

# 3D Visualization and Analysis of Ecological Networks on WWW

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## ABSTRACT

Food webs describe who eats whom among species within a habitat, and these networks depicting food chains have long been a central paradigm for understanding simple and complex networks in many scientific and social arenas. The structure of the feeding links within diverse food webs typically generates highly complex and dense networks whose details are critical to the behavior of ecosystems. Due to these issues, food webs are it is both difficult and very important to visualize and study food webs. In this paper, we describe 3D visualizations of food webs that address these difficulties with cylindrical node placement, minimal edge-crossing and link length, hierarchical node aggregation, and color-schemes representing different characteristics (trophic level, connectivity, generality, vulnerability, taxonomy, and biomass) of network nodes and links. These visualizations simplify the complexity, illuminate insightful information and provide an effective analysis on top of ecological Semantic Web. We describe our deployment of “Webs on the Web” (WoW) visualization and analysis tools on the world wide web to facilitate food-web research, collaboration and education. Given the variety of 3D visualization technologies on the WWW, our WoW visualization pipeline based on semantic web supports diverse formats and adapts to users’ preferences by employing XML and a flexible architecture. Currently, WoW uses XML to semantically markup food web data (FoodWebML), extracts visual information into X3D format and then uses the information for direct display on VRML/X3D browsers or feeds into a Shockwave 3D visualization.

**Keywords:** food webs, graph visualization, web3D, XML

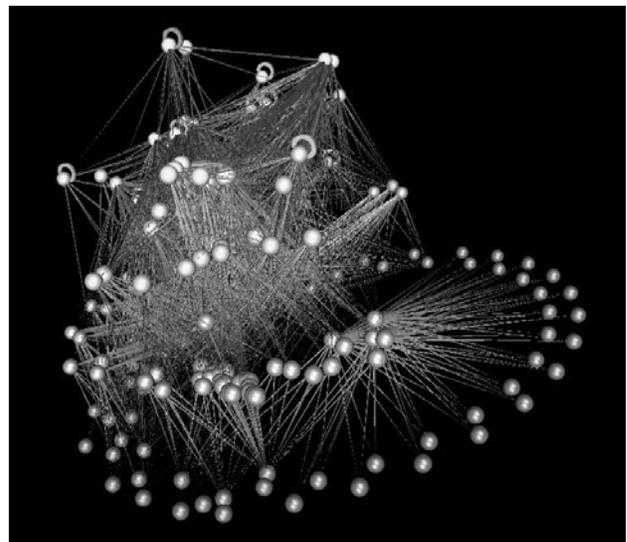
## 1. INTRODUCTION

Many aspects of our daily life, applications or natural phenomena such as human relationships, website administration, and ecological food webs can be represented and modeled as networks comprised of nodes and links between them. The ability to quantitatively describe, analyze, and visualize such networks has become increasingly important [2][4][11]. As networks get larger and more complex, network visualization plays crucial role in analyzing and understanding the network.

However, network visualizations also face several challenges with respect to their clarity, usability, intuitiveness, ability to be viewed with a fixed window and ability to discern nodes and links, especially as the number of elements (nodes or links) increases [6].

General aesthetic guidelines for graph layout such as using straight, uniform length links, minimal edge link crossings, and even distribution of nodes are helpful for visualizing networks, but these guidelines may be inadequate for large dense networks. In [12] that focuses on handling millions of elements, initial graph layout is quickly computed and then users are allowed to select additional algorithms to improve layout. This approach enables users to interact with large graph and comprehend overall structure. Different edge lengths are used for representing weights and edge crossings and uneven node distribution were allowed for more intuitive results. However, the algorithm currently works well only with relatively planar graphs whose topology is close to tree structures.

Several approaches to visualizing large networks employ multi-scaling where the user chooses among different



**Fig. 1** – 3D Visualization of the food web of Little Rock Lake, Wisconsin (181 nodes and 2375 links). The network shows strong connectivity, an average link (in-coming & out-going) per node is 26.24.

