraction, it was reduced to 18540 polygons (10.9%) as well.

Because of the much smaller size of the phalanx compared to the ilium (roughly 18% if maximum lengths are compared), it appears unreasonable to demand the same degree of absolute accuracy for digital files of both. Acceptable error should be expressed not as an absolute value (e.g., 2.5 mm), but as a percentage of total size (e.g., 2.5% of largest dimension). Therefore, the phalanx files were 3D compared using two different scales: the same scale that was used for the ilium and humerus (0 – +/- 5 mm deviation, with the

minimum displayed deviation greater than +/- 0.5 mm), and a scale with one fifth the values: 0 – +/- 1mm, minimum displayed > +/- 0.1 mm.

The NURBS file 3D deviation maps for both scales are given in Figure 10. Although the average deviation is very small at ~ 0.1 mm, maximum deviations of slightly over 2.5 mm occur at the sharp dorsal edge of the proximal articulation surface and on the medial distal condyle. However, these are three localized deviations that do not appear to alter the general shape of the edge if the 5 mm scale is used to assess the differences (Figure 10.1). Using the tighter 1 mm scale, in contrast, exposes deviations of 0.5% maximum specimen length along all edges (Figure 10.2) and shows that this deviation is continuous along the dorsal margin
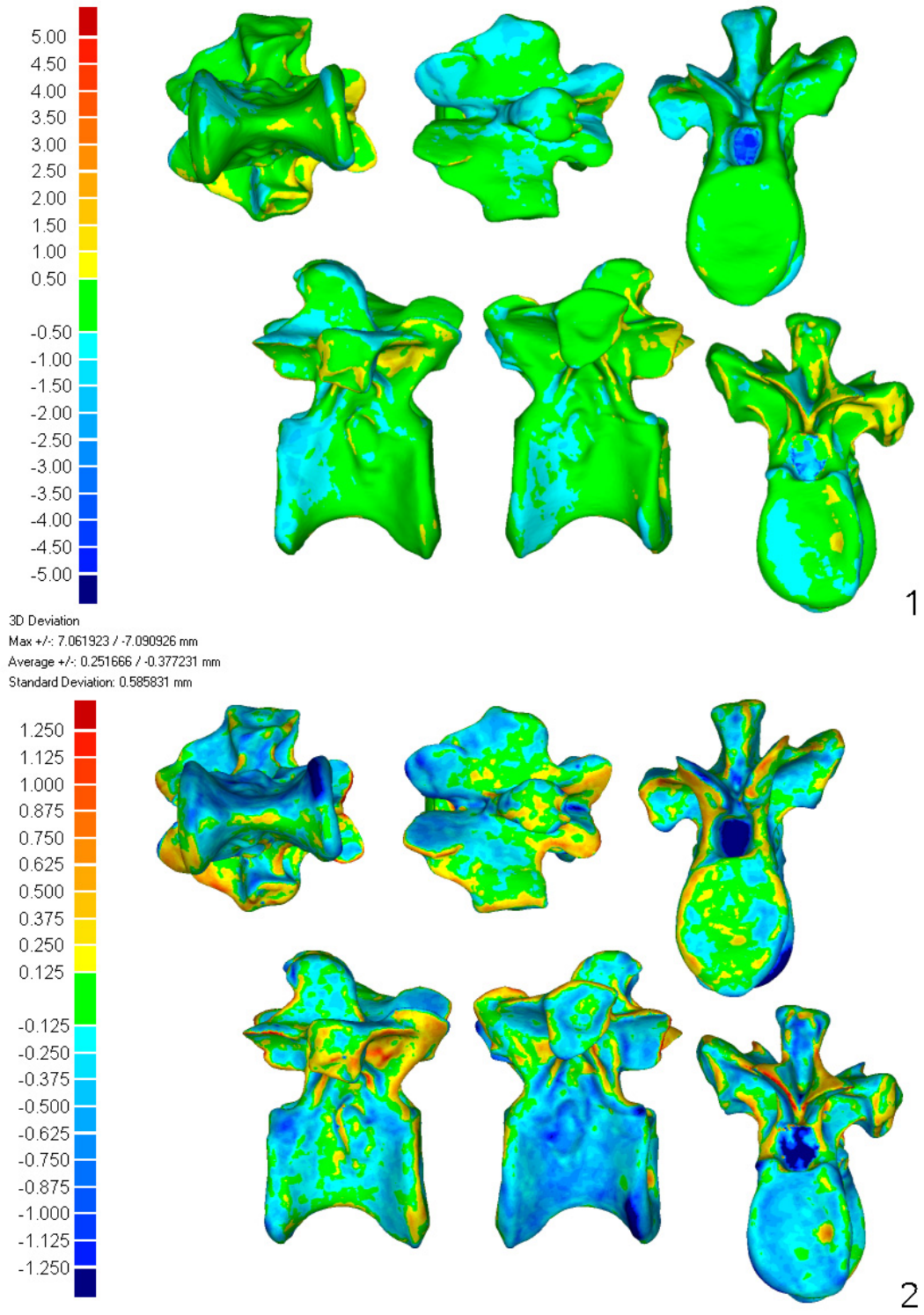
15

FIGURE 12. 3D deviation maps from Geomagic® of dorsal 2 of GPIT 1 *Plateosaurus engelhardti* (centrum length 79 mm). (1) pointcloud-based file compared to CT file using 5 mm scale. (2) as (1), but using 1.25 mm scale.

and the distal condyle. This means that the compound error when measuring across these two points may exceed 1% of maximum length.

The point cloud file deviations are shown in Figure 11.1 (5 mm scale) and Figure 11.2 (1 mm scale). Here, average deviation is more than double that of the NURBS file, and the errors are widely spread over the bone surfaces. Maximum deviation, though, is much lower, expect for one artifact on the ventral side near the proximal end.

Dorsal 2: The CT data, which had the same wrinkling problems as the ilium file, was reduced to 28266 triangles for use in the virtual skeleton. It shall serve here as an example of an object with a complex shape combined with a small file size. The mechanical digitizing file, with 51582 points (41592 after removal of obviously erroneous points), was meshed in Geomagic® and required some filling of holes. It took nearly 12 minutes to create. Spikes were removed on an average setting. Now the file contained 8611 polygons. It was now reduced to 28266 polygons (32.83%), to fit the CT based file. The size is now 1.381 MB. Figure 12 shows the 3D deviation, both using the 5 mm scale (Figure 12.1) and a size adjusted scale running from +/- 0.125 mm to +/- 1.25 mm (Figure 12.2). The standard deviation at less than 0.4 mm is tolerable, but many edges show strong deviation along their entire lengths. The maximum deviation of over 7 mm occurs along the sharp edges of the left postzygapophysis. These deviations indicate that the problem rests with the meshing of the point cloud in places where interpoint distances are similar between points on the same surface and points on different surfaces (upper and lower face of the zygapophysal process). Note that the point cloud file has an artificially constructed neural canal, while the canal of the fossil is filled with matrix. High deviations in this area are to be expected and meaningless for digitizing accuracy.

Discussion of 3D deviation analyses

In general, the 3D deviation analyses show that – at the file size of mechanical digitizing with point clouds or NURBS curves – the accuracy of both CT and mechanical digitizing data is sufficiently similar to allow using the various formats interchangeably for most applications. At the maximum resolution of CT data available to us, the deviations are probably marginally larger. However, comparing the reduced CT files of all four bones to the maximum sized ones in 3D deviation analyses resulted in differences only in places where

there were extremely fine cracks,

there were very fine connections between internal and external surfaces (irrelevant for mechanical digitizing), or

there were 'wrinkling' artifacts present in the high-resolution surface, apparently caused by the overlap of neighboring slices.

These differences all remained under 0.1% of the greatest length of the bone. Therefore, the reduced CT files can serve as an accurate model of the high-resolution files.

Our sample number is low, but except for very large bones or extremely thin structures (e.g., sauropod vertebral laminae) all typical problems are represented by the sample. Generally, it is possible to mechanically digitize mid-sized to large bones (>20 cm greatest length) with errors below 0.5% of the maximum length or 1 mm. While one of the files we used to assess the accuracy of our methods, the dorsal 2 file, is close to this size class and shows significantly higher errors, it is important to note that this point cloud file was our first attempt at digitizing a vertebra at all. The deviations, spread out over nearly all the surface, and consistently positive or negative over relatively wide areas of the bone, are apparently caused by insufficiently accurate calibration of the digitizer between the different point cloud parts. The complex shape of the specimen and our inexperience in mechanical digitizing lead to a high number of recalibrations, along with the instable support of the specimen in a sandbox. The deviations evident in Figure 12.2 underscore the importance of both stable support for the specimen and as few recalibrations as possible during the digitizing process. Files smaller than 20 cm maximum length are probably better digitized using point clouds.

