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Review

Computer-aided interactive three-dimensional reconstruction of the embryonic human heart

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ABSTRACT

Despite the fact that development of the human embryo heart is of considerable clinical importance, there is still disagreement over the process and the timing of events. It is likely that some of the conflicting accounts may have arisen from difficulties in describing and visualising 3-dimensional structures from 2-dimensional sections. To help overcome this problem and to improve our understanding of the development of the heart, we have devised techniques for the production of interactive 3D models reconstructed from serial histological sections of human embryos. Our method uses commercial software designed for the creation of 3D models and virtual reality environments. The ability to construct interactive visual images which both illustrate and communicate complex 3D information contributes to our understanding of the complex developmental changes occurring in embryogenesis.

Key words: Computer reconstruction; 3-dimensional modelling.

INTRODUCTION

Despite the fact that development of the human embryo heart is of considerable clinical importance, there is still disagreement over the process and the timing of events (Anderson, 1992; Ferreira et al. 1992; Anderson & Wilcox, 1993). It is likely that some of the conflicting accounts may have arisen from difficulties in describing and visualising three dimensional (3D) structures from two dimensional sections. To help comprehend developmental changes, we have developed techniques for reconstructing serially sectioned human embryos to create computer generated interactive 3D models (McLachlan et al. 1997). Since we have ready access to serially sectioned human embryos we wished to realise the potential of this valuable resource by creating models of embryonic hearts which are useful in teaching and research. By utilising our existing expertise, standard equipment and commercially available software, we felt it would be possible to make models of any embryo or embryonic structure relatively quickly and also to disseminate our results easily.

3D computer reconstruction of sectioned embryo material is being carried out by other groups (Keri & Ahnelt, 1991; Doyle et al. 1993; Verbeek et al. 1995; Ringwald et al. 1994). However, such approaches can require sophisticated computing expertise and specialist hardware which may give rise to a number of problems. Thus advanced computer hardware can be expensive and specially written software may only be effective in the hands of its authors.

In order to address some of these issues, we have developed a method for creating 3D computer reconstructions which uses commercial graphics software to create interactive 3D models. These can be viewed on Macintosh and IBM compatible personal computers. The ability to construct interactive visual images which both illustrate and communicate complex 3D information contributes to our understanding of the complicated developmental changes occurring during embryogenesis. This paper details the methods we have employed, firstly by describing 3D reconstruction in general and then by describing our own specific approach to modelling the embryonic heart.

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GENERAL DESCRIPTION OF THE PROCESS OF COMPUTER AIDED 3D MODELLING

The conversion of a real 3-dimensional object into a 3D computer model can be divided into 4 basic stages; deconstruction, analysis, reconstruction and presentation.

Deconstruction

Deconstruction of a generic solid object can be achieved in various ways depending on the nature of the object, with the end result being a series of slices (Fig. 1). A clay model, or paraffin wax or resin embedded tissue may be physically cut into sections; images of sections of a living person can be generated using a CT scanner. The number and thickness of sections determines the potential spatial resolution of any reconstruction on the axis of sectioning.

Analysis

Any modelling technique requires analysis of the original sections in order to determine how they are to be reassembled. It is necessary to identify features of interest across a series of sections and decide how these regions need to connect and bifurcate in the completed computer model, in other words to establish the topological relationships (Fig. 2*a*). A structure which bifurcates must be represented by two separate components in the 3D modelling software.

Reconstruction

After analysis and planning, the sections are reassembled to construct a wire frame model of the original 3D object (Fig. 2). This process involves digitising the sections and aligning the resulting data sets in 3 dimensions. Alignment of the sections is an