Graph	Average link per node	Number of nodes(S)	Number of links(L)	Connectivity ( $L/S^2$ )
[12] Fig.7	2.035	167	172	0.0061
[6] Fig.1	1.981	219	218	0.0045
[6] Fig.7	1.955	289	291	0.0034
Broom web	4.805	154	370	0.0156
El Verde web	19.358	156	1510	0.0620
LittleRock Lake web	26.243	181	2375	0.0724

**Table.1** Food web graphs have highly connected nodes compared to nodes in other graph.

ranges (e.g., all of the U.S. or just one state) that reveal different levels of detail and subsetting where particular small modules of the network are focused upon. These approaches make use of the high connectivity within subsets of large networks combined with low connectivity between subsets that often characterizes "small-world" networks. [9][18]. Breaking down large networks into smaller subsets may be effective for analyzing local properties, but focusing on such subsets limits more comprehensive understanding of the whole structure. In addition, nodes or species within ecology food webs tend to be closely and highly connected but relatively unclustered which prevent food webs from being "small worlds" and from being effectively visualized by focusing on clusters (figure 1). Ecology food webs are unlike large networks usually found in Information Visualization, build much more highly connected than large networks usually found in information visualization networks (table 1). Strong connectivity is resulted from each node basal (i.e., plants) or "grandchildren" nodes in the children level gets being connected with multiple "children" nodes above in parent level (multiple inheritance style) which in turn are connected to and multiple "parental" nodes at higher trophic levels in the grand children level while large networks like file system networks tend to have each node in the children level gets multiple nodes in grandchildren level but usually single or low connectance to parent level. (single inheritance style or tree structure).. There can also be many connections between children and also between parents. With such high connectivity, edge density and crossing prevent networks from being clearly intuitively rendered in 2D. In 3D, graph layout and node placement algorithms can provide more insight by using the additional dimension to minimize occlusion when viewed from multiple viewpoints.

In this paper, we discuss visualization of highly connected networks using ecological food webs as an example. Our algorithm responds to network structure and takes advantage of domain specific knowledge to intuitively layout for food web researchers. This food web visualizations is being developed as an analysis and visualization components of ecological network study that include a central data repository for collaborative research and education. The importance of food web network stud and issues of 3D visualization on the WWW are discussed in section 2. Algorithms and the results of

graph layout, clustering, and analysis using color-schemes and histograms are explained in section 3. System architecture is explained in section 4 with focus as a visualization component of central repository system. On-going and future researches are discussed in section 5.

## 2. BACKGROUND

### 2.1. Ecological Network Research

The study of ecological networks, particularly in the form of food webs, has been and continues to be a central paradigm for research into the relationships between ecosystem complexity and stability. A food web describes the network of feeding interactions among taxa within a particular habitat. Quantitative, mathematical approaches have been used to describe general aspects of food-web network structure, dynamics, and stability since the 1970's [8]. However, much of the early work was based on highly simplified data and analytically tractable but biologically implausible assumptions and models. Recently, more detailed ecological data and new approaches to network analysis have supported advances in the description of general properties of complex food-web structure [3][5][13].

While it was relatively easy to depict aspects of early species-poor food-web data with hand drawn 2D wiring networks, such images did little to augment analytical aspects of ecological research. The species diversity, complex network structures, and dynamics that characterize current food-web data and research require a much more sophisticated approach to visualization. Because of the complexity of the data, a visualization framework that abstracts and illustrates food-web network structure and dynamics can play a critical role in understanding, explaining, and predicting important aspects of bio-complexity.

Like other networks, food webs are fundamentally characterized as a set of nodes with links that connect the nodes. In this case, the nodes represent species (or groups of species) and the links represent feeding interactions, and are often referred to as "trophic links." Trophic links occur between consumer species and the resource species that they eat. Thus, a food web consists of  $L$  directed trophic links between  $S$  nodes. There are  $S^2$  possible and  $L$  actual link, so connectance ( $C$ ) is computed as the fraction of all possible links that are realized ( $L/S^2$ ) and represents a standard measure of food web complexity (table 1).

### 2.2. 3D Visualizations on the WWW

Central repositories for a wide range of scientific data have been extremely important for many research endeavors, for example in genomics and paleobiology. Data compiled in centralized repositories can play an important role in ecological research and the conservation and management of ecosystems because no single researcher is an expert in all, or even most of the organisms found in any particular habitat. The integration of analysis and visualization tools with centralized data repositories can dramatically increase the utility of

databases and thus increase voluntary use, participation, and collaboration among dispersed researchers, as well as facilitating community inspection and validation of data and theory. Due to the high connectivity of food webs compared to many other kinds of networks, 3D visualization and animation is likely to attract researchers to central repository by helping researchers gain new insights and develop new hypotheses regarding the structure and dynamics of complex food webs.