There is no general pattern of one of the two mechanical digitizing methods being more accurate or faster. NURBS digitizing suffers when the specimen is small or has a very complex shape, but surprisingly the pedal phalanx NURBS file is more accurate over large amounts of the surface than the point cloud file. However, in the NURBS file errors concentrate in specific crucial areas, namely the extreme edges of articular surfaces. Which of the two methods is more suitable to a given task depends on what that task is. Research that uses volumetric data is probably better served by the NURBS file, while investigations concerning the exact shape of articular surfaces, e.g., motion range analyses, should be conducted using point cloud based files.
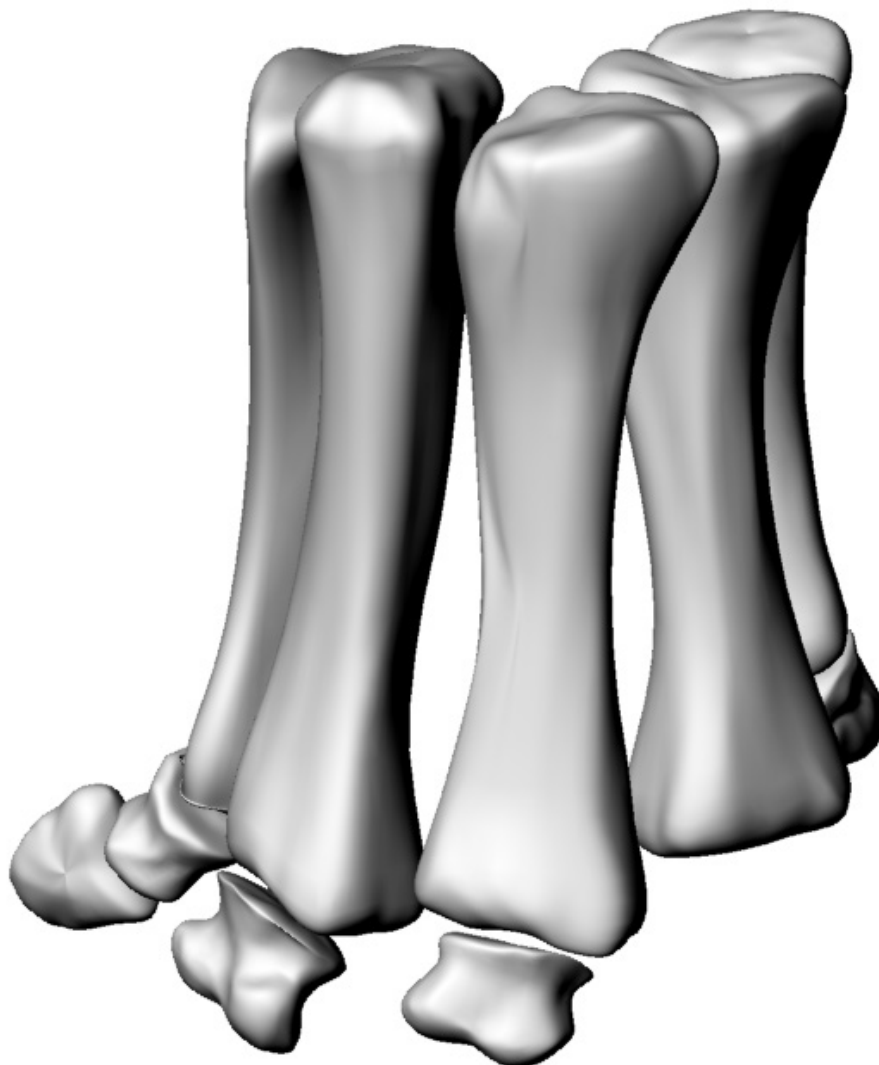
FIGURE 13. Digital mount of NURBS files of the left hand of *Giraffatitan (Brachiosaurus) brancai* MB.R.2249 R9 – R17. Length of metacarpal 3 390 mm. Total file size 4.4 MB.

BENEFITS AND LIMITATIONS OF MECHANICALLY DIGITIZED DATA

The obvious benefit of digital data is the ease with which it can be copied, shared and stored, and compared to real bones and casts. Mechanical digitizing data has smaller file sizes than unreduced CT or laser scan based data, and is, therefore, even easier to email, upload, or use in a CAD software.

Due to the sizes and weights involved, manipulation of real bones, especially sauropod bones, to ascertain joint mobility, is problematic even with only two elements. Trying to manually sort together partial skeletons such as a sauropod manus with-

out sandbags or extensive custom-cut styrofoam supports is impossible. Digital files, on the other hand, can easily be used for this purpose, e.g., in Rhinoceros® (see Figure 13, digitally mounted hand of *Giraffatitan* (*Brachiosaurus*) *brancai* [MB.R.2249 R9 through R17] and Wilhite 2003a, 2003b, and 2005; Mallison 2007) or other CAD programs (e.g., Allen 2008). Paper drawings also work well, but are limited to two dimensions, while digital data can be freely rotated, sectioned, and rearranged as desired. Figure 14 shows a CAD mount of a complete *Plateosaurus* skeleton as it could be posed in a museum mount. Here, the correct articulation of a large number of elements can be
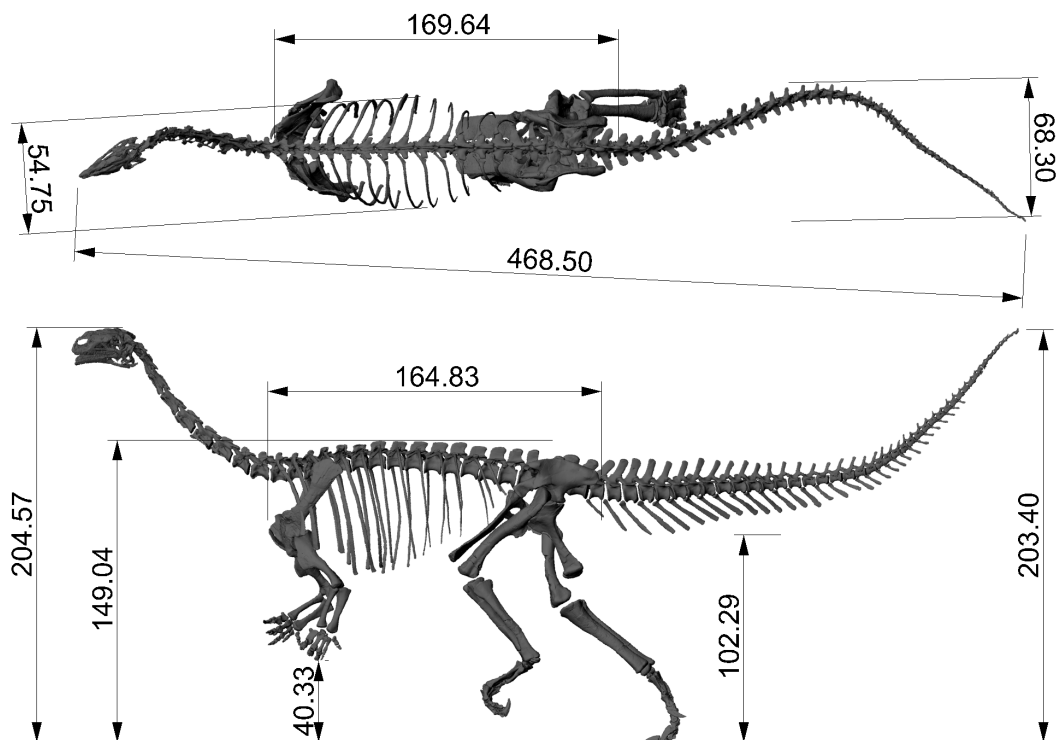
FIGURE 14. Digital mount of CT based files of the complete skeleton of GPIT 1 *Plateosaurus engelhardti*. The animal is posed running quickly, as might be done for a museum exhibition mount. Various dimensions are measured and marked directly on the digital skeleton in cm.

checked easily, and exact measurements from all dimensions can be taken with a mouse click before any work is done with the real bones. Exhibit design and arrangement can be accurately planned and altered easily at any time. While the *Plateosaurus* skeleton in Figure 14 is derived from CT data, the same work could also be done using NURBS bodies from mechanical digitizing.

Sharing data with researchers abroad can be problematic with conventional methods, too. Either expensive travels are required, or casts or originals must be shipped at great cost. Digital files can be sent via email or on CDs/DVDs instead, given sufficient resolution for the planned project. They also do not require storage room, in contrast to casts.

Digital files can also be accurately and quickly scaled to produce proportionally correct composite skeletons, while physical scale models must be molded by hand, a process that requires considerable time and resources. Skeleton drawings of the type made famous by the work of Paul (1987, 1996, 1997, 2003) usually also include only two dimensions – the width of the animal is not indicated. Even if a top view or a cross section drawing is available (Leahy 2003; Paul 2003), much interpretation is needed. Often the operator has no choice but to guess the third dimension in many places, incurring significant inaccuracies in the model. Sometimes, lateral and cross-section views of the same animal contradict each other (Paul 1987: *Plateosaurus engelhardti*, see Mallison 2007). Digital bones, in contrast, allow articulating a digital three-dimensional skeleton. It can be rotated to view it from any aspect, sectioned to facilitate modeling sections otherwise hidden by broader neighboring areas, and has the added benefit compared to measurements that errors become easy to spot. Also, the exact articular surface geometries are depicted, whereas a drawing can hardly detail a sloping or curving surface well.

Digital bones can also be used to produce exact casts of the original bones without subjecting them to molding – a process that may damage the fossils even if great care is taken to minimize the physical stresses exerted. For example, Research Casting International created rapid prototyping copies of the MFN *Kentrosaurus* mount. These were used instead of the real bones to build the armature for the new mount in order to reduce the risk of damaging the original material. Obviously,

specimens must be handled carefully, which is true both for moving them for CT or laser scanning and for mechanical digitizing. Extremely fragile bones are best scanned with touch-free methods and not suited for mechanical digitizing. However, aside from minimal scratches on the surfaces of lacquer-covered specimens, we never damaged any bones during our digitizing.

The biggest limitation of digital data is the lack of detailed representation of surface features and colorations. Also, the smaller the files are the rougher the resolution will be, reducing detail. Hence, for delicate objects, CT data or high resolution laser scans have a clear advantage over mechanical digitizing as described here and by Wilhite (2003b). Additionally, all research that requires information not encoded in the digital files can only be done by studying the real bones. This problem can be somewhat amended by adding color photographs of surface colors and features to the digital file.

For a detailed discussion of the benefits and problems of digital data, also see Wilhite (2003a).

CONCLUSIONS

Mechanical digitizing with a Microscribe 3D digitizer provides a cheap and easy alternative to complicated high-resolution digitizing techniques such as CT scanning and laser scanning, at an accuracy sufficient for most research and curatorial tasks. The accuracy of mechanical digitizing data is comparable to CT data of similar file sizes. Mechanical digitizing provides a far superior database for digital 3D skeleton creation than photographs, measurements, or drawings of bones.

We find that for medium accuracy or complex topographies, point cloud based digitizing works best, while very large objects can be rapidly digitized at slightly lower accuracy using NURBS curves. Costs are much lower than CT or laser scanning, especially if only NURBS elements are used, while point cloud digitizing requires one additional computer program. The main cost factor, however, is the digitizer. The work time requirements are comparable or below those of high-detail techniques. A custom-made and adjustable holder for specimens eases the workload of digitizing significantly, by allowing 360° access.

Mechanical digitizing data can easily be shared by email or on websites with other researchers around the world. Computing power requirements and post-digitizing workload are comparatively low, when using our methods for NURBS digitizing, and all equipment is easily transported in a single suitcase. Thus digitizing can take place in collections worldwide. Transport of specimens to hospitals or other institutions with CT scanners is not required. The risk of loss and damage to specimens is reduced somewhat. However, the digitizing process itself increases the risk of damage more than CT or laser scanning, and thus excludes the use of the techniques on fragile specimens.

The biggest drawbacks of mechanical digitizing are the inability to acquire color data and the limited resolution. However, we found that the resolution is nearly comparable to CT scan-based data at similar overall file sizes.

Three-dimensional digital files can be used for a wide variety of research studies, including ontogenetic and biomechanical aspects, and are useful for museum display and curatorial aspects. However, data from mechanical digitizing is limited to reproduction of the general shape of bones, not high resolution surface detail such as rugosities. Delicate structures, especially thin edges below 2 mm thickness, may be significantly deformed in the digital files, and internal surfaces can not be depicted at all. Also, post-digitizing file editing can consume additional time. These factors should be kept in mind before projects based on mechanically digitized data are planned.