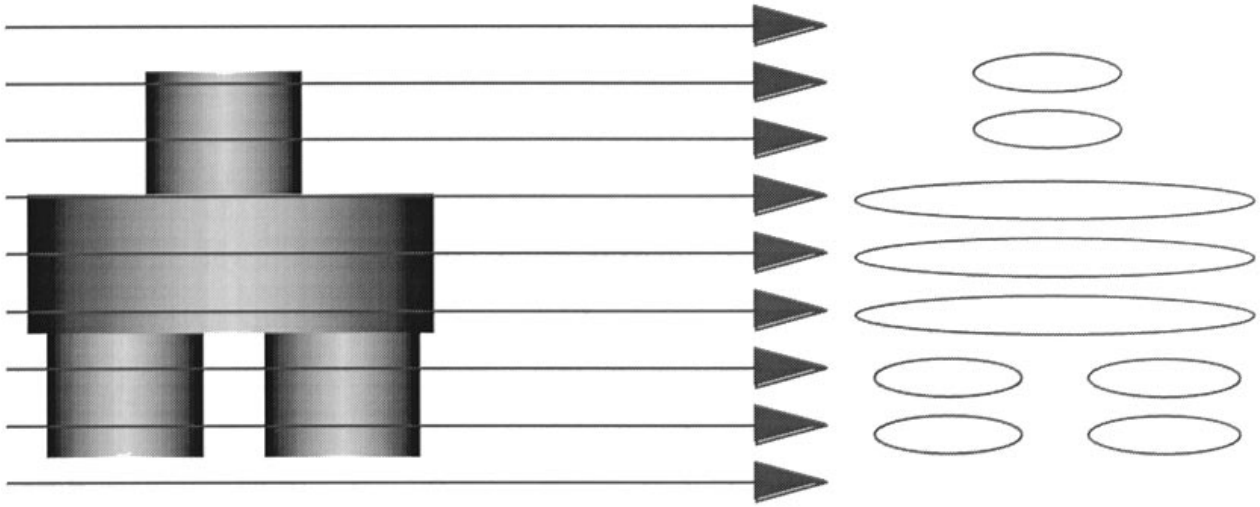


Fig. 1. Schematic model illustrating the principles of deconstruction of a simple solid object.

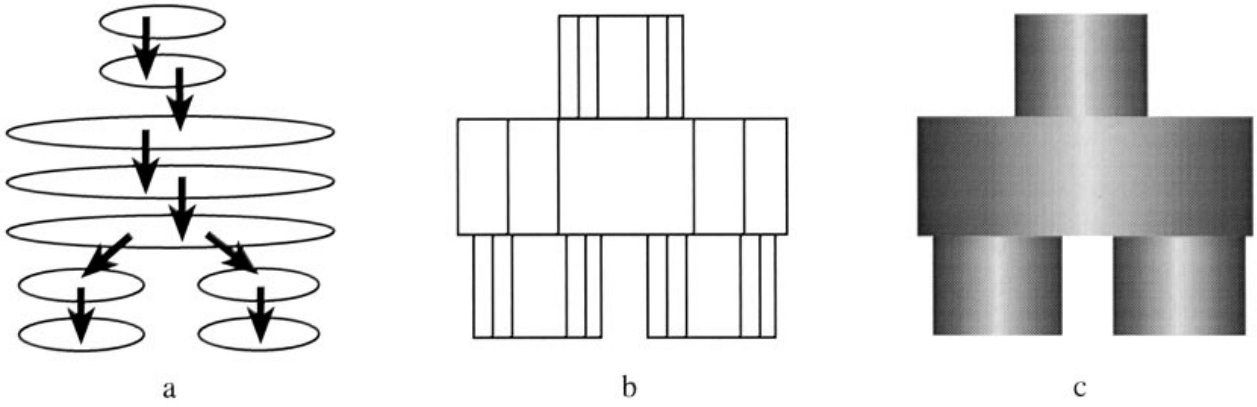


Fig. 2. After alignment (*a*), the components are linked to create a wire frame model (*b*). Finally a surface or skin is applied, to which tone, colour and texture can be added (*c*).