When providing 3D visualization on the WWW, a central issue includes 3D format selection for universal acceptance due to the lack of 3D standardization on the WWW. Unlike images such as gif or jpg formats that are supported by all WWW browsers, 3D formats are not natively supported. There are different advantages and disadvantages among different approaches such as VRML/X3D, Java Applet/Java Web Start with JOGL, MPEG4, and proprietary Plug-ins [17]. Considering that the goal of this project includes reaching as many researchers as possible and as well as serving as an educational tool, our approach is to support the different preferences of individuals by generating diverse formats with minimal overhead, allowing individuals to make the choice of preferred format. At the same time, we plan to experiment and study performance and usability issues of different 3D formats on the WWW to contribute to web3D standardization. To support diverse formats with minimal overheads, we have developed XML applications to describe visualization data (FoodWebML) as well as graphics user interfaces (GUIML). Streamability, data cache, client-server task separation, XML applications, and flexible pipeline architectures are briefly discussed in section 4.

### 3. VISUALIZATION AND ANALYSIS

Most properties (e.g., fractions of species at top, intermediate and basal trophic levels, the means and variabilities of generality, vulnerability and food-chain length, and the degree of cannibalism, omnivory, looping and trophic similarity) are derived from relations of species and their binary links, not from additional information. Therefore, we nodes to embed such properties intuitively into the 3D structure of food webs. The algorithms are inspired by domain knowledge (such as using trophic level as y axis but do not depend on domain specific information, so can be easily applicable to other highly connected networks).

In section 3.1, we describe the importance of the graph layout and node placement in 3D space and its key algorithms. In section 3.2, we discuss hierarchical aggregation or clustering and in section 3.3, we focus on analysis of node properties by using color-scheme. In section 3.4, other analysis tools including simulation, annotation, and search will be presented.

#### 3.1 Graph layout/3D node placement

We represent nodes (species) as sphere and links as cones, with the cone tapered from predator to prey. We experimented different coordinate systems to represent

food webs, but cylindrical coordinate system (with coordinates  $r, \theta, y$ ) generates most intuitive structure due to our natural familiarity with food chains.

*Vertical (y) axis* is aligned with trophic levels: “basal species” or species eat no other organisms such as most plants at the bottom on trophic level one while their direct and indirect consumers are at higher levels. In other words, the  $y$ -axis represents trophic level of the species. Among the many methods for computing trophic levels exist in the ecological literature, we use the “prey-averaged” trophic level recently shown to be a computationally efficient and highly accurate algorithm [15].

A food webs is mathematically represented by a two-dimensional binary matrix(the connection matrix) with elements  $l_{ij}$  among  $S$  rows and  $S$  columns measuring links in a food web with  $S$  species. For column  $j$  and row  $i$ ,  $l_{ij}$  is 1 if species  $j$  consumes species  $i$  and 0 if not. The number of elements equal to 1 is the number links ( $L$ ) in the food web. A food chain is defined as a linked path, excluding loops, from a consuming species to a basal species.

*Radius* indicates the number of connections attached to the node. Nodes that are less highly connected are placed further from the center of the visualization and more highly connected nodes are placed toward the core. This prevents the many links of the more connected nodes from obscuring views and allows more nodes to be seen from the outside of the network, especially the less connected or more “specialized” nodes.