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Appendix A – The digitizing techniques in detail

Setting things up

Before digitizing begins, the digitizer, computer, foot pedal and the object to be digitized must be readied. Experience shows the following order works best:

1. Sort the specimens by size and stability. Determine which can be placed on the holder and which are too large or fragile.

2. Set up the holder (if used). Place the digitizer behind it, as it is very hard to push the tip steadily across the bone surface, but easy to pull it.

3. Place the computer so that you can both reach the keyboard and see the screen while digitizing. Make sure that you can reach across and under the specimen if using the holder.

4. Start the Rhinoceros® program and load a template file. Using the 'Centimeters.3dm' file is recommended. Save this file with the file name intended for the finished file, include the specimen type (e.g., 'dex radius') and number (e.g., 'MB.R.1664') in the file name. Set the tolerances for the file according to the object size. Example values:

   Absolute tolerance: 0.01 units (0.001 for small bones)

   Relative tolerance: 0.1 percent

   Angle tolerance: 0.1 degree

   Higher accuracy values lead to significantly longer computation times, including the risk of program crashes on less powerful computers, for little gain.

5. Prepare the first specimen for digitizing: Check the range of the digitizer arm and decide on coordinate placement and curve directions (see below). Usually, curves should be roughly orthogonal to the long axis of the bone. Then decide on seam line and coordinate placement. Mark the bone accordingly.

6. Calibrate the digitizer to the first set of coordinates.

7. Start digitizing.

8. After data collection is completed, immediately create a surface in Rhinoceros® (Geomagic® for point clouds) and check for accuracy. Only if the surface is roughly satisfactory, remove markings from bone. Otherwise redigitize non-satisfactory areas.

We recommend digitizing several curves in quick succession, without consulting the laptop monitor often, instead of checking each new curve for accuracy immediately. A smooth, uninterrupted work flow is key to short digitizing times.

Coordinate placement, recalibration and seam line placement

Coordinates and recalibration (multiple coordinate sets): Before digitizing can begin, coordinates for recalibration must be marked on the specimen as well as (when using closed curves, see below) a seam line (line through the contacts of all curves start and end points). In most cases, thorough planning of the placement of coordinates and the seam line is necessary to avoid complicated recalibrations of the digitizer. Sometimes, it is not possible to avoid a recalibration, but reducing the number of instances necessary will result in fewer inaccuracies. Also, the fewer different sets of coordinates are used the smaller the inaccuracies.

For small and medium sized specimens, approximately up to a size of 80 cm greatest length (110 cm for the Microscribe® GL), a single set of coordinates located roughly halfway down the length of the bone is sufficient. Three coordinates on the specimen are needed: an origin point (O_1) for the origin of the coordinate system and two points (X_1, Y_1) to determine the direction of the x- and y-axis respectively. These can be placed in any relation to each other except for a straight line, because Rhinoceros® translates into a Cartesian coordinate system internally. Thus there is no need to place the coordinates in a right triangle. It is advisable to space them at least 5 cm apart in easily accessible locations to reduce the influence of the unavoidable slight inaccuracies during recalibration. Multiple coordinate sets allow digitizing very large objects; theoretically there is no size limit.

Coordinates should usually be placed (see Appendix C) so that one set ($C_{set}1=O_1$, X_1, Y_1) is accessible in all positions the specimen will have to be placed in during digitizing. If this is not possible, a second set ($C_{set}2=O_2$, X_2, Y_2) must be placed so that it can be reached with the digitizer after calibration through $C_{set}1$. This means that two sets of coordinates should be placed at approximately 1/4 and 3/4 of the length of the bone to allow maximum range for the digitizer.

Complex bone shapes, or large flat bones (e.g., sauropod ilia) may require more sets of coordinates. $C_{set}2$, 3, etc. should all be accessible from $C_{set}1$ to minimize inaccuracies. Thus $C_{set}1$ should be placed roughly halfway down the bone, with sets of higher number to both sides.

Small or ball-shaped flat bones (e.g. calcanei, dermal scutes) tend not to rest stably on the holder unless placed horizontally. Here it proved best to use one set of coordinates placed on the narrow edges, digitize curves as concentric rings on the upper surface, then flip the bone over onto the other side and digitize concentric curves there (Figures 15), using the same coordinate set $C_{set}1$.

Seam line: The seam line is an imaginary line connecting all curve starts and ends when digitizing using closed curves (Figures 6 and 15). Proper placement of the seam line is equally important as the placement of the coordinates. The seam line needs not be digitized, but should be marked on the bone. It should run on a relatively flat area of the bone, where the lofted surface will show little change in topology. Also, the bone should rest stably on the holder (or against other support) with the seam line positioned downwards (on the side opposite to the digitizer and the operator when other support is used); otherwise access to it from both directions will be difficult. It can be helpful to digitize a short open curve down part of the seam line to gain a reference in Rhinoceros®. This helps selecting the curves for lofting properly if selection by hand is necessary. When digitizing closed curves, the seam line must always be placed on the side of the bone away from the digitizer, otherwise the reach of the digitizer arm will not be sufficient to draw the curve completely.

Gathering data - open and closed curves, point clouds.

Open curves: Open curves run across one side of the specimen as subparallel lines, requiring access to only one side of the specimen. Wilhite (2003b) used this technique exclusively. A loft over open curves results in a surface. Open lofts may, but need not, start and end with a point object. Joining these surfaces into closed bodies (solids) is often difficult, thus this technique is not recommended.

Closed curves: The most important improvement we made compared to the technique of Wilhite (2003a, 2003b) is the use of closed curves. This means that each curve reaches 360° around the bone as an infinite loop (Figure 2), allowing a closed loft over the entire bone in one step. Thus,

there is no need to assemble two surfaces into one body, a process very difficult in Rhinoceros®. This saves effort, increases accuracy, and reduces costs by making the purchase of a separate editing program unnecessary. Additionally, a closed loft does not possess a visible seam that has to be manually smoothed over in Rhinoceros®. It requires, in addition to closed curves, a start and an end point at each end of the loft. These points can be digitized at any time before, after or in between curves. When the bone it too large to be digitized without moving the digitizer, the points should be digitized together with the neighboring curves, to avoid recalibrations for just one point. If several separate lofts are combined to model complex shapes, surfaces open at one or both ends can be used. These require one or no points, respectively.

In order to achieve a surface with minimum artificial distortion, all curve ends must meet the respective curve starting points with minimum overlap and shift along the seam line (Figure 16), and point in roughly the same direction (have similar tangency). To achieve this it is useful to mark starting points on the bone by taping a strip of adhesive tape (masking tape) along the intended seam line (usually the long axis of the bone) and mark curve starts by a lengthwise line with cross marks. This has the additional benefit of reducing wriggling of the seam line, avoiding a common source of massive lofting artifacts. To avoid overlap a small gap of 1 or 2 mm should be left between curve start and end, which Rhinoceros® closes automatically when the foot pedal is released. Also, to minimize distortion at the bone ends, it is often advisable to cover at least a circle with r=2.5 cm at each end with masking tape and draw the first and last few curves onto the tape prior to digitizing (Figure 6). The end-points should also be marked here.

Composite closed curves: Some bones are so large that drawing closed curves around them is impossible due to the constricted range of the digitizer arm, e.g. sauropod ilia, or bones that are held in fixed mounts. Here, it is advisable to create closed curves by digitizing them in parts. Each part is an open curve, and the parts are joined together using the *'match'* and *'join'* commands. In theory, there is no size limit for this method! The only drawback is the need for extremely accurate digitizing at the contact points of partial curves. This requires extensive marking of the bone prior to digitizing, as each separate contact point must be marked. Also, it is often necessary to redistribute
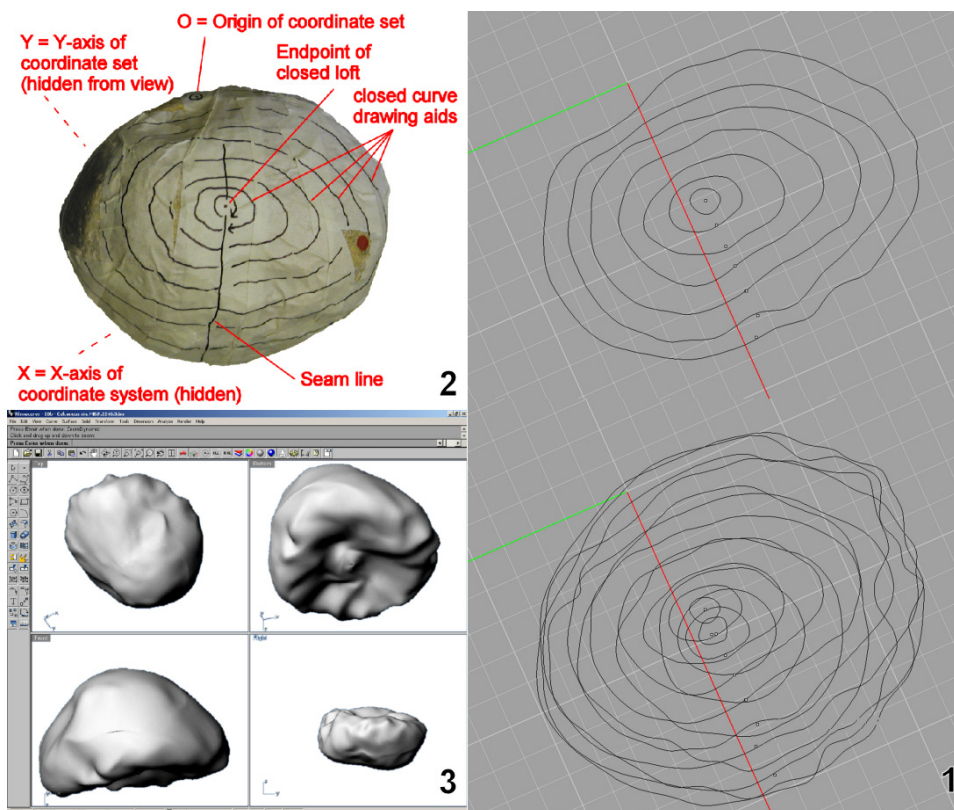
FIGURE 15. Digitizing small round or flat specimens. *Giraffatitan (Brachiosaurus) brancai* MB.R.2246 left calcaneum. (1) Curves from digitizing; top half shows first set digitized before the bone was turned upside down. Bottom half shows complete set. (2) Photograph of the specimen readied for digitizing. Important markings are labeled. (3) Four views of the final 3D file from Rhinoceros®. Greatest length of the bone is 125 mm.

the sampling points of the curve more regularly after joining the various parts. This can be done via the *'rebuild'* command and slightly decreases accuracy. Note that in case of a bone mounted with a metal rod that closely follows the shaft longitudinally, it is also possible to digitize with closed curves and edit the curve control points to remove the armature instead of using composite curves.