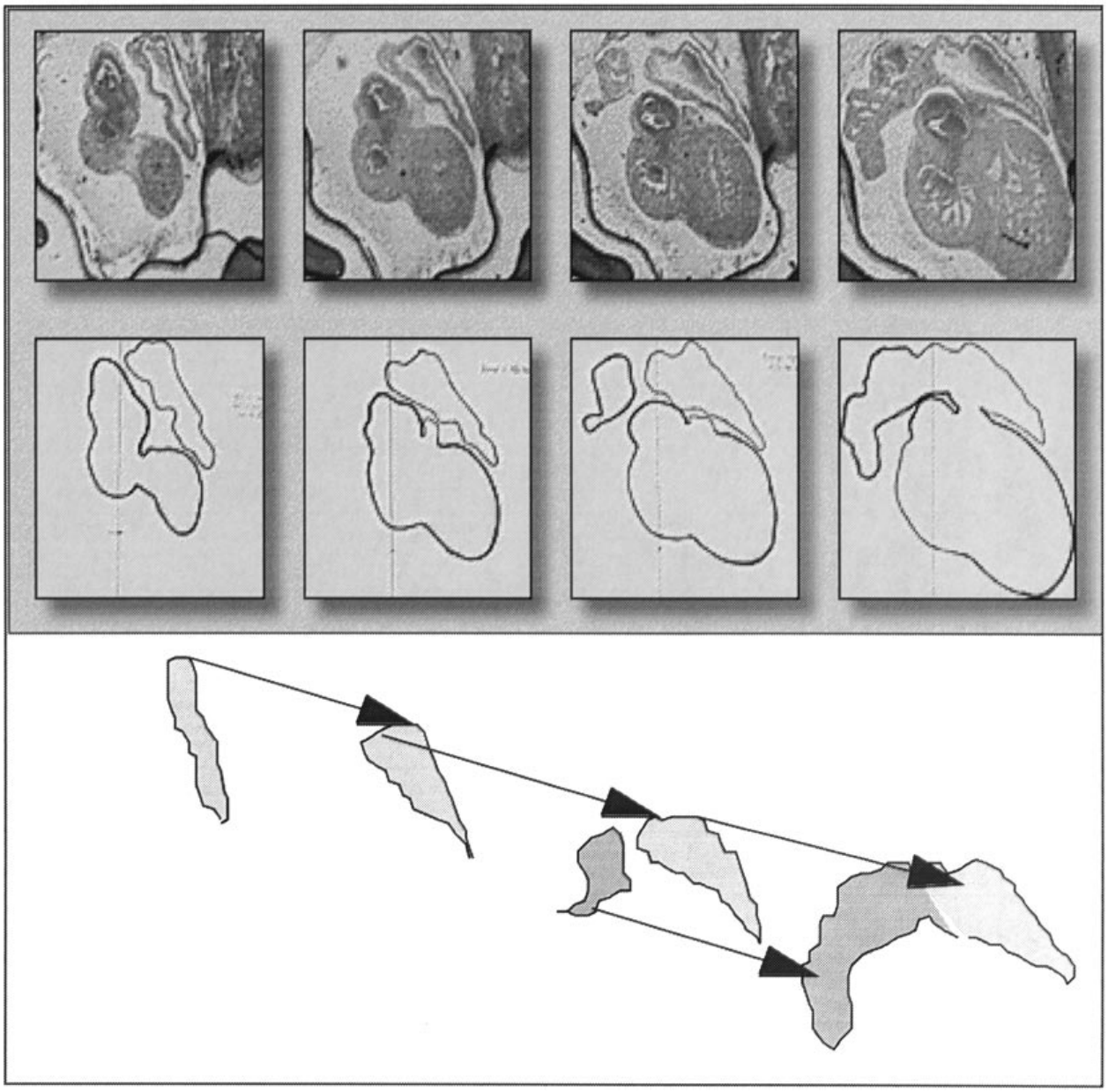


Fig. 3. Drawings are studied from a topological point of view in order to plan where 3D shapes in the final model would need to bifurcate.

import issue which is considered below in the context of the reconstruction of the heart.

After alignment (Fig. 2*a*), the components of the original object defined on the digitised tracings are linked to create a wire frame model (Fig. 2*b*). Finally a surface or skin is applied, to which tone, colour and texture can be added (Fig. 2*c*). The finished model is then rendered with computer generated lighting.

Presentation

The 3D model should be presented in a way which makes it easily accessible to potential users. One useful way of achieving this is by creating an interactive animation, which allows the model to be manipulated in virtual space. Animations can be viewed on a workstation, on videotape, or via the Internet.

METHODS

The process of reconstructing the embryonic heart follows the same protocol as described in general terms above (see also McLachlan et al. 1997, and Scarborough et al. 1997).

Deconstruction

The serially sectioned embryos used in this study are from the Walmsley Collection, School of Biological

and Medical Sciences, University of St Andrews and the Boyd Collection, Department of Anatomy, University of Cambridge (Aiton et al. 1996). Details of these collections are available via the British Universities Human Embryo Database (http://embryos.st-andrews.ac.uk).