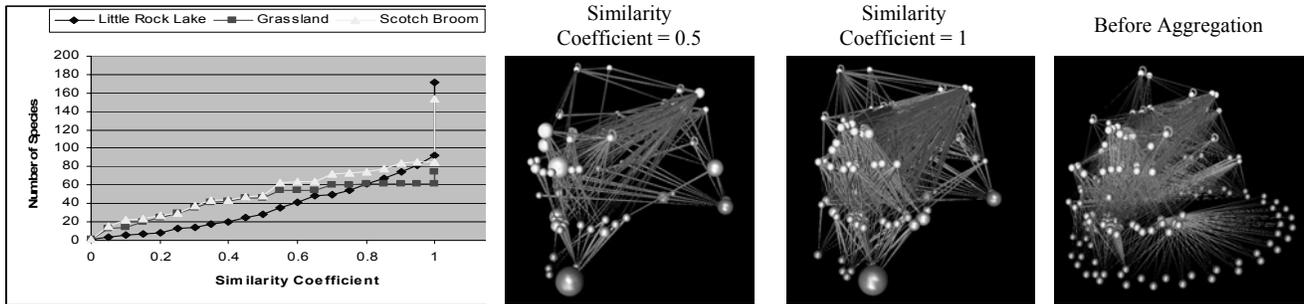
We use the value of  $\theta$  to more closely place functionally related nodes next to each other. Since feeding is the most meaningful relation in food webs, we place species that are consumed by same nodes more closely. This reduces total link length up to 43% in one food webs and an average of 33%, in several food webs compared to alternative algorithms for  $\theta$ . Visual cluttering is also reduced along with total link length. This makes it easier to recognize relations between prey and predators and provides a type of locality [16] of food web links that illuminate “guilds” of species engaged in similar functional relationships in the network without explicit annotation.

This algorithm for calculating  $\theta$  finds groups of similar nodes in each trophic level and then places them close together. We iterate the process till no groups share same components.

#### 3.2 Aggregation/Clustering

Clustering is important for large or complex network not only to reduce visual clustering for better navigation, but also organize nodes into meaningful cluster and add analysis intuitiveness to researchers [10]. We developed both structure-based clustering that depends on only their node and link relations and content-based clustering that is derived from additional information of each node – taxonomy information from each species.

##### 3.2.1 Structure-based clustering - Trophic Similarity



**Fig. 2.** Hierarchical aggregation of food web by trophic similarity is shown. Aggregation rate in each food web is determined by similarity

Quantitative patterns in food webs have been the subject of the controversy for several years [10]. The clustering species into trophic similarity helps ecologists to investigate resolution-related issues with statistics commonly used to describe the patterns. To cluster species in the raw food web, the nodes are hierarchically clustered based on the amount of trophic overlap between taxa [10]. A trophic overlap similarity index ( $I$ ) between every pair of node is calculated using an algorithm defined by Jaccard [7] :

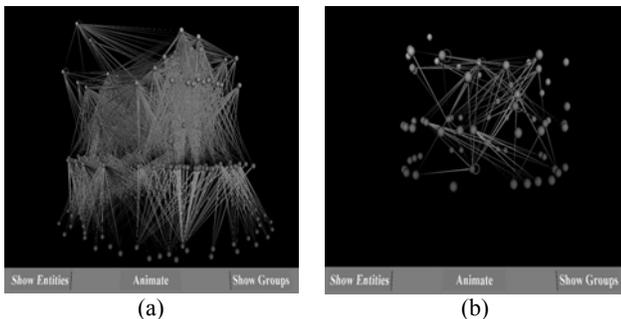
$$I = c/(a+b+c)$$

where  $c$  = number of predators and prey common to the two nodes,  $a$  = number of predators and prey unique to one node, and  $b$  = number of predators and prey unique to the other node. When the two nodes have the same set of predators and prey,  $I = 1$ . When the two nodes have no common predators or common prey,  $I = 0$ .

Trophic species are based purely on network structure. More aggregated species based on lumping species with a user designated  $I < 1$  can be generated (Fig. 2).

### 3.2.2 Content-based clustering - Taxonomic Aggregation

We also provide a content-based clustering we call taxonomic aggregation. Considering that each species naturally belongs to hierarchical taxonomy starting as species and ending at kingdom, taxonomic aggregation provides well structured, naturally organized, multi-level clustering. The number of nodes can be systematically reduced by taxonomic aggregation [19]. Each species may be identified taxonomically according to sub-species, species, genus, family, etc. Each node will be clustered into the level specified by user (figure 3). Same linkage criteria used at trophic similarity is employed for linking



**Fig. 3.** Little Rock Lake's food web viewed in VRML format; (a) shows nodes resolved to the species level and (b) shows nodes grouped to the family level.

groups of clustered nodes. This could also hide overwhelming degrees of complexity to give additional information in hierarchically organized way [6]. FoodWebML, the XML application that stores food web data allows the definition of different types of aggregations using group-level elements [17] and the clustering process is animated using VRML and available at [www.foodwebs.org].