Points: Single points are collected using the *'point'* command. They are useful to mark coordinates and as start and end points for closed lofts. The *'points'* command can also be used, but if the digitizer tip is not kept very still, a string of point objects will be digitized. We recommend deleting surplus points, as they can lead to confusion and lofting errors.

Point clouds: With the *'digsketch'* command point clouds (Figures 3 and 4) can be digitized continuously or in several parts, without having to worry about slipping off the object with the digitizer tip. Complex shapes can be sampled better with point clouds than with curves. Also, complete reach around the object is not necessary, nor planning

partial curves for joining into closed ones. This is useful when bones are mounted closely together and can not be taken off the mount for digitizing.

The object is placed on a stable support, e.g. placed in a sandbox. Very small objects can be held in place on the table with two fingertips. Coordinates must be marked so that they are accessible in all positions necessary for digitizing the complete bone. Now, point clouds are digitized over the entire accessible surface. Usually, several percent of all points digitized are erroneous. These can, however, usually be spotted easily, and quickly removed. Then the object is turned over, the digitizer recalibrated, and the remaining surfaces are digitized. Experience tells that drawing the digitizer tip along all edges repeatedly is advisable; larger flat areas can be painted in roughly with a to and fro movement of the digitizer. Note that near sharp edges, such as cristae or the edges of transverse processes, artifacts will appear near the edges of the flat surfaces if the sampling distance on the surface is not significantly smaller than the thickness of the bone.

25

Meshing then erroneously connects points from both sides to each other instead of to the points at the edge (Figure 5). Geomagic® produces fewer meshing errors that Rhinoceros®. The sampling distance should be at most 0.2 times the distance of the surfaces to avoid this. During digitizing, it is advisable to create meshes from time to time in order to judge which areas need further digitizing. It is also possible to digitize with this preliminary mesh visible, best in 'Shaded' viewport mode, which facilitates the task. Alternative, the mesh can be created in Geomagic® and viewed while digitizing, as Rhinoceros® will accept digitizer input even if it is running as a background process (see Appendix E).

Although curves for lofting can be created from these points by a variety of methods, using the 'wrap' function in Geomagic® usually is the best option to create a polygon mesh. If some areas prove troublesome, separate meshes can be created for parts of the point cloud and then combined. The gaps can be filled with the 'FillHoles' function of Geomagic®.

Editing raw data

Editing curves: Curves can be edited to remove artifacts in them or to join several curves into one (commands: '*controlPts*', '*rebuild*', '*match*', '*join*'). The concept of 'control points' and their use is explained below. As this editing changes the original input data as few changes as possible should be made.

Editing point clouds: Point clouds can be edited to remove points that are either incorrectly collected during digitizing or supernumerary. In Rhinoceros®, point clouds are 'groups' of points. Each consists of all points collected during one period of sampling (keeping the foot pedal pressed). In order to edit single points in a cloud, the cloud must be selected and separated (command '*explode*'). Erroneous points are best spotted by rotating the view until it is nearly parallel with the bone surface. Erroneous points will now be visible above the main bulk and can be deleted (Figure 17.1). Remember to also check the inside of the point cloud for stray points! To remove these it is advisable to select and hide ('*hide*') the ends of the point cloud in order to create a clear background against which the erroneous points can be easily spotted.

If a digitizing error is detected during the digitizing of the point cloud (that is while the foot pedal is still pressed), the tip of the digitizer should be removed a generous distance from the bone before the foot pedal is released. This way the
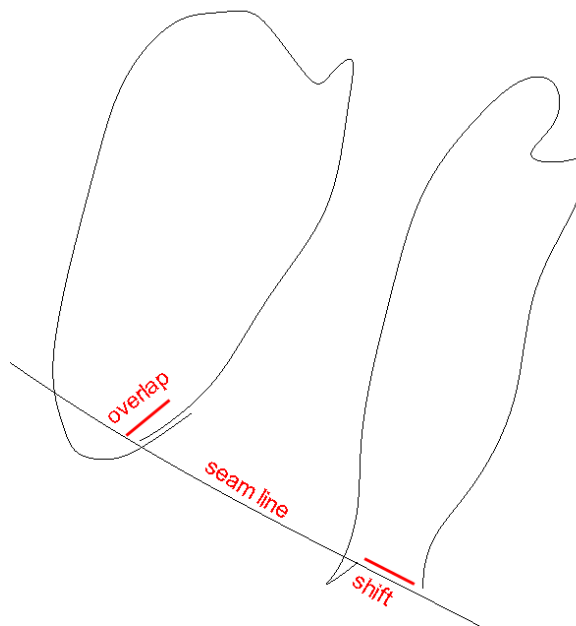

FIGURE 16. Example of NURBS curves in Rhinoceros® showing 'shift' and 'overlap' errors.

group of points that contains the faulty points has a 'trail' of points leading away from the surface that is quite conspicuous and facilitates finding and removing that specific group (Figure 17.2).

Creating bodies - lofting and joining surfaces

Surfaces from curves: Lofting a surface over closed curves (command '*loft*') is the easiest way to create surfaces for digitized objects in Rhinoceros®. A loft that, in addition to the curves, contains a point object at one end will be closed at that end, but still be a surface, not a body. A loft that both starts and ends with a point will create a body, not a surface. This method requires the least post-digitizing data editing. In order to loft, the respective curves must be selected and the proper loft option chosen. Here, different versions of Rhinoceros® differ markedly. Often, Rhinoceros3.0® does not reliably sort curves correctly, so each point/curve must be selected by hand in the proper order, starting with one endpoint, then the closest curve, then the next etc. to the other end of the bone. In Rhinoceros 2.0® and earlier version, each curve has a direction that is not automatically adjusted during lofting. It is necessary to select each curve at the same side of the seam line; otherwise the surface will fold into itself. Rhinoceros 3.0® sorts the directions automatically, usually correctly. Rhinoceros 4.0® sorts curves correctly, but usually misplaces the endpoints, sorting each point

with the wrong end of the bone, so curves and points must be selected in the correct order by hand for closed lofts. The 'closed loft' option creates the same errors and should not be used.

Note that large bones digitized at high accuracy will lead to long computation times for lofting. It may be advisable to increase the tolerances values in the file preferences before lofting, as this will not add a significant error but speed up lofting by up to 90%. Additionally, we have experienced program crashes at high accuracies, which can be avoided by downgrading the accuracy after data collection and before lofting.

Surfaces from point clouds: Meshing is done automatically via the '*Meshfrompoints*' command in Rhinoceros®. Much more accurate results can be achieved in Geomagic®, using the 'Wrap' function. If the resulting mesh shows many inaccuracies, deleting it and editing the point cloud for a new meshing is best. If there are few errors in the created surface, it is best to delete erroneous mesh facets ('*Deletemeshfaces*') and fill the resulting holes via the '*fillhole*' command in Rhinoceros®. In Geomagic®, faulty areas can be selected directly and removed by pressing 'Del'. The holes can be filled using the 'Fill Holes' function.

In Rhinoceros®, tolerance settings should remain tight for meshing, as low values will result in significant errors.

Joining and editing surfaces: Several **NURBS surfaces** can be joined into one via the '*joinsrf*' command. Alternatively, for smoother contacts, it is possible to use '*blendsrf*'. This requires that the surfaces touch along all their common edge. As this cannot be reliably achieved when digitizing several surfaces on one object due to the invariable drift of the digitizer and the inaccuracies of the operator's hand movements, edge contact must be created artificially in Rhinoceros 3.0®. We could not evaluate the mesh edit tools in Rhinoceros 4.0 because the program regularly crashed (updated until 9/2008).

Sometimes it is extremely difficult to join partial surfaces in Rhinoceros®, or close openings in partial lofts. Also, cropped NURBS bodies can be difficult to 'cap' properly. In this case, the NURBS surface(s) should be transferred into an STL polymesh. Further editing can then take place in Geomagic®.

Control points: Surface editing via the various options in Rhinoceros® is usually too time consuming and difficult to be useful, except for the use of control points. Any 'surface' or 'body' (i.e. 'closed surface') can be edited in Rhinoceros® via its 'control points'. These are point objects representing coefficients of the NURBS function of a curve (called 'nodes' in many other programs). Moving them in 3D space alters the curve function, changing the shape of the curve and the associated NURBS surface. In order to change the form of a body, the control points must be turned on ('*Cpoints*'). Now, they can be selected and moved the same way any point object can be moved in Rhinoceros®. A lofted body has hundreds or thousands of control points along the surface isocurves, which are essentially identical to the curves the body was lofted from. Editing larger areas by hand is a tedious process, but small deformations or digitizing errors can be easily removed. Rebuilding the individual curves with a smaller number of points before lofting makes editing of the lofted surface easier, but the accuracy can suffer significantly if the number of points is reduced too much.

Since a 'control point' is a coefficient of a NURBS function, the surface will not always pass through the point object visual on the screen, and care should be taken to always move neighboring points together. Otherwise, the surface topology will show artifacts resulting from the rapid 'swinging' of the underlying spline function. If, e.g., one point is moved by 5 mm, then the two neighboring points should each be moved in the same direction by a few millimeters, too.

