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Interactive Anatomy Online

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Technological developments in the field of medical imaging are increasing at an exponential rate. There are now literally hundreds of researchers and clinicians generating three-dimensional (3D) visualizations of anatomical structures using magnetic resonance imaging, computed tomography and serial sections (Fig. 1). The creation and use of 3D visualizations has revolutionized the study of anatomy and physiology. These 3D pictures have also provided researchers and clinicians with new tools to diagnose disease, to train surgeons through “virtual” operations, and to examine minute, complex and internal structures. Because reconstructions are nearly exact digital copies of real biological objects, researchers can use 3D images to analyze, identify and more accurately measure the distances, landmark coordinates, surfaces and volumes associated with anatomical structures.

The accessibility, durability and usability of digital reconstructions are just as noteworthy as their importance to advancing anatomical research. Digital images can be stored, duplicated and accessed easily through databases. They can be electronically exchanged almost instantly between colleagues. And digital images can be cut and dissected electronically, then subsequently restored to provide a renewable and near permanent anatomical resource. The latter is especially important if the subjects under study are living, fragile, large or unique (e.g., fossils). This is in comparison to traditional specimen dissection, which results in the destruction of study materials.

Hence, a digital library can provide several useful functions. For instance, virtual dissection presents a viable alternative to actual dissection if the “experience” is realistic enough to be useful. To insure usability, users must be able to execute the following actions simply and efficiently: 1) “dissect” visualizations by showing and hiding layers, 2) resize and rotate images about the x-, y-, and z-axes simultaneously (via mouse clicks and drags), and 3) enlarge, reduce and move the images about the screen.

If the digital library is available to all Internet users at no cost, is platform and browser independent, and does not require any proprietary software, then it also provides a cost-effective means for studying specimens for research, educa-

tion and medical applications. Then if the library provides other advantages, such as the ability to study tiny structures not typically seen in gross dissection and the capability to customize image colors and textures, then it actually is a superior alternative to the traditional laboratory dissection. Further, by allowing users to contribute their own 3D images, and enabling queries by anatomic part and taxonomic reference (common and scientific names), it can serve as a community resource for collaboration, education and research.

The scientific community and general public can best

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The MorphologyNet®
Digital Library of Anatomy
Interactive anatomy online

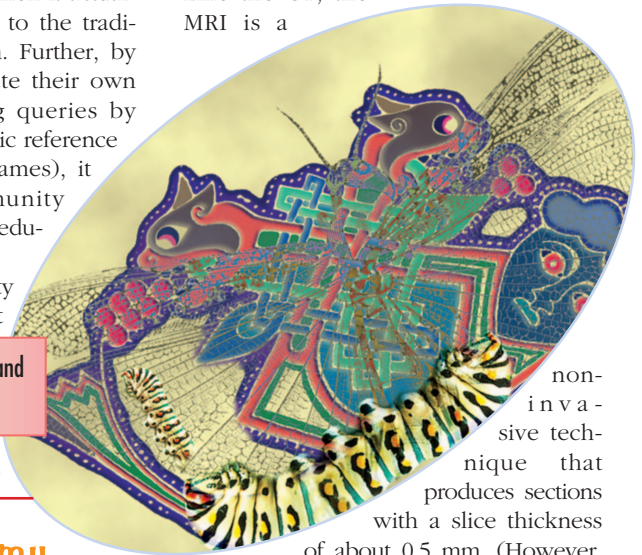
take advantage of the benefits of 3D digital reconstructions if they are stored in a web-accessible, easy-to-access database. Here we describe *MorphologyNet®*, a web-based digital library of realistic, 3D interactive and customizable images of anatomy currently in development at the University of Missouri-Rolla (Fig. 2).

Generating 3D anatomical reconstructions

There are three popular and complementary methods used to generate 3D reconstructions of anatomy: computed tomography (CT), magnetic resonance imaging (MRI) and histological serial sectioning. Computed tomography is a high-performance x-ray technique that permits a 3D object to be digitized non-invasively from 0.5 mm thick slices. The slice thickness provides excellent resolution for larger objects (e.g., humans, large mammals, etc.). X-rays are ideal for reconstructing bony structures, but require a contrasting agent to be present in the biological specimen (which must be injected while the specimen is alive) if soft tissue information is to be captured. Thus, CT is inefficient for reconstructing small objects and soft tissues of non-living specimens.