### 3.3 Node color

Since human perception responds strongly to color scheme, color has been popular approach in information visualization, but may not have been intensively utilized in network visualization due to limits on the amount of information that can usefully interpreted by human perception [9]. In food webs, we used a color scheme that complements 3D structure to render effective a visual aid to the network properties that ecologists and other network scientists feel is important. For example, node color varies with the trophic level of the node. Link color also varies with the trophic level of the prey species. This means that omnivores, or species that consume prey from more than one trophic level, are visible because the large diameter end of links of different colors connect to the node.

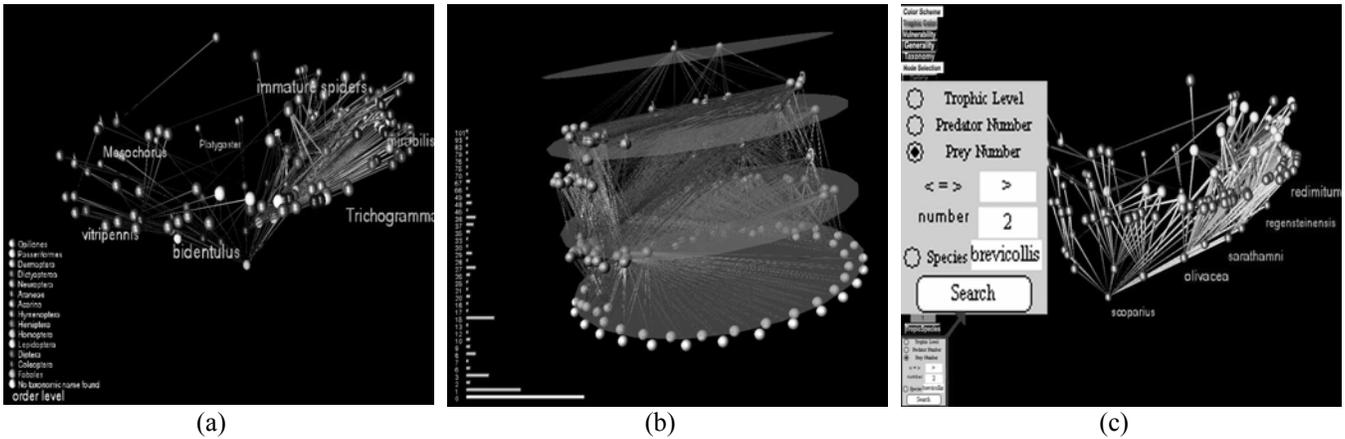
#### 3.3.1 Trophic level color

Trophic level color is used for both node and link as default color of food web visualization. Trophic level is represented through 'y' axis and trophic level color at the same time: trophic level color is used to support distinction of trophic level as shown in figure 1.

### 3.4. Species extinction simulation (Cascading extinctions)

Recent scientific studies show the relation of food web robustness with species loss, species richness, omnivory, most-connected species, or least-connected species using cascading extinction simulation [3]. For most food webs, removing the least-connected species results in minimal secondary extinctions, but significant exceptions occur. Our system simulates the cascading extinctions due to dynamics or to user designated species loss. Node deletion causes deletion of the link(s) attached to it.

### 3.5. Node annotation and Depth cue



**Fig.4** (a) Annotations of species name are shown in green color on nodes selected by user. (b) shows depth cue in Little Rock Lake web (c) shows node search results of Scotch Broom web that node which has more than 2 prey is high-lighted; Other nodes and links are gray-scaled

Annotation provides additional information to node during visualization. Users may get lost easily during navigation and annotation provides both a description of the node and also navigation cues for users. Currently species' taxonomic or common name can be shown attached to each node upon clicking of node by user when 'annotation selection' is on. User also can choose 'All annotation on' to see all species name on each node at the same time. Figure 4.a shows annotations of selected nodes. When semantic web is completed to support visualization, users will be provided hyper links to multimedia objects on top of annotations. We also provide additional depth cue. Since the visualization is based on cylindrical coordinate, we use layers of circular disk to enhance the depth cue of node positions in 3D (figure 4.b).

### 3.6. Node search

When there are many nodes and many properties of nodes, advanced search within the food web is useful for users. Not only node search supports single node search based on taxa, diverse searches can be used to accomplish queries. Some searches enable users to find certain nodes by manipulating query conditions using the combination of trophic level, number of predators and prey, and species name. Queried nodes will be shown in selected color scheme and others will be grayed out. Semantic query to be added will work beyond regular query search. Current search performs mostly on client side with pre-fetched information.