Polygon meshes are easy to combine in Geomagic®. The 'FillHoles' function allows building 'bridges' between them. In order to do so, the meshes must first be merged using the 'Merge Polygon Objects' command. The remaining openings can be filled with the 'FillHoles' command.
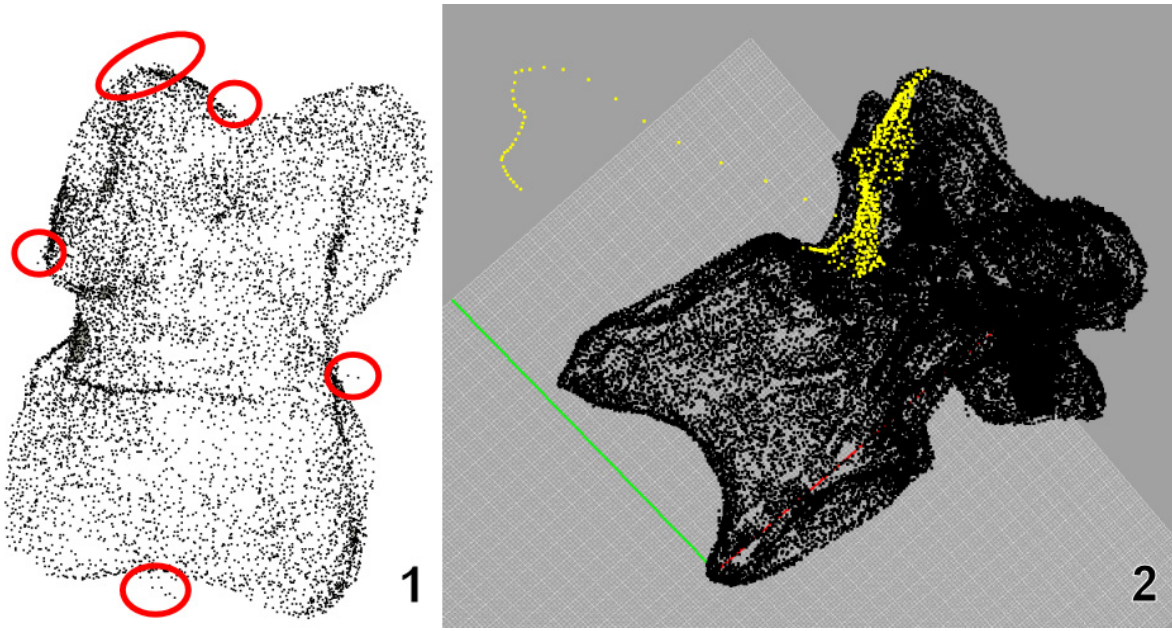
FIGURE 17. GPIT 1 *Plateosaurus engelhardti* (1) Pointcloud file of left pedal phalanx II-1 (length 73 mm) prior to editing. Red circles mark obvious erroneous points. (2) Pointcloud file of dorsal 2 (centrum length 79 mm) during digitizing. Yellow points: pointcloud with digitizing errors noted while the points were being digitized. The 'trail' of points leading to the top left was intentionally created to allow easy recognition of the flawed pointcloud during later editing.

Appendix B – Application of techniques to different types of specimens

Digitizing with closed curves – general remarks

Plan coordinate and seam line position prior to digitizing and mark them. Keep the limited range of the digitizer arm in mind! When aiming for a closed loft, remember to digitize start and end points! Closed curves may lead to artifacts, usually along the seam line or in places where neighboring curves are of significantly different lengths or their distance and direction varies greatly. The same is true if closed curves overlap or shift at the seam line. Here, using the 'Simplify: Rebuild…' option of the '*loft*' command dialog box can reduce or remove the problem. Alternatively, the curves can be edited prior to lofting via the '*rebuild*' command, and/or by editing their 'control points'.

Digitizing with closed curves – small bones (simple shapes)

Small bones up to 10 cm maximum length tend to be hard to digitize for a number of reasons. They shift position easily, drawing curves on or around them at relatively regular intervals without overlap alone is hard, and ensuring that these curves accurately reproduce small surface features makes the task of drawing curves free-handed too cumbersome. Using the fossil holder reduces the first problem. Still, care must be taken not to put pressure on the specimen with the tip of the digitizer as this may shift the bone. As it is hard to place a small bone on the holder stably while still being able to reach both upper and lower surfaces, we recommend first digitizing only the upper half with concentric closed curves in a horizontal plane (Figure 15.1), then flipping the bone over and repeating the procedure for the other half. This requires a coordinate set $C_{set}1$ placed on the circumference of the bone (Figure 15.2).

The problem of drawing curves properly - especially closed curves - can be solved by extensive marking of the bone. For this, much or all of the bone is covered in painter's adhesive tape or masking tape and the seam line and curves are drawn onto it (Figure 15.2). It is also possible to only mark partial curves or markers for curve passage over radially placed strips of tape if the bone is too large for complete wrapping. It is of paramount importance to select a tape that can be removed completely without damaging the bone. The resulting curve set can be lofted normally (Figure 15.3).

Digitizing with closed curves – medium sized bones

For medium sized elements (up to around 90 cm maximum length), curves should be placed roughly perpendicularly to the long axis of the bone, with the seam line on the lower side. The specially constructed holder again proved best, as it keeps the specimen from shifting while allowing easy access. Usually, it will not prevent access to important features and curves placed directly to the left and right of the fittings are sufficient to give an accurate surface. If not, it is necessary to shift the bone a few centimeters and recalibrate the digitizer before adding curves into the gaps. See Figure 6 for an example of this setup.

Digitizing with closed curves – large bones

Drawing closed curves requires that it is possible to reach around the specimen on both sides down to the seam line. For very large specimens, especially relatively slender longbones like tibiae and radii of sauropods, it is advisable to place the specimen close to vertical by leaning it against a solid structure, with a cut-to-fit styrofoam spacer to create a gap in between. Some bones, especially sauropod longbones, rest stably in this position on their articular ends. If necessary, the lower end can be secured with wooden wedges and small sandbags or in a sandbox. Thus, bending moments on the shaft are minimal, reducing the risk of damage. The digitizer may have to be set up on a wooden box or a chair in front of the bone to achieve a sufficient vertical reach; care must be given to stability. For large specimens, a forklift or similar adjustable tool can be used. This allows digitizing the top end and shaft with curves sub-parallel to the ground; then the fossil must be turned upside down, the digitizer recalibrated and the bottom end added. The seam line here runs down the 'back' of the bone, opposite the digitizer and operator during the first part, but facing the digitizer during the second part. When using early versions of Rhinoceros®, care must be given to either digitize the curves in the opposite direction after rotating the specimen (seam line now at front) or change curve direction in Rhinoceros® before or during lofting.

Digitizing with composite closed curves (very large bones and/or complex bone shapes)

Bones that are too large in circumfence for closed curves or encased in supports that make reaching around them impossible can be digitized

by drawing sets of open curves. Each curve in a set ends at the starting point of a curve from another set. The matching curves are then merged into one closed curve. Two or more curves together must fully surround the bone the way a closed curve would. This requires extensive marking of the bone to minimize overlap and shift between touching curves (Figure 16). It is advisable to place the contact line between curves at places with low curvature (i.e. flat bone surfaces) to minimize artifacts and leave a very small gap between curves. The partial curves then must be joined into closed curves using the '*match*' and '*join*' commands. Then, a closed loft can be made over the entire bone.

Usually, it is necessary to rebuild matched curves using the *'rebuild'* command to avoid artifacts, as the control points will be unevenly distributed along each curve. An additional advantage of rebuilding curves is the ability to somewhat reduce the number of control points, making both the final file smaller and editing *via* control points simpler. This must be executed carefully, as too large a reduction in control point numbers can induce significant shape changes in the curves.

Digitizing bones as composite bodies with separate curve sets - complex bone shapes

Some bone shapes cannot be represented by one loft over closed curves. In these cases, it is possible to digitize parts of the bone, loft surfaces over these parts, and then combine them into one body in Rhinoceros®. Examples are the articular heads of sauropod ribs, where one set of closed curves cannot easily be drawn around both heads. Digitizing as large a part as possible with curves in one direction, then adding a second set of curves for the missing parts is usually the best option, although it is sometimes preferable to aim to minimize the suture length between the parts.

Several points must be kept in mind when planning a composite body:

- The separate parts must together contain the entire surface or volume of the specimen when using open surfaces or closed surfaces, respectively; otherwise there will be gaps or holes. If holes cannot be avoided, they should be in flat areas of the bone, where filling them up in Rhinoceros® is easy and carries a low risk of error.

- Boolean operations on bodies (3D volumes) are much easier to conduct than joining operations on surfaces.

- The separate lofts must overlap enough or contact each other exactly to allow joining the bodies in Rhinoceros®.

- The overlap area should not contain repeat intersections between surfaces/bodies as these tend to confuse Rhinoceros® and make merging impossible. It is helpful to close lofted bodies by placing the end point inside the bone by manually adding it in Rhinoceros®. This guarantees overlap with only one section contact.

- It is advisable to digitize a closed curve along the contact line of the parts to be joined. This facilitates creation of a cutting plane, which allows cropping the parts to an exact fit. Ideally, the contact line allows the use of a flat plane for cutting.

- To create holes in a body (e.g., foramina in ischia or coracoids) it can be easier to digitize and loft an air volume and subtract it from the main body by a Boolean operation than splitting the main body into parts and joining them.

- Remember to set the tolerances tight enough, otherwise cutting and joining surfaces may not work properly.

Using **open curves** and **multiple lofts**: A closed curve should additionally be digitized along each suture line to facilitate closing each open loft into a closed body before joining the adjacent bodies.

Using **closed curves** and **multiple lofts**: A closed curve should additionally be digitized along each suture line to facilitate cropping both adjacent bodies to avoid problems when joining them.

When it is not possible to digitize one closed curve around the end of the surface it is possible to digitize it in parts, and then join them into one curve using the '*match*' command.

These methods often fail for joining surfaces, due to problems with joining cropped surfaces. We strongly recommend using multiple closed lofts (bodies) and uniting them with Boolean operations.

Ideally, complex shapes should be digitized using point clouds. If that is not possible or desirable, the above procedure can also be used in a variant that delivers a polygon mesh instead of a NURBS object as the final result: Digitizing takes place with separate curve sets, then all surfaces are 'meshed', after which the meshes can be joined in Geomagic®.

Digitizing with point clouds/meshes (small bones with complex shapes, partially inaccessible bones)

Any bone too small to rest stably on the holder and/or with a shape too complex to be easily digitized by the above method for small bones using closed curves should be placed either on clay/PlayDoh® or in a sandbox. The '*Digsketch*' command allows collection of point clouds. Care must be taken to ensure that the distance between closest points on the same surface is always significantly smaller than the distance to points on any other surface; otherwise artifacts will be produced during meshing. '*Meshfrompoints*' produces a polygon mesh that can be edited via the '*deletemeshfaces*' and '*fillhole*' commands. Reducing the mesh count in Rhinoceros® is usually not advisable, as the errors incurred are significant. Both meshing and editing of the mesh are better carried out in Geomagic® (see Appendix D). This is especially true for filling gaps in the mesh.

Theoretically, Geomagic® also supports the Microscribe 3D digitizer. For unknown reasons, we were not able to make the digitizer connect to the program correctly. Despite this technical problem, Geomagic® can be a helpful tool during digitizing of point clouds. It is possible to collect data with the digitizer in Rhinoceros® while the other program is displayed on the screen (see Appendix E). Therefore, one can digitize points in Rhinoceros®, intermittently mesh them in Geomagic®, and then go on collecting data to fill the gaps shown in the mesh in Rhinoceros® while the mesh in Geomagic® is actually visible on the screen. Due to the far better ability to selectively collect data where it is needed, this process can save up to 30% of the digitizing time. Also, errors will show up earlier, allowing faster correction.