In order to illustrate the development of the embryonic heart, we selected 5 serially sectioned embryos for reconstruction (1.8, 8, 10, 12.5 and 18 mm). As an example, in order to reconstruct the heart of the 18 mm embryo, we examined 1344 sections and located the heart in 200. Since the embryo was sectioned at an interval of 7 μm, we elected to analyse every 8th section, giving a sampling interval of 49 μm. Embryos from the Walmsley Collection were drawn directly from the histological sections using a projection microscope. Embryos from the Boyd Collection were traced from projected 35 mm slides. Scale bars, registration marks, and section intervals were added directly to the tracings which were then digitised using a UMAX PowerLook flatbed scanner and Adobe Photoshop 4.0 giving a set of 30 to 50 PICT image files for each model. Tracing by an embryologist is essential since automated edge recognition techniques, possible with some 3D reconstruction methods, cannot readily be used with low contrast histological material.

Analysis

The tracings were studied from an anatomical point of view in order to plan carefully which regions of the drawings would represent distinct components of the model, for example the outlines of the atria, ventricles and great vessels were colour coded to facilitate identification during the reconstruction process. Less obviously, it was also essential to consider where topological changes occurred in the finished model; it was particularly important to identify structures which connect or bifurcate, for example where 2 parts of the atrium join (Fig. 3). Macromedia FreeHand 5.5

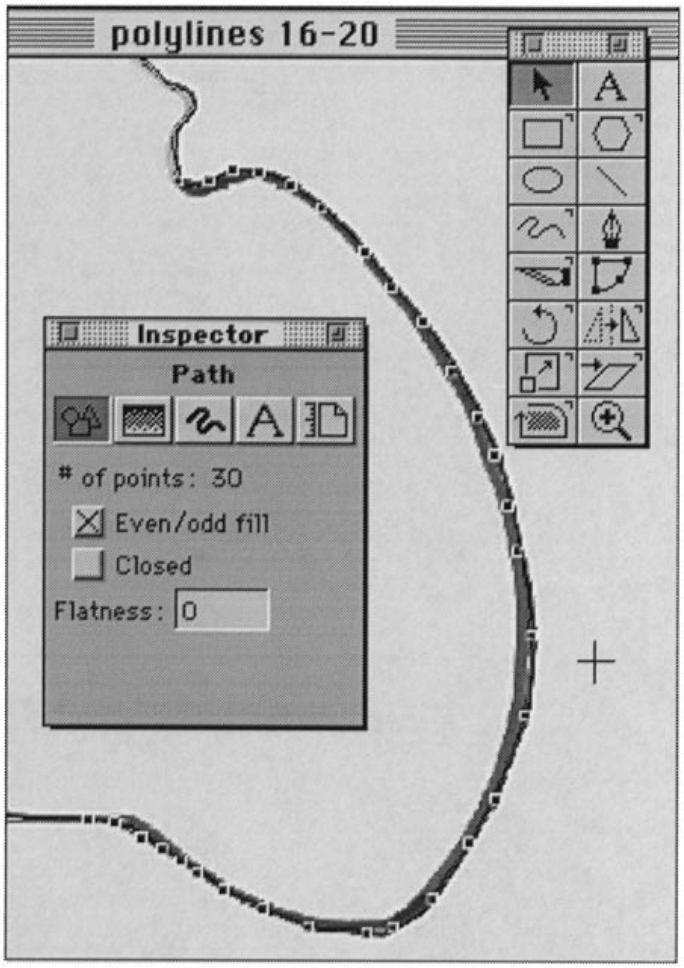
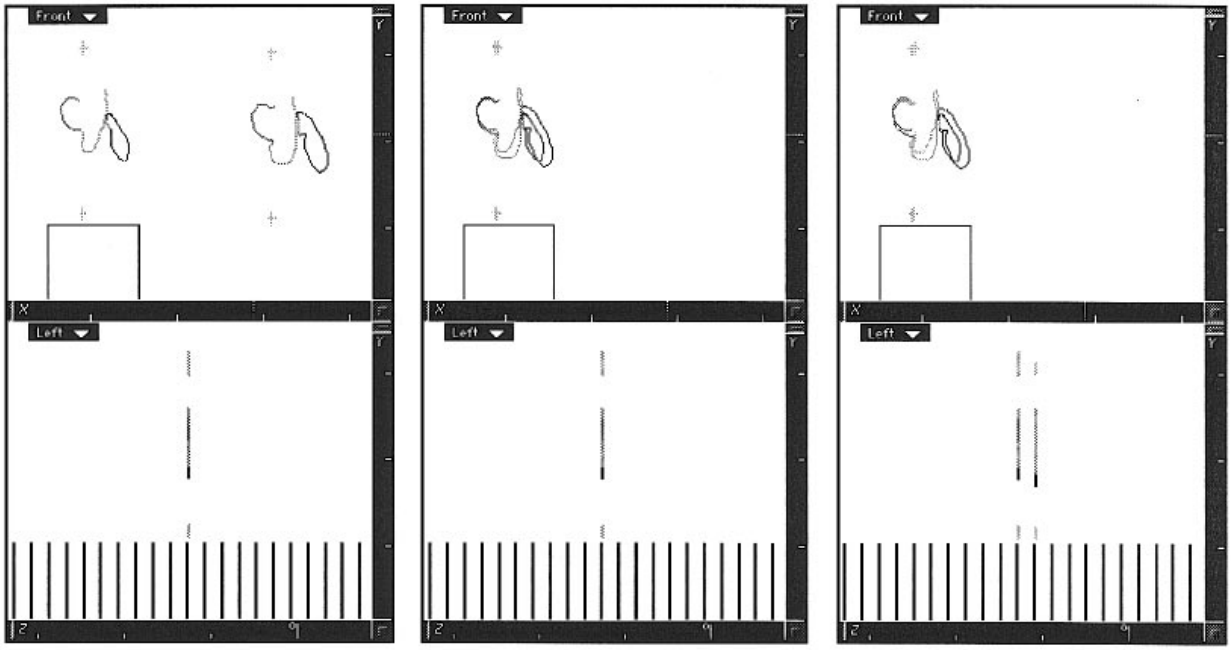