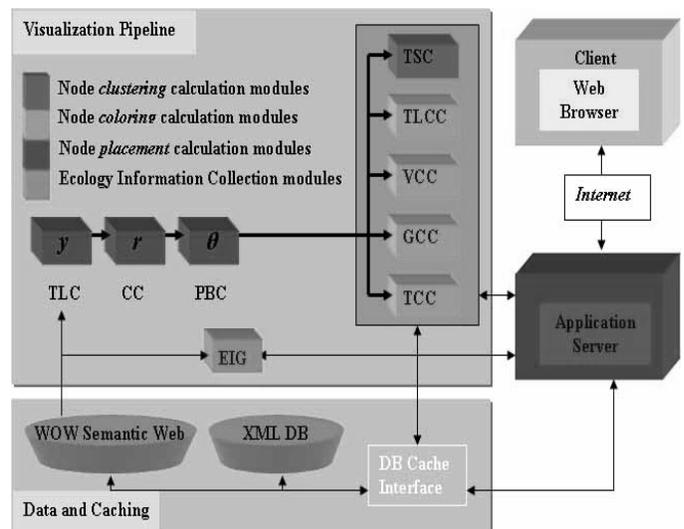
## 4. WOW ARCHITECTURE DESIGN

The WOW architecture design focuses on flexibility, extensibility as well as performance and usability because we anticipate that central repositories serving as data bank will soon accommodate analysis and 3D visualization tools on top of them. Our architecture design and computational/visualization components is designed to be easily reusable in different environments as shown in Fig 5. We also aim to provide different 3D visualization formats on the client side with minimal overhead and are currently experimenting with VRML and Shockwave. For graphics data representation with some caching

mechanism embedded, we developed and implemented an XML application called FoodwebML. We also found that graphics user interfaces should be described in neutral format to minimize the developer's overhead for porting, so GUIML was designed and is currently under development.

### 4.1 FoodWebML

One advantage of XML over HTML is the separation of contents from presentation. Another advantage would be that XML serves well for heterogeneous data base description. In our approach, FoodWebML is used to describe ontology of food web data and also contain intermediate or final visualization components as a cache. When visualization is being processed through the pipeline, intermediate data such as trophic levels or visual information node (color, size, geometry, position) are computed and saved back to FoodWebML, so they can be easily reused in the future when any change is made to food web data or its properties. FoodWebML contains contents and presentation (visual info) in one XML application, but they are clearly separated internally. Visual nodes within FoodWebML can be easily translated to X3D/VRML. When used with Shockwave Lingo,



**Fig. 5** Wow architecture.

visual nodes are sent out in streaming fashion, so clients receive nodes and links closer to viewer and render while the rest is arriving and being updated [17].

#### 4.2 Visualization Pipeline

Our current pipeline stays in the server side. While processing visualization, FoodWebML stores intermediate data as a cache within the pipeline and the resulting visualization information is sent to the client according to the format that user wants. This approach is efficient, especially for frequent access to the same food web that reuses up-to-date cached information. An alternative is moving the visualization pipeline to the client side where client receives only food web data and processes the analyses and visualizations intensively without making any connection to server. Both are supported with current server pipeline. We are developing java version client using JOGL and Java Web Start as a thick client for intensive users. Our server side pipeline is easily ported to the client side.

#### 5. CONCLUSION AND FUTURE WORK

We describe our on-going effort on 1. highly connected food-web visualization with clustering, positioning and coloring, 2. developing flexible visualization pipeline, 3. FoodWebML and GUIML for supporting diverse 3D formats on the WWW, available at <http://www.foodwebs.org/networks.html>. We are currently working on a semantic web data bank for food webs and an interface between the data bank and visualization pipeline, Java client using JOGL and Java Web Start, and GUIML. When GUIML and Java client is completed, we plan to do usability study using surveys on 3D network visualization and formats on the WWW. Due to the lack of standard of Web3D, the usability study will contribute to develop the standard of 3D on WWW and embedded systems. Many other attributes of food web must be studied and then the system should be extended to other application area. Animations and simulations will be added for research and educational purposes.

#### ACKNOWLEDGEMENT

This project is being funded by National Science Foundation Div. Of Biological Infrastructure, Biological Databases and Information, No. DBI-0234980.

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