Marking surface features

Rugosities, damaged or discolored areas, articular surfaces or muscle attachment scars can be marked on the surface by drawing a closed curve around them. This curve can later be projected onto the lofted surface. While this data will usually be lost when exporting the 3D bodies into other programs, some formats allow retention.

Also, a very thin body can be constructed from the curve via the '*extrude*' command; this will be preserved in all formats. Rhinoceros® allows changing the color of these markings to make them more conspicuous. Alternatively, the area can be covered with a point cloud, from which a polygon mesh can be created.

Composite bones from partially preserved specimens

Here, an explanation is given for combining two parts; a higher number can be combined by repetition. There are two methods for combining data from two specimens. It is possible to select at least three landmarks, which are present on both objects, and digitize them as coordinates for a coordinate system, then digitize the specimens after calibrating to these landmarks. This works well if there are e.g. small foramina or sutural contacts with ontogenetically stable positions present on the bones. Otherwise, the landmarks can be digitized as points, point cloud or NURBS curve data on both objects, and the data sets can be aligned later. Optimally, only one set of closed curves is needed, with the last curve of one specimen subparallel to the first of the second specimen. If only a contralateral element is available to complete a partial specimen, it is possible to digitize one part including the landmarks and then mirror it before digitizing the other element.

If no landmarks are present, it is possible to just digitize the specimen without calibrating from one to the other, then copy and paste them into one file and move one until it appears to fit the other. This process works well if there are cristae or spinae present, or any other feature on the bone that allows easy 3D orientation of the separate parts. For both methods it is possible to scale ('*scale*' command) one part isometrically to fit the other. If a large size difference exists, it may be necessary to scale the element differently for various axes to compensate for the allometric growth common in vertebrates, which is possible with the '*scale2D*' and '*scale1D*' commands. For this, the bone should be aligned with the coordinate axes of Rhinoceros®. In any case, a note should be added to the file indicating the composite nature of the model.

Appendix C – Step-by-step instructions for Rhinoceros® for digitizing and model creation techniques

Abbreviations used herein:

TIP – tip of the digitizer arm

RFP – right foot pedal

LFP – left foot pedal

If asked to 'at the command line enter…', ensure that Rhinoceros® is ready for a new command (not already processing a command) and type the exact phrase given, then press the ENTER or RETURN key on the keyboard. 'Select' means click the appropriate box with the mouse so that a tick appears in the box, 'deselect' means to click the box so there is no tick in it.

'*Menu:*' refers to the pull-down menus at the top of the Rhinoceros® screen. Select the menu title given, and then select the (sub-)entry/-ies given after the arrow(s) -->.

For most commands, icons are available in Rhinoceros®. In the standard workplace setup, only a few are visible. These are referred to in the text. To make others available, refer to the in-program help.

Commands are not case sensitive in Rhinoceros®, thus '*points*' and '*Points*' are equivalent.

Note for users of earlier versions of Rhinoceros than 3.0 SR4: As opposed to Rhinoceros 3.0® SR4 and later versions, earlier versions do not automatically repeat the '*digsketch*' command. It is necessary, after digitizing a curve or point(s), to press the left foot pedal (LFP) once to repeat the command. Also, any version before Service Release 4 (SR4) will not support polygon mesh creation via the '*meshfrompoints*' command.

Note for users of more recent versions of Rhinoceros (4.0 and updates): Rhinoceros 4.0 has a slightly different user interface, therefore some commands are available from a different 'Menu' than in earlier versions. The basic functions have not changed, and all techniques described herein can still be used.

Digitizing preparations

To **begin digitizing** it is recommended to open a new file via the 'New' icon. This displays a selection of template files with varying units. For this study, the 'centimeters.3dm' template was used for all objects. This sets the scale of the coordinate axes as centimeters. Digitizing distance for curves should be selected accordingly. Open the file properties page (*Menu:* File --> Properties), select 'Units' and set the **tolerances** to values suitable for the task.

Example values:

Absolute tolerance: 0.01 units (0.001 for small bones)

Relative tolerance: 0.1 percent

Angle tolerance: 0.1 degree

Tolerances should be at least an order of magnitude higher than the smallest value used in any operation on the data. Joining surfaces, e.g., requires distances smaller than 0.01 mm as the surfaces themselves are a theoretical 0.01 mm thick. Thus, absolute tolerance should be set to 0.001 mm. Angle tolerance should be equally low, as joining lines between surfaces otherwise will show as kinks.

It is possible to create a new **custom template** file that includes appropriate tolerance settings. See the Rhinoceros® help file for details on how to save a file as a template.

Digitizing coordinates, (re-)calibration with and without moving the digitizer or specimen

Initial setup and initial calibration: Before digitizing, mark three coordinates on the specimen.

1. Place the digitizer so it can reach all three coordinates.

2. Connect the digitizer to Rhinoceros® (*Menu:* Tools --> 3-D Digitizer --> Connect, or enter '*digcalibrate*' in the command line), select Digitizer type (Rhinoceros® suggests the Faro Digitizer; if using a different one, press 'f' and RETURN, then the first letter for your type of digitizer, confirm selections with RETURN). Rhinoceros® 4.0 offers a selection menu instead.

3. When asked to 'Enter origin with digitizer' in the command line, place the tip of the digitizer (TIP) on the mark for the origin (O_1) on the specimen and press the right foot pedal (RFP).

4. When asked to 'Enter X-Axis with digitizer' in the command line, place TIP on the mark for the x-axis (X_1) on the specimen and press RFP.

5. When asked to 'Enter Y-Axis with digitizer' in the command line, place TIP on the mark for

the y-axis (Y_1) on the specimen and press RFP.

6. When asked to 'Enter origin in Rhinoceros® (…)', press RETURN

Now the digitizer is ready for digitizing curves or points. The origin of the displayed coordinate system in Rhinoceros® coincides with O_1 on the bone; the X-axis in Rhinoceros® runs in the direction of X_1. Note that the coordinate system is automatically transferred into a Cartesian system. Therefore, the Y-axis in Rhinoceros® runs only roughly in the direction of Y_1.

Recalibration: To calibrate the digitizer back to the $C_{set}1$ (O_1,X_1,Y_1) proceed as follows:

1. In the command line, enter '*digcalibrate*' or choose '*Menu:* Tools --> 3-D Digitizer --> Calibrate'

2. Proceed as above, starting with step 3.

The digitizer is now recalibrated to the original coordinate set $C_{set}1$.

Using several sets of coordinates: When using several sets of coordinates, it is important to mark each set on the bone as well as in Rhinoceros® to avoid mixing them up. We found it easiest not to add text or change object names, but connect each set with a polyline and change the color of each X point. X_1 was left unchanged (black), X_2 changed to white, X_3 to red etc., following the default order of colors in Rhinoceros® layers. If this simple convention is kept, recalibration takes less time than with any other method, while mix-ups can be avoided.

In order to use several sets, mark <u>all</u> sets on the bone, calibrate the digitizer to $C_{set}1$ as above, and then proceed as follows:

1. In the command line, enter '*point*'.

2. Place the TIP on O_2, press and release RFP. Watch the screen to note where the point appears. If necessary, shift the view using the 'pan' tool.

3. Press [space] or RFP to repeat the '*point*' command. Repeat 2. to digitize X_2 and Y_2, note where they are on the screen. Press ESC after digitizing Y_2.

4. At the command line enter '*Polyline*'.

5. On the screen, with the mouse select X_2, O_2, and Y_2 in this order, press ENTER. To facilitate this, make sure that 'OSnap' is on and set to 'Points'. See Rhinoceros® help for the use

of 'OSnap'. A polyline will appear with O_2 at the meeting point of the two sections.

6. On the screen, select X_2 (make sure the other points are deselected), press F3 and change the color of X_2.

7. Repeat 2. to 6. until all sets have been digitized.

To **calibrate the digitizer to a different set** (e.g., set 2), make sure the second set of coordinates has been digitized as points as described above. Place the digitizer so it can reach all three point of the set to calibrate to and proceed as follows:

1. At the command line enter '*digcalibrate*'

2. When asked to 'Enter origin with digitizer' in the command line, place TIP on the mark for the origin (O_2) of this set on the specimen and press the right foot pedal (RFP).

3. When asked to 'Enter X-Axis with digitizer' in the command line, place TIP on the mark for the x-axis (X_2) on the specimen and press RFP.

4. When asked to 'Enter Y-Axis with digitizer' in the command line, place TIP on the mark for the y-axis (Y_2) on the specimen and press RFP.

5. When asked to 'Enter origin in Rhinoceros® (…)', use the mouse to select O_2 in Rhinoceros®. To facilitate this, check that 'Osnap (points)' is on.

6. When asked to 'Enter X-Axis in Rhinoceros® (…)', use the mouse to select X_2 in Rhinoceros®.

7. When asked to 'Enter Y-axis in Rhinoceros® (…)', use the mouse to select Y_2 in Rhinoceros®.

The digitizer is now calibrated to $C_{set}2$.

Digitizing and editing curves, points and pointclouds

Neighboring curves must be of similar length and should be roughly parallel. Large differences in length or distance produce artifacts. Also, curves may not cross each other.

Digitizing points: The digitizer must be properly connected and calibrated before data can be gathered.

1. At the command line enter '*points*' or click the appropriate icon in the 3d digitizing toolbar.

2. Place TIP at the desired location for the point and press RFP

3. To digitize more than one point, repeat 2.

4. To end data collection, press 'Esc'.

Digitizing point clouds: A point cloud is a group of points that can be digitized in one continuous motion and is automatically grouped in Rhinoceros®. Ungrouping works best via the '*explode*' command.

The digitizer must be properly connected and calibrated before data can be gathered.

1. At the command line enter '*pointcloud*' or click the appropriate icon in the 3d digitizing toolbar. It is also possible to enter '*digsketch*' and select the appropriate options.

2. Choose the desired sampling density by pressing '*d*', [ENTER], and entering the number followed by [ENTER].

3. Place TIP at the desired location for the point and press and keep pressed RFP.

4. Move TIP across area for which points are to be digitized.

5. Release RFP to end point data collection.

6. To digitize more than one point cloud, repeat 2. to 4.

7. To end data collection, press 'Esc'.

Digitizing open curves: The digitizer must be properly connected and calibrated before data can be gathered.

1. At the command line enter '*digsketch*' or select '*Menu:* Tool --> 3D Digitizer --> Sketch Curve'.

2. In the command line deselect 'Points' by pressing 'p' followed by ENTER and similarly select 'Curves' and deselect 'Closed Curves'. Choose the distance at which points are to be placed on the curves by Rhinoceros®. Note that this distance depends on the scale of the template file you chose! Usually, 0.1 to 0.7 proved to be acceptable values, for very large objects with hardly any sudden curvature changes even a value of 1 is acceptable (using the centimeter template; change value accordingly if using other templates). Enter the value by changing the 'Point Spacing' value.