Fig. 4. Polygonal line segments are drawn on to the digitised tracings using Macromedia FreeHand.



a b c

Fig. 5. The vector graphics are transfered to the 3D modelling package Strata StudioPro (*a*) and the registration marks on the digitised tracings aligned in the x-y plane (*b*) and correctly spaced on the armature in the z axis (*c*).

was used to draw polygonal line segments over the digitised tracings to create object graphics (vector as opposed to pixel graphics files) (Fig. 4). Using the original coloured tracings as a plan, the same colour coding was used to define the anatomical and topological boundaries. After redrawing all the traced slices in this way, the resulting images, consisting of coloured polygonal line segments, were exported as Adobe Illustrator 3.0 files for transfer to the 3D modelling software.

Reconstruction

Using Strata StudioPro Blitz 1.75+, the 2D polygonal drawings were aligned and spaced in 3 dimensions (Fig. 5). Alignment of the sections requires information about section thickness and sampling interval as well as matching registration marks between adjacent sections. Historically, sectioned human embryos rarely had external fiducial points added for the purpose of section registration. In addition, paraffin wax embedded sections of soft tissues are often subject to extensive deformation during the sectioning process (David et al. 1998). In consequence, we are unable to use automatic registration techniques, or algorithms designed to minimise mismatches between sections (Kaufman et al. 1997). Our method of registration is therefore based on aligning integral features in the original sectioned material (e.g. notochord), based on expert interpretation of the section features.

To achieve this alignment and section spacing, an 'armature' was modelled using the digitised scale bar to define a set of planes reflecting the separations of the original histological sections (Fig. 5) Working along the sections, similarly coloured line segments were first linked and then skinned (Fig. 6). These processes connect a line segment on one section with the equivalent line segment on the next using a polygon net. This procedure is analogous to stretching canvas over the ribs of an aeroplane wing. In this way, the line segments were formed into a 3 dimensional wire frame model.

Presentation as an Interactive Animation

Physically handling a 3D structure facilitates an understanding of complex spatial relationships. QuickTime Virtual Reality (QTVR) software can be used to create interactive animations which enable the viewer to manipulate a computer generated object in 3 dimensions. This virtual reality experience creates the sensation of physically handling a solid object.

After previewing the prototype, the wire frame model was rendered using the colour coding which had previously been applied. The rendering process involves placing 'cameras' and light sources around the model to produce images of apparently solid objects. A variety of rendering settings can be employed, producing images of increasing quality at the expense of extending the computing time required.