Magnetic resonance imaging works by aligning the nuclei of the subject's hydrogen atoms with the scanner's magnetic field. The nuclei are displaced out of their normal position using radio waves, and

then allowed to align back to their normal position. During the realignment process, the nuclei send out signals that are captured by a scanner and are translated into a 3D visualization of the scanned area. Like the CT, the MRI is a



non-invasive technique that produces sections with a slice thickness of about 0.5 mm. (However, resolution and slice thickness can vary greatly depending on the strength of the magnet and the power of the scanner.) Contrast agents are often required to better identify soft tissue. But the MRI offers better contrast of soft tissues than the CT (and does not include the negative affects of ionizing x-rays generated from the CT scans). Unfortunately, MRI reconstructions are very expensive relative to CT. Thus, they are cost prohibitive for most researchers and educators.

Histological serial section reconstructions are made by embedding specimens in a dense medium such as paraffin or glass. The specimens are physically sliced (with a microtome or cryotome). The sections (e.g., for major tissue types such as nerve, muscle and bone) are then stained and photographed with a digital high-resolution camera (usually attached to a transmission or scanning electron microscope, depending upon the size of the object). As with CT and MRI scans, specialized software is used to link the 2D images of the sections together into a 3D model. Histological sectioning has the benefits of representing all tissue types (including soft tissues) and allowing the examination of very small structures (i.e., the typical histological section is about 8 mm thick). Unfortunately, histological sectioning requires the destruction of the original specimen and, thus, is highly invasive.

Other 3D anatomy projects on the web

Currently, there are several web-

based projects designed to study anatomical structure. The *Anatomical Structure Viewer*® of the *Visible Human Server*® is an excellent resource that provides 3D viewing of human-based models via mouse controls. This viewer offers several interesting features including predefined viewing angles, the ability to record movies and a keyword search utility for model loading.

The *Virtual Frog Dissection Kit*® uses Internet requests in which mouse clicks on an HTML page are translated into image update queries. In addition, this project supports layer structures that allow the user to perform virtual dissections and rotations. However, there is only a single frog model available for investigation.

Digital Morphology® is arguably the best 3D digital anatomy database available, with an impressive collection of reconstructions of both living and extinct species. Each specimen can be viewed via 3D movies and/or a Java-based slice viewer. However, it lacks the ability to split objects into layers. Also, most objects cannot be rotated, enlarged or reduced.

Unfortunately, nearly all of the current web-based anatomical viewer projects suffer from one or more problems: 1) they focus on a single model organism (e.g., human, frog), or 2) they are designed for elementary and secondary education, and thus are too simplistic for research use, or 3) they provide only limited model interactivity. In addition, none of the projects

allows users to upload their own images; thus, they have limited functionality as a community resource/clearinghouse.

MorphologyNet

To overcome these limitations, we are developing *MorphologyNet*®. This web-based digital library will include the following features (e.g., Fig. 3): 1) visualizations that can be “dissected” by showing and hiding layers; 2) visualizations that can be resized and rotated in all axes simultaneously; 3) visualizations that can be enlarged, reduced and moved about the page; 4) the texture map, color and translucency of the individual objects comprising each visualization will be modifiable; 5) the library is Internet accessible and platform- and browser-independent; 6) access is free and no proprietary software is required; 7) the library allows users to contribute their own 3D images, and 8) users can query the library by anatomic part and/or taxonomic reference.

Challenges to developing MorphologyNet

Several challenges had to be addressed to fulfill the stated requirements for the *MorphologyNet*® project. First, to satisfy the requirements of web-accessibility, platform- and implementation-independence, and freedom from proprietary software, the viewer was developed as a Java applet (i.e., a Java program that can be embedded in a web page).

However, without a high security level, a Java applet can be an open door that lets malicious code enter any computer system with an Internet browser. Thus, to satisfy security (and other file access issues) for the *MorphologyNet*® viewer, jar signing was employed. Jar signing is a security technique in which a jar (a “Java archive”) file that contains executable code is given a public and private key. This technique allows the end-user to know where the jar file originated from and gives the user the option to accept the applet as trusted. Jar signing provides the means for an applet to connect securely to external URLs, access local files and instantiate classes from downloaded bytes. For *MorphologyNet*®, jar signing also allows the functionality of the

viewer to be extended by providing a means to access plugins such as file loaders, landmark algorithms, vertex algorithms, user controls, and device controls—all programs (developed by the *MorphologyNet*® team or by other members of the user community) that can interface with the *MorphologyNet*® code.