3. Place TIP at the desired starting location for the curve and press and keep pressed RFP.

4. Move TIP along the intended path of the curve

5. When TIP has reached the end location release RFP.

6. To digitize more than one closed curve repeat 3. to 5.

7. To end data collection, press 'Esc'.

Digitizing closed curves: The digitizer must be properly connected and calibrated before data can be gathered.

1. At the command line enter '*digsketch*' or select '*Menu:* Tool --> 3D Digitizer --> Sketch Curve'.

2. In the command line deselect 'Points' by pressing 'p' followed by ENTER and similarly select 'Curves' and select 'Closed Curves'. Choose the distance at which points are to be placed on the curves by Rhinoceros®. Note that this distance depends on the scale of the template file you chose! Usually, 0.1 to 0.7 proved to be acceptable values, for very large objects with hardly any sudden curvature changes even a value of 1 is acceptable (using the centimeter template; change value accordingly if using other templates). Enter the value by changing the 'Point Spacing' value.

3. Place TIP at the desired starting location for the curve (a point on the seam line) and press and keep pressed RFP.

4. Move TIP along the intended path of the curve

5. When TIP has almost reached the starting location again (1 to 2 mm gap) release RFP.

6. To digitize more than one closed curve repeat 3. to 5.

7. To end data collection, press 'Esc'.

Note: A small gap should be left between the start and end of a curve to guarantee a smooth connection at the seam. Failure to do so can lead to overlap, which produces artifacts on the lofted surface. Also, the start and end points should not show shift along the seam line, as this also leads to artifacts.

Editing kinks and artifacts out of curves: This option should be used sparingly and can produce massive artifacts!

1. Rotate a viewport so that the viewplane is as parallel to the main orientation of the curve as possible. This means that the curve ideally will lie flat on the viewplane.

2. At the command prompt enter '*CPlanetoView*' to make the construction plane parallel with your view.

3. Select the curve to edit

4. Turn edit points on by clicking the icon at the lower left in the toolbar

5. Carefully select points and drag them to adjust the curve. Watch the changes in several viewports with different directions to avoid introducing deformations in the third axis.

Joining open curves into closed curves: Make sure the curves ends are close to each other. To 'match' several curves sets, always select the first and second curve in the same order to achieve equally directed closed curves with seam points aligned in one row.

1. At the command line enter '*match*'

2. Select the first curve near the end that is supposed to be connected to the other curve. If only one of the curves is to be adjusted by Rhinoceros®, this curve must be the one that stays unchanged.

3. Select the second curve near the end that is supposed to be matched to the first curve. If only one of the curves is to be adjusted by Rhinoceros®, this second curve must be the one that gets changed.

4. In the match dialog box, select the appropriate options. We recommend selecting 'curvature', 'average curve' and deselect 'join'. 'average curve' adjusts both curves instead of only curve 2, leading to the distortion being more spread out but lesser in degree, reducing artifacts.

5. Repeat this process until all contact points have been matched.

6. At the command line, enter '*join*', then select the curves near the contact point.

Note: In Rhinoceros 2.0®, it is possible to use the 'join' option in the 'match' options dialog. This does not work for Rhinoceros 3.0® as the curve can only be joined in one place with this option, while the second contact point will remain open.

Rebuilding curves: Especially curves closed using the 'match' command have a very uneven distribution of their edit points. This tends to produce artifacts on lofts using these curves. In order to equally distribute the points on a curve the 'rebuild' command can be used.

1. At the command line enter '*rebuild*'

2. Select the curve you want to rebuild. If several curves are to be rebuilt to the same standards

(same number of points), these curves can be selected at the same time.

3. Select the appropriate options. Usually, the same number of points that the curve already possesses should be chosen. However, reductions of 50% may be tolerable.

4. To rebuild more than one curve, repeat 1. to 3.

Curves of similar length can be selected and rebuilt in groups.

Lofting surfaces (open and closed)

A flat, 'open' surface resembles a sheet of paper, a closed surface open at the ends forms a tube and a closed surface with closed ends results in a 3D body. It may be necessary to lower tolerances in the file properties to shorten computing time for lofting. Usually, this will not significantly reduce the accuracy of the lofted surface.

Selecting curves automatically and manually for a loft (for all lofting options): Rhinoceros 3.0® may sorts curves into the proper order when a group of curves is selected at the same time (automatic selection). This can be done by dragging a box over the curves with the mouse. Dragging from left to right will select only those curves that are completely within the dragged box, dragging from right to left will select all curves that are entirely or partially in the box. Rhinoceros 3.0® will also attempt to sort curve directions and adjust the seam line. Remember to de-select all other elements such as coordinates.

If the loft contains both curves and points (start and end of closed lofts), the automatic sorting will usually fail, especially in Rhinoceros 3.0® SR4 and Rhinoceros 4.0®. If automatic sorting does not work (i.e., the resulting surface curves back onto itself or shows other defects), curves must be selected manually. Here, the potential for mistakes is quite large, and care must be given to the following points.

- All curves must be clicked with the mouse at the same end. Otherwise, version of Rhinoceros® earlier than 3.0 may attempt to form a surface that connects two opposite ends.

- All curves must have the same direction (must have been digitized or later edited to have the same direction). Rhinoceros 2.0® does not automatically sort curve directions, while later versions usually sorts them correctly.

- Curves must be selected one by one from one end of the bone to the other, otherwise the surface will fold back onto itself.

- For closed lofts, the end points must be selected first and last, with the curves in between in proper order.

Lofting a flat surface: An open, flat loft requires as a minimum two curves.

1. At the command line enter '*Loft*'
2. Select the appropriate curves
3. Press ENTER
4. Select the lofting options desired in the options box (see below)
5. Press ENTER
6. Click 'Shade all viewports' and check the surface for accuracy.

Lofting a closed surface open at one or both ends: A closed surface requires closed curves. If an end is supposed to be closed, a point is required at that end. This method lets Rhinoceros® automatically adjust the seam points and directions of the curves; if the curves were digitized as advised above this should be free of problems.

1. At the command line enter '*Loft*'
2. Select the appropriate curves and the end-point (if appropriate)
3. Press ENTER
4. Check that the selected curves all have the same direction (arrow at seam line); switch directions of odd curves
5. Select the lofting options desired in the options box (see below)
6. Press ENTER
7. Click 'Shade all viewports' and check the surface for accuracy.

Lofting a body (a closed surface closed at both ends): A closed surface requires closed curves. A point is required at each end. This method lets Rhinoceros® automatically adjust the seam points and directions of the curves; if the curves were digitized as advised above this should be free of problems.

1. 1. At the command line enter '*Loft*'
2. Select the appropriate curves and both end-points, starting with one endpoints, then selecting the curves in correct order, and selecting the second endpoint last.
3. Press ENTER

4. Check that the selected curves all have the same direction (arrow at seam line); switch directions of odd curves
5. Select the lofting options desired in the options box (see below)
6. Press ENTER
7. Click 'Shade all viewports' and check the surface for accuracy.
8. Select 'Analyze --> Mass Properties --> Volume' and compare the given volume with a rough estimate to ensure that the loft actually resulted in the correct 3D body. Sometimes, the body will be open at some point and the surface folded back unto itself – the 3D body is hollowed out; this will result in a minuscule volume!

Using the various 'Loft' options: A variety of options is available in the loft dialog box:

For '**Style**', there are:

Normal - Uses chord-length parameterization in the loft direction. This is usually the best option to choose.

Loose - results in a smother surface, but allows the surface to move away from the curves. This option should be used as rarely as possible, as it will significantly change the external appearance of smaller bones.

Tight - Uses square root of chord-length parameterization in the loft direction which results in the surface sticking closely to the curves. This option tends to result in sharp changes of direction near the articular ends of bones.

For '**Simplify**', there are:

Do not simplify - preferred option.

Rebuild with control points - Rebuilds the shape curves before lofting. This is especially helpful if the curves change direction in small intervals a lot which can produce artifacts.

Refit within units - Refits the shape curves to a tolerance value before lofting. Use same as the previous option.

Troubleshooting: If the surface does not look correct, check the following:

- Have all curves necessary been selected? Have all necessary end points been selected? If not, delete the surface and loft again.

- Do all curves have the same direction? If not, delete the surface and loft again and change the directions.

- Does any one curve show excessive differences from its neighbors (erroneous curve)? If so, delete the surface and loft again without the troublesome curve. Alternatively, rebuild curves with the '*rebuild*' command, each with a number of points intermediate between the original number and that of the other curve.

- Do all curves look OK but the surface has odd wrinkles and twists? If so, delete the surface and try various 'Simplify' options of the loft dialog in a new loft. Or try rebuilding curves near the artifacts of the surface, and then loft again. Also, try adjusting the 'seam line' visible during lofting setup by dragging the points on all curves so that the seam line has no kinks.

Editing and joining surfaces and bodies

Some helpful Rhinoceros® commands are given a short description here - for a tutorial on editing and combining surfaces please refer to the in-program help.

Joining bodies smoothly in Rhinoceros® can be difficult, so we advise against using multiple bodies whenever possible. Check that the tolerance levels are set to suitable values. Remember that you can copy and paste bodies, so that one body can be deleted when used as a cutting object and still become part of the final assembly.

Joining two bodies:

1. At the command line enter '*BooleanUnion*' or select the icon from the toolbar at the left of the screen.
2. Select both bodies
3. Press ENTER

Subtracting one body from another:

1. At the command line enter '*BooleanDifference*' or select the icon from the toolbar at the left of the screen (right-click BooleanUnion and select the second icon in the pop-up box)
2. Select the body from which to subtract the other body and press ENTER

3. Select the body to subtract and press ENTER.

Intersecting two bodies: results in only the overlap being preserved.

1. At the command line enter '*BooleanIntersection*' or select the icon from the toolbar at the left of the screen (right-click BooleanUnion and select the third icon in the pop-up box)
2. Select the bodies to intersect and press ENTER

Creating a surface from a curve:

1. Select the curve
2. At the command line enter '*patch*' and press enter.
3. As trimmed surfaces cannot by joined and tend to be difficult to use for cutting both surfaces and bodies we recommend to deselect 'trim automatically' in the dialog box.
4. Click OK.

Using a surface as a cutting object to trim surfaces or bodies:

1. At the command line enter '*Split*' (keeps the cut of pieces as separate objects) or '*Trim*' (deletes the cut off pieces).
2. Select the object to split/trim. If trimming, click the part that should remain.
3. Select the cutting/trimming object.
4. Press ENTER.