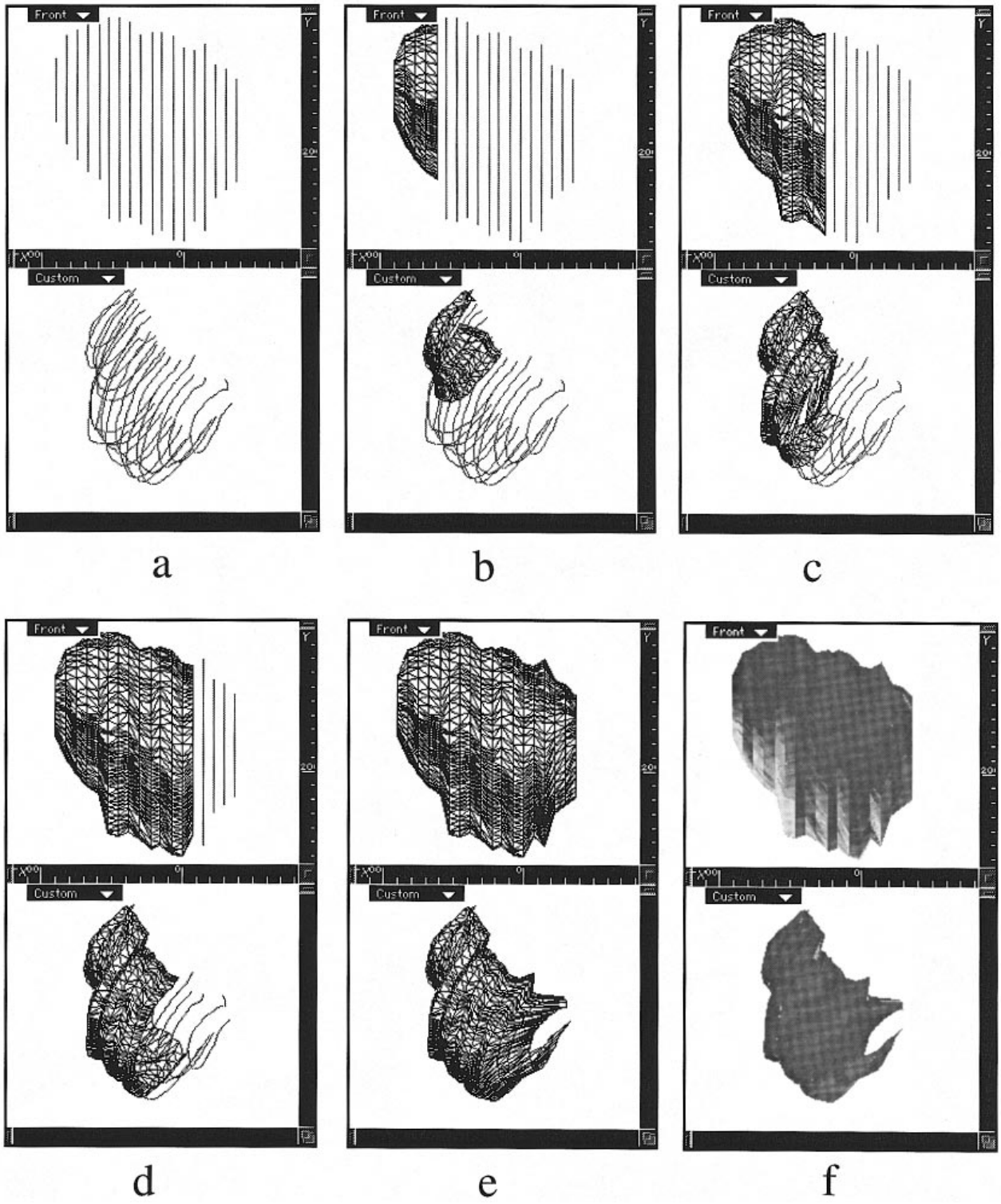


Fig. 6. Aligned sections of the exterior surface of the heart (*a*) are skinned (*b–d*) to make a wire frame model (*e*), before shading is applied and the surface of the model is rendered (*f*).