A second, more interesting challenge for the *MorphologyNet*® project is the development of a web-accessible database that can efficiently store multimedia image data and retrieve images. The database uses five criteria: 1) species’ scientific or common name, 2) developmental/growth stage, 3) anatomical part, 4) *MorphologyNet*® accession number, and 5) contributor’s name.

For example, a *MorphologyNet*® user should have the ability to retrieve an image by taxonomic reference (e.g., “all visualizations of leopard frogs” or “all visualizations of *Rana pipiens*”), by anatomical reference (e.g., “all visualizations of a jaw”), by developmental stage (e.g., “all visualizations of tadpoles”), and by any combination of those criteria (e.g., “all visualizations of jaws of tadpoles in the family Ranidae”). Therefore, taxonomy (e.g., family, genus, species), developmental descriptors (e.g., “tadpole”, “larval stage”), and hierarchical anatomy (e.g., head, jaw, mandible) must be represented and interrelated in the *MorphologyNet*® database.

The relational database is the most commonly used for traditional business applications. But, this model is not the most appropriate for applications involving entities with complex structures (including multimedia data) and complex hierarchical inter-object relationships. Instead, object-oriented databases (which model both object state and behavior) are currently the *de facto* standard for engineering design and manufacturing (CAD/CAM/CAE) applications that require the ability to represent and manipulate a visual object in terms of a hierarchy of sub-objects. For example, a real-world object such as an *automobile* can be conceptualized and implemented better as an instance of an *object class* in an object-oriented database (made up of many *automobile part* class objects) rather than as a *tuple* (or an algebraically computed sequence of related tuples) in a relational database. As best described by technology-industry analyst Esther Dyson, “Using relational tables to store objects is like driving your car home and then disassembling it to put it in the garage. It can be assembled again in the morning, but one eventually asks whether this is the most efficient way

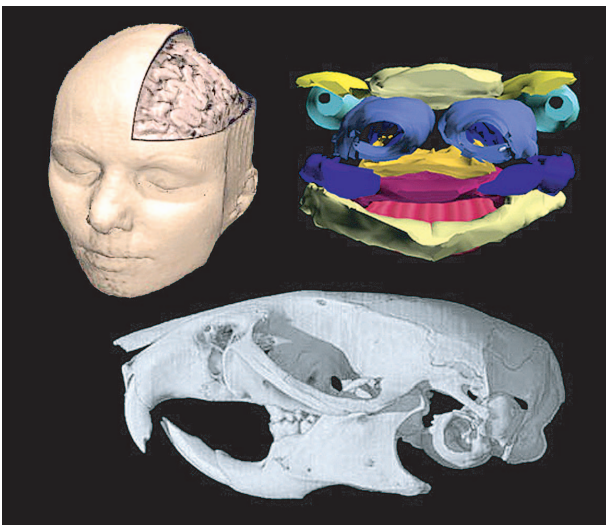


Fig. 1 Three-dimensional reconstructions (not to scale) generated from different imaging sources. Clockwise from upper left: MRI scans of human head (Jörg Meyer, CoMED: Computer Aided Image Processing for Medical Applications, University of California-Irvine), histological serial sections of the internal anatomy a frog head (Anne Maglia, *MorphologyNet*®, University of Missouri-Rolla), and CT scans of a mouse skull (Timothy Rowe, *Digital Morphology*® at the University of Texas).

to park a car."

The *MorphologyNet*® database is being developed with a commercial object-oriented database management system called ObjectStore®. The *MorphologyNet*® user-interface includes both a text-based query window and a visual query system to facilitate queries by any combination of the aforementioned criteria. (That is the ability to select a species from a hierarchical tree of taxonomy or by an anatomical part from a generalized 2D anatomical image and so forth.)

These queries are then translated into an appropriate statement in the object query language (OQL) of the database management system and the desired results are displayed. It is expected that this process of retrieving visualizations via the hierarchical and orthogonal relationships among their related attributes will be more efficient than the execution of a complex (and computationally expensive) series of join operations over several tables in a relational database.