Creating a curve on a surface (for 3D model creation, can also be used as a cutting object)

1. Select the surface.
2. Select 'Curve-->Free-Form-->Interpolate on Surface'.
3. Click on the surface at the start of the curve.
4. Click close to this first point in order to get tight control of the direction of the curve start.
5. Add more points to describe the surface.
6. Place the last clicks near each other to control the curvature exactly at the end of the curve.
7. Press ENTER.

Appendix D - Guide to point cloud and polygon mesh editing in Geomagic Qualify®

Note: Many actions are not reversible in Geomagic Qualify ®, or only until the next action has been completed. Take care to save your data often and with altered filenames! Note: instructions here refer to version 8.0 of Geomagic®. Other version may require slightly different command inputs.

Transferring data from Geomagic® to Rhinoceros® and back. Both Geomagic® and Rhinoceros® use program-specific file types. Neither program can reliably import the other program's specific files. Therefore, data must be saved in formats that can be read by both programs, for which standardized file types are advisable. Point clouds can be saved as IGES files (*.igs), while polygon meshes are best saved as binary Stereolithography files (*.stl).

Creating polygon meshes from point clouds

1. Load the point cloud file. Acceptable formats are e.g. *.obj and *.igs

2. Choose a selection tool ('Edit-->Selection Tools-->) and select erroneous points.

3. Delete selected points by pressing [Del]. Unmark the selection by pressing [Ctrl]+[C].

4. Select the wrapping tool ('Points-->Wrap') and choose the 'Surface' wrap type.

5. Check the 'advanced options' box and set the meshing quality to maximum.

6. Click 'OK'

Removing artifacts from and smoothing a polygon mesh. Smoothing via the 'smooth' command cleans up the surface in one work step. Less aggressive are 'Remove Noise' and 'Remove Spikes'. They allow the user to control the degree of smoothing, and 'Remove Noise' also has options to show the deviation between the original and the smoothed version.

Smoothing a polygon mesh:

1. Select 'Polygons-->Smooth'.

2. Click 'OK'.

Removing spikes: This tool works well for little pyramidal shapes on the surface caused by points that lie slightly outwards or inwards of the plane of the neighboring points.

1. Select 'Polygons-->Remove Spikes'.

2. Set the slider to the desired degree of smoothness.

3. Click 'Apply'.

4. Check the result. Repeat 2. and 3. until satisfied, then click 'OK'.

Removing noise:

1. Select 'Polygons-->Remove Noise'.

2. Set parameters as desired.

3. In order to see deviations, mark 'Show Deviations'. Set colors and values as required.

4. Click 'Apply'. If marked, the deviations are now shown as color changes according to the options chosen.

5. Repeat 2. to 4. until satisfied, then click 'OK'.

Reducing the polygon number in a mesh

The shape of the bone is preserved better if the reduction is done in small steps. Thus, reducing to 80% several times is better than going down to 20% in one instance.

1. Select 'Polygons-->Decimate'.

2. Set either the target number of polygons or the target percentage desired.

3. Mark 'Fix Boundaries' to preserve the extreme points and edges of the object. If this option is not selected, edges will be smoothed over.

4. Click 'Apply'.

5. Check the result. When satisfied, click 'OK'.

Removing artifacts on a polygon mesh

Removing artifacts and other erroneous triangles will leave holes in the object. They can be filled using the 'Fill Holes' tool.

1. Choose a selection tool ('Edit-->Selection Tools-->)

2. Choose the proper selection mode ('Edit-->….). Selecting 'Backface mode' allows selecting both triangle fronts and backs, deselecting it allows selecting polygons from the outside only. 'Select visible only' selects visible triangles only, while 'Select through' selects any triangle that is in the direct line of projection, whether it is visible or hidden by other polygons.

CAUTION - It is easy to accidentally delete triangles on the reverse side of the model when using 'Select Through'

3. Select erroneous triangles. Holding down [CTRL] while clicking removes triangles from the selection.

4. Press [DEL].

Erroneous triangles can also be removed while using the 'Fill Holes' tool (see there). Especially useful is the option removing floating data.

Filling holes: Note that it is usually advisable to first clean up a polygon mesh and then fill the holes. This is faster, as many small holes will be filled automatically by the 'Smooth', 'Remove Spikes' and 'Remove Noise' commands.

1. Start the 'Fill Holes' mode ('Polygons-->Fill Holes')

2. Select the appropriate mode:

'Fill' fills holes completely. Select the appropriate options and click on the

boundary of a hole to fill it.

'Fill partial' allows defining a stretch of boundary along which the hole will

be filled. The rest of the hole stays open. Click on the boundary in two places, then click that part of the boundary were the fill should take place.

'Create bridges' creates strips of polygons between two selected edges. Click

on one edge for the bridge start, then on another for the bridge end.

'Delete' allows removing triangles based on various selection options. Checking the 'floating data' box allows removing triangles that have no connection to the external surface.

'Move' allows changing the shape of a bridge created in 'Create Bridge' mode.

Click the place where you want to apply the change, click and drag the arrow into the correct direction and set the shape and extension of the shape. Click 'Next' to confirm a move and start a new one.

3. Decide whether you want to use curvature based or flat filling. Check or uncheck the corresponding box accordingly. Flat filling creates a surface as planar as possible, while curvature based filling attempts to keep the tangency of the hole closing surface as constant as possible.

4. If satisfied with the fillings, click 'OK'. Otherwise, discard them by clicking 'Cancel'.

Sectioning polygon meshes. Cuts can be executed in two ways: with a plane or along a curve. The former option is not very useful if the resulting sections are used in kinetic modeling, as large gaps will appear when sections with straight cut-

offs rotate versus each other. A curve allows creation of saddle-shaped cuts, so that rotary joints are almost gap-free.

Using curves, there are two options: to create closed objects (bodies) or open objects (surfaces). Creating closed bodies usually results in small gaps between neighboring objects and is more work intensive. Creating open objects is faster, but carries a high risk of artifacts at the edges if the openings are closed using the 'Fill Holes' function. The higher the resolution of the file is, the weaker the artifacts will be.

Using curves as cutting object to create closed section object:

1. The import the STL file.

2. Rotate it so that the view axis is parallel to the intended cut.

3. Select 'Polygon-->Section by Curve'.

4. Draw a curve from control points by clicking on the model. It is important to imagine how the two sections-to-be will be positioned after having rotated versus each other in kinetic modeling and place the curve accordingly. A circular arc would be ideal, but it is not easy to draw one given the tools offered by Geomagic®. [Ctrl-Z] removes the last point. This curve can NOT be saved!

5. Click 'Create' to see a preview of the curve on the model

6. Click 'Intersect Extrusion. This extrudes the curve to the depth given in the 'Profile Curve --> Depth' field. Usually, Geomagic® suggests a sufficient depth, lower depths will not penetrate the model fully.

7. Mark 'Delete Selection' and 'Fill Intersection'.

8. 'Reverse Selection' allows changing the part to be deleted and the part to be kept.

9. Click 'OK'

Now, one part has been cut away from the rest of the model along the extruded curve. It is advisable to rename and save it (right-click the part in the model manager window and choose the appropriate option). In order to create the contacting part, proceed as follows:

1. Into the same file, import the STL with the 'File-->Import' command.

2. In the model manager, select both the section created before and the complete part (hold 'Ctrl' to select both while clicking).

3. Rotate the viewport so that the cutting surface is parallel to the view axis.

4. Deselect the finished section by holding down 'Ctrl' and clicking the part again. It is now shown in ghosted view mode.

5. Select 'Polygon-->Section by Curve'.

6. Draw a curve along the cut line. Try to follow the boundary of the already created part as exactly as possible.

7. Click 'Intersect Extrusion. This extrudes the curve to the depth given in the 'Profile Curve --> Depth' field. Usually, Geomagic® suggests a sufficient depth, lower depths will not penetrate the full model.

8. Mark 'Delete Selection' and 'Fill Intersection'.

9. 'Reverse Selection' allows changing the part to be deleted and the part to be kept.

10. Click 'OK'

Now, the next part has been created. Depending on how close the two cutting curves correlate, there will be a small gap or overlap between the parts.

Using curves as cutting object to create open section object:

1. Import the STL file

2. Rotate it so that the view axis is parallel to the intended cut.

3. Select 'Polygon-->Section by Curve'.

4. Draw a curve from control points by clicking on the model. It is important to imagine how the two sections-to-be will be positioned after having rotated versus each other in kinetic modeling and place the curve accordingly. A circular arc would be ideal, but it is not easy to draw one in the fashion offered by Geomagic®. [Ctrl-Z] removes the last point. This curve can NOT be saved!

5. Click 'Create' to see a preview of the curve on the model

6. Click 'Intersect Extrusion. This extrudes the curve to the depth given in the 'Profile Curve --> Depth' field. Usually, Geomagic® suggests a sufficient depth, lower depths will not penetrate the full model.

7. Unmark 'Delete Selection'

8. Click 'OK'

Now the object has been split along the curve. Each part can be separately selected, e.g. with the lasso selection tool, and turned into a separate object ('Edit-->Selection to Object…'). In order to fill the holes, use the 'Polygons-->Fill Holes' function. Use 'Flat fill' and 'Create bridges' to build flat fills for both sides that correspond to each other.

Appendix E - Combined techniques for Rhinoceros® and Geomagic®

Note: instructions here refer to versions 3.0 of Rhinoceros® and 8.0 of Geomagic®. Other version may require slightly different command inputs.

Collecting pointclouds in Rhinoceros® using partial mesh display in Geomagic®. While sampling a specimen with pointclouds it is often hard to judge if there are any unsampled parts left, and if the sampling density is sufficient near sudden topology changes. Given sufficient computing power the following procedure makes this process easier.

Both Rhinoceros® and Geomagic® must be running. The digitizer must be properly connected in Rhinoceros® and calibrated before data can be gathered.

1. Begin digitizing the surface normally

2. After a while, save the file in IGES format (*.igs)

3. Load this file in Geomagic® and mesh the pointcloud as described above.

4. Rotate this file so that the screen view coincides with the operator's view of the real specimen.

5. Ready Rhinoceros® for continued digitizing (e.g.: if necessary, enter *'digsketch'*).

6. Shift the screen display to Geomagic® by pressing the MS Windows® hotkey [Alt]+[Tab]. Do not click anywhere in the Geomagic® window with the mouse!

7. Continue digitizing, using the partial surface visible in Geomagic® as a guide. Control the input through the foot pedal exclusively.

8. Shift back to Rhinoceros® periodically using the MS Windows® hotkey [Alt]+[Tab].

9. Repeat 2. to 8. until digitizing is complete

10. Save the final file in any desired format in Rhinoceros®.