Normally, rendering was completed at the highest possible quality and a series of images was captured (photographed electronically) from a predefined sequence of camera positions. Although Strata Studio-Pro has an integral facility to shoot such a sequence of images, in practice we found that this facility was cumbersome and therefore we developed our own protocols. Typically, we found that adequate coverage was accomplished using a vertical pan of 180°, composed of 7 camera arcs. On each arc, the camera

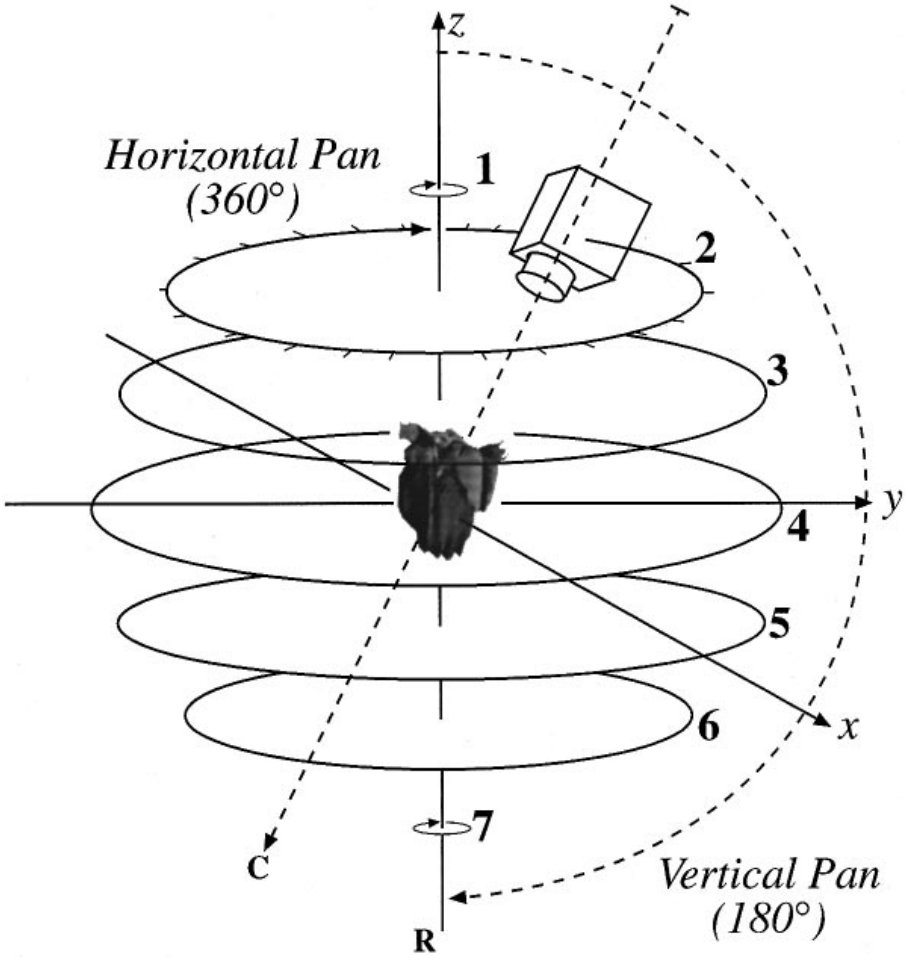


Fig. 7. Illustration of the camera movements used to create a Quicktime VR animation from a 3D model. 1–7, camera paths; C, example of the camera axis; R, axis of rotation.

was moved around 360° of horizontal pan in 24 steps (Fig. 7).

Each series of rendered images was saved as a QuickTime Movie prior to the construction of the QuickTime VR animation. Frame sequences were edited together using Adobe Premiere 4.0 and the navigable data, which converts a QuickTime Movie into a QuickTime VR animation, was added using Apple's Navigable Movie Player software. A QuickTime VR animation created in this way can be viewed subsequently using Apple's QTVR Player, which allows the model to be manipulated interactively in 3 dimensions.

A customised control interface was produced by adapting 'NavMovie XCMD Stack', a HyperCard stack which is included in the QuickTime VR Authoring Tools Suite 1.0 development software (Fig. 8). QuickTime VR Object files of the embryonic hearts were typically 10–30 Mb in size, though this is, of course, dependant upon the final pixel dimensions of the animation. Since QuickTime VR viewers are freely available for both Macintosh and Windows operating systems, it is simple to port VR Object files to other computer platforms.