Morphologynet's future

Additional challenges lie ahead for the *MorphologyNet*® project, especially those related to increasing the functionality of the viewer and to incorporating community-developed functionalities into the viewer (via plugins). Several functions would enhance the usability of the project for anatomical research, such as linear and geometric measurement and analysis tools (e.g., Euclidean distance, thin-plate spline deformation grids and Procruste distance). Although several of these functionalities are being developed by the *MorphologyNet*® team, it is hoped that user demand for additional functionality will encourage community contribution of other plugins.

Additionally, the current *MorphologyNet*® plugin architecture should be expanded to more readily accommodate the incorporation of certain types of plugins. Plugins inherit information from public program interfaces. Currently, when the *MorphologyNet*® viewer executes plugin code, it does so in a predefined manner that causes the plugin to react passively.

A more sophisticated strategy would be defining plugin roles using an XML descriptor. This method would allow developers to define the execution order of plugins. It also would provide the ability to chain plugins so that input could be passed to and from distributed libraries. In this way, the public interfaces to the viewer would advance from being a simple set of functions to being an interaction vocabu-

lary. This would further increase the modularity and customizability of the viewer: it could allow a user to tailor the functionality of the viewer based on the particular resources selected. For example, while one user might want a lightweight viewer that can be embedded in a presentation, another user may desire a robust suite of morphometric tools to use for complex shape analysis.

The current prototype implementation (of *MorphologyNet*®) houses six 3D reconstructions of frogs generated from serial sections. But we are working with several researchers worldwide to incorporate their reconstructions of other organisms (e.g., humans, turtles, salamanders, etc.) from serial sections, CTs, and MRIs into the library. Also, we are actively generating new reconstructions to add to the digital library. We anticipate that the newest release of *MorphologyNet*® (expected July 2005) will include many more images and much of the functionality described in this article. Future developments such as these will increase the accessibility, usability and usefulness of *MorphologyNet*®. As a result, it will facilitate anatomical research, provide innovative educational resources, and promote communication, data-sharing and plugin contributions among a community of scientists and the general public.

Read more about it

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About the authors

Jennifer Leopold is an Assistant Professor in the Department of Computer Science at the University of Missouri-Rolla. Her research interests range broadly in human-computer interaction and end-user programming environments,

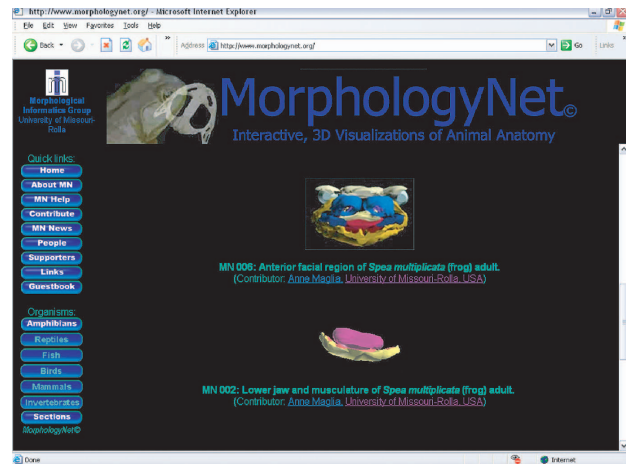


Fig. 2 The *MorphologyNet*® web interface



Fig. 2 The *MorphologyNet*® web interface

with particular focus on web-based and multimodal user interfaces, and visual programming languages. She pursues many of those interests through research projects in the field of bioinformatics. She is interested in developing and studying the use of software tools that will allow "public programmers" to use powerful information technology to enhance their research, without the need for traditional programming training.

Anne Maglia is an Assistant Professor in the Department of Biological Sciences at the University of Missouri-Rolla. Her research program includes several projects in which she develops and applies information technology to biological questions, including the generation of 3D digital reconstructions of animal anatomy, the development of predictive models of species distributions, and the use of data-mining techniques to identify character non-independence in phylogenetic data.

Thomas Hoeft graduated with his Master's Degree in Computer Science at the University of Missouri-Rolla in December 2004. He is currently employed as a bioinformatics programmer at Pacific Northwest National Laboratory in Richland, Washington.