MODIFICATIONS TO THE METHOD

The approach to modelling the embryonic heart we have described above has been successfully applied to the reconstruction of other embryonic structures including the craniocervical joint (David et al. 1998). Most recently we have successfully used form·Z RenderZone 2.9.5 to model the human vomeronasal organ using similar techniques to those required for Strata StudioPro. This programme is available for both Macintosh and Windows 95 platforms. When using form·Z RenderZone we have found it possible to input the tracings directly into the 3D modelling programme using a Wacom digitising tablet and puck with significant time saving. QuickTime VR animations are relatively easy to produce in form·Z RenderZone and the software now supports the export of models in VRML 2.0 format (Virtual

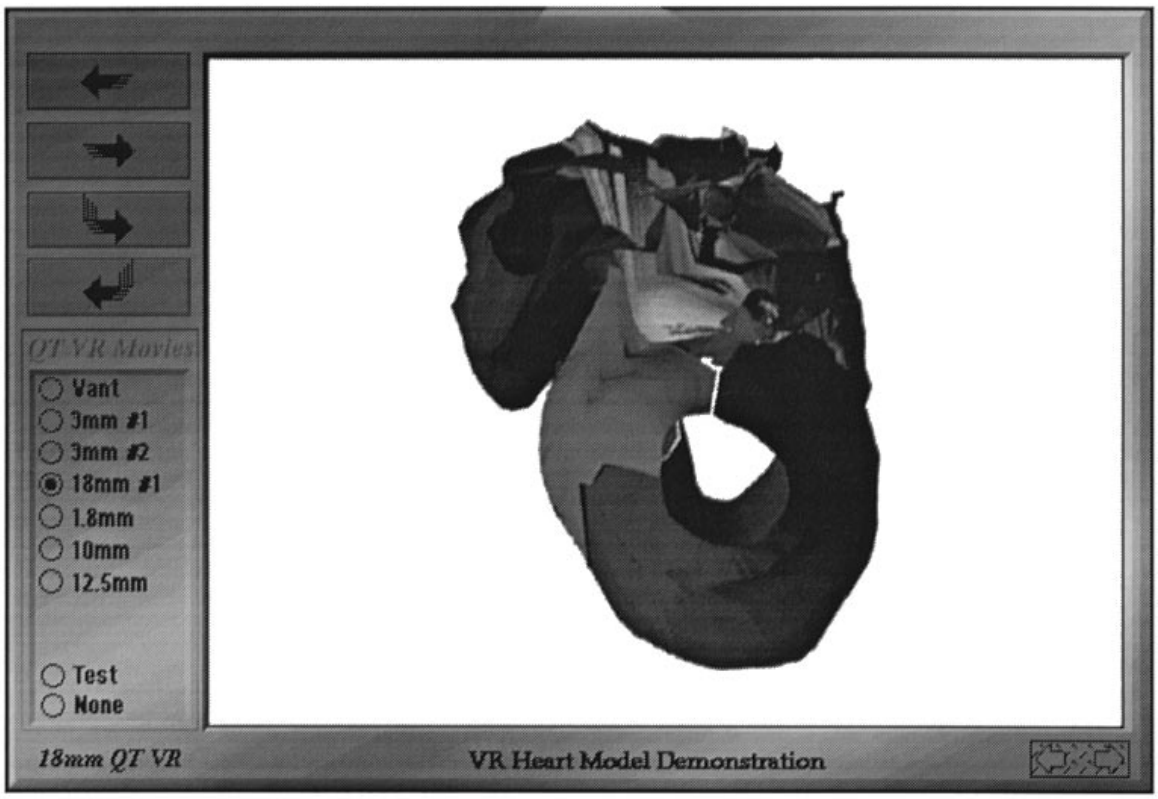


Fig. 8. Customised interface created in HyperCard used to view the reconstructed models of the heart.

Reality Modelling Language) which is extensively used to distribute 3D models on the Internet.

A selection of the models created using these methods is available and can be accessed and downloaded from the World Wide Web (http://embryos.st-andrews.ac.uk/download.html

CONCLUSIONS

Different approaches to reconstruction are being used by research groups attempting to image biological specimens in 3 dimensions. The methods that we describe here illustrate one possible approach using serially sectioned histological material which proved to be effective in the hands of embryologists and anatomists as opposed to computer scientists